CLUSTERING OF FATTY ACIDS COMPOSITION, SENSORY QUALITY AND PROTEOMIC BIOMARKERS OF YOUNG CHAROLAIS BULLS

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Abstract – Fatty acid composition, meat sensory quality and muscle biomarkers of tenderness and intramuscular fat content were characterized for the *Longissimus thoracis* of young Charolais bulls. Each dataset was grouped into homogeneous clusters in order to constitute different synthetic quantitative variables, which were further combined in Global Indexes. The innovative statistical approach used allowed a clear discrimination of muscle biomarkers that are linked not only with tenderness and adiposity but also with other sensory qualities and with fatty acids composition. This seems very useful for an early selection of carcasses depending on the characteristics expected for meat samples.

Key Words – Fatty acid composition, Meat quality, Muscle biomarkers, Prediction, Quality management

I. INTRODUCTION

Gene expression controls the biological characteristics of muscles and thanks to advances in genomics, researchers have identified a number of genes that are associated with different meat quality traits as well as underlying biological mechanisms [1]. In the present report, the links between sensory quality, fatty acid composition of meat and abundances of a list of muscle biomarkers, previously designed to predict tenderness and intramuscular fat, were evaluated. The interlinking of the three datasets aimed to establish a pool of biomarkers that could predict meat quality traits of young Charolais bulls and allow to select early carcasses that have an optimal tradeoff between sensory and nutritional quality.

II. MATERIALS AND METHODS

A total of 15 Charolais young bulls were slaughtered at an average of 700 kg. Twenty-nine biomarkers (Table 1) were combined on m. *Longissimus thoracis* using Reverse Phase Protein Array (RPPA, [2]). Intramuscular fat content, fatty acid composition (NV ; 16 variables) and sensory qualities parameters (SQ; 9 variables, Table 1) were also evaluated as previously described by Mialon *et al.* [3]). To identify the biomarkers that should be useful to predict SQ and NV, we used the R package ClustOfVar, specially developed to arrange variables into homogeneous clusters and to allow dimension reduction and variable selection [4]. The clustering of variables led to Intermediate Scores (IS) that were characterized by the variables having a square correlation with the central synthetic variable of the cluster greater than 0.50. Then, 4 Global Indexes (GI) were established by the combination of the IS to evaluate the interactions between biomarkers and meat quality (SQ and/or NV). The three best GI are summarized in Table 2.

III. RESULTS AND DISCUSSION

Among the Global Indexes identified, **GI1** is of great interest. The first two axes of the PCA explained 71% of the variability (Figure 1), mainly characterized by an opposition between meat quality traits related to palatability (OL, BF and GF, see Table 1), FHL1 and α-Tubulin (positive), and ENO1 and ENO3 (negative). According to Lin and Hsu, [5], FHL1 may be linked to growth development and oxidative metabolism. Moreover, ENO1 and 3, seem to be linked to fatty acids deposition in bovine, in agreement with a previous link reported between ENO3, muscle metabolism and fat deposition in pig [6]. Furthermore, tubulin-lipid interactions by a lipid-specificity manner (by blocking the voltage-dependent anion channel of mitochondria), was reported [7]. For instance, the involvement of these proteins in lipid metabolism could explain the link with the flavor sensory descriptors. **For GI2**, 67% of the variability was explained (Figure 1). The 1st PC opposed COX activity, HSP20, HSP27 and TNNT1 to residues attribute (negatively correlated (r^2=-0.41) with

tenderness in this study), PKG1 and MyHC-IIx biomarkers. These results confirm the positive link already established between tenderness and oxidative metabolism (namely COX) in this muscle and this type of cattle [8]. Similarly, the 2nd PC opposed ALDH1A1 and PKG1 (having a great role in mitochondria) to µ-calpain and MLC1F (structure and proteolysis). Finally, **the GI3** revealed inverse relationships between tenderness and the activities of LDH and PFK, but also between tenderness and nutritional value of meat (higher PUFA and CLA contents with a lower n6/n3 ratio).

Table 1. Variables characterizing each element of the triptych

Biomarkers (BIOM) by RPPA assay	ENO1, ENO3, HSP20, 27, 40, 70-1A and 70-8, µ-calpain, MLC1F, CRYAB, PRDX6, MDH1, DJ-1, TNNT1, SOD1, ACTIN 2, ACTININ 3, α-ACTIN, MyHC-IIx, MyHC-I, ALDOA, TRIM72, TTN, α-Tubulin, PYBG, PKG1, FHL1, ALDH1A1, TPI1
Sensory quality and metabolism (SQ)	Scores of Global Tenderness (GT), Juiciness (J), Overall and Bovine Flavor (OF-BF), Residue, Overall Liking (OL) Activities of metabolic enzymes : Lactate Dehydrogenase (LDH), Cyochrome-c Oxydase (COX), PhosphoFructoKinase (PFK)
Nutritional value (NV) by fatty acids	Fatty acids and lipids contents: fatty acids (FA), Saturated FA (SFA), Mono Unsaturated FA (MUFA), Poly Unsaturated FA (PUFA), Conjugated Linoleic Acids (CLA), C16:0, C18:1, C18:1tr, PUFAn-6, PUFAn-3, C22:5n-3cis, C20:5n-3cis, Ratio: C16:0/C18:0, PUFA/SFA, PUFAn-6/PUFAn-3, C18:2n-6/C18:3n-3

Table 2. Description of Global Indices

	Details of GI	Details of each SI
GI1	SQ2 (+) BIOM1 (+)	**SQ2 :** OF (+), OL (+), BF (+) **BIOM1 :** FHL1 (+), α-Tubulin (+), ENO1 (-), ENO3 (-)
GI2	SQ3 (+), BIOM2 (+) BIOM3 (-)	**SQ3 :** COX (+), Residue (-) **BIOM2 :** MyHC-IIx (-), HSP27 (+), TNNT1 (+), ALDH1A1 (+) **BIOM3 :** PKG1 (+), HSP20 (-), µ-calpain (-), MLC1F (-)
GI3	SQ1 (-) NV1 (+), NV2 (-)	**SQ1 :** GT (+), LDH (-), PFK (-) **NV1:** C16/C18 (+), Lipids (+), FA (+), C16:0 (+), SFA (+), MUFA (+), C18:1trans (+), C18:1 (+), CLA (+), PUFAn6 (+), PUFA (+), PUFA/SFA (-) **NV2 :** n6/n3 (+), C18:2n6 (+), C18:3n3 (+), C20:5n3 (-), C22:5n3 (-), PUFAn3 (-)

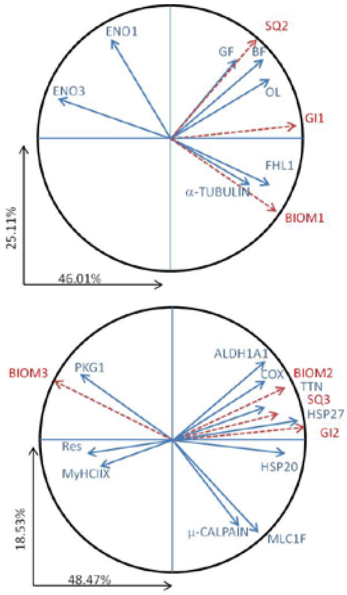

Figure 1. Projection of the variables that were used in the construction of GI1 (up) and GI2 (down) on to the first two axes of the PCAs

IV. CONCLUSION

Proteins previously identified as biomarkers of meat tenderness and adiposity are also linked with other sensory qualities and with fatty acid composition. They provide elements to better understand the biological mechanisms related to these qualities.

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