

GEPHE SUMMARY

		Gephebase Gene		GepheID
lactate dehydrogenase-B (Ldh-B) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+lactate+dehydrogenase-B+(Ldh-B)+#gephebase-summary-title)			GP00000533	
Published		Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

		Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+#gephebase-summary-title)				
		Trait		
Stress response (https://www.gephebase.org/search-criteria?/and+Trait+Stress+response+#gephebase-summary-title)				
		Trait State in Taxon A		
Fundulus heteroclitus - Northern populations				
		Trait State in Taxon B		
Fundulus heteroclitus - Southern populations				
		Ancestral State		
Data not curated				
		Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific+#gephebase-summary-title)				
Taxon A			Taxon B	
	Latin Name			Latin Name
Fundulus heteroclitus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Fundulus+heteroclitus+#gephebase-summary-title)		Fundulus heteroclitus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Fundulus+heteroclitus+#gephebase-summary-title)		
	Common Name			Common Name
mummichog		mummichog		
	Synonyms			Synonyms
mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)		mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)		
	Rank			Rank
species		species		
	Lineage			Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidae; Fundulidae; Fundulus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidae; Fundulidae; Fundulus		
	Parent			Parent
Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8077)		Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8077)		
	NCBI Taxonomy ID			NCBI Taxonomy ID
8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8078)		8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8078)		
	is Taxon A an Intraspecies?			is Taxon B an Intraspecies?
No		No		

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Fundulus heteroclitus
ldhb		P20373 (http://www.uniprot.org/uniprot/P20373)	
	Synonyms		GenebankID or UniProtKB
ldhb; Ldh-B		L23795 (https://www.ncbi.nlm.nih.gov/nuccore/L23795)	
-	String		
	Sequence Similarities		
Belongs to the LDH/MDH superfamily. LDH family.			
	GO - Molecular Function		
GO:0004459 : L-lactate dehydrogenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004459)			
	GO - Biological Process		
GO:0005975 : carbohydrate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0005975)			
GO:0019752 : carboxylic acid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019752)			

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

Cis-regulatory ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Cis-regulatory^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

Aberration Type

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

Molecular Details of the Mutation

unknown - candidate 1 bp change in southern populatin generates mammary tumor virus glucocorticoid responsive element

Experimental Evidence

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

Main Reference

Adaptive variation in lactate dehydrogenase-B gene expression: role of a stress-responsive regulatory element. (2000) (<https://pubmed.ncbi.nlm.nih.gov/10841559>)

Authors

Schulte PM; Glemet HC; Fiebig AA; Powers DA

Abstract

Although changes in gene regulation may play an important role in adaptive evolution, there have been few attempts to investigate the molecular mechanisms responsible for adaptively significant variation in gene expression. Here we describe the mechanism underlying an adaptive difference in the expression of the lactate dehydrogenase-B gene (Ldh-B) between northern and southern populations of the fish *Fundulus heteroclitus*. Ldh-B regulatory sequences from northern and southern individuals, coupled to a luciferase reporter gene, were introduced into the livers of live fish. Deletion studies indicated that sequence changes between 400 and 500 bp upstream of the transcription start site resulted in a 2-fold difference in reporter gene transcription. These sequence changes can account for the previously observed 2-fold difference in Ldh-B transcription between populations. Variation in transcription factors did not play an important role. Sequences within the functionally important region resemble a mammary tumor virus glucocorticoid responsive element (MTV-GRE) in southern alleles, whereas northern alleles differ from the consensus by 1 bp. To test the hypothesis that this element is involved in the variation between populations of *F. heteroclitus*, we exposed transiently transgenic fish containing Ldh-B regulatory sequence/reporter gene constructs to handling stress or injected cortisol. Both treatments increased reporter gene transcription driven by southern alleles but not northern alleles, as expected if an MTV-GRE sequence were involved. This finding suggests that sequence variation in a GRE is the cause of the adaptive differences in Ldh-B gene expression between populations and demonstrates that small changes in gene regulatory sequences can have important evolutionary consequences.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS