RESEARCHABSTRACT

pork checkoff

ANIMAL SCIENCE

Title: Identification of quantitative trait nucleotides (QTN) for pork tenderness – **NPB #08-105**

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Scientific Abstract

Genome scans have identified QTL for tenderness on pig chromosome 2. The QTL have been fine-mapped to the calpastatin locus. In this study we genotyped one hundred thirty polymorphisms in promoter regions and evaluated these with previous markers and changes in amino acids. We identified five SNPs that were consistently highly associated with tenderness measures across four different populations of industry-relevant pigs. Five polymorphic sites demonstrated binding to nuclear extracts in electrophoretic mobility shift assays and two of these were allele-specific in their ability to bind nuclear proteins. At the polymorphic sites that bound protein, the SNPs were not in linkage disequilibrium with each other and may independently affect calpastatin expression.

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