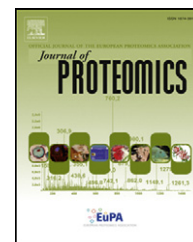


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Review

Meat science: From proteomics to integrated omics towards system biology

Angelo D'Alessandro, Lello Zolla*

Department of Ecological and Biological Sciences, University of Tuscia, Largo dell'Università, snc, 01100 Viterbo, Italy

ARTICLE INFO

Article history:

Received 22 August 2012

Accepted 26 October 2012

Available online 6 November 2012

Keywords:

Farm animal

System biology

Muscle to meat conversion

Proteomics

Integrated omics

ABSTRACT

Since the main ultimate goal of farm animal raising is the production of proteins for human consumption, research tools to investigate proteins play a major role in farm animal and meat science. Indeed, proteomics has been applied to the field of farm animal science to monitor *in vivo* performances of livestock animals (growth performances, fertility, milk quality etc.), but also to further our understanding of the molecular processes at the basis of meat quality, which are largely dependent on the *post mortem* biochemistry of the muscle, often in a species-specific way. *Post mortem* alterations to the muscle proteome reflect the biological complexity of the process of “muscle to meat conversion,” a process that, despite decades of advancements, is all but fully understood.

This is mainly due to the enormous amounts of variables affecting meat tenderness *per se*, including biological factors, such as animal species, breed specific-characteristic, muscle under investigation. However, it is rapidly emerging that the tender meat phenotype is not only tied to genetics (livestock breeding selection), but also to extrinsic factors, such as the rearing environment, feeding conditions, physical activity, administration of hormonal growth promotants, pre-slaughter handling and stress, *post mortem* handling.

From this intricate scenario, biochemical approaches and systems-wide integrated investigations (metabolomics, transcriptomics, interactomics, phosphoproteomics, mathematical modeling), which have emerged as complementary tools to proteomics, have helped establishing a few milestones in our understanding of the events leading from muscle to meat conversion. The growing integration of omics disciplines in the field of systems biology will soon contribute to take further steps forward.

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* Corresponding author at: Tuscia University, Largo dell'Università snc, 01100 Viterbo, Italy. Tel.: +39 0761 357 100; fax: +39 0761 357 630.
E-mail address: zolla@unitus.it (L. Zolla).

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1. Proteomics and farm animal science: a special focus on meat science

Research tools to investigate proteins play a major role in meat science, since the ultimate end objective of farm livestock raising is the production of proteins for human consumption. Within the framework of protein-oriented investigations, proteomics has achieved a leading role over the last two decades, owing to a long series of technological innovations in the fields of protein separation (through chromatography and electrophoresis), mass spectrometry and bioinformatics and their application to farm animal science-relevant issues [1–4]. In addition, the more extensive publication of species genomes is making the proteomic approach in animal science more viable [1,2], especially as far as protein identification through mass spectrometry and database interrogation are concerned.

The flourishing of the field of farm animal proteomics is also confirmed by the constant growth and spread of international initiatives. The European Cooperation in Science and Technology (COST) farm animal proteomics (Action FA1002) [2] is an initiative that has been promoted by the EU with the goal to apply proteomics in animal science in order to reach a deeper understanding of the phenotype, physiology, pathophysiology and productivity of land and water raised farm animals.

To date, proteomics has been applied to the field of farm animal science to monitor *in vivo* performances of livestock animals (growth performances, fertility, milk quality etc. [1–7]), but also to further our understanding of the molecular processes at the basis of meat quality, which are largely dependent on the *post mortem* biochemistry of the muscle, often in a species-specific way [8]. Indeed, one of the major goals of proteomics in the field of farm animal science is to shed light on skeletal muscle biochemistry [9] and to deepen our understanding of the physiological changes taking place at the protein level following harvest. *Post mortem* alterations to the muscle proteome reflect the biological complexity of the process often referred to as “muscle to meat conversion” [8].

1.1. Proteomics and swine science and meat investigations

The pig (*Sus scrofa domestica*) is one of the most important domestic animals, with global populations estimated to be 1 billion pigs (www.thepigsite.com and www.zoosavvy.com), while pig meat represents an essential protein source to the human diet, although its consumption is often hampered by religious constraints, as it happens for example in Muslim countries. Pig has been selectively bred to fulfill different purposes, including features like growth performances, prolificacy (Chinese breeds such as the Meishan), backfat thickness for the production of lard and smoked ham production (Casertana and Iberian/Alentejano pig), meat leanness (commercial lines based on Large White and Landrace breeds), feed conversion rate, muscle growth development and size, adaptation to harsh rearing environments and stress, flavor and taste-affecting traits, like boar taint and the suitability for biomedical research (Yucatan or the Göttingen minipigs) [10].

Investigations in the field of swine farming range from insemination to slaughter and industrial pork production [10].

The control of pig reproduction and the extensive use of artificial insemination have been a key feature of pig production over the last decades. Several experimental articles and reviews address the post-fecundation events: from zygote formation and implantation, to embryo development and birth, there exists a collection of complex physiological processes, dependent on variables and conditionings both inherent to the animal and to environmental factors (the interested reader is referred to the reviews by Oestrup et al. [11], Waclawik [12] and Croy and co-workers [13]). Briefly, proteomics has been successfully applied to several aspects of both male and female reproduction as well as the interaction between the sperm and oocytes [14]. Spermatozoa’s surface proteins play a major role in the process of fecundation of the oocyte. In a recent study, sperm surface proteins were purified, identified and their changes were monitored during the different stages of maturation in the epididymis [15]. Proteomics approaches have been also applied

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