

GEPHE SUMMARY

| | | | |
|--|----------------|------------|--------------|
| SCN8A (Nav1.6) (https://www.gephebase.org/search-criteria?/and+Gene) | Gephebase Gene | GP00001657 | GepheID |
| Gephebase="SCN8A (Nav1.6)"#gephebase-summary-title) | | | Main curator |
| Published | Entry Status | Prigent | |

PHENOTYPIC CHANGE

| | | | |
|--|---|---------|-----------------------------|
| Physiology (https://www.gephebase.org/search-criteria?/and+Trait) | Trait Category | | |
| Category="Physiology"#gephebase-summary-title) | | | |
| Xenobiotic resistance (TTX) (<a (ttx)"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=" resistance="" xenobiotic="">https://www.gephebase.org/search-criteria?/and+Trait="Xenobiotic resistance (TTX)"#gephebase-summary-title) | Trait | | |
| TTX-Sensitive <i>Amphisma pryeri</i> | Trait State in Taxon A | | |
| TTX-Resistant natricine clade (<i>Afronatrix</i> ; <i>Rhabdophis</i> ; <i>Xenocrophis</i>) | Trait State in Taxon B | | |
| Taxon A | Ancestral State | | |
| Intergenic or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic) | Taxonomic Status | | |
| Status="Intergenic or Higher"#gephebase-summary-title) | | | |
| | Taxon A | Taxon B | |
| | Latin Name | | Latin Name |
| <i>Hebius pryeri</i> | Natricinae | | |
| (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Hebius pryeri"#gephebase-summary-title) | (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Natricinae"#gephebase-summary-title) | | |
| | Common Name | | Common Name |
| Pryer's keelback | - | | |
| | Synonyms | | Synonyms |
| <i>Amphisma pryeri</i> ; <i>Tropidonotus pryeri</i> ; Pryer's keelback; <i>Amphisma pryeri</i> (Boulenger, 1887) | Natricidae | | |
| | Rank | | Rank |
| species | subfamily | | |
| | Lineage | | 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; Colubridae; | 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; Colubridae | | |
| <i>Natricinae</i> ; <i>Hebius</i> | Colubridae (colubrid snakes) - (Rank: family) | | Parent |
| | (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8578) | | |
| <i>Hebius</i> () - (Rank: genus) | 169862 | | NCBI Taxonomy ID |
| (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1591003) | (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 169862) | | |
| 1159330 | | | is Taxon B an Intraspecies? |
| (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1159330) | No | | |
| | | | is Taxon A an Intraspecies? |
| No | | | |

GENOTYPIC CHANGE

| | | |
|--|-------------------------|--|
| SCN8A | Generic Gene Name | UniProtKB <i>Afronatrix anoscopus</i> |
| - | Synonyms | A0A1B0Z7B0 (http://www.uniprot.org/uniprot/A0A1B0Z7B0) |
| - | String | 0 |
| - | Sequence Similarities | |
| Belongs to the sodium channel (TC 1.A.1.10) family. | 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: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 (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

V1709I (reversion) in DIV (loss of 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; Geffney SL; Hanifin CT; Toledo G; Vonk FJ; Richardson MK; Brodie ED; Pfreder 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.

Copyright © 2016 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

Related Genes

1 (SCN4A (Nav1.4)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~1159330~/and+Trait=Xenobiotic resistance/or+Taxon ID=~169862~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Non-null mutation