

GEPHE SUMMARY

	Gephebase Gene	GephelD
ebony (https://www.gephebase.org/search-criteria/?and+GeneGephebase=%22ebony%22#gephebase-summary-title)	GP00002024	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

	Trait Category
Morphology (https://www.gephebase.org/search-criteria/?and+TraitCategory=%22Morphology%22#gephebase-summary-title)	Trait
Coloration (abdomen; male) (https://www.gephebase.org/search-criteria/?and+Trait=%22Coloration+(abdomen;%20male)%22#gephebase-summary-title)	Trait State in Taxon A
dark posterior male abdomen	Trait State in Taxon B
light posterior male abdomen	Ancestral State
Taxon A	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria/?and+TaxonomicStatus=%22Interspecific%22#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Drosophila yakuba (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%22Drosophila+yakuba%22#gephebase-summary-title)		Drosophila santomea (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%22Drosophila+santomea%22#gephebase-summary-title)	
-	Common Name	-	Common Name
Drosophila yakuba Burla, 1954	Synonyms	-	Synonyms
species	Rank	species	Rank
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; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	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; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent
7245 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7245)	NCBI Taxonomy ID	129105 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=129105)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

e	Generic Gene Name	UniProtKB Drosophila melanogaster
ebony; CG3331	Synonyms	GenebankID or UniProtKB
-	String	0
	Sequence Similarities	
GO:0000036 : acyl carrier activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000036)	GO - Molecular Function	
GO:0003833 : beta-alanyl-dopamine synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003833)		
GO:0031177 : phosphopantetheine binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031177)		
GO:0048085 : adult chitin-containing cuticle pigmentation	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048085>)
GO:0042417 : dopamine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042417>)
GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)
GO:0048082 : regulation of adult chitin-containing cuticle pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048082>)
GO:0048066 : developmental pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048066>)
GO:0043042 : amino acid adenylylation by nonribosomal peptide synthase
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043042>)
GO:0007593 : chitin-based cuticle sclerotization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007593>)
GO:0048067 : cuticle pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048067>)
GO:0001692 : histamine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001692>)
GO:0045475 : locomotor rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0045475>)
GO:0006583 : melanin biosynthetic process from tyrosine
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006583>)
GO:0048022 : negative regulation of melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048022>)
GO:0042440 : pigment metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042440>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

100-999 bp

Molecular Details of the Mutation

insertion of a partial 481 bp fragment related to a transposable element of the helitron class - maybe other causing mutations as well at this ebony locus (including one fixed amino acid change whose phenotypic effect has not been investigated) - increased expression associated with lighter pigmentation

Experimental Evidence

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

Main Reference

Changes throughout a Genetic Network Mask the Contribution of Hox Gene Evolution. (2019) (<https://pubmed.ncbi.nlm.nih.gov/31257142>)

Authors

Liu Y; Ramos-Womack M; Han C; Reilly P; Brackett KL; Rogers W; Williams TM; Andolfatto P; Stern DL; Rebeiz M

Abstract

Hox genes pattern the anterior-posterior axis of animals and are posited to drive animal body plan evolution, yet their precise role in evolution has been difficult to determine. Here, we identified evolutionary modifications in the Hox gene Abd-B that dramatically altered its expression along the body plan of *Drosophila santomea*. Abd-B is required for pigmentation in *Drosophila yakuba*, the sister species of D. \ddot{A} santomea, and changes to Abd-B expression would be predicted to make large contributions to the loss of body pigmentation in D. \ddot{A} santomea. However, manipulating Abd-B expression in current-day D. \ddot{A} santomea does not affect pigmentation. We attribute this epistatic interaction to four other genes within the D. \ddot{A} santomea pigmentation network, three of which have evolved expression patterns that do not respond to Abd-B. Our results demonstrate how body plans may evolve through small evolutionary steps distributed throughout Hox-regulated networks. Polygenicity and epistasis may hinder efforts to identify genes and mechanisms underlying macroevolutionary traits.

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Additional References

RELATED GEPHE

Related Genes

5 (Abdominal-B, pdm3, tan, yellow, bab) (<https://www.gephbase.org/search-criteria/?or+Taxon+ID=^7245^/and+Trait=Coloration/or+Taxon+ID=^129105^/and+Trait=Coloration/and+groupHaplotypes=true#gephbase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait @SeveralMutationsWithEffect @TE

