Molecular signatures of beef tenderness

Ground-breaking integromics analysis co-ordinated by TEAGASC has led to the publication of the world's first and most robust set of beef tenderness biomarkers and major molecular signatures.

Background

Meeting consumer demands for consistency and high quality is an important challenge for the meat sector. Currently, there is no rapid, objective method available for estimating the eating quality of beef, either in the live animal or in the carcass. Addressing this gap in knowledge and technology would not only assist in generating higher-quality product but would also contribute to improved efficiency for the beef industry in Ireland and ultimately worldwide. To accomplish this, the underlying mechanisms responsible for creating the most important meat quality traits must be defined. A number of attempts have been made to achieve this immense challenge over the past decades, specifically the study of meat quality variation using high-throughput protein analytical platforms, also known as proteomics. One research area where proteomics has been of particular interest is in the discovery of meat quality biomarkers. Considering the vastness of the data collected thus far, and the need to establish a biologically meaningful and comprehensive list of biomarkers for tenderness, the aim of our study was to apply an integrative 'omics' ('integromics') approach to integrate worldwide proteomics datasets (Gagaoua *et al.*, 2021). The final aim was to identify the major molecular signatures of beef meat tenderness, which in turn will lead to the optimisation of management systems for guaranteed quality.

Integromics meta-analysis to gather putative protein biomarkers

Many large omics datasets, especially proteomics, have been generated in the quest to identify molecular signatures for meat tenderness. To broaden our understanding about the biological mechanisms underpinning meat tenderisation across a large number of proteomics studies, a systematic computerised literature search was performed, followed by an integromics and holistic meta-analysis to determine the current status of protein biomarker discovery targeting beef tenderness. This study is the first of its kind to provide clarity on the most consistently and robustly identified biomarkers of beef tenderness. It gathers data from 28 independent proteomics-based experiments (888 animals including bulls, cows, heifers and steers) from which a comprehensive list of 124 proteins was initially identified to create the first worldwide repertoire of beef tenderness biomarkers.

Multistep bioinformatics analyses including Gene Ontology annotations, pathway and process enrichment, and literature mining were applied to the database to reveal the major pathways and mechanisms underlying the conversion of muscle into tender meat.

Interconnectedness of the molecular signatures underpinning beef tenderness

Protein network analysis delivered a functional annotation of the 124 proteins from striploin and provided key insights into the interconnectedness among various pathways and processes in the muscle that are pivotal in producing high-quality beef. Six interconnected pathways were identified: (i) muscle contraction and structure development; (ii) energy metabolism; (iii) cellular responses to stress; (iv) response to oxidative stress; (v) proteolysis; and, (vi) regulation of cellular processes, binding, apoptosis and transport.

This analysis revealed the importance of the changing integrity of muscle contractile and structure proteins, energy metabolism enzymes, heat stress proteins and oxidative stress proteins in the determination of beef tenderness, in that order of importance. Interestingly, our analyses revealed that these major pathways and proteins directly or indirectly impinge on apoptosis (programmed cell death) onset in post-mortem muscle, which may be initiated by mitochondrial degradation signals.
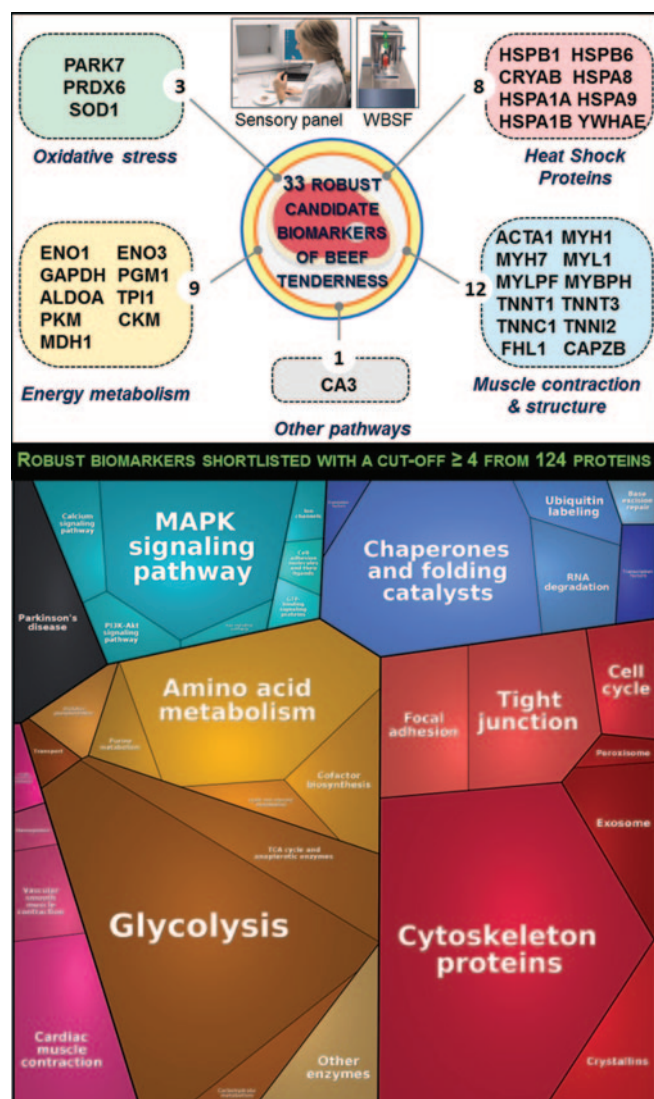
FIGURE 1: *Major pathways and list of the 33 robust biomarkers of beef tenderness, from five main biological pathways, shortlisted with a cut-off ≥ 4 from 124 proteins (Gagaoua et al., 2021).*

A robust list of putative biomarkers of beef tenderness released

From the list of 124 putative protein biomarkers, a cut-off of two or more datasets (≥ 2) was applied to identify common proteins across studies regardless of the animal category, leading to a panel of 64 proteins that were reported in at least two independent proteomic experiments. From these, we shortlisted a panel of 33 robust candidates (**Figure 1**) worthy of evaluation using targeted or untargeted data-independent acquisition proteomic methods to develop future predictive tools. Among the putative list of biomarkers, we further searched for potential quantitative trait loci (QTL) by interrogating the public library of the Animal QTL Database, which contains cattle QTL and associated data curated from published scientific articles. As a result, 18 QTLs among the candidate biomarkers were identified for tenderness score and shear force at different chromosomes.

Benefits to the beef industry

Our integromics study revealed the importance of omics tools and the power provided by data integration approaches such as this. The data gathered demonstrated how protein dynamics across the different metabolic pathways are associated with the development of tenderness early post mortem and during the ageing process. Anticipated downstream applications for the beef industry will see shortlisted protein biomarkers informing carcass management systems for delivering consistency in beef tenderness while at the same time leading to the development of prediction equations enabling rapid evaluation of beef tenderness potential.

References

Gagaoua, M., Terlouw, E.M.C., Mullen, AM., Franco, D., Warner, R.D., Lorenzo, J.M., *et al.* (2021). 'Molecular signatures of beef tenderness: underlying mechanisms based on integromics of protein biomarkers from multi-platform proteomics studies'. *Meat Science* 172: 108311. Available from: https://doi.org/10.1016/j.meatsci.2020.108311.

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