

GEPHE SUMMARY

	Gephebase Gene	GephelD
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Na/K-ATPase alpha-subunit "#gephebase-summary-title")	GP00000705	Main curator
Published	Entry Status	Martin

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
Rhyssomatus lineaticollis	Ancestral State
Taxon A	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Interspecific">#gephebase-summary-title")	

Taxon A	Latin Name	Taxon B	Latin Name
Coleoptera (#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Coleoptera">#gephebase-summary-title)		Rhyssomatus lineaticollis (#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Rhyssomatus+lineaticollis">#gephebase-summary-title)	
beetles	Common Name	-	Common Name
beetles	Synonyms	Rhyssomatus lineaticollis (Say, 1824)	Synonyms
order	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Coleoptera; Polyphaga; Cucujiformia; Curculionoidea; Curculionidae; Molytinae; Cleogonini; Rhyssomatus	Lineage
Holometabola () - (Rank: cohort) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33392)	Parent	Rhyssomatus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=672673)	Parent
7041 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7041)	NCBI Taxonomy ID	1206597 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1206597)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

K+ ATPase alpha subunit	Generic Gene Name	UniProtKB Danaus plexippus
Na+	Synonyms	GenebankID or UniProtKB
-	String	0
	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)		

No (#gephebase-summary-title)	Presumptive Null
Coding (#gephebase-summary-title)	Molecular Type
SNP (#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
C104Y	Molecular Details of the Mutation
Candidate Gene (#gephebase-summary-title)	Experimental Evidence

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

Parallel molecular evolution in an herbivore community. (2012) (https://pubmed.ncbi.nlm.nih.gov/23019645)	Main Reference
Zhen Y; Aardema ML; Medina EM; Schumer M; Andolfatto P	Authors
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 (ATP \downarrow \pm), 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 ATP \downarrow \pm 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.	Abstract
	Additional References

RELATED GEPHE

6 (ABCB1, Acetylcholinesterase (Ace-2), Acetylcholinesterase (Ace), para (kdr), nAChR, resistance to dieldrin) (#gephebase-summary-title)	Related Genes
3 (#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS