MEAT METABOLOME OF CATTLE FROM DIFFERENT GENETIC GROUPS SUPPLEMENTED WITH POLYUNSATURATED FATTY ACIDS

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I. INTRODUCTION

Diet and animal genotype can modify the muscle and fat metabolism of beef cattle, affecting growth rate and site and amount of intramuscular fat (IMF) [1], which are related to the meat quality and consequently to the consumer's acceptance of the meat [2]. Some metabolites are formed during the animal metabolism, characterizing evidence of the occurrence of biochemical activity and fingerprints from specific cellular processes [3]. Due to this, the metabolomics analysis allows a correlation between biochemical and phenotypic changes [3]. Thus, the aim of this work was to evaluate the effects of diets with or without polyunsaturated fatty acids (PUFA) supplementation on meat metabolome of cattle from different genetic predispositions for IMF deposition.

II. MATERIALS AND METHODS

Thirty *Bos indicus* (BI; Nellore) and thirty crossbred *Bos indicus* x *Bos indicus* (CB; Angus x Nellore) (368 ± 28 kg body weight; 24 mo old) were allocated in individual pens according to the initial body weight (block) in a randomized block design with a 2 x 2 factorial arrangement (diet x genetic group) and 15 replications per treatment. Animals were fed for 133 d to one of two high concentration diets: control diet (CO; TDN = 78.9%; EE = 3.11%) and soybean oil diet (SB; TDN = 82.3%; EE = 6.45%). Diets contained corn silage (10%), sugarcane bagasse (5%), corn grain (58% for CO and 54.5% for SB), citrus pulp (16%), soybean meal (9%), urea (1.2%), mineral salt (0.8%) and soybean oil (0% for CO and 3.5% for SB). At the end of feeding period, animals were slaughtered and the Longissimus muscle was sampled between 12th and 13th ribs for evaluating meat metabolome by nuclear magnetic resonance (NMR). The ^{1}H NMR spectra were acquired on a Bruker Avance 14.1 T spectrometer (600.13 MHz for ^{1}H). For the meat metabolome analysis, ^{1}H NMR data ranging from 0.00 to 10.00 ppm were converted to ASCII files using Bruker TopSpin 3.5 and were aligned using the icoshift algorithm. Chenomx software was used to calculate the metabolites levels measured by ^{1}H NMR. Means were compared by Student's t test, and differences were considered statistically significant when $P \leq 0.05$. Effects of main factors and interaction were evaluated using the mixed procedure of SAS.

III. RESULTS AND DISCUSSION

No interaction between diet and genetic group was observed for any meat metabolome. The concentration of 3 and 10 metabolites (from 31 metabolites identified) differed significantly between animals fed different dietary PUFA concentrations (Table 1) and between different genetic groups (Table 2), respectively. Moreover, the concentration of 5 metabolites tended ($P < 0.10$) to be significantly different between diets. Generally, amino acids contribute to various gustatory sensations [4]. Sweetness can be associated with alanine, glutamine and glycine; bitterness is associated with isoleucine, leucine, phenylalanine, tyrosine and valine; and a glutamate is typically associated with umami [4]. In this sense, consumers ranked higher meat flavor for animals fed CO than fed SO diet ($P = 0.0444$), as well as they ranked higher meat flavor for BI beef than CB beef ($P = 0.0533$; Figure 1). All of these water-soluble metabolites are contributing to cooked meat flavor, to a greater or lesser extent, as precursors in the Maillard reactions [5]. Therefore, both results of effects of diet and genetic on metabolites suggest that carnosine, which was observed in higher abundance in the meat of animals fed CO than SB (3.71 fold) and in BI beef than CB (1.55 fold), may play a more important role in influencing consumer preference in beef flavor.

Table 1 Metabolites that differ significantly ($P < 0.10$) in beef samples, according to the diets[1]

Metabolite	CO	SO	SEM	*P* value
Isoleucine	0.13	0.17	0.023	0.0843
Glutamine	2.10	1.65	0.247	0.0931
Glutamate	0.41	0.32	0.071	0.0897
Glycerol	1.65	2.81	0.229	0.0004
Carnosine	12.01	3.24	0.962	0.0052
Carnitine	1.50	1.89	0.216	0.0633
Betaine	0.73	1.28	0.086	<0.0001
Fumarate	0.12	0.09	0.015	0.0561

[1] CO = basal diet without soybean oil inclusion; SO = basal diet containing 3.5% soybean oil inclusion in replacing of ground corn grain.

Table 2 Metabolites that differ significantly in the beef samples, according to the genetic groups[1]

Metabolite	BI	CB	SEM	*P* value
Alanine	1.09	1.94	0.193	<0.0001
Acetate	0.18	0.10	0.017	0.0015
Succinate	0.06	0.04	0.008	0.0297
Methionine	0.80	1.14	0.092	0.0117
Glutamate	0.44	0.29	0.071	0.0020
Creatinine	0.50	0.72	0.052	0.0051
Glycine	0.76	1.23	0.071	<0.0001
Glucose	4.36	2.54	0.353	<0.0001
Carnosine	12.97	8.37	0.962	<0.0001
IMP	0.94	0.56	0.093	0.0047

[1] BI = *Bos indicus*; CB = crossbred *Bos taurus* x *Bos indicus*.

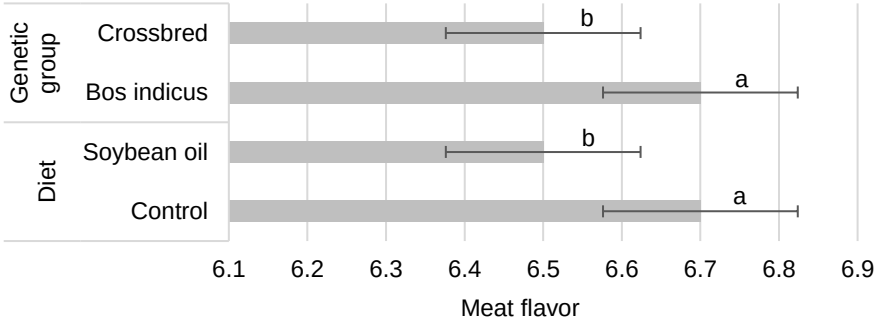

Figure 1 – Effect of diet and genetic group on meat flavor evaluated by consumer sensory panel (1 - dislike extremely; 9 - like extremely)

IV. CONCLUSION

Diet and genetic group change the meat metabolome, suggesting that some metabolites in the meat are related to the increase of consumer`s acceptance of meat flavor.

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