GEPHE SUMMARY

Gephebase Gene
MSH4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MSH4^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001665
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
MSH4
Synonyms
-
String
9913.ENSBTAP00000024552 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9913.ENSBTAP00000024552)
Sequence Similarities
Belongs to the DNA mismatch repair MutS family.
GO - Molecular Function
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0008094 : DNA-dependent ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008094)
GO:0003684 : damaged DNA binding

UniProtKB Bos taurus
E1BK76 (http://www.uniprot.org/uniprot/E1BK76)
GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0003684)
GO:0030983 : mismatched DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0030983)

GO - Biological Process

GO:0001541 : ovarian follicle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001541)
GO:0007283 : spermatogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0007283)
GO:0007292 : female gamete generation
(https://www.ebi.ac.uk/QuickGO/term/GO:0007292)
GO:0051026 : chiasma assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0051026)
GO:0007131 : reciprocal meiotic recombination
(https://www.ebi.ac.uk/QuickGO/term/GO:0007131)
GO:0045143 : homologous chromosome segregation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045143)
GO:0006298 : mismatch repair (https://www.ebi.ac.uk/QuickGO/term/GO:0006298)
GO:0000712 : resolution of meiotic recombination intermediates
(https://www.ebi.ac.uk/QuickGO/term/GO:0000712)

GO - Cellular Component

GO:0000228 : nuclear chromosome (https://www.ebi.ac.uk/QuickGO/term/GO:0000228)
GO:0000795 : synaptonemal complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0000795)
GO:0032300 : mismatch repair complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032300)
GO:0032301 : MutSalpha complex (https://www.ebi.ac.uk/QuickGO/term/GO:0032301)
GO:0005713 : recombination nodule (https://www.ebi.ac.uk/QuickGO/term/GO:0005713)

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 3. Associated SNP located in the intron 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, FMN1, GCLM, 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

MSH4 is a meiosis-specific MutS homologue that affects crossing over