

GEPHE SUMMARY

scabrous (https://www.gephebase.org/search-criteria/?and+Gene Gephebase="scabrous">#gephebase-summary-title)	Gephebase Gene	GP00001025	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

	Trait Category	Trait	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category="Morphology">#gephebase-summary-title)			
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	Latin Name	Taxon B	Latin Name
Drosophila melanogaster (#gephebase-summary-title)		Drosophila melanogaster (#gephebase-summary-title)	
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melanogaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melanogaster	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; Ephydriodea; 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; Ephydriodea; 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 Infraspecies?		is Taxon B an Infraspecies?

GENOTYPIC CHANGE

sca	Generic Gene Name	UniProtKB Drosophila melanogaster
AAA28880; AAA58455; anon-EST:Liang-38; CG17579; clone 38; Dmel\CG17579; FBpp0086968; FBpp0086969; mAb sca1; Sca; Sca1b	Synonyms	P21520 (http://www.uniprot.org/uniprot/P21520)
7227.FBpp0086969 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0086969)	String	GenebankID or UniProtKB
-	Sequence Similarities	AE013599 (https://www.ncbi.nlm.nih.gov/nuccore/AE013599)
-	GO - Molecular Function	
GO:0008407 : chaeta morphogenesis	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008407>)
GO:0007399 : nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>)
GO:0007219 : Notch signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007219>)
GO:0048749 : compound eye development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048749>)
GO:0046331 : lateral inhibition (<https://www.ebi.ac.uk/QuickGO/term/GO:0046331>)
GO:0007460 : R8 cell fate commitment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007460>)
GO:0045468 : regulation of R8 cell spacing in compound eye
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045468>)
GO:0008587 : imaginal disc-derived wing margin morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008587>)
GO:0016318 : ommatidial rotation (<https://www.ebi.ac.uk/QuickGO/term/GO:0016318>)
GO:0016321 : female meiosis chromosome segregation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016321>)
GO:0097305 : response to alcohol (<https://www.ebi.ac.uk/QuickGO/term/GO:0097305>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0005770 : late endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005770>)

Presumptive Null

Unknown ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=%27Unknown%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%27Unknown%27#gephebase-summary-title))

Molecular Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Unknown%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Unknown%27#gephebase-summary-title))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Unknown%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27Unknown%27#gephebase-summary-title))

Molecular Details of the Mutation

unknown; but different sites than for abdomen association

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Linkage%20Mapping%27#gephebase-summary-title))

Main Reference

Naturally occurring variation in bristle number and DNA polymorphisms at the scabrous locus of *Drosophila melanogaster*. (1994) (<https://pubmed.ncbi.nlm.nih.gov/7992053>)

Authors

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

Abstract

The association between quantitative genetic variation in bristle number and molecular variation at a candidate neurogenic locus, scabrous, was examined in *Drosophila melanogaster*. Approximately 32 percent of the genetic variation in abdominal bristle number (21 percent for sternopleural bristle number) among 47 second chromosomes from a natural population was correlated with DNA sequence polymorphisms at this locus. Several polymorphic sites associated with large phenotypic effects occurred at intermediate frequency. Quantitative genetic variation in natural populations caused by alleles that have large effects at a few loci and that segregate at intermediate frequencies conflicts with the classical infinitesimal model of the genetic basis of quantitative variation.

Additional References

RELATED GEPHE

Related Genes

7 (achaete-scute complex, Delta, Dopa-decarboxylase, hairy (h), poils au dos (pad), smooth, Catecholamines up) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%277227%27/and+Trait=Bristle number/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+TaxonID=%277227%27/and+Trait=Bristle%20number/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%27scabrous%27/and+Taxon ID=%277227%27/or+Gene Gephebase=%27scabrous%27/and+Taxon ID=%277227%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene%20Gephebase=%27scabrous%27/and+Taxon%20ID=%277227%27/or+Gene%20Gephebase=%27scabrous%27/and+Taxon%20ID=%277227%27#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS