

GEPHE SUMMARY

	Gephebase Gene		GepheID
Delta (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Delta~#gephebase-summary-title)		GP00000217	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)			
	Trait		
Bristle number (thorax) (https://www.gephebase.org/search-criteria?/and+Trait=~Bristle+number+(thorax)~#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		Taxon B	
	Latin Name		Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)		Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)	
	Common Name		Common Name
fruit fly		fruit fly	
	Synonyms		Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)		7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	
	is Taxon A an Infrappecies?		is Taxon B an Infrappecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
DI		P10041 (http://www.uniprot.org/uniprot/P10041)	
	Synonyms		GenebankID or UniProtKB
0495/20; 0926/11; 1053/14; 1119/09; 1304/03; 1423/11; 1440/11; 1485/04; anon-WO0118547.269; C1; CG3619; CT12133; D; delta; delta D1; dl; DL; dmDelta; Dmel\CG3619; E(l)s2; EC3-5; l(3)05151; l(3)92Ab; l(3)j8C3		AY437234 (https://www.ncbi.nlm.nih.gov/nuccore/AY437234)	
	String		
7227.FBpp0083153 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0083153)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0005102 : signaling receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005102)			

GO:0005509 : calcium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005509>)

GO:0005112 : Notch binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005112>)

GO - Biological Process

GO:0007155 : cell adhesion (<https://www.ebi.ac.uk/QuickGO/term/GO:0007155>)

GO:0007419 : ventral cord development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007419>)

GO:0008407 : chaeta morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008407>)

GO:0007399 : nervous system development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>)

GO:0007422 : peripheral nervous system development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007422>)

GO:0007423 : sensory organ development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007423>)

GO:0008284 : positive regulation of cell proliferation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008284>)

GO:0007219 : Notch signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007219>)

GO:0007015 : actin filament organization

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007015>)

GO:0048800 : antennal morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048800>)

GO:0007475 : apposition of dorsal and ventral imaginal disc-derived wing surfaces

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007475>)

GO:0008356 : asymmetric cell division

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008356>)

GO:0007298 : border follicle cell migration

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007298>)

GO:0001708 : cell fate specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0001708>)

GO:0042676 : compound eye cone cell fate commitment

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042676>)

GO:0048749 : compound eye development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048749>)

GO:0046667 : compound eye retinal cell programmed cell death

(<https://www.ebi.ac.uk/QuickGO/term/GO:0046667>)

GO:0007451 : dorsal/ventral lineage restriction, imaginal disc

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007451>)

GO:0007398 : ectoderm development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007398>)

GO:0042067 : establishment of ommatidial planar polarity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042067>)

GO:0001736 : establishment of planar polarity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0001736>)

GO:0030718 : germ-line stem cell population maintenance

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030718>)

GO:0008347 : glial cell migration (<https://www.ebi.ac.uk/QuickGO/term/GO:0008347>)

GO:0007480 : imaginal disc-derived leg morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007480>)

GO:0036011 : imaginal disc-derived leg segmentation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0036011>)

GO:0007476 : imaginal disc-derived wing morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007476>)

GO:0008586 : imaginal disc-derived wing vein morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008586>)

GO:0007474 : imaginal disc-derived wing vein specification

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007474>)

GO:0046331 : lateral inhibition (<https://www.ebi.ac.uk/QuickGO/term/GO:0046331>)

GO:0007498 : mesoderm development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007498>)

GO:0050768 : negative regulation of neurogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0050768>)

GO:0007314 : oocyte anterior/posterior axis specification

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007314>)

GO:0030720 : oocyte localization involved in germarium-derived egg chamber formation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030720>)

GO:0048477 : oogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0048477>)

GO:0030707 : ovarian follicle cell development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030707>)

GO:0030713 : ovarian follicle cell stalk formation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030713>)

GO:0045931 : positive regulation of mitotic cell cycle

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045931>)

GO:0007464 : R3/R4 cell fate commitment

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007464>)

GO:0045465 : R8 cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0045465>)

GO:0007460 : R8 cell fate commitment

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007460>)

GO:0045468 : regulation of R8 cell spacing in compound eye

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045468>)
GO:0016330 : second mitotic wave involved in compound eye morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016330>)
GO:0048863 : stem cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048863>)
GO:0048190 : wing disc dorsal/ventral pattern formation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048190>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005768 : endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005768>)
GO:0031410 : cytoplasmic vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0031410>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
GO:0005912 : adherens junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0005912>)
GO:0030139 : endocytic vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0030139>)
GO:0035003 : subapical complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0035003>)

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

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

Molecular Details of the Mutation

unknown; associated site in intron 2

Experimental Evidence

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

Main Reference

Two sites in the Delta gene region contribute to naturally occurring variation in bristle number in Drosophila melanogaster. (1998) (<https://pubmed.ncbi.nlm.nih.gov/9611209>)

Authors

Long AD; Lyman RF; Langley CH; Mackay TF

Abstract

A restriction enzyme survey of a 57-kb region including the gene Delta uncovered 53 polymorphic molecular markers in a sample of 55 naturally occurring chromosomes. A permutation test, which assesses the significance of the molecular marker with the largest effect on bristle variation in four genetic backgrounds relative to permuted data-sets, found two sites that were independently associated with variation in bristle number. A common site in the second intron of Delta affected only sternopleural bristle number, and another common site in the fifth intron affected only abdominal bristle number in females. Under an additive genetic model, the polymorphism in the second intron may account for 12% of the total genetic variation in sternopleural bristle number due to third chromosomes, and the site in the fifth intron may account for 6% of the total variation in female abdominal bristle number due to the third chromosomes. These results suggest the following: (1) models that incorporate balancing selection are more consistent with observations than deleterious mutation-selection equilibrium models, (2) mapped quantitative trait loci of large effect may not represent a single variable site at a genetic locus, and (3) linkage disequilibrium can be used as a tool for understanding the molecular basis of quantitative variation.

Additional References

No evidence for an association between common nonsynonymous polymorphisms in delta and bristle number variation in natural and laboratory populations of Drosophila melanogaster. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15020426>)

RELATED GEPHE

Related Genes

7 (achaete-scute complex, Dopa-decarboxylase, hairy (h), poils au dos (pad), scabrous, smooth, Catecholamines up) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~7227~/and+Trait=Bristle number/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

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

EXTERNAL LINKS

COMMENTS