GEPHE SUMMARY

Gephebase Gene

SCN9A (Nav1.7) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SCN9A (Nav1.7)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001644

Main curator

Prigent

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 Anolis carolinensis

Trait State in Taxon B

TTX-Resistant (Henophidia) Boa constrictor & Python molurus

Ancestral State

Taxon A

Taxonomic Status

Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#gephebase-summary-title)

Taxon A

Latin Name

Anolis carolinensis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anolis carolinensis^#gephebase-summary-title)

Common Name

green anole

Synonyms

green anole; Carolina anole; Anolis carolinensis (Voigt, 1832); UCMZ 53793; UCMZ:53793

Rank

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; Iguania; Dactyloidae; Anolis

Parent

Anolis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28376)

NCBI Taxonomy ID

28377 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28377)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Henophidia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Henophidia^#gephebase-summary-title)

Common Name

-

Synonyms

Boidea; Booidea

Rank

superfamily

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

Parent

Serpentes (snakes) - (Rank: infraorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8570)

NCBI Taxonomy ID

34979 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34979)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

SCN9A

Synonyms

PN1; ETHA; NENA; SFNP; FEB3B; NE-NA; GEFSP7; HSAN2D; Nav1.7

String

9606.ENSP00000386306 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000386306)

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)

UniProtKB Homo sapiens

Q15858 (http://www.uniprot.org/uniprot/Q15858)

GenebankID or UniProtKB

()

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)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

M1392T in DIII (15x resistance)

Experimental Evidence

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

	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 â^¼170 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 â^¼38 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.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

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=^34979^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Non-null mutation. According to phylogeny could be parallelism or convergence too