

GEPHE SUMMARY

CHRNA1 (<https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^CHRNA1^#gephebase-summary-title>)

Gephebase Gene: GP00001720

Entry Status: Courtier

Published

GepheID: Main curator

PHENOTYPIC CHANGE

Physiology (<https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title>)

Trait Category

Xenobiotic resistance (snake venom) ([https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+\(snake+venom\)^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(snake+venom)^#gephebase-summary-title))

Trait

Other Carnivora

Trait State in Taxon A

Resistance to Erabu Sea Snake (Laticauda semifasciata) - Egyptian cobra

Trait State in Taxon B

Taxon A

Ancestral State

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

Taxonomic Status

Taxon A	Latin Name	Taxon B	Latin Name
Carnivora (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Carnivora^#gephebase-summary-title)	Naja haje (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Naja+haje^#gephebase-summary-title)		
carnivores	Common Name	-	Common Name
carnivores	Synonyms	ZMB 2820; ZMB:2820	Synonyms
order	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria	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; Elapidae; Elapinae; Naja	Lineage
Laurasiatheria () - (Rank: superorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=314145)	Parent	Naja () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8638)	Parent
33554 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33554)	NCBI Taxonomy ID	8639 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8639)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

CHRNA1

Generic Gene Name: P02708 (<http://www.uniprot.org/uniprot/P02708>)

ACHRA; ACHRD; CHRNA; CMS1A; CMS1B; CMS2A; FCCMS; SCCMS; CHNRA

Synonyms: ()

String: 9606.ENSP00000261007
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000261007)

Sequence Similarities: Belongs to the ligand-gated ion channel (TC 1.A.9) family. Acetylcholine receptor (TC 1.A.9.1) subfamily. Alpha-1/CHRNA1 sub-subfamily.

GO - Molecular Function: GO:0042166 : acetylcholine binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0042166>)
GO:0015464 : acetylcholine receptor activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0015464>)
GO:0022848 : acetylcholine-gated cation-selective channel activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0022848>)

UniProtKB Homo sapiens

GenebankID or UniProtKB

GO:0005216 : ion channel activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0005216>)
 GO:1904315 : transmitter-gated ion channel activity involved in regulation of postsynaptic membrane potential (<https://www.ebi.ac.uk/QuickGO/term/GO:1904315>)

GO - Biological Process

GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
 GO:0007268 : chemical synaptic transmission (<https://www.ebi.ac.uk/QuickGO/term/GO:0007268>)
 GO:0007271 : synaptic transmission, cholinergic (<https://www.ebi.ac.uk/QuickGO/term/GO:0007271>)
 GO:0034220 : ion transmembrane transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0034220>)
 GO:0046716 : muscle cell cellular homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0046716>)
 GO:0050881 : musculoskeletal movement (<https://www.ebi.ac.uk/QuickGO/term/GO:0050881>)
 GO:0050877 : nervous system process (<https://www.ebi.ac.uk/QuickGO/term/GO:0050877>)
 GO:0007528 : neuromuscular junction development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007528>)
 GO:0050905 : neuromuscular process (<https://www.ebi.ac.uk/QuickGO/term/GO:0050905>)
 GO:0007274 : neuromuscular synaptic transmission (<https://www.ebi.ac.uk/QuickGO/term/GO:0007274>)
 GO:0070050 : neuron cellular homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0070050>)
 GO:0019228 : neuronal action potential (<https://www.ebi.ac.uk/QuickGO/term/GO:0019228>)
 GO:0042391 : regulation of membrane potential (<https://www.ebi.ac.uk/QuickGO/term/GO:0042391>)
 GO:0035094 : response to nicotine (<https://www.ebi.ac.uk/QuickGO/term/GO:0035094>)
 GO:0003009 : skeletal muscle contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0003009>)
 GO:0048630 : skeletal muscle tissue growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0048630>)

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:0030054 : cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0030054>)
 GO:0043005 : neuron projection (<https://www.ebi.ac.uk/QuickGO/term/GO:0043005>)
 GO:0045211 : postsynaptic membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0045211>)
 GO:0045202 : synapse (<https://www.ebi.ac.uk/QuickGO/term/GO:0045202>)
 GO:0005892 : acetylcholine-gated channel complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0005892>)
 GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
 GO:0099060 : integral component of postsynaptic specialization membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0099060>)
 GO:0031594 : neuromuscular junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0031594>)

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

Phe189Asn - The inhibitory effect on the pharmacological action of the toxin is primarily attributed to the presence of glycosylation at position N189.

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	Phe	Asn	189

Main Reference

Cobra (*Naja* spp.) nicotinic acetylcholine receptor exhibits resistance to Erabu sea snake (*Laticauda semifasciata*) short-chain alpha-neurotoxin. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15170255>)

Authors

Takacs Z; Wilhelmsen KC; Sorota S

Abstract

Snake alpha-neurotoxins of Elapidae venoms are grouped into two structural classes, short-chain and long-chain alpha-neurotoxins. While these two classes share many chemical and biological characteristics, there are also distinct dissimilarities between them, including their binding site on the nicotinic acetylcholine receptor (nAChR), specificity among species of Chordata, and the

associated pharmacological effects. In the present study we test the hypothesis that structural motifs that evolved to confer natural resistance against conspecific long-chain alpha-neurotoxins in Elapidae snakes also interfere with the biological action of short-chain alpha-neurotoxins. We expressed functional nAChRs that contains segments or single residues of the Elapidae nAChR ligand binding domain and tested the effect of short-chain alpha-neurotoxin erabutoxin-a (ETX-a) from the Erabu sea snake *Laticauda semifasciata* on the acetylcholine-induced currents as measured by two-microelectrode voltage clamp. Our results show that the Elapidae nAChR alpha subunit segment T(154)-L(208) ligand binding domain has an inhibitory effect on the pharmacological action of ETX-a. This effect is primarily attributed to the presence of glycosylation at position N(189). If the glycosylation is removed from the T(154)-L(208) segment, the nAChR will be inhibited, however, to a lesser extent than seen in the mouse. This effect correlates with the variations in alpha-neurotoxin sensitivity of different species and, importantly, reflects the evolutionary conservation of the binding site on the nAChR polypeptide backbone per se. Phylogenetic analysis of alpha-neurotoxin resistance suggests that alpha-neurotoxin-resistant nAChR evolved first, which permitted the evolution of snake venom alpha-neurotoxins. A model describing alpha-neurotoxin resistance in Elapidae snakes is presented.

[Additional References](#)

RELATED GEPHE

No matches found.

[Related Genes](#)

4 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~CHRNA1~/and+Taxon+ID=~33554~/or+Gene+Gephebase=~CHRNA1~/and+Taxon+ID=~8639~#gephebase-summary-title>)

[Related Haplotypes](#)

EXTERNAL LINKS

COMMENTS