GEPHE SUMMARY

Gephebase Gene
achaete-scute complex (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^achaete-scute complex^#gephebase-summary-title)

GepheID
GP00000049

Entry Status
Published

Main curator
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 quadrilineata

Ancestral State
Data not curated

Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Drosophila quadrilineata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila quadrilineata^#gephebase-summary-title)

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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila; immigrans group; quadrilineata subgroup

Parent
quadrilineata subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 157052)

NCBI Taxonomy ID
387621 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 387621)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
sc

Synonyms
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

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

UniProtKB Drosophila melanogaster
P10084 (http://www.uniprot.org/uniprot/P10084)

GenebankID or UniProtKB
AAF45499.1 (https://www.ncbi.nlm.nih.gov/nuccore/AAF45499.1)

(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)

Molecular Type

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

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

Not identified

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Two or four bristles: functional evolution of an enhancer of scute in Drosophilidae. (2006) (https://pubmed.ncbi.nlm.nih.gov/17105353)

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 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/or+Taxon ID=^387621^/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=^387621^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Cluster of paralogous transcription factors