

GEPHE SUMMARY

	Gephebase Gene	GepheID
achaete-scute complex (<a +achaete-scute+complex+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+achaete-scute+complex+"#gephebase-summary-title)	GP00000047	
	Entry Status	Martin
Published		Main curator

PHENOTYPIC CHANGE

	Trait Category		
Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)		Trait	
Bristle number (abdomen) (<a +bristle+number+(abdomen)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Bristle+number+(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 (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)		Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
sc		P10084 (http://www.uniprot.org/uniprot/P10084)
	Synonyms	GenebankID or UniProtKB
AS-C T4; AS-C T4sc; ascT4; bHLHc28; CG3827; Dmel\CG3827; DROACS2; EG:198A6.1; Hw; l(1)1Ba; Sc; sc/T4; scalpha; scute/sisterlessB; SC_DA; sis b; sis-b; sisb; sisB; T4; T4 AS-C		AAF45499.1 (https://www.ncbi.nlm.nih.gov/nuccore/AAF45499.1)
	String	
7227.FBpp0070072 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0070072)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)		
GO:0003700 : DNA-binding transcription factor activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)
GO:0046982 : protein heterodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046982>)
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 - Biological Process

GO:0007419 : ventral cord development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007419>)
GO:0007417 : central nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007417>)
GO:0022416 : chaeta development (<https://www.ebi.ac.uk/QuickGO/term/GO:0022416>)
GO:0008407 : chaeta morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008407>)
GO:0035883 : enteroendocrine cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035883>)
GO:0061382 : Malpighian tubule tip cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061382>)
GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0007399 : nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>)
GO:0007400 : neuroblast fate determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007400>)
GO:0030182 : neuron differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030182>)
GO:0007422 : peripheral nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007422>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0007346 : regulation of mitotic cell cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007346>)
GO:0050767 : regulation of neurogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050767>)
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:0007423 : sensory organ development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007423>)
GO:0007530 : sex determination (<https://www.ebi.ac.uk/QuickGO/term/GO:0007530>)
GO:0007540 : sex determination, establishment of X:A ratio
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007540>)

GO - Cellular Component

GO:0090575 : RNA polymerase II transcription factor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090575>)
GO:0005667 : transcription factor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005667>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
Indel (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Indel~#gephebase-summary-title)	Aberration Type
1-10 kb	Indel Size
indel MC21 in promoter region of scute	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence
Both naturally occurring insertions of transposable elements and intermediate frequency polymorphisms at the achaete-scute complex are associated with variation in bristle number in <i>Drosophila melanogaster</i> . (2000) (https://pubmed.ncbi.nlm.nih.gov/10757767)	Main Reference
Long AD; Lyman RF; Morgan AH; Langley CH; Mackay TF	Authors
A restriction enzyme survey of a 110-kb region including the achaete scute complex (ASC) examined 14 polymorphic molecular markers in a sample of 56 naturally occurring chromosomes. Large insertions as a class were associated with a reduction in both sternopleural and abdominal bristle number, supporting deleterious mutation-selection equilibrium models for the maintenance of quantitative genetic variation. Two polymorphic sites were independently associated with variation in bristle number measured in two genetic backgrounds as assessed by a permutation test. A 6-bp deletion near sc alpha is associated with sternopleural bristle number variation in both sexes and a 3.4-kb insertion between sc beta and sc gamma is associated with abdominal bristle number variation in females. Under an additive genetic model, the small deletion polymorphism near sc alpha accounts for 25% of the total X chromosome genetic variation in sternopleural bristle number, and the 3.4 kb insertion accounts for 22% of the total X chromosome variation in female abdominal bristle number. The observation of common polymorphisms associated with variation in bristle number is more parsimoniously explained by models that incorporate balancing selection or assume variants affecting bristle number are neutral, than mutation-selection equilibrium models.	Abstract

RELATED GEPHE

Related Genes

7 (Delta, 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

3 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^achaete-scute complex^/and+Taxon ID=^7227^/or+Gene Gephebase=^achaete-scute complex^/and+Taxon ID=^7227^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

Cluster of paralogous transcription factors