GEPHE SUMMARY

Gephebase Gene

AHR2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^AHR2^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002669

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

Ahr

Synonyms

Ah; In; Ahh; Ahre; bHLHe76

String

10090.ENSMUSP00000112137 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000112137)

Sequence Similarities

-

GO - Molecular Function

GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0046982 : protein heterodimerization activity

UniProtKB Mus musculus

P30561 (http://www.uniprot.org/uniprot/P30561)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0046982)
GO:0043565 : sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0008134 : transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0044212 : transcription regulatory region DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0044212)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific
(https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0004879 : nuclear receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004879)
GO:0070888 : E-box binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070888)
GO:1990837 : sequence-specific double-stranded DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:1990837)
GO:0051879 : Hsp90 protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051879)
GO:0051087 : chaperone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051087)
GO:0001223 : transcription coactivator binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001223)
GO:0017162 : aryl hydrocarbon receptor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0017162)
GO:0035326 : enhancer binding (https://www.ebi.ac.uk/QuickGO/term/GO:0035326)
GO:0017025 : TBP-class protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0017025)
GO:0001094 : TFIID-class transcription factor complex binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001094)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006357 : regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
GO:0006355 : regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045892 : negative regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0045893 : positive regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0035162 : embryonic hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035162)
GO:0001541 : ovarian follicle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001541)
GO:0030850 : prostate gland development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030850)
GO:0032922 : circadian regulation of gene expression
(https://www.ebi.ac.uk/QuickGO/term/GO:0032922)
GO:0014070 : response to organic cyclic compound
(https://www.ebi.ac.uk/QuickGO/term/GO:0014070)
GO:0010468 : regulation of gene expression
(https://www.ebi.ac.uk/QuickGO/term/GO:0010468)
GO:0006805 : xenobiotic metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006805)
GO:0008217 : regulation of blood pressure
(https://www.ebi.ac.uk/QuickGO/term/GO:0008217)
GO:0008015 : blood circulation (https://www.ebi.ac.uk/QuickGO/term/GO:0008015)
GO:0001974 : blood vessel remodeling
(https://www.ebi.ac.uk/QuickGO/term/GO:0001974)
GO:0006366 : transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0006366)
GO:0001889 : liver development (https://www.ebi.ac.uk/QuickGO/term/GO:0001889)
GO:0048608 : reproductive structure development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048608)
GO:0043010 : camera-type eye development
(https://www.ebi.ac.uk/QuickGO/term/GO:0043010)
GO:0048745 : smooth muscle tissue development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048745)
GO:0000902 : cell morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0000902)
GO:0050880 : regulation of blood vessel size
(https://www.ebi.ac.uk/QuickGO/term/GO:0050880)
GO:0030183 : B cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030183)
GO:0045793 : positive regulation of cell size
(https://www.ebi.ac.uk/QuickGO/term/GO:0045793)
GO:0071320 : cellular response to cAMP
(https://www.ebi.ac.uk/QuickGO/term/GO:0071320)
GO:0009636 : response to toxic substance
(https://www.ebi.ac.uk/QuickGO/term/GO:0009636)
GO:0007049 : cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0007049)

GO:0009410 : response to xenobiotic stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009410)
GO:0001568 : blood vessel development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001568)
GO:0001782 : B cell homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0001782)
GO:0001922 : B-1 B cell homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0001922)
GO:0048514 : blood vessel morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048514)
GO:0001569 : branching involved in blood vessel morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0001569)
GO:0019933 : cAMP-mediated signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0019933)
GO:0003214 : cardiac left ventricle morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0003214)
GO:1904613 : cellular response to 2,3,7,8-tetrachlorodibenzodioxine
(https://www.ebi.ac.uk/QuickGO/term/GO:1904613)
GO:1904682 : cellular response to 3-methylcholanthrene
(https://www.ebi.ac.uk/QuickGO/term/GO:1904682)
GO:1904322 : cellular response to forskolin
(https://www.ebi.ac.uk/QuickGO/term/GO:1904322)
GO:0003243 : circumferential growth involved in left ventricle morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0003243)
GO:0061009 : common bile duct development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061009)
GO:0048732 : gland development (https://www.ebi.ac.uk/QuickGO/term/GO:0048732)
GO:0072102 : glomerulus morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0072102)
GO:0002376 : immune system process
(https://www.ebi.ac.uk/QuickGO/term/GO:0002376)
GO:0060993 : kidney morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060993)
GO:0002260 : lymphocyte homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0002260)
GO:0060547 : negative regulation of necrotic cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0060547)
GO:0003085 : negative regulation of systemic arterial blood pressure
(https://www.ebi.ac.uk/QuickGO/term/GO:0003085)
GO:0045906 : negative regulation of vasoconstriction
(https://www.ebi.ac.uk/QuickGO/term/GO:0045906)
GO:0040010 : positive regulation of growth rate
(https://www.ebi.ac.uk/QuickGO/term/GO:0040010)
GO:0045899 : positive regulation of RNA polymerase II transcriptional preinitiation complex
assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0045899)
GO:0035166 : post-embryonic hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035166)
GO:0030888 : regulation of B cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0030888)
GO:0060420 : regulation of heart growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0060420)
GO:0048536 : spleen development (https://www.ebi.ac.uk/QuickGO/term/GO:0048536)
GO:0043029 : T cell homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0043029)
GO:0060841 : venous blood vessel development
(https://www.ebi.ac.uk/QuickGO/term/GO:0060841)

GO - Cellular Component

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:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005667 : transcription factor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005667)
GO:0032991 : protein-containing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032991)
GO:0034751 : aryl hydrocarbon receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0034751)
GO:0034752 : cytosolic aryl hydrocarbon receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0034752)
GO:0034753 : nuclear aryl hydrocarbon receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0034753)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

10-100 kb

Molecular Details of the Mutation

70 kb deletion that removes parts of the two genes AHR1a and AHR2a

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 (AIP, 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

@Introgression from Fundulus heteroclitus. Knockdown of AHR2a is protective of toxicity - @Fitness