

GEPHE SUMMARY

Gephebase Gene

ebony

Entry Status

Published

GepheID

GP00001544

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Morphology

Trait

Coloration (male-specific)

Trait State in Taxon A

D. m. malerkotliana with darker male abdominal pigmentation

Trait State in Taxon B

D. m. pallens with light colored male abdominal pigmentation

Ancestral State

Unknown

Taxonomic Status

Intraspecific

	Taxon A	Taxon B
Latin Name	<i>Drosophila malerkotliana</i>	<i>Drosophila malerkotliana</i>
Common Name	-	-
Synonyms	-	-
Rank	species	species
Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalytratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; ananassae subgroup; bipectinata species complex	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalytratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; ananassae subgroup; bipectinata species complex
Parent	bipectinata species complex () - (Rank: no rank)	bipectinata species complex () - (Rank: no rank)
NCBI Taxonomy ID	30036	30036
is Taxon A an Intraspecies?	Yes	Yes
Taxon A Description	D. m. malerkotliana with darker male abdominal pigmentation	D. m. pallens with light colored male abdominal pigmentation

GENOTYPIC CHANGE

Generic Gene Name

e

Synonyms

ebony; CG3331

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0000036 : acyl carrier activity

GO:0003833 : beta-alanyl-dopamine synthase activity

GO:0031177 : phosphopantetheine binding

GO - Biological Process

GO:0048085 : adult chitin-containing cuticle pigmentation

GO:0042417 : dopamine metabolic process

UniProtKB *Drosophila melanogaster*

O76858

GenebankID or UniProtKB

GO:0007623 : circadian rhythm
GO:0048082 : regulation of adult chitin-containing cuticle pigmentation
GO:0048066 : developmental pigmentation
GO:0043042 : amino acid adenylation by nonribosomal peptide synthase
GO:0007593 : chitin-based cuticle sclerotization
GO:0048067 : cuticle pigmentation
GO:0001692 : histamine metabolic process
GO:0045475 : locomotor rhythm
GO:0006583 : melanin biosynthetic process from tyrosine
GO:0048022 : negative regulation of melanin biosynthetic process
GO:0042440 : pigment metabolic process

GO - Cellular Component
GO:0005737 : cytoplasm

Presumptive Null
No

Molecular Type
Cis-regulatory

Aberration Type
SNP

Molecular Details of the Mutation
5 changes including 4 SNP and 1bp indel in the first intron

Experimental Evidence
Linkage Mapping

Main Reference
[Genetic Convergence in the Evolution of Male-Specific Color Patterns in Drosophila. \(2016\)](#)

Authors
Signor SA; Liu Y; Rebeiz M; Kopp A

Abstract
Convergent evolution provides a type of natural replication that can be exploited to understand the roles of contingency and constraint in the evolution of phenotypes and the gene networks that control their development. For sex-specific traits, convergence offers the additional opportunity for testing whether the same gene networks follow different evolutionary trends in males versus females. Here, we use an unbiased, systematic mapping approach to compare the genetic basis of evolutionary changes in male-limited pigmentation in several pairs of *Drosophila* species that represent independent evolutionary transitions. We find strong evidence for repeated recruitment of the same genes to specify similar pigmentation in different species. At one of these genes, *ebony*, we observe convergent evolution of sexually dimorphic and monomorphic expression through cis-regulatory changes. However, this functional convergence has a different molecular basis in different species, reflecting both parallel fixation of ancestral alleles and independent origin of distinct mutations with similar functional consequences. Our results show that a strong evolutionary constraint at the gene level is compatible with a dominant role of chance at the molecular level.

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[Additional References](#)

RELATED GEPHE

[Related Genes](#)
[2 \(Abdominal-B, yellow\)](#)
[Related Haplotypes](#)
No matches found.

COMMENTS

@ILS or @Introgression - @SexualTrait - A large QTL on 3R (3R1) including *ebony*; *ebony* is not expressed in segments that are completely black in darker species while it is expressed in a wider pattern in light colored taxa. Involvement of *ebony* demonstrated by RNAi experiments and evidence of cis-regulatory differences by sequencing of transcript in F1 hybrid. The causative variants in *ebony* may be due either to parallel fixation of ancestral alleles or to interspecific introgression (with the couple *D. bipectinata*-*D. parabipectinata*). For the light forms (*D. bipectinata* & *D. m. pallens*) phylogenetic analysis supports a sorting of ancestral polymorphisms.