

GEPHE SUMMARY

Gephebase Gene		GepheID
hairy (h) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~hairy(h)^#gephebase-summary-title)	GP00000436	
Entry Status		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	
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	
h		P14003 (http://www.uniprot.org/uniprot/P14003)	
Synonyms		GenebankID or UniProtKB	
8247; bHLHb39; bHLHc14; brr; CG6494; dDr1; Dmel\CG6494; H; Hair; hry; HRY; l(3)08247; l(3)rM384		AY055840 (https://www.ncbi.nlm.nih.gov/nuccore/AY055840)	
String			
7227.FBpp0099504 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0099504)			
Sequence Similarities			
-			
GO - Molecular Function			
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)			
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000977>)
GO:0043565 : sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)
GO:0008134 : transcription factor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008134>)
GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)
GO:0070888 : E-box binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0070888>)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001078>)
GO:1990837 : sequence-specific double-stranded DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990837>)
GO:0003714 : transcription corepressor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003714>)

GO - Biological Process

GO:0007399 : nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>)
GO:0050767 : regulation of neurogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050767>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0007219 : Notch signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007219>)
GO:0001756 : somitogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0001756>)
GO:0007460 : R8 cell fate commitment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007460>)
GO:0007431 : salivary gland development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007431>)
GO:0001666 : response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0001666>)
GO:0000902 : cell morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0000902>)
GO:0061024 : membrane organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061024>)
GO:0007424 : open tracheal system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007424>)
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:0031323 : regulation of cellular metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031323>)
GO:0007435 : salivary gland morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007435>)
GO:0035290 : trunk segmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0035290>)
GO:0035239 : tube morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0035239>)

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](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Unknown+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

Molecular Details of the Mutation

unknown; complex promoter indel variation shows high-association

Experimental Evidence

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

Main Reference

hairy: A quantitative trait locus for drosophila sensory bristle number. (2002) (<https://pubmed.ncbi.nlm.nih.gov/12242230>)

Authors

Robin C; Lyman RF; Long AD; Langley CH; Mackay TF

Abstract

Advances in medicine, agriculture, and an understanding of evolution depend on resolving the genetic architecture of quantitative traits, which is challenging since variation for complex traits is caused by multiple interacting quantitative trait loci (QTL) with small and conditional effects. Here, we show that the key developmental gene, hairy (h), is a QTL for *Drosophila* sternopleural bristle number, a model quantitative trait. Near-isoallelic lines (NIL) for the h gene region exhibited significant variation in bristle number and failed to complement a hairy mutation. Sequencing 10 h alleles from a single population revealed 330 polymorphic sites in approximately 10 kb. Genotypes for 25 of these and 14 additional sites in the flanking regions were determined for the 57 NIL and associated with variation in bristle number in four genetic backgrounds. A highly significant association was found for a complicated insertion/deletion polymorphism upstream of the transcription start site. This polymorphism, present in 17.5% of the h alleles, was associated with an increase of 0.5 bristle and accounted for 31% of the genetic variance in bristle number in the NIL.

Additional References

7 (achaete-scute complex, Delta, Dopa-decarboxylase, poils au dos (pad), scabrous, smooth, Catecholamines up) ([https://www.gephebase.org/search-criteria?/or+TaxonID=^7227^/and+Trait=Bristle number/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+TaxonID=^7227^/and+Trait=Bristle+number/and+groupHaplotypes=true#gephebase-summary-title))

No matches found.

EXTERNAL LINKS

COMMENTS