

GEPHE SUMMARY

MC1R (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="MC1R">#gephebase-summary-title)	Gephebase Gene	GP00000627	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait		
Coloration (scales) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (scales)#gephebase-summary-title)	Trait State in Taxon A		
Aspidoscelis inornata	Trait State in Taxon B		
Aspidoscelis inornata	Ancestral State		
Data not curated	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific">#gephebase-summary-title)			
Taxon A		Taxon B	
Aspidoscelis inornatus (#gephebase-summary-title)	Latin Name	Aspidoscelis inornatus (#gephebase-summary-title)	Latin Name
Little striped whiptail	Common Name	Little striped whiptail	Common Name
Aspidoscelis inornata; Cnemidophorus inornatus; Little striped whiptail; Cnemidophorus inornatus Baird 1859	Synonyms	Aspidoscelis inornata; Cnemidophorus inornatus; Little striped whiptail; Cnemidophorus inornatus Baird 1859	Synonyms
species	Rank	species	Rank
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; Laterata; Teiioidea; Teiidae; Aspidoscelis; Aspidoscelis sexlineata group	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; Laterata; Teiioidea; Teiidae; Aspidoscelis; Aspidoscelis sexlineata group	Lineage
Aspidoscelis sexlineata group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=212530)	Parent	Aspidoscelis sexlineata group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=212530)	Parent
68352 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=68352)	NCBI Taxonomy ID	68352 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=68352)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

MC1R	Generic Gene Name	UniProtKB Homo sapiens
CMM5; MSH-R; SHEP2; MSHR	Synonyms	GenebankID or UniProtKB
9606.ENSP00000451605 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000451605)	String	AAT90190 (https://www.ncbi.nlm.nih.gov/nuccore/AAT90190)
Belongs to the G-protein coupled receptor 1 family.	Sequence Similarities	
GO:0008528 : G protein-coupled peptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008528)	GO - Molecular Function	
GO:0004977 : melanocortin receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004977)		
GO:0004980 : melanocyte-stimulating hormone receptor activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0004980>)

GO:0031625 : ubiquitin protein ligase binding

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031625>)

GO - Biological Process

GO:0007275 : multicellular organism development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)

GO:0045944 : positive regulation of transcription by RNA polymerase II

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)

GO:0042438 : melanin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042438>)

GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)

GO:0007186 : G protein-coupled receptor signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007186>)

GO:0051897 : positive regulation of protein kinase B signaling

(<https://www.ebi.ac.uk/QuickGO/term/GO:0051897>)

GO:0019233 : sensory perception of pain

(<https://www.ebi.ac.uk/QuickGO/term/GO:0019233>)

GO:0007189 : adenylate cyclase-activating G protein-coupled receptor signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007189>)

GO:0035556 : intracellular signal transduction

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)

GO:0007187 : G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide

second messenger (<https://www.ebi.ac.uk/QuickGO/term/GO:0007187>)

GO:0032720 : negative regulation of tumor necrosis factor production

(<https://www.ebi.ac.uk/QuickGO/term/GO:0032720>)

GO:0010739 : positive regulation of protein kinase A signaling

(<https://www.ebi.ac.uk/QuickGO/term/GO:0010739>)

GO:0090037 : positive regulation of protein kinase C signaling

(<https://www.ebi.ac.uk/QuickGO/term/GO:0090037>)

GO:0009650 : UV protection (<https://www.ebi.ac.uk/QuickGO/term/GO:0009650>)

GO:0070914 : UV-damage excision repair

(<https://www.ebi.ac.uk/QuickGO/term/GO:0070914>)

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>)

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

I170T

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	-	-	-

Main Reference

Adaptive reptile color variation and the evolution of the Mc1r gene. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15446431>)

Authors

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Abstract

The wealth of information on the genetics of pigmentation and the clear fitness consequences of many pigmentation phenotypes provide an opportunity to study the molecular basis of an ecologically important trait. The melanocortin-1 receptor (Mc1r) is responsible for intraspecific color variation in mammals and birds. Here, we study the molecular evolution of Mc1r and investigate its role in adaptive intraspecific color differences in reptiles. We sequenced the complete Mc1r locus in seven phylogenetically diverse squamate species with melanistic or blanched forms associated with different colored substrates or thermal environments. We found that patterns of amino acid substitution across different regions of the receptor are similar to the patterns seen in mammals, suggesting comparable levels of constraint and probably a conserved function for Mc1r in mammals and reptiles. We also found high levels of silent-site heterozygosity in all species, consistent with a high mutation rate or large long-term effective population size. Mc1r polymorphisms were strongly associated with color differences in Holbrookia maculata and Aspidoscelis inornata. In A. inornata, several observations suggest that Mc1r mutations may contribute to differences in color: (1) a strong association is observed between one Mc1r amino acid substitution and dorsal color; (2) no significant population structure was detected among individuals from these populations at the mitochondrial ND4 gene; (3) the distribution of allele frequencies at Mc1r deviates from neutral expectations; and (4) patterns of linkage disequilibrium at Mc1r are consistent with recent selection. This study provides comparative data on a nuclear gene in reptiles and highlights the utility of a candidate-gene approach for understanding the evolution of genes involved in vertebrate adaptation.

Additional References

Molecular and functional basis of phenotypic convergence in white lizards at White Sands. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20080544>)

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS