

GEPHE SUMMARY

cortex (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~cortex~#gephebase-summary-title)	Gephebase Gene	GP00002418	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)	Trait Category		
Coloration (wing) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+(wing)~#gephebase-summary-title)	Trait		
wild-type coloration	Trait State in Taxon A		
spot on the apex of the wings - Wild wing spot (Ws) mutant	Trait State in Taxon B		
Unknown	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)	Taxonomic Status		

Taxon A	Latin Name	Taxon B	Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Bombyx+mori~#gephebase-summary-title)	Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Bombyx+mori~#gephebase-summary-title)	Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Bombyx+mori~#gephebase-summary-title)	Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Bombyx+mori~#gephebase-summary-title)
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; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; 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; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; 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

cort	Generic Gene Name	Q960N3 (http://www.uniprot.org/uniprot/Q960N3)	UniProtKB Drosophila melanogaster
CG11330; cor; Cort; Dmel\CG11330	Synonyms	()	GenebankID or UniProtKB
7227.FBpp0078949 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0078949)	String		
Belongs to the WD repeat CORT family.	Sequence Similarities		
GO:0010997 : anaphase-promoting complex binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010997)	GO - Molecular Function		
GO:0097027 : ubiquitin-protein transferase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0097027)			
GO:0048477 : oogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048477)	GO - Biological Process		

GO:0045143 : homologous chromosome segregation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045143)
 GO:0031145 : anaphase-promoting complex-dependent catabolic process
 (https://www.ebi.ac.uk/QuickGO/term/GO:0031145)
 GO:0007349 : cellularization (https://www.ebi.ac.uk/QuickGO/term/GO:0007349)
 GO:0007343 : egg activation (https://www.ebi.ac.uk/QuickGO/term/GO:0007343)
 GO:0007144 : female meiosis I (https://www.ebi.ac.uk/QuickGO/term/GO:0007144)
 GO:0007147 : female meiosis II (https://www.ebi.ac.uk/QuickGO/term/GO:0007147)
 GO:0007143 : female meiotic nuclear division
 (https://www.ebi.ac.uk/QuickGO/term/GO:0007143)
 GO:0007279 : pole cell formation (https://www.ebi.ac.uk/QuickGO/term/GO:0007279)
 GO:1905786 : positive regulation of anaphase-promoting complex-dependent catabolic
 process (https://www.ebi.ac.uk/QuickGO/term/GO:1905786)
 GO:1904668 : positive regulation of ubiquitin protein ligase activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:1904668)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Mapping to a 100-kb-long region which contains the cortex gene.

Experimental Evidence

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

Main Reference

Mapping and recombination analysis of two moth colour mutations, Black moth and Wild wing spot, in the silkworm *Bombyx mori*. (2016) (https://pubmed.ncbi.nlm.nih.gov/26219230)

Authors

Ito K; Katsuma S; Kuwazaki S; Jouraku A; Fujimoto T; Sahara K; Yasukochi Y; Yamamoto K; Tabunoki H; Yokoyama T; Kadono-Okuda K; Shimada T

Abstract

Many lepidopteran insects exhibit body colour variations, where the high phenotypic diversity observed in the wings and bodies of adults provides opportunities for studying adaptive morphological evolution. In the silkworm *Bombyx mori*, two genes responsible for moth colour mutation, *Bm* and *Ws*, have been mapped to 0.0 and 14.7 cM of the *B. mori* genetic linkage group 17; however, these genes have not been identified at the molecular level. We performed positional cloning of both genes to elucidate the molecular mechanisms that underlie the moth wing- and body-colour patterns in *B. mori*. We successfully narrowed down *Bm* and *Ws* to ~2-Mb-long and 100-kb-long regions on the same scaffold *Bm_scaf33*. Gene prediction analysis of this region identified 77 candidate genes in the *Bm* region, whereas there were no candidate genes in the *Ws* region. Fluorescence in-situ hybridisation analysis in *Bm* mutant detected chromosome inversion, which explains why there are no recombination in the corresponding region. The comparative genomic analysis demonstrated that the candidate regions of both genes shared synteny with a region associated with wing- and body-colour variations in other lepidopteran species including *Biston betularia* and *Heliconius* butterflies. These results suggest that the genes responsible for wing and body colour in *B. mori* may be associated with similar genes in other Lepidoptera.

Additional References

RELATED GEPHE

Related Genes

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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase="cortex"/and+Taxon ID="7091"/or+Gene Gephebase="cortex"/and+Taxon ID="7091"#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@Parallelism