GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00001812

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 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?

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 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