GEPHE SUMMARY

Gephebase Gene

PRKG2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PRKG2^#gephebase-summary-title)

GepheID

GP00002274

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Body size (dwarfism) (https://www.gephebase.org/search-criteria?/and+Trait=^Body size (dwarfism)^#gephebase-summary-title)

Trait State in Taxon A

Angus - normal size

Trait State in Taxon B

Angus - dwarf (recessive)

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)

Common Name

cattle

Synonyms

Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

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; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent

Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID

9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)

Common Name

cattle

Synonyms

Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

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; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent

Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID

9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

PRKG2

Synonyms

PKG2; cGK2; cGKII; PRKGR2

String

9606.ENSP00000264399 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000264399)

Sequence Similarities

Belongs to the protein kinase superfamily. AGC Ser/Thr protein kinase family. cGMP subfamily.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0030553 : cGMP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030553)
GO:0004692 : cGMP-dependent protein kinase activity

UniProtKB Homo sapiens

Q13237 (http://www.uniprot.org/uniprot/Q13237)

GenebankID or UniProtKB

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(https://www.ebi.ac.uk/QuickGO/term/GO:0004692)
GO:0004672 : protein kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004672)

GO - Biological Process

GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0006468 : protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:0072659 : protein localization to plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0072659)
GO:0051186 : cofactor metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0051186)
GO:2001226 : negative regulation of chloride transport
(https://www.ebi.ac.uk/QuickGO/term/GO:2001226)
GO:0036289 : peptidyl-serine autophosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0036289)

GO - Cellular Component

GO:0016324 : apical plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016324)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0031965 : nuclear membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0031965)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#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

Nonsense

Molecular Details of the Mutation

c.2032C>T p.R678*

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Arg	STP	678

Main Reference

A nonsense mutation in cGMP-dependent type II protein kinase (PRKG2) causes dwarfism in American Angus cattle. (2009) (https://pubmed.ncbi.nlm.nih.gov/19887637)

Authors

Koltes JE; Mishra BP; Kumar D; Kataria RS; Totir LR; Fernando RL; Cobbold R; Steffen D; Coppieters W; Georges M; Reecy JM

Abstract

Historically, dwarfism was the major genetic defect in U.S. beef cattle. Aggressive culling and sire testing were used to minimize its prevalence; however, neither of these practices can eliminate a recessive genetic defect. We assembled a 4-generation pedigree to identify the mutation underlying dwarfism in American Angus cattle. An adaptation of the Elston-Steward algorithm was used to overcome small pedigree size and missing genotypes. The dwarfism locus was fine-mapped to BTA6 between markers AFR227 and BM4311. Four candidate genes were sequenced, revealing a nonsense mutation in exon 15 of cGMP-dependant type II protein kinase (PRKG2). This C/T transition introduced a stop codon (R678X) that truncated 85 C-terminal amino acids, including a large portion of the kinase domain. Of the 75 mutations discovered in this region, only this mutation was 100% concordant with the recessive pattern of inheritance in affected and carrier individuals (log of odds score = 6.63). Previous research has shown that PRKG2 regulates SRY (sex-determining region Y) box 9 (SOX9)-mediated transcription of collagen 2 (COL2). We evaluated the ability of wild-type (WT) or R678X PRKG2 to regulate COL2 expression in cell culture. Real-time PCR results confirmed that COL2 is overexpressed in cells that overexpressed R678X PRKG2 as compared with WT PRKG2. Furthermore, COL2 and COL10 mRNA expression was increased in dwarf cattle compared with unaffected cattle. These experiments indicate that the R678X mutation is functional, resulting in a loss of PRKG2 regulation of COL2 and COL10 mRNA expression. Therefore, we present PRKG2 R678X as a causative mutation for dwarfism cattle.

Additional References

RELATED GEPHE

Related Genes

5 (aggrecan, GH, LCORL, PLAG1, RNF11) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9913^/and+Trait=Body size/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^PRKG2^/and+Taxon ID=^9913^/or+Gene Gephebase=^PRKG2^/and+Taxon ID=^9913^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS