GEPHE SUMMARY

Gephebase Gene
PRDM9 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PRDM9^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001640
Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Recombination rate (male) (https://www.gephebase.org/search-criteria?/and+Trait=^Recombination rate (male)^#gephebase-summary-title)
Trait State in Taxon A
Sperm Crossing-over Rate 1
Trait State in Taxon B
Sperm Crossing-over Rate 2
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
Bulls from the Netherlands and New-Zealand

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
Bulls from the Netherlands and New-Zealand

GENOTYPIC CHANGE

Generic Gene Name
PRDM9
Synonyms
ZNF596
String
-
Sequence Similarities
-
GO - Molecular Function
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0003676 : nucleic acid binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003676)
GO - Biological Process
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO - Cellular Component

UniProtKB Bos taurus
A6QNW2 (http://www.uniprot.org/uniprot/A6QNW2)
GenebankID or UniProtKB
()

-

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

variation in the C-terminal tandem array of Cys2His2 zinc-finger domains: 22 domains > 20 domains decreasing 6-fold Genome wide hot window usage in Crossing Over

Experimental Evidence

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

Main Reference

Genetic variants in REC8, RNF212, and PRDM9 influence male recombination in cattle. (2012) (https://pubmed.ncbi.nlm.nih.gov/22844258)

Authors

Sandor C; Li W; Coppieters W; Druet T; Charlier C; Georges M

Abstract

We use >250,000 cross-over events identified in >10,000 bovine sperm cells to perform an extensive characterization of meiotic recombination in male cattle. We map Quantitative Trait Loci (QTL) influencing genome-wide recombination rate, genome-wide hotspot usage, and locus-specific recombination rate. We fine-map three QTL and present strong evidence that genetic variants in REC8 and RNF212 influence genome-wide recombination rate, while genetic variants in PRDM9 influence genome-wide hotspot usage.

Additional References

RELATED GEPHE

Related Genes

11 (CEP55, CPLX1, FMN1, GCLM, MSH4, NEK9, PABPN1, 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

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^PRDM9^/and+Taxon ID=^9913^/or+Gene Gephebase=^PRDM9^/and+Taxon ID=^9913^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS