Quest for plasma biomarkers for beef tenderness

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Take home message We have made an *in-silico* identification of 63 candidate plasma biomarkers for beef tenderness by a meta-analysis of published data.

Introduction A challenge for the ruminant sector is to predict and manage the complex phenotypic traits related to meat production and quality especially tenderness a top priority for the beef industry. Meat quality is a complex phenotype that can be evaluated only after slaughtering and ageing. Previous research efforts have investigated the potential of muscle-derived markers to assess meat quality (Picard *et al*., 2015; Cassar-Malek and Picard, 2016). However, their evaluation requires post-mortem muscle sampling or biopsies in the living animals. Thus, the identification of low invasive biomarkers is an issue for the beef sector. In this study, we hypothesized that available published data may help identifying candidate plasma biomarkers for beef quality.

Materials & methods Proteomic, transcriptomic and genetic muscle data related to beef tenderness (with significant correlation, differential abundance in extreme groups, or gene polymorphism) were collected from 54 publications including 1 GEO dataset (GSE9256) and computed according to Bonnet *et al*. (2016). Aggregation of the Gene Names (GN) from 3 datasets (proteomics, transcriptomics and genetics) were analysed using ProteINSIDE (http://www.proteinside.org/) to find biological information and predict secretion through a signal P sequence (SignalP score ≥ 0.5; TargetP score ≤ 2) or through a non-classical pathway without signal P (TargetP score ≤ 2). The lists of secreted proteins (named SignalP, other secreted) and cytoplasmic proteins were compared to a list of bovine plasma proteins from publications and experimental data (n=1106).

Results & discussion. The numbers of GN included in each dataset are shown in Table 1. Among the total 681 unique GN, 145 corresponded to secreted proteins, and 543 to cytoplasmic proteins. The comparison of the GO annotations revealed 73 common GO Biological Pathways (BP) between the datasets (oxidation-reduction process, response to oxidative stress, apoptotic process, proteolysis, lipid metabolic process, response to hypoxia, transport) consistent with tenderness mechanisms (Cassar-Malek and Picard, 2016). Twenty-four of the secreted proteins and 39 of the cytoplasmic proteins were hypothetically released in the bovine plasma. In both repertoires the GO BP were mainly related to oxidation-reduction process and neutrophil degranulation. Moreover, glycolytic process, ATP metabolic and apoptotic process, response to oxidative stress and extracellular matrix were specific to cytoplasmic plasma proteins whereas transport, lipid metabolic process and response to hypoxia were more specifically associated with secreted plasma proteins.

Table 1 Candidate plasma proteins secreted by muscle as computed from proteomic, transcriptomic or genetic data.

Dataset	Nb of unique GN	Signal P	Other secreted	Cytoplasmic	Secreted + Plasma	Cytoplasmic + Plasma
[Proteomics] n= 25 publications	156	10	31	115	11	20
[Transcriptomics] n= 9 publications	226	28	13	185	4	10
[Genetics] n= 20 publications	328	47	20	261	9	13
[General bilan] (unique Gene Names)	710 (681)	85 (83)	64 (62)	561 (543)	24	39

Conclusion Meta-analysis and bioinformatic analysis of published data enabled to identify putative plasma biomarkers for beef tenderness. Their detection in the plasma proteome of cattle from extreme groups of tenderness is on-going.

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References

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