

Across the great divide: Proteomics becoming an essential tool for animal and veterinary sciences

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Graphical abstract



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Since 2012, when the first and latest Thematic Issue of the Journal of Proteomics devoted to animal proteomics was published [[1](#)], there have been significant advances in the area, both in the extent of the applications and also in the use of more advanced technologies to this niche area of proteomic science. Although still not used as widely as in other areas of life sciences, such as biomedicine, the benefits of proteomics to extending the boundaries of knowledge in animal and veterinary science is being widely recognised. This has occurred to such an extent that an up-to-date Thematic Issue is fully justified and, as its predecessor, it should be influential in stimulating

further interest and use by animal science researchers in the use of this particular technology. Indeed, it would be of great value if this issue could simultaneously encourage experts in animal and veterinary sciences to overcome any hesitation in seeking to apply advantages of proteomic analysis in their research and not only in research on farm animals but also in investigations of companion animals in health and disease. Furthermore, we hope to encourage those with extensive expertise in proteomics to recognise there is a considerable value and reward in applying their hard won expertise in alternative areas of comparative proteomics where surprising and illuminating findings await their endeavours. Accompanying the Thematic Issue is a position paper that examines the development of proteomics as applied to animal sciences beyond the boundary imposed by focussing on laboratory animal studies [2]. Herein, we introduce the papers included in the Thematic Issue in relation to their context in animal science and their implication for the future development of the field. The papers in the Issue describe the application of proteomics not only to terrestrial farm animals but also to fish in aquaculture and to companion animals. Species covered are cattle, sheep, goats, pigs, chicken, fish, dogs, cats and horses and topics include a wide range of physiological and pathophysiological phenomena, from reproduction to host responses to infection and nutritional studies.

Farm animal breeding is nowadays often based on assisted reproductive technologies (ART). Proteomics is able to assist, for instance by increasing the knowledge about the composition and physiology of female reproductive fluids [3]. Metabolomics data from plasma analysis may additionally provide valuable information about successful transfer of *in vitro* produced embryos [4]. Ruminant production is highly influenced by climate and seasonal changes, especially in tropical and sub-tropical regions. Increased knowledge about animal physiology of different breeds under these conditions gained by –omics is supposed to contribute not only to animal health, but also to their productivity and to higher quality of meat and dairy products [5]. Supplementation of animal feed by particular amino acids influences the proteome and metabolome of both the skeletal muscles and the blood of pre-weaned calves, for instance the level of antioxidant proteins [6]. Protein changes in beef can be traced back to animal stress [7], and protein biomarkers for beef tenderness have meanwhile been found [8]. Mammary gland secretions in the dry period and milk production have been studied over time [9] as well as the influence of *Staphylococcus aureus* infection

on the milk proteome and peptidome of cows and goats [10,11]. Another product of small ruminants, wool of sheep, showed distinct proteome and fibre characteristics in a comparison of three particular genetic breeds from Portugal [12].

The manuscripts included in this issue dealing with pigs show an even larger variety in topics: They span from the proteome changes induced by exposure to the mycoestrogen zearalenone in the pig intestine [13] to a targeted proteome study on serum amyloid A isoforms in infection [14] and investigations of several brain areas in pigs raised under environmental enrichment [15]. Primary immune cells from transgenic pigs with a stable diabetic phenotype allowed the study of an early stage of diabetes mellitus [16]. Less known is about chicken leukocytes and therefore an approach was undertaken to better characterize a commonly used monoclonal antibody and to determine its true target [17]. Like in cattle, also in fish feed supplementation with amino acids, this time tryptophan, had an impact on physiology, metabolism and the proteome [18]. In addition, alteration in diet composition (linseed oil enrichment) caused changes in the liver phosphoproteome of a carnivorous marine fish [19].

Compared to other animal species, there is less in-depth information about protein components in equine body fluids, although different diseases would call for it [20]. Information is also lacking in equine sperm cryopreservation [21], the role of granulocytes in an autoimmune disease (equine recurrent uveitis) [22] and protein changes in chondrocytes during osteochondrosis [23]. In all those case, LC-MS based proteomics helped to collect more data on altered protein profiles.

Not all body fluids of dogs are equally well studied, as compiled for the less investigated ones in [24]. Among them is cerebrospinal fluid, whose protein composition was the topic of interest when comparing three different types/treatments of epilepsy [25]. Like in humans, also in the dog proteome and metabolome profiling of urine is a good means to diagnose chronic kidney disease [26]. Both, pyometra [27] and chronic valve disease [28] leave their traces in canine serum, the first mainly in acute phase protein levels, while not all detected changes in the latter disease were similar to those known in human pathophysiology. Together with protein from coagulation cascades, inflammation markers were also the main altered serum components in a study of feline congestive heart failure due to primary cardiomyopathy [29].

This Thematic Issue captures an essence of the expanding scope of research being performed in animal sciences, making use of the additional insights that are forthcoming from the use of current proteomic technology. This process should expand with the growing experience of a new generation of animal scientists who are familiar with the potential and technicalities of implementation. In combination with metabolomics which is also expanding in uses in animal sciences and the more established genomic and transcriptomic technologies, animal and veterinary sciences research will be able to take a truly systems biology approach to further explore fundamental and applied avenues of research, making significant contributions to the society.

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