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BOOK OF ABSTRACTS



The potential of gel-based proteomics approaches to study changes in the sarcoplasmic muscle proteome of lamb meat

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Over the past few decades, several factors affecting lamb meat quality from "farm-to-fork" have been investigated. The causes and phenomena behind lamb meat quality variability, however, remain not fully understood and in-depth exploratory studies are needed. The current developments in a broad range of analytical techniques allow a comprehensive understanding of the molecular mechanisms with the aim of both monitoring and improving animal welfare and quality products. Among the most recent foodomics methods, we applied in this study gel-based proteomics to better understand the potential role of feeding strategies in modulating the mechanisms affecting post-mortem protein changes during storage. Therefore, twenty-two male lambs were randomly assigned to two experimental treatments. Lambs of the control group (C) received a maize-barley without any supplement, whereas the hazelnut group (H), in a circular economy perspective, received a hazelnut skin by-product as a maize partial replacer in the concentrate diet. After slaughter, samples of *Longissimus thoracis et lumborum* muscle (LTL) were collected and stored at 4°C for 4 and 7 days.

In line with the current knowledge, SDS-PAGE analysis evidenced 5 proteins as significantly changing by the treatment. Meat from the hazelnut group showed a higher abundance of pyruvate kinase (PKM; $P < 0.001$), glycogen phosphorylase (PYGM; $P < 0.001$), triosephosphate isomerase (TPI1; $P < 0.01$; at 0 and 4 days) and phosphoglycerate mutase 1 (PGAM1; $P < 0.001$; at 0 days) compared to the control. During storage, meat from the hazelnut group showed an increase in the number of protein bands accompanied by a significant decrease in GAPDH ($P < 0.01$) and PGAM1 ($P < 0.05$), and an increase in PYGM ($P < 0.05$) after 7 days of storage. Two-dimensional electrophoresis (2DE), by confirming the SDS-PAGE results, allowed to go in-depth of these results and depicted a progressive increase in the number of protein spots in the hazelnut group during storage time. Ten protein spots, corresponding to 41 proteoforms mainly involved in glycolytic processes, responses to oxidative stress, and immune and endocrine system were found to change significantly in their abundance as a result of the dietary treatment and/or storage time. The use of proteomics seemed to be a powerful approach to deepen our understanding of the molecular mechanism involved in the post-mortem processes linked with lamb meat quality variation.

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