

## Symposium: Growth and Development: The Molecular Basis for Feed Efficiency

**767 Mitochondrial efficiency in lines of mice divergently selected for heat loss.** J. M. McDonald\* and M. K. Nielsen, *University of Nebraska, Lincoln.*

Divergent selection (high=MH, low=ML, and control=MC) for heat loss was applied in mice in three replicates. After 16 generations (G) of selection, no selection was practiced for 26 generations; another 9 generations of selection ensued; then selection was relaxed again. A total of 25 generations occurred, and at G51, differences of 55% in heat loss 34% in feed intake:BW<sup>0.75</sup> in mature males existed between MH and ML mice. Rates of mitochondrial respiration states, degree of coupling and mitochondrial efficiency were measured in liver tissue of G58 mature males using a Clark-type oxygen electrode in an attempt to explain part of the line differences in feed intake. Body weight, body composition, feed intake and liver weight were also measured. Data from 69 mice (total for MH, ML and MC) in Replicate 1 and 67 in Replicate 2 were analyzed with contrasts used to test selection response (MH – ML) and asymmetry of response ( $[(MH+ML)/2 - MC]$ ). There were no significant differences in body weight or percents lean and fat between MH and ML mice ( $P>0.15$ ). However, liver:BW of MH mice was approximately 5.6% larger than in ML mice ( $P<0.06$ ). Selection response ( $P<0.01$ ) in feed intake:BW was similar to that observed at G51 with MH mice consuming 31.7% more than ML mice. States 2 and 4 respiration rates approached significance ( $P=0.09$  and  $P=0.12$ , respectively) with rates for MH mice greater than for ML mice. Differences in State 3 respiration failed to show significance. No differences existed in the degree of coupling, expressed as respiratory control ratio. ADP:O ratio in ML mice averaged 27.2% greater than in MH mice ( $P=0.03$ ), indicating greater mitochondrial efficiency in the liver for ML mice. Asymmetry of response was not observed for any of the characteristics ( $P>0.10$ ). Across all lines, a correlation of -0.32 was observed between feed intake:BW and ADP:O, however within lines this correlation failed to exist. These data indicate that efficiency of mitochondrial respiration explains a portion of the difference in feed intake between mice of the MH and ML lines.

**Key Words:** Mice, Heat Loss, Mitochondrial Efficiency

**768 The molecular basis for feed efficiency in beef cattle.** S. S. Moore\*<sup>1</sup>, E. L. Sherman<sup>1</sup>, J. D. Nkrumah<sup>2</sup>, F. D. Mujabi<sup>1</sup>, Z. Wang<sup>1</sup>, and P. Stothard<sup>1</sup>, <sup>1</sup>*University of Alberta, Edmonton, AB, Canada*, <sup>2</sup>*Merial Limited, Duluth, GA.*

Feed intake and feed efficiency are economically important traits in beef cattle as feed is the highest variable cost in production. Feed efficiency can be measured as feed conversion ratio (FCR, intake per unit gain) or residual feed intake (RFI, measured as DMI corrected for BW and growth rate, and sometimes a measure of body composition, usually carcass fatness, RFIbf). In an effort to fine map the genes underlying feed intake and feed efficiency we have used an increasing density of genetic markers to identify quantitative trait loci (QTL). QTL discovery was carried out as a whole genome scan on 400 to 500 steers, depending on analysis, that comprised 20 half sib families. The number of genome wide markers used for the scans increased from an initial 450, to 3,000 and eventually 51,000 SNP. Various statistical approaches were used for analysis and these included single and multiple marker regressions to estimate SNP effects as well as linear mixed models for QTL mapping.

To date we have identified 48 putative SNP markers for residual feed intake. Validation of these markers is ongoing in independent populations of animals with available individual animal intake records. The identification of narrow QTL regions will aid greatly in the identification and testing of positional candidate genes underlying traits associated with feed intake and efficiency in cattle.

**Key Words:** Residual Feed Intake, Feed Efficiency, Beef Cattle

**769 Associations between mitochondrial function and feed efficiency in poultry and livestock species.** W. G. Bottje\*<sup>1</sup> and G. E. Carstens<sup>2</sup>, <sup>1</sup>*University of Arkansas, Fayetteville*, <sup>2</sup>*Texas A&M University, College Station.*

Meeting future global demands for animal protein in the face of rising feed costs, emerging bioenergy policies and environmental concerns will require substantive improvements in feed efficiency to maintain viable meat production systems in the U.S. In livestock and poultry, genetic variation exists in feed consumed above and below predicted requirements for production and maintenance, which can be quantified as the difference between actual and expected feed intake based on size and weight gain (residual feed intake; RFI). While research has established that inter-animal variation in RFI is favorably linked with variation in total energy expenditure, our understanding of the cellular and biochemical mechanisms responsible for bioenergetic processes associated with feed efficiency is incomplete. There is evidence that mitochondrial function, respiration, and/or biochemistry are linked to the phenotypic expression of feed efficiency (FE; g gain to g feed) and RFI in livestock and poultry. This paper will provide a short overview of biochemical mechanisms controlling mitochondrial energy metabolism and function, and will review the literature that examines the role that these important mitochondrial-linked biological processes could play in accounting for genetic and phenotypic variation in feed efficiency. Enhanced understanding of the mechanisms controlling mitochondrial function will provide useful insight into development of physiological biomarkers and genetic markers that are predictive for RFI or FE in livestock and poultry. Development of new selection tools will enhance the accuracy of identifying livestock and poultry with superior genetic merit for RFI, thereby improving the economic and environmental sustainability of U.S. meat-production systems.

**Key Words:** Mitochondria, Residual Feed Intake, Feed Efficiency

**770 Physiological basis for residual feed intake.** R. M. Herd\*<sup>1</sup> and P. F. Arthur<sup>2</sup>, <sup>1</sup>*NSW Department of Primary Industries, Armidale, Australia*, <sup>2</sup>*NSW Department of Primary Industries, Camden, Australia.*

Residual feed intake (RFI) is a measure of feed efficiency that is independent of level of production and hence a useful new trait for studying the physiological mechanisms underlying variation in feed efficiency. Five major physiological processes are likely to contribute to variation in RFI; being processes associated with intake of feed, digestion of feed, metabolism (anabolism and catabolism associated with and including variation in body composition), activity, and thermoregulation. Studies on Angus steers following divergent selection for RFI estimated that heat

production from metabolic processes, body composition and activity explained 73% of the variation in RFI. The proportion of variation in RFI that these processes explain are: protein turnover, tissue metabolism and stress (37%), digestibility (10%), heat increment and fermentation (9%), physical activity (9%), body composition (5%) and feeding patterns (2%). Other studies in cattle and studies in poultry similarly found these processes to be important in explaining RFI. The physiological mechanisms identified so far are based on very few studies, some of which have small sample sizes. The genomic basis to variation in these physiological processes remains to be determined. Early studies have shown many hundred genes to be associated with differences in RFI, perhaps in hindsight not surprising given the diversity of physiological processes involved. Further research is required to better understand the mechanisms responsible for the variation in RFI in target populations and to marry the physiological information with molecular genetics information which will become the basis for commercial tests for genetically-superior animals.

**Key Words:** Feed Efficiency, Body Composition, Genomics

**771 Physiological basis for residual feed intake in pigs.** C. de Lange\* and G. vanderVoort, *University of Guelph, Guelph, ON, Canada.*

Selection for residual feed intake in growing pigs is an important means to improve pork production efficiencies. Differences in pork production

efficiencies between pigs can be attributed largely to between-animal variation in the composition of growth (fat tissue vs lean tissue vs visceral organs), energy and nutrient requirements for body protein deposition, and basal energy expenditure. Visceral organ mass, an important predictor of whole body energy expenditure in growing pigs, is influenced by factors associated with feed (feed intake level and diet composition), environment (i.e. disease) and pig genotype. In isotope tracer studies it has been shown that variation in the ratio between whole body protein synthesis, an important contributor to whole body energy expenditure, and body protein deposition varies between extreme pig genotypes. Between-animal variation in this ratio should be explored further within lines of pigs. Basal energy expenditure can be defined as the available energy requirements at the tissue level to support body functions that are not related to growth and feed intake. Basal energy expenditure, in contrast to maintenance energy requirements, is largely independent of feeding level, diet composition, composition and rate of growth and can thus be related more easily to animal characteristics. The contribution of animal activity to between-animal variability in basal energy expenditure appears quite substantial and deserves further exploring. Key aspects of animal activity in ad libitum fed pigs are time spend standing, feeding frequency and eating rate. At the cellular level, special consideration should be give to the efficiency of oxidative phosphorylation which is influenced by uncoupling proteins, and maintenance of ion gradients across membranes. A better understanding of the biology of energy and nutrient utilization may lead to means to improve the efficiencies of pork production, including the identification of genetic markers that may be used in pig breeding strategies.

**Key Words:** Residual Feed Intake, Energetic Efficiency, Growing Pigs