GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002021

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

Abd-B

Synonyms

BX-C; 9; Abd B; abd-B; Abd-b; ABD-B; Abd0B; abdB; Abdb; AbdB; ABDB; AbdB(CA) [[26]]; AbdB-I; AbdB-II; AbdBm; Adb-B; AdbB; bex; CG10291; CG11648; DmAbdB; Dmel\CG11648; Droabdb; DROABDB; FAB; Fab-6; Fab-7; Fab-8; Fab7; iab; IAB 5; iab-5; iab-6; iab-7; Iab-7; iab-8; iab5; IAB5; iab6; iab7; IAB7; iab8; IAB8; iab8.9; iab9; l(3)89Ed; Mc; Mcp; MCP; pH189; Sab; Tab; tuh-3; twig; Uab-5[Sab]

String

7227.FBpp0082826 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0082826)

Sequence Similarities

Belongs to the Abd-B homeobox family.

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity

UniProtKB Drosophila melanogaster

P09087 (http://www.uniprot.org/uniprot/P09087)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0000980 : RNA polymerase II distal enhancer sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000980)
GO:0000976 : transcription regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000976)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0007507 : heart development (https://www.ebi.ac.uk/QuickGO/term/GO:0007507)
GO:0008584 : male gonad development (https://www.ebi.ac.uk/QuickGO/term/GO:0008584)
GO:0007548 : sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0007548)
GO:0007621 : negative regulation of female receptivity (https://www.ebi.ac.uk/QuickGO/term/GO:0007621)
GO:0048071 : sex-specific pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048071)
GO:0030539 : male genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0030539)
GO:0035215 : genital disc development (https://www.ebi.ac.uk/QuickGO/term/GO:0035215)
GO:0048066 : developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0007486 : imaginal disc-derived female genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0007486)
GO:0035225 : determination of genital disc primordium (https://www.ebi.ac.uk/QuickGO/term/GO:0035225)
GO:0007431 : salivary gland development (https://www.ebi.ac.uk/QuickGO/term/GO:0007431)
GO:0035277 : spiracle morphogenesis, open tracheal system (https://www.ebi.ac.uk/QuickGO/term/GO:0035277)
GO:0007424 : open tracheal system development (https://www.ebi.ac.uk/QuickGO/term/GO:0007424)
GO:0008354 : germ cell migration (https://www.ebi.ac.uk/QuickGO/term/GO:0008354)
GO:0007494 : midgut development (https://www.ebi.ac.uk/QuickGO/term/GO:0007494)
GO:0035224 : genital disc anterior/posterior pattern formation (https://www.ebi.ac.uk/QuickGO/term/GO:0035224)
GO:0035263 : genital disc sexually dimorphic development (https://www.ebi.ac.uk/QuickGO/term/GO:0035263)
GO:0030540 : female genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0030540)
GO:0035261 : external genitalia morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0035261)
GO:0007506 : gonadal mesoderm development (https://www.ebi.ac.uk/QuickGO/term/GO:0007506)
GO:0007484 : imaginal disc-derived genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0007484)
GO:0048094 : male pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048094)
GO:0009997 : negative regulation of cardioblast cell fate specification (https://www.ebi.ac.uk/QuickGO/term/GO:0009997)
GO:0045705 : negative regulation of salivary gland boundary specification (https://www.ebi.ac.uk/QuickGO/term/GO:0045705)
GO:0045843 : negative regulation of striated muscle tissue development (https://www.ebi.ac.uk/QuickGO/term/GO:0045843)
GO:0061101 : neuroendocrine cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0061101)
GO:0007280 : pole cell migration (https://www.ebi.ac.uk/QuickGO/term/GO:0007280)
GO:1902339 : positive regulation of apoptotic process involved in morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:1902339)
GO:0048087 : positive regulation of developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048087)
GO:0007379 : segment specification (https://www.ebi.ac.uk/QuickGO/term/GO:0007379)
GO:0007385 : specification of segmental identity, abdomen (https://www.ebi.ac.uk/QuickGO/term/GO:0007385)
GO:0046693 : sperm storage (https://www.ebi.ac.uk/QuickGO/term/GO:0046693)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

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

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

Molecular Details of the Mutation

change in the iab5 cis-regulatory element (15kb long)- exact causing mutation(s) unknown - decreased AbdB abdominal expression

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.

Copyright Â© 2019 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

Related Genes

5 (ebony, 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