

GEPHE SUMMARY

HSP90 (<a +hsp90+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+HSP90+"#gephebase-summary-title)	Gephebase Gene	GP00002437	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

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 Category		
Developmental time (<a +developmental+time+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Developmental+time+"#gephebase-summary-title)	Trait		
Locusta migratoria - slower development and higher developmental synchrony	Trait State in Taxon A		
Locusta migratoria - faster development and higher developmental synchrony	Trait State in Taxon B		
	Ancestral State		
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)	Taxonomic Status		
	Taxon A	Taxon B	
Locusta migratoria (<a +locusta+migratoria+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Locusta+migratoria+"#gephebase-summary-title)	Latin Name	Locusta migratoria (<a +locusta+migratoria+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Locusta+migratoria+"#gephebase-summary-title)	Latin Name
migratory locust	Common Name	migratory locust	Common Name
migratory locust; Locusta migratoria (Linnaeus, 1758)	Synonyms	migratory locust; Locusta migratoria (Linnaeus, 1758)	Synonyms
species	Rank	species	Rank
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	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	Lineage
Locusta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7003)	Parent	Locusta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7003)	Parent
7004 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7004)	NCBI Taxonomy ID	7004 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7004)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

daf-21	Generic Gene Name	Q18688 (http://www.uniprot.org/uniprot/Q18688)	UniProtKB Caenorhabditis elegans
C47E8.5	Synonyms		GenebankID or UniProtKB
6239.C47E8.5.2 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=6239.C47E8.5.2)	String		
Belongs to the heat shock protein 90 family.	Sequence Similarities		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	GO - Molecular Function		
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)			

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.

RELATED GEPHE

No matches found.

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS

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