PROTEIN BIOMARKERS IDENTIFIED IN SUBCUTANEOUS FAT FROM ZEBU CATTLE CAN BE ASSOCIATED WITH ENDOCRINE HORMONES

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I. OBJECTIVES

This work aimed to correlate the significant electrophoretic bands of subcutaneous fat proteins with productive, biologics, and qualitative phenotypes, such as weight gain, hormones, marbling, and subcutaneous fat deposition measured by carcass ultrasound. It also aimed to identify the proteins involved in these biological processes.

II. MATERIALS AND METHODS

One hundred and five Nelore bulls (initial weight of 350 kg ± 15 kg) 20 mo of age were confined for 100 d and fed with the same diet (27:73 forage/concentrate). The animals were slaughtered, and subcutaneous fat samples were collected and immediately frozen in liquid nitrogen. The animals were ranked based on their parent's Expected Progeny Difference for precocity and growth, and 14 animals were selected with either Highest Expected Progeny Difference ($N = 7$) or Lowest Expected Progeny Difference ($N = 7$) deposition of subcutaneous fat to form the groups that were tested for differential proteomic analysis. The present study analyzed the protein profile of subcutaneous fat by dodecyl sulfate-polyacrylamide gel electrophoresis and detected 3 electrophoretic bands differentially abundant (bands 24, 30, and 32) between the groups evaluated. The bands were excised from the gel and submitted to protein identification by liquid chromatography-tandem mass spectrometry. Correlations were estimated by Pearson's correlation coefficient (r) within and between groups and considered significant at $P < 0.05$.

Table 1.
Top over-representation KEGG pathways (FDR <0.05) for the list of proteins identified for each band differentially abundant between high and low group for deposition of subcutaneous fat in Nelore cattle

Band	KEGG	Description	Protein
24	bta01210	2-oxocarboxylic acid metabolism	ACY1, CS, IDH1
	bta00061	Fatty acid biosynthesis	ACSL1, FASN
	bta00020	Citrate cycle	CS, IDH1, SUCLG2
30	bta00620	Pyruvate metabolism	LDHA, LDHB, MDH1, MDH2, PDHB
	bta00270	Cysteine and methionine metabolism	LDHA, LDHB, MDH1, MDH2, MPST
	bta00020	Citrate cycle	MDH1, MDH2, PDHB
32	bta03050	Proteasome	PSMA1, PSME1, PSME2

III. RESULTS

Independent of groups, the serum insulin content was positively correlated with band 30 ($r = 0.63$), while beef marbling was positively correlated with band 24 ($r = 0.76$) and band 30 ($r = 0.65$). The results showed a great positive correlation between the serum insulin content and band 30 ($r = 0.93$) for group Lowest Expected Progeny Difference. Correlations within the group Highest Expected Progeny Difference revealed a great negative correlation between band 32 and average daily weight gain ($r = -0.85$) and total weight gain ($r = -0.84$). The list of proteins identified in each band was submitted to over-representation analysis using WebGestalt web tool. The top enriched pathways (false discovery rate < 0.05) found are shown in Table 1.

IV. CONCLUSION

This study revealed that there is a strong relationship between the subcutaneous fat protein profile and the insulin serum hormonal profile, independent and within the groups evaluated. The proteins involved in the citrate cycle pathway may influence subcutaneous fat deposition. Besides that, the proteins involved in the proteasome pathway can be related to animal growth. Thus, the exploration of proteins present in subcutaneous fat will allow a better understanding of the metabolic pathways involved in fat deposition, animal production, carcass, and beef quality.