GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001158

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Bombyx mandarina -wild

Trait State in Taxon B

Bombyx mori - domesticated

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

Common Name

wild silkworm

Synonyms

Bombyx mori mandarina; Theophila mandarina; wild silkworm; Bombyx mandarina (Moore, 1872)

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

7092 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7092)

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

ple

Synonyms

CG10118; DH65B; Dmel\CG10118; DTH; dTH1; dTH65B; Pale; pale/ple; Ple; th; Th; TH; VII

String

7227.FBpp0076666 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0076666)

Sequence Similarities

Belongs to the biopterin-dependent aromatic amino acid hydroxylase family.

GO - Molecular Function

GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)
GO:0004511 : tyrosine 3-monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004511)

GO - Biological Process

UniProtKB Drosophila melanogaster

P18459 (http://www.uniprot.org/uniprot/P18459)

GenebankID or UniProtKB

ACU82844 (https://www.ncbi.nlm.nih.gov/nuccore/ACU82844)

GO:0048085 : adult chitin-containing cuticle pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048085)
GO:0042417 : dopamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042417)
GO:2000274 : regulation of epithelial cell migration, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:2000274)
GO:0008344 : adult locomotory behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0008344)
GO:0006585 : dopamine biosynthetic process from tyrosine
(https://www.ebi.ac.uk/QuickGO/term/GO:0006585)
GO:0048082 : regulation of adult chitin-containing cuticle pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048082)
GO:0009611 : response to wounding (https://www.ebi.ac.uk/QuickGO/term/GO:0009611)
GO:0040040 : thermosensory behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0040040)
GO:0043052 : thermotaxis (https://www.ebi.ac.uk/QuickGO/term/GO:0043052)
GO:0035220 : wing disc development
(https://www.ebi.ac.uk/QuickGO/term/GO:0035220)
GO:0006584 : catecholamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006584)
GO:0048066 : developmental pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0007619 : courtship behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007619)
GO:0008049 : male courtship behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0008049)
GO:0048067 : cuticle pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048067)
GO:0042416 : dopamine biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042416)
GO:0042136 : neurotransmitter biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042136)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0030424 : axon (https://www.ebi.ac.uk/QuickGO/term/GO:0030424)
GO:0043204 : perikaryon (https://www.ebi.ac.uk/QuickGO/term/GO:0043204)

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

Variation in intron; possibly loss of AbdA binding site

Experimental Evidence

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

Main Reference

Evidence of selection at melanin synthesis pathway loci during silkworm domestication. (2011) (https://pubmed.ncbi.nlm.nih.gov/21212153)

Authors

Yu HS; Shen YH; Yuan GX; Hu YG; Xu HE; Xiang ZH; Zhang Z

Abstract

The domesticated silkworm (Bombyx mori) was domesticated from wild silkworm (Bombyx mandarina) more than 5,000 years ago. During domestication, body color between B. mandarina and B. mori changed dramatically. However, the molecular mechanism of the silkworm body color transition is not known. In the present study, we examined within- and between-species nucleotide diversity for eight silkworm melanin synthesis pathway genes, which play a key role in cuticular pigmentation of insects. Our results showed that the genetic diversity of B. mori was significantly lower than that of B. mandarina and 40.7% of the genetic diversity of wild silkworm was lost in domesticated silkworm. We also examined whether position effect exists among melanin synthesis pathway genes in B. mandarina and B. mori. We found that the upstream genes have significantly lower levels of genetic diversity than the downstream genes, supporting a functional constraint hypothesis (FCH) of metabolic pathway, that is, upstream enzymes are under greater selective constraint than downstream enzymes because upstream enzymes participate in biosynthesis of a number of metabolites. We also investigated whether some of the melanin synthesis pathway genes experienced selection during domestication. Neutrality test, coalescent simulation, as well as network and phylogenetic analyses showed that tyrosine hydroxylase (TH) gene was a domestication locus. Sequence analysis further suggested that a putative expression enhancer (Abd-B-binding site) in the intron of TH gene might be disrupted during domestication. TH is the rate-limiting enzyme of melanin synthesis pathway in insects. Real-time polymerase chain reaction assay did show that the relative expression levels of TH gene in B. mori were significantly lower than that in B. mandarina at three different developmental stages, which is consistent with light body color of domesticated silkworm relative to wild silkworm. Therefore, we speculated that expression change of TH gene may contribute to the body color transition from B. mandarina to B. mori. Our results emphasize the exceptional role of gene expression regulation in morphological transition of domesticated animals.

Additional References

RELATED GEPHE

Related Genes

1 (Carotenoid-binding protein (CBP)) (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