2016 Reciprocal Meat Conference – Muscle and Lipid Biology and BioChemistry

Meat and Muscle Biology™

Investigation of Metabolomic Profiles to Understand the Effect of Postmortem Aging on Color and Lipid Oxidation Stabilities of Different Bovine Muscles

D. Ma[1]*, B. R. Cooper[2], J.-H. Oh[3], H. Chun[3], and Y. H. B. Kim[1]

[1]Department of Animal Science, Purdue University, West Lafayette, IN, USA; [2]Bindley Bioscience Center, Purdue University, West Lafayette, IN, USA; [3]Department of Statistics, Purdue University, West Lafayette, IN, USA

Keywords: beef color, lipid oxidation, metabolomics, postmortem aging
Meat and Muscle Biology 1(2):147 **doi:10.221751/rmc2016.141**

Objectives

Postmortem aging is extensively practiced in the meat industry mainly due to its beneficial impacts on eating quality attributes. However, depletion of antioxidant compounds during aging may lead postmortem muscles to be more oxidation susceptible, resulting in intensified discoloration and/or off-flavor development. Identifying key metabolites that are related to oxidative quality deterioration will provide critical insights for the industry to develop practical strategies to prevent oxidation-related quality defects. The objective of this study was to identify key metabolites that could be associated with oxidation stabilities of aged bovine muscles by using a novel HPLC-MS based global metabolomics approach.

Materials and Methods

At 1-d postmortem, three muscles (*longissimus dorsi* (LD), *semimembranosus* (SM) and *psoas major* (PM)) from 7 beef carcasses were divided into 3 sections, vacuum-packaged, and assigned for 9, 16, and 23 d of aging. After each aging time, steaks made from each sections were overwrap PVC-packaged and displayed for 7 d. Meat color, lipid oxidation (TBARS) and non-heme iron were measured and previously reported. Selected samples ($n = 4$) at d 0 (prior to display) of each aging time were analyzed by HPLC-ESI-MS metabolomics. The experiment was a split-plot design. The relative abundance of metabolites was quantified and normalized for statistical inference, which was analyzed by PROC MIXED of SAS (SAS Inst. Inc., Cary, NC) for the main effects of aging, muscle types, and their interaction. Spearman correlation and principal component analysis (PCA) were conducted by using R software.

Results

The metabolomics platform detected 1,012 compounds, among which 243 were significantly ($p < 0.05$ with FDR correction) responsive to either aging or muscle treatment. Primary metabolites being identified include carnitines, free amino acids, nucleotides, vitamins/coenzymes, and glucuronides. NAD showed positive correlation to redness of meat color ($r = 0.672$) and negative correlation to discoloration ($r = –0.535$), TBARS ($r = –0.554$), and non-heme iron ($r = –0.667$), indicating its relevance to myoglobin redox stability and/or lipid oxidation stability. A group of carnitines that decreased with aging was associated with decreased redness ($r = –0.67$) and intensified discoloration ($r = 0.70$), which may be explained by its role in the mitochondria matrix and/or its potential antioxidation property. Glucuronides were increased with extended aging, and associated with discoloration ($r = 0.56$) and non-heme iron accumulation ($r = 0.65$). Some nucleotides, nucleosides and free amino acids were more liberated with aging and positively correlated to chemical/phenotypic oxidation indicators. The PCA plots showed clear clustering among 3 aging treatments (PC1 33%) or muscle types (PC2 21%).

Conclusion

The results from the current study suggest that some metabolites could be associated with oxidation stabilities of beef muscles. In particular, our study confirmed the relevance of NAD and NADH in myoglobin redox stability. Further, we identified potential compounds, such as carnitines and glucuronides, which could be related to color/lipid oxidation stabilities of aged beef muscles. Further research on elaborating the direct involvement of those metabolites in meat quality traits as potential biomarkers and their underlying biochemical process should be warranted.