MEAT METABOLOME OF NELLORE MALE WITH DIVERGENT GENETIC POTENTIAL FOR GROWTH

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I. INTRODUCTION

Cattle herds have largely applied the genetic selection in beef cattle in order to increase performance and meat production. One of the prominent genetic tools is the Expected Progeny Difference (EPD), which has led the genetic selection of many production traits [1]. According to genetic selection, muscle metabolism can differ among animals with divergent growth rate and consequently alter metabolites due to different patterns of growth [2]. In this sense, metabolomics can be an important evaluation to detect some differences on metabolite concentration in meat of animals with divergent genetic potential for growth. Therefore, the hypothesize of this study is that animals with divergent potential for post-weaning growth have differences on meat metabolism and metabolites, and the aim of this study was to evaluate the meat metabolome of Nellore male with divergent genetic potential for post-weaning growth.

II. MATERIALS AND METHODS

Longissimus samples from 74 feedlot finished Nellore bulls of high and low genetic potential for growth were collected 24 hours' postmortem. The genetic potential was measured by expected progeny differences, which the High potential for growth animals presented EPD between 4.4 to 13.8 kg of increases on body weight (BW) compared to the average BW of the herd at 18 months' age; and the Low potential for growth animals presented EPD between -9.92 kg to 4.0 kg of BW also compared to the herd average BW. Expected progeny differences (EPD) were evaluated by BW measured on the post-weaning (from 7 to 18 months) period, at pasture system. After finishing period and slaughter, samples were vacuum packed and frozen at -80°C for posterior metabolite extraction and metabolome analysis. The metabolite extraction was performed as described by Beckonert et al., [3] and the internal chemical shift standard used was the sodium 3-trimethylsilyl-2,2,3,3-d4-propionate (TMSP-d4, from Cambridge Isotopes, Leicestershire, UK) to metabolite quantification. The nuclear magnetic resonance (^{1}H NMR) was used for metabolome evaluation, through the Bruker Avance 600 NMR spectrometer. The data preprocessing and Principal Component Analysis (PCA) from ^{1}H NMR were performed using MATLAB R2016b from normalized and mean-centering data. Chenomx software was used to calculate the metabolite levels as measured by ^{1}H NMR. The metabolite quantification statistics were performed using the SAS software and data were analyzed as a completely randomized design by the MIXED procedure.

III. RESULTS AND DISCUSSION

The high-resolution NMR spectra of the polar metabolite of meat samples identified and quantified 31 compounds. The metabolites in higher concentration were lactate (62.3±7.6 μmol·g^{-1}), creatine (23.33±5.56 μmol·g^{-1}), and carnosine (12.18±3.55 μmol·g^{-1}). The other metabolites in lower concentration were fumarate and succinate (Krebs cycle intermediates), amino acids, sugars and organic acids. Figure 1 shows the score plot of the principal component of analysis (PCA) for the NMR data. PC1 and PC2 represent 41.48% and 22.56% of the variance, explaining 64.04% of the total variance. The score plot did not show any clustering between high and low EPD for growth. Thus suggesting similarities in metabolome, among animals with divergent genetic potential for growth. There was just a tendency for lower ($P = 0.089$) β-alanine in animals with high EPD compared to low group (0.21 vs 0.14 μmol·g^{-1}, respectively).

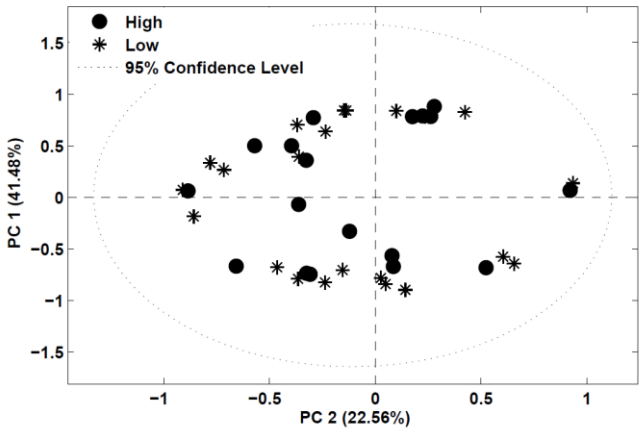

Figure 1. Meat polar metabolome PCA

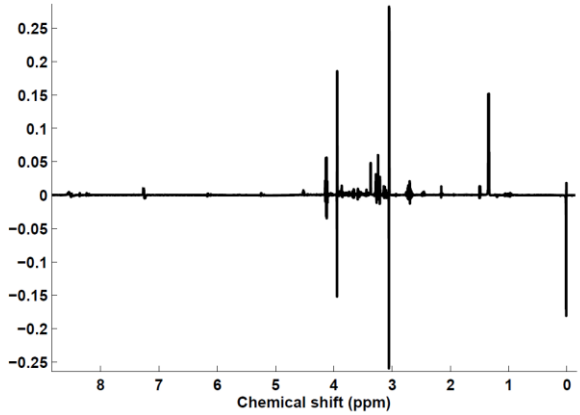

Figure 2. Loading plots of meat metabolome

Initially, we had expected some differences on meat metabolome according to the genetic potential for growth. Whereas, animals with greater potential for growth had a higher performance during post-weaning period than those with lower potential for growth; and according to Florini et al. [2], energy metabolism in skeletal muscle is under strong endocrinological control and it can change the concentrations of key hormones and metabolites. However, despite divergent potential for growth, there were no changes on performance among groups during finishing period [4], as consequence, the metabolism and consequently metabolites on muscle was also similar between treatments. Suggesting that genetic potential for growth measured from post-weaning until 18 months' age could not change some traits evaluated at the end of finishing period. Lopes et al. [5], who conceived each EPD reflects an animal's genetic merit for only a single trait at a time, reported the same. As consequence, animals selected for growth post-weaning could not reflected differences in carcass, meat production and metabolome at the end of finishing period.

CONCLUSION

Post-weaning growth potential does not affect the meat metabolome from Nellore young bulls.

ACKNOWLEDGEMENTS

The authors would like to thanks the EMBRAPA and FAPESP by the financial support (2016/01320-7).

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