

GEPHE SUMMARY

Gephebase Gene

yellow

Entry Status

Published

GepheID

GP00001961

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Morphology

Trait

Coloration (body; wing)

Trait State in Taxon A

population of *Drosophila melanogaster* from Uman (Ukraine) - wild-type

Trait State in Taxon B

population of *Drosophila melanogaster* from Uman (Ukraine) - yellow body and yellow wings

Ancestral State

Taxon A

Taxonomic Status

Intraspecific

Taxon A

Latin Name

Drosophila melanogaster

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; *Drosophila melanogaster* Meigen, 1830; *Sophophora melanogaster* (Meigen, 1830); *Drosophila melangaster*

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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; *Drosophila*; *Sophophora*; melanogaster group; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup)

NCBI Taxonomy ID

7227

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Drosophila melanogaster

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; *Drosophila melanogaster* Meigen, 1830; *Sophophora melanogaster* (Meigen, 1830); *Drosophila melangaster*

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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; *Drosophila*; *Sophophora*; melanogaster group; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup)

NCBI Taxonomy ID

7227

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

y

Synonyms

CG3757; Dmel\CG3757; EG:125H10.2; T6; Y

String

7227.FBpp0070070

Sequence Similarities

Belongs to the major royal jelly protein family.

GO - Molecular Function

-

GO - Biological Process

GO:0042438 : melanin biosynthetic process

GO:0048082 : regulation of adult chitin-containing cuticle pigmentation

GO:0048066 : developmental pigmentation

GO:0048067 : cuticle pigmentation

UniProtKB *Drosophila melanogaster*

P09957

GenebankID or UniProtKB

GO:0006583 : melanin biosynthetic process from tyrosine
GO:0048065 : male courtship behavior, veined wing extension
GO:0060179 : male mating behavior

GO - Cellular Component

GO:0005737 : cytoplasm
GO:0005576 : extracellular region
GO:0070451 : cell hair

Presumptive Null

No

Molecular Type

Cis-regulatory

Aberration Type

Inversion

Inversion Size

100-1000 kb

Molecular Details of the Mutation

y[2-717] - Inversion that occurred between two hobo elements: one located 129 bp from the start site of yellow transcription and the other in the distal telomere region. The yellow phenotype is caused by the separation of the body and wing enhancers from the transcription unit.

Experimental Evidence

Candidate Gene

Main Reference

[hobo-induced rearrangements are responsible for mutation bursts at the yellow locus in a natural population of Drosophila melanogaster. \(2000\)](#)

Authors

Zakharenko LP; p6acheva EM; Romanova OA; Zakharov IK; Voloshina MA; Kochieva EZ; Simonova OB; Golubovsky MD; Georgiev P

Abstract

In 1981 recurrent local bursts of mutability of the yellow gene were observed in a natural population of *Drosophila melanogaster* from Uman' (Ukraine). A series of y2-like mutations in the yellow gene were recovered during the period 1982 to 1991. Most of the mutants display the y2-phenotype, i.e. mutant yellow color of wings and body cuticle. Ninety-nine y2 mutants were shown to be generated by an inversion that occurred between two hobo elements, one located 129 bp from the start site of yellow transcription, and the other in the distal telomere region. The y2 phenotype was caused by the separation of the body and wing enhancers from the transcription unit. Many of the y2-like alleles were highly unstable and reverted to y+, which again, gave rise to y2-like mutants. We found that the y2->y+>y2 transitions were generated by repeated inversions between the two hobo elements mentioned. The y2 and y+ alleles lost their instability after deletion of the hobo element present at the tip of the X chromosome.

Additional References

RELATED GEPHE

Related Genes

4 (bab, bab1, ebony, wingless (wg))

Related Haplotypes

1

EXTERNAL LINKS

COMMENTS

@TE hobo element <http://flybase.org/reports/FBal0104919>