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Aging-Induced Changes in Sarcoplasmic Proteome of 3 Beef Hindquarter Muscles with Differential Color Stability

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Objectives

Fresh beef color is critical to consumers' purchase decisions. Beef color stability is muscle-specific, and the muscle-specific variations in sarcoplasmic proteome influence beef color. Post-mortem aging is a common practice employed by beef industry for improving beef tenderness and palatability. However, the color attributes and sarcoplasmic proteome of beef muscles undergo changes during aging. The objective of this study was to examine the changes in the sarcoplasmic proteome profile of 3 differentially color-stable muscles from beef hindquarters during postmortem aging.

Materials and Methods

Longissimus lumborum (LL), psoas major (PM), and semitendinosus (ST) muscles were obtained from both sides of 8 (n = 8) beef carcasses (USDA Choice, 24 h post-mortem). Muscles were further divided into 2 equal-length sections and vacuum-packaged. The vacuum-packaged muscle sections were randomly assigned to aging at 2°C for either 0, 7, 14, or 21 d. On each aging period, muscle sections were fabricated into 2.5-cm thick steaks, individually over-wrapped, and allocated to refrigerated storage for 0, 3, or 6 d. Samples for proteome analysis obtained during fabrication were frozen at –80°C. On each storage day, lightness (L*), redness (a*), yellowness (b*), hue (trueness of red), chroma (saturation index), pH, and metmyoglobin reducing activity (MRA) were evaluated. The instrumental color, pH, and MRA data were analyzed using MIXED procedure in SAS (SAS Inst. Inc., Cary, NC). Sarcoplasmic proteome was analyzed using 2-dimensional electrophoresis (pH 5 to 8; 13.5% acrylamide gels). The images of Coomassie Blue-stained gels were obtained and analyzed. Protein spots exhibiting 1.5–fold intensity difference ($P < 0.05$) were considered differentially abundant and were subjected to tryptic digestion and tandem mass spectrometry for identification

Results

The results indicated that instrumental color attributes and biochemical parameters during storage were influenced by muscle source and aging ($P < 0.05$). LL and ST had greater ($P < 0.05$) surface redness (a* value) than PM, whereas the color stability (R630/580) followed the order: LL > ST > PM. Aging also influenced surface redness with 7-d aged steaks demonstrating greatest values ($P < 0.05$). Proteome analysis identified differentially abundant glycolytic enzymes between the treatments (muscle source and aging days; $P < 0.05$) indicating muscle-specific changes in sarcoplasmic proteins during aging. The glycolytic enzymes identified (triosephosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase, enolase, and phosphoglucomutase-1) were more abundant ($P < 0.05$) in color-stable LL and ST compared to color-labile PM.

Conclusion

Our results indicated that the color attributes and sarcoplasmic proteome profile of beef LL, PM, and ST were influenced by aging for 21 d. Furthermore, the aging-induced changes in the sarcoplasmic proteome profile and color traits were muscle-specific. The differentially abundant glycolytic enzymes could be used as biomarkers for beef color, and for developing muscle-specific processing strategies to improve beef color stability.

