GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002662

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

Lifespan (https://www.gephebase.org/search-criteria?/and+Trait=^Lifespan^#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

Doa

Synonyms

0844/02; CG1658; CG31049; CG33204; CG33553; CG42320; Dmel\CG42320; doa; DOA; DOA/CLK2; l(3)01705; l(3)S084402; l(3)s2784; Msu

String

7227.FBpp0289029 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0289029)

Sequence Similarities

Belongs to the protein kinase superfamily. CMGC Ser/Thr protein kinase family. Lammer subfamily.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0004674 : protein serine/threonine kinase activity

UniProtKB Drosophila melanogaster

P49762 (http://www.uniprot.org/uniprot/P49762)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0004674)
GO:0004672 : protein kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004672)
GO:0004713 : protein tyrosine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004713)
GO:0016301 : kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016301)
GO:0106310 : protein serine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0106310)
GO:0004712 : protein serine/threonine/tyrosine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004712)

GO - Biological Process

GO:0007399 : nervous system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007399)
GO:0007548 : sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0007548)
GO:0006468 : protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:0048749 : compound eye development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048749)
GO:0018993 : somatic sex determination
(https://www.ebi.ac.uk/QuickGO/term/GO:0018993)
GO:0046777 : protein autophosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0046777)
GO:0007601 : visual perception (https://www.ebi.ac.uk/QuickGO/term/GO:0007601)
GO:0045752 : positive regulation of Toll signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0045752)
GO:0009306 : protein secretion (https://www.ebi.ac.uk/QuickGO/term/GO:0009306)
GO:0010508 : positive regulation of autophagy
(https://www.ebi.ac.uk/QuickGO/term/GO:0010508)
GO:0050896 : response to stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:0050896)
GO:0007350 : blastoderm segmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0007350)
GO:0042051 : compound eye photoreceptor development
(https://www.ebi.ac.uk/QuickGO/term/GO:0042051)
GO:2000255 : negative regulation of male germ cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:2000255)
GO:0002225 : positive regulation of antimicrobial peptide production
(https://www.ebi.ac.uk/QuickGO/term/GO:0002225)
GO:0000381 : regulation of alternative mRNA splicing, via spliceosome
(https://www.ebi.ac.uk/QuickGO/term/GO:0000381)
GO:0043484 : regulation of RNA splicing
(https://www.ebi.ac.uk/QuickGO/term/GO:0043484)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)

Presumptive Null

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

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Natural alleles at the Doa locus underpin evolutionary changes in Drosophila lifespan and fecundity. (2022) (https://pubmed.ncbi.nlm.nih.gov/36350205)

Authors

Hoedjes KM; Kostic H; Keller L; Flatt T

Abstract

'Evolve and resequence' (E&R) studies in Drosophila melanogaster have identified many candidate loci underlying the evolution of ageing and life history, but experiments that validate the effects of such candidates remain rare. In a recent E&R study we have identified several alleles of the LAMMER kinase Darkener of apricot (Doa) as candidates for evolutionary changes in lifespan and fecundity. Here, we use two complementary approaches to confirm a functional role of Doa in life-history evolution. First, we used transgenic RNAi to study the effects of Doa at the whole-gene level. Ubiquitous silencing of expression in adult flies reduced both lifespan and fecundity, indicating pleiotropic effects. Second, to characterize segregating variation at Doa, we examined four candidate single nucleotide polymorphisms (SNPs; Doa-1, -2, -3, -4) using a genetic association approach. Three candidate SNPs had effects that were qualitatively consistent with expectations based on our E&R study: Doa-2 pleiotropically affected both lifespan and late-life fecundity; Doa-1 affected lifespan (but not fecundity); and Doa-4 affected late-life fecundity (but not lifespan). Finally, the last candidate allele (Doa-3) also affected lifespan, but in the opposite direction from predicted.

Additional References

RELATED GEPHE

Related Genes

3 (Catecholamines up, Dopa-decarboxylase, InR) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Lifespan/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Four candidate single nucleotide polymorphisms (SNPs; Doa-1 -2 -3 -4) were tested using a genetic association approach. Three candidate SNPs had effects that were qualitatively consistent with expectations based on our E&R study: Doa-2 pleiotropically affected both lifespan and late-life fecundity; Doa-1 affected lifespan (but not fecundity); and Doa-4 affected late-life fecundity (but not lifespan). The last candidate allele (Doa-3) also affected lifespan but in the opposite direction from predicted.