GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002024

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

dark posterior male abdomen

Trait State in Taxon B

light posterior male abdomen

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Drosophila yakuba Burla, 1954

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; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

7245 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7245)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Drosophila santomea (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila santomea^#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; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

129105 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 129105)

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

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

Aberration Type

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

Insertion Size

100-999 bp

Molecular Details of the Mutation

insertion of a partial 481 bp fragment related to a transposable element of the helitron class - maybe other causing mutations as well at this ebony locus (including one fixed amino acid change whose phenotypic effect has not been investigated) - increased expression associated with lighter pigmentation

Experimental Evidence

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

Main Reference

Changes throughout a Genetic Network Mask the Contribution of Hox Gene Evolution. (2019) (https://pubmed.ncbi.nlm.nih.gov/31257142)

Authors

Liu Y; Ramos-Womack M; Han C; Reilly P; Brackett KL; Rogers W; Williams TM; Andolfatto P; Stern DL; Rebeiz M

Abstract

Hox genes pattern the anterior-posterior axis of animals and are posited to drive animal body plan evolution, yet their precise role in evolution has been difficult to determine. Here, we identified evolutionary modifications in the Hox gene Abd-B that dramatically altered its expression along the body plan of Drosophila santomea. Abd-B is required for pigmentation in Drosophila yakuba, the sister species of D.Â santomea, and changes to Abd-B expression would be predicted to make large contributions to the loss of body pigmentation in D.Â santomea. However, manipulating Abd-B expression in current-day D.Â santomea does not affect pigmentation. We attribute this epistatic interaction to four other genes within the D.Â santomea pigmentation network, three of which have evolved expression patterns that do not respond to Abd-B. Our results demonstrate how body plans may evolve through small evolutionary steps distributed throughout Hox-regulated networks. Polygenicity and epistasis may hinder efforts to identify genes and mechanisms underlying macroevolutionary traits.

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Additional References

RELATED GEPHE

Related Genes

5 (Abdominal-B, pdm3, tan, yellow, bab) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7245^/and+Trait=Coloration/or+Taxon ID=^129105^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait @SeveralMutationsWithEffect @TE