

GEPHE SUMMARY

	Gephebase Gene	GephelD
Carotenoid-binding protein (CBP) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Carotenoid-binding protein (CBP)^#gephebase-summary-title)	GP00000169	Main curator
	Entry Status	Martin
Published		

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=Morphology^#gephebase-summary-title)	Trait	
Coloration (silk) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (silk)^#gephebase-summary-title)	Trait State in Taxon A	
Bombyx mandarina	Trait State in Taxon B	
Bombyx mori - various strains	Ancestral State	
Taxon A	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=Domesticated^#gephebase-summary-title)		
Taxon A	Latin Name	Latin Name
Bombyx mandarina (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bombyx+mandarina^#gephebase-summary-title)		
wild silkworm	Common Name	Common Name
Bombyx mori mandarina; Theophila mandarina; wild silkworm; Bombyx mandarina (Moore, 1872)	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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent	Parent
7092 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7092)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

-	Generic Gene Name	UniProtKB Bombyx mori
-	Synonyms	GenebankID or UniProtKB
-	String	
7091.BGIBMGA007585-TA (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7091.BGIBMGA007585-TA)	Sequence Similarities	
Belongs to the RRM NCBP2 family.	GO - Molecular Function	
GO:0000339 : RNA cap binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000339)	GO - Biological Process	
GO:0031047 : gene silencing by RNA (https://www.ebi.ac.uk/QuickGO/term/GO:0031047)		
GO:0045292 : mRNA cis splicing, via spliceosome		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045292>)

GO - Cellular Component

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

GO:0005846 : nuclear cap binding complex

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005846>)

Presumptive Null

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

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Amplification%#gephebase-summary-title>)

Aberration Type

Complex Change (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Complex+Change%#gephebase-summary-title>)

Molecular Details of the Mutation

Copy Number Variation (up to 20 copies in *B. mori* ; only one in the wild form; *B. mandarina*)

Experimental Evidence

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

Main Reference

Diversity in copy number and structure of a silkworm morphogenetic gene as a result of domestication. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21242537>)

Authors

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Abstract

The carotenoid-binding protein (CBP) of the domesticated silkworm, *Bombyx mori*, a major determinant of cocoon color, is likely to have been substantially influenced by domestication of this species. We analyzed the structure of the CBP gene in multiple strains of *B. mori*, in multiple individuals of the wild silkworm, *B. mandarina* (the putative wild ancestor of *B. mori*), and in a number of other lepidopterans. We found the CBP gene copy number in genomic DNA to vary widely among *B. mori* strains, ranging from 1 to 20. The copies of CBP are of several types, based on the presence of a retrotransposon or partial deletion of the coding sequence. In contrast to *B. mori*, *B. mandarina* was found to possess a single copy of CBP without the retrotransposon insertion, regardless of habitat. Several other lepidopterans were found to contain sequences homologous to CBP, revealing that this gene is evolutionarily conserved in the lepidopteran lineage. Thus, domestication can generate significant diversity of gene copy number and structure over a relatively short evolutionary time.

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Additional References

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

RELATED GEPHE

Related Genes

1 (Tyrosine hydroxylase) (<https://www.gephebase.org/search-criteria/?or+Taxon+ID=%7092%and+Trait=Coloration/or+Taxon+ID=%7091%and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS