OPTIMIZATION OF SAMPLING TIME FOR THE DETECTION OF PROTEOMIC CHANGES RELATED TO BEEF QUALITY

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I. INTRODUCTION

Meat scientists show increasing interest in the identification of animal-based biomarkers of meat quality. In this field proteomics is a promising tool since the muscle proteome provides useful information about the process of conversion of the muscle into meat [1,2]. However, the muscle proteomic profile shows significant changes during the first 24 h *postmortem (pm)*. The objective of this work was to identify the optimum *pm* sampling time for the detection of the protein biomarkers with higher correlation to beef quality.

II. MATERIALS AND METHODS

Muscle samples were obtained from the *Longissimus dorsi* of twenty four yearling bulls of the "Asturiana de los Valles" breed at 2h, 8h and 24h *pm* for proteomic analysis of the sarcoplasmic extracts: protein separation by 1D-SDS-PAGE, quantification by image analysis (ImageQuant TL software) and identification of all the protein bands by MALDI-TOF/TOF MS. Meat quality traits (pH-24h, drip loss-24h, colour (L*, a*, b*-24h) and toughness (WBSF-14 days) were measured as described by Sierra et al. [1]. The relationships between meat quality traits and the protein profile obtained at different sampling times were calculated by bivariate Pearson's correlations and multiple linear regressions, using SPSS Software.

III. RESULTS AND DISCUSSION

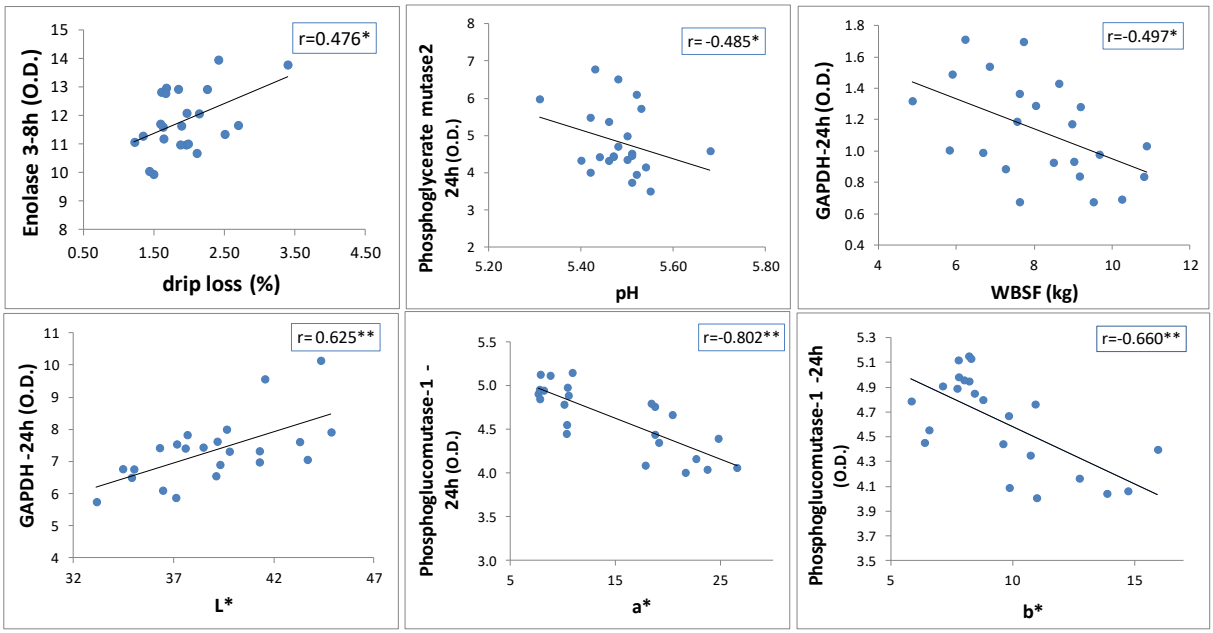

Figure 1. Best bivariate correlations (higher r) between meat quality traits and protein biomarkers.

A total of 26 proteins were identified in the sarcoplasmic extracts, most of them with metabolic function. The best correlations between these proteins and the meat quality traits were found with data obtained from muscle extracts taken at 8h (for drip loss) and 24h *pm* (for pH, WBSF, CIE-L*, a*, b*) (Fig. 1).

The multiple regression analysis improved the accuracy of the prediction of drip loss and some meat colour variables (L*, b*) (Table 1) and showed again that the best prediction models, that is, those with higher variance explanation (adjusted R^2) and lower prediction error (SEP), were obtained with the protein profile taken from the muscle at 8h *pm* (drip loss) and 24h *pm* (meat colour).

Table 1. Statistics of multiple regression models with higher accuracy of prediction of meat quality traits.

Dependent variable	Proteome sampling time *(pm)*	r	Adj-R^2	SEP	Independent variables included[a]
Drip loss (%)	8h	0.610	0.310***	0.408	ENO3, Glycogen debranching enzyme
L* (Lightness)	24h	0.927	0.806***	1.436	GAPDH, Glycogen debranching enzyme, ALDOA, PK, Serotransferrin
b* (yellowness)	24h	0.883	0.780***	1.394	PGM, AK-1, PFK-M, CK

[a] Variables are shown in order of entrance in the prediction model. ENO3: β-enolase, GAPDH: glyceraldehyde-3-phosphate dehydrogenase; ALDOA: fructose-bisphosphate aldolase A, PK: piruvate kinase isoform X1, PGM: phosphoglucomutase-1, AK-1: adenylate kinase isoenzyme 1, PFK-M: ATP-dependent 6-phosphofructokinase muscle type, CK: creatine kinase

These relationships indicate that in this study the proteins involved in glycolytic metabolism (Phosphoglycerate mutase-2, ENO3, GAPDH, ALDOA, PK, PFK-M) and muscle energy homeostasis (PGM, Glycogen debranching enzyme, AK-1, CK) played a major role in the determination of beef quality attributes. In addition, our results show that the accuracy of the predictions depends on the muscle sampling time for the determination of the protein biomarkers, due to the great metabolic changes that occur in the muscle cell during the first 24 h after exsanguination [3]. Most previous studies have been performed on muscle samples obtained at very short *pm* time (30 min to 2 h) [2,4] but our data indicate that the protein profile measured at 8 or 24 h *pm* has higher correlation with beef quality traits.

IV. CONCLUSION

Many studies are focused on the search for protein biomarkers underlying the process of meat quality acquisition. Most of the previous research has been performed on muscle samples obtained at very early (≤ 2h) post-slaughtering time, however our results suggest that the cell metabolic processes with influence on meat quality need a time lapse of at least 8 h to be clearly developed and therefore the optimum sampling time of the muscle sarcoplasmic protein biomarkers is comprised in the range between 8 h to 24 h *pm*.

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