

GEPHE SUMMARY

		Gephebase Gene		GepheID
metallothionein (MtnA) (https://www.gephebase.org/search-criteria?/and+Gene)			GP00002018	
Gephebase="metallothionein (MtnA)"#gephebase-summary-title)				Main curator
Published		Entry Status	Courtier	

PHENOTYPIC CHANGE

		Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait)				
Category="Physiology"#gephebase-summary-title)		Trait		
Oxidative stress resistance (https://www.gephebase.org/search-criteria?/and+Trait="Oxidative stress resistance"#gephebase-summary-title)				
Drosophila melanogaster		Trait State in Taxon A		
Drosophila melanogaster		Trait State in Taxon B		
Taxon A		Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)		Taxonomic Status		
Status="Intraspecific"#gephebase-summary-title)				
Taxon A			Taxon B	
		Latin Name		
Drosophila melanogaster			Drosophila melanogaster	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Drosophila melanogaster"#gephebase-summary-title)			(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Drosophila melanogaster"#gephebase-summary-title)	
		Common Name		
fruit fly			fruit fly	
		Synonyms		
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster			Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
		Rank		
species			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			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)			melanogaster subgroup () - (Rank: species subgroup)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)			(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
		NCBI Taxonomy ID		
7227			7227	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)			(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	
		is Taxon A an Intraspecies?		
No			No	
		is Taxon B an Intraspecies?		

GENOTYPIC CHANGE

		Generic Gene Name		UniProtKB Drosophila melanogaster
MtnA			P04357 (http://www.uniprot.org/uniprot/P04357)	
		Synonyms		
anon-WO0153538.42; anon-WO0153538.44; anon-WO0153538.49; BcDNA:GH18460; CG9470; Dmel\CG9470; DrosMtn; Mtn; MTN; mtnA			()	
		String		
7227.FBpp0081636				
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0081636)				
		Sequence Similarities		
Belongs to the metallothionein superfamily. Type 5 family.				
		GO - Molecular Function		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)				
		GO - Biological Process		
GO:0010038 : response to metal ion (https://www.ebi.ac.uk/QuickGO/term/GO:0010038)				

GO:0055065 : metal ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0055065>)

GO - Cellular Component

-	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
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)	Deletion Size
10-99 bp	Molecular Details of the Mutation
49bp deletion in the MtnA 3'UTR	Experimental Evidence
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)	Main Reference
An Indel Polymorphism in the MtnA 3' Untranslated Region Is Associated with Gene Expression Variation and Local Adaptation in <i>Drosophila melanogaster</i> . (2016) (https://pubmed.ncbi.nlm.nih.gov/27120580)	Authors
Catal��n A; Glaser-Schmitt A; Argyridou E; Duchon P; Parsch J	Abstract
Insertions and deletions (indels) are a major source of genetic variation within species and may result in functional changes to coding or regulatory sequences. In this study we report that an indel polymorphism in the 3' untranslated region (UTR) of the metallothionein gene MtnA is associated with gene expression variation in natural populations of <i>Drosophila melanogaster</i> . A derived allele of MtnA with a 49-bp deletion in the 3' UTR segregates at high frequency in populations outside of sub-Saharan Africa. The frequency of the deletion increases with latitude across multiple continents and approaches 100% in northern Europe. Flies with the deletion have more than 4-fold higher MtnA expression than flies with the ancestral sequence. Using reporter gene constructs in transgenic flies, we show that the 3' UTR deletion significantly contributes to the observed expression difference. Population genetic analyses uncovered signatures of a selective sweep in the MtnA region within populations from northern Europe. We also find that the 3' UTR deletion is associated with increased oxidative stress tolerance. These results suggest that the 3' UTR deletion has been a target of selection for its ability to confer increased levels of MtnA expression in northern European populations, likely due to a local adaptive advantage of increased oxidative stress tolerance.	Additional References

RELATED GEPHE

1 (Jheh1-Jheh2-Jheh3 complex) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Oxidative stress resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

signatures of a @SelectiveSweep in the MtnA region within populations from northern Europe. The 3' UTR deletion is associated with increased oxidative stress tolerance. These results suggest that the 3' UTR deletion has been a target of selection for its ability to confer increased levels of MtnA expression in northern European populations; likely due to a local adaptive advantage of increased oxidative stress tolerance. - <http://flybase.org/reports/FBa0338143>