

GEPHE SUMMARY

	Gephebase Gene	GephelD
SCN8A (Nav1.6) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SCN8A (Nav1.6)^#gephebase-summary-title)	GP00001656	Main curator
	Entry Status	Prigent
Published		

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology^#gephebase-summary-title")	Trait
Xenobiotic resistance (TTX) (https://www.gephebase.org/search-criteria?/and+Trait=Xenobiotic+resistance+(TTX)^#gephebase-summary-title)	Trait State in Taxon A
TTX-Sensitive <i>Helicops angulatus</i>	Trait State in Taxon B
TTX-Resistant <i>dipsadine Lygophis anomalus</i>	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
<i>Helicops angulatus</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Helicops+angulatus^#gephebase-summary-title)	Common Name	<i>Lygophis anomalus</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Lygophis+anomalus^#gephebase-summary-title)	Common Name
-	Synonyms	-	Synonyms
<i>Helicops angulatus</i> (Linnaeus, 1758)	Rank	Coronella anomala; Liophis anomala; Liophis anomalus; Lygophis anomalus (Guenther, 1858); BMNH 1946.1.9.13; BMNH:1946.1.9.13	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Serpentes; Colubroidea; Dipsadidae; <i>Helicops</i>	Parent	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Serpentes; Colubroidea; Dipsadidae; <i>Lygophis</i>	Parent
<i>Helicops</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=46306)	NCBI Taxonomy ID	<i>Lygophis</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1159288)	NCBI Taxonomy ID
121331 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=121331)		1159289 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1159289)	
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

SCN8A	Generic Gene Name	UniProtKB Lygophis anomalus
-	Synonyms	GenebankID or UniProtKB
-	String	0
Belongs to the sodium channel (TC 1.A.1.10) family.	Sequence Similarities	
GO:0005244 : voltage-gated ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005244)	GO - Molecular Function	
GO:0005248 : voltage-gated sodium channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005248)		
GO:0034765 : regulation of ion transmembrane transport (https://www.ebi.ac.uk/QuickGO/term/GO:0034765)	GO - Biological Process	

GO - Cellular Component

GO:0001518 : voltage-gated sodium channel complex
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0001518>)

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

V1709I (reversion) in DIV domain (loss of resistance)

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	-	-	-

Historical Contingency in a Multigene Family Facilitates Adaptive Evolution of Toxin Resistance. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27291053>)

Main Reference

McGlothlin JW; Kobiela ME; Feldman CR; Castoe TA; Geffeney SL; Hanifin CT; Toledo G; Vonk FJ; Richardson MK; Brodie ED; Pfrender ME; Brodie ED

Authors

Novel adaptations must originate and function within an already established genome [1]. As a result, the ability of a species to adapt to new environmental challenges is predicted to be highly contingent on the evolutionary history of its lineage [2-6]. Despite a growing appreciation of the importance of historical contingency in the adaptive evolution of single proteins [7-11], we know surprisingly little about its role in shaping complex adaptations that require evolutionary change in multiple genes. One such adaptation, extreme resistance to tetrodotoxin (TTX), has arisen in several species of snakes through coevolutionary arms races with toxic amphibian prey, which select for TTX-resistant voltage-gated sodium channels (Nav) [12-16]. Here, we show that the relatively recent origins of extreme toxin resistance, which involve the skeletal muscle channel Nav1.4, were facilitated by ancient evolutionary changes in two other members of the same gene family. A substitution conferring TTX resistance to Nav1.7, a channel found in small peripheral neurons, arose in lizards ~4170 million years ago (mya) and was present in the common ancestor of all snakes. A second channel found in larger myelinated neurons, Nav1.6, subsequently evolved resistance in four different snake lineages beginning ~438 mya. Extreme TTX resistance has evolved at least five times within the past 12 million years via changes in Nav1.4, but only within lineages that previously evolved resistant Nav1.6 and Nav1.7. Our results show that adaptive protein evolution may be contingent upon enabling substitutions elsewhere in the genome, in this case, in paralogs of the same gene family.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Non-null mutation