

GEPHE SUMMARY

	Gephebase Gene	GephelD
eve (#gephebase-summary-title)	GP00001986	Main curator
	Entry Status	Courtier
Published		

PHENOTYPIC CHANGE

Trait Category		Trait	
Physiology (#gephebase-summary-title)			
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 (#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Drosophila melanogaster (#gephebase-summary-title))		Drosophila melanogaster (#gephebase-summary-title))	
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	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; Ephydriodea; 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; Ephydriodea; 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	7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

eve	Generic Gene Name	UniProtKB Drosophila melanogaster
	Synonyms	GenebankID or UniProtKB
10.5; 10.9; 14.10; 20.35; CG2328; dm-eve; Dmel\CG2328; E(eve); Eve; EVE; eve2; even; F; I(2)46Ce; I(2)46CFg; I(2)46CFh; I(2)46CFj; I(2)46CFp; I(2)46Cg; V; VI		
7227.FBpp0087478 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0087478)	String	
Belongs to the even-skipped homeobox family.	Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	GO - Molecular Function	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		

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.gephbase.org/search-criteria/?and+Presumptive+Null=^No^#gephbase-summary-title>)

Molecular Type

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

Aberration Type

Deletion (<https://www.gephbase.org/search-criteria/?and+Aberration+Type=^Deletion^#gephbase-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.gephbase.org/search-criteria/?and+Experimental+Evidence=^Candidate+Gene^#gephbase-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 $\approx 1/4250$ bp, sit on distinct haplotypes, and segregate at appreciable frequency. The Hb8^l is at 5 to 35% frequency in the new world, but also shows cosmopolitan distribution. There is depletion of sequence variation on the Hb8^l-carrying haplotype. Quantitative genetic tests indicate that Hb8^l 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 Hb8^l. 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.gephbase.org/search-criteria/?or+Taxon+ID=^7227^/and+Trait=Developmental+time/and+groupHaplotypes=true#gephbase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

This mutation appears to affect developmental time, but not viability of offspring. The evehb8^{-/-} deletion polymorphism shows a cosmopolitan distribution. There is no significant relation between latitude and frequency of evehb8^{-/-} in 13 samples from the east coast of North America. - <http://flybase.org/reports/FBal0296117>