GEPHE SUMMARY

Gephebase Gene
SCARB1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SCARB1^#gephebase-summary-title)

GepheID
GP00001905

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (silk; carotenoids) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (silk; carotenoids)^#gephebase-summary-title)

Trait State in Taxon A
Bombyx mori - wild-type

Trait State in Taxon B
Bombyx mori - Yellow cocoon (C) mutant - white cocoons - defect in the cellular uptake of lutein - silk gland selectively transporting beta-carotene

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758

Rank
species

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

Parent
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)

NCBI Taxonomy ID
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7091)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758

Rank
species

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

Parent
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)

NCBI Taxonomy ID
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7091)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Cameo2

Synonyms
Cameo2; BmSCRB4

String
-

Sequence Similarities
Belongs to the CD36 family.

GO - Molecular Function
-

GO - Biological Process
-

GO - Cellular Component
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)

UniProtKB Bombyx mori
D2KXB3 (http://www.uniprot.org/uniprot/D2KXB3)

GenebankID or UniProtKB
()

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