

GEPHE SUMMARY

Gephebase Gene
FMN1

Entry Status
Published

GepheID
GP00001662

Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Recombination rate

Trait State in Taxon A
Holstein cattle

Trait State in Taxon B
Holstein cattle

Ancestral State
Unknown

Taxonomic Status
Domesticated

Taxon A

Latin Name
Bos taurus

Common Name
cattle

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

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)

NCBI Taxonomy ID
9913

is Taxon A an Intraspecies?
Yes

Taxon A Description
Holstein cattle

Taxon B

Latin Name
Bos taurus

Common Name
cattle

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

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)

NCBI Taxonomy ID
9913

is Taxon B an Intraspecies?
Yes

Taxon B Description
Holstein cattle

GENOTYPIC CHANGE

Generic Gene Name
FMN1

Synonyms
LD; FMN

String
9606.ENSP00000333950

Sequence Similarities
Belongs to the formin homology family. Cappuccino subfamily.

GO - Molecular Function
GO:0003779 : actin binding
GO:0017124 : SH3 domain binding
GO:0008017 : microtubule binding

GO - Biological Process
GO:0010467 : gene expression
GO:0048705 : skeletal system morphogenesis
GO:0035136 : forelimb morphogenesis

UniProtKB Homo sapiens
Q68DA7

GenebankID or UniProtKB

GO:0035137 : hindlimb morphogenesis
GO:0045010 : actin nucleation
GO:0051127 : positive regulation of actin nucleation
GO:0051894 : positive regulation of focal adhesion assembly
GO:0072092 : ureteric bud invasion

GO - Cellular Component

GO:0005886 : plasma membrane
GO:0005737 : cytoplasm
GO:0005634 : nucleus
GO:0005912 : adherens junction
GO:0005884 : actin filament

Presumptive Null

No

Molecular Type

Unknown

Aberration Type

Unknown

Molecular Details of the Mutation

On chromosome 10. Associated SNP located upstream of the gene

Experimental Evidence

Association Mapping

Main Reference

Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. (2015)

Authors

Ma L; O'Connell JR; VanRaden PM; Shen B; Padhi A; Sun C; Bickhart DM; Cole JB; Null DJ; Liu GE; Da Y; Wiggans GR

Abstract

Meiotic recombination is an essential biological process that generates genetic diversity and ensures proper segregation of chromosomes during meiosis. From a large USDA dairy cattle pedigree with over half a million genotyped animals, we extracted 186,927 three-generation families, identified over 8.5 million maternal and paternal recombination events, and constructed sex-specific recombination maps for 59,309 autosomal SNPs. The recombination map spans for 25.5 Morgans in males and 23.2 Morgans in females, for a total studied region of 2,516 Mb (986 kb/cM in males and 1,085 kb/cM in females). The male map is 10% longer than the female map and the sex difference is most pronounced in the subtelomeric regions. We identified 1,792 male and 1,885 female putative recombination hotspots, with 720 hotspots shared between sexes. These hotspots encompass 3% of the genome but account for 25% of the genome-wide recombination events in both sexes. During the past forty years, males showed a decreasing trend in recombination rate that coincided with the artificial selection for milk production. Sex-specific GWAS analyses identified PRDM9 and CPLX1 to have significant effects on genome-wide recombination rate in both sexes. Two novel loci, NEK9 and REC114, were associated with recombination rate in both sexes, whereas three loci, MSH4, SMC3 and CEP55, affected recombination rate in females only. Among the multiple PRDM9 paralogues on the bovine genome, our GWAS of recombination hotspot usage together with linkage analysis identified the PRDM9 paralogue on chromosome 1 to be associated in the U.S. Holstein data. Given the largest sample size ever reported for such studies, our results reveal new insights into the understanding of cattle and mammalian recombination.

Additional References

RELATED GEPHE

Related Genes

11 (CEP55, CPLX1, GCLM, MSH4, NEK9, PABPN1, PRDM9, REC114, REC8, RNF212, SMC3)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS