Abstract #2

Genome scan and gene enrichment analyses of meat tenderness in an Angus-Brahman cattle population

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Genome wide association combined with gene enrichment analyses will not only identify genomic regions of large effect but will also have the potential to help with identifying the challenging small effect chromosomal regions. The objective of this study was to apply this methodology to meat tenderness related traits in an Angus-Brahman cattle population. Animals used in the study belong to the multibreed Angus-Brahman herd from University of Florida. Two steaks from the *Longissimus dorsi* muscle were sampled from each animal. Objective tenderness was measured by Warner-Bratzler Shear Force (WBSF) on 673 steaks, and tenderness and connective tissue amount (CTA) were measured through a trained sensory panel on 496 steaks. Animals were genotyped with the Bovine GGP F250 array Data processing and analysis were performed using the Genetics Q-K analysis workflow of JMP-Genomics 6.0 software. All SNPs with uncorrected p-value ≥ 0.05 were included in a gene enrichment analysis. Only genes expressed in bovine skeletal muscle were included in subsequent analyses. The correlation between all the SNPs within each gene was calculated and SNPs were considered correlated when $r^2 > \pm 0.3$. Genes, whose SNPs are all correlated, were included once in the final gene list and genes with more than one uncorrelated SNP were included multiple times (as many as the number of uncorrelated SNPs) in the final gene list. A total number of 5,980 markers assigned to 2,134 genes for WBSF; 5,844 markers in 2,191 genes for sensory panel tenderness; and 5,710 markers in 2,060 genes for CTA were significant in the WGA studies. The final gene lists had 1,503, 1,343, and 1,402 genes for WBSF, tenderness, and CTA, respectively. The pathways GO:0005789, GO: 0000122, GO:0005743, GO:0045944 were identified as enriched. This study found an enrichment of genes in four GO terms and some of them are involved in regulation of transcription and cell growth and proliferation.