

GEPHE SUMMARY

| | | |
|---|----------------|--------------|
| | Gephebase Gene | GephelD |
| SCN8A (Nav1.6) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SCN8A (Nav1.6)^#gephebase-summary-title) | GP00001652 | Main curator |
| | Entry Status | Prigent |
| Published | | |

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 Other Viperidae (<i>Protobothrops flavoviridis</i>) | Trait State in Taxon B |
| TTX-Resistant Viperidae (<i>Agkistrodon contortrix</i> & <i>Crotalus scutulatus</i>) | Ancestral State |
| Taxon A | Taxonomic Status |

| Taxon A | Latin Name | Taxon B | Latin Name |
|--|-----------------------------|---|-----------------------------|
| <i>Protobothrops flavoviridis</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Protobothrops+flavoviridis^#gephebase-summary-title) | Common Name | <i>Viperidae</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Viperidae^#gephebase-summary-title) | Common Name |
| - | Synonyms | - | Synonyms |
| <i>Bothrops flavoviridis</i> ; <i>Trimeresurus flavoviridis</i> ; <i>habu</i> ; <i>Bothrops flavoviridis</i> Hallowell 1861 | Rank | - | Rank |
| species | Lineage | family | 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; Viperidae; Crotalinae; <i>Protobothrops</i> | Parent | 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 | Parent |
| <i>Protobothrops</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 103943) | NCBI Taxonomy ID | Colubroidea () - (Rank: superfamily) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34989) | NCBI Taxonomy ID |
| 88087 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 88087) | | 8689 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8689) | is Taxon B an Infraspecies? |
| No | is Taxon A an Infraspecies? | No | |

GENOTYPIC CHANGE

| | | |
|--|-------------------------|--|
| SCN8A | Generic Gene Name | UniProtKB <i>Agkistrodon contortrix</i> |
| - | Synonyms | A0A1BoZ7A5 (http://www.uniprot.org/uniprot/A0A1BoZ7A5) |
| - | String | GenebankID or UniProtKB |
| - | Sequence Similarities | 0 |
| - | GO - Molecular Function | |
| GO:0005216 : ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005216) | GO - Biological Process | |
| - | GO - Cellular Component | |
| GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021) | | Presumptive Null |
| No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title) | | |

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%5BCoding%5D#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%5BCoding%5D#gephebase-summary-title))

Molecular Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%5BSNP%5D#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%5BSNP%5D#gephebase-summary-title))

Aberration Type

Nonsynonymous

Molecular Details of the Mutation

I1709V in DIV (2x resistance)

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%5BCandidate Gene%5D#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%5BCandidate%20Gene%5D#gephebase-summary-title))

| 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; Geffeney 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 ~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

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Non-null mutation