

# GEPHE SUMMARY

	Gephebase Gene	GephelD
Chit beta-GlcNAcase ( <a href="https://www.gephebase.org/search-criteria/?and+Gene">https://www.gephebase.org/search-criteria/?and+Gene</a> Gephebase=^Chit beta-GlcNAcase^#gephebase-summary-title)	GP00002401	Main curator
Published	Entry Status	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 fineness ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=^Silk">https://www.gephebase.org/search-criteria/?and+Trait=^Silk</a> fineness^#gephebase-summary-title)	Trait State in Taxon A		
Bombyx mori - coarse silk	Trait State in Taxon B		
Bombyx mori - fine silk	Ancestral State		
Taxon A	Taxonomic Status		
Domesticated ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic">https://www.gephebase.org/search-criteria/?and+Taxonomic</a> Status=^Domesticated^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Bombyx mori ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Bombyx">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Bombyx</a> mori^#gephebase-summary-title)		Bombyx mori ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Bombyx">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Bombyx</a> mori^#gephebase-summary-title)	
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) ( <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	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
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	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
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Xiafang strain, Qiubai strain	Taxon A Description	Suxiu strain, Chunfeng strain	Taxon B Description

## GENOTYPIC CHANGE

-	Generic Gene Name	UniProtKB Bombyx mori
-	Synonyms	GenebankID or UniProtKB Bombyx mori
-	String	P49010 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/P49010">https://www.ncbi.nlm.nih.gov/nuccore/P49010</a> )
7091.BGIBMGA005899-TA ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7091.BGIBMGA005899-TA">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7091.BGIBMGA005899-TA</a> )	Sequence Similarities	
Belongs to the glycosyl hydrolase 20 family.	GO - Molecular Function	
GO:0004563 : beta-N-acetylhexosaminidase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004563">https://www.ebi.ac.uk/QuickGO/term/GO:0004563</a> )		
GO:0102148 : N-acetyl-beta-D-galactosaminidase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0102148">https://www.ebi.ac.uk/QuickGO/term/GO:0102148</a> )		

## GO - Biological Process

GO:0006032 : chitin catabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006032>)

GO:0000272 : polysaccharide catabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000272>)

## GO - Cellular Component

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

BmChit  $\beta$ -GlcNAcase gene is expressed at a significantly higher level in fine silk strains (Suxiu, Chunfeng) compared to coarse silk strains. CRISPR-cas9 mediated knockout of the BmChit  $\beta$ -GlcNAcase gene produced coarser silk.

Experimental Evidence

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

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.

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Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS