

GEPHE SUMMARY

	Gephebase Gene	GephelD
achaete-scute complex (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^achaete-scute complex^#gephebase-summary-title)	GP00000048	Main curator
Published	Entry Status	Martin

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)	Latin Name	Latin Name
fruit fly	Common Name	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melanogaster	Synonyms	Synonyms
species	Rank	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	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
sc	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	P10084 (http://www.uniprot.org/uniprot/P10084)	
7227.FBpp0070072 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0070072)	String	AAF45499.1 (https://www.ncbi.nlm.nih.gov/nuccore/AAF45499.1)
-	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		

[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
 GO:0046982 : protein heterodimerization activity
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0046982>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0046982)
 GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0000977>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
 GO:0043565 : sequence-specific DNA binding
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
 GO:0008134 : transcription factor binding
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0008134>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0008134)

GO - Biological Process

GO:0007419 : ventral cord development
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007419>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0007419)
 GO:0007417 : central nervous system development
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007417>\)](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
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0008407>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0008407)
 GO:0035883 : enteroendocrine cell differentiation
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0035883>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0035883)
 GO:0061382 : Malpighian tubule tip cell differentiation
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0061382>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0061382)
 GO:0043066 : negative regulation of apoptotic process
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
 GO:0007399 : nervous system development
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0007399)
 GO:0007400 : neuroblast fate determination
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007400>\)](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
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007422>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0007422)
 GO:0045944 : positive regulation of transcription by RNA polymerase II
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
 GO:0007346 : regulation of mitotic cell cycle
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007346>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0007346)
 GO:0050767 : regulation of neurogenesis
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0050767>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0050767)
 GO:0006357 : regulation of transcription by RNA polymerase II
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0006357>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
 GO:0006355 : regulation of transcription, DNA-templated
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
 GO:0007423 : sensory organ development
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007423>\)](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
[\(<https://www.ebi.ac.uk/QuickGO/term/GO:0007540>\)](https://www.ebi.ac.uk/QuickGO/term/GO:0007540)

GO - Cellular Component

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

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Cis-regulatory%22#gephebase-summary-title>)

Aberration Type

Indel (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22Indel%22#gephebase-summary-title>)

Indel Size

1-9 bp

Molecular Details of the Mutation

indel MC22 in promoter region of scute

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Linkage+Mapping%22#gephebase-summary-title>)

Main Reference

How repeatable are associations between polymorphisms in achaete-scute and bristle number variation in *Drosophila?*. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17277365>)

Authors

Gruber JD; Genissel A; Macdonald SJ; Long AD

Abstract

Currently, the relevance of common genetic variants--particularly those significantly associated with phenotypic variation in laboratory studies--to standing phenotypic variation in the wild is poorly understood. To address this, we quantified the relationship between achaete-scute complex (ASC) polymorphisms and *Drosophila* bristle number phenotypes in several new population samples. MC22 is a biallelic, nonrepetitive-length polymorphism 97 bp downstream of the scute transcript. It has been previously shown to be associated with sternopleural bristle number variation in both sexes in a set of isogenic lines. We replicated this association in a large cohort of wild-caught *Drosophila melanogaster*. We also detected a significant association at MC22 in an outbred population maintained under laboratory conditions for approximately 25 years, but the phenotypic effects in this sample were opposite from the direction estimated in the initial study. Finally, no significant associations were detected in a second large wild-caught cohort or in a set of 134 nearly isogenic lines. Our ability to repeat the initial association in wild samples suggests that it was not spurious. Nevertheless, inconsistent results from the other three panels suggest that the relationship between polymorphic genetic markers and loci contributing to continuous variation is not a simple one.

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%20&Trait=Bristle number%20and%20groupHaplotypes=true#gephebase-summary-title)
Related Haplotypes
3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%7227%20&Trait=Achaete-Scute Complex%20and%20Taxon ID=%7227%20#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Cluster of paralogous transcription factors