

# Gene Associations with Country Ham Quality, Quantity and Color Traits

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### Summary and Implications

The demand for country hams or dry-cured hams has been on the rise in recent years in the U.S., which provides a new market for pork producers. In this study, three genes involved in the regulation of fatty acid synthesis and anti-oxidative enzyme transcription were investigated for associations with country ham quality, quantity, and color traits. These processes are important for meat quality. Differences in the animals' genetic sequence, single nucleotide polymorphisms (SNPs) were detected in each gene and association analyses were performed. Several significant associations were found and include, but are not limited to, cured weight, ham yield, moisture and salt percentage. The findings in this study provide evidence that pigs carrying favorable variants of these genes could be selected for use in improvements in country ham production.

### Introduction

The curing of pork in the United States dates back hundreds of years with techniques that have been refined and passed down for generations. A country ham is meat taken from the ham or hind leg of a pig and is cured by salting the fresh pork followed by further process steps such as drying, aging, and smoking. The consumer demand for these products has increased substantially in recent years, which opened a new window of opportunity for pig producers worldwide. This high value product requires high quality fresh meat to avoid processing problems.

The three genes, *SREBP-1* (a transcription factor involved in the regulation of fatty acid synthesis and anti-oxidative enzyme transcription) and its regulating genes, *SCAP* and *SIP*, work together in the SREBP pathway for lipid homeostasis. Fatty acid synthesis and antioxidative enzymes greatly affect the majority of meat quality traits, therefore the regulation of these processes are extremely important.

The study objective was to investigate *SREBP-1* and its regulating genes, *SCAP* and *SIP* and find genetic markers called single nucleotide polymorphisms (SNPs). These

SNPs are small genetic changes or variations that occur when a single nucleotide (A, T, C, or G) in the genetic sequence is altered. For example, the nucleotide letter A replaces one of the three other nucleotide letters: C, G, or T. These differences were then determined for each animal for each gene and association analyses were conducted to see if there were any associations between these genes and several meat quality traits in a sample of country hams.

### Materials and Methods

Traits were collected and recorded in the fresh hams and after the dry-curing period in a set of 299 Southern style (dry-cured) hams obtained from Clifty Farm Country Hams (Paris, TN). DNA was extracted from a muscle sample of the ham muscle from each animal. Variations in each of the three gene sequences were analyzed. Association studies were conducted for all genes individually and analyzed for gene-gene interaction using a standard statistical approach.

### Results and Discussion

All genes were found to be significantly associated with several fresh and dry-cured ham traits. Genotypes from *SIP* and the gene interactions between *SREBP1xSIP* were significantly associated with cured weight (*SIP*,  $P<0.05$  and *SREBP1xSIP*,  $P<0.05$ ), ham yield (*SIP*,  $P<0.05$  and *SREBP1xSIP*,  $P<0.05$ ), and ham circumference (*SIP*,  $P<0.05$  and *SREBP1xSIP*,  $P<0.001$ ). The significant associations with color traits on fresh and cured hams include fresh Minolta and Hunter A scores (*SREBP1*,  $P<0.05$ ), cured Minolta B (*SREBP1xSIP*,  $P<0.01$ ) and cured Hunter B (*SIP*,  $P<0.05$  and *SREBP1xSIP*,  $P<0.01$ ). Significant associations with cured ham quality traits were also found and they are moisture (*SCAPxSIP*,  $P<0.02$ ), salt percentage (*SCAPxSREBP1*,  $P<0.05$ ) and lipid content (*SIP*,  $P<0.10$ ) was nearly significant.

This study demonstrates that these genetic markers could be used in selection of the pigs carrying favorable variants of these genes, and used for country ham production.

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