GEPHE SUMMARY

Gephebase Gene
bab1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^bab1^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00000130

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Drosophila melanogaster

Trait State in Taxon B
Drosophila melanogaster

Ancestral State
Data not curated

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
U01333 (https://www.ncbi.nlm.nih.gov/nuccore/U01333)

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

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

multiple cis-regulatory changes in at least 3 regions: a promoter; a tissue-specific enhancer and a Polycomb response element.

Experimental Evidence

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

Main Reference

Quantitative trait loci responsible for variation in sexually dimorphic traits in Drosophila melanogaster. (2003) (https://pubmed.ncbi.nlm.nih.gov/12618413)

Authors

Kopp A; Graze RM; Xu S; Carroll SB; Nuzhdin SV

Abstract

To understand the mechanisms of morphological evolution and species divergence, it is essential to elucidate the genetic basis of variation in natural populations. Sexually dimorphic characters, which evolve rapidly both within and among species, present attractive models for addressing these questions. In this report, we map quantitative trait loci (QTL) responsible for variation in sexually dimorphic traits (abdominal pigmentation and the number of ventral abdominal bristles and sex comb teeth) in a natural population of Drosophila melanogaster. To capture the pattern of genetic variation present in the wild, a panel of recombinant inbred lines was created from two heterozygous flies taken directly from nature. High-resolution mapping was made possible by cytological markers at the average density of one per 2 cM. We have used a new Bayesian algorithm that allows QTL mapping based on all markers simultaneously. With this approach, we were able to detect small-effect QTL that were not evident in single-marker analyses. Our results show that at least for some sexually dimorphic traits, a small number of QTL account for the majority of genetic variation. The three strongest QTL account for >60% of variation in the number of ventral abdominal bristles. Strikingly, a single QTL accounts for almost 60% of variation in female abdominal pigmentation. This QTL maps to the chromosomal region that Robertson et al. have found to affect female abdominal pigmentation in other populations of D. melanogaster. Using quantitative complementation tests, we demonstrate that this QTL is allelic to the bric a brac gene, whose expression has previously been shown to correlate with interspecific differences in pigmentation. Multiple bab alleles that confer distinct phenotypes appear to segregate in natural populations at appreciable frequencies, suggesting that intraspecific and interspecific variation in abdominal pigmentation may share a similar genetic basis.

Additional References

Composite effects of polymorphisms near multiple regulatory elements create a major-effect QTL. (2011) (https://pubmed.ncbi.nlm.nih.gov/21249179)

Mutation #2

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

multiple cis-regulatory changes in at least 3 regions: a promoter; a tissue-specific enhancer and a Polycomb response element.

Experimental Evidence

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

Main Reference

Quantitative trait loci responsible for variation in sexually dimorphic traits in Drosophila melanogaster. (2003) (https://pubmed.ncbi.nlm.nih.gov/12618413)

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Additional References

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Mutation #3

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

multiple cis-regulatory changes in at least 3 regions: a promoter; a tissue-specific enhancer and a Polycomb response element.

Experimental Evidence

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

Main Reference

Quantitative trait loci responsible for variation in sexually dimorphic traits in Drosophila melanogaster. (2003) (https://pubmed.ncbi.nlm.nih.gov/12618413)

Authors

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Abstract

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Additional References

Composite effects of polymorphisms near multiple regulatory elements create a major-effect QTL. (2011) (https://pubmed.ncbi.nlm.nih.gov/21249179)

RELATED GEPHE

Related Genes

5 (bab, 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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^bab1^/and+Taxon ID=^7227^/or+Gene Gephebase=^bab1^/and+Taxon ID=^7227^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@SexualTrait