

## GEPHE SUMMARY

TMEM154 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+TMEM154+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+TMEM154+Gephebase-summary-title</a> )	Gephebase Gene	GP00002242	GepheID
Published	Entry Status	Martin	Main curator

## PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+Gephebase-summary-title</a> )	Trait Category		
Pathogen resistance (lentivirus) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Pathogen+resistance+(lentivirus)+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Pathogen+resistance+(lentivirus)+Gephebase-summary-title</a> )	Trait		
Susceptible to ovine progressive pneumonia virus (OPPV)	Trait State in Taxon A		
Resistant to ovine progressive pneumonia virus (OPPV)	Trait State in Taxon B		
	Ancestral State		
	Taxon A		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific+Gephebase-summary-title</a> )	Taxonomic Status		
	Taxon A		Taxon B
	Latin Name		Latin Name
Ovis aries ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Ovis+aries+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Ovis+aries+Gephebase-summary-title</a> )	Latin Name	Ovis aries ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Ovis+aries+Gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Ovis+aries+Gephebase-summary-title</a> )	Latin Name
sheep	Common Name	sheep	Common Name
Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries Linnaeus, 1758	Synonyms	Ovis ammon aries; Ovis orientalis aries; Ovis ovis; sheep; domestic sheep; lambs; wild sheep; Ovis aries Linnaeus, 1758	Synonyms
species	Rank	species	Rank
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	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	Lineage
Ovis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9935">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9935</a> )	Parent	Ovis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9935">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9935</a> )	Parent
9940 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940</a> )	NCBI Taxonomy ID	9940 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9940</a> )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

TMEM154	Generic Gene Name	Q6P9G4 ( <a href="http://www.uniprot.org/uniprot/Q6P9G4">http://www.uniprot.org/uniprot/Q6P9G4</a> )	UniProtKB Homo sapiens
-	Synonyms	O	GenebankID or UniProtKB
9606.ENSP00000302144 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000302144">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000302144</a> )	String		
-	Sequence Similarities		
-	GO - Molecular Function		
-	GO - Biological Process		
-	GO - Cellular Component		
GO:0016021 : integral component of membrane ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016021">https://www.ebi.ac.uk/QuickGO/term/GO:0016021</a> )			

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

Presumptive Null

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

Molecular Type

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

Aberration Type

Nonsynonymous

SNP Coding Change

Mutation at conserved position associated to resistance in homozygous state

Molecular Details of the Mutation

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

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Glu	Lys	35

Main Reference

Reduced lentivirus susceptibility in sheep with TMEM154 mutations. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22291605>)

Authors

Heaton MP; Clawson ML; Chitko-Mckown CG; Leymaster KA; Smith TP; Harhay GP; White SN; Herrmann-Hoesing LM; Mousel MR; Lewis GS; Kalbfleisch TS; Keen JE; Laegreid WW

Abstract

Visna/Maedi, or ovine progressive pneumonia (OPP) as it is known in the United States, is an incurable slow-acting disease of sheep caused by persistent lentivirus infection. This disease affects multiple tissues, including those of the respiratory and central nervous systems. Our aim was to identify ovine genetic risk factors for lentivirus infection. Sixty-nine matched pairs of infected cases and uninfected controls were identified among 736 naturally exposed sheep older than five years of age. These pairs were used in a genome-wide association study with 50,614 markers. A single SNP was identified in the ovine transmembrane protein (TMEM154) that exceeded genome-wide significance (unadjusted  $p$ -value  $3 \times 10^{-9}$ ). Sanger sequencing of the ovine TMEM154 coding region identified six missense and two frameshift deletion mutations in the predicted signal peptide and extracellular domain. Two TMEM154 haplotypes encoding glutamate (E) at position 35 were associated with infection while a third haplotype with lysine (K) at position 35 was not. Haplotypes encoding full-length E35 isoforms were analyzed together as genetic risk factors in a multi-breed, matched case-control design, with 61 pairs of 4-year-old ewes. The odds of infection for ewes with one copy of a full-length TMEM154 E35 allele were 28 times greater than the odds for those without ( $p$ -value  $< 0.0001$ , 95% CI 5-1,100). In a combined analysis of nine cohorts with 2,705 sheep from Nebraska, Idaho, and Iowa, the relative risk of infection was 2.85 times greater for sheep with a full-length TMEM154 E35 allele ( $p$ -value  $< 0.0001$ , 95% CI 2.36-3.43). Although rare, some sheep were homozygous for TMEM154 deletion mutations and remained uninfected despite a lifetime of significant exposure. Together, these findings indicate that TMEM154 may play a central role in ovine lentivirus infection and removing sheep with the most susceptible genotypes may help eradicate OPP and protect flocks from reinfection.

Additional References

## RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

## EXTERNAL LINKS

## COMMENTS

@AllelicSeries : two deletion - frameshift haplotypes exist in populations but were not tested for association with resistance. <https://omia.org/OMIA001694/9940/>