

SCN9A (Nav1.7) (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~SCN9A (Nav1.7)*#gephebase-summary-title)	Gephebase Gene	GP00001643	GepheID
Published	Entry Status	Prigent	Main curator

Physiology (#Physiology ^#gephebase-summary-title)		Trait Category	
Xenobiotic resistance (TTX) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (TTX)^#gephebase-summary-title)		Trait	
TTX-Sensitive <i>Anolis carolinensis</i>		Trait State in Taxon A	
TTX-Resistant <i>Ramphotyphlops bituberculatus</i>		Trait State in Taxon B	
Taxon A		Ancestral State	
Interspecific (#Interspecific ^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Anolis carolinensis (#gephebase-summary-title)	Latin Name	Anilius bituberculatus (#gephebase-summary-title)	Latin Name
green anole	Common Name	prong-snouted blind snake	Common Name
green anole; Carolina anole; Anolis carolinensis (Voigt, 1832); UCMZ 53793; UCMZ:53793	Synonyms	Ramphotyphlops bituberculatus; Typhlops bituberculatus; prong-snouted blind snake; Typhlops bituberculatus Peters 1863; ZMB 4723; ZMB:4723	Synonyms
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; Iguania; Dactyloidae; Anolis	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; Typhlopoidea; Typhlopidae; Anilius	Lineage
Anolis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28376)	Parent	Anilius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1539840)	Parent
28377 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28377)	NCBI Taxonomy ID	261707 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=261707)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

SCN9A	Generic Gene Name	Q15858 (http://www.uniprot.org/uniprot/Q15858)	UniProtKB Homo sapiens
PN1; ETHA; NENA; SFNP; FEB3B; NE-NA; GEFSP7; HSAN2D; Nav1.7	Synonyms	0	GenebankID or UniProtKB
9606.ENSPP00000386306 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000386306)	String		
	Sequence Similarities		
Belongs to the sodium channel (TC 1.A.1.10) family. Nav1.7/SCN9A subfamily.			
	GO - Molecular Function		
GO:0031402 : sodium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031402)			
GO:0005244 : voltage-gated ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005244)			
GO:0005248 : voltage-gated sodium channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005248)			

GO - Biological Process

GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)
GO:0006954 : inflammatory response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0019228 : neuronal action potential (<https://www.ebi.ac.uk/QuickGO/term/GO:0019228>)
GO:0009791 : post-embryonic development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009791>)
GO:0019233 : sensory perception of pain (<https://www.ebi.ac.uk/QuickGO/term/GO:0019233>)
GO:0034765 : regulation of ion transmembrane transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0034765>)
GO:0086010 : membrane depolarization during action potential (<https://www.ebi.ac.uk/QuickGO/term/GO:0086010>)
GO:0035725 : sodium ion transmembrane transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0035725>)
GO:0048266 : behavioral response to pain (<https://www.ebi.ac.uk/QuickGO/term/GO:0048266>)
GO:0009636 : response to toxic substance (<https://www.ebi.ac.uk/QuickGO/term/GO:0009636>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005887 : integral component of plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0030424 : axon (<https://www.ebi.ac.uk/QuickGO/term/GO:0030424>)
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
M1392A in DIII domain (not tested)	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; Geffkeney SL; Hanifin CT; Toledo G; Vonk FJ; Richardson MK; Brodie ED; Pfreder 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 ~170 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
2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~SCN9A (Nav1.7)~/and+Taxon ID=~28377~/or+Gene Gephebase=~SCN9A (Nav1.7)~/and+Taxon ID=~261707~#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation