

GEPHE SUMMARY

Gephebase Gene		GepheID
Couch potato (<a +couch+potato+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Couch+potato+"#gephebase-summary-title)	GP00000191	
Entry Status		Main curator
Published		

PHENOTYPIC CHANGE

Trait Category			
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
Trait			
Diapause (<a +diapause+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Diapause+"#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 (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
Taxon A		Taxon B	
Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)		Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)	
Common Name		Common Name	
fruit fly		fruit fly	
Synonyms		Synonyms	
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
Rank		Rank	
species		species	
Lineage		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; Acalypterae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup		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; Acalypterae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	
Parent		Parent	
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)		7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	
is Taxon A an Infrappecies?		is Taxon B an Infrappecies?	
No		No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster	
cpo		Q01617 (http://www.uniprot.org/uniprot/Q01617)	
Synonyms		GenebankID or UniProtKB	
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		Z14312 (https://www.ncbi.nlm.nih.gov/nuccore/Z14312)	
String			
7227.FBpp0303306 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303306)			
Sequence Similarities			
-			
GO - Molecular Function			
GO:0003729 : mRNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003729)			
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

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

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Pleiotropy @GxE - <http://flybase.org/reports/FBa0263640> - <http://flybase.org/reports/FBa0263641> - <http://flybase.org/reports/FBa0261205>

