GEPHE SUMMARY

Gephebase Gene
ebony (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ebony^#gephebase-summary-title)

GepheID
GP00000250

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (posterior abdomen) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (posterior abdomen)^#gephebase-summary-title)

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 (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Drosophila auraria (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila auraria^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
species

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

Parent
montium subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32352)

NCBI Taxonomy ID
47315 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47315)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Drosophila auraria - Japan ; dark

Taxon B

Latin Name
Drosophila auraria (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila auraria^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
species

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

Parent
montium subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32352)

NCBI Taxonomy ID
47315 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47315)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Drosophila auraria - Japan ; light

GENOTYPIC CHANGE

Generic Gene Name
e

Synonyms
ebony; CG3331

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0000036 : acyl carrier activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000036)
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)

UniProtKB Drosophila melanogaster
O76858 (http://www.uniprot.org/uniprot/O76858)

GenebankID or UniProtKB
()

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=^No^#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

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=^Candidate Gene^#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=^47315^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism