

GEPHE SUMMARY

CHRNA1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^CHRNA1^#gephebase-summary-title)	Gephebase Gene	GP00000184	GepheID
Published	Entry Status	Courtier	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)	Trait		
Other Carnivora	Trait State in Taxon A		
Mellivora capensis	Trait State in Taxon B		
Taxon A	Ancestral State		
Intergenic or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intergenic+or+Higher^#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Carnivora (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Carnivora^#gephebase-summary-title)	Latin Name	Mellivora capensis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Mellivora+capensis^#gephebase-summary-title)	Latin Name
carnivores	Common Name	ratel	Common Name
carnivores	Synonyms	ratel; honey badger	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; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Mustelidae; Mellivoriane; Mellivora	Lineage
Laurasiatheria () - (Rank: superorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=314145)	Parent	Mellivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9663)	Parent
33554 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33554)	NCBI Taxonomy ID	9664 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9664)	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)	UniProtKB Homo sapiens
ACHRA; ACHRD; CHRNA; CMS1A; CMS1B; CMS2A; FCCMS; SCCMS; CHNRA	Synonyms	()	GenebankID or UniProtKB
9606.ENSPO0000261007 (http://string-db.org/newstring_.../show_network_section.pl?identifier=9606.ENSPO0000261007)	String		
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.	Sequence Similarities		
GO:0042166 : acetylcholine binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042166)	GO - Molecular Function		
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)			

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 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

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

Trp187Arg + Phe189Leu

Molecular Details of the Mutation

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	Phe	Leu	189

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Abstract

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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="+9664^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

Related Haplotypes

EXTERNAL LINKS

COMMENTS

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

