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SREBP pathway genes as candidate markers in country ham production

Benedicte Renaville
Università di Udine

Kimberly L. Glenn
Iowa State University

Benny E. Mote
Iowa State University

Bin Fan
Iowa State University

Kenneth J. Stalder
Iowa State University, stalder@iastate.edu

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Abstract
Country hams are dry-cured products from the Southeastern region of the USA. This high value product requires quality fresh meat to avoid later processing problems. The marker SREBF1 is a transcription factor involved in the regulation of fatty acid synthesis and anti-oxidative enzyme transcription. The SREBF1 gene and its regulators, SCAP and MBTPS1, were investigated for associations with several meat quality traits in country hams. After single nucleotide polymorphism (SNP) identification, PCR-RFLP tests were designed for one polymorphism in each of the three investigated genes. Meat quality and physical traits were collected on 299 fresh hams. Significant associations were found with ham yield (MBTPS1, PSREBF1×MBTPS1, PMBTPS1, PSREBF1×MBTPS1, PSREBF1, PMBTPS1, PSREBF1×MBTPS1, PSCAP×MBTPS1, PSREBF1×SCAP, PSREBF1, SCAP and MBTPS1 are associated with some country ham quality traits. Breeders could use these gene tests to improve their animals, which would in turn improve country ham processing and other desired production goals.

Keywords
Pig, SREBF1, MBTPS1, SCAP, SNP

Disciplines
Agriculture | Animal Sciences | Genetics and Genomics | Meat Science

Comments

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Authors
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SREBP pathway genes as candidate markers in country ham production

Benedicte Renaville,1 Kimberly L. Glenn,2 Benny E. Mote,2 Bin Fan,1 Kenneth J. Stalder,1 Max F. Rothschild2
1Dipartimento di Scienze degli Alimenti, Università di Udine, Italy
2Department of Animal Science and the Center for Integrated Animal Genomics, State University, Iowa, USA

Introduction

Country hams are American dry-cured hams produced throughout the Southeastern part of the U.S. in states like Kentucky, Tennessee, North Carolina and Virginia. These country hams differ from the traditional dry-cured hams produced in Italy and Spain in that they utilize considerably shorter curing periods and the inclusion of a smoking step after curing (Ramos et al., 2007). In 2005, approximately 3.4 million country hams were processed and the retail value of these hams exceeded 340 million dollars (Stalder et al., 2006). This production requires high meat quality as inconsistent pork quality can often lead to variation in water holding capacity (yield) and muscle colour of dry-cured hams (Stalder et al., 2005).

Sterol regulatory element binding proteins (SREBPs) belong to the original basic helix-loop-helix leucine zipper family of transcription factors (Eberle et al., 2004). Three SREBPs have been characterized: SREBP-1a, -1c, and -2, which stimulate transcription of more than 30 genes involved in the uptake and synthesis of cholesterol, fatty acids, triglycerides, and phospholipids (Horton et al., 2003). The binding protein SREBP-1c preferentially activates lipogenic genes, whereas SREBP-2 acts more specifically on cholesterol biosynthesis genes (Ameniya-Kudo et al., 2002). Furthermore, SREBP-1a regulates both metabolic pathways. The same gene (SREBF1) encodes for SREBP-1c and SREBP-1a (Shimano, 2001) but this last protein is a more potent transcriptional activator than SREBP-1c, due to its longer NH2-terminal transactivation domain (Eberle et al., 2004).

The precursors of the SREBPs are retained in the ER membranes through a tight association with the SREBP cleavage activating protein (SCAP) (Nohturfft et al., 1998). Under the appropriate conditions, SCAP escorts the SREBP precursors from the ER to the Golgi apparatus where two functionally distinct proteases, site 1 protease (S1P, locus symbol: MBTPS1) and site 2 protease (S2P), sequentially cleave the precursor protein releasing the active nuclear isoform of SREBP (nSREBPs) in the cytoplasm (Wang et al., 1994; Sakai et al., 1998).

The objective of this paper was to identify SNPs in the pig SREBF1, SCAP and MBTPS1 genes and evaluate whether these SNPs are associated with country ham quality parameters.

Abstract

Country hams are dry-cured products from the Southeastern region of the USA. This high value product requires quality fresh meat to avoid later processing problems. The marker SREBF1 is a transcription factor involved in the regulation of fatty acid synthesis and anti-oxidative enzyme transcription. The SREBF1 gene and its regulators, SCAP and MBTPS1, were investigated for associations with several meat quality traits in country hams. After single nucleotide polymorphism (SNP) identification, PCR-RFLP tests were designed for one polymorphism in each of the three investigated genes. Meat quality and physical traits were collected on 299 fresh hams. Significant associations were found with ham yield (MBTPS1, P<0.05 and SREBF1 x MBTPS1, P<0.05) and ham circumference (MBTPS1, P<0.05 and SREBF1 x MBTPS1, P<0.01), Hunter A colour score on fresh meat (SREBF1, P<0.05), Hunter B colour score on cured meat (MBTPS1, P<0.05 and SREBF1 x MBTPS1, P<0.01), moisture (SCAP x MBTPS1, P<0.05) and salt percentage (SREBF1 x SCAP, P<0.05). Our findings provide initial evidence that SNPs in SREBF1, SCAP and MBTPS1 are associated with some country ham quality traits. Breeders could use these gene tests to improve their animals, which would in turn improve country ham processing and other desired production goals.

Materials and methods

Animals and ham processing

Hams were obtained from two pork harvesting facilities that routinely supply fresh hams to Clifty Farm Country Hams (Paris, TN, USA). All hams (321) were derived from commercially crossbred individuals, but information regarding the individual contribution of the breeds used in establishing the cross was not available. Since pigs were not tracked during the harvesting process or cutting of the carcass into primal cuts, including into hams, it was not possible to determine the sex of the animals from which the hams were derived. In order to avoid sampling the same animal twice, all hams were collected from the left side of the carcass only. In order to minimize variation due to initial ham weight, only hams between 8.5 and 10.5 kg were utilized in this study. Despite the large number of hams sampled, hams were processed for only two days, in order to minimize day of harvest effects.

Fresh ham evaluation

On each fresh ham, several physical and quality traits were recorded, including weight, circumference (measured using a flexible cloth measuring tape around the section of each ham presenting the greatest circumfer-
ence), depth (measured at the thickest part of the ham), objective colour scores, marbling and firmness scores. The latter two traits were evaluated using the U.S. National Pork Producers Council guidelines (NPPC, 2000). All these traits were evaluated on the semimembranosus muscle of each ham face at approximately 48 hours after slaughter. Objective colour scores were measured using a Minolta Chroma Meter (Ramsey, NJ, USA) with a 50 mm aperture, using Standard Illuminant C light source and 0° viewing angle geometry. The Minolta Chroma Meter was calibrated against a white tile standard prior to use. The values recorded included Minolta and Hunter L, a, and b scores and were only recorded in the first day of data collection because of machine malfunction on day 2. Since the Minolta and Hunter measures of colour often correlate closely with each other (Stalder et al., 2005), only the results for Hunter scores are presented here. In addition, a sample of the semimembranosus was collected from each ham to obtain pH, lipid percentage and dry matter percentage. Approximately 75 g of the semimembranosus sample collected was homogenized using a standard food processor until it was finely ground. For pH determination, the pH meter (model IQ150, IQ Scientific Instruments, CA, USA) probe was inserted, after calibration, into the ground ham sample and two pH values were obtained from each sample and averaged. Lipid percentage was determined using a modified lipid extraction procedure based on the method described by Folch et al. (1957). In order to calculate dry matter, a sample of ground pork (1 g) was incubated at 80°C and weighed several times until the sample reached constant weight and was considered dry. Dry matter was then expressed as a percentage of initial sample weight.

**Dry-cure processing**

All hams were processed following standard commercial curing procedures in place at Clifty Farm Country Hams, including application of a salt mixture, curing time, curing temperature and humidity. The curing mixture included salt, sodium nitrate, sugar and other spices, and was applied to all hams. Afterwards, the hams were refrigerated at approximately 2.5 to 4.0°C for 5 days. Then, the hams were re-salted and refrigerated again for 44 days. Upon completion of the initial curing process, the hams were washed and then dried in chambers for a period of 20 days. These chambers were at 15°C and 58-60% relative humidity. The final step included smoking for 8 days at a temperature of 38°C. The general curing procedures adopted for country hams have been described previously (Stalder et al., 2006). In order to maintain individual ham identification through the curing process, each ham was individually identified using a commercially available tagging system (Laser®3™, Koch Supplies, North Kansas City, MO, USA).

**Cured ham evaluation**

Upon completion of the curing process, all hams were weighed and yield was calculated as the weight of the cured ham divided by the weight of the fresh ham. Slices (9 mm thick) from each ham were cut perpendicular to the femur using a band saw. Afterwards, the same objective colour scores described above were evaluated on the semimembranosus muscle from a slice obtained from approximately the centre of each cured ham. The semimembranosus was chosen to be evaluated after the completion of the curing process, since the face of the ham is extremely dry due to curing and is not representative of the quality found in the high value centre cuts. A sample of each slice was retained for further analytical determinations including moisture and salt content. First, the cured ham samples were finely ground using the procedures described above. Moisture was determined from a 50 g ground sample using the procedures described for evaluating fresh ham dry matter percentage. The salt content was calculated using 10 g samples analyzed with a Sodium Ion Selective Electrode attached to a Model 225 pH-ISE meter (Denver Instrument Company, Arvada, CO, USA) with a standard curve verified by AOAC (1990) standard method.

**Molecular genetic marker evaluation**

The DNA was extracted from the fresh muscle samples using a standard DNA extraction method. In order to account for genes that are known to have a major impact on pork quality, all samples were initially genotyped for the porcine stress syndrome gene (RYRI - ryanodine receptor 1 gene, usually indicated as the HAL 1843™ mutation) and for the RN- or Napole genotype using the procedures described by Fuji et al. (1991) and Milan et al. (2000), respectively. New genetic markers were developed using single nucleotide polymorphisms (SNPs) identified in SREBF1, SCAP and MBTPS1. Initially, primer sets were used for each of these genes in order to amplify PCR fragments from each gene. SREBF1 primer set (Table 1) was designed from the corresponding human SREBF1 exon 6 genomic sequence, SCAP primer set was described in Qiu et al., (2006) (Forward primer: GCAGCGCCGGGACAGTGG; reverse primer: TGATGCCCGAGCCACCTCCTC) and amplified intron 13 of the SCAP gene. MBTPS1 primers were designed from the consensus regions of exon 5 (Forward primer: TGAAGGAGACCAACTGA) and exon 6 (reverse primer: CTGATCTGAGGAAAACTCT) of the human (accession numbers in ensemble ENSE0000945694 and ENSE0000945695) and mouse (accession numbers: ENSMUSE0000319523 and ENSMUSE0000319518) MBTPS1 gene. After PCR optimization of these primer sets, PCR products were sequenced for each gene using an ABI automated DNA sequencer (Applied Biosystems, Foster City, CA, USA). The genomics sequences of the amplified fragments have been deposited into GenBank, and accession numbers are FJ904278, FJ904279 and FJ904280 for SREBF1, SCAP and MBTPS1, respectively. The sequence comparisons between animals were used to identify SNPs. The sequences were analyzed using Sequencher software version 3.0 (Gene Codes, Ann Arbor, MI, USA). In order to ensure that the sequences obtained came from the investigated genes, they were blasted against human and mouse genomes. After identification of the polymorphisms present in each gene, new primer sets were designed in order to create PCR-RFLP tests for those polymorphisms found within recognition sites of restriction enzymes. The sequences of these primer sets for each gene are presented in Table 1. These PCR-RFLP tests were used to genotype the whole dataset. Amplifications were performed using 12.5 ng of porcine DNA, 1x PCR buffer, 2.5 mM of MgCl2, 0.125 mM each dNTP, 0.3 mM of each primer and 0.35 U Taq polymerase (Promega, Madison, WI, USA). The PCR conditions consisted of an initial step at 94°C for 3 minutes followed by 40 cycles of 94°C for 30 seconds, specific annealing temperature for each primer set (Table 1) for 30 seconds and 72°C for 30 seconds. The final extension step consisted of 3 minutes at 72°C. Digestions were performed using the restriction enzyme for each PCR-RFLP test (Table 1) following the recommendations of the manufacturer. The locations of the SNPs within the genes, as well as the fragment sizes for each allele, are also presented in Table 1.

**Statistical analyses**

Single locus and multiple genotype associations were analyzed using the General Linear Model of the SAS software package (SAS Institute, release 9.1, Cary, NC, USA) with a model that included ham source, day of sampling and marker genotype (SREBF1, SCAP, MBTPS1 and the two-way interactions among these markers) as fixed effects. The model used for the analysis of cured weight was dif-
ferent because initial ham weight was included as a linear covariate. For the objective colour scores determined on the fresh hams, the model included only ham source and marker genotypes, because these traits were collected only on the first day of sampling. Information on other effects, such as sex or sire, was not available for the dataset analyzed. Samples from animals that were carriers or homozygous for the unfavourable allele at the RYR1 (RYR1 c.1843T allele) and PRKAG3 (PRKAG3 p.200Q allele) loci were removed from the dataset before the association analyses. Results from the analyses performed showed significant associations between MBTPS1 and the interaction between SREBF1 and MBTPS1 (SREBF1xMBTPS1) with cured weight, yield and circumference (Table 2). The SNP c.736+78C>T (dbSNP accession no: ss120258599) within MBTPS1 genotype was associated with significantly higher cured weight, yield and circumference values when compared with genotype TT (P<0.05) (Table 3). The SREBF1 c.1158+118A>G (dbSNP accession no: ss120258595) polymorphism was associated with Hunter A scores measured on fresh meat (Table 2) with the AA genotype associated with significantly (P<0.05) redder meat (Table 3). Both MBTPS1 and the interaction SREBF1xMBTPS1 were associated with Hunter B scores of cured ham. The SCAPxMBTPS1 and SCAPxSREBF1 gene

Table 1. Genes analyzed, primers, PCR annealing temperature, restriction enzymes used, PCR-RFLP fragment sizes and allele frequencies in a study of the association between genetic markers and fresh and dry-cured ham processing characteristics.

<table>
<thead>
<tr>
<th>Marker*</th>
<th>dbSNP accession No.</th>
<th>Primer</th>
<th>Primer sequence</th>
<th>Fragment size (bp)</th>
<th>Annealing temp. (°C)</th>
<th>Restriction enzyme</th>
<th>Fragment sizes (bp) and allele frequency (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SREBF1</td>
<td>c.1158+118A&gt;G</td>
<td>SREBF-F</td>
<td>ATG CCT GCC TGC CCT AAC</td>
<td>503</td>
<td>60</td>
<td>NlaIII</td>
<td>503 (allele G: 29.7%) 373+130 (allele A: 70.3%)</td>
</tr>
<tr>
<td>SCAP</td>
<td>c.2616C&gt;T</td>
<td>SCAP-F</td>
<td>CTC TGC GCC TGC CCT AAC</td>
<td>381</td>
<td>62</td>
<td>BglII</td>
<td>381 (allele C: 60.8%) 246+155 (allele T: 39.2%)</td>
</tr>
<tr>
<td>MBTPS1</td>
<td>c.736+78C&gt;T</td>
<td>MBTPS1-F</td>
<td>GCC AACACGACCACCGAG</td>
<td>363</td>
<td>59</td>
<td>Ddel</td>
<td>345+18 (allele T: 74.9%) 228+117+18 (allele C: 25.1%)</td>
</tr>
</tbody>
</table>

*The genes analysed were: Sterol regulatory element binding transcription factor 1 (SREBF1), SREBF chaperone (SCAP) and membrane-bound transcription factor peptidase, site 1 (MBTPS1).

Table 2. P-values for the effects of SREBF1, SCAP and MBTPS1 on fresh and cured ham traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>SREBF1</th>
<th>SCAP</th>
<th>MBTPS1</th>
<th>SREBF1xSCAP</th>
<th>SREBF1xMBTPS1</th>
<th>SCAPxMBTPS1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cured weight, kg</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
</tr>
<tr>
<td>Yield, %</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
</tr>
<tr>
<td>Circumference, cm</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>&lt;0.10</td>
<td>&lt;0.01</td>
<td>ns</td>
</tr>
<tr>
<td>Lipid percentage, %</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.10</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Fresh Hunter a</td>
<td>&lt;0.05</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Cured Hunter L</td>
<td>&lt;0.10</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Cured Hunter b</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>&lt;0.01</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Moisture, %</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Salt content, %</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>&lt;0.05</td>
<td>ns</td>
<td>ns</td>
</tr>
</tbody>
</table>

Green weight, Depth (cm), Marbling, Firmness, pH, Dry matter (%), Fresh Hunter L and b and Cured Hunter a were not significant at P<0.05.

Table 3. Genotypic least square means (± standard errors) for SREBF1, SCAP and MBTPS1 in fresh and cured ham traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>SREBF1</th>
<th>SCAP</th>
<th>MBTPS1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cured weight, kg</td>
<td>7.32±0.09</td>
<td>7.25±0.05</td>
<td>7.31±0.03</td>
</tr>
<tr>
<td>Yield, %</td>
<td>78.71±0.94</td>
<td>77.95±0.50</td>
<td>76.59±0.36</td>
</tr>
<tr>
<td>Circumference, cm</td>
<td>72.00±0.72</td>
<td>71.74±0.38</td>
<td>72.06±0.28</td>
</tr>
<tr>
<td>Lipid percentage, %</td>
<td>2.46±0.34</td>
<td>2.37±0.18</td>
<td>2.38±0.13</td>
</tr>
<tr>
<td>Fresh Hunter a</td>
<td>7.12±0.35</td>
<td>8.14±0.30</td>
<td>8.63±0.26</td>
</tr>
<tr>
<td>Cured Hunter L</td>
<td>5.86±0.19</td>
<td>5.65±0.10</td>
<td>5.52±0.07</td>
</tr>
<tr>
<td>Moisture, %</td>
<td>63.86±0.50</td>
<td>64.65±0.31</td>
<td>64.55±0.23</td>
</tr>
<tr>
<td>Salt content, %</td>
<td>5.40±0.39</td>
<td>5.29±0.21</td>
<td>5.26±0.15</td>
</tr>
</tbody>
</table>

*Mean values with different letters were significantly different; P<0.05.
interactions showed significant associations with moisture and salt percentage, respectively (Table 2). In addition, a suggestive association (P<0.1) with lipid content was also detected for SNP MBTPS1 c.736+78C>T. For this marker, genotype TC had higher lipid content than animals with the TT genotype (P<0.05) (Table 3). No associations were found between the SCAP c.2616C>T (dbSNP accession no: ss120258396) polymorphism and the investigated ham traits, although the interaction of this marker with the other ones resulted in significant associations (Table 2).

Discussion

The SREBP-1 is a transcription factor which regulates the expression of various genes implicated in fatty acid synthesis such as (Stearyl-CoA Desaturase and Fatty Acid Synthase) and in cholesterol uptake affecting the expression of the LDL receptor (Espenshade and Hughes, 2007) and HDL receptor SR-BI (Lopez and McLean, 1999). SREBP also controls adiponectin expression (Rahmouni and Sigmund, 2008), which regulates lipid catabolism. The release of the nuclear active form of SREBP is regulated by various proteins including SCAP and S1P (gene locus: MBTPS1) and these genes mediate the effects of SREBP. In Japanese Black cattle, a mutation in SREBF1 was associated with meat fatty acid composition (Hoashi et al., 2007). An association between the studied SNPs and lipid content was expected considering the importance of the SREBP pathway in the regulation of fatty acid synthesis. Indeed, an association between the MBTPS1 gene and lipid content nearly reached significance. This lack of significance might be due to the limited number of samples used in this study. Moreover, it was not possible to correct the data for sex effect, which might have affected our results. Indeed, some authors reported that sex can influence fat content with castrated males being fatter than females (Candek-Potokar et al., 2002; Edwards et al., 2008; Latorre et al., 2008); others, however, found little or no effect (Barton-Gade, 1987; Cisneros et al., 1996).

MBTPS1 polymorphism and the interaction SREBF1xMBTPS1 had significant effects on cured ham weight, ham yield and ham circumference. These effects may result from a secondary effect of the intramuscular fat content modification. Indeed, fat content modifies water holding capacity and, therefore, ham yield (Candek-Potokar et al., 2002). This could also explain the effects of SCAPxMBTPS1 on moisture and of SREBFxSCAP on salt content.

The SREBP is also known to induce expression of enzymes involved in the protection against oxidative stress like cysteine sulfenic acid decarboxylase, glutathione S-transferase and heme oxygenase 1 (HMOX-1) (Horton et al., 2003; Kallin et al., 2007). The HMOX-1 catalyzes the degradation of heme into biliverdin, which is subsequently transformed into bilirubin by biliverdin reductase. Further, HMOX-1, which is up-regulated by different types of cellular stresses, also presents potent antioxidant properties that are associated with the release of carbon monoxide, iron, and biliverdin from the heme molecule (Poss and Tonegawa, 1997; Otterbein et al., 2003). The SREBP pathway genes (SREBF1, SCAP and MBTPS1) can affect the presence of anti-oxidative enzymes which might explain the observed association of SNPs with meat colour after slaughter.

The observed association of the SREBF1 c.1158+118A>G SNP on Hunter A colour score may result from a difference in the muscle fibre type. Indeed, slow twitch fibres are more prone to use lipids instead of glucose as an energy source and thus require more myoglobin, resulting in meat which is more red in colour. Moreover, SREBF1 is also involved in the regulation of aldolase C, an enzyme of the glycolytic pathway (Horton et al., 2003), thus improving the use of glucose as energy supply by muscle fibres.

Most of the significant associations in the present study were obtained from the interaction of genes, suggesting that these genes could be associated in defining a few ham traits. Indeed, we observed significant associations of SREBF1xMBTPS1 on quantity traits and cured colour, of SCAPxMBTPS1 on moisture and of SCAPxSREBF1 on salt content.

Conclusions

Our findings provide initial evidence that mutations in some SREBP pathway genes are associated with U.S country ham quality and therefore, demonstrate that these genetic markers could be used in selection programs in which pigs will be utilized in country ham production. They may also be useful for dry cured hams produced in other countries such as Italy, but further investigation of these genes on other dry cured ham production seems warranted.

References


Horton, J.D., Shah, N.A., Warrington, J.A., Anderson, N.N., Park, S.W., Brown, M.S.,


