GEPHE SUMMARY

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

GepheID
GP00002048

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

Trait State in Taxon A
red abdomen - higher expression of Abd-B

Trait State in Taxon B
black abdomen - lower expression of Abd-B

Ancestral State
Unknown

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

Taxon A

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

Common Name
-

Synonyms
Bombus edwardsii

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Bombinae; Bombini; Bombus; Pyrobombus

Parent
Pyrobombus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 144703)

NCBI Taxonomy ID
207638 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 207638)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
Bombus edwardsii

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Bombinae; Bombini; Bombus; Pyrobombus

Parent
Pyrobombus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 144703)

NCBI Taxonomy ID
207638 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 207638)

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

UniProtKB Drosophila melanogaster
P09087 (http://www.uniprot.org/uniprot/P09087)

GenebankID or UniProtKB
()

(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

4kb region - probably several mutations according to recombinants with intermediate phenotypes

Experimental Evidence

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

Main Reference

A homeotic shift late in development drives mimetic color variation in a bumble bee. (2019) (https://pubmed.ncbi.nlm.nih.gov/31043564)

Authors

Tian L; Rahman SR; Ezray BD; Franzini L; Strange JP; Lhomme P; Hines HM

Abstract

Natural phenotypic radiations, with their high diversity and convergence, are well-suited for informing how genomic changes translate to natural phenotypic variation. New genomic tools enable discovery in such traditionally nonmodel systems. Here, we characterize the genomic basis of color pattern variation in bumble bees (Hymenoptera, Apidae, Bombus), a group that has undergone extensive convergence of setal color patterns as a result of MÃ¼llerian mimicry. In western North America, multiple species converge on local mimicry patterns through parallel shifts of midabdominal segments from red to black. Using genome-wide association, we establish that a cis-regulatory locus between the abdominal fate-determining Hox genes, abd-A and Abd-B, controls the red-black color switch in a western species, Bombus melanopygus Gene expression analysis reveals distinct shifts in Abd-B aligned with the duration of setal pigmentation at the pupal-adult transition. This results in atypical anterior Abd-B expression, a late developmental homeotic shift. Changing expression of Hox genes can have widespread effects, given their important role across segmental phenotypes; however, the late timing reduces this pleiotropy, making Hox genes suitable targets. Analysis of this locus across mimics and relatives reveals that other species follow independent genetic routes to obtain the same phenotypes.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Mimicry