

Molecular Markers Associated with Improved Yield and Quality of Dry-Cured Hams

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Summary and Implications

The effect of three cathepsin genes on several processing characteristics of fresh and dry-cured hams was investigated. The results of the association studies conducted for all genes indicated that the variants of all genes significantly affect several of the phenotypic traits analyzed. These markers can now be used to select pigs carrying the preferred variants for dry-cured ham production.

Introduction

High quality processed pork products (dry-curing) have traditionally been produced in the Mediterranean region, in countries like Italy, Spain and Portugal. Similar dry-cure or country style cured products have been produced in the southeastern part of the U.S. for many generations. The consumer demand for these products has increased substantially in recent years, which opened a new window of opportunity for pig producers worldwide. Even in the U.S., importation of dry-cured has increased from Italy, Spain and other European countries. Local production of products similar to those imported is also beginning. Furthermore, the high market prices that these products reach make them a very attractive product for a lucrative niche market. In order to meet these new consumer requirements, pig producers need to adopt new strategies that will allow the selection of the animals carrying the most desirable genotypes for enhanced pork quality. For this purpose, a sound understanding of the genetic factors controlling pork meat quality is needed.

Meat quality traits pose a different challenge for pig breeders due to the fact that they can only be measured after the animal has been slaughtered. This is a situation where molecular markers associated with increased meat quality are most useful. Molecular genetics allows several good biological candidate genes affecting meat quality traits to be studied at the DNA level. Polymorphisms in these genes can be identified and used to develop genetic tests that in turn can be used to select the animals carrying the most desirable genotypes. To date, several major genes affecting pork meat quality have already been identified (e.g. halothane and RN genes) and are currently used by the pig industry.

Cathepsins are lysosomal enzymes involved in the proteolysis process observed during the dry curing process of hams. Therefore, the genes coding for these enzymes can be viewed as good candidate genes to explain variation associated with the production of dry-cured hams. The objectives of this study were to analyze the effect of three cathepsin genes (cathepsins B, F and Z) on several processing characteristics of fresh and dry-cured hams.

Materials and Methods

Phenotypic data was collected in a set of Southern style (dry-cured) hams obtained from Clifty Farm Country Hams (Paris, TN). The dataset included traits recorded in the fresh hams and after the dry-curing period. A muscle sample of the semimembranosus was excised from the center cut slices and used to harvest DNA. Genotypes for all genes were obtained using Polymerase Chain Reaction – Restriction Fragment Length Polymorphism (PCR-RFLP) procedures developed in our group (cathepsins B and Z) or published in the literature (cathepsin F). Association studies were conducted for all genes using two different statistical models, one for fresh ham traits, and another for cured ham traits.

Results and Discussion

The association analysis conducted revealed significant effects of all genes on several fresh (Table 1) and dry-cured (Table 2) ham traits. Cathepsin Z (CTS_Z) genotypes significantly affected several fresh and dry-cured ham traits. In particular, this gene influenced several traits related to growth (circumference, depth and weight of the fresh ham). Furthermore, the CTS_Z genotype 22 was found to be associated not only with higher fresh but also with cured ham weight and higher yield. Finally, the CTS_Z variants also had a significant effect on several ham quality traits, such as firmness and pH. Similar results were detected for cathepsin F (CTS_F). In fact, CTS_F gene variants had a significant effect on fresh and dry-cured ham weight, as well as on average marbling, intramuscular fat and pH of the cured ham. The fresh ham traits analyzed were not influenced by the cathepsin B (CTS_B) variants. However, this locus had a significant effect on several important dry-cured ham traits, including cured weight, yield, weight loss and moisture content.

This study indicates that the variants at these three cathepsin genes are associated with increased quality characteristics of fresh and dry-cured hams. Therefore, these genes can be used by the swine industry as tools to select pigs with characteristics more suitable for dry-cured ham production.

Acknowledgements

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Table 1 – Association of cathepsin genotypes with fresh ham traits

Trait	Gene		
	CTSB	CTSF	CTSZ
Circumference	0.436	0.226	0.132
Depth	0.808	0.345	0.006
Temperature	0.427	0.132	0.467
Green weight	0.301	0.002	0.016
Raw Minolta L	0.588	0.690	0.456
Raw Hunter L	0.594	0.687	0.452
Raw Minolta Y	0.615	0.693	0.415
Average color	0.218	0.435	0.260
Average marbling	0.571	0.105	0.925
Average firmness	0.742	0.244	0.114
pH	0.323	0.701	0.107

Significant (P < 0.10) and suggestive (P < 0.15) P-values are indicated in bold

Table 2 – Association of cathepsin genotypes with dry-cured ham traits

Trait	Gene		
	CTSB	CTSF	CTSZ
Final weight	0.083	0.086	0.053
Cut weight	0.089	0.134	0.189
IM Fat	0.492	0.135	0.715
Cut Minolta L	0.507	0.509	0.473
% change Minolta L	0.349	0.981	0.285
Cut Hunter L	0.810	0.596	0.711
% change Hunter L	0.812	0.857	0.538
Cut Minolta Y	0.760	0.835	0.474
% change Minolta Y	0.816	0.721	0.350
Yield	0.084	0.346	0.111
Yield 2	0.089	0.410	0.964
Moisture	0.080	0.526	0.190
Loss	0.107	0.386	0.127
Loss 2	0.129	0.461	0.949
% loss	0.094	0.349	0.130
% loss 2	0.089	0.410	0.964
Cured moisture	0.503	0.973	0.258
Salt %	0.692	0.297	0.424
Cured ham pH	0.715	0.090	0.236

Significant (P < 0.10) and suggestive (P < 0.15) P-values are indicated in bold