

## GEPHE SUMMARY

**Gephebase Gene**  
AHR2

**Entry Status**  
Published

**GepheID**  
GP00001806

**Main curator**  
Courtier

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Xenobiotic resistance (pollution)

**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

### Taxon A

**Latin Name**  
*Fundulus heteroclitus*

**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; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Ovalentaria; Atherinomorpha; Cyprinodontiformes; Cyprinodontoides; Fundulidae; Fundulus

**Parent**  
Fundulus () - (Rank: genus)

**NCBI Taxonomy ID**  
8078

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Fundulus heteroclitus*

**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; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Ovalentaria; Atherinomorpha; Cyprinodontiformes; Cyprinodontoides; Fundulidae; Fundulus

**Parent**  
Fundulus () - (Rank: genus)

**NCBI Taxonomy ID**  
8078

**is Taxon B an Intraspecies?**  
Yes

**Taxon B Description**  
population T1

## GENOTYPIC CHANGE

**Generic Gene Name**  
Ahr

**Synonyms**  
Ah; In; Ahh; Ahre; bHLHe76

**String**  
10090.ENSMUSP00000112137

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0042803 : protein homodimerization activity  
GO:0003700 : DNA-binding transcription factor activity  
GO:0046982 : protein heterodimerization activity  
GO:0043565 : sequence-specific DNA binding  
GO:0008134 : transcription factor binding  
GO:0044212 : transcription regulatory region DNA binding

**UniProtKB Mus musculus**  
P30561

**GenebankID or UniProtKB**  
Q90505

GO:0003677 : DNA binding  
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific  
GO:0004879 : nuclear receptor activity  
GO:0070888 : E-box binding  
GO:1990837 : sequence-specific double-stranded DNA binding  
GO:0051879 : Hsp90 protein binding  
GO:0051087 : chaperone binding  
GO:0001223 : transcription coactivator binding  
GO:0017162 : aryl hydrocarbon receptor binding  
GO:0035326 : enhancer binding  
GO:0017025 : TBP-class protein binding  
GO:0001094 : TFIIID-class transcription factor complex binding

#### GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II  
GO:0006357 : regulation of transcription by RNA polymerase II  
GO:0006355 : regulation of transcription, DNA-templated  
GO:0000122 : negative regulation of transcription by RNA polymerase II  
GO:0045892 : negative regulation of transcription, DNA-templated  
GO:0045893 : positive regulation of transcription, DNA-templated  
GO:0035162 : embryonic hemopoiesis  
GO:0001541 : ovarian follicle development  
GO:0030850 : prostate gland development  
GO:0032922 : circadian regulation of gene expression  
GO:0014070 : response to organic cyclic compound  
GO:0010468 : regulation of gene expression  
GO:0006805 : xenobiotic metabolic process  
GO:0008217 : regulation of blood pressure  
GO:0008015 : blood circulation  
GO:0001974 : blood vessel remodeling  
GO:0006366 : transcription by RNA polymerase II  
GO:0001889 : liver development  
GO:0048608 : reproductive structure development  
GO:0043010 : camera-type eye development  
GO:0048745 : smooth muscle tissue development  
GO:0000902 : cell morphogenesis  
GO:0050880 : regulation of blood vessel size  
GO:0030183 : B cell differentiation  
GO:0045793 : positive regulation of cell size  
GO:0071320 : cellular response to cAMP  
GO:0009636 : response to toxic substance  
GO:0007049 : cell cycle  
GO:0009410 : response to xenobiotic stimulus  
GO:0001568 : blood vessel development  
GO:0001782 : B cell homeostasis  
GO:0001922 : B-1 B cell homeostasis  
GO:0048514 : blood vessel morphogenesis  
GO:0001569 : branching involved in blood vessel morphogenesis  
GO:0019933 : cAMP-mediated signaling  
GO:0003214 : cardiac left ventricle morphogenesis  
GO:1904613 : cellular response to 2,3,7,8-tetrachlorodibenzodioxine  
GO:1904682 : cellular response to 3-methylcholanthrene  
GO:1904322 : cellular response to forskolin  
GO:0003243 : circumferential growth involved in left ventricle morphogenesis  
GO:0061009 : common bile duct development  
GO:0048732 : gland development  
GO:0072102 : glomerulus morphogenesis  
GO:0002376 : immune system process  
GO:0060993 : kidney morphogenesis  
GO:0002260 : lymphocyte homeostasis  
GO:0060547 : negative regulation of necrotic cell death  
GO:0003085 : negative regulation of systemic arterial blood pressure  
GO:0045906 : negative regulation of vasoconstriction  
GO:0040010 : positive regulation of growth rate  
GO:0045899 : positive regulation of RNA polymerase II transcriptional preinitiation complex assembly  
GO:0035166 : post-embryonic hemopoiesis  
GO:0030888 : regulation of B cell proliferation  
GO:0060420 : regulation of heart growth  
GO:0048536 : spleen development  
GO:0043029 : T cell homeostasis  
GO:0060841 : venous blood vessel development

#### GO - Cellular Component

GO:0005737 : cytoplasm  
GO:0005829 : cytosol  
GO:0005634 : nucleus  
GO:0005667 : transcription factor complex  
GO:0032991 : protein-containing complex  
GO:0034751 : aryl hydrocarbon receptor complex  
GO:0034752 : cytosolic aryl hydrocarbon receptor complex  
GO:0034753 : nuclear aryl hydrocarbon receptor complex

#### Presumptive Null

Yes

#### Molecular Type

Gene Loss

#### Aberration Type

Deletion

#### 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

#### Main Reference

The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. (2016)

#### 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)

## RELATED GEPHE

#### Related Genes

1 (AIP)

#### Related Haplotypes

2

## COMMENTS

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