Variations in intramuscular fat content and profile in Angus x Nellore steers under different feeding strategies contribute to color and tenderness development in longissimus thoracis

Daniel Antonelo[1], Mariane Beline[1], Saulo Silva[1], Juan Gómez[1], Christina Ferreira[2], Xue Zhang[3], Bruna Pavan[1], Larissa Koulicoff[4], Alessandra Rosa[1], Rodrigo Goulart[1], David Gerrard[5], Surendranath Suman[6], Wes Schilling[3], Julio Balieiro[1]

[1] University of Sao Paulo, Pirassununga, Brazil
[2] Purdue University, West Lafayette, USA
[3] Mississippi State University, Mississippi State, USA
[4] Kansas State University, Manhattan, USA
[5] Virginia Tech University, Blacksburg, USA
[6] University of Kentucky, Lexington, USA

Introduction: Muscle from cattle reared under different finishing regimes (FR; grain vs. forage) and growth rate (GR) may have divergent metabolic signatures that are reflective of their inherent differences in biochemical processes that may impact its subsequent transformation into high quality beef. Thus, the aim of this study was to evaluate the muscle lipid profiles from cattle differing in FR and GR and correlate them to beef color and tenderness.

Materials and Methods: Thirty-six contemporary ½ Angus x ½ Nellore crossbred steers (330 ± 30 kg body weight [BW], 12 ± 1-mo-old) were randomly assigned to one of four treatments (n = 9 steers/treatment): 1) feedlot, high GR (F-H); 2) feedlot, low GR (F-L); 3) pasture, high GR (P-H); and 4) pasture, low GR (P-L). Average BW of 530 kg was reached within each treatment after 116, 228, 262 and 292 d of feeding with an ADG of 1.51, 0.94, 0.76, and 0.62 kg/d for F-H, F-L, P-H, and P-L animals, respectively. Samples were excised from the longissimus thoracis (LT) muscle at 24 h postmortem for total intramuscular fat (IMF) and lipidomic analysis. One 2.5-cm thick LT muscle sample was collected between the 12th and 13th ribs for analyses of instrumental color (L*, a*, and b*) and Warner Bratzler shear force (WBSF). Targeted lipid profiling was performed using discovery Multiple Reaction Monitoring (MRM)-profiling method. Beef quality data were analyzed in a completely randomized design considering treatment as fixed effects and the animal as the experimental unit. The relative ion intensity data (MRMs) were uploaded to Metaboanalyst 5.0 and normalized by auto-scaling. Principal component analysis, heatmaps, and quantitative enrichment analysis were performed using the lipid dataset for each sample. Pearson's correlation analysis was performed between beef quality traits and lipid compounds.

Results: Steaks from F-H animals had greater L* ($P < 0.001$), a* ($P = 0.002$), and b* ($P < 0.001$) values than steaks from other treatments. Steaks from F-H also had higher IMF ($P = 0.001$) deposition than P-H and P-L animals, but were not different from F-L animals ($P > 0.05$). F-L animals had a greater L* ($P < 0.05$) and similar IMF ($P > 0.05$) when compared to P-H and P-L animals, which did not differ for beef quality traits. In addition, P-H and P-L animals yielded steaks with greater WBSF (less tender) values than F-H and F-L animals ($P < 0.05$). Of the 1,366 ion transitions (MRMs) scanned, 440 were 440 were found to have an intensity of at least 1.3-fold higher than the blank sample. Relative ion intensity data indicated that 172, 97, 117, and 82 lipids were differentially abundant ($P < 0.05$) between F-H × P-L, F-L × P-H, F-H × F-L, and P-H × P-L comparisons, respectively, especially triacylglycerol (TG), phosphatidylcholine (PC), phosphatidylethanolamine (PE), sphingomyelin (SM), and acyl-carnitine (AC) classes. Distinct clusters between feeding strategies for the lipid dataset indicated that glycerolipid metabolism ($P = 0.004$), phospholipid metabolism ($P = 0.009$), sphingolipid metabolism ($P = 0.050$) and mitochondrial beta-oxidation of long chain saturated fatty acids ($P = 0.073$) pathways differed due to finishing regime and growth rate. Seven (3 AC, 2 PC, 1 PE, and 1 SM), 43 (featuring 22 TG, 9 AC, and 5 PG) and 132 (featuring 85 TG, 27 PC, and 15 PE) lipids had moderate ($-0.4 > r > 0.4$) and significant ($P \leq 0.05$) correlation with L*, a* and WBSF, respectively.

Conclusions: Results indicated that FR is the main factor that is responsible for altering IMF deposition and phospholipid profiles, which in turn contribute to the development of lightness and tenderness in beef. Moreover, GR was the main factor that affected TG deposition and profile, which was positively correlated with the redness of the beef.

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