GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001806

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 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

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

Common Name

mummichog

Synonyms

mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)

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

8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8078)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

mummichog

Synonyms

mummichog; Atlantic killifish; killifish; Fundulus heteroclitus (Linnaeus, 1766)

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

8078 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8078)

is Taxon B an Infraspecies?

Yes

Taxon B Description

population T1

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

UniProtKB Mus musculus

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

GenebankID or UniProtKB

Q90505 (https://www.ncbi.nlm.nih.gov/nuccore/Q90505)

(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0046982 : protein heterodimerization activity
(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

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

AHR2 mediates cardiac teratogenesis of polycyclic aromatic hydrocarbons and PCB-126 in Atlantic killifish (Fundulus heteroclitus). (2010) (https://pubmed.ncbi.nlm.nih.gov/20605646)

RELATED GEPHE

Related Genes

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

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^AHR2^/and+Taxon ID=^8078^/or+Gene Gephebase=^AHR2^/and+Taxon ID=^8078^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Knockdown of AHR2a is protective of toxicity - @Parallelism @Fitness