

GEPHE SUMMARY

Gephebase Gene		GepheID
Tyrosine hydroxylase (<a +tyrosine+hydroxylase+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Tyrosine+hydroxylase+"#gephebase-summary-title)	GP00001158	
Entry Status	Courtier	Main curator
Published		

PHENOTYPIC CHANGE

Trait Category			
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	
Coloration (body) (<a +coloration+(body)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<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)			
Taxon A		Taxon B	
Latin Name		Latin Name	
Bombyx mandarina (<a +bombyx+mandarina+"#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+mandarina+"#gephebase-summary-title)		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)	
Common Name		Common Name	
wild silkworm		domestic silkworm	
Synonyms		Synonyms	
Bombyx mori mandarina; Theophila mandarina; wild silkworm; Bombyx mandarina (Moore, 1872)		domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	
Rank		Rank	
species		species	
Lineage		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		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		Parent	
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)		Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
7092 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7092)		7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?	
No		No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster	
ple		P18459 (http://www.uniprot.org/uniprot/P18459)	
Synonyms		GenebankID or UniProtKB	
CG10118; DH65B; Dmel\CG10118; DTH; dTH1; dTH65B; Pale; pale/ple; Ple; th; Th; VII		ACU82844 (https://www.ncbi.nlm.nih.gov/nuccore/ACU82844)	
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			

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](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Cis-regulatory ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Cis-regulatory+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

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](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

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](https://www.gephebase.org/search-criteria?/or+Taxon ID=))

Related Haplotypes

No matches found.

EXTERNAL LINKS

