

GEPHE SUMMARY

| | | | |
|---|----------------|------------|--------------|
| CEP55 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CEP55^#gephebase-summary-title) | Gephebase Gene | GP00001667 | GephelD |
| | Entry Status | Prigent | Main curator |
| Published | | | |

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 | Taxon B | Latin Name |
| Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bos+taurus^#gephebase-summary-title) | | Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bos+taurus^#gephebase-summary-title) | |
| 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 |
| | Lineage | | 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 | | 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 | |
| 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 Infraspecies? | Yes | is Taxon B an Infraspecies? |
| Holstein cattle | Taxon A Description | Holstein cattle | Taxon B Description |

GENOTYPIC CHANGE

| | | |
|---|-------------------------|-------------------------|
| CEP55 | Generic Gene Name | UniProtKB Bos taurus |
| - | Synonyms | GenebankID or UniProtKB |
| 9913.ENSBTAPO00000006763 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9913.ENSBTAPO00000006763) | String | 0 |
| - | 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 | | |

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Associated SNP located near the gene

Experimental Evidence

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

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

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS