

GEPHE SUMMARY

	Gephebase Gene		GepheID
Growth Hormone Receptor (<a +growth+hormone+receptor+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Growth+Hormone+Receptor+"#gephebase-summary-title)	GP00000416		
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Milk yield (<a +milk+yield+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Milk+yield+"#gephebase-summary-title)			
	Trait State in Taxon A		
Bos bovis		Trait State in Taxon B	
Bos bovis			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Bos taurus (<a +bos+taurus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bos+taurus+"#gephebase-summary-title)		Bos taurus (<a +bos+taurus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bos+taurus+"#gephebase-summary-title)	
	Common Name		Common Name
cattle		cattle	
	Synonyms		Synonyms
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus		Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	
	Rank		Rank
species		species	
	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	
	Parent		Parent
Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9903)		Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9903)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9913)		9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9913)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Mus musculus
Ghr		P16882 (http://www.uniprot.org/uniprot/P16882)	
	Synonyms		GenebankID or UniProtKB
GHBP; GHR/BP		AAU94310 (https://www.ncbi.nlm.nih.gov/nuccore/AAU94310)	
	String		
10090.ENSMUSP00000069457 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000069457)			
	Sequence Similarities		
Belongs to the type I cytokine receptor family. Type 1 subfamily.			
	GO - Molecular Function		
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)			
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)			
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)			
GO:0017046 : peptide hormone binding			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0017046>)
GO:0019903 : protein phosphatase binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019903>)
GO:0019955 : cytokine binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019955>)
GO:0004896 : cytokine receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004896>)
GO:0019838 : growth factor binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019838>)
GO:0004903 : growth hormone receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004903>)
GO:0042169 : SH2 domain binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0042169>)

GO - Biological Process

GO:0009755 : hormone-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009755>)
GO:1901215 : negative regulation of neuron death
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901215>)
GO:0050731 : positive regulation of peptidyl-tyrosine phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050731>)
GO:0032870 : cellular response to hormone stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032870>)
GO:0032355 : response to estradiol (<https://www.ebi.ac.uk/QuickGO/term/GO:0032355>)
GO:0040014 : regulation of multicellular organism growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0040014>)
GO:0006897 : endocytosis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006897>)
GO:0048009 : insulin-like growth factor receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048009>)
GO:0006631 : fatty acid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006631>)
GO:0040018 : positive regulation of multicellular organism growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0040018>)
GO:0006103 : 2-oxoglutarate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006103>)
GO:0042976 : activation of Janus kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042976>)
GO:0000187 : activation of MAPK activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000187>)
GO:0000255 : allantoin metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000255>)
GO:0006101 : citrate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006101>)
GO:0006600 : creatine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006600>)
GO:0046449 : creatinine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046449>)
GO:0060396 : growth hormone receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060396>)
GO:0042445 : hormone metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042445>)
GO:0006549 : isoleucine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006549>)
GO:0007259 : JAK-STAT cascade (<https://www.ebi.ac.uk/QuickGO/term/GO:0007259>)
GO:0006107 : oxaloacetate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006107>)
GO:0046427 : positive regulation of JAK-STAT cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046427>)
GO:0006105 : succinate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006105>)
GO:0019530 : taurine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019530>)
GO:0006573 : valine metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006573>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0043235 : receptor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0043235>)
GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)
GO:0043025 : neuronal cell body (<https://www.ebi.ac.uk/QuickGO/term/GO:0043025>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
GO:0036464 : cytoplasmic ribonucleoprotein granule
(<https://www.ebi.ac.uk/QuickGO/term/GO:0036464>)
GO:0009897 : external side of plasma membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009897>)
GO:0070195 : growth hormone receptor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070195>)
GO:0019898 : extrinsic component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019898>)

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

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

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title>)

Nonsynonymous

Phe279Tyr

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

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

The role of the bovine growth hormone receptor and prolactin receptor genes in milk, fat and protein production in Finnish Ayrshire dairy cattle. (2006)
(<https://pubmed.ncbi.nlm.nih.gov/16751675>)

Viitala S; Szyda J; Blott S; Schulman N; Lidauer M; Mäntä-Tanila A; Georges M; Vilkki J

Main Reference

Authors

Abstract

We herein report new evidence that the QTL effect on chromosome 20 in Finnish Ayrshire can be explained by variation in two distinct genes, growth hormone receptor (GHR) and prolactin receptor (PRLR). In a previous study in Holstein-Friesian dairy cattle an F279Y polymorphism in the transmembrane domain of GHR was found to be associated with an effect on milk yield and composition. The result of our multimarker regression analysis suggests that in Finnish Ayrshire two QTL segregate on the chromosomal region including GHR and PRLR. By sequencing the coding sequences of GHR and PRLR and the sequence of three GHR promoters from the pooled samples of individuals of known QTL genotype, we identified two substitutions that were associated with milk production traits: the previously reported F-to-Y substitution in the transmembrane domain of GHR and an S-to-N substitution in the signal peptide of PRLR. The results provide strong evidence that the effect of PRLR S18N polymorphism is distinct from the GHR F279Y effect. In particular, the GHR F279Y has the highest influence on protein percentage and fat percentage while PRLR S18N markedly influences protein and fat yield. Furthermore, an interaction between the two loci is suggested.

Additional References

The F279Y polymorphism of the GHR gene and its relation to milk production and somatic cell score in German Holstein dairy cattle. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21660490>)

RELATED GEPHE

2 (ABCG2, Prolactin receptor) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~9913~/and+Trait=Milk yield/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS