

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)	Gephebase Gene	GP00001680	GepheID
Published	Entry Status	Courtier	Main curator

	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	
	Trait
Bristle number (genitalia; leg sex comb) (https://www.gephebase.org/search-criteria?/and+Trait=^Bristle number (genitalia; leg sex comb)^#gephebase-summary-title)	
	Trait State in Taxon A
Two hypandrial bristles	
	Trait State in Taxon B
No hypandrial bristles ; Additional sex comb teeth	
	Ancestral State
Taxon A	
	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Interspecific^#gephebase-summary-title)	

GENOTYPIC CHANGE	
sc	Generic Gene Name UniProtKB Drosophila melanogaster P10084 (http://www.uniprot.org/uniprot/P10084) GenebankID or UniProtKB
AS-C T4; AS-C T4 ^{sc} ; ascT4; bHLHc28; CG3827; Dmel\CG3827; DROACS2; EG:198A6.1; Hw; l(1)tBa; Sc; sc/T4; scalpha; scute/sisterlessB; SC_DA; sis b; sis-b; sisb; sisB; T4; T4 AS-C	Synonyms AAF45499.1 (https://www.ncbi.nlm.nih.gov/nuccore/AAF45499.1)
7227.FBpp0070072 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0070072)	String
-	Sequence Similarities
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)	GO - Molecular Function
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>)

Mutation #1

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

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

Molecular Details of the Mutation

T1775 G - decreases scute expression in the developing genitalia and thus reduces the number of hypandrial bristles. Also increases scute expression in the developing leg and thus increases the number of sex comb teeth. The mutation alters a binding site for Abd-B.

Experimental Evidence

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

Main Reference

Correlated Evolution of Two Copulatory Organs via a Single cis-Regulatory Nucleotide Change. (2018) (<https://pubmed.ncbi.nlm.nih.gov/30344115>)

Authors

Nagy O; Nuez I; Savisaar R; Peluffo AE; Yassin A; Lang M; Stern DL; Matute DR; David JR; Courtier-Orgogozo V

Abstract

Diverse traits often covary between species [1-3]. The possibility that a single mutation could contribute to the evolution of several characters between species [3] is rarely investigated as relatively few cases are dissected at the nucleotide level. Drosophila santomea has evolved additional sex comb sensory teeth on its legs and has lost two sensory bristles on its genitalia. We present evidence that a single nucleotide substitution in an enhancer of the scute gene contributes to both changes. The mutation alters a binding site for the Hox protein Abdominal-B in the developing genitalia, leading to bristle loss, and for another factor in the developing leg, leading to bristle gain. Our study suggests that morphological evolution between species can occur through a single nucleotide change affecting several sexually dimorphic traits. VIDEO ABSTRACT.

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Additional References

Mutation #2

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

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

Molecular Details of the Mutation

T1429G - decreases scute expression in the developing genitalia and thus reduces the number of hypandrial bristles. No effect on sex comb tooth number.

Experimental Evidence

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

Main Reference

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Authors

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Additional References

Mutation #3

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

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

Molecular Details of the Mutation

A1407G - decreases scute expression in the developing genitalia and thus reduces the number of hypandrial bristles. No effect on sex comb tooth number.

Experimental Evidence

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

Main Reference

Correlated Evolution of Two Copulatory Organs via a Single cis-Regulatory Nucleotide Change. (2018) (<https://pubmed.ncbi.nlm.nih.gov/30344115>)

Authors

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait - Several genes contribute to the trait change and several cis-regulatory mutations within scute contribute to the reduction in scute expression

