GEPHE SUMMARY

Gephebase Gene
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Na/K-ATPase alpha-subunit^#gephebase-summary-title)
Entry Status
Draft

GepheID
GP00002361
Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Xenobiotic resistance (cardiac glycosides) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (cardiac glycosides)^#gephebase-summary-title)
Trait State in Taxon A
-
Trait State in Taxon B
-
Ancestral State
Taxon A
Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name
-
Common Name
-
Synonyms
-
Rank
-
Lineage
-
Parent
-
NCBI Taxonomy ID
-
is Taxon A an Infraspecies?
No

Taxon B

Latin Name
-
Common Name
-
Synonyms
-
Rank
-
Lineage
-
Parent
-
NCBI Taxonomy ID
-
is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
K+ ATPase alpha subunit
Synonyms
Na+
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:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0005391 : sodium:potassium-exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005391)
GO - Biological Process
-
GO - Cellular Component
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)

UniProtKB Danaus plexippus
R4ZHW8 (http://www.uniprot.org/uniprot/R4ZHW8)
GenebankID or UniProtKB
()

Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)
Molecular Type
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)
Aberration Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)
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-Ãlvarez S; Del Pilar RodrÃguez-OrdoÃ±ez 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 Î±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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Additional References

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No matches found.

Related Haplotypes

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EXTERNAL LINKS

COMMENTS