

GEPHE SUMMARY

	Gephebase Gene	GepheID
bab (https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%bab%#gephebase-summary-title)	GP00002008	
	Entry Status	Main curator
Published	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;%20female)%#gephebase-summary-title)	Trait State in Taxon A
Drosophila melanogaster - light pigmentation	Trait State in Taxon B
Drosophila yakuba - darker pigmentation; lower expression levels of bab	Ancestral State
Unknown	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=Interspecific%#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Drosophila+melanogaster%#gephebase-summary-title)		Drosophila yakuba (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Drosophila+yakuba%#gephebase-summary-title)	
fruit fly	Common Name	-	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Drosophila yakuba Burla, 1954	Synonyms
Species	Rank	Species	Rank
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	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	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID	7245 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7245)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
bab1		Q9W0K7 (http://www.uniprot.org/uniprot/Q9W0K7)
	Synonyms	GenebankID or UniProtKB
anon-WO0118547.639; bab; BAB; BAB-1; bab-I; Bab1; BAB1; bric-a-brac; CG13910; CG9097; Dmel\CG9097	0	
	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)		

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>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%22Cis-regulatory%22#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%22Unknown%22#gephebase-summary-title>)

Molecular Details of the Mutation

causing mutation(s) unknown. Cis-regulatory element assayed with a GFP reporter in *D. melanogaster*.

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%22Candidate+Gene%22#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-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=%227227%22+and+Trait=Coloration/or+Taxon+ID=%227245%22+and+Trait=Coloration/+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

5 (<https://www.gephebase.org/search-criteria/?or+Gene+Gephebase=%22bab%22+and+Taxon+ID=%227227%22/or+Gene+Gephebase=%22bab%22+and+Taxon+ID=%227245%22#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

@SexualTrait

