

GEPHE SUMMARY

	Gephebase Gene	GephelD
AIP (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=AIP^#gephebase-summary-title)	GP00001812	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		
Xenobiotic resistance (pollution) (https://www.gephebase.org/search-criteria?/and+Trait=Xenobiotic+resistance+(pollution)^#gephebase-summary-title)	Trait State in Taxon A		
Fundulus heteroclitus - sensitive - lives in non-polluted sites	Trait State in Taxon B		
Fundulus heteroclitus - tolerant - adapted to polluted sites	Ancestral State		
Taxon A		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=Intraspecific^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	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)	
mummichog	Common Name	mummichog	Common Name
mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)	Synonyms	mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleoste; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleoste; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphacea; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidei; Fundulidae; Fundulus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleoste; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleoste; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphacea; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidei; Fundulidae; Fundulus	
Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8077)	Parent	Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8077)	Parent
8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8078)	NCBI Taxonomy ID	8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8078)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name		
Aip	O08915 (http://www.uniprot.org/uniprot/O08915)		UniProtKB Mus musculus
Ara9; Xap2; Fkbp16; AA408703; AW476050; D19Bwg1412e	Synonyms		GenebankID or UniProtKB
10090.ENSMUSP00000025767 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000025767)	String	0	
	Sequence Similarities		
GO:0051082 : unfolded protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051082)	GO - Molecular Function		
GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)			
GO:0017162 : aryl hydrocarbon receptor binding			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0017162>)
GO:0036004 : GAF domain binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0036004>)
GO - Biological Process
GO:0006805 : xenobiotic metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006805>)
GO:0051344 : negative regulation of cyclic-nucleotide phosphodiesterase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051344>)
GO:0022417 : protein maturation by protein folding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0022417>)
GO:0006626 : protein targeting to mitochondrion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006626>)
GO:0010738 : regulation of protein kinase A signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010738>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0034751 : aryl hydrocarbon receptor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034751>)

Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes^#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

exact mutation(s) unknown - very good candidate gene according to association mapping and knowledge about the physiology

Experimental Evidence

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

Main Reference

The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27940876>)

Authors

Reid NM; Proestou DA; Clark BW; Warren WC; Colbourne JK; Shaw JR; Karchner SI; Hahn ME; Nacci D; Oleksiak MF; Crawford DL; Whitehead A

Abstract

Atlantic killifish populations have rapidly adapted to normally lethal levels of pollution in four urban estuaries. Through analysis of 384 whole killifish genome sequences and comparative transcriptomics in four pairs of sensitive and tolerant populations, we identify the aryl hydrocarbon receptor-based signaling pathway as a shared target of selection. This suggests evolutionary constraint on adaptive solutions to complex toxicant mixtures at each site. However, distinct molecular variants apparently contribute to adaptive pathway modification among tolerant populations. Selection also targets other toxicity-mediating genes and genes of connected signaling pathways; this indicates complex tolerance phenotypes and potentially compensatory adaptations. Molecular changes are consistent with selection on standing genetic variation. In killifish, high nucleotide diversity has likely been a crucial substrate for selective sweeps to propel rapid adaptation.

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Additional References

RELATED GEPHE

Related Genes

1 (AHR2) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^8078^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism @Fitness