

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")	GP00000712	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=^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 (#gephebase-summary-title")	

Taxon A	Latin Name	Taxon B	Latin Name
Insecta (#gephebase-summary-title")		Aphis nerii (#gephebase-summary-title")	
true insects	Common Name	oleander aphid	Common Name
true insects	Synonyms	Aphis (Aphis) nerii; oleander aphid; Aphis nerii Boyer de Foscolombe, 1843	Synonyms
class	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda	Lineage	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	Lineage
Hexapoda (insects) - (Rank: subphylum) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6960)	Parent	Aphis () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 464929)	Parent
50557 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 50557)	NCBI Taxonomy ID	100479 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 100479)	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)		

Mutation #1

No (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)	Molecular Type
SNP (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)	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 (ATP \ddagger \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 \ddagger \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.

Additional References

Mutation #2

No (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)	Molecular Type
SNP (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)	Experimental Evidence

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

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

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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-Cyp28d2, cyp6d2, cyp6g1, GSS (glutathione synthetase), GSTE1-E10 cluster, kin of ire (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%20and+Trait=Xenobiotic resistance/or+Taxon ID=%100479%20and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%50557%20and+Trait=Xenobiotic+resistance/or+Taxon%20ID=%100479%20and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

11 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%5BNa/K-ATPase alpha-subunit%5D and+Taxon ID=%50557%20and+Trait=Xenobiotic resistance/or+Taxon ID=%100479%20and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene%20Gephebase=%5BNa/K-ATPase%5D%20alpha-subunit%20and+Taxon%20ID=%50557%20and+Trait=Xenobiotic+resistance/or+Taxon%20ID=%100479%20and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect