GEPHE SUMMARY

Gephebase Gene
NUDT7 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^NUDT7^#gephebase-summary-title)

GepheID
GP00000741

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Meat color (https://www.gephebase.org/search-criteria?/and+Trait=^Meat color^#gephebase-summary-title)

Trait State in Taxon A
Sus scrofa - red meat pig and red meat wild boar

Trait State in Taxon B
Sus scrofa - white meat

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
Sus scrofa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Sus scrofa^#gephebase-summary-title)

Common Name
pig

Synonyms
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofus

Rank
species

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

Parent
Sus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9822)

NCBI Taxonomy ID
9823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Sus scrofa domesticus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Sus scrofa domesticus^#gephebase-summary-title)

Common Name
domestic pig

Synonyms
Sus domestica; Sus domesticus; Sus scrofa domestica; domestic pig

Rank
subspecies

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

Parent
Sus scrofa (pig) - (Rank: species) (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)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Nudt7

Synonyms
1300007B24Rik; 2210404C19Rik

String
10090.ENSMUSP00000073213 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000073213)

Sequence Similarities
Belongs to the Nudix hydrolase family. PCD1 subfamily.

GO - Molecular Function
GO:0030145 : manganese ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030145)
GO:0005102 : signaling receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005102)
GO:0000287 : magnesium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000287)
GO:0003986 : acetyl-CoA hydrolase activity

UniProtKB Mus musculus
Q99P30 (http://www.uniprot.org/uniprot/Q99P30)

GenebankID or UniProtKB
BAH82842 (https://www.ncbi.nlm.nih.gov/nuccore/BAH82842)

(https://www.ebi.ac.uk/QuickGO/term/GO:0003986)
GO:0016818 : hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (https://www.ebi.ac.uk/QuickGO/term/GO:0016818)
GO:0030515 : snoRNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030515)

GO - Biological Process

GO:0046356 : acetyl-CoA catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0046356)
GO:0050873 : brown fat cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0050873)
GO:0015938 : coenzyme A catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0015938)
GO:0009132 : nucleoside diphosphate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009132)

GO - Cellular Component

GO:0005777 : peroxisome (https://www.ebi.ac.uk/QuickGO/term/GO:0005777)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

Fine mapping of quantitative trait loci for meat color on Sus scrofa chromosome 6: analysis of the swine NUDT7 gene. (2010) (https://pubmed.ncbi.nlm.nih.gov/19749013)

Authors

Taniguchi M; Hayashi T; Nii M; Yamaguchi T; Fujishima-Kanaya N; Awata T; Mikawa S

Abstract

In the livestock industry, meat color has become important because consumer acceptance is subject to the appearance of the product in the marketplace. Our previous analyses of a whole genome QTL scan for various meat qualities using 2 F(2) families from Japanese wild boar (known as a red meat) x Large White and from Duroc x Chinese Jinhua suggested that a meat color (heme content) QTL is located on SSC6. The objective of this study was to fine-map this SSC6 meat color QTL and subsequently investigate positional candidate genes for polymorphisms that may cause changes in meat color. Therefore, we conducted interval mapping on SSC6 using an additional 9 gene markers through combined analyses of the 2 F(2) families of Japanese wild boar x Large White (353 progeny) and Duroc x Chinese Jinhua (204 progeny). Comparative analysis with humans, mice, and cattle suggested that there were 10 functional genes in the region. Among these genes, we suggested that a novel pig gene encoding a nudix (nucleoside diphosphate linked moiety X)-type motif 7 (NUDT7, a member of the nudix hydrolases) is a strong candidate for the QTL because the mouse Nudt7 is reported to hydrolyze succinyl-CoA, a substrate of the reaction limiting the rate of heme biosynthesis. We therefore determined the pig NUDT7 gene sequence including the 5′ promoter region and explored genetic polymorphisms between Japanese wild boar and Large White. We identified 116 polymorphisms within the NUDT7 CDS or in the 5′ region. None of the AA substitutions were associated with the meat color QTL; however, 3 polymorphisms were found in putative transcription factor recognition sites. We then investigated the differential expression of NUDT7 in Japanese wild boar and Large White by allele-specific quantitative real-time PCR. The expression level of the Large White type allele was greater than that of the Japanese wild-boar-type allele. Consequently, we speculated that the difference in meat color between Japanese wild boar and Large White is caused partly by differential expression of this candidate gene. Upregulation of NUDT7 expression in muscle may reduce succinyl-CoA content and thus reduce the level of heme biosynthesis.

Additional References

Overexpression of NUDT7, a candidate quantitative trait locus for pork color, downregulates heme biosynthesis in L6 myoblasts. (2010) (https://pubmed.ncbi.nlm.nih.gov/20619544)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS