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RELATIONSHIP BETWEEN INDIVIDUAL DIFFERENCES IN SKELETAL MUSCLE PROTEOLYSIS INDUCED BY PRE-SLAUGHTER FASTING AND CHICKEN MEAT QUALITY AFTER AGING IN BROILER CHICKENS

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I. INTRODUCTION

Pre-slaughter fasting is a common practice in the poultry meat industry, as it can excrete gastrointestinal content to reduce the risk of microbial contamination [1-3]. However, fasting induces skeletal muscle proteolysis by enhancing the activities of several muscle proteases and proteasomes [3,4]. Our previous study suggested that skeletal muscle proteolysis levels are related to postmortem chicken meat quality, especially glutamic acid content and umami taste [5], while the relationship between individual differences in skeletal muscle proteolysis levels and meat quality after aging remains poorly understood. This study aimed to investigate the effect of pre-slaughter fasting on individual differences in skeletal muscle proteolysis levels and their relationship with meat quality after aging, with a specific focus on the free amino acid contents and muscle proteases and proteasomes in the pectoralis major muscle of broiler chickens.

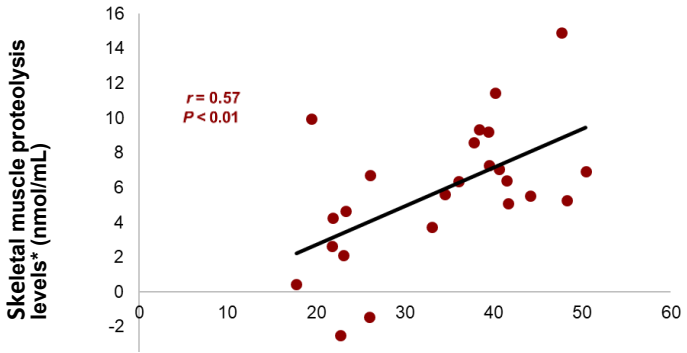


Figure 1. Relationship between skeletal muscle proteolysis levels and glutamic acid concentrations in the pectoralis major muscle in broiler chickens. Reference: [5], * an indicator of skeletal muscle proteolysis: post-fasting minus pre-fasting plasma N^{τ}-methylhistidine concentrations.

II. MATERIALS AND METHODS

Fifty broiler chicks (Ross 308) at 0 days of age were used in this study and reared until 42 days of age. The chickens were fed a semi-purified diet based on corn and soybean meals, along with *ad libitum* access to water, until 41 days of age. At 41 days, all experimental chickens were fasted for 16 hours and then slaughtered at 42 days. Blood samples were collected from the wing vein just before fasting and again just prior to slaughter. Pectoralis major muscles were collected at slaughter and after 48 hours of aging (4°C). Plasma concentrations of N^{τ}-methylhistidine (MeHis), an indicator of skeletal muscle proteolysis levels, and free amino acid content in the pectoralis major muscle after aging were analyzed by the UHPLC system (NexeraX2, Shimadzu Co., Ltd., Japan). The mRNA expressions of some muscle proteases and proteasomes were analyzed using qPCR. Data were analyzed using the SAS (version 9.4, SAS Institute, Cary, NC). Pearson's correlation coefficients were analyzed using the PROC CORR procedures. The study protocols and procedures were approved by the Animal Care and Use Committee of Okayama University (approval number: OKU-2023601).

III. RESULTS AND DISCUSSION

The skeletal muscle proteolysis levels (changes in plasma MeHis concentrations), calculated by post-fasting minus pre-fasting, ranged from −1.0 to 12.7 nmol/mL (mean ± SD: 3.6 ± 3.01), indicating considerable individual differences. The glutamic acid (Glu) contents in the pectoralis major muscles after 48 hours of aging ranged from 9.7 to 45.8 mg/100g (mean ± SD: 18.0 ± 7.34). These results suggest that, even though broiler chickens experienced the same duration of pre-slaughter fasting, there were individual differences in muscle proteolysis levels and Glu contents in the pectoralis major muscle in broilers. Interestingly, a positive correlation was observed between skeletal muscle proteolysis levels and Glu content in the pectoralis major muscle after 48 hours of aging ($P < 0.05$), and the result was consistent with our previous study [5]. There were positive correlations between skeletal muscle protein degradation levels and the mRNA expression levels of proteasomes (Atrogin-1 and Murf-1) at slaughter ($P < 0.05$). In addition, positive correlations were also found between Glu content in the pectoralis major muscle after aging and the mRNA expression levels of proteases (cathepsin L-like, H, and calpain 2, 11) ($P < 0.05$).

IV. CONCLUSION

These findings suggest that individual differences in skeletal muscle proteolysis levels at slaughter may influence postmortem meat quality (e.g., Glu contents). Understanding this relationship could help improve the consistency of meat quality and potentially benefit poultry producers.

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