

## GEPHE SUMMARY

<p>ccdc170 (<a href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=^ccdc170^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+GeneGephebase=^ccdc170^#gephebase-summary-title</a>)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00002363</p> <p>Santos</p>	<p>GepheID</p> <p>Main curator</p>
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## PHENOTYPIC CHANGE

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

<p>Ccdc170</p> <p>Gm221</p> <p>10090.ENSMUSP00000115997 (<a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000115997">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000115997</a>)</p> <p>-</p> <p>GO - Molecular Function</p> <p>GO:0008017 : microtubule binding (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0008017">https://www.ebi.ac.uk/QuickGO/term/GO:0008017</a>)</p> <p>GO - Biological Process</p> <p>GO:0000226 : microtubule cytoskeleton organization (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000226">https://www.ebi.ac.uk/QuickGO/term/GO:0000226</a>)</p> <p>GO - Cellular Component</p> <p>GO:0005794 : Golgi apparatus (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005794">https://www.ebi.ac.uk/QuickGO/term/GO:0005794</a>)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p>	<p>D3YXL0 (<a href="http://www.uniprot.org/uniprot/D3YXL0">http://www.uniprot.org/uniprot/D3YXL0</a>)</p> <p>()</p> <p>UniProtKB Mus musculus</p> <p>GenebankID or UniProtKB</p>
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GO:0036064 : ciliary basal body (<https://www.ebi.ac.uk/QuickGO/term/GO:0036064>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

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Experimental Evidence

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

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

No matches found.

Related Genes

No matches found.

Related Haplotypes

## EXTERNAL LINKS

## COMMENTS