

GEPHE SUMMARY

Gephebase Gene
CHRNA1

Entry Status
Published

GepheID
GP00000184

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Xenobiotic resistance (snake venom)

Trait State in Taxon A
Other Carnivora

Trait State in Taxon B
Mellivora capensis

Ancestral State
Taxon A

Taxonomic Status
Intergeneric or Higher

Taxon A

Latin Name
Carnivora

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)

NCBI Taxonomy ID
33554

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Mellivora capensis

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; Mellivorinae; Mellivora

Parent
Mellivora () - (Rank: genus)

NCBI Taxonomy ID
9664

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
CHRNA1

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

String
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
GO:0015464 : acetylcholine receptor activity
GO:0022848 : acetylcholine-gated cation-selective channel activity
GO:0005216 : ion channel activity
GO:1904315 : transmitter-gated ion channel activity involved in regulation of postsynaptic membrane potential

GO - Biological Process
GO:0007165 : signal transduction
GO:0007268 : chemical synaptic transmission

UniProtKB Homo sapiens
P02708

GenebankID or UniProtKB

GO:0007271 : synaptic transmission, cholinergic
 GO:0034220 : ion transmembrane transport
 GO:0046716 : muscle cell cellular homeostasis
 GO:0050881 : musculoskeletal movement
 GO:0050877 : nervous system process
 GO:0007528 : neuromuscular junction development
 GO:0050905 : neuromuscular process
 GO:0007274 : neuromuscular synaptic transmission
 GO:0070050 : neuron cellular homeostasis
 GO:0019228 : neuronal action potential
 GO:0042391 : regulation of membrane potential
 GO:0035094 : response to nicotine
 GO:0003009 : skeletal muscle contraction
 GO:0048630 : skeletal muscle tissue growth

GO - Cellular Component

GO:0005886 : plasma membrane
 GO:0005887 : integral component of plasma membrane
 GO:0030054 : cell junction
 GO:0043005 : neuron projection
 GO:0045211 : postsynaptic membrane
 GO:0045202 : synapse
 GO:0005892 : acetylcholine-gated channel complex
 GO:0009986 : cell surface
 GO:0099060 : integral component of postsynaptic specialization membrane
 GO:0031594 : neuromuscular junction

Mutation #1

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Trp187Arg + Phe189Leu

Experimental Evidence

Candidate Gene

	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)

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 α -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 α -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

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Trp187Arg + Phe189Leu

Experimental Evidence

Candidate Gene

	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

COMMENTS

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