A candidate proteomic signature from the plasma of Charolais bulls to phenotype feed efficiency

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Take home message We have identified a set of candidate biomarkers for feed efficiency in the plasma proteome of young Charolais bulls underlying the contribution of non-productive functions such as immunity.

Introduction The measurement of the feed efficiency (FE) requires an individual and strict control of the ingestion and performances of animals at least over a period of 70 days. We aimed at developing biomarkers from low invasive samples the combination of which will predict FE individual variations.

Material & methods We examined the plasma proteome of two groups of Charolais young bulls according to their residual feed intake (RFI) and feed conversion efficiency (FCE) metrics (Meale *et al.*, 2017). The study included 17 extremes animals: n=9 positive RFI vs n= 8 low RFI negative (0.69 vs -0.75 kg/j). Prior to nano LC-MS/MS analysis, the plasma samples were depleted of high-abundance proteins using the Proteominer technology (Cassar-Malek *et al*, 2015). Statistical analysis of data included ANOVA, Principal Components Analysis (PCA) and correlation analysis (Pearson). Lists of proteins were analysed using ProteINSIDE (http://www.proteinside.org/) to mine biological information. Gene Ontology (GO) enrichment tests (P value_Benjamini Hochberg < 0.05) were done with human orthologs to take advantage of the most complete annotation available for molecular functions and biological processes. A similar workflow was applied to the same animals ranked according to their FCE (0.17 [low FCE] vs 0.23 [high FCE] kg/kg).

Results & discussion A PCA analysis of all data was applied to remove outliers (n=2/per RFI group) from further analysis. Then a differential abundance according to RFI was revealed for 51 proteins (P <0.1) including 4 uncharacterised proteins. A correlation between plasma abundance and RFI values was detected for 24 proteins out of the 51 proteins (-0.795 <r2 <+0.806). Nine of the 51 differential proteins- 5 of the proteins correlated to RFI- were detected in a repertoire of secreted proteins identified by computation of published RFI omic datasets (Cassar-Malek and Bonnet, this symposium). These proteins are candidate biomarkers for RFI. The top GO Molecular Functions of the differential proteins were: calcium ion binding, serine-type endopeptidase inhibitor activity, lipid binding, carbohydrate binding, growth factor activity, regulation of insulin-like growth factor receptor signaling pathway. GO Biological Processes were mainly related to immunity (immune response, innate immune response), inflammatory response, complement and coagulation cascades, protein modification (protein folding, proteolysis, negative regulation of endopeptidase activity) and lipid metabolism (lipid transport, triglyceride and cholesterol homeostasis). These findings agree with the recent report that non-productive functions including immunity may contribute to inter-individual variations in feed efficiency in pig (Gondret *et al.*, 2017) and cattle (Weber *et al.*, 2016; Alexandre *et al*, 2015).

Examination of proteomic data according to the FCE index revealed 21 differentially abundant proteins and 7 correlated proteins (-0.599< r2 < +0,637). Comparison of FCE and RFI datasets showed that 6 proteins out of the 9 identified above as candidate RFI biomarkers are specific for RFI while 3 of them are common to both RFI and FCE.

Conclusion This is the first study identifying candidate biomarkers for feed efficiency in the plasma of cattle. It opens perspectives for biomarkers validation and high-throughput evaluation of this trait in ruminants.

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