GEPHE SUMMARY

Gephebase Gene

HSP90 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^HSP90^#gephebase-summary-title)

GepheID

GP00002437

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

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

Trait State in Taxon A

Locusta migratoria - slower development and higher developmental synchrony

Trait State in Taxon B

Locusta migratoria - faster development and higher developmental synchrony

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Locusta migratoria (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Locusta migratoria^#gephebase-summary-title)

Common Name

migratory locust

Synonyms

migratory locust; Locusta migratoria (Linnaeus, 1758)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Polyneoptera; Orthoptera; Caelifera; Acrididea; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta

Parent

Locusta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7003)

NCBI Taxonomy ID

7004 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7004)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Locusta migratoria (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Locusta migratoria^#gephebase-summary-title)

Common Name

migratory locust

Synonyms

migratory locust; Locusta migratoria (Linnaeus, 1758)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Polyneoptera; Orthoptera; Caelifera; Acrididea; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta

Parent

Locusta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7003)

NCBI Taxonomy ID

7004 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7004)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

daf-21

Synonyms

C47E8.5

String

6239.C47E8.5.2 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 6239.C47E8.5.2)

Sequence Similarities

Belongs to the heat shock protein 90 family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
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:0097718 : disordered domain specific binding (https://www.ebi.ac.uk/QuickGO/term/GO:0097718)

UniProtKB Caenorhabditis elegans

Q18688 (http://www.uniprot.org/uniprot/Q18688)

GenebankID or UniProtKB

()

GO:0140662 : ATP-dependent protein folding chaperone
(https://www.ebi.ac.uk/QuickGO/term/GO:0140662)
GO:0035259 : nuclear glucocorticoid receptor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0035259)
GO:1990634 : protein phosphatase 5 binding
(https://www.ebi.ac.uk/QuickGO/term/GO:1990634)

GO - Biological Process

GO:0006457 : protein folding (https://www.ebi.ac.uk/QuickGO/term/GO:0006457)
GO:0006935 : chemotaxis (https://www.ebi.ac.uk/QuickGO/term/GO:0006935)
GO:0050829 : defense response to Gram-negative bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0050829)
GO:0008340 : determination of adult lifespan
(https://www.ebi.ac.uk/QuickGO/term/GO:0008340)
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:0050821 : protein stabilization (https://www.ebi.ac.uk/QuickGO/term/GO:0050821)
GO:0007049 : cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0007049)
GO:0040024 : dauer larval development
(https://www.ebi.ac.uk/QuickGO/term/GO:0040024)
GO:0006470 : protein dephosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006470)
GO:0032516 : positive regulation of phosphoprotein phosphatase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0032516)
GO:0022417 : protein maturation by protein folding
(https://www.ebi.ac.uk/QuickGO/term/GO:0022417)
GO:0045859 : regulation of protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0045859)
GO:0061077 : chaperone-mediated protein folding
(https://www.ebi.ac.uk/QuickGO/term/GO:0061077)
GO:0002119 : nematode larval development
(https://www.ebi.ac.uk/QuickGO/term/GO:0002119)
GO:0006611 : protein export from nucleus
(https://www.ebi.ac.uk/QuickGO/term/GO:0006611)
GO:0050920 : regulation of chemotaxis
(https://www.ebi.ac.uk/QuickGO/term/GO:0050920)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0045121 : membrane raft (https://www.ebi.ac.uk/QuickGO/term/GO:0045121)
GO:0032991 : protein-containing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032991)
GO:0048471 : perinuclear region of cytoplasm
(https://www.ebi.ac.uk/QuickGO/term/GO:0048471)
GO:0101031 : chaperone complex (https://www.ebi.ac.uk/QuickGO/term/GO:0101031)
GO:1990565 : HSP90-CDC37 chaperone complex
(https://www.ebi.ac.uk/QuickGO/term/GO:1990565)
GO:0008287 : protein serine/threonine phosphatase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0008287)

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

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

Insertion Size

-

Molecular Details of the Mutation

an Lm1 SINE insertion in the third exon of the Hsp90 gene produces an alternative splicing form associated with faster development and higher developmental synchrony. Found by scanning Lm1 insertions in natural locust populations.

Experimental Evidence

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

Main Reference

Transposable Element-Mediated Balancing Selection at Hsp90 Underlies Embryo Developmental Variation. (2017) (https://pubmed.ncbi.nlm.nih.gov/28138075)

Authors

Chen B; Zhang B; Xu L; Li Q; Jiang F; Yang P; Xu Y; Kang L

Abstract

Understanding the roles of transposable elements (TEs) in the evolution of genome and adaptation is a long-sought goal. Here, we present a new model of TE co-option, in which a TE is harnessed by an essential gene and confers local adaptation through heterozygote advantage. We characterized a human Alu-like TE family, the Lm1 elements, in the genome of the migratory locust Locusta migratoria that harbors 0.7 million copies of the elements. Scanning Lm1 insertions in the natural locust populations revealed the widespread high polymorphism of Lm1. An Lm1 was recruited into the coding region of Heat-shock protein 90 (Hsp90), an important molecular chaperone for diverse signal transduction and developmental pathways. Only heterozygotes of the allele are present in natural populations. Allele frequency increases with decreased latitudes in east coastal China, even increasing up to 76% in southern populations. Regions flanking the Lm1 insertion display clear signatures of a selective sweep linked to Lm1. The Lm1-mediated Hsp90 mutation is consequential for the embryonic development of locust. Heterozygous embryos develop faster than the wild type, particularly when cued by long-day parental photoperiod. The heterozygotes also present a reduced within-population variation in embryonic development, i.e., high developmental synchrony of embryos. The naturally occurring Hsp90 mutation could facilitate multivoltinism and developmental synchronization of the locust in southern tropical region. These results revealed a genetic mechanism behind microevolutionary changes in which balancing selection may have acted to maintain the heterozygote advantage through TE co-option in essential genes.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE @SelectiveSweep