

## GEPHE SUMMARY

**Gephebase Gene**  
ebony

**Entry Status**  
Published

**GepheID**  
GP00000250

**Main curator**  
Courtier

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

**Trait**  
Coloration (posterior abdomen)

**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

	Taxon A	Taxon B
<b>Latin Name</b>	<i>Drosophila auraria</i>	<i>Drosophila auraria</i>
<b>Common Name</b>	-	-
<b>Synonyms</b>	-	-
<b>Rank</b>	species	species
<b>Lineage</b>	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; Acalytratae; Ephydroidea; 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; Acalytratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium subgroup
<b>Parent</b>	montium subgroup () - (Rank: species subgroup)	montium subgroup () - (Rank: species subgroup)
<b>NCBI Taxonomy ID</b>	47315	47315
<b>is Taxon A an Intraspecies?</b>	Yes	Yes
<b>Taxon A Description</b>	Drosophila auraria - Japan ; dark	Drosophila auraria - Japan ; light

## GENOTYPIC CHANGE

**Generic Gene Name**  
e

**Synonyms**  
ebony; CG3331

**String**  
-

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0000036 : acyl carrier activity  
GO:0003833 : beta-alanyl-dopamine synthase activity  
GO:0031177 : phosphopantetheine binding

**GO - Biological Process**  
GO:0048085 : adult chitin-containing cuticle pigmentation  
GO:0042417 : dopamine metabolic process  
GO:0007623 : circadian rhythm

**UniProtKB Drosophila melanogaster**  
O76858

**GenebankID or UniProtKB**

GO:0048082 : regulation of adult chitin-containing cuticle pigmentation  
GO:0048066 : developmental pigmentation  
GO:0043042 : amino acid adenylation by nonribosomal peptide synthase  
GO:0007593 : chitin-based cuticle sclerotization  
GO:0048067 : cuticle pigmentation  
GO:0001692 : histamine metabolic process  
GO:0045475 : locomotor rhythm  
GO:0006583 : melanin biosynthetic process from tyrosine  
GO:0048022 : negative regulation of melanin biosynthetic process  
GO:0042440 : pigment metabolic process

GO - Cellular Component  
GO:0005737 : cytoplasm

#### Presumptive Null

No

#### Molecular Type

Cis-regulatory

#### Aberration Type

Unknown

#### 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

##### Main Reference

Genetic Changes to a Transcriptional Silencer Element Confers Phenotypic Diversity within and between *Drosophila* Species. (2015)

##### 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](#))

#### Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@Parallelism