

GEPHE SUMMARY

	Gephebase Gene	GephelD
Doublesex (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Doublesex^#gephebase-summary-title)	GP00000235	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=Morphology^#gephebase-summary-title)		Trait
Bristle number (male sex comb tooth number) (https://www.gephebase.org/search-criteria?/and+Trait=^Bristle+number+(male+sex+comb+tooth+number)^#gephebase-summary-title)		Trait State in Taxon A
Other Drosophila spp.		Trait State in Taxon B
Drosophila melanogaster/obscura group - Sex combs		Ancestral State
Data not curated		Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)		

Taxon A		Taxon B	
	Latin Name		Latin Name
Sophophora (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Sophophora^#gephebase-summary-title)		obscura group (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^obscura+group^#gephebase-summary-title)	
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
-	Rank	-	Rank
subgenus	Lineage	species group	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		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	
Drosophila (fruit flies) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7215)	Parent	Sophophora () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32341)	Parent
32341 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32341)	NCBI Taxonomy ID	32355 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32355)	NCBI Taxonomy ID
-	is Taxon A an Infraspecies?	-	is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

dsx	Generic Gene Name	UniProtKB Drosophila melanogaster
CG11094; Dmdsx; Dmel\CG11094; Dsx; DSX; dsxF; dsxM; Hr; ix-62c	Synonyms	P23023 (http://www.uniprot.org/uniprot/P23023)
7227.FBpp0303107 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303107)	String	GenebankID or UniProtKB
-	Sequence Similarities	AAB99948 (https://www.ncbi.nlm.nih.gov/nuccore/AAB99948)
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)	GO - Molecular Function	
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)		
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		

GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001078>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006357 : regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006357>)
GO:0007530 : sex determination (<https://www.ebi.ac.uk/QuickGO/term/GO:0007530>)
GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0046660 : female sex differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046660>)
GO:0048086 : negative regulation of developmental pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048086>)
GO:0048071 : sex-specific pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048071>)
GO:0035215 : genital disc development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035215>)
GO:0007485 : imaginal disc-derived male genitalia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007485>)
GO:0016199 : axon midline choice point recognition
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016199>)
GO:0007619 : courtship behavior (<https://www.ebi.ac.uk/QuickGO/term/GO:0007619>)
GO:0045497 : female analia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045497>)
GO:0019101 : female somatic sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019101>)
GO:0007486 : imaginal disc-derived female genitalia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007486>)
GO:0045496 : male analia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045496>)
GO:0008049 : male courtship behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008049>)
GO:0045433 : male courtship behavior, veined wing generated song production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045433>)
GO:0046661 : male sex differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046661>)
GO:0045498 : sex comb development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045498>)
GO:0018993 : somatic sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018993>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

No (<https://www.gephbase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephbase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephbase.org/search-criteria?/and+Molecular+Type=%22Cis-regulatory%22#gephbase-summary-title>)

Aberration Type

Complex Change (<https://www.gephbase.org/search-criteria?/and+Aberration+Type=%22Complex+Change%22#gephbase-summary-title>)

Molecular Details of the Mutation

Acquisition of Scr binding sites in enhancer

Experimental Evidence

Candidate Gene (<https://www.gephbase.org/search-criteria?/and+Experimental+Evidence=%22Candidate+Gene%22#gephbase-summary-title>)

Main Reference

Evolution of sex-specific traits through changes in HOX-dependent doublesex expression. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21886483>)

Authors

Tanaka K; Barmina O; Sanders LE; Arbeitman MN; Kopp A

Abstract

Almost every animal lineage is characterized by unique sex-specific traits, implying that such traits are gained and lost frequently in evolution. However, the genetic mechanisms responsible for these changes are not understood. In *Drosophila*, the activity of the sex determination pathway is restricted to sexually dimorphic tissues, suggesting that spatial regulation of this pathway may contribute to the evolution of sex-specific traits. We examine the regulation and function of doublesex (*dsx*), the main transcriptional effector of the sex determination pathway, in the development and evolution of *Drosophila* sex combs. Sex combs are a recent evolutionary innovation and show dramatic diversity in the relatively few *Drosophila* species that have them. We show that *dsx* expression in the presumptive sex comb region is activated by the HOX gene *Sex combs reduced* (*Scr*), and that the male isoform of *dsx* up-regulates *Scr* so that both genes become expressed at high levels in this region in males but not in females. Precise spatial regulation of *dsx* is essential for defining sex comb position and morphology. Comparative analysis of *Scr* and *dsx* expression reveals a tight correlation between sex comb morphology and the expression patterns of both genes. In species that primitively lack sex combs, no *dsx* expression is observed in the homologous region, suggesting that the origin and diversification of this structure were linked to the gain of a new *dsx* expression domain. Two other, distantly related fly lineages that independently evolved novel male-specific structures show evolutionary gains of *dsx* expression in the corresponding tissues, where *dsx* may also be controlled by *Scr*. These findings suggest that changes in the spatial regulation of sex-determining genes are a key mechanism that enables the evolution of new sex-specific traits, contributing to some of the most dramatic examples of phenotypic diversification in nature.

Additional References

Related Genes

9 (achaete-scute complex, Delta, Dopa-decarboxylase, hairy (h), poils au dos (pad), scabrous, smooth, Catecholamines up, tartan) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%2732341%27/and+Trait=Bristle number/or+Taxon ID=%2732355%27/and+Trait=Bristle number/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%2732341%27/and+Trait=Bristle%20number/or+Taxon%20ID=%2732355%27/and+Trait=Bristle%20number/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait Artyom's unpublished data supports the association between Dsx and sex comb tooth number