

tyrosinase-related protein 1 (TYRP1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~tyrosinase-related+protein+1+(TYRP1)^#gephebase-summary-title)	Gephebase Gene	GP00002237	GepheID
Published	Entry Status	Martin	Main curator

Trait Category		Trait		Trait State in Taxon A		Trait State in Taxon B		Ancestral State		Taxonomic Status	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)		Coloration (coat) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+coat^#gephebase-summary-title)		darker Merino fiber		lighter Awassi fiber		Taxon A		Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	
Taxon A		Taxon B		Taxon A		Taxon B		Taxon A		Taxon B	
Ovis aries (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Ovis+aries^#gephebase-summary-title)		Ovis aries (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Ovis+aries^#gephebase-summary-title)		sheep		sheep		Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries Linnaeus, 1758		Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries Linnaeus, 1758	
Common Name		Common Name		Synonyms		Synonyms		Rank		Rank	
species		species		Lineage		Lineage		Parent		Parent	
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		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)		Ovis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9935)		NCBI Taxonomy ID		NCBI Taxonomy ID	
9940 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940)		9940 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940)		is Taxon A an Infrapopulation?		is Taxon B an Infrapopulation?		No		No	

	Generic Gene Name	UniProtKB Mus musculus
Tyrp1		P07147 (http://www.uniprot.org/uniprot/P07147)
	Synonyms	GenebankID or UniProtKB
b; isa; Oca3; TRP1; Tyrp; TRP-1; brown; Tyrp-1		ABG76825 (https://www.ncbi.nlm.nih.gov/nucore/ABG76825)
	String	
10090.ENSMUSP00000006151 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000006151)		
	Sequence Similarities	
Belongs to the tyrosinase family.		
	GO - Molecular Function	
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)		
GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		

GO:0004497 : monooxygenase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004497>)

GO - Biological Process

GO:0032438 : melanosome organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032438>)
GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)
GO:0048023 : positive regulation of melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048023>)
GO:0006583 : melanin biosynthetic process from tyrosine
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006583>)
GO:0030318 : melanocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030318>)
GO:0043438 : acetoacetic acid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043438>)
GO:0006582 : melanin metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006582>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0030669 : clathrin-coated endocytic vesicle membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030669>)
GO:0010008 : endosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010008>)
GO:0042470 : melanosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0042470>)
GO:0033162 : melanosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033162>)

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

c.2240C>G p.A746V

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	Ala	Val	746

Main Reference

QTL and association analysis for skin and fibre pigmentation in sheep provides evidence of a major causative mutation and epistatic effects. (2013)
(<https://pubmed.ncbi.nlm.nih.gov/23451726>)

Authors

Raadsma HW; Jonas E; Fleet MR; Fullard K; Gongora J; Cavanagh CR; Tammen I; Thomson PC

Abstract

The pursuits of white features and white fleeces free of pigmented fibre have been important selection objectives for many sheep breeds. The cause and inheritance of non-white colour patterns in sheep has been studied since the early 19th century. Discovery of genetic causes, especially those which predispose pigmentation in white sheep, may lead to more accurate selection tools for improved apparel wool. This article describes an extended QTL study for 13 skin and fibre pigmentation traits in sheep. A total of 19 highly significant, 10 significant and seven suggestive QTL were identified in a QTL mapping experiment using an Awassi×Merino backcross sheep population. All QTL on chromosome 2 exceeded a LOD score of greater than 4 (range 4.4-30.1), giving very strong support for a major gene for pigmentation on this chromosome. Evidence of epistatic interactions was found for QTL for four traits on chromosomes 2 and 19. The ovine TYRP1 gene on OAR 2 was sequenced as a strong positional candidate gene. A highly significant association ($P < 0.01$) of grandparental haplotypes across nine segregating SNP/microsatellite markers including one non-synonymous SNP with pigmentation traits could be shown. Up to 47% of the observed variation in pigmentation was accounted for by models using TYRP1 haplotypes and 83% for models with interactions between two QTL probabilities, offering scope for marker-assisted selection for these traits.

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Additional References

RELATED GEPHE

Related Genes

2 (Agouti (ASIP), MC1R) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~9940~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

3 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~tyrosinase-related protein 1 \(TYRP1\)~/and+Taxon ID=~9940~/or+Gene Gephebase=~tyrosinase-related protein 1 \(TYRP1\)~/and+Taxon ID=~9940~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~tyrosinase-related protein 1 (TYRP1)~/and+Taxon ID=~9940~/or+Gene Gephebase=~tyrosinase-related protein 1 (TYRP1)~/and+Taxon ID=~9940~#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@AllelicSeries <https://omia.org/OMIA001249/9940/>