

GEPHE SUMMARY

	Gephebase Gene		GepheID
Nav1.7 sodium channel (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] Nav1.7 sodium channel [^] #gephebase-summary-title)		GP00000736	Main curator
Published	Entry Status	Courtier	

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		
Thamnophis sirtalis - sensitive			
	Trait State in Taxon B		
Thamnophis sirtalis - resistant - Willow creek			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Intraspecific [^] #gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Thamnophis sirtalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Thamnophis sirtalis [^] #gephebase-summary-title)		Thamnophis sirtalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Thamnophis sirtalis [^] #gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
FMNH 73660; FMNH:73660		FMNH 73660; FMNH:73660	
	Rank		Rank
species		species	
	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; Natricinae; Thamnophis		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; Natricinae; Thamnophis	
	Parent		Parent
Thamnophis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34999)		Thamnophis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34999)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
35019 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35019)		35019 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35019)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
SCN9A		Q15858 (http://www.uniprot.org/uniprot/Q15858)	GenebankID or UniProtKB
	Synonyms		
PN1; ETHA; NENA; SFNP; FEB3B; NE-NA; GEFSP7; HSN2D; 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>)
 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>)

Mutation #1

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

Asp1393Glu + Ala1681Gly + Asp1684Asn + Gly1685Tyr Molecular Details of the Mutation

The Asp→Glu substitution has been previously described in Nav1.4 from two snake species, the resistant *Th. atratus* (Feldman et al. 2009) and the putatively resistant *Amphispma pryeri* (Feldman et al. 2012) and replacements at this site lead to minor changes in TTX-binding affinity (Terlau et al. 1991; Choudhary et al. 2003) but this specific replacement has not been empirically tested for its effects on TTX binding.

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	Asp	Glu	1393

Parallel evolution of tetrodotoxin resistance in three voltage-gated sodium channel genes in the garter snake *Thamnophis sirtalis*. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25135948>) Main Reference

McGlothlin JW; Chuckalovcak JP; Janes DE; Edwards SV; Feldman CR; Brodie ED; Pfrender ME; Brodie ED Authors

Members of a gene family expressed in a single species often experience common selection pressures. Consequently, the molecular basis of complex adaptations may be expected to involve parallel evolutionary changes in multiple paralogs. Here, we use bacterial artificial chromosome library scans to investigate the evolution of the voltage-gated sodium channel (Nav) family in the garter snake *Thamnophis sirtalis*, a predator of highly toxic *Taricha* newts. Newts possess tetrodotoxin (TTX), which blocks Nav's, arresting action potentials in nerves and muscle. Some *Thamnophis* populations have evolved resistance to extremely high levels of TTX. Previous work has identified amino acid sites in the skeletal muscle sodium channel Nav1.4 that confer resistance to TTX and vary across populations. We identify parallel evolution of TTX resistance in two additional Nav paralogs, Nav1.6 and 1.7, which are known to be expressed in the peripheral nervous system and should thus be exposed to ingested TTX. Each paralog contains at least one TTX-resistant substitution identical to a substitution previously identified in Nav1.4. These sites are fixed across populations, suggesting that the resistant peripheral nerves antedate resistant muscle. In contrast, three sodium channels expressed solely in the central nervous system (Nav1.1-1.3) showed no evidence of TTX resistance, consistent with protection from toxins by the blood-brain barrier. We also report the exon-intron structure of six Nav paralogs, the first such analysis for snake genes. Our results demonstrate that the molecular basis of adaptation may be both repeatable across members of a gene family and predictable based on functional considerations.

Abstract

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Mutation #2

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

Aberration Type 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

Asp1393Glu + Ala1681Gly + Asp1684Asn + Gly1685Tyr

- The Ala→Gly substitution occurs at the channel's selectivity filter, and is also found in four different paralogs in TTX-bearing pufferfishes, where it provides 1.5-fold resistance to TTX and 11-fold resistance to saxitoxin (Jost et al. 2008). Despite its location, this substitution does not affect ion selectivity, but delays recovery from slow inactivation (Wu et al. 2013), suggesting the possibility that it evolved to compensate for other changes to the channel's pore.

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	Ala	Gly	1681

Main Reference

Parallel evolution of tetrodotoxin resistance in three voltage-gated sodium channel genes in the garter snake *Thamnophis sirtalis*. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25135948>)

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Additional References

Mutation #3

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

Asp1393Glu + Ala1681Gly + Asp1684Asn + Gly1685Tyr

- The Asp→Asn substitution occurs in a highly TTX-resistant (600X) isoform of Nav1.4 found in California *Th. sirtalis* (Geffeney et al. 2005) and on its own should confer approximately 30- to 40-fold resistance to TTX (Penzotti et al. 1998; Choudhary et al. 2003).

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	Asp	Asn	1684

Main Reference

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Mutation #4

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

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

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

Nonsynonymous SNP Coding Change

Asp1393Glu + Ala1681Gly + Asp1684Asn + Gly1685Tyr Molecular Details of the Mutation
 - The Gly→Tyr substitution is previously undescribed and untested but substitutions in this location are often found in TTX-resistant species (Geffeney et al. 2005; Jost et al. 2008; Feldman et al. 2012). This residue is located in the outer portion of the pore, and the replacement of glycine's hydrogen with tyrosine's large aromatic side chain may conceivably interfere with the ability of TTX to access its binding site in the pore.

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Gly	Tyr	1685

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RELATED GEPHE

2 (Nav1.6 sodium channel, SCN4A (Nav1.4)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID="35019"/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon ID=)) Related Genes

No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect

