

GEPHE SUMMARY

AHR2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~AHR2~#gephebase-summary-title)	Gephebase Gene	GP00001809	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait Category	
Xenobiotic resistance (pollution; polychlorinated biphenyls; PCBs) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic+resistance+(pollution;+polychlorinated+biphenyls;+PCBs)~#gephebase-summary-title)		Trait	
Atlantic tomcod - sensitive		Trait State in Taxon A	
Atlantic tomcod - tolerant		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Microgadus tomcod (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Microgadus+tomcod~#gephebase-summary-title)		Microgadus tomcod (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Microgadus+tomcod~#gephebase-summary-title)	
Atlantic tomcod		Atlantic tomcod	
Atlantic tomcod		Atlantic tomcod	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Paracanthomorphacea; Zeiogadaria; Gadariae; Gadiformes; Gadoidei; Gadidae; Microgadus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Paracanthomorphacea; Zeiogadaria; Gadariae; Gadiformes; Gadoidei; Gadidae; Microgadus	
Microgadus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34822)		Microgadus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34822)	
34823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34823)		34823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34823)	
No		Yes	
		population in Hudson river	

GENOTYPIC CHANGE

Ahr		Generic Gene Name	UniProtKB Mus musculus
Ah; In; Ahh; Ahre; bHLHe76		Synonyms	GenebankID or UniProtKB
10090.ENSMUSP00000112137 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000112137)		String	
-		Sequence Similarities	
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)		GO - Molecular Function	

GO:0003700 : DNA-binding transcription factor activity
(<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 : TFIIID-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>)

Yes (#gephebase-summary-title)	Presumptive Null
Coding (#gephebase-summary-title)	Molecular Type
Deletion (#gephebase-summary-title)	Aberration Type
1-9 bp	Deletion Size

6-bp deletion - (nts 1314 to 1319 in exon 10; TTCCTC) that resulted in a two-amino acid (Phe-Leu) deletion located 43 amino acids downstream of the amino terminal of the AHR2 ligand binding domain	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title)	Experimental Evidence
Mechanistic basis of resistance to PCBs in Atlantic tomcod from the Hudson River. (2011) (https://pubmed.ncbi.nlm.nih.gov/21330491)	Main Reference
Wirgin I; Roy NK; Loftus M; Chambers RC; Franks DG; Hahn ME	Authors
The mechanistic basis of resistance of vertebrate populations to contaminants, including Atlantic tomcod from the Hudson River (HR) to polychlorinated biphenyls (PCBs), is unknown. HR tomcod exhibited variants in the aryl hydrocarbon receptor 2 (AHR2) that were nearly absent elsewhere. In ligand-binding assays, AHR2-1 protein (common in the HR) was impaired as compared to widespread AHR2-2 in binding TCDD (2,3,7,8-tetrachlorodibenzo-p-dioxin) and in driving expression in reporter gene assays in AHR-deficient cells treated with TCDD or PCB126. We identified a six-base deletion in AHR2 as the basis of resistance and suggest that the HR population has undergone rapid evolution, probably due to contaminant exposure. This mechanistic basis of resistance in a vertebrate population provides evidence of evolutionary change due to selective pressure at a single locus.	Abstract
	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

Knockdown of AHR2 is protective of toxicity in killifish