GROWTH AND DEVELOPMENT: JOINT MEAT SCIENCE & MUSCLE BIOLOGY, AND GROWTH & DEVELOPMENT—APPLICATIONS OF PROTEOMICS IN ANIMAL PRODUCTION

0377 Proteomics in animal science. J. Lippolis*, *National Animal Disease Center, Ruminant Disease of Cattle Research Unit , Ames, IA.*

The ultimate goal of proteomics is to detect and quantify the tens of thousands of proteins from a specific cell, tissue, or fluid. To observe protein expression, location, interaction, and modification under different experimental conditions would aid the understanding of the molecular mechanisms critical for cellular functions. In the context of animal health, better understanding of cellular functions would be the basis for rational therapeutic designs to target pathogens and correct disease conditions. The unique advantage of this technology is that a fairly large number of proteins can be identified and quantitated at one time, without any prior knowledge that any specific protein might exist in a sample. Analyzing a proteomic dataset can often lead to surprising results, and the unexpected may be the most interesting observation. In fact, most shotgun proteomic experiments are not typical "hypothesis driven" experiments, but may be better described as experiments designed to find a hypothesis. In these experiments hundreds if not thousands of proteins can be identified whose expression is altered by a defined experimental condition. Some changes in protein expression observed in a proteomics experiment may be expected and even well characterized. However, some may be unexpected or unknown and lead to new hypothesis for the connections between protein expression and cellular processes. Utilization of this technology with its potential for discovery, balanced with its limitations, is a useful tool in animal health research.

0378 Functional proteomics: Elucidation of molecular mechanisms of physiological variations of fat depots in beef cattle. J. M. Romao[1], M. He[2], T. McAllister[2], and L. L. Guan[1]*, [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada,* [2]*Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

Adipose tissue plays an important role in energetics, meat quality and animal productivity, but the factors that regulate fat metabolism in beef cattle are unclear. Recent transcriptomics has identified hundreds of genes that may influence fat deposition in bovine adipocytes, but the phenotypic traits of fat are ultimately determined by the functional proteins that regulate adipogenesis and lipolysis. It is evident that gene expression does not always correspond to the levels of functional proteins produced due to differences in translation efficiency and post-translational modification. Using high throughput Label Free Quantification (LC-MS/MS), we have attempted to identify the global changes in protein expression in bovine subcutaneous and visceral fat depots of steers fed different diets at different stages of physiological maturity. Our results revealed that the proteomic profile of bovine adipocytes differs among fat depots, reflecting functional and physiological differences such as the higher metabolic activity of visceral fat. Changes in lipid profiles in the diet, altered proteomic profiles in subcutaneous fat and provide insight into mechanisms whereby the fatty acid composition of adipose tissue may be favourable altered. Moreover, proteomic changes in subcutaneous adipose tissue of feedlot cattle between 12and 15 months reflected increased adipocyte growth and proliferation, but fatty acid synthesis declined as steers approached finishing weight. These findings suggest that the rate of fatty acids synthesis is not static during growth, revealing a coordinated balance between subcutaneous fat mass and the cellular abundance of lipogenic proteins which regulate the rate and degree of fat deposition in beef cattle. Additional work suggested that miRNAs within bovine adipose tissue may play an important role in the controlling the expression of regulatory proteins within fat depots. Consequently, proteins and miRNAs may serve as markers for future selection of cattle based on their ability to generate favourable levels of adipose tissue with desirable fatty acid profiles within beef meat.

0379 Use of proteomics in animal health and disease research. P. D. Eckersall*, *Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Bearsden Rd, Glasgow, G61 1QH, UK.*

Proteomics is the application of advanced protein analytical methods to determine the individual protein components in a biological sample from cells, tissue or fluid. These technologies have application wherever proteins are investigated and are essential for a full systems biology approach for integration of omic technologies to address myriad research questions. While there have been great strides made in the applications of proteomics in research into human disease and for in vitro study there has been relatively limited application in farm animal health and disease. However the value of proteomic investigation is being recognized in animal research. The combination of two dimension electrophoresis and mass spectrometry was the initial approach to proteomic investigation and remains a powerful technology for proteome characterisation and biomarker discovery. In our laboratory, investigation of bovine nasal secretion to assess its value as a non-invasive medium for diagnosis of bovine respiratory disease has revealed the presence of glutathione S-transferase as a significant component of the secretion. γ-Glutamyl transferase and alkaline phosphatase have also been identified in nasal secretion with active host defence mechanisms being suggested. Recently non-gel based proteomics combining liquid chromatography with mass spectrometry have seen major application in farm animal research. Quantitative proteomics shows great promise in providing multiplexed assay systems for the simultaneous assay of numerous low abundance protein biomarkers. For example, it has been shown that the concentrations of cytokines, acute phase proteins and bioactive peptides can be monitored in the same micro-litre volume of milk during bovine mastitis, using standards of specific peptides derived from the respective proteins with great potential for research into this important disease (Bislev et al., 2012 J Prot Res 11:1832). Undoubtedly, the use of proteomics will become an established and valuable tool for animal health and disease research in the near future.

0380 Use of proteomics for livestock improvement.

E. Huff-Lonergan, S. M. Lonergan, S. Cruzen, K. Grubbs, J. Dekkers, N. Gabler, J. Selsby, and L. Baumgard, *Department of Animal Science, Iowa State University, Ames.*

Proteomics is a very broad term that includes a wide variety of techniques to characterize the entire protein profile of the cell or tissue (referred to as the proteome). Proteomic tools provide insight into the relative abundance of specific proteins, protein modifications (including proteolysis, phosphorylation, glycosolation, etc.), subcellular localization of specific proteins, interaction partners and protein sequence information. One of the challenges that face researchers is that differences that are noted are all with respect to a particular point in time. The very nature of the proteome dictates this because the proteome is dynamic, especially in respect to posttranslational modifications. Proteomics is very powerful in helping understand the role of proteins in various tissues/cells, it is however a challenging tool to use if the desired outcome is truly to identify the entire complement of proteins in a cell. Investigators should focus first on their research question before commencing any experiment, but this might be even more important in the “global” experiments that utilize any of the new integrated “omics” approaches. Often, researchers will choose to narrow their focus and look more specifically at a particular organelle or subcellular fraction. This decision cannot be made lightly, and interpretation of the results must take into consideration the techniques employed as well as all of the steps involved in sample preparation. The creative use of appropriate proteomics techniques has the potential to reveal many subtle changes in protein profiles that can aid in characterizing the physiological response to a wide variety of stressors to identify factors impact animals’ ability to cope. In addition, proteomic techniques can be a valuable adjunct to studies that seek to understand innate differences in production characteristics.