

GEPHE SUMMARY

	Gephebase Gene		GepheID
Myostatin (MSTN = GDF8) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00000696	
Gephebase="Myostatin (MSTN = GDF8)"#gephebase-summary-title)			Main curator
Published	Entry Status	Martin	

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait)			
Category="Morphology"#gephebase-summary-title)	Trait		
Muscular mass (double muscling) (<a (double="" href="https://www.gephebase.org/search-criteria?/and+Trait=" mass="" muscling)"#gephebase-summary-title"="" muscular="">https://www.gephebase.org/search-criteria?/and+Trait="Muscular mass (double muscling)"#gephebase-summary-title)			
Sus scrofa	Trait State in Taxon A		
Sus scrofa - Pietrain	Trait State in Taxon B		
Data not curated	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic)	Taxonomic Status		
Status="Domesticated"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Sus scrofa		Sus scrofa domesticus	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Sus scrofa"#gephebase-summary-title)		(<a domesticus"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" scrofa="" sus="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Sus scrofa domesticus"#gephebase-summary-title)	
	Common Name		Common Name
pig		domestic pig	
	Synonyms		Synonyms
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofa		Sus domestica; Sus domesticus; Sus scrofa domestica; domestic pig	
species	Rank		Rank
		subspecies	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia;		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia;	
Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;		Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;	
Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria;		Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria;	
Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus		Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus; Sus scrofa	
	Parent		Parent
Sus () - (Rank: genus)		Sus scrofa (pig) - (Rank: species)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9822)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9825)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
9823		9825	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9823)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9825)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		Sus scrofa - Pietrain	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
MSTN		O14793 (http://www.uniprot.org/uniprot/O14793)	
	Synonyms		GenebankID or UniProtKB
GDF8; MSLHP		AAR18245 (https://www.ncbi.nlm.nih.gov/nucleotide/AAR18245)	
	String		
9606.ENSP00000260950			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000260950)			
	Sequence Similarities		
Belongs to the TGF-beta family.			
	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: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>)

Unknown ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?and+Presumptive+Null=~Unknown)) Presumptive Null
Cis-regulatory ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?and+Molecular+Type=~Cis-regulatory)) Molecular Type
SNP ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?and+Aberration+Type=~SNP)) Aberration Type
Possible promoter disruption : changes the G nucleotide at position 8 of the MEF3 binding site into an A nucleotide, thus disrupting the MEF3 binding site Molecular Details of the Mutation
Candidate Gene ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?and+Experimental+Evidence=~Candidate+Gene)) Experimental Evidence
Characterization of the complete porcine MSTN gene and expression levels in pig breeds differing in muscularity. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18822098>) Main Reference

Myostatin (MSTN), a transforming growth factor beta superfamily member, is an essential factor for the growth and development of muscle mass. The protein functions as a negative regulator of muscle growth and is related to the so-called double-muscling phenotype in cattle, where a series of mutations renders the gene inactive. One particular breed of pigs, the Belgian PiÅ©train, also shows a heavily muscled phenotype. The similarity of muscular phenotypes between the double-muscled cattle and PiÅ©train pigs indicated that MSTN may be a candidate gene for muscular hypertrophy in pigs. In this study, we sequenced and analysed the complete MSTN gene from 45 pigs of five different breeds, including the heavily muscled PiÅ©train breed at one extreme and the Meishan and Wild boar breeds at the other extreme. In total, 7626 bp of the porcine MSTN gene were sequenced, including the 5' and 3' UTR. Fifteen polymorphic loci were found, three of which were located in the promoter region, five in intron 1 and seven in intron 2. Most mutations were found when comparing the obtained MSTN sequence with porcine MSTN sequences already published. However, one polymorphism located at position 447 of the porcine MSTN promoter had a very high allele frequency in the PiÅ©train pig breed and disrupted a putative myocyte enhancer factor 3 binding site. Real-time PCR using Sybr Green showed that this mutation was associated with expression levels of the MSTN gene in *m. longissimus dorsi* at an age of 4 weeks.

Additional References

RELATED GEPHE

Related Genes

1 (Insulin-like growth factor 2 (IGF2)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9823^/and+Trait=Muscular mass/or+Taxon ID=^9825^/and+Trait=Muscular mass/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism <https://omia.org/OMIA000683/9823/>