GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00002670

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

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

Trait State in Taxon A

Fundulus grandis - sensitive - lives in non-polluted sites

Trait State in Taxon B

Fundulus grandis - 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

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

Common Name

Gulf killifish

Synonyms

Gulf killifish; Fundulus grandis Baird & Girard, 1853

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidei; Fundulidae; Fundulus

Parent

Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8077)

NCBI Taxonomy ID

34779 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34779)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

Gulf killifish

Synonyms

Gulf killifish; Fundulus grandis Baird & Girard, 1853

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Cyprinodontiformes; Cyprinodontoidei; Fundulidae; Fundulus

Parent

Fundulus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8077)

NCBI Taxonomy ID

34779 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34779)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

Aip

Synonyms

Ara9; Xap2; Fkbp16; AA408703; AW476050; D19Bwg1412e

String

10090.ENSMUSP00000025767 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000025767)

Sequence Similarities

-

GO - Molecular Function

GO:0051082 : unfolded protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051082)
GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)
GO:0017162 : aryl hydrocarbon receptor binding

UniProtKB Mus musculus

O08915 (http://www.uniprot.org/uniprot/O08915)

GenebankID or UniProtKB

()

(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 Fst 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

Adaptive introgression enables evolutionary rescue from extreme environmental pollution. (2019) (https://pubmed.ncbi.nlm.nih.gov/31048485)

Authors

Oziolor EM; Reid NM; Yair S; Lee KM; Guberman VerPloeg S; Bruns PC; Shaw JR; Whitehead A; Matson CW

Abstract

Radical environmental change that provokes population decline can impose constraints on the sources of genetic variation that may enable evolutionary rescue. Adaptive toxicant resistance has rapidly evolved in Gulf killifish (Fundulus grandis) that occupy polluted habitats. We show that resistance scales with pollution level and negatively correlates with inducibility of aryl hydrocarbon receptor (AHR) signaling. Loci with the strongest signatures of recent selection harbor genes regulating AHR signaling. Two of these loci introgressed recently (18 to 34 generations ago) from Atlantic killifish (F. heteroclitus). One introgressed locus contains a deletion in AHR that confers a large adaptive advantage [selection coefficient (s) = 0.8]. Given the limited migration of killifish, recent adaptive introgression was likely mediated by human-assisted transport. We suggest that interspecies connectivity may be an important source of adaptive variation during extreme environmental change.

Additional References

RELATED GEPHE

Related Genes

3 (AHR2, ARNT-1c, ARNT-L2a) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^34779^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Fitness Probably @Introgression from Fundulus heteroclitus