2008

Gene Associations with Country Ham Quality, Quantity and Color Traits

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Recommended Citation

Glenn, Kimberly; Renaville, Benedicte; Mote, Benny E.; Fan, Bin; Stalder, Kenneth J.; and Rothschild, Max F. (2008) "Gene Associations with Country Ham Quality, Quantity and Color Traits," *Animal Industry Report: AS 654, ASL R2347.* Available at: https://lib.dr.iastate.edu/ans_air/vol654/iss1/96

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This swine is available in Animal Industry Report: https://lib.dr.iastate.edu/ans_air/vol654/iss1/96
Gene Associations with Country Ham Quality, Quantity and Color Traits

A.S. Leaflet R2347

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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 antioxidative 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 analyzes 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 antioxidative 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 analyzes 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.

Acknowledgements
Support was provided by Iowa State University Department of Animal Science, the Center for Integrated Animal Genomics and the College of Agriculture and State of Iowa and Hatch funding.