POSTMORTEM PROTEOMIC CHANGES IN NORMAL AND WOODY BROILER BREAST MUSCLE

X. Zhang[1*], M. W. Schilling[1], W. Zhai[2], S. P. Suman[3], S. Li[3], J. Chen[4], H. Zhu[4], and D. S. Antonelo[5],
[1]*Food Science, Nutrition, and Health Promotion, Mississippi State University, Mississippi State, MS, USA*,

[2]*Department of Poultry Science, Mississippi State University, Mississippi State, MS, USA*,

[3]*Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, USA*,

[4]*Proteomics Core Facility, University of Kentucky, Lexington, KY, USA*,

[5]*Department of Animal Nutrition and Production, University of São Paulo, Pirassununga, Brazil*,

*xz206@msstate.edu

I. OBJECTIVES

Woody breast (WB) is a stress-related pectoral myopathy in fast-growing broilers. WB muscle exhibits changes in energy homeostasis, osmotic balance, protease/lipase system, and proteins compared to normal breast (NB). These antemortem differences can influence the biochemical changes postmortem. In the current study, the proteomic profiles in NB and WB were studied early postmortem (0–24 h after death) in order to characterize proteome changes in live muscle, pre-rigor muscle, and post-rigor muscle to improve our knowledge regarding the postmortem biochemical changes exerted by the WB condition.

II. MATERIALS AND METHODS

A total of 128 one-day-old mixed-sex chicks were selected and randomly assigned to 8 pens that were evenly distributed in a chicken house at the Poultry Research Farm at Mississippi State University (IACUC-16-542). At 8 wk of age, live male broilers were evaluated by palpation for WB myopathy. Four birds with NB were sampled from 4 pens (1 bird per pen), and 4 birds with WB were sampled from the rest of 4 pens (1 bird per pen). Birds were euthanized using CO_2 gas. The muscle from the cranial portion of the right breast was collected and snap-frozen in liquid nitrogen at death (0 min), 15 min, 4 h, and 24 h postmortem. To confirm the manual palpation technique, the WB defects were evaluated at each time point, where 0 = normal, 1 = slight, 2 = moderate, and 3 = severe. Three NB samples ($n = 3$) that were scored 0 and 1, and three WB samples ($n = 3$) that were scored 2 and 3 throughout 24 h were selected for proteomic analysis. Whole muscle proteins were separated using two-dimensional gel electrophoresis (6 gels per treatment) and identified using liquid chromatography-tandem mass spectrometry. A 1.5-fold change threshold in abundance between samples collected at 4 time points was considered significant ($P < 0.05$) using the Student's *t* test.

III. RESULTS

Four proteins, including EH domain-containing protein 2, elongation factor 2, phosphoglycerate mutase 1, and T-complex protein 1 subunit gamma, were changed in both NB and WB muscles during postmortem storage. Twenty proteins were uniquely changed in either NB (6 proteins) or WB (14 proteins) postmortem muscles, indicating the differences in their postmortem metabolism. In postmortem WB meat, the changes in protein degradation products were observed as indicated by the presence of desmin fragment, ovotransferrin chain A, and troponin I chain I. In addition, a few glycolytic proteins in WB consisted of post-

translational modified postmortem, including enolase, phosphoglucomutase-1, phosphoglycerate mutase 1, and pyruvate kinase.

IV. CONCLUSION

WB meat exhibited a greater number of changes in structural proteins, metabolic proteins, stress-related proteins, and transport proteins. In addition, WB had a greater rate of postmortem metabolism and a greater number of post-translational modifications postmortem due to the differences in antemortem conditions that exist in NB and WB. These differences indicate a faster and more oxidative muscle to meat conversion process for WB. These protein biomarkers and their post-translational modification products improve our knowledge of the biochemical processes in postmortem WB meat and provide novel insights into the development of WB and the potential strategies to reduce WB incidence, such as alleviating oxidative stress and regulating protein degradation and oxidation.

Keywords: postmortem change, protein degradation, proteomics, woody breast