

## GEPHE SUMMARY

	Gephebase Gene	GephelD
glutamine synthetase 2 (GS) ( <a href="https://www.gephebase.org/search-criteria/?and+Gene">https://www.gephebase.org/search-criteria/?and+Gene</a> Gephebase=^glutamine synthetase 2 (GS)^#gephebase-summary-title)	GP00002405	
	Entry Status	Main curator
Published	Courtier	

## PHENOTYPIC CHANGE

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

## GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
Gs2		
CG1743; Dmel\CG1743; gs-c; gs2; GS2; GsII	Synonyms	GenebankID or UniProtKB
7227.FBpp0073344 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0073344">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0073344</a> )	String	
Belongs to the glutamine synthetase family.	Sequence Similarities	
GO:0005524 : ATP binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005524">https://www.ebi.ac.uk/QuickGO/term/GO:0005524</a> ) GO:0004356 : glutamate-ammonia ligase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004356">https://www.ebi.ac.uk/QuickGO/term/GO:0004356</a> )	GO - Molecular Function	
GO:0006538 : glutamate catabolic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006538">https://www.ebi.ac.uk/QuickGO/term/GO:0006538</a> )	GO - Biological Process	

GO:0006542 : glutamine biosynthetic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006542">https://www.ebi.ac.uk/QuickGO/term/GO:0006542</a> )	
GO:0045213 : neurotransmitter receptor metabolic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0045213">https://www.ebi.ac.uk/QuickGO/term/GO:0045213</a> )	
GO:0007416 : synapse assembly ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0007416">https://www.ebi.ac.uk/QuickGO/term/GO:0007416</a> )	GO - Cellular Component
GO:0005737 : cytoplasm ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005737">https://www.ebi.ac.uk/QuickGO/term/GO:0005737</a> )	Presumptive Null
No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title</a> )	Molecular Type
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title</a> )	Aberration Type
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title</a> )	Molecular Details of the Mutation
-	Experimental Evidence
Association Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title</a> )	Main Reference
The evolutionary road from wild moth to domestic silkworm. (2018) ( <a href="https://pubmed.ncbi.nlm.nih.gov/29967484">https://pubmed.ncbi.nlm.nih.gov/29967484</a> )	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 <i>Bombyx mori</i> , 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) ( <a href="https://pubmed.ncbi.nlm.nih.gov/36153338">https://pubmed.ncbi.nlm.nih.gov/36153338</a> )	

## RELATED GEPHE

6 (asparagine synthetase (AS), E2F1, Fkh, glutamate dehydrogenase (GDH), glutamate synthase (GOGAT), sage) ( <a href="https://www.gephebase.org/search-criteria?/or+TaxonID=^7091^/and+Trait=Silk yield/and+groupHaplotypes=true#gephebase-summary-title">https://www.gephebase.org/search-criteria?/or+TaxonID=^7091^/and+Trait=Silk yield/and+groupHaplotypes=true#gephebase-summary-title</a> )	Related Genes
No matches found.	Related Haplotypes

## EXTERNAL LINKS

## COMMENTS