2016 Reciprocal Meat Conference – Muscle and Lipid Biology and BioChemistry

Meat and Muscle Biology™

Proteomic Biomarkers for Color in Beef Longissimus Lumborum Aged for 21 Days

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Keywords: beef color, longissimus lumborum, proteome, wet-aging
Meat and Muscle Biology 1(2):149 **doi:10.221751/rmc2016.143**

Objectives

Meat color is highly critical to fresh beef marketability as it influences consumer purchase decisions at the point-of-sale. Longissimus lumborum (LL) is an economically important and color-stable muscle in beef hindquarter which has been extensively studied with respect to color biochemistry. Previous research indicated that sarcoplasmic proteome influences fresh beef color. Post-mortem aging employed to improve beef tenderness and palatability can influence color as well as the sarcoplasmic proteome. Our objective was to examine color attributes and sarcoplasmic proteome profile of beef LL during wet-aging, and to identify potential biomarkers for beef color attributes.

Materials and Methods

LL muscles were obtained from both sides of eight (n = 8) beef carcasses (USDA Choice, 24 h post-mortem). LL from each side was further divided into two equal-length sections and vacuum-packaged. The vacuum-packaged muscle sections were randomly assigned to aging at 2°C for either 0 (LL0), 7 (LL7), 14 (LL14), or 21 (LL21) days. On each aging period, muscle sections were fabricated into 2.5-cm thick steaks. Samples for proteome analysis obtained during fabrication were frozen at –80°C. After respective aging, the steaks were allowed to bloom for 2 h, and lightness (L^*), redness (a^*), yellowness (b^*), hue (trueness of red), chroma (saturation index), pH, and metmyoglobin reducing activity (MRA) were evaluated. The color data, pH, and MRA were analyzed using MIXED procedure in SAS (SAS Inst. Inc., Cary, NC). Sarcoplasmic proteome was analyzed using two-dimensional electrophoresis (pH 5 to 8; 13.5% acrylamide gels). The images of Coomassie Blue-stained gels were obtained using VersaDoc and were analyzed by PDQuest software. The influence of aging on proteome profile was examined by comparing LL0 against rest of the aging days. Protein spots exhibiting 1.5–fold intensity difference and associated with $P <$ 0.05 in a pairwise Student's t test were considered to be differentially abundant and were subjected to tryptic digestion and tandem mass spectrometry for identification.

Results

The LL0 exhibited lower ($P < 0.05$) surface redness (a^*), lightness (L^*), yellowness (b^*), hue, and chroma than samples from other aging days. However, pH and MRA were similar ($P > 0.05$) on all aging days. Proteome analyses revealed that adenylate kinase isoenzyme 1 was more abundant in LL7, whereas creatine kinase M-type, β-enolase, phosphoglucomutase-1, heat shock cognate 71 kDa protein, and alanine aminotransferase 1 were more abundant in LL14. Comparison of LL0 and LL21 proteomes revealed greater abundance of α-enolase in LL21, whereas malate dehydrogenase and glyceraldehyde-3-phosphate dehydrogenase were more abundant in LL0.

Conclusion

Our results indicated that beef LL demonstrates lower surface redness, lightness, yellowness, hue, and chroma on d 0 of aging compared to the other aging periods. Majority of the differentially abundant proteins observed in LL during aging are chaperones and enzymes associated with energy metabolism. Chaperones have been reported to prevent protein denaturation and aggregation in biological systems, whereas metabolic enzymes are well-known to play a critical role on beef color biochemistry. Therefore, these findings indicated that differentially abundant sarcoplasmic proteins could be utilized as potential biomarkers for color attributes in fresh beef LL.

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