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Associations between 44 gene-associated markers and meat tenderness in Limousin steers

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Beef tenderness is a major factor influencing consumer satisfaction which can only be quantitatively measured using Warner-Bratzler Shear Force (WBSF) after carcasses are harvested and samples have been aged for fourteen days and then cooked. Because of the logistic difficulty and cost of this process, researchers have begun developing genetic markers which identify beef cattle with the propensity to produce tender meat. In this project, 44 single nucleotide polymorphisms (SNPs) representing 11 genes were scored in 131 Limousin steers with available WBSF, growth and carcass composition data. Genotypes were determined using a Beckman Coulter GenomeLab SNPStream system. The primary genes of interest in this study were CAPN1 which encodes the μ -calpain protein which posthumously degrades myofibrils and CAST which encodes the calpain inhibitor, calpastatin. While SNP loci in both of these genes are currently being commercialized to the beef industry, none appear to be causal for effects on meat tenderness. This project was designed to examine alternate SNPs within these genes to identify markers that may have greater commercial value. SNPs located within the genes: LOX, OPN, ABCG2, DGAT1, GHR, LEP, TG, SST and APM were also analyzed, since these genes have previously been associated with variation in growth and carcass composition traits in beef cattle. A commercial test which combines several of these SNPs would greatly benefit the industry by effectively identifying genetically superior breeding and slaughter animals.

