

GEPHE SUMMARY

ccdc170 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="ccdc170">#gephebase-summary-title)	Gephebase Gene	GP00002363	GephelD
Published	Entry Status	Santos	Main curator

PHENOTYPIC CHANGE

	Trait Category	Trait	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)			
Coloration (#gephebase-summary-title)	Trait State in Taxon A		
Diamond morph	Trait State in Taxon B		
Chevron morph	Ancestral State		
Unknown	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific">#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Anolis sagrei (#gephebase-summary-title")		Anolis sagrei (#gephebase-summary-title")	
Brown anole	Common Name	Brown anole	Common Name
Norops sagrei; Brown anole; Anolis sagrei Dumeril & Bibron, 1837; Anolis sagrei Dumelir & Bibron, 1837; MNHN 2340; MNHN:2340	Synonyms	Norops sagrei; Brown anole; Anolis sagrei Dumeril & Bibron, 1837; Anolis sagrei Dumelir & Bibron, 1837; MNHN 2340; MNHN:2340	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; Toxicofera; Iguania; Dactyloidae; Anolis	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; Toxicofera; Iguania; Dactyloidae; Anolis	Lineage
Anolis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28376)	Parent	Anolis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 28376)	Parent
38937 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38937)	NCBI Taxonomy ID	38937 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 38937)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Ccdc170	Generic Gene Name	D3YXLo (http://www.uniprot.org/uniprot/D3YXLo)	UniProtKB Mus musculus
Gm221	Synonyms	0	GenebankID or UniProtKB
10090.ENSMUSP00000115997 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000115997)	String		
-	Sequence Similarities		
GO:0008017 : microtubule binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008017)	GO - Molecular Function		
GO:0000226 : microtubule cytoskeleton organization (https://www.ebi.ac.uk/QuickGO/term/GO:0000226)	GO - Biological Process		
GO:0005794 : Golgi apparatus (https://www.ebi.ac.uk/QuickGO/term/GO:0005794)	GO - Cellular Component		

GO:0036064 : ciliary basal body (<https://www.ebi.ac.uk/QuickGO/term/GO:0036064>)

Presumptive Null

Unknown ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown))

Molecular Type

Unknown ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Unknown))

Aberration Type

Unknown ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown))

Molecular Details of the Mutation

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Experimental Evidence

Association Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping))

Main Reference

A single locus regulates a female-limited color pattern polymorphism in a reptile. (2022) (<https://pubmed.ncbi.nlm.nih.gov/35263124/>)

Authors

Feiner N; Brun-Usan M; Andrade P; Pranter R; Park S; Menke DB; Geneva AJ; Uller T

Abstract

Animal coloration is often expressed in periodic patterns that can arise from differential cell migration, yet how these processes are regulated remains elusive. We show that a female-limited polymorphism in dorsal patterning (diamond/chevron) in the brown anole is controlled by a single Mendelian locus. This locus contains the gene CCDC170 that is adjacent to, and coexpressed with, the Estrogen receptor-1 gene, explaining why the polymorphism is female limited. CCDC170 is an organizer of the Golgi-microtubule network underlying a cell's ability to migrate, and the two segregating alleles encode structurally different proteins. Our agent-based modeling of skin development demonstrates that, in principle, a change in cell migratory behaviors is sufficient to switch between the two morphs. These results suggest that CCDC170 might have been co-opted as a switch between color patterning morphs, likely by modulating cell migratory behaviors.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS