

GEPHE SUMMARY

	Gephebase Gene	GephelD
CAST (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CAST^#gephebase-summary-title)	GP00000170	Main curator
Published	Entry Status	Martin

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait
Meat tenderness (https://www.gephebase.org/search-criteria?/and+Trait=^Meat tenderness^#gephebase-summary-title)	Trait State in Taxon A
Sus scrofa	Trait State in Taxon B
Sus scrofa	Ancestral State
Data not curated	Taxonomic Status

Domesticated (<https://www.gephebase.org/search-criteria?/and+Taxonomic>
Status=^Domesticated^#gephebase-summary-title)

Taxon A	Latin Name	Taxon B	Latin Name
Sus scrofa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Sus+scrofa^#gephebase-summary-title)		Sus scrofa domesticus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Sus+scrofa+domesticus^#gephebase-summary-title)	
pig	Common Name	domestic pig	Common Name
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofa	Synonyms	Sus domestica; Sus domesticus; Sus scrofa domestica; domestic pig	Synonyms
species	Rank	subspecies	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus; Sus scrofa	Lineage
Sus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9822)	Parent	Sus scrofa (pig) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)	Parent
9823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)	NCBI Taxonomy ID	9825 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9825)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

CAST	Generic Gene Name	UniProtKB Homo sapiens
BS-17; PLACK	Synonyms	GenebankID or UniProtKB
-	String	
Belongs to the protease inhibitor I27 (calpastatin) family.	Sequence Similarities	
GO:0003723 : RNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003723)	GO - Molecular Function	
GO:0045296 : cadherin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0045296)		
GO:0010859 : calcium-dependent cysteine-type endopeptidase inhibitor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0010859)		
GO:0004866 : endopeptidase inhibitor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004866)		
GO:0002020 : protease binding (https://www.ebi.ac.uk/QuickGO/term/GO:0002020)	GO - Biological Process	
GO:0097340 : inhibition of cysteine-type endopeptidase activity		

(https://www.ebi.ac.uk/QuickGO/term/GO:0097340)	
GO:2000675 : negative regulation of type B pancreatic cell apoptotic process	
(https://www.ebi.ac.uk/QuickGO/term/GO:2000675)	
GO:1990709 : presynaptic active zone organization	
(https://www.ebi.ac.uk/QuickGO/term/GO:1990709)	
GO - Cellular Component	
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)	Presumptive Null
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)	Molecular Type
GO:0005783 : endoplasmic reticulum	Aberration Type
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)	Molecular Details of the Mutation
No (https://www.gephebase.org/search-criteria/?and+Presumptive Null=%22No%22#gephebase-summary-title)	Experimental Evidence
Cis-regulatory (https://www.gephebase.org/search-criteria/?and+Molecular Type=%22Cis-regulatory%22#gephebase-summary-title)	Main Reference
Unknown (https://www.gephebase.org/search-criteria/?and+Aberration Type=%22Unknown%22#gephebase-summary-title)	Authors
4 candidate SNPs in putative enhancers with nuclear factor-binding properties	Abstract
Linkage Mapping (https://www.gephebase.org/search-criteria/?and+Experimental Evidence=%22Linkage Mapping%22#gephebase-summary-title)	Additional References
Predictive markers in calpastatin for tenderness in commercial pig populations. (2011) (https://pubmed.ncbi.nlm.nih.gov/21454860)	
Nonneman D; Lindholm-Perry AK; Shackelford SD; King DA; Wheeler TL; Rohrer GA; Bierman CD; Schneider JF; Miller RK; Zerby H; Moeller SJ	
The identification of predictive DNA markers for pork quality would allow US pork producers and breeders to select genetically superior animals more quickly and efficiently for the production of consistent, high-quality meat. Genome scans have identified QTL for tenderness on SSC 2, which have been fine-mapped to the calpastatin locus. The objectives of this study were to identify the sequence variation in calpastatin that likely affects tenderness in commercial-level pig populations and to develop definitive DNA markers that are predictive of pork tenderness for use in marker-assisted selection programs. We resequenced the calpastatin regulatory and transcribed regions in pigs with divergently extreme shear force values to identify possible mutations that could affect tenderness. A total of 194 SNP were identified in this sequence, and 31 SNP were found in predicted transcription factor binding sites. We tested 131 polymorphisms in our research population and a subset (40) of these in samples of industry pigs for their association with objective measures of tenderness. We identified 4 SNP that were consistently associated with pork tenderness in all the populations studied, representing 2,826 pigs from 4 distinct populations. Gel shift assays were designed for these SNP and 12 other polymorphic sites. Six sites demonstrated a gel shift when probes were incubated with nuclear extract from muscle, heart, or testis. Four of these sites, a specificity protein 1 (Sp1) site around nucleotides 12978 and 12979, a potential thyrotroph embryonic factor (Tef) site at nucleotide 25587, an unknown site at nucleotide 48699, and myocyte enhancer factor-2 (Mef-2)/TATA sites with SNP at positions 49223 and 49228 were allele specific in binding nuclear proteins. The allele frequencies for the tender alleles were similar (0.11 to 0.36) in the 4 different commercial populations. These 4 SNP were not in complete linkage disequilibrium with each other and may independently affect calpastatin expression, tenderness, or both. These markers should be predictive of pork tenderness in industry populations.	

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS