GEPHE SUMMARY

Gephebase Gene sage (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^sage^#gephebase-summary-title)

GepheID
GP00002410

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Silk yield (https://www.gephebase.org/search-criteria?/and+Trait=^Silk yield^#gephebase-summary-title)

Trait State in Taxon A
Bombyx mori - local breed

Trait State in Taxon B
Bombyx mori - breeds with improved silk yield

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758

Rank
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

Parent
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)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758

Rank
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

Parent
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)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
sage

Synonyms
bHLHc7; CG12952; Dmel\CG12952; Sage; Dmel_CG12952

String
7227.FBpp0081462 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0081462)

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)

UniProtKB Drosophila melanogaster
Q9VHG3 (http://www.uniprot.org/uniprot/Q9VHG3)

GenebankID or UniProtKB
()

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 (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

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

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#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS