

## GEPHE SUMMARY

	Gephebase Gene	GephelD
ebony ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase="ebony">#gephebase-summary-title)	GP00000250	Main curator
Published	Entry Status	Courtier

## PHENOTYPIC CHANGE

	Trait Category		
Morphology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category="Morphology">#gephebase-summary-title)	Trait		
Coloration (posterior abdomen) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+(posterior+abdomen)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+(posterior+abdomen)^#gephebase-summary-title</a> )	Trait State in Taxon A		
Drosophila auraria - Japan ; dark	Trait State in Taxon B		
Drosophila auraria - Japan ; light	Ancestral State		
Taxon A	Taxonomic Status		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status="Intraspecific">#gephebase-summary-title)	Drosophila auraria ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title</a> )	Taxon B	
Taxon A	Latin Name		Latin Name
Drosophila auraria ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title</a> )	Drosophila auraria ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+auraria^#gephebase-summary-title</a> )	Taxon B	
-	Common Name		Common Name
-	Synonyms		Synonyms
-	Rank		Rank
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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium 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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium subgroup	Taxon B	
montium subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32352">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32352</a> )	Parent		Parent
47315 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47315">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47315</a> )	NCBI Taxonomy ID		NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
Drosophila auraria - Japan ; dark	Taxon A Description		Taxon B Description
	Drosophila auraria - Japan ; light		

## GENOTYPIC CHANGE

e	Generic Gene Name	UniProtKB Drosophila melanogaster
ebony; CG3331	Synonyms	GenebankID or UniProtKB
-	String	
-	Sequence Similarities	
	GO - Molecular Function	
GO:0000036 : acyl carrier activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000036">https://www.ebi.ac.uk/QuickGO/term/GO:0000036</a> )		
GO:0003833 : beta-alanyl-dopamine synthase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003833">https://www.ebi.ac.uk/QuickGO/term/GO:0003833</a> )		
GO:0031177 : phosphopantetheine binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0031177">https://www.ebi.ac.uk/QuickGO/term/GO:0031177</a> )		

## GO - Biological Process

GO:0048085 : adult chitin-containing cuticle pigmentation  
 (<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.gephebase.org/search-criteria/?and+Presumptive+Null=%27No%27#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%27Cis-regulatory%27#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%27Unknown%27#gephebase-summary-title>)

Molecular Details of the Mutation

Inactivation of a conserved silencer resulting in gain-of-expression; the increase in ebony expression in the light strain occurred primarily through mutations affecting the ebony male-specific silencer element

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%27Candidate+Gene%27#gephebase-summary-title>)

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

## Related Genes

1 (bab) (<https://www.gephebase.org/search-criteria/?or+Taxon+ID=%2747315%27&Trait=Coloration&groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@Parallelism

