

GEPHE SUMMARY

RXFP2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="RXFP2">#gephebase-summary-title)	Gephebase Gene	GP00001019	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Horns absence (https://www.gephebase.org/search-criteria?/and+Trait=^Horns absence="#gephebase-summary-title")	Trait State in Taxon A
Ovis aries	Trait State in Taxon B
Ovis aries	

Trait #2	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology">#gephebase-summary-title)	Trait
Somatic sex change (https://www.gephebase.org/search-criteria?/and+Trait=^Somatic%20sex%20change #gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

Data not curated	Ancestral State	
	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Domesticated">#gephebase-summary-title)		
Taxon A	Latin Name	Taxon B
Ovis aries (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Ovis aries="#gephebase-summary-title)		Latin Name
sheep	Common Name	
Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries Linnaeus, 1758	Synonyms	
species	Rank	
	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; Caprinae; Ovis		
Ovis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9935)	Parent	
9940 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9940)	NCBI Taxonomy ID	NCBI Taxonomy ID
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
No		

GENOTYPIC CHANGE

RXFP2	Generic Gene Name	UniProt Homo sapiens
LGR8; GREAT; GPR106; INSL3R; LGR8.1; RXFPR2	Synonyms	GenebankID or UniProtKB
9606.ENSP00000298386 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000298386)	String	AGS77194 (https://www.ncbi.nlm.nih.gov/nuccore/AGS77194)
Belongs to the G-protein coupled receptor 1 family.	Sequence Similarities	
GO:0017046 : peptide hormone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017046)	GO - Molecular Function	
GO:0008528 : G protein-coupled peptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008528)		
GO:0016500 : protein-hormone receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016500)		
GO:0043066 : negative regulation of apoptotic process (https://www.ebi.ac.uk/QuickGO/term/GO:0043066)	GO - Biological Process	
GO:0009755 : hormone-mediated signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0009755)		
GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)		
GO:0008584 : male gonad development (https://www.ebi.ac.uk/QuickGO/term/GO:0008584)		
GO:0008285 : negative regulation of cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008285)		
GO:0043950 : positive regulation of cAMP-mediated signaling (https://www.ebi.ac.uk/QuickGO/term/GO:0043950)		
GO:0007189 : adenylate cyclase-activating G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007189)		
GO:0007193 : adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007193)		
GO:0007190 : activation of adenylate cyclase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0007190)		
GO:0001556 : oocyte maturation (https://www.ebi.ac.uk/QuickGO/term/GO:0001556)	GO - Cellular Component	
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)		Presumptive Null
GO:0005887 : integral component of plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005887)		
No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)		Molecular Type
Gene Amplification (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Amplification%#gephebase-summary-title)		Aberration Type
Insertion (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Insertion%#gephebase-summary-title)		Insertion Size
1-10 kb		
1833-bp genomic insertion located in the 3'-UTR region of RXFP2		Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Linkage+Mapping%#gephebase-summary-title)		Experimental Evidence
Life history trade-offs at a single locus maintain sexually selected genetic variation. (2013) (https://pubmed.ncbi.nlm.nih.gov/23965625)		Main Reference
Johnston SE; Gratten J; Berenos C; Pilkington JG; Clutton-Brock TH; Pemberton JM; Slate J		Authors
Sexual selection, through intra-male competition or female choice, is assumed to be a source of strong and sustained directional selection in the wild. In the presence of such strong directional selection, alleles enhancing a particular trait are predicted to become fixed within a population, leading to a decrease in the underlying genetic variation. However, there is often considerable genetic variation underlying sexually selected traits in wild populations, and consequently, this phenomenon has become a long-discussed issue in the field of evolutionary biology. In wild Soay sheep, large horns confer an advantage in strong intra-sexual competition, yet males show an inherited polymorphism for horn type and have substantial genetic variation in their horn size. Here we show that most genetic variation in this trait is maintained by a trade-off between natural and sexual selection at a single gene, relaxin-like receptor 2 (RXFP2). We found that an allele conferring larger horns, Ho(+), is associated with higher reproductive success, whereas a smaller horn allele, Ho(P), confers increased survival, resulting in a net effect of overdominance (that is, heterozygote advantage) for fitness at RXFP2. The nature of this trade-off is simple relative to commonly proposed explanations for the maintenance of sexually selected traits, such as genic capture ('good genes') and sexually antagonistic selection. Our results demonstrate that by identifying the genetic architecture of trait variation, we can determine the principal mechanisms maintaining genetic variation in traits under strong selection and explain apparently counter-evolutionary observations.	Abstract	
A 1.8-kb insertion in the 3'-UTR of RXFP2 is associated with polledness in sheep. (2015) (https://pubmed.ncbi.nlm.nih.gov/26103004)		Additional References

RELATED GEPHE

No matches found.

Related Genes

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

<https://omia.org/OMIA000483/9940/>