GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001999

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 - increased 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?

No

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

-

GO - Biological Process

-

GO - Cellular Component

-

UniProtKB

()

GenebankID or UniProtKB

()

Presumptive Null

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

-

Experimental Evidence

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

Main Reference

Both allelic variation and expression of nuclear and cytoplasmic transcripts of Hsr-omega are closely associated with thermal phenotype in Drosophila. (1998) (https://pubmed.ncbi.nlm.nih.gov/9482901)

Authors

McKechnie SW; Halford MM; McColl G; Hoffmann AA

Abstract

Inducible heat shock genes are considered a major component of the molecular mechanisms that confer cellular protection against a variety of environmental stresses, in particular high temperature extremes. We have tested the association between expression of the heat shock RNA gene hsr-omega and thermoresistance by generating thermoresistant lines of Drosophila melanogaster after application of two distinct regimes of laboratory selection. One set of lines was selected for resistance to knockdown by heat stress and the other was similarly selected but before selection a mild heat exposure known to increase resistance (heat hardening) was applied. A cross between resistant and susceptible lines confirmed our earlier observation that increased thermal tolerance cosegregates with allelic variation in the hsr-omega gene. This cosegregating variation is attributed largely to two haplotype groups. Using quantitative reverse transcription-PCR, we find evidence for divergent phenotypic responses in the two selection regimes, involving both structural and regulatory changes in hsr-omega. Lines selected after hardening showed increased levels of the cytoplasmic transcript but decreased levels of the nuclear transcript. Lines selected without hardening showed decreased levels of the cytoplasmic transcript. The allelic frequency changes at hsr-omega could not by themselves account for the altered transcription patterns. Our results support the idea that the functional RNA molecules transcribed from hsr-omega are an important and polymorphic regulatory component of an insect thermoresistance phenotype.

Additional References

The Drosophila heat shock hsr-omega gene: an allele frequency cline detected by quantitative PCR. (1999) (https://pubmed.ncbi.nlm.nih.gov/10555288)

RELATED GEPHE

Related Genes

1 (hsp70Ba) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Temperature tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

No UniProtKB entry for this long non-coding RNA - http://flybase.org/reports/FBal0052269 - http://flybase.org/reports/FBal0052270