Nonruminant Nutrition Symposium: Nutrigenomics

157 Practical uses of nutrigenomics and gene expression patterns to develop and evaluate nutritional strategies. K. A. Dawson*, *Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition*, *Nicholasville, KY*.

In addition to providing information on the regulation of physiological activities; applications of nutrigenomic and transcriptomic techniques are providing new tools for evaluating the value and effectiveness of nutritional strategies in domestic livestock. Detailed studies of gene expression patterns associated with different forms and levels of selenium in animal diets have begun to elucidate the critical hidden effects of specific mineral forms in several species. While it is clear that diets which use selenium incorporated into growing yeast (selenium yeast) can significantly and uniquely influence the expression of genes associated with recognized antioxidant systems, such materials also have other significant effects on genes and metabolic pathways that influence basic cellular repair mechanisms, the production of stress proteins, energy production systems, immunological systems, neurological function and reproductive systems. Tissue specific gene expression patterns determined with standardized microarrays clearly indicate major differences in various dietary forms of selenium and can be used to differentiate the effects of selenium yeast from those associated with sodium selenite. Such genomics tools have allowed for an understanding of the effects of specific nutrients in unprecedented detail and have opened new frontiers in nutrition and dietary manipulations. Gene expression patterns also provide useful tools for initially comparing dietary treatments and can be used to rapidly screen for key nutritional effects and to evaluate supplementation strategies. Using these comparison techniques, it has been possible to compare alternative antioxidant systems that can partially replace traditional dietary ingredients like vitamin E in animal feed. In chickens, the value of comparing the effects of diets using gene expression patterns and marker genes has been validated by examining more traditional methods for determining antioxidant status in the serum and by examining meat quality. In the future, Nutrigenomics approaches will undoubtedly improve the efficiency of techniques for evaluating dietary formulations and provide basic biochemical information that will lead to a new understanding of basic nutritional principles.

158 Early life nutritional conditioning with dietary phosphorus. C. M. Ashwell*[1] and R. Angel[2], [1]*Department of Poultry Science, North Carolina State University*, *Raleigh*, [2]*Department of Animal and Avian Sciences, University of Maryland*, *College Park*.

The recent technologies that have led to the new field of functional genomics are providing a clearer understanding of how organisms interact with their environment and in particular their diet. We are beginning to learn how the diet may have long-term influence on performance and health. A form of epigenetic regulation has been recently described called fetal "programming." We have observed similar apparent programming by dietary manipulation in the perinatal period of the chicken. When birds are challenged with a diet low in phosphorus (P) for 90 h immediately post-hatch they obtain the ability to better utilize P later in life. This increased utilization of P (1.24-fold, $P < 0.001$) from the diet can partially be explained by an enduring increase (2.4-fold, $P < 0.05$) in the expression of the intestine-specific Na/P cotransporter (NaPcoT) IIb gene during programming as well as later in life when fed P restricted diets. The resulting data provide the first evidence for neonatal programming of gene expression in an oviparous species. Studies are ongoing to determine if the mechanism of persistent responses of gene expression to stimuli are epigenetic in nature. If epigenetic regulation is involved in dietary conditioning the opportunities for nutrition to impact both the animal and its offspring are almost limitless.

159 Using nutrigenomics to elucidate interrelationships in trace mineral metabolism. S. L. Hansen*[1], J. W. Spears[2], and R. S. Fry[2], [1]*Iowa State University*, *Ames*, [2]*North Carolina State University*, *Raleigh*.

Nutrigenomics is the study of dietary influence on gene expression. This presentation will focus on the area of trace mineral metabolism and the information that can be gained through the use of nutrigenomics. Numerous interactions between certain trace minerals may occur as minerals compete for intestinal absorption and transport throughout the body. Because of these interactions it has become apparent that it is no longer appropriate to examine the metabolism of a single mineral without consideration for the mineral "ionome" as a whole. Nutrigenomics presents a new way of looking at an old problem; while we have known for many years about the antagonistic relationship between minerals such as iron, manganese, and copper, it is only in recent years that specific gene products have been identified as potential points of interaction between these elements. For example, in 2 experiments where weaned pigs were fed varying levels of dietary iron, a strong negative relationship between dietary iron and tissue manganese concentration was observed. Using quantitative-PCR it was found that intestinal expression of divalent metal transporter 1 (dmt1) was depressed in pigs fed high dietary iron. Elucidating points of interaction, such as dmt1, which is a transporter for both iron and manganese, allows nutritionists to more accurately formulate diets. Utilizing nutrigenomics in the field of mineral metabolism has many potential benefits, including redefining mineral requirements of animals in the face of a new generation of plant and animal genetics, and diminishing environmental impacts by decreasing excessive oral supplementation of minerals. In summary, nutrigenomics provides biological targets at which to aim studies of animal trace mineral metabolism, which should increase our knowledge of mineral interactions and lead to more accurate dietary mineral recommendations.

Key Words: interactions, minerals, nutrigenomics

160 A functional genomics view of selenium in energy metabolism, obesity, and diabetes. X. G. Lei*, *Cornell University*, *Ithaca, NY*.

The trace element Se and Se-dependent glutathione peroxidase-1 (GPX1) have been considered to protect against diabetes. Intriguingly, we found a spontaneous development of type 2 diabetes-like phenotypes in GPX1 overexpressing mice at 6 mo of age. Later, other laboratories demonstrated similar deleterious effects of overexpression of other antioxidant proteins on sensitizing mice to diabetes. Most striking, 8 major human studies have recently shown hyperglycemic, hypolipidemic, and pro-diabetic effects of Se supplement. Because pigs are an excellent model for human nutrition, we have conducted a series of experiments to elucidate functional genomics of porcine selenoproteins in glucose and lipid metabolism. We first identified all 25 porcine selenoproteins using *in silico* cloning followed by PCR. We then determined the effects of dietary Se deficiency and excess on gene expression of all 25 selenoproteins in various tissues of pigs using quantitative real-time Q-PCR. Recently, we induced obesity in pigs by feeding them with a high-fat diet and determined effects of obesity on gene expression of the 25 selenoproteins. Our results indicate that gene expression of

13 selenoproteins was altered by dietary Se deficiency or excess non-unilaterally. The induced-obesity enhanced or decreased gene expression of 17 selenoproteins in various tissues of pigs. Microarray data have been generated from the dietary Se and fat experiments to establish systems biology related to body energy metabolism, selenogenome, and porcine genome. Our findings will reveal novel metabolic roles of Se in energy metabolism, obesity, and diabetes.

NIH DK 53018, NSFC Projects 30628019, 30700585, and 30871844, and the Chang Jiang Scholars Program.

Key Words: energy metabolism, gene expression, genomics