

GEPHE SUMMARY

	Gephebase Gene		GepheID
AHR (https://www.gephebase.org/search-criteria?/and+GeneGephebase=AHR^#gephebase-summary-title)		GP00001810	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=Physiology^#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (polycyclic aromatic hydrocarbons; TCDD) (https://www.gephebase.org/search-criteria?/and+Trait=Xenobiotic resistance (polycyclic aromatic hydrocarbons; TCDD)^#gephebase-summary-title)			
	Trait State in Taxon A		
Mus musculus - sensitive			
	Trait State in Taxon B		
Mus musculus - tolerant			
	Ancestral State		
Unknown			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Mus musculus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=Mus musculus^#gephebase-summary-title)		Mus musculus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=Mus musculus^#gephebase-summary-title)	
	Common Name		Common Name
house mouse		house mouse	
	Synonyms		Synonyms
house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid		house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus	
	Parent		Parent
Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)		Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)		10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Mus musculus
Ahr		P30561 (http://www.uniprot.org/uniprot/P30561)	
	Synonyms		GenebankID or UniProtKB Mus musculus
Ah; In; Ahh; Ahre; bHLHe76			
	String		P30561 (https://www.ncbi.nlm.nih.gov/nuccore/P30561)
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 (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>)

	Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
alanine at position 375 mutated into valine; decreases the affinity 4-fold	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ala	Val	375

Main Reference

Analysis of the four alleles of the murine aryl hydrocarbon receptor. (1994) (<https://pubmed.ncbi.nlm.nih.gov/7969080>)

Authors

Poland A; Palen D; Glover E

Abstract

The cDNAs for the four murine aryl hydrocarbon (Ah) receptor alleles were cloned and sequenced, and the deduced amino acid sequences were compared. The Ahb-1 allele encodes a protein of 805 amino acids, the Ahd and Ahb-2 alleles encode proteins of 848 amino acids, and the Ahb-3 allele encodes a protein of 883 amino acids. The alleles differ by eight point mutations in the common open reading frame (the initial 805 amino acids) and by additional sequences at the carboxyl end. The amino halves of the proteins, containing a spliced leader sequence, a basic helix-loop-helix motif, and two 50-amino acid repeats (PAAS), have identical sequences except for a single amino acid change in the second PAAS box. The Ahd allele, which has a lower ligand binding affinity, differs from the Ahb-2 receptor by only two amino acids. Mutagenesis experiments with these cloned cDNAs, using in vitro transcription and translation and 2-[125I]iodo-7,8-dibromodibenzo-p-dioxin binding, indicate that the low ligand binding affinity of the Ahd allele is attributable to a valine at residue 375; changing this amino acid to an alanine, as in the Ahb-2 protein, enhances the affinity 4-fold. For in vitro translated Ahb-1 and Ahb-2 alleles the Kd values were approximately 6-10 pM and for Ahd the Kd value was approximately 37 pM. Using 5' truncation and mutations to produce 3' translation truncation sites, we mapped the ligand binding region for the Ahb-1 allele.

Additional References

RELATED GEPHE

Related Genes

2 (Vkorc1, Na/K-ATPase alpha-subunit) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~10090^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Mutation in AHR2 is protective of toxicity in killifish and in tomcod