GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00002423

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Drosophila melanogaster - pale female abdominal pigmentation

Trait State in Taxon B
Drosophila melanogaster - dark female abdominal pigmentation

Ancestral State
Taxon A

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)

UniProtKB Drosophila melanogaster
Q9W0K7 (http://www.uniprot.org/uniprot/Q9W0K7)

GenebankID or UniProtKB
()

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=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

a 56-bp deletion that removes two binding sites for Abdominal B (Abd-B), a direct activator of bab, is present in a cis-regulatiry region of bab1 (within the first intron of bab1) in the Dark line.

Experimental Evidence

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

Main Reference

bric Ã brac (bab), a central player in the gene regulatory network that mediates thermal plasticity of pigmentation in Drosophila melanogaster. (2018) (https://pubmed.ncbi.nlm.nih.gov/30067846)

Authors

De Castro S; Peronnet F; Gilles JF; Mouchel-Vielh E; Gibert JM

Abstract

Drosophila body pigmentation has emerged as a major Evo-Devo model. Using two Drosophila melanogaster lines, Dark and Pale, selected from a natural population, we analyse here the interaction between genetic variation and environmental factors to produce this complex trait. Indeed, pigmentation varies with genotype in natural populations and is sensitive to temperature during development. We demonstrate that the bric Ã brac (bab) genes, that are differentially expressed between the two lines and whose expression levels vary with temperature, participate in the pigmentation difference between the Dark and Pale lines. The two lines differ in a bab regulatory sequence, the dimorphic element (called here bDE). Both bDE alleles are temperature-sensitive, but the activity of the bDE allele from the Dark line is lower than that of the bDE allele from the Pale line. Our results suggest that this difference could partly be due to differential regulation by AbdB. bab has been previously reported to be a repressor of abdominal pigmentation. We show here that one of its targets in this process is the pigmentation gene tan (t), regulated via the tan abdominal enhancer (t_MSE). Furthermore, t expression is strongly modulated by temperature in the two lines. Thus, temperature sensitivity of t expression is at least partly a consequence of bab thermal transcriptional plasticity. We therefore propose that a gene regulatory network integrating both genetic variation and temperature sensitivity modulates female abdominal pigmentation. Interestingly, both bDE and t_MSE were previously shown to have been recurrently involved in abdominal pigmentation evolution in drosophilids. We propose that the environmental sensitivity of these enhancers has turned them into evolutionary hotspots.

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 @GxE - The 56 bp deletion is likely to be a recent and rare allele, perhaps deleterious, present at low frequency at least in some Canadian populations.