## GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001986

Main curator

Courtier

## PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Drosophila melanogaster

Trait State in Taxon B

Drosophila melanogaster - slower embryonic development - allele hb8delta

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

eve

Synonyms

10.5; 10.9; 14.10; 20.35; CG2328; dm-eve; Dmel\CG2328; E(eve); Eve; EVE; eve2; even; F; l(2)46Ce; l(2)46CFg; l(2)46CFh; l(2)46CFj; l(2)46CFp; l(2)46Cg; V; VI

String

7227.FBpp0087478 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0087478 )

Sequence Similarities

Belongs to the even-skipped homeobox family.

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

UniProtKB Drosophila melanogaster

P06602 (http://www.uniprot.org/uniprot/P06602)

GenebankID or UniProtKB

()

GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0000980 : RNA polymerase II distal enhancer sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000980)

GO - Biological Process

GO:0007417 : central nervous system development (https://www.ebi.ac.uk/QuickGO/term/GO:0007417)
GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0007507 : heart development (https://www.ebi.ac.uk/QuickGO/term/GO:0007507)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045165 : cell fate commitment (https://www.ebi.ac.uk/QuickGO/term/GO:0045165)
GO:0008045 : motor neuron axon guidance (https://www.ebi.ac.uk/QuickGO/term/GO:0008045)
GO:0007366 : periodic partitioning by pair rule gene (https://www.ebi.ac.uk/QuickGO/term/GO:0007366)
GO:0035289 : posterior head segmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0035289)
GO:0035290 : trunk segmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0035290)
GO:0007517 : muscle organ development (https://www.ebi.ac.uk/QuickGO/term/GO:0007517)
GO:0001709 : cell fate determination (https://www.ebi.ac.uk/QuickGO/term/GO:0001709)
GO:0007350 : blastoderm segmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0007350)
GO:0003007 : heart morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0003007)
GO:1901739 : regulation of myoblast fusion (https://www.ebi.ac.uk/QuickGO/term/GO:1901739)
GO:0008595 : anterior/posterior axis specification, embryo (https://www.ebi.ac.uk/QuickGO/term/GO:0008595)
GO:0009997 : negative regulation of cardioblast cell fate specification (https://www.ebi.ac.uk/QuickGO/term/GO:0009997)
GO:0007512 : adult heart development (https://www.ebi.ac.uk/QuickGO/term/GO:0007512)
GO:0007376 : cephalic furrow formation (https://www.ebi.ac.uk/QuickGO/term/GO:0007376)
GO:0007377 : germ-band extension (https://www.ebi.ac.uk/QuickGO/term/GO:0007377)
GO:0050770 : regulation of axonogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0050770)

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

72bp deletion that removes one of the hb protein-binding sites in the stripe 3+7 enhancer of eve. The deletion also removes half of a putative slp1 protein-binding site.

Experimental Evidence

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

Main Reference

Naturally occurring deletions of hunchback binding sites in the even-skipped stripe 3+7 enhancer. (2014) (https://pubmed.ncbi.nlm.nih.gov/24786295)

Authors

Palsson A; Wesolowska N; ReynisdÃ³ttir S; Ludwig MZ; Kreitman M

Abstract

Changes in regulatory DNA contribute to phenotypic differences within and between taxa. Comparative studies show that many transcription factor binding sites (TFBS) are conserved between species whereas functional studies reveal that some mutations segregating within species alter TFBS function. Consistently, in this analysis of 13 regulatory elements in Drosophila melanogaster populations, single base and insertion/deletion polymorphism are rare in characterized regulatory elements. Experimentally defined TFBS are nearly devoid of segregating mutations and, as has been shown before, are quite conserved. For instance 8 of 11 Hunchback binding sites in the stripe 3+7 enhancer of even-skipped are conserved between D. melanogaster and Drosophila virilis. Oddly, we found a 72 bp deletion that removes one of these binding sites (Hb8), segregating within D. melanogaster. Furthermore, a 45 bp deletion polymorphism in the spacer between the stripe 3+7 and stripe 2 enhancers, removes another predicted Hunchback site. These two deletions are separated by â^¼250 bp, sit on distinct haplotypes, and segregate at appreciable frequency. The Hb8Î" is at 5 to 35% frequency in the new world, but also shows cosmopolitan distribution. There is depletion of sequence variation on the Hb8Î"-carrying haplotype. Quantitative genetic tests indicate that Hb8Î" affects developmental time, but not viability of offspring. The Eve expression pattern differs between inbred lines, but the stripe 3 and 7 boundaries seem unaffected by Hb8Î". The data reveal segregating variation in regulatory elements, which may reflect evolutionary turnover of characterized TFBS due to drift or co-evolution.

Additional References

## RELATED GEPHE

Related Genes

1 (InR) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Developmental time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

This mutation appears to affect developmental time, but not viability of offspring. The evehb8Î” deletion polymorphism shows a cosmopolitan distribution. There is no significant relation between latitude and frequency of evehb8Î” in 13 samples from the east coast of North America. - http://flybase.org/reports/FBal0296117