METABOLOMICS PROFILING OF MEAT EXUDATE TO UNDERSTAND THE IMPACT OF POSTMORTEM AGING ON OXIDATIVE STABILITY OF BEEF MUSCLES

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I. INTRODUCTION

Postmortem aging is a common practice to increase meat palatability. However, extended aging period may result in adverse impacts on color and oxidative stability of meat, subsequently inducing rapid discoloration and/or off-flavor development [1]. Therefore, developing aging strategies that specifically monitor ideal aging times for different muscles will be beneficial for the meat industry to minimize oxidation–related quality defects, while maximizing positive aging impacts on eating quality attributes of fresh meat. Meat purge is an easy-to-obtain aqueous matrix, which is naturally released from fresh meat during storage. Despite its potential as an excellent analytical matrix to determine meat quality attributes, very few studies have addressed the value of analysing the meat exudate for assessing meat quality [2-3]. Further, little to no research is available characterizing the chemical changes in metabolites present in beef exudates to determine muscle-specific biochemical mechanisms associated with oxidative stability of different muscles during aging. Therefore, the objective of this study was to characterize the major metabolites present in beef exudate and determine the relationship between identified metabolites and color and lipid oxidative stability of beef muscles during aging. This study was further investigation of our recent published study [1], where we found that different muscle type and aging period could differently affect oxidative stability as well as the metabolomics profile of the meat.

II. MATERIALS AND METHODS

Beef loin (*M. Longissimus lumborum,* LD) and tenderloin (*M. Psoas major,* PM) from one side of 8 carcasses were obtained at 2 d postmortem, cut into 3 sections and vacuum packaged. Sections were then randomly assigned into 3 different aging periods (9, 16 and 23 d). At the end of each aging, purge was collected from each package and immediately frozen at -80 ºC for the metabolomics analysis. Steaks were collected from each section for instrumental and sensory color analyses and chemical analyses, such as 2-thiobarbituric acid reactive substances (TBARS), non-heme iron content (NHI) and conjugated diene (CD) as previously reported [1]. Purge samples (n =6) were prepared and were analyzed by UPLC-ESI-MS metabolomics. Mass chromatogram peaks were obtained using time of flight mass spectrometry and annotated using METLIN and HMDB database. The relative abundance of metabolites was quantified and normalized for the statistical analyses. Data were analyzed by split-plot ANOVA using PROC Mixed from SAS, and LS means were separated ($P<0.05$). Principle component analysis (PCA) was conducted by using R software.

III. RESULTS AND DISCUSSION

A total of 517 metabolites were detected from meat exudate samples, in which 170 metabolites were found to be significantly different between treatments ($P<0.05$). The PCA analysis exhibited distinct clusters of the metabolites of each treatments, separating each muscle type and aging period (Fig. 1). This result was in agreement with our previous finding, where different muscle types resulted in different liberation of metabolites in fresh muscle with aging [1]. At 23 d, higher abundance of antioxidant related compound, such as L-arginine and Quinone, were observed in the meat exudate samples from LD compared to PM ($P<0.05$). Homocysteine, an oxidative stress inducer, was found to be more abundant in PM compared to LD ($P<0.05$). Furthermore, propionyl carnitine, a known antioxidant, was more present in PM at 9 d and significantly decreased ($P<0.05$) at 23d, which would be likely associated with the rapid decrease in color and lipid oxidative of PM samples with extended aging [1]. Taken together, these identified metabolites in exudate samples from different beef muscles with aging were in good agreement with our previous results of beef steak samples. In the study, lower extents of discoloration, TBARS, CD and NHI were observed in LD compared to PM with aging [1].

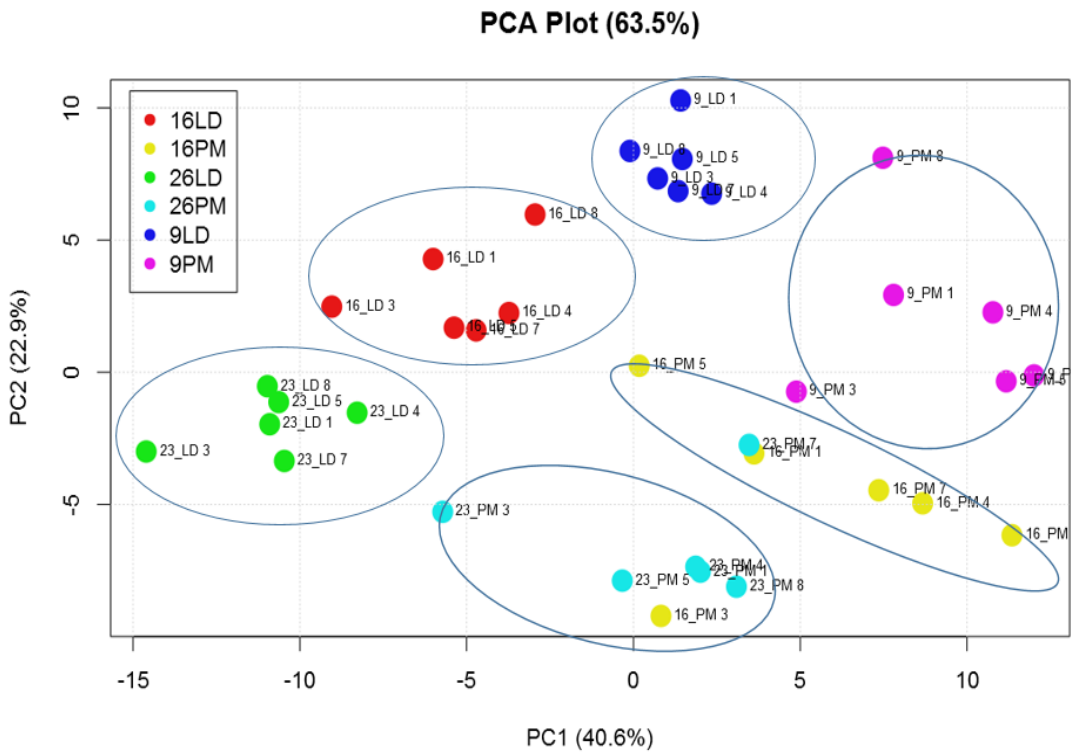

Figure 1. PCA analysis of identified metabolites (P<0.05) in exudate samples from different muscles (*Longissimus lumborum*, LD and *Psoas major*, PM) with various aging times (9, 16, and 23 days).

IV. CONCLUSION

The results from the current study suggest that metabolomics profiling of meat exudate could clearly distinguish compounds from different muscles with different aging periods. Meat purge collected from different aging periods and muscles revealed some oxidative stability-related compounds, which could possibly explain the results from the beef muscle samples, where muscle-specific aging response to color and oxidative stability was found. Together, the results indicate that meat exudate analysis could be a potentially viable analytical matrix to predict meat quality attributes. Further studies to confirm the feasibility of using these identified metabolites as potential biomarkers through analyzing comprehensive data correlation and targeted compound quantification would be highly warranted. A part of findings and further implications of the present study have been filed for the provisional patent application (US #68203).

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