

	Gephebase Gene		GepheID
Agouti (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Agouti^#gephebase-summary-title)		GP00000058	
	Entry Status	Martin	Main curator
Published			

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)		Trait Category
Coloration (coat; dorso-ventral) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration (coat; dorso-ventral)~#gephebase-summary-title)		Trait
Sus scrofa- Mangalitza		Trait State in Taxon A
Sus scrofa - Pi_strain		Trait State in Taxon B
Data not curated		Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)		Taxonomic Status
Taxon A	Taxon B	
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)	Latin Name
pig	domestic pig	Common Name
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofuscus	Sus domestica; Sus domesticus; Sus scrofa domestica; domestic pig	Synonyms
species	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	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)	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)	9825 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9825)	NCBI Taxonomy ID
is Taxon A an Intraspecies?	is Taxon B an Intraspecies?	
Yes	Yes	
Sus scrofa- Mangalitza	Sus scrofa - Pi_strain	Taxon A Description
		Taxon B Description

Asip	Generic Gene Name	Q03288 (http://www.uniprot.org/uniprot/Q03288)	UniProtKB Mus musculus
As; ASP; A<y>; ASIP; a	Synonyms	AAF22158 (https://www.ncbi.nlm.nih.gov/nuccore/AAF22158)	GenebankID or UniProtKB
10090.ENSMUSP00000029123 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000029123)	String		
-	Sequence Similarities		
GO:0031779 : melanocortin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031779) GO:0031781 : type 3 melanocortin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031781) GO:0031782 : type 4 melanocortin receptor binding	GO - Molecular Function		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031782>)

GO - Biological Process

GO:0008343 : adult feeding behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008343>)
GO:0006091 : generation of precursor metabolites and energy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006091>)
GO:0071514 : genetic imprinting (<https://www.ebi.ac.uk/QuickGO/term/GO:0071514>)
GO:0009755 : hormone-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009755>)
GO:0042438 : melanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042438>)
GO:0032438 : melanosome organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032438>)
GO:0032402 : melanosome transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032402>)
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:0040030 : regulation of molecular function, epigenetic
(<https://www.ebi.ac.uk/QuickGO/term/GO:0040030>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0005623 : cell (<https://www.ebi.ac.uk/QuickGO/term/GO:0005623>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

The mutation causing the black-and-tan pigmentation phenotype of Mangalitza pigs maps to the porcine ASIP locus but does not affect its coding sequence. (2006)
(<https://pubmed.ncbi.nlm.nih.gov/16416091>)

Authors

DrÃ¶gemÃ¶ller C; Giese A; Martins-Wess F; Wiedemann S; Andersson L; Brenig B; Fries R; Leeb T

Abstract

The gene for agouti signaling protein (ASIP) is centrally involved in the expression of coat color traits in animals. The Mangalitza pig breed is characterized by a black-and-tan phenotype with black dorsal pigmentation and yellow or white ventral pigmentation. We investigated a Mangalitza x PiÃ©train cross and observed a coat color segregation pattern in the F2 generation that can be explained by virtue of two alleles at the MC1R locus and two alleles at the ASIP locus. Complete linkage of the black-and-tan phenotype to microsatellite alleles at the ASIP locus on SSC 17q21 was observed. Corroborated by the knowledge of similar mouse coat color mutants, it seems therefore conceivable that the black-and-tan pigmentation of Mangalitza pigs is caused by an ASIP allele a(t), which is recessive to the wild-type allele A. Toward positional cloning of the a(t) mutation, a 200-kb genomic BAC/PAC contig of this chromosomal region has been constructed and subsequently sequenced. Full-length ASIP cDNAs obtained by RACE differed in their 5' untranslated regions, whereas they shared a common open reading frame. Comparative sequencing of all ASIP exons and ASIP cDNAs between Mangalitza and PiÃ©train pigs did not reveal any differences associated with the coat color phenotype. Relative qRT-PCR analyses showed different dorsoventral skin expression intensities of the five ASIP transcripts in black-and-tan Mangalitza. The a(t) mutation is therefore probably a regulatory ASIP mutation that alters its dorsoventral expression pattern.

Additional References

RELATED GEPHE

Related Genes

3 (Kit (type III receptor protein-tyrosine kinase), MC1R, tyrosinase-related protein 1 (TYRP1)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9823^/and+Trait=Coloration/or+Taxon ID=^9825^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

