GEPHE SUMMARY

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

GepheID
GP00001721

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Other Carnivora

Trait State in Taxon B
domestic pig - looks like resistant to venom - domestic pigs can prey on a variety of venomous snakes and survive snakebite

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

Common Name
carnivores

Synonyms
carnivores

Rank
order

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria

Parent
Laurasiatheria () - (Rank: superorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 314145)

NCBI Taxonomy ID
33554 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33554)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
pig

Synonyms
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofus

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus

Parent
Sus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9822)

NCBI Taxonomy ID
9823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
CHRNA1

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

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
P02708 (http://www.uniprot.org/uniprot/P02708)

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)

Mutation #1

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

W187R

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	Trp	Arg	187

Main Reference

Why the honey badger don't care: Convergent evolution of venom-targeted nicotinic acetylcholine receptors in mammals that survive venomous snake bites. (2015) (https://pubmed.ncbi.nlm.nih.gov/25796346)

Authors

Drabeck DH; Dean AM; Jansa SA

Abstract

Honey badgers (Mellivora capensis) prey upon and survive bites from venomous snakes (Family: Elapidae), but the molecular basis of their venom resistance is unknown. The muscular nicotinic cholinergic receptor (nAChR), targeted by snake Î±-neurotoxins, has evolved in some venom-resistant mammals to no longer bind these toxins. Through phylogenetic analysis of mammalian nAChR sequences, we show that honey badgers, hedgehogs, and pigs have independently acquired functionally equivalent amino acid replacements in the toxin-binding site of this receptor. These convergent amino acid changes impede toxin binding by introducing a positively charged amino acid in place of an uncharged aromatic residue. In venom-resistant mongooses, different replacements at these same sites are glycosylated, which is thought to disrupt binding through steric effects. Thus, it appears that resistance to snake venom Î±-neurotoxin has evolved at least four times among mammals through two distinct biochemical mechanisms operating at the same sites on the same receptor.

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Additional References

Mutation #2

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

F189L

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	Leu	189

Main Reference

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

4 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^CHRNA1^/and+Taxon ID=^33554^/or+Gene Gephebase=^CHRNA1^/and+Taxon ID=^9823^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS