

Gephebase Gene		GepheID
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Na/K-ATPase alpha-subunit*#gepbase-summary-title)	GP00000701	Main curator
Entry Status	Courtier	
Published		

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=~Physiology~#gephebase-summary-title)		Trait Category	Xenobiotic resistance (cardiac glycosides) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (cardiac glycosides)~#gephebase-summary-title)		Trait
Leptodactylus latrans (formerly known as Leptodactylus ocellatus) - sensitive		Trait State in Taxon A	Leptodactylus latrans (formerly known as Leptodactylus ocellatus) - resistant		Trait State in Taxon B
Taxon A		Ancestral State	Taxon B		Ancestral State
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Intraspecific~#gephebase-summary-title)		Taxonomic Status
Taxon A		Latin Name	Taxon B		Latin Name
Leptodactylus ocellatus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Leptodactylus ocellatus~#gephebase-summary-title)		Leptodactylus ocellatus	Leptodactylus ocellatus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Leptodactylus ocellatus~#gephebase-summary-title)		Leptodactylus ocellatus
argus frog		Common Name	argus frog		Common Name
argus frog; wrestler frog		Synonyms	argus frog; wrestler frog		Synonyms
species		Rank	species		Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae; Leptodactylinae; Leptodactylus		Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae; Leptodactylinae; Leptodactylus		Lineage
Leptodactylus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47563)		Parent	Leptodactylus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47563)		Parent
209673 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 209673)		NCBI Taxonomy ID	209673 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 209673)		NCBI Taxonomy ID
is Taxon A an Intraspecies?		No	is Taxon B an Intraspecies?		No

Atp1a1	Generic Gene Name	Q8VDN2 (http://www.uniprot.org/uniprot/Q8VDN2)	UniProtKB Mus musculus
Atpa-1; BC010319	Synonyms	FJ976618 (https://www.ncbi.nlm.nih.gov/nucleotide/FJ976618)	GeneBankID or UniProtKB
10090.ENS MUSP00000039657 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENS MUSP00000039657)	String		
Sequence Similarities			
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIC subfamily.			
GO - Molecular Function			
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)			
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)			
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)			
GO:0043548 : phosphatidylinositol 3-kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043548)			
GO:0005391 : sodium:potassium-exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005391)			

GO:0051087 : chaperone binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0051087>)
GO:0019904 : protein domain specific binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019904>)
GO:0030506 : ankyrin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0030506>)
GO:0016791 : phosphatase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0016791>)
GO:0030955 : potassium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0030955>)
GO:0031402 : sodium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0031402>)
GO:1990239 : steroid hormone binding (<https://www.ebi.ac.uk/QuickGO/term/GO:1990239>)

GO - Biological Process

GO:0071383 : cellular response to steroid hormone stimulus (<https://www.ebi.ac.uk/QuickGO/term/GO:0071383>)
GO:0006813 : potassium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)
GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)
GO:0071260 : cellular response to mechanical stimulus (<https://www.ebi.ac.uk/QuickGO/term/GO:0071260>)
GO:0042493 : response to drug (<https://www.ebi.ac.uk/QuickGO/term/GO:0042493>)
GO:0008217 : regulation of blood pressure (<https://www.ebi.ac.uk/QuickGO/term/GO:0008217>)
GO:0015991 : ATP hydrolysis coupled proton transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015991>)
GO:0030007 : cellular potassium ion homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0030007>)
GO:0006883 : cellular sodium ion homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006883>)
GO:1990573 : potassium ion import across plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:1990573>)
GO:0036376 : sodium ion export across plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0036376>)
GO:0090662 : ATP hydrolysis coupled transmembrane transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0090662>)
GO:0060081 : membrane hyperpolarization (<https://www.ebi.ac.uk/QuickGO/term/GO:0060081>)
GO:0086009 : membrane repolarization (<https://www.ebi.ac.uk/QuickGO/term/GO:0086009>)
GO:0031947 : negative regulation of glucocorticoid biosynthetic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0031947>)
GO:0045822 : negative regulation of heart contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0045822>)
GO:0045823 : positive regulation of heart contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0045823>)
GO:0045989 : positive regulation of striated muscle contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0045989>)
GO:0086004 : regulation of cardiac muscle cell contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0086004>)
GO:0002028 : regulation of sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0002028>)
GO:0002026 : regulation of the force of heart contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0002026>)

GO - Cellular Component

GO:0016021 : integral component of membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0016324 : apical plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016324>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0032991 : protein-containing complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)
GO:0005783 : endoplasmic reticulum (<https://www.ebi.ac.uk/QuickGO/term/GO:0005783>)
GO:0005768 : endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005768>)
GO:0016323 : basolateral plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016323>)
GO:0005901 : caveola (<https://www.ebi.ac.uk/QuickGO/term/GO:0005901>)
GO:0030315 : T-tubule (<https://www.ebi.ac.uk/QuickGO/term/GO:0030315>)
GO:0014069 : postsynaptic density (<https://www.ebi.ac.uk/QuickGO/term/GO:0014069>)
GO:0014704 : intercalated disc (<https://www.ebi.ac.uk/QuickGO/term/GO:0014704>)
GO:0043209 : myelin sheath (<https://www.ebi.ac.uk/QuickGO/term/GO:0043209>)
GO:0042383 : sarcolemma (<https://www.ebi.ac.uk/QuickGO/term/GO:0042383>)
GO:0005890 : sodium:potassium-exchanging ATPase complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0005890>)

Mutation #1

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null= "No`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Coding^#gephebase-summary-title>)

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^SNP^#gephebase-summary-title>)

Nonsynonymous

Q111R

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Candidate+Gene^#gephebase-summary-title>)

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Gln	Arg	111

Positive Darwinian selection results in resistance to cardioactive toxins in true toads (Anura: Bufonidae). (2009) (<https://pubmed.ncbi.nlm.nih.gov/19465576>)

Moore DJ; Halliday DC; Rowell DM; Robinson AJ; Keogh JS

Main Reference

Authors

Abstract

Members of the Family Bufonidae, true toads, are famous for their endogenously synthesized cardioactive steroids that serve as defensive toxins. Evolution of resistance to these toxins is not understood. We sequenced a key region of the toxin’s binding site in the Na(+)/K(+) ATPase for relevant taxa representing Hyloidea (including bufonids), Ranoidea and Archaeobatrachia and tested for positive selection in a phylogenetic context. Bufonidae were distinct from other Hyloidea at 4-6 of 12 sites and, with one exception, had a homologous amino acid sequence. Melanophryniscus stelzneri had a distinct sequence, consistent with other independent evidence for a differentiated toxin. Tests within Bufonidae detected positive selection within the binding region, providing, to our knowledge, the first evidence of this type for positive selection within Amphibia. There was no evidence for positive selection on Bufonidae or M. stelzneri lineages. Sequence change in Leptodactylus ocellatus, a leptodactylid predator of Bufonidae, provides a molecular basis for predator resistance possibly associated with gene duplication.

Additional References

Widespread convergence in toxin resistance by predictable molecular evolution. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26372961>)

Mutation #2

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>)

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^SNP^#gephebase-summary-title>)

Nonsynonymous

N122D

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Candidate+Gene^#gephebase-summary-title>)

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asn	Asp	122

Positive Darwinian selection results in resistance to cardioactive toxins in true toads (Anura: Bufonidae). (2009) (<https://pubmed.ncbi.nlm.nih.gov/19465576>)

Moore DJ; Halliday DC; Rowell DM; Robinson AJ; Keogh JS

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Members of the Family Bufonidae, true toads, are famous for their endogenously synthesized cardioactive steroids that serve as defensive toxins. Evolution of resistance to these toxins is not understood. We sequenced a key region of the toxin’s binding site in the Na(+)/K(+) ATPase for relevant taxa representing Hyloidea (including bufonids), Ranoidea and Archaeobatrachia and tested for positive selection in a phylogenetic context. Bufonidae were distinct from other Hyloidea at 4-6 of 12 sites and, with one exception, had a homologous amino acid sequence. Melanophryniscus stelzneri had a distinct sequence, consistent with other independent evidence for a differentiated toxin. Tests within Bufonidae detected positive selection within the binding region, providing, to our knowledge, the first evidence of this type for positive selection within Amphibia. There was no evidence for positive selection on Bufonidae or M. stelzneri lineages. Sequence change in Leptodactylus ocellatus, a leptodactylid predator of Bufonidae, provides a molecular basis for predator resistance possibly associated with gene duplication.

Additional References

Widespread convergence in toxin resistance by predictable molecular evolution. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26372961>)

No matches found.

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect - Ujvari et al. 2015 show that the change is intraspecific