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)

GepheID
GP00000706

Entry Status
Published

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
Other beetles

Trait State in Taxon B
Tetraopes tetraophthalmus

Ancestral State
Taxon A

Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name
Coleoptera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Coleoptera^#gephebase-summary-title)

Common Name
beetles

Synonyms
beetles

Rank
order

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola

Parent
Holometabola () - (Rank: cohort) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33392)

NCBI Taxonomy ID
7041 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7041)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Tetraopes tetrophthalmus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Tetraopes tetrophthalmus^#gephebase-summary-title)

Common Name
red milkweed beetle

Synonyms
red milkweed beetle; Tetraopes tetrophthalmus (Forster, 1771); Tetraopes tetraophtalmus; Tetraopes tetraophthalmus; Tetraopes tetropthalmus

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Coleoptera; Polyphaga; Cucujiformia; Chrysomeloidea; Cerambycidae; Lamiinae; Tetraopini; Tetraopes

Parent
Tetraopes () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 50524)

NCBI Taxonomy ID
1206596 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1206596)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Atp1a1

Synonyms
Atpa-1; BC010319

String
10090.ENSMUSP00000039657 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000039657)

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

UniProtKB Mus musculus
Q8VDN2 (http://www.uniprot.org/uniprot/Q8VDN2)

GenebankID or UniProtKB
()

(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)

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

Q111L + I315V

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	Gln	Leu	111

Main Reference

Parallel molecular evolution in an herbivore community. (2012) (https://pubmed.ncbi.nlm.nih.gov/23019645)

Authors

Zhen Y; Aardema ML; Medina EM; Schumer M; Andolfatto P

Abstract

Numerous insects have independently evolved the ability to feed on plants that produce toxic secondary compounds called cardenolides and can sequester these compounds for use in their defense. We surveyed the protein target for cardenolides, the alpha subunit of the sodium pump, Na(+),K(+)-ATPase (ATPÎ±), in 14 species that feed on cardenolide-producing plants and 15 outgroups spanning three insect orders. Despite the large number of potential targets for modulating cardenolide sensitivity, amino acid substitutions associated with host-plant specialization are highly clustered, with many parallel substitutions. Additionally, we document four independent duplications of ATPÎ± with convergent tissue-specific expression patterns. We find that unique substitutions are disproportionately associated with recent duplications relative to parallel substitutions. Together, these findings support the hypothesis that adaptation tends to take evolutionary paths that minimize negative pleiotropy.

Additional References

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

Mutation #2

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

Q111L + I315V

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	Ile	Val	315

Main Reference

Parallel molecular evolution in an herbivore community. (2012) (https://pubmed.ncbi.nlm.nih.gov/23019645)

Authors

Zhen Y; Aardema ML; Medina EM; Schumer M; Andolfatto P

Abstract

Numerous insects have independently evolved the ability to feed on plants that produce toxic secondary compounds called cardenolides and can sequester these compounds for use in their defense. We surveyed the protein target for cardenolides, the alpha subunit of the sodium pump, Na(+),K(+)-ATPase (ATPÎ±), in 14 species that feed on cardenolide-producing plants and 15 outgroups spanning three insect orders. Despite the large number of potential targets for modulating cardenolide sensitivity, amino acid substitutions associated with host-plant specialization are highly clustered, with many parallel substitutions. Additionally, we document four independent duplications of ATPÎ± with convergent tissue-specific expression patterns. We find that unique substitutions are disproportionately associated with recent duplications relative to parallel substitutions. Together, these findings support the hypothesis that adaptation tends to take evolutionary paths that minimize negative pleiotropy.

Additional References

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

Related Genes

6 (ABCB1, Acetylcholinesterase (Ace-2), Acetylcholinesterase (Ace), para (kdr), nAChR, resistance to dieldrin) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7041^/and+Trait=Xenobiotic resistance/or+Taxon ID=^1206596^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Na/K-ATPase alpha-subunit^/and+Taxon ID=^7041^/or+Gene Gephebase=^Na/K-ATPase alpha-subunit^/and+Taxon ID=^1206596^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect