

GEPHE SUMMARY

<p>bab (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~bab~#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00002610</p> <p>Courtier</p>	<p>GepheID</p> <p>Main curator</p>
---	---	-----------------------------------	------------------------------------

PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)</p> <p>Coloration (abdomen; female) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration (abdomen; female)~#gephebase-summary-title)</p> <p>Drosophila melanogaster - light pigmentation</p> <p>Drosophila melanogaster - darker pigmentation</p> <p>Unknown</p> <p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)</p>		<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila melanogaster~#gephebase-summary-title)</p> <p>Common Name</p> <p>fruit fly</p> <p>Synonyms</p> <p>Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)</p> <p>NCBI Taxonomy ID</p> <p>7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila melanogaster~#gephebase-summary-title)</p> <p>Common Name</p> <p>fruit fly</p> <p>Synonyms</p> <p>Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)</p> <p>NCBI Taxonomy ID</p> <p>7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>
--	--	---	--	--

GENOTYPIC CHANGE

<p>bab1</p> <p>anon-WO0118547.639; bab; BAB; BAB-1; bab-I; Bab1; BAB1; bric-a-brac; CG13910; CG9097; Dmel\CG9097</p> <p>7227.FBpp0072538 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0072538)</p> <p>Sequence Similarities</p> <p>-</p> <p>GO - Molecular Function</p> <p>GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)</p> <p>GO:0003680 : AT DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003680)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Drosophila melanogaster</p> <p>Q9W0K7 (http://www.uniprot.org/uniprot/Q9W0K7)</p> <p>GenebankID or UniProtKB</p> <p>()</p>
--	--	---

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

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Presumptive Null

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

Molecular Type

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

Aberration Type

F mutation = GA>TT and L mutation A>G in an enhancer of bab

Molecular Details of the Mutation

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

Experimental Evidence

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

Main Reference

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

Authors

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-À-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

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Presumptive Null

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

Molecular Type

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

Aberration Type

F mutation = GA>TT and L mutation A>G in an enhancer of bab

Molecular Details of the Mutation

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

Experimental Evidence

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

Main Reference

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

Authors

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-À-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

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