

Na/K-ATPase alpha-subunit ( <a href="https://www.gepibase.org/search-criteria?/and+Gene">https://www.gepibase.org/search-criteria?/and+Gene</a> )	Gepibase Gene	GepheID
Gepibase= <sup>^</sup> Na/K-ATPase alpha-subunit <sup>^</sup> #gepibase-summary-title)	GP00002361	Main curator
Draft	Entry Status	Courtier

[illegible]

Generic Gene Name	UniProtKB Danaus plexippus
K+ ATPase alpha subunit	R4ZHW8 ( <a href="http://www.uniprot.org/uniprot/R4ZHW8">http://www.uniprot.org/uniprot/R4ZHW8</a> )
Synonyms	GenebankID or UniProtKB
Na+	0
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 ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005524">https://www.ebi.ac.uk/QuickGO/term/GO:0005524</a> )	
GO:0046872 : metal ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046872">https://www.ebi.ac.uk/QuickGO/term/GO:0046872</a> )	
GO:0005391 : sodium:potassium-exchanging ATPase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005391">https://www.ebi.ac.uk/QuickGO/term/GO:0005391</a> )	
GO - Biological Process	
-	
GO - Cellular Component	
GO:0016021 : integral component of membrane ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016021">https://www.ebi.ac.uk/QuickGO/term/GO:0016021</a> )	
Presumptive Null	
No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title</a> )	
Molecular Type	
Coding ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title</a> )	
Aberration Type	
SNP ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title</a> )	
SNP Coding Change	

Nonsynonymous

Molecular Details of the Mutation

-

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Concerted evolution reveals co-adapted amino acid substitutions in NaK-ATPase of frogs that prey on toxic toads. (2021) (<https://pubmed.ncbi.nlm.nih.gov/33887183>)

Authors

Mohammadi S; Yang L; Harpak A; Herrera-Álvarez S; Del Pilar Rodríguez-Ordóñez M; Peng J; Zhang K; Storz JF; Dobler S; Crawford AJ; Andolfatto P

Abstract

Although gene duplication is an important source of evolutionary innovation, the functional divergence of duplicates can be opposed by ongoing gene conversion between them. Here, we report on the evolution of a tandem duplication of Na,K-ATPase subunit 1 (ATP1A1) shared by frogs in the genus *Leptodactylus*, a group of species that feeds on toxic toads. One ATP1A1 paralog evolved resistance to toad toxins although the other retained ancestral susceptibility. Within species, frequent non-allelic gene conversion homogenized most of the sequence between the two copies but was counteracted by strong selection on 12 amino acid substitutions that distinguish the two paralogs. Protein-engineering experiments show that two of these substitutions substantially increase toxin resistance, whereas the additional 10 mitigate their deleterious effects on ATPase activity. Our results reveal how examination of neo-functionalized gene duplicate evolution can help pinpoint key functional substitutions and interactions with the genetic backgrounds on which they arise.

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