P129. LIPID ANALYSIS OF BEEF MEAT: CAN MALDI-TOF MASS SPECTROMETRY BE USED TO DEFINE DIFFERENTIAL PROFILES FOR BOVINE BREEDS FED UNDER DISTINCT FAT CONTENT DIET?

Verbisck, N. V.[1*], Perestrelo, A. A.[2], Ferraz, A. L. J.[2], De Paula, L. C.[3], Bonin, M. N.[3], Medeiros, S. R. [4], Mele, M. [5], Almeida, R. G.[1], Feijó, G. L. D.[1]

[1]Embrapa Beef Cattle, Brazil, [2]Mato Grosso do Sul State University-UEMS, Brazil, [3]Federal University of Mato Grosso do Sul-UFMS, Brazil, [4] Embrapa Southeast Livestock, Brazil, [5] University of Pisa, Italy.

Lipid constitution of bovine muscle tissue is affected by several factors, including genetics and diet (1). We have previously characterized the intramuscular fatty acid composition of Nellore and Brangus bovine breeds fed with contrasting fat levels (2). MALDI-TOF mass spectrometry (MS) has been used to characterize intact lipid components in bovine muscle (3). The aim of this study is to use MALDI-TOF MS to differentiate bovine muscle from different breeds under distinct fat diets. Nellore (n = 11) and Brangus (n = 12) bulls were randomly assigned to a low (LFD) or a high fat diet (HFD): 3.2% versus 6.4% ether extract. The diets had similar energy and protein levels and were composed by sorghum silage (30% dry matter), soybean hulls, ground corn, soybean meal, urea and a mineral mixture. HFD additional fat derived from cottonseed (18% dry matter), in substitution to ground corn (31% versus 52%, on HFD and LFD, respectively). The experiment lasted 71 days and *Longissimus dorsi* muscle samples were processed for lipid analysis by MALDI-TOF MS. Folch method was used to lipid extraction from 15 g of muscle tissue and lipid concentration within samples ranged from 8.7 to 44.14 mg/mL. Total lipids (1 uL) were directly spotted in MALDI plate with dihydroxybenzoic acid (DHB) and 9-aminoacridine (9-AA) as matrices (4,5). Mass spectra were acquired from m/z 680 to 1580 in the negative-ion reflectron mode with an Autoflex mass spectrometer (Bruker Daltonics). As a rule, 9-AA ionization yielded more peaks and with higher intensity than DHB. Several m/z could be assigned as glycerophospholipids in LIPID MAPS® Lipidomics Gateway search, however the resolving power of MALDI-TOF is not enough for lipid identification, despite good resolution (~0.2 FWHM) of our peaks. We then processed Nellore LFD, Nellore HFD, Brangus LFD and Brangus HFD mass spectra profiles with ClinProTools™ software (Bruker Daltonics) for fishing biomarkers but no differences could be assigned. More analysis shall be performed but so far the answer to the aforementioned title question is no. To further explore our samples next step will be the use of Solid Phase Extraction (SPE) and Thin Layer Chromatography (TLC) hyphenated to MALDI-MS to improve our mass spectra profiles regarding phospholipid moiety analysis.

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