METABOLOMIC FINGERPRINTING OF NELLORE CALVES WITH GENETIC VARIATION FOR MEAT TENDERNESS

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I. INTRODUCTION

Nellore (*Bos taurus indicus*) is the most representative breed in the Brazilian cattle herd. However, these animals have less tender meat compared to taurine breeds [1]. Within the breed itself, there is great variation for this trait, which creates an opportunity for research and selection of Nellore animals with more tender meat. This characteristic has been increasingly valued by consumers. Tenderness has been a target of selection in genetic improvement programs, but there is a continuous need to integrate new evaluation and prediction methods to meet consumer market trends. Metabolomics emerges as an alternative to better understand the metabolism of meat tenderness, allowing for the development of new technologies to evaluate and predict tenderness. Therefore, the aim of this study was to assess whether genetic selection of bulls for meat tenderness influences the metabolism of their progeny at birth.

II. MATERIALS AND METHODS

The experimental procedures were conducted in accordance with the Institutional Animal Care of the College of Animal Science and Food Engineering at the University of Sao Paulo (9249180123). One hundred male Nelore calves were divided into two groups based on the genetic variation of the bull (progenitor), selected through expected difference in progeny (EPD) for meat tenderness: Higher EPDs (Tender, n=50) and Lower EPDs (Tough, n=50). At birth, blood samples were collected and subjected to the protocol described by [2], and the resulting filtrate was taken for nuclear magnetic resonance spectroscopy (^{1}H-RMN). The spectra were uploaded to the web tool NMRProcFlow (version 1.4.24, https://nmrprocflow.org/), processed and divided into uniform bucketings of 0.05 ppm width, totaling 112 buckets, which were used for statistical analysis. The data were analyzed in the web tool MetaboAnalyst (Version 6.0, https://www.metaboanalyst.ca/MetaboAnalyst/) using principal component analysis (PCA) and Volcano Plot.

III. RESULTS AND DISCUSSION

There was an overlap between the groups in the PCA analysis, indicating similarity between them. However, in the Volcano plot, it was possible to observe some metabolites responsible for differentiating the groups (Table 1 and Figure 1). Animals in the tender group showed a higher concentration of lactate (P = 0.03), which may indicate greater substrate availability for energy production through gluconeogenic pathways [3]. In contrast, the tough group exhibited higher concentrations of threonine (P = 0.01) and ribose (P = 0.01), suggesting protein and carbohydrate catabolism aimed at energy production [4]. Generally, metabolites have been used to differentiate the degree of tenderness in meat post-slaughter [5,6]. However, in our study, these differences have not yet been correlated with tenderness, but rather with genetic selection for this trait. This could potentially

lead to a deeper and more comprehensive understanding of meat tenderness development from early stages of life.

Table 1 –Metabolites found in the tender and tough treatments.

Metabolites	FC	Log2(FC)	P value	-log10(p)
Threonine	1.5307	0.61417	0.01279	1.8931
Ribose	1.5642	0.64544	0.013142	1.8813
Lactate	0.69936	-0.5159	0.030317	1.5183
Citrate	0.73732	-0.43965	0.079036	1.1022
Tyrosine	0.70248	-0.50948	0.090928	1.0413

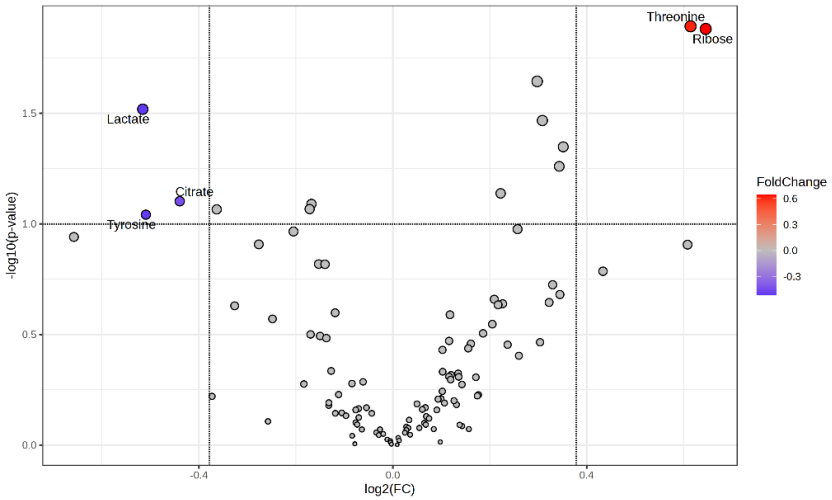

Figure 1. Volcano plot of Nellore calves at birth in the tender and tough groups.

IV. CONCLUSION

Genetic variation for meat tenderness influenced the metabolic fingerprint of the serum of Nellore calves at birth.

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