

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)	GP00000048		
	Entry Status	Martin	Main curator
Published			

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 (thorax) (<a +bristle+number+(thorax)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<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
1-9 bp	Indel Size
indel MC22 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
How repeatable are associations between polymorphisms in achaete-scute and bristle number variation in Drosophila?. (2007) (https://pubmed.ncbi.nlm.nih.gov/17277365)	Main Reference
Gruber JD; Genissel A; Macdonald SJ; Long AD	Authors

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~/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