

	Gephebase Gene	GepheID
Myostatin (MSTN = GDF8) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Myostatin (MSTN = GDF8)^#gephebase-summary-title)	GP00000694	Main curator
Published	Entry Status: Martin	

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)	Trait Category
Muscular mass (double muscling) (https://www.gephebase.org/search-criteria?/and+Trait=^Muscular mass (double muscling)^#gephebase-summary-title)	Trait
Ovis aries	Trait State in Taxon A
Ovis aries; Norwegian Spaelsau	Trait State in Taxon B
Taxon A	Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)	Taxonomic Status
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
species	species
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)
No	Yes
	Taxon B Description
	Ovis aries; Norwegian Spaelsau

MSTN	Generic Gene Name	O14793 (http://www.uniprot.org/uniprot/O14793)	UniProtKB Homo sapiens
GDF8; MSLHP	Synonyms	CAR63506 (https://www.ncbi.nlm.nih.gov/nucore/CAR63506)	GenebankID or UniProtKB
9606.ENSPP00000260950 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000260950)	String		
Belongs to the TGF-beta family.	Sequence Similarities		
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)	GO - Molecular Function		
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)			

GO:0008201 : heparin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0008201>)
GO:0005125 : cytokine activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0005125>)
GO:0008083 : growth factor activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0008083>)
GO:0005102 : signaling receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005102>)
GO:0005160 : transforming growth factor beta receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005160>)

GO - Biological Process

GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0048468 : cell development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048468>)
GO:0010862 : positive regulation of pathway-restricted SMAD protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010862>)
GO:0042981 : regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042981>)
GO:0043408 : regulation of MAPK cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043408>)
GO:0060395 : SMAD protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060395>)
GO:0043627 : response to estrogen (<https://www.ebi.ac.uk/QuickGO/term/GO:0043627>)
GO:0046716 : muscle cell cellular homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046716>)
GO:0045471 : response to ethanol (<https://www.ebi.ac.uk/QuickGO/term/GO:0045471>)
GO:0033574 : response to testosterone
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033574>)
GO:0007179 : transforming growth factor beta receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007179>)
GO:0009408 : response to heat (<https://www.ebi.ac.uk/QuickGO/term/GO:0009408>)
GO:0071549 : cellular response to dexamethasone stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071549>)
GO:0007517 : muscle organ development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007517>)
GO:0014839 : myoblast migration involved in skeletal muscle regeneration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014839>)
GO:0046627 : negative regulation of insulin receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046627>)
GO:0033673 : negative regulation of kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033673>)
GO:0014741 : negative regulation of muscle hypertrophy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014741>)
GO:0045662 : negative regulation of myoblast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045662>)
GO:2000818 : negative regulation of myoblast proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000818>)
GO:0051898 : negative regulation of protein kinase B signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051898>)
GO:1902725 : negative regulation of satellite cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:1902725>)
GO:1902723 : negative regulation of skeletal muscle satellite cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:1902723>)
GO:0048632 : negative regulation of skeletal muscle tissue growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048632>)
GO:0022602 : ovulation cycle process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0022602>)
GO:0010592 : positive regulation of lamellipodium assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010592>)
GO:0010759 : positive regulation of macrophage chemotaxis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010759>)
GO:0051602 : response to electrical stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051602>)
GO:0009629 : response to gravity (<https://www.ebi.ac.uk/QuickGO/term/GO:0009629>)
GO:0014850 : response to muscle activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014850>)
GO:0014732 : skeletal muscle atrophy (<https://www.ebi.ac.uk/QuickGO/term/GO:0014732>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+Yes^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

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

Aberration Type

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

1bp insertion resulting in premature stop codon at position 49

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title)	Main Reference
An insertion in the coding region of the myostatin (MSTN) gene affects carcass conformation and fatness in the Norwegian Spaelsau (Ovis aries). (2009) (https://pubmed.ncbi.nlm.nih.gov/19505313)	
Boman IA; VÅrge DI	Authors
A phenotype of increased muscle mass (IMM) and reduced fat, comparable to reported effects of deleterious mutations in the myostatin gene (MSTN), has been observed in the Norwegian Spaelsau breed. However, the genotyping of five AI rams producing descendants with this phenotype, failed to reveal any of the known functional MSTN mutations.	Abstract
In the present study, the coding region of the MSTN gene was sequenced in a Spaelsau ram lamb with this particular phenotype. A one base-pair insertion mutation (c.120insA) producing a premature stop codon in amino acid position 49 was identified. The consequence of this mutation is that the bioactive carboxy-terminal end of the protein is not translated, and a completely non-functional myostatin protein is produced. Among the 98 available AI rams of this breed, all five individuals having descendants with this particular phenotype were found to be heterozygous for the c.120insA mutation. The probability that these five selected AI rams should be heterozygous carriers of the c.120insA mutation purely by chance was calculated to be 3.1 x 10 ⁻⁷ . In total, 7 AI rams were found to be heterozygous carriers of c.120insA. The estimated breeding values (EBVs) for EUROP carcass conformation and fat class for these 7 individuals also points towards a strong phenotypic effect of this mutation.	
Based upon the completely deleterious effect this novel c.120insA mutation has on myostatin protein function, and the documented phenotypic effect of comparable MSTN mutations in Norwegian White Sheep and other species, we conclude that this mutation is the functional explanation underlying the IMM phenotype in Norwegian Spaelsau. The allele distribution among the 98 genotyped AI rams support this conclusion, and also suggests that c.120insA is the most common reason for this phenotype in the Norwegian Spaelsau breed.	Additional References

RELATED GEPHE

1 (Callipyge (CLPG1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~9940~/and+Trait=Muscular mass/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~Myostatin (MSTN = GDF8)~/and+Taxon ID=~9940~/or+Gene Gephebase=~Myostatin (MSTN = GDF8)~/and+Taxon ID=~9940~#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS