

GEPHE SUMMARY

	Gephebase Gene		GepheID
Ultrabithorax (Ubx) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Ultrabithorax (Ubx)^#gephebase-summary-title)	GP00001161		
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)			
	Trait		
Trichome pattern (leg) (https://www.gephebase.org/search-criteria?/and+Trait=~Trichome+pattern (leg)^#gephebase-summary-title)			
	Trait State in Taxon A		
Drosophila melanogaster			
	Trait State in Taxon B		
Drosophila simulans			
	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
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila melanogaster^#gephebase-summary-title)		Drosophila simulans (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila simulans^#gephebase-summary-title)	
	Common Name		Common Name
fruit fly		-	
	Synonyms		Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		-	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)		7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240)	
	is Taxon A an Infrasppecies?		is Taxon B an Infrasppecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
Ubx		P83949 (http://www.uniprot.org/uniprot/P83949)	
	Synonyms		GenebankID or UniProtKB
abx; bx; BX-C; bxd; bxd[D]; bxl; Bxl; bx[D]; Cbx; CG10388; Dm Ubx; Dmel\CG10388; DmUbx; DUBx; Hm; l(3)89Eb; pbx; Uab; ubx; UBx; UBX; Ubx1b		EDX12647 (https://www.ncbi.nlm.nih.gov/nuccore/EDX12647)	
	String		
7227.FBpp0082793 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0082793)			
	Sequence Similarities		
Belongs to the Antp homeobox family.			
	GO - Molecular Function		
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)			
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			

GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0000980 : RNA polymerase II distal enhancer sequence-specific DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0000980>)
GO:0003705 : transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003705>)
GO:0019904 : protein domain specific binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019904>)
GO:0000987 : proximal promoter sequence-specific DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0000987>)
GO:0001221 : transcription cofactor binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0001221>)

GO - Biological Process

GO:0006355 : regulation of transcription, DNA-templated (<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0007507 : heart development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007507>)
GO:0009952 : anterior/posterior pattern specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0009952>)
GO:0000122 : negative regulation of transcription by RNA polymerase II (<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
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:0007480 : imaginal disc-derived leg morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0007480>)
GO:0010092 : specification of animal organ identity (<https://www.ebi.ac.uk/QuickGO/term/GO:0010092>)
GO:0007482 : haltere development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007482>)
GO:0001706 : endoderm formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0001706>)
GO:0007424 : open tracheal system development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007424>)
GO:0007525 : somatic muscle development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007525>)
GO:0061327 : anterior Malpighian tubule development (<https://www.ebi.ac.uk/QuickGO/term/GO:0061327>)
GO:0001709 : cell fate determination (<https://www.ebi.ac.uk/QuickGO/term/GO:0001709>)
GO:0035052 : dorsal vessel aortic cell fate commitment (<https://www.ebi.ac.uk/QuickGO/term/GO:0035052>)
GO:0007501 : mesodermal cell fate specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0007501>)
GO:0007494 : midgut development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007494>)
GO:0042694 : muscle cell fate specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0042694>)
GO:0060969 : negative regulation of gene silencing (<https://www.ebi.ac.uk/QuickGO/term/GO:0060969>)
GO:0048636 : positive regulation of muscle organ development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048636>)
GO:0042659 : regulation of cell fate specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0042659>)
GO:0045570 : regulation of imaginal disc growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0045570>)
GO:0007384 : specification of segmental identity, thorax (<https://www.ebi.ac.uk/QuickGO/term/GO:0007384>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0005667 : transcription factor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0005667>)
GO:0017053 : transcriptional repressor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0017053>)
GO:0032993 : protein-DNA complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0032993>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#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
A role of Ultrabithorax in morphological differences between Drosophila species. (1998) (https://pubmed.ncbi.nlm.nih.gov/9853753)	Authors
Stern DL	Abstract

The mechanisms underlying the evolution of morphology are poorly understood. Distantly related taxa sometimes exhibit correlations between morphological differences and patterns of gene expression, but such comparisons cannot establish how mechanisms evolve to generate diverse morphologies. Answers to these questions require resolution of the nature of developmental evolution within and between closely related species. Here I show how the detailed regulation of the Hox gene *Ultrabithorax* patterns trichomes on the posterior femur of the second leg in *Drosophila melanogaster*, and that evolution of *Ultrabithorax* has contributed to divergence of this feature among closely related species. The *cis*-regulatory regions of *Ultrabithorax*, and not the protein itself, appear to have evolved. This study provides experimental evidence that *cis*-regulatory evolution is one way in which conserved proteins have promoted morphological diversity.

Additional References

RELATED GEPHE

Related Genes

1 (mir-92a) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~7227~/and+Trait=Trichome pattern/or+Taxon ID=~7240~/and+Trait=Trichome pattern/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~7227~/and+Trait=Trichome+pattern/or+Taxon+ID=~7240~/and+Trait=Trichome+pattern/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS