

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category= [^] Physiology [^] #gephebase-summary-title)	Trait Category		
Xenobiotic resistance (TTX) (<a href="https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (TTX)<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=[^]Xenobiotic resistance (TTX)[^]#gephebase-summary-title)	Trait		
TTX-Sensitive <i>Helicops angulatus</i>	Trait State in Taxon A		
TTX-Resistant dipsadine <i>Lygophis anomalus</i>	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Interspecific [^] #gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
	Latin Name	Latin Name	
<i>Helicops angulatus</i> (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Helicops angulatus<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Helicops angulatus[^]#gephebase-summary-title)	Latin Name	<i>Lygophis anomalus</i> (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Lygophis anomalus<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Lygophis anomalus[^]#gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
	Synonyms		Synonyms
<i>Helicops angulatus</i> (Linnaeus, 1758)	Common Name	<i>Coronella anomala</i> ; <i>Liophis anomalus</i> ; <i>Liophis anomalus</i> ; <i>Lygophis anomalus</i> (Guenther, 1858); BMNH 1946.1.9.13; BMNH:1946.1.9.13	Common Name
species	Rank	species	Rank
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; Helicops	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; Lygophis	Lineage
<i>Helicops</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=46306)	Parent	<i>Lygophis</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1159288)	Parent
121331 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=121331)	NCBI Taxonomy ID	1159289 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1159289)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

SCN8A	Generic Gene Name	A0A1B0Z7F2 (http://www.uniprot.org/uniprot/A0A1B0Z7F2)	UniProtKB <i>Lygophis anomalus</i>
-	Synonyms	0	GenebankID or UniProtKB
-	String		
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:0001518 : voltage-gated sodium channel complex
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0001518>)

Presumptive Null

No ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null+No))

Molecular Type

Coding ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type+Coding))

Aberration Type

SNP ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type+SNP))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

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

Experimental Evidence

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

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

Main Reference

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

Authors

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

Abstract

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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation