

## GEPHE SUMMARY

**Gephebase Gene**  
achaete-scute complex

**Entry Status**  
Published

**GepheID**  
GP00000049

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

**Trait**  
Bristle number (thorax)

**Trait State in Taxon A**  
Drosophila melanogaster

**Trait State in Taxon B**  
Drosophila quadrilineata

**Ancestral State**  
Data not curated

**Taxonomic Status**  
Interspecific

### Taxon A

**Latin Name**  
*Drosophila melanogaster*

**Common Name**  
fruit fly

**Synonyms**  
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

**Rank**  
species

**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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

**Parent**  
melanogaster subgroup () - (Rank: species subgroup)

**NCBI Taxonomy ID**  
7227

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Drosophila quadrilineata*

**Common Name**  
-

**Synonyms**  
Drosophila quadrilineata de Meijere, 1911

**Rank**  
species

**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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila; immigrans group; quadrilineata subgroup

**Parent**  
quadrilineata subgroup () - (Rank: species subgroup)

**NCBI Taxonomy ID**  
387621

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
sc

**Synonyms**  
AS-C T4; AS-C T4sc; ascT4; bHLHc28; CG3827; Dmel\CG3827; DROACS2; EG:198A6.1; Hw; I(1)1Ba; Sc; sc/T4; scalpha; scute/sisterlessB; SC\_LDA; sis b; sis-b; sisB; T4; T4 AS-C

**String**  
7227.FBpp0070072

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific  
GO:0003700 : DNA-binding transcription factor activity  
GO:0046982 : protein heterodimerization activity  
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding  
GO:0043565 : sequence-specific DNA binding  
GO:0008134 : transcription factor binding

**UniProtKB Drosophila melanogaster**  
P10084

**GenebankID or UniProtKB**  
AAF45499.1

#### GO - Biological Process

GO:0007419 : ventral cord development  
GO:0007417 : central nervous system development  
GO:0022416 : chaeta development  
GO:0008407 : chaeta morphogenesis  
GO:0035883 : enteroendocrine cell differentiation  
GO:0061382 : Malpighian tubule tip cell differentiation  
GO:0043066 : negative regulation of apoptotic process  
GO:0007399 : nervous system development  
GO:0007400 : neuroblast fate determination  
GO:0030182 : neuron differentiation  
GO:0007422 : peripheral nervous system development  
GO:0045944 : positive regulation of transcription by RNA polymerase II  
GO:0007346 : regulation of mitotic cell cycle  
GO:0050767 : regulation of neurogenesis  
GO:0006357 : regulation of transcription by RNA polymerase II  
GO:0006355 : regulation of transcription, DNA-templated  
GO:0007423 : sensory organ development  
GO:0007530 : sex determination  
GO:0007540 : sex determination, establishment of X:A ratio

#### GO - Cellular Component

GO:0090575 : RNA polymerase II transcription factor complex  
GO:0005667 : transcription factor complex

#### Presumptive Null

No

#### Molecular Type

Cis-regulatory

#### Aberration Type

Unknown

#### Molecular Details of the Mutation

Not identified

#### Experimental Evidence

Candidate Gene

#### Main Reference

Two or four bristles: functional evolution of an enhancer of scute in *Drosophilidae*. (2006)

#### Authors

Marcellini S; Simpson P

#### Abstract

Changes in cis-regulatory sequences are proposed to underlie much of morphological evolution. Yet, little is known about how such modifications translate into phenotypic differences. To address this problem, we focus on the dorsocentral bristles of *Drosophilidae*. In *Drosophila melanogaster*, development of these bristles depends on a cis-regulatory element, the dorsocentral enhancer, to activate scute in a cluster of cells from which two bristles on the posterior scutum arise. A few species however, such as *D. quadrilineata*, bear anterior dorsocentral bristles as well as posterior ones, a derived feature. This correlates with an anterior expansion of the scute expression domain. Here, we show that the *D. quadrilineata* enhancer has evolved, and is now active in more anterior regions. When used to rescue scute expression in transgenic *D. melanogaster*, the *D. quadrilineata* enhancer is able to induce anterior bristles. Importantly, these properties are not displayed by homologous enhancers from control species bearing only two posterior bristles. We also provide evidence that upstream regulation of the enhancer, by the GATA transcription factor Pannier, has been evolutionarily conserved. This work illustrates how, in the context of a conserved trans-regulatory landscape, evolutionary tinkering of pre-existing enhancers can modify gene expression patterns and contribute to morphological diversification.

#### Additional References

## RELATED GEPHE

#### Related Genes

7 (Delta, Dopa-decarboxylase, hairy (h), poils au dos (pad), scabrous, smooth, Catecholamines up)

#### Related Haplotypes

3

## COMMENTS

Cluster of paralogous transcription factors