GEPHE SUMMARY

Gephebase Gene
CEP55 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CEP55^#gephebase-summary-title)

GepheID
GP00001667

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Holstein cattle

Trait State in Taxon B
Holstein cattle

Ancestral State
Unknown

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?
Yes

Taxon A Description
Holstein cattle

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?
Yes

Taxon B Description
Holstein cattle

GENOTYPIC CHANGE

Generic Gene Name
CEP55

Synonyms
-

String
9913.ENSBTAP00000006763 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9913.ENSBTAP00000006763)

Sequence Similarities
-

GO - Molecular Function
-

GO - Biological Process
GO:0000281 : mitotic cytokinesis (https://www.ebi.ac.uk/QuickGO/term/GO:0000281)
GO:0014066 : regulation of phosphatidylinositol 3-kinase signaling

UniProtKB Bos taurus
E1B8M0 (http://www.uniprot.org/uniprot/E1B8M0)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0014066)
GO:1904888 : cranial skeletal system development
(https://www.ebi.ac.uk/QuickGO/term/GO:1904888)
GO:0045184 : establishment of protein localization
(https://www.ebi.ac.uk/QuickGO/term/GO:0045184)
GO:0061952 : midbody abscission (https://www.ebi.ac.uk/QuickGO/term/GO:0061952)
GO:0072001 : renal system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0072001)
GO:0000920 : septum digestion after cytokinesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0000920)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0030496 : midbody (https://www.ebi.ac.uk/QuickGO/term/GO:0030496)
GO:0005813 : centrosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005813)
GO:0090543 : Flemming body (https://www.ebi.ac.uk/QuickGO/term/GO:0090543)
GO:0045171 : intercellular bridge (https://www.ebi.ac.uk/QuickGO/term/GO:0045171)

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

Associated SNP located near 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 (CPLX1, FMN1, 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