GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00000184

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

Mellivora capensis

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

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

Common Name

ratel

Synonyms

ratel; honey badger

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; Carnivora; Caniformia; Mustelidae; Mellivoriane; Mellivora

Parent

Mellivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9663)

NCBI Taxonomy ID

9664 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9664)

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)
GO:0005216 : ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005216)

UniProtKB Homo sapiens

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

GenebankID or UniProtKB

()

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

Trp187Arg + Phe189Leu

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.

Copyright Â© 2015 Elsevier Ltd. All rights reserved.

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

Trp187Arg + Phe189Leu

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

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.

Copyright Â© 2015 Elsevier Ltd. All rights reserved.

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=^9664^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect ; Parallel changes in a 3rd lineage thought to be venom resistant (pigs)