

GEPHE SUMMARY

ebony (<a +ebony+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+ebony+"#gephebase-summary-title)	Gephebase Gene	GP00000251	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)	Trait Category		
Coloration (posterior abdomen) (<a +coloration+(posterior+abdomen)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Coloration+(posterior+abdomen)+"#gephebase-summary-title)	Trait		
Drosophila jambulina - Dark	Trait State in Taxon A		
Drosophila serrata - Light (Loss of Abdominal Pigmentation)	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)	Taxonomic Status		

Taxon A	Latin Name	Taxon B	Latin Name
Drosophila jambulina (<a +drosophila+jambulina+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+jambulina+"#gephebase-summary-title)	Drosophila serrata (<a +drosophila+serrata+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+serrata+"#gephebase-summary-title)		
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
species	Rank	Drosophila serrata Malloch, 1927	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; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium 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; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium subgroup; Drosophila serrata species complex	Lineage
montium subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32352)	Parent	Drosophila serrata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=446045)	Parent
111875 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=111875)	NCBI Taxonomy ID	7274 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7274)	NCBI Taxonomy ID
No	is Taxon A an Infrasppecies?	No	is Taxon B an Infrasppecies?

GENOTYPIC CHANGE

e	Generic Gene Name	UniProtKB Drosophila melanogaster
ebony; CG3331	Synonyms	O76858 (http://www.uniprot.org/uniprot/O76858)
-	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 adenylation 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 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

loss of the ebony male-specific silencer function - increased expression of ebony

Experimental Evidence

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

Main Reference

Genetic Changes to a Transcriptional Silencer Element Confers Phenotypic Diversity within and between Drosophila Species. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26115430>)

Authors

Johnson WC; Ordway AJ; Watada M; Pruitt JN; Williams TM; Rebeiz M

Abstract

The modification of transcriptional regulation has become increasingly appreciated as a major contributor to morphological evolution. However, the role of negative-acting control elements (e.g. silencers) in generating morphological diversity has been generally overlooked relative to positive-acting "enhancer" elements. The highly variable body coloration patterns among Drosophilid insects represents a powerful model system in which the molecular alterations that underlie phenotypic diversity can be defined. In a survey of pigment phenotypes among geographically disparate Japanese populations of *Drosophila auraria*, we discovered a remarkable degree of variation in male-specific abdominal coloration. In testing the expression patterns of the major pigment-producing enzymes, we found that phenotypes uniquely correlated with differences in the expression of *ebony*, a gene required for yellow-colored cuticle. Assays of *ebony*'s transcriptional control region indicated that a lightly pigmented strain harbored cis-regulatory mutations that caused correlated changes in its expression. Through a series of chimeric reporter constructs between light and dark strain alleles, we localized function-altering mutations to a conserved silencer that mediates a male-specific pattern of *ebony* repression. This suggests that the light allele was derived through the loss of this silencer's activity. Furthermore, examination of the *ebony* gene of *D. serrata*, a close relative of *D. auraria* which secondarily lost male-specific pigmentation revealed the parallel loss of this silencer element. These results demonstrate how loss-of-function mutations in a silencer element resulted in increased gene expression. We propose that the mutational inactivation of silencer elements may represent a favored path to evolve gene expression, impacting morphological traits.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Parallelism

