GEPHE SUMMARY

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

GepheID
GP00002418

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

Trait State in Taxon A
wild-type coloration

Trait State in Taxon B
spot on the apex of the wings - Wild wing spot (Ws) mutant

Ancestral State
Unknown

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
cort

Synonyms
CG11330; cor; Cort; Dmel\CG11330

String
7227.FBpp0078949 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0078949)

Sequence Similarities
Belongs to the WD repeat CORT family.

GO - Molecular Function
GO:0010997 : anaphase-promoting complex binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010997)
GO:0097027 : ubiquitin-protein transferase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0097027)

GO - Biological Process
GO:0048477 : oogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048477)

UniProtKB Drosophila melanogaster
Q960N3 (http://www.uniprot.org/uniprot/Q960N3)

GenebankID or UniProtKB
()

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 14.7â€‰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