

GEPHE SUMMARY

FMN1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+^FMN1^#gephebase-summary-title)	Gephebase Gene	GP00001662	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+^Physiology^#gephebase-summary-title)	Trait Category		
Recombination rate (https://www.gephebase.org/search-criteria?/and+Trait+^Recombination+rate^#gephebase-summary-title)	Trait		
Holstein cattle	Trait State in Taxon A		
Holstein cattle	Trait State in Taxon B		
Unknown	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+^Domesticated^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
	Latin Name		Latin Name
Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Bos+taurus^#gephebase-summary-title)	Latin Name	Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Bos+taurus^#gephebase-summary-title)	Latin Name
cattle	Common Name	cattle	Common Name
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	Synonyms	Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	Synonyms
species	Rank	species	Rank
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	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	Lineage
Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9903)	Parent	Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9903)	Parent
9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9913)	NCBI Taxonomy ID	9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9913)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Holstein cattle	Taxon A Description	Holstein cattle	Taxon B Description

GENOTYPIC CHANGE

FMN1	Generic Gene Name	Q68DA7 (http://www.uniprot.org/uniprot/Q68DA7)	UniProtKB Homo sapiens
LD; FMN	Synonyms	0	GenebankID or UniProtKB
9606.ENSPO0000333950 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSPO0000333950)	String		
Belongs to the formin homology family. Cappuccino subfamily.	Sequence Similarities		
GO:0003779 : actin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003779)	GO - Molecular Function		
GO:0017124 : SH3 domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017124)			
GO:0008017 : microtubule binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008017)			
	GO - Biological Process		

GO:0010467 : gene expression (<https://www.ebi.ac.uk/QuickGO/term/GO:0010467>)
 GO:0048705 : skeletal system morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0048705>)
 GO:0035136 : forelimb morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0035136>)
 GO:0035137 : hindlimb morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0035137>)
 GO:0045010 : actin nucleation (<https://www.ebi.ac.uk/QuickGO/term/GO:0045010>)
 GO:0051127 : positive regulation of actin nucleation
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0051127>)
 GO:0051894 : positive regulation of focal adhesion assembly
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0051894>)
 GO:0072092 : ureteric bud invasion (<https://www.ebi.ac.uk/QuickGO/term/GO:0072092>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
 GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
 GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
 GO:0005912 : adherens junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0005912>)
 GO:0005884 : actin filament (<https://www.ebi.ac.uk/QuickGO/term/GO:0005884>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

Unknown (<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>)

Molecular Details of the Mutation

On chromosome 10. Associated SNP located upstream of the gene

Experimental Evidence

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

Main Reference

Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26540184>)

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) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9913^/and+Trait=Recombination rate/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS