

COMPARATIVE TRANSCRIPTOMIC PROFILE FOR MEAT TENDERNESS IN A MULTIBREED ANGUS-BRAHMAN POPULATION

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I. OBJECTIVES

The aim of this study was to evaluate the transcriptome profile of *Longissimus dorsi* muscle from multibreed Angus-Brahman cattle with divergent phenotypes for meat tenderness.

II. MATERIALS AND METHODS

Animals from 4 breed groups (BG) from the University of Florida multibreed Angus-Brahman herd were used: BG1 = 80% > 100% Angus; BG2 = 65% > 79.0% Angus; BG3 = 40% > 59% Angus; and BG4 = 0.0% > 19% Angus. Two extreme groups were identified within each BG based on the Warner-Bratzler shear force (WBSF) values (LOW and HIGH). A total of 47 animals slaughtered in 2016 and 2017 with *Longissimus dorsi* muscle RNA-Seq data were used to identify differentially expressed genes (DEG). A Generalized Mixed Linear model was used to identify DEG, assuming link function with negative binomial distribution. The model included the fixed effects of the BG, WBSF class, BG × WBSF class interaction, and the random effects of birth year. The DEG annotation was performed using *Ensembl* Release 99 file, and the Database for Annotation, Visualization and Integrated Discovery 6.8 was used to identify Gene Ontology terms and pathways with significant enrichment scores. A false discovery rate < 10% was used for DEG and Gene Ontology analyses.

III. RESULTS

The WBSF LSMeans and standard deviation for the LOW groups within each BG were as follows: 2.77 ± 0.24 kg (BG1, *n* = 8), 3.11 ± 0.28 kg (BG2, *n* = 5), 3.12 ± 0.47 kg (BG3, *n* = 7), and 3.22 ± 0.55 kg (BG4, *n* = 5). The WBSF LSMeans and standard deviation for the HIGH groups within each BG were as follows: 5.00 ± 0.62 kg (BG1, *n* = 4), 5.04 ± 0.78 kg (BG2, *n* = 5), 5.41 ± 0.36 kg (BG3, *n* = 7), and 6.00 ± 0.50 kg (BG4, *n* = 6). There were no significant BG × WBSF class interaction effects. There were 266 significant DEG for the main effect of BG. Regression analysis of the transcripts counts on Angus percentage showed that 129 of the 266 DEG had a linear reduction in expression as the percentage of Angus increased from 0% to 100%, and 135 DEG had a linear increase in expression as the percentage of Angus increased. For the main effect of BG, the most significant pathways were related with general metabolism ($P = 7.81 \times 10^{-8}$), longevity regulating ($P = 1.26 \times 10^{-4}$), and proton pump inhibitor ($P = 1.48 \times 10^{-4}$). There were 2,038 significant DEG for the WBSF class main effect. A correlations analysis between WBSF values and transcript counts identified 353 and 47 DEG with correlation higher than -0.50 and 0.5, respectively. The most significant pathways for the WBSF class main effect DEG were related with transport to the Golgi and subsequent modifications ($P = 1.91 \times 10^{-12}$), vesicle-mediated Transport ($P = 4.14 \times 10^{-10}$), and Metabolism of Proteins ($P = 1.34 \times 10^{-9}$).

IV. CONCLUSION

Our results suggest that (i) effect of WBSF class acts independently of breed composition, (ii) there are significant differences in transcript count between BG, and (iii) there are significant differences in transcript count between the LOW and HIGH WBSF groups.

Keywords: beef quality, RNA profile, RNA-Seq, Warner-Bratzler shear force