GEPHE SUMMARY

Gephebase Gene
mir-92a (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^mir-92a^#gephebase-summary-title)

GepheID
GP00000661

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Drosophila melanogaster

Trait State in Taxon B
Drosophila melanogaster

Ancestral State
Data not curated

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

Taxon A

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

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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?
No

Taxon B

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

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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
-

Synonyms
-

String
-

Sequence Similarities
-

GO - Molecular Function
-

GO - Biological Process
-

GO - Cellular Component
-

UniProtKB
()

GenebankID or UniProtKB
NR_048486.1 (https://www.ncbi.nlm.nih.gov/nuccore/NR_048486.1)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

Not identified

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

Evolution of mir-92a underlies natural morphological variation in Drosophila melanogaster. (2013) (https://pubmed.ncbi.nlm.nih.gov/23453955)

Authors

Arif S; Murat S; Almudi I; Nunes MD; Bortolamiol-Becet D; McGregor NS; Currie JM; Hughes H; Ronshaugen M; Sucena Ã‰; Lai EC; SchlÃ¶tterer C; McGregor AP

Abstract

Identifying the genetic mechanisms underlying phenotypic change is essential to understanding how gene regulatory networks and ultimately the genotype-to-phenotype map evolve. It is recognized that microRNAs (miRNAs) have the potential to facilitate evolutionary change [1-3]; however, there are no known examples of natural morphological variation caused by evolutionary changes in miRNA expression. Therefore, the contribution of miRNAs to evolutionary change remains unknown [1, 4]. Drosophila melanogaster subgroup species display a portion of trichome-free cuticle on the femur of the second leg called the "naked valley." It was previously shown that Ultrabithorax (Ubx) is involved in naked valley variation between D. melanogaster and D. simulans [5, 6]. However, naked valley size also varies among populations of D. melanogaster, ranging from 1,000 up to 30,000 Î¼m(2). We investigated the genetic basis of intraspecific differences in the naked valley in D. melanogaster and found that neither Ubx nor shavenbaby (svb) [7, 8] contributes to this morphological difference. Instead, we show that changes in mir-92a expression underlie the evolution of naked valley size in D. melanogaster through repression of shavenoid (sha) [9]. Therefore, our results reveal a novel mechanism for morphological evolution and suggest that modulation of the expression of miRNAs potentially plays a prominent role in generating organismal diversity.

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Additional References

RELATED GEPHE

Related Genes

1 (Ultrabithorax (Ubx)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Trichome pattern/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS