

Nonruminant Nutrition

Are We Ready for Nutritional Genomics?

321 Microarray and proteomic technology for nutrition research. K. E. Webb, Jr.*¹, E. A. Wong, and H. Jiang, *Virginia Tech, Blacksburg, VA.*

For decades, biochemical and physiological and, more recently, molecular approaches have been employed exhaustively and effectively in the quest to better understand nutrient utilization. A greater understanding of gene regulation and the interactions among their encoded proteins will enable the further extension of knowledge concerning nutritional physiology. The same genes are present in all cells in the body, however, differential expression of a subset of genes determines a cell's function. Multiple genes are responsible for most physiological processes, including nutritional processes such as digestion and absorption. Interactions among gene products are complicated and highly orchestrated. Functional genomics, through microarray hybridization, allows the coordinated assessment of changes in mRNA abundance for thousands of genes simultaneously in a cell or tissue in relation to changing physiological status. Microarrays can be valuable in understanding transcriptional regulation across the genome. mRNA are essential for translation of proteins, however, the presence of the mRNA for a protein does not necessarily mean that the protein is expressed. Further, proteins can persist in cells long after their mRNA are no longer present. Therefore, besides abundance of steady-state mRNA, it is necessary to monitor changes in the expression of proteins. Functional proteomics, the global analysis of gene expression at the protein level, allows the simultaneous evaluation of expression of hundreds or thousands of proteins and possible post-translational modifications of these proteins in cells or tissues using high-resolution, two-dimensional gel electrophoresis. Individually, microarray and proteomic technologies can provide vast amounts of information about gene function in relation to nutritional physiology which can assist in understanding prevailing concepts, enable discover-

ies, and/or facilitate the development of new hypotheses. Combined, they can be immensely powerful. These are new paradigms for examining gene expression in food-producing animals.

Key Words: Microarrays, Proteomics, Nutritional physiology

322 How do these tools help study nutrient function? X. G. Lei*¹, *Cornell University.*

In a post-genome-sequencing era, gene-chip and proteomic tools are being increasingly applied to study nutrient function and metabolism. Our laboratory has studied in vivo antioxidant functions and signaling of selenium. Using the selenium-dependent glutathione peroxidase (GPX1) knockout mice, we found that minute hepatic GPX1 activity attenuated the pro-oxidant-induced apoptosis, a mixed form of cell death that shares apoptosis and necrosis. To illustrate the underlying signal pathways, we determined the impact of minute GPX1 activity on the time-course of the pro-oxidant-induced expression of 23 apoptosis-related signal molecules in livers of the GPX1 knockout mice and the wild-type mice. Total liver RNA was isolated using the RNAqueousTM kit (Ambion, Austin, TX), and detected using the Mouse Apoptosis-1 GEArray kit (Super Array, Inc., Bethesda, MD). A total of 11 out of the 23 genes in the Array gave distinct and reproducible signals. The largest difference in mRNA levels between the two groups of mice was the DNA damage-inducible GADD45, followed by consistent protein responses. Our results unveil a novel signal mechanism for the GPX1 protection against oxidative cell death, and exemplify the usefulness of the genomic tools in studying nutrient function.

Key Words: Selenium, Gene knockout, Microarray

Animal Behavior and Well-Being

Influence of Production Practices on Behavior and Well-Being

323 Reaction of Holstein dairy cattle to a looming person as a temperament assessment tool. J. L. Lanier¹ and T. Grandin*¹, *Colorado State University.*

A population of registered, artificially inseminated Holstein dairy cows (n=263) was used to determine if temperament as measured by reaction to a looming person was associated with average milk production. Individual reaction to a looming person was assessed while the cow was restrained in outdoor head stanchion during the morning feeding. An unfamiliar observer stood 1 m (3 feet) directly in front of each cow's head, keeping the shoulder pointed towards the cow's head, waited 15 s, then calmly leaned sideways towards the cow allowing the inner arm to dangle. Reaction was rated as 1) non-reactive - no reaction, or stretched to sniff observer, 2) mildly reactive - pulled away from observer, did not pull against head stanchion, or 3) highly reactive - pulled against head stanchion or head remained pulled against stanchion throughout test. Milk production values from the current lactation were used. Results were expected a priori for more reactive cows to have lower productivity. One-way analysis of variance with a contrast was used to compare the average production yield of highly reactive cows to the combined average of the mildly and non-reactive cows. Very reactive cows had 47.3 kg less productivity mature equivalent fat compared to the non- and mildly reactive cow average (P = 0.05). No association was found for all other production values. The temperament assessment could have been improved by comparing the cows' reaction to a familiar looming person as well. The use of temperament assessment combined with current production traits could assist dairy producers in their herd management.

Key Words: Dairy cattle, Milk production, Temperament

324 Orientation of beef cattle grazing foothill winter range in Montana. B. Olson*¹, *Montana State University.*

Cattle may graze foothill winter range in northern areas as an alternative to feeding hay, although this exposes them to potential thermal stress. Consequently, cattle may orient to maximize heat gain or to minimize heat loss depending on ambient weather. Our objective was

to determine how mature cattle orient while grazing winter range. During two winters (Winter 1 1996-1997; Winter 2 1997-1998), we recorded orientation of cattle (n = 32) at 30-min intervals from dawn to dusk 3d each wk for approximately 7 wk. Circular statistics, including mean vector (body orientation relative to direction) and vector length (variation around mean vector), were used to characterize orientation. Stepwise multiple regression was used with mean vector and vector length as response variables, and solar radiation, net radiation, temperature, relative humidity, wind velocity, and wind direction as predictor variables. Mean vector was approximately east-west (Winter 1, 80°, Winter 2, 100°; body perpendicular to the sun low in the winter sky), although coefficients of determination were low, especially in the second winter (Winter 1, R² = 0.14; Winter 2, R² = 0.03). Vector lengths increased with increasing solar radiation, especially at cold temperatures (Winter 1, R² = 0.24; Winter 2 R² = 0.17), indicating more cattle were assuming the same orientation under these conditions. Cattle oriented perpendicular to the sun's rays intercept about 80% more direct radiation than cattle facing the sun. On relatively warm, sunny days, radiation absorbed by cattle can range from 4 to 6x (280-420 W m⁻²) basal metabolic heat production (70 W m⁻²). A simple thermal balance model, including net radiation, ambient temperature, cattle surface temperature, latent and sensible heat loss, conduction, storage, and metabolic heat, indicates that net radiation can greatly affect thermal energy gains and losses under different weather conditions.

Key Words: winter, thermal balance, behavior

325 Relationships between daily feed intake and feeding behaviours in feedlot steers. J.A. Basarab*¹, E.K. Okine², and K.L. Lyle¹, *¹Western Forage Beef Group, Lacombe Research Centre, Lacombe, Alberta, Canada, ²University of Alberta, Edmonton, Alberta, Canada.*

This study was conducted to quantify the relationship between daily feed intake and feeding behaviors in feedlot steers. Seventy-five spring born steer calves (330 kg; SD=40 kg), 15 from each of the M1, M2, M3, M4 and TX BeefBooster strains, were adjusted to a high-barley diet (22.0%