GEPHE SUMMARY

Gephebase Gene

SCRB15 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SCRB15^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001904

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 - Flesh mutant - silk gland selectively transporting more lutein and thus being more orange

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

SCRB15

Synonyms

SCRB15

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

K7ZRZ1 (http://www.uniprot.org/uniprot/K7ZRZ1)

GenebankID or UniProtKB

()

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)

Insertion Size

1-10 kb

Molecular Details of the Mutation

In the F mutant SCRB15 mRNA structure was severely disrupted due to a 1.4 kb genomic insertion in a coding exon

Experimental Evidence

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

Main Reference

CD36 homolog divergence is responsible for the selectivity of carotenoid species migration to the silk gland of the silkworm Bombyx mori. (2013) (https://pubmed.ncbi.nlm.nih.gov/23160179)

Authors

Sakudoh T; Kuwazaki S; Iizuka T; Narukawa J; Yamamoto K; Uchino K; Sezutsu H; Banno Y; Tsuchida K

Abstract

Dietary carotenoids are absorbed in the intestine and delivered to various tissues by circulating lipoproteins; however, the mechanism underlying selective delivery of different carotenoid species to individual tissues remains elusive. The products of the Yellow cocoon (C) gene and the Flesh (F) gene of the silkworm Bombyx mori determine the selectivity for transport of lutein and Î²-carotene, respectively, to the silk gland. We previously showed that the C gene encodes Cameo2, a CD36 family member, which is thought to function as a transmembrane lipoprotein receptor. Here, we elucidated the molecular identity of the F gene product by positional cloning, as SCRB15, a paralog of Cameo2 with 26% amino acid identity. In the F mutant, SCRB15 mRNA structure was severely disrupted, due to a 1.4 kb genomic insertion in a coding exon. Transgenic expression of SCRB15 in the middle silk gland using the binary GAL4-UAS expression system enhanced selective Î²-carotene uptake by the middle silk gland, while transgenic expression of Cameo2 enhanced selective lutein uptake under the same GAL4 driver. Our findings indicate that divergence of genes in the CD36 family determines the selectivity of carotenoid species uptake by silk gland tissue and that CD36-homologous proteins can discriminate among carotenoid species.

Additional References

RELATED GEPHE

Related Genes

9 (apontic-like, Bm-iAANAT, cardinal, cortex, SCARB1, 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