GEPHE SUMMARY

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

GepheID
GP00001547

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
D. parabipectinata with darker male abdominal pigmentation

Trait State in Taxon B
D. bipectinata with light colored male abdominal pigmentation

Ancestral State
Unknown

Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name
Drosophila parabipectinata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila parabipectinata^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; ananassae subgroup; bipectinata species complex

Parent
bipectinata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 186282)

NCBI Taxonomy ID
186283 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 186283)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Drosophila bipectinata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila bipectinata^#gephebase-summary-title)

Common Name
-

Synonyms
Drosophila bipectinata Duda, 1923

Rank
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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; ananassae subgroup; bipectinata species complex

Parent
bipectinata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 186282)

NCBI Taxonomy ID
42026 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 42026)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
e

Synonyms
ebony; CG3331

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0000036 : acyl carrier activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000036)
GO:0003833 : beta-alanyl-dopamine synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003833)
GO:0031177 : phosphopantetheine binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031177)

GO - Biological Process
GO:0048085 : adult chitin-containing cuticle pigmentation

UniProtKB Drosophila melanogaster
O76858 (http://www.uniprot.org/uniprot/O76858)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0048085)
GO:0042417 : dopamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042417)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0048082 : regulation of adult chitin-containing cuticle pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048082)
GO:0048066 : developmental pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0043042 : amino acid adenylylation by nonribosomal peptide synthase
(https://www.ebi.ac.uk/QuickGO/term/GO:0043042)
GO:0007593 : chitin-based cuticle sclerotization
(https://www.ebi.ac.uk/QuickGO/term/GO:0007593)
GO:0048067 : cuticle pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048067)
GO:0001692 : histamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001692)
GO:0045475 : locomotor rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0045475)
GO:0006583 : melanin biosynthetic process from tyrosine
(https://www.ebi.ac.uk/QuickGO/term/GO:0006583)
GO:0048022 : negative regulation of melanin biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0048022)
GO:0042440 : pigment metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042440)

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

unknown

Experimental Evidence

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

Main Reference

Genetic Convergence in the Evolution of Male-Specific Color Patterns in Drosophila. (2016) (https://pubmed.ncbi.nlm.nih.gov/27546578)

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

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

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. QTL was first determined in comparison with D. m. malerkotliana; but difference in ebony expression is observed between D. bipectinata and D. parabipectinata. The causative variants in ebony may be due either to parallel fixation of ancestral alleles or to interspecific introgression (with the couple D. m. malerkotliana-D. m. pallens). For the light forms (D. bipectinata & D. m. pallens) phylogenetic analysis supports a sorting of ancestral polymorphisms.