

Published	Entry Status	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)	GP00000046
			Main curator

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)		Trait Category	
Bristle number (abdomen; female-limited) (https://www.gephebase.org/search-criteria?/and+Trait=~Bristle number (abdomen; female-limited)~#gephebase-summary-title)		Trait	
Drosophila melanogaster		Trait State in Taxon A	
Drosophila melanogaster		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila melanogaster~#gephebase-summary-title)	Latin Name	Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila melanogaster~#gephebase-summary-title)	Latin Name
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; Ephydroidea; 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; Ephydroidea; 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 Intraspecies?	No	is Taxon B an Intraspecies?

sc	Generic Gene Name	UniProtKB Drosophila melanogaster
	Synonyms	GenebankID or UniProtKB
AS-C T4; AS-C T4 ^{sc} ; 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		P10084 (http://www.uniprot.org/uniprot/P10084) AAF45499.1 (https://www.ncbi.nlm.nih.gov/nuccore/AAF45499.1)
7227.FBpp0070072 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0070072)	String	
-	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>)

	Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
	Aberration Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title)	
	Insertion Size
1-10 kb	
	Molecular Details of the Mutation
transposon insertion in non-coding region	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	
	Main Reference
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)	
	Authors
Long AD; Lyman RF; Morgan AH; Langley CH; Mackay TF	
	Abstract

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.

Additional References

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