

GEPHE SUMMARY

	Gephebase Gene	GephelD
SMC3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SMC3^#gephebase-summary-title)	GP00001666	Main curator
Published	Entry Status	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		Taxon B
Bos taurus	Latin Name	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bos+taurus^#gephebase-summary-title)		
cattle	Common Name	Common Name
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	Synonyms	Synonyms
species	Rank	Rank
Bos (oxen, cattle) - (Rank: genus)	Lineage	Lineage
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)		
9913	NCBI Taxonomy ID	NCBI Taxonomy ID
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Yes	Taxon A Description	Taxon B Description
Holstein cattle	Holstein cattle	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Bos taurus
SMC3		
CSPG6; SMC-3; SMC3L1	Synonyms	GenebankID or UniProtKB
9913.ENSBTAP00000043550 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9913.ENSBTAP00000043550)	String	
Belongs to the SMC family. SMC3 subfamily.	Sequence Similarities	
	GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0070840 : dynein complex binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070840)		
	GO - Biological Process	

GO:0051301 : cell division (<https://www.ebi.ac.uk/QuickGO/term/GO:0051301>)
GO:0051321 : meiotic cell cycle (<https://www.ebi.ac.uk/QuickGO/term/GO:0051321>)
GO:0006281 : DNA repair (<https://www.ebi.ac.uk/QuickGO/term/GO:0006281>)
GO:0051276 : chromosome organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051276>)
GO:0006275 : regulation of DNA replication
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006275>)

GO - Cellular Component

GO:0000775 : chromosome, centromeric region
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000775>)
GO:0000785 : chromatin (<https://www.ebi.ac.uk/QuickGO/term/GO:0000785>)
GO:0016363 : nuclear matrix (<https://www.ebi.ac.uk/QuickGO/term/GO:0016363>)
GO:0030893 : meiotic cohesin complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030893>)
GO:0097431 : mitotic spindle pole (<https://www.ebi.ac.uk/QuickGO/term/GO:0097431>)

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 26. Associated SNP located upstream

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 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 (CEP55, CPLX1, FMN1, GCLM, MSH4, NEK9, PABPN1, PRDM9, REC114, REC8, RNF212) (<https://www.gephebase.org/search-criteria?/or+TaxonID=^9913^/and+Trait=Recombination rate/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

SMC3 encodes a protein related to meiotic chromosomes and synaptonemal complexes