

GEPHE SUMMARY

	Gephebase Gene		GepheID
glutamate synthase (GOGAT) (https://www.gephebase.org/search-criteria?/and+Gene		GP00002407	
Gephebase="glutamate synthase (GOGAT)"#gephebase-summary-title)			Main curator
	Entry Status	Courtier	
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait			
Category="Physiology"#gephebase-summary-title)	Trait		
Silk yield (<a a="" href="https://www.gephebase.org/search-criteria?/and+Trait=" silk="" yield"#gephebase-summary-title)<="">			
	Trait State in Taxon A		
Bombyx mori - local strains			
	Trait State in Taxon B		
Bombyx mori - domesticated strains			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic			
Status="Domesticated"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Bombyx mori		Bombyx mori	
(<a a="" bombyx="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" mori"#gephebase-summary-title)<="">		(<a a="" bombyx="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" 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)		Bombyx () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7091		7091	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 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	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
GS		M9NFH8 (http://www.uniprot.org/uniprot/M9NFH8)	
	Synonyms		GenebankID or UniProtKB
GS; Dmel\CG9674; CG9674; Dmel_CG9674		Q0KIX8 (https://www.ncbi.nlm.nih.gov/nuccore/Q0KIX8)	
	String		
7227.FBpp0297083			
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0297083			
)			
	Sequence Similarities		
Belongs to the glutamate synthase family.			
	GO - Molecular Function		
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)			
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)			
GO:0050660 : flavin adenine dinucleotide binding			
(https://www.ebi.ac.uk/QuickGO/term/GO:0050660)			
GO:0010181 : FMN binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010181)			
GO:0051538 : 3 iron, 4 sulfur cluster binding			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0051538>)
GO:0016040 : glutamate synthase (NADH) activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016040>)
GO:0015930 : glutamate synthase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015930>)

GO - Biological Process

GO:0006537 : glutamate biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006537>)
GO:0019676 : ammonia assimilation cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019676>)
GO:0097054 : L-glutamate biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097054>)

GO - Cellular Component

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Presumptive Null

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

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#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 the domesticated strains at the larval stage

Experimental Evidence

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

Main Reference

The evolutionary road from wild moth to domestic silkworm. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29967484>)

Authors

Xiang H; Liu X; Li M; Zhu Y; Wang L; Cui Y; Liu L; Fang G; Qian H; Xu A; Wang W; Zhan S

Abstract

The Silk Road, which derives its name from the trade of silk produced by the domestic silkworm *Bombyx mori*, was an important episode in the development and interaction of human civilizations. However, the detailed history behind silkworm domestication remains ambiguous, and little is known about the underlying genetics with respect to important aspects of its domestication. Here, we reconstruct the domestication processes and identify selective sweeps by sequencing 137 representative silkworm strains. The results present an evolutionary scenario in which silkworms may have been initially domesticated in China as trimoulting lines, then subjected to independent spreads along the Silk Road that gave rise to the development of most local strains, and further improved for modern silk production in Japan and China, having descended from diverse ancestral sources. We find that genes with key roles in nitrogen and amino acid metabolism may have contributed to the promotion of silk production, and that circadian-related genes are generally selected for their adaptation. We additionally identify associations between several candidate genes and important breeding traits, thereby advancing the applicable value of our resources.

Additional References

High-resolution silkworm pan-genome provides genetic insights into artificial selection and ecological adaptation. (2022) (<https://pubmed.ncbi.nlm.nih.gov/36153338>)

RELATED GEPHE

Related Genes

6 (asparagine synthetase (AS), E2F1, Fkh, glutamate dehydrogenase (GDH), 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