

GEPHE SUMMARY

SCARB1 (<a +scarb1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+SCARB1+"#gephebase-summary-title)	Gephebase Gene	GP00001905	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)	Trait Category		
Coloration (silk; carotenoids) (<a +coloration+(silk;+carotenoids)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Coloration+(silk;+carotenoids)+"#gephebase-summary-title)	Trait		
Bombyx mori - wild-type	Trait State in Taxon A		
Bombyx mori - Yellow cocoon (C) mutant - white cocoons - defect in the cellular uptake of lutein - silk gland selectively transporting beta-carotene	Trait State in Taxon B		
	Ancestral State		
Domesticated (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Bombyx mori (<a +bombyx+mori+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bombyx+mori+"#gephebase-summary-title)	Latin Name	Bombyx mori (<a +bombyx+mori+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bombyx+mori+"#gephebase-summary-title)	Latin Name
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; Dityrsia; 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; Dityrsia; Obtectomera; Bombycoidea; Bombycidae; Bombycinae; Bombyx	Lineage
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent	Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID	7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

Cameo2	Generic Gene Name	D2KXB3 (http://www.uniprot.org/uniprot/D2KXB3)	UniProtKB Bombyx mori
Cameo2; BmSCRB4	Synonyms	0	GenebankID or UniProtKB
-	String		
Belongs to the CD36 family.	Sequence Similarities		
-	GO - Molecular Function		
-	GO - Biological Process		
-	GO - Cellular Component		
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)			

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

difference in expression levels - three non synonymous mutations are also observed in the coding region - the gene is also named Cameo2

Experimental Evidence

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

Main Reference

A CD36-related transmembrane protein is coordinated with an intracellular lipid-binding protein in selective carotenoid transport for cocoon coloration. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20053988>)

Authors

Sakudoh T; Iizuka T; Narukawa J; Sezutsu H; Kobayashi I; Kuwazaki S; Banno Y; Kitamura A; Sugiyama H; Takada N; Fujimoto H; Kadono-Okuda K; Mita K; Tamura T; Yamamoto K; Tsuchida K

Abstract

The transport pathway of specific dietary carotenoids from the midgut lumen to the silk gland in the silkworm, *Bombyx mori*, is a model system for selective carotenoid transport because several genetic mutants with defects in parts of this pathway have been identified that manifest altered cocoon pigmentation. In the wild-type silkworm, which has both genes, Yellow blood (Y) and Yellow cocoon (C), lutein is transferred selectively from the hemolymph lipoprotein to the silk gland cells where it is accumulated into the cocoon. The Y gene encodes an intracellular carotenoid-binding protein (CBP) containing a lipid-binding domain known as the steroidogenic acute regulatory protein-related lipid transfer domain. Positional cloning and transgenic rescue experiments revealed that the C gene encodes Cameo2, a transmembrane protein gene belonging to the CD36 family genes, some of which, such as the mammalian SR-BI and the fruit fly *ninaD*, are reported as lipoprotein receptors or implicated in carotenoid transport for visual system. In C mutant larvae, Cameo2 expression was strongly repressed in the silk gland in a specific manner, resulting in colorless silk glands and white cocoons. The developmental profile of Cameo2 expression, CBP expression, and lutein pigmentation in the silk gland of the yellow cocoon strain were correlated. We hypothesize that selective delivery of lutein to specific tissue requires the combination of two components: 1) CBP as a carotenoid transporter in cytosol and 2) Cameo2 as a transmembrane receptor on the surface of the cells.

Additional References

RELATED GEPHE

Related Genes

9 (apontic-like, Bm-iAANAT, cardinal, cortex, SCRB15, Wnt1, Carotenoid-binding protein (CBP), Tyrosine hydroxylase, UGT86 (Bm-UGT10286)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7091^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Cameo2 is the silkworm ortholog of vertebrate SCARB1