

GEPHE SUMMARY

SCN9A (Nav1.7) (#https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+SCN9A+Nav1.7) Gephebase=^SCN9A (Nav1.7)^#gephebase-summary-title	Gephebase Gene	GP00001649	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology)	Trait Category		
Xenobiotic resistance (TTX) (#https://www.gephebase.org/search-criteria?/and+Trait+Xenobiotic+resistance+TTX)	Trait		
TTX-Sensitive <i>Ophisaurus gracilis</i>	Trait State in Taxon A		
TTX-Resistant <i>Anolis carolinensis</i>	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Interspecific)	Taxonomic Status		
	Taxon A	Taxon B	
<i>Dopasia gracilis</i> (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Dopasia+gracilis)	Latin Name	<i>Anolis carolinensis</i> (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Anolis+carolinensis)	Latin Name
Burmese glass lizard	Common Name	green anole	Common Name
<i>Ophisaurus gracilis</i> ; <i>Pseudopus gracilis</i> ; Burmese glass lizard; <i>Pseudopus gracilis</i> Gray 1845; BMNH 1946.8.29.28; BMNH:1946.8.29.28	Synonyms	green anole; Carolina anole; <i>Anolis carolinensis</i> (Voigt, 1832); UCMZ 53793; UCMZ:53793	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; Anguimorpha; Neoanguimorpha; Anguioidea; Anguinae; <i>Dopasia</i>	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; Iguania; Dactyloidae; <i>Anolis</i>	Lineage
<i>Dopasia</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1469810)	Parent	<i>Anolis</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28376)	Parent
182351 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=182351)	NCBI Taxonomy ID	28377 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28377)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

SCN9A	Generic Gene Name	Q15858 (http://www.uniprot.org/uniprot/Q15858)	UniProtKB Homo sapiens
PN1; ETHA; NENA; SFNP; FEB3B; NE-NA; GEFSP7; HSN2D; Nav1.7	Synonyms	()	GenebankID or UniProtKB
9606.ENSP00000386306 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000386306)	String		
Belongs to the sodium channel (TC 1.A.1.10) family. Nav1.7/SCN9A subfamily.	Sequence Similarities		
GO:0031402 : sodium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031402)	GO - Molecular Function		
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

D1684A (most probably N>A) in DIV domain (150x 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; Geffeny 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 ~ 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.

Abstract

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation