

GEPHE SUMMARY

Couch potato (https://www.gephebase.org/search-criteria/?and+Gene Gephebase^Couch potato^#gephebase-summary-title)	Gephebase Gene	GP00000191	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category^Physiology^#gephebase-summary-title)	Trait Category
Diapause (https://www.gephebase.org/search-criteria/?and+Trait^Diapause^#gephebase-summary-title)	Trait
Drosophila melanogaster	Trait State in Taxon A
Drosophila melanogaster	Trait State in Taxon B
Data not curated	Ancestral State
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status^Intraspecific^#gephebase-summary-title)	Taxonomic Status

Taxon A	Latin Name	Taxon B	Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms^Drosophila melanogaster^#gephebase-summary-title)		Drosophila melanogaster (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms^Drosophila melanogaster^#gephebase-summary-title)	
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms
species	Rank	species	Rank
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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	NCBI Taxonomy ID	7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

cpo	Generic Gene Name	UniProtKB Drosophila melanogaster
1824; 3603; 5339; 6015; BcDNA:AT31405; CG12349; CG18434; cg18435; CG18435; CG31243; CG42457; CG43738; Cpo; CPO; Dmel\CG43738; E(sda)N; l(3)01432; l(3)6015; l(3)j4A1; l(3)j4D4; l(3)j7E2; l(3)j9B3; l(3)rJ553; l(3)s2336; Line N; ORE-17	Synonyms	Q01617 (http://www.uniprot.org/uniprot/Q01617)
7227.FBpp0303306 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303306)	String	GenebankID or UniProtKB
-	Sequence Similarities	Z14312 (https://www.ncbi.nlm.nih.gov/nuccore/Z14312)
GO:0003729 : mRNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003729)	GO - Molecular Function	
GO:0035614 : snRNA stem-loop binding		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035614>)

GO - Biological Process

GO:0007275 : multicellular organism development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)

GO:0007268 : chemical synaptic transmission

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007268>)

GO:0022611 : dormancy process (<https://www.ebi.ac.uk/QuickGO/term/GO:0022611>)

GO:0000398 : mRNA splicing, via spliceosome

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000398>)

GO:0035206 : regulation of hemocyte proliferation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035206>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Ile462Lys

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ile	Lys	462

Main Reference

An amino acid polymorphism in the couch potato gene forms the basis for climatic adaptation in *Drosophila melanogaster*. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18852464>)

Authors

Schmidt PS; Zhu CT; Das J; Batavia M; Yang L; Eanes WF

Abstract

Diapause is the classic adaptation to seasonality in arthropods, and its expression can result in extreme lifespan extension as well as enhanced resistance to environmental challenges. Little is known about the underlying evolutionary genetic architecture of diapause in any organism. *Drosophila melanogaster* exhibits a reproductive diapause that is variable within and among populations; the incidence of diapause increases with more temperate climates and has significant pleiotropic effects on a number of life history traits. Using quantitative trait mapping, we identified the RNA-binding protein encoding gene couch potato (*cpo*) as a major genetic locus determining diapause phenotype in *D. melanogaster* and independently confirmed this ability to impact diapause expression through genetic complementation mapping. By sequencing this gene in samples from natural populations we demonstrated through linkage association that variation for the diapause phenotype is caused by a single Lys/Ile substitution in one of the six *cpo* transcripts. Complementation analyses confirmed that the identified amino acid variants are functionally distinct with respect to diapause expression, and the polymorphism also shows geographic variation that closely mirrors the known latitudinal cline in diapause incidence. Our results suggest that a naturally occurring amino acid polymorphism results in the variable expression of a diapause syndrome that is associated with the seasonal persistence of this model organism in temperate habitats.

Additional References

RELATED GEPHE

Related Genes

1 (timeless (tim)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Diapause/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Pleiotropy @GxE - <http://flybase.org/reports/FBal0263640>- <http://flybase.org/reports/FBal0263641> - <http://flybase.org/reports/FBal0261205>

