GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002004

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

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

T32 population - collected in Chad; Africa in 1977

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.

GO - Molecular Function

UniProtKB Drosophila melanogaster

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

GenebankID or UniProtKB

()

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 1447 bp fragment corresponding to the 39 end of a jockey element is inserted 107 bps upstream of the hsp70Ba transcription start site in the T strain. The insertion intervenes between HSEs 2 and 3; displacing HSEs 3 and 4 as well as three GAGA elements.

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/FBal0147840.html