PREDICTION OF BEEF CARCASS QUALITY CLUSTERS FROM MUSCLE BIOMARKERS

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Abstract – The aim of this study was to predict carcass quality clusters from the relative abundance of 20 biomarkers of meat tenderness and adiposity measured from *rectus abdominis* muscle samples. The carcass quality clusters were determined from 3 carcass traits: cold carcass weight, dressing percentage and conformation score, measured on 75 heifer carcasses. The prediction model established, using the ordered multinomial logistic regression, displayed that an increase in the abundance of Heat Shock Protein 27 and Enolase 3 could allow to improve carcass quality. This model with a success of 57.3%, allowed to discriminate with an accuracy of 72.2%, carcasses with the lowest quality. New data will be required to confirm our results.

Key Words – EUROP classification system, Logistic regression, Skeletal muscle proteins

I. INTRODUCTION

In Europe, the carcass quality is evaluated from 3 main parameters: cold carcass weight, conformation and fat score [1]. A difficulty encountered by the meat sector stakeholders is the variability of the carcass quality and their aim is to be able to control this variability. In recent 10 years, different studies had identified skeletal muscle proteins (biomarkers) allowing to predict the beef meat tenderness [2] and more recently, meat adiposity. However, no studies had observed the link between the carcass traits and the abundance of these biomarkers. The aims of this study were to determine carcass quality clusters and to identify biomarkers related to these clusters from a prediction model.

II. MATERIALS AND METHODS

This study concerned the data of 75 carcasses from crossed Charolais x Aubrac heifers reared in many farms and slaughtered in the same industrial slaughterhouse. Carcasses were characterized by 3 parameters: cold carcass weight, dressing percentage and conformation score. The conformation was evaluated using the EUROP grid system [1]. On each carcass right-hand side, full *rectus abdominis* (RA) muscles were removed 24-hour *post-mortem*. On each RA muscle, a sample of 5 g was collected to measure the relative abundances of 20 biomarkers, using the Reverse Phase Protein Array method [3]. From the 3 carcass parameters, carcass quality clusters were determined, using analysis for mixed data completed by a hierarchical clustering on principal components (HCPC) with R software. Logistic regression was used to predict the clusters obtained from the biomarker abundances. The model interpretation was realized from the odd ratio (OR) values and this prediction quality was analysed from 3 parameters: the success rate, the sensitivity and the accuracy. According to the reference cluster, the OR determine the chance which had carcasses to move to the superior carcass cluster when the abundance of one biomarker present in the predicted model increases of one unit while the other considered biomarkers are fixed at the means values.

III. RESULTS AND DISCUSSION

The HCPC allowed to determine 3 ordered carcass quality clusters (Table 1). The Clust-Low was the reference cluster because carcasses in this cluster had the lower weight and conformation score among other clusters. To predict these clusters from the biomarker abundances, the prediction model was established using the ordered multinomial logistic regression. As the heifers were issued from different farms, this factor was in random effect in the predicted model developed. Only the abundances of 2 biomarkers: Heat Shock Protein 27 (HSP27) and Enolase (ENO3) were retained in our model (Table 2). The success rate of this model was only 57.3%, nevertheless it has a high accuracy (72.2%) to predict the carcasses characterised by a low quality (Clust-Low), in the good cluster. On the other hand, this model had more difficulty to predict both other clusters (Table 1). The OR of this model displayed that an increase in the abundances of HSP27 and ENO3 allowed improving the carcass quality (Table 2). In fact, if the abundance of HSP27

or ENO3 increases, carcasses will have 5.4 or 1.6 times respectively more chances to move to the superior carcass quality cluster.

Table 1 Carcass clusters description and goodness of fit measures p for the predicted model

	Carcass quality clusters		
	Clust-Low	Clust-Medium	Clust-High
Cluster traits			
Weight (kg)	$382^{c} \pm 33$	$428^{b} \pm 22$	$460^{a} \pm 25$
Dressing% (%)	$57.2^{b} \pm 2.1$	$58,4^{b} \pm 1,4$	$59,8^{a} \pm 2.0$
Conformation (scale 1-15)	$9.8^{c} \pm 0.4$	$11^{b} \pm 0$	$12.1^{a} \pm 0.3$
Prediction quality of the model			
Sensibility (%)	61.9	51.8	59.3
Accuracy (%)	72.2	46.7	59.2

Table 2 Predicted model description

Independent variable	Coefficient	OR
Intercept		
Clust-Low vs Clust-Mean	-1.03	
Clust-Mean vs Clust-High	0.92	
HSP27	0.01*	5.45
ENO3	0.34^{NS}	1.57

OR = odd ratio; NS = nonsignificant; * $P < 0.05$

ENO3 is involved in glucose metabolism and is known to play a role in muscle development and regeneration. In accordance with our results higher glycolytic properties are observed in cattle with high muscle growth and carcass yield such as the Blonde d'Aquitaine and Belgian Blue [4]. The HSP27 is implicated in the cell development, differentiation and survival. In our knowledge, the relation between HSP27 and carcass traits had not been studied, in cattle. However, in mice Kammoun *et al.*[5] observed that the HSP27 KO mice had delayed growth with lower body weight than controls at the start of growth. However, the differences disappeared with the aging of the mice. This result displays that this protein had an impact on the mice growth and could have the same impact in cattle.

IV. CONCLUSION

This study is original because to our knowledge, it is first time that the link between proteomic biomarkers of meat qualities and carcass traits is observed. Our results report that a higher carcass quality was concomitant with higher abundances of ENO3 and HSP27 in the RA muscle. These proteins should be helpful to predict carcass quality, which remains to be confirmed by the validation of this model with other data.

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