## GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002611

Main curator

Courtier

## PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Drosophila melanogaster - dark 1 allele

Trait State in Taxon B

Drosophila melanogaster - dark 2 allele

Ancestral State

Unknown

Taxonomic Status

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

### Taxon A

Latin Name

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

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227 )

is Taxon A an Infraspecies?

No

### Taxon B

Latin Name

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

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227 )

is Taxon B an Infraspecies?

No

## GENOTYPIC CHANGE

Generic Gene Name

bab1

Synonyms

anon-WO0118547.639; bab; BAB; BAB-1; bab-I; Bab1; BAB1; bric-a-brac; CG13910; CG9097; Dmel\CG9097

String

7227.FBpp0072538 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0072538 )

Sequence Similarities

-

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0003680 : AT DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003680)

UniProtKB Drosophila melanogaster

Q9W0K7 (http://www.uniprot.org/uniprot/Q9W0K7)

GenebankID or UniProtKB

()

## GO - Biological Process

GO:0006357 : regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0006357)

GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)

GO:0007548 : sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0007548)

GO:0006351 : transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006351)

GO:0048085 : adult chitin-containing cuticle pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048085)

GO:0007455 : eye-antennal disc morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0007455)

GO:0046660 : female sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0046660)

GO:0007478 : leg disc morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0007478)

GO:0048086 : negative regulation of developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048086)

GO:0048092 : negative regulation of male pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048092)

GO:0048070 : regulation of developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048070)

GO:0048071 : sex-specific pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048071)

## GO - Cellular Component

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

Mutation #1

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

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

Molecular Details of the Mutation

D mutation = G>C and M mutation

Experimental Evidence

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

Main Reference

Recurrent modification of a conserved cis-regulatory element underlies fruit fly pigmentation diversity. (2013) (https://pubmed.ncbi.nlm.nih.gov/24009528)

Authors

Rogers WA; Salomone JR; Tacy DJ; Camino EM; Davis KA; Rebeiz M; Williams TM

Abstract

The development of morphological traits occurs through the collective action of networks of genes connected at the level of gene expression. As any node in a network may be a target of evolutionary change, the recurrent targeting of the same node would indicate that the path of evolution is biased for the relevant trait and network. Although examples of parallel evolution have implicated recurrent modification of the same gene and cis-regulatory element (CRE), little is known about the mutational and molecular paths of parallel CRE evolution. In Drosophila melanogaster fruit flies, the Bric-Ã -brac (Bab) transcription factors control the development of a suite of sexually dimorphic traits on the posterior abdomen. Female-specific Bab expression is regulated by the dimorphic element, a CRE that possesses direct inputs from body plan (ABD-B) and sex-determination (DSX) transcription factors. Here, we find that the recurrent evolutionary modification of this CRE underlies both intraspecific and interspecific variation in female pigmentation in the melanogaster species group. By reconstructing the sequence and regulatory activity of the ancestral Drosophila melanogaster dimorphic element, we demonstrate that a handful of mutations were sufficient to create independent CRE alleles with differing activities. Moreover, intraspecific and interspecific dimorphic element evolution proceeded with little to no alterations to the known body plan and sex-determination regulatory linkages. Collectively, our findings represent an example where the paths of evolution appear biased to a specific CRE, and drastic changes in function were accompanied by deep conservation of key regulatory linkages.

Additional References

Mutation #2

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

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

Molecular Details of the Mutation

D mutation = G>C and M mutation

Experimental Evidence

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

Main Reference

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Abstract

The development of morphological traits occurs through the collective action of networks of genes connected at the level of gene expression. As any node in a network may be a target of evolutionary change, the recurrent targeting of the same node would indicate that the path of evolution is biased for the relevant trait and network. Although examples of parallel evolution have implicated recurrent modification of the same gene and cis-regulatory element (CRE), little is known about the mutational and molecular paths of parallel CRE evolution. In Drosophila melanogaster fruit flies, the Bric-Ã -brac (Bab) transcription factors control the development of a suite of sexually dimorphic traits on the posterior abdomen. Female-specific Bab expression is regulated by the dimorphic element, a CRE that possesses direct inputs from body plan (ABD-B) and sex-determination (DSX) transcription factors.

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Additional References

## RELATED GEPHE

Related Genes

5 (bab1, ebony, tan, yellow, wingless (wg)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

5 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^bab^/and+Taxon ID=^7227^/or+Gene Gephebase=^bab^/and+Taxon ID=^7227^#gephebase-summary-title)

## EXTERNAL LINKS

## COMMENTS

@SexualTrait