GEPHE SUMMARY

Gephebase Gene

hsp70Ba (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^hsp70Ba^#gephebase-summary-title)

GepheID

GP00002006

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Drosophila melanogaster - wild-type tolerance

Trait State in Taxon B

Drosophila melanogaster - lower tolerance - Arv/Zim allele

Ancestral State

Taxon A

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?

Yes

Taxon B Description

The Arv/Zim populations were founded from crosses of parents from California and Zimbabwe and were cultured at 18.8C for 5 years before experimentation.

GENOTYPIC CHANGE

Generic Gene Name

Hsp70Ba

Synonyms

CG31449; dhsp70; dHsp70; Dm-hsp70; Dmel\CG31449; Hsp 70; hsp-70; Hsp-70; hsp70; Hsp70; HSP70; hsp70 87C; hsp70 Ba; Hsp70(87C); hsp70b; hsp70B; Hsp70B; hsp70ba; hsp70Ba

String

7227.FBpp0082107 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0082107)

Sequence Similarities

Belongs to the heat shock protein 70 family.

UniProtKB Drosophila melanogaster

Q8INI8 (http://www.uniprot.org/uniprot/Q8INI8)

GenebankID or UniProtKB

()

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0031072 : heat shock protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0031072)
GO:0051082 : unfolded protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0051082)
GO:0016887 : ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016887)
GO:0042623 : ATPase activity, coupled
(https://www.ebi.ac.uk/QuickGO/term/GO:0042623)
GO:0051787 : misfolded protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0051787)
GO:0044183 : protein folding chaperone
(https://www.ebi.ac.uk/QuickGO/term/GO:0044183)

GO - Biological Process

GO:0001666 : response to hypoxia (https://www.ebi.ac.uk/QuickGO/term/GO:0001666)
GO:0034605 : cellular response to heat
(https://www.ebi.ac.uk/QuickGO/term/GO:0034605)
GO:0009408 : response to heat (https://www.ebi.ac.uk/QuickGO/term/GO:0009408)
GO:0034620 : cellular response to unfolded protein
(https://www.ebi.ac.uk/QuickGO/term/GO:0034620)
GO:0051085 : chaperone cofactor-dependent protein refolding
(https://www.ebi.ac.uk/QuickGO/term/GO:0051085)
GO:0035080 : heat shock-mediated polytene chromosome puffing
(https://www.ebi.ac.uk/QuickGO/term/GO:0035080)
GO:0042026 : protein refolding (https://www.ebi.ac.uk/QuickGO/term/GO:0042026)
GO:0006986 : response to unfolded protein
(https://www.ebi.ac.uk/QuickGO/term/GO:0006986)

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)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

A non-autonomous 1383bp P-element is inserted 97bp upstream of the Hsp70Ba transcription start site. The P-element intervenes between the second and third heat shock response elements (HSEs).

Experimental Evidence

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

Main Reference

Modification of heat-shock gene expression in Drosophila melanogaster populations via transposable elements. (2003) (https://pubmed.ncbi.nlm.nih.gov/12519916)

Authors

Lerman DN; Michalak P; Helin AB; Bettencourt BR; Feder ME

Abstract

We report multiple cases in which disruption of hsp70 regulatory regions by transposable element (TE) insertions underlies natural variation in expression of the stress-inducible molecular chaperone Hsp70 in Drosophila melanogaster. Three D. melanogaster populations from different continents are polymorphic for jockey or P element insertions in the promoter of the hsp70Ba gene. All three TE insertions are within the same 87-bp region of hsp70Ba promoter, and we suggest that the distinctive promoter architecture of hsp genes may make them vulnerable to TE insertions. Each of the TE insertions reduces Hsp70 levels, and RNase protection assays demonstrate that such insertions can reduce transcription of the hsp70Ba gene. In addition, the TEs alter two measures of organismal fitness, inducible thermotolerance and female reproductive success. Thus, transposition can create quantitative genetic variation in gene expression within populations, on which natural selection can act.

Additional References

RELATED GEPHE

Related Genes

1 (lncRNA:Hsr omega) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Temperature tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^hsp70Ba^/and+Taxon ID=^7227^/or+Gene Gephebase=^hsp70Ba^/and+Taxon ID=^7227^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@TE - http://flybase.org/reports/FBal0147841.html