

GEPHE SUMMARY

	Gephebase Gene		GepheID
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene)		GP00000712	
Gephebase= [^] Na/K-ATPase alpha-subunit [^] #gephebase-summary-title)			Main curator
Published	Entry Status	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)			
Criteria= [^] Xenobiotic resistance (cardiac glycosides) [^] #gephebase-summary-title)	Trait State in Taxon A		
Other insects			
	Trait State in Taxon B		
Aphis pisum and Aphis nerii			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)			
Status= [^] Interspecific [^] #gephebase-summary-title)			

Taxon A	Latin Name	Taxon B	Latin Name
Insecta (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Insecta [^] #gephebase-summary-title)		Aphis nerii (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Aphis nerii [^] #gephebase-summary-title)	
Common Name		Common Name	
true insects		oleander aphid	
Synonyms		Synonyms	
true insects		Aphis (Aphis) nerii; oleander aphid; Aphis nerii Boyer de Foscolombe, 1843	
Rank		Rank	
class		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidomorpha; Aphidoidea; Aphididae; Aphidinae; Aphidini; Aphis; Aphis	
Parent		Parent	
Hexapoda (insects) - (Rank: subphylum) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6960)		Aphis () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=464929)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
50557 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=50557)		100479 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=100479)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Danaus plexippus
K+ ATPase alpha subunit		R4ZHW8 (http://www.uniprot.org/uniprot/R4ZHW8)	
	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 (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)			

Mutation #1

No ([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)) Presumptive Null

Coding ([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)) Molecular Type

SNP ([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)) Aberration Type

Nonsynonymous SNP Coding Change

Y308C + T797A Molecular Details of the Mutation

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Tyr	Cys	308

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 (ATP1±), 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 ATP1± 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

Mutation #2

No ([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)) Presumptive Null

Coding ([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)) Molecular Type

SNP ([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)) Aberration Type

Nonsynonymous SNP Coding Change

Y308C + T797A Molecular Details of the Mutation

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Thr	Ala	797

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Additional References

73 (ABCA2, Aminopeptidase N (APN), cadherin, CYP337B3, Ha_BtR, para (kdr), tetraspanin, ABCC2, ABCB1, ABCB4, CYP9J26, CYP9M6, resistance to dieldrin, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), MAP4K4, nAChR, RYR, CYP321A8, CYP9A186, GSTe, CYP9A, acetyl-CoA carboxylase (ACC), Acetylcholinesterase (Ace-2), CYP6CM1, CYP6CY3, CYP6CY3-CYP6CY4, esterase E4, esterase FE4, SAP-2, Cpm1, esterase A8 and B8, esterase B4, esterase B5, esterase B1, CYP6AY1, CYP6ER1, esterase NI-EST1, GST, CYP6FU1, Acetylcholinesterase (Ace), CYP6D1, esterase isozyme E7 = E3, alcohol dehydrogenase (Adh), Aldehyde dehydrogenase (Aldh), CG11699, Cyp12d1, Cyp28d1, Cyp28d1-Cyp28d2, cyp6d2, cyp6g1, GSS (glutathione synthetase), GSTE1-E10 cluster, kin of irre (kire), PHGPx, RnrS, SOD1, Ugt86Dd, esterase isozyme E3, esterase B1 + esterase A, esterase B1 = esterase beta1, CYP6AB3, CYP6P9 cluster (CYP6P9a and CYP6P9b), CYP6P9; CYP6P4 cluster, esterase type I, Nav1 sodium channel, CHKov1, CYP6B1, CYP6B4, FMO1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^50557^/and+Trait=Xenobiotic resistance/or+Taxon ID=^100479^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

11 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Na/K-ATPase alpha-subunit^/and+Taxon ID=^50557^/or+Gene Gephebase=^Na/K-ATPase alpha-subunit^/and+Taxon ID=^100479^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect