sorted into three marketing groups based on projected days to USDA low Choice quality grade and fed a common high concentrate diet in twelve slatted-floor pens (10 head per pen). Ultrasound measurements (backfat (uBF), rump fat (uRmpFt), ribeye area (uREA), and intramuscular fat (IMF)), were taken at approximately one year of age. At the projected days to finish, each marketing group was harvested in a commercial packing facility. Carcass data (HCW, backfat over the 12-13th rib (BF), marbling score (MRB), and ribeye area (REA)) was collected for comparison with ultrasound data. The 9-10-11th rib section was removed and dissected into edible and non-edible portions. Chemical fat was determined by ether extract of the edible portion and used to compute carcass fat (CF) and empty body fat (EBF). The observed EBF averaged 23.7%. Multiple regression analysis indicated that carcass measurements explained 73% of the variation in EBF (EBF = 16.0583 + 5.6352*BF + 0.01781* HCW + 1.0486*MRB - 0.1239*REA). Because carcass traits are not available on bulls intended for breeding, another equation using computed HCW (cHCW; using a previously published equation between HCW and SBW) and ultrasound measurements was developed (EBF = 41.0437*uBF - 0.1384*uREA + 0.0867*cHCW - 0.0897*uBF*cHCW - 2.4225). This equation accounted for 62% of the variation in EBF. An equation previously developed to estimate EBF from carcass traits of steers over predicted the observed EBF of these bulls (28.2 vs. 23.7%, respectively). Carcass traits are sufficient to estimate EBF in yearling bulls, but further investigation is required to improve equations for EBF using ultrasound measures.±

Key Words: Beef bulls, Ultrasound, Body Composition

Meat Science and Muscle Biology: Novel Technologies in Muscle Biology/Fresh Meat Research

175 Adipocytes, myofibers, and cytokine biology: New horizons in the regulation of growth and body composition. M. Spurlock*, S. Jacobi, J. Davis, N. Gabler, and K. Ajuwon, *Purdue University*, *West Lafayette, IN*.

Muscle growth in meat animals is a complex process governed by integrated signals emanating from multiple endocrine and immune cells. A generalized phenomenon among meat animal industries is that animals commonly fail to meet their genetic potential for growth in commercial production settings. Therefore, understanding the impact of stress and disease on muscle growth potential is essential to improving production efficiency. The adipocyte in particular seems to be well positioned as an interface between energy status and immune function, and may thus regulate myofiber growth through a combination of signals which influence fatty acid oxidation, glucose uptake and insulin sensitivity. Adipocytes are active participants in the innate immune response, and as such, produce a number of metabolic regulators, including leptin, adiponectin, and proinflammatory cytokines. Specifically, adipocytes respond directly to bacterial lipopolysaccharide by producing IL-6 and TNFÎ±. However, adipocytes are also the sole source of the anti-inflammatory hormone, adiponectin, which regulates the nuclear factor kappa-B transcription factor, locally, and in myofibers. The production of such molecules strategically positions inter- and intra-muscular adipocytes to act as immunological sensors to regulate direct and indirect responses of myofibers to inflammatory signals. In this talk, we will establish critical immunological aspects of the adipocyte, and build specific linkages between these processes, cytokine production, and energy metabolism at the myofiber and whole-animal level. Finally, specific research needs will be emphasized.

Key Words: Adipocyte, Myofiber, Cytokine

176 Gene expression profiling: Insights into skeletal muscle growth and development. D. Moody, C. Stahl, and J. Reecy*, *Iowa State University*, *Ames*.

It has been appreciated for a long time that skeletal muscle has an incredible ability to adapt to the genetic and physiological demands placed upon it. However, it has only been with the advent of high-throughput gene expression analysis that a systems-based understanding of these adaptations has begun to be appreciated. For example, compensatory growth in response to an imposed load is an important and well-known biological adaptation of skeletal muscle. Skeletal muscle hypertrophy results in increased amino acid transport, satellite cell proliferation, protein accretion, and involves fiber-type switching. However, we are only beginning to understand the systemic changes in hypertrophying muscle at the molecular level. An initial gene expression profiling experiment of work overloaded skeletal muscle has led us to describe the requirement for JAK2 signaling in myoblast proliferation and differentiation. In addition, gene expression profiling has also led to the discovery of new gene families associated with muscle hypertrophy. For example, gene expression analysis of skeletal muscle following administration of the beta-adrenergic receptor agonist clenbuterol revealed a significant decrease in RNA abundance of multiple members of the novel ankyrin repeat and SOCS-box containing (ASB) gene family. Furthermore, while the need of dietary P for both soft-tissue and bone growth has been well documented, the mechanisms by which this nutrient is involved in regulating growth has only begun to be elucidated. Current research is focused on identifying these mechanisms as well as nutrition by genetic interactions, which may affect them. These results provide new information concerning changes in gene expression associated with skeletal muscle growth and development, and provide candidate genes for future hypothesis-based testing.

Key Words: Microarray, Genetic, Nutrition

177 Use of transgenic mouse models to understand proteolytic degradation systems in muscle. M. Spencer*, *University of California*, *Los Angeles*.

Investigations into mechanisms involved in muscle wasting and growth have traditionally relied on the use of inhibitors against the different proteolytic systems present in muscle. These studies, while informative, do not always provide specific information about the role of individual proteases within a class or about the contribution of different family members. Genetically modified mice, in which genes are either knocked out or overexpressed are useful tools to circumvent these problems. We have generated several lines of genetically modified mice and have used them to address questions of muscle wasting, remodeling and disease. Mice lacking (knock out) or overexpressing (transgenic) proteins of the calpain and ubiquitin ligase families are generated, characterized and then subjected to perturbations that elicit muscle wasting. These studies have shown that calpains act upstream of ubiquitin ligases in the processes of muscle wasting and growth.

Key Words: Calpain, Ubiquitin, Muscle Growth

178 Application of proteomics in meat research. R. Lametsch*, *The Royal Veterinary and Agricultural University, Department of Food Science*, *Frederiksberg, Denmark*.

The large progress in biotechnology in recent years has resulted in the development of new scientific research areas such as genomics and proteomics, which are used to study the complex patterns of gene and protein expression in cells and tissue. The technologies developed within genomics and proteomics have mainly been used in life science, e.g. to develop new drugs and diagnostic tools. However, they also have a large potential in food science as gene expression and protein composition of plants and animals have a major impact on the yield and quality of the final food products. Proteomics is the study of the proteome which is defined as the protein complement expressed by the genome of an organism.

For the consumer and the meat industry variation in meat tenderness is a well known problem. Although it is an area with high attention the mechanisms leading to tender, and sometimes unexpectedly tough, meat are not fully understood. Meat tenderizes during post mortem storage and it is well established that post mortem protein degradation plays a major role in the tenderization process. During the post mortem proteolytic processes several muscle proteins are degraded, but the number and identity of the proteins that are degraded is partly unknown. Moreover, it is still unclear which proteolytic enzymes are involved and how they are regulated. We apply proteomics to study the mechanism involved in the tenderization process in meat and to identify specific markers for the post mortem proteolytic processes. Several protein fragments that result from post mortem proteolysis have been identified and it has also been possible to assign which part of the full-length proteins the fragments were revealed from. This information was used to construct the cleavage pattern of some of the proteins involved in meat tenderization. More importantly, some of the identified fragments were significant correlated to meat texture. We also apply proteomics to study the regulation of the calpain-system, which takes part in the tenderization process.

Key Words: Proteomics, Meat, Tenderness

Nonruminant Nutrition: Weanling Pig Nutrition and Methodology

179 Fermented soybean meal as a protein source in nursery diets replacing dried skim milk. S. W. Kim*, R. D. Mateo, and F. Ji, *Texas Tech University*, *Lubbock, TX*.

Two studies were conducted to evaluate if fermented soybean meal (FSBM) successfully replace the use of dried skim milk (DSM) in nursery diets. Fermentation of soybean meal was done by *Aspergillus Oryzae GB-107*. Previous studies demonstrated that this fermentation process reduces trypsin inhibitor contents and the size of soybean peptide. In Exp. 1, 192 newly weaned pigs (21.5 ± 0.1 d, 6.35 ± 0.10 kg) were allotted to one of four dietary treatments by increasing FSBM (0, 3, 6, and 9%) whereas reducing DSM (25, 22, 19, and 16%). Each treatment had six pens with eight pigs per pen. All diets contained 1.53% lysine, 0.87% methionine+cysteine, 1.03% threonine, 0.28% tryptophan, and 3.40 Mcal/kg ME. Pigs were fed the diets for two weeks. Body weight and feed intake were measured weekly. Diarrhea score was recorded daily during the entire feeding period. Average daily gain and feed intake were the same ($P > 0.05$) among the pigs fed the diets with 0, 3, and 6% FSBM. Pigs fed a diet with 9% FSBM had a lower ($P < 0.05$) ADG and ADFI than pigs with 0% FSBM. Diarrhea scores were the same ($P > 0.05$) among the treatments. In Exp. 2, 144 newly weaned pigs (22.1 ± 0.1 d, 6.52 ± 0.11 kg) were allotted to one of three dietary treatments by increasing FSBM (0, 5, and 10%) while reducing DSM (40, 32.4, and 24.8%). Lactose was added at 0, 3.8, and 7.6%, respectively, in order to match lactose content equal to 23.5% for all diets. All diets contained 1.58% lysine, 0.91% methionine+cysteine, 1.03% threonine, 0.29% tryptophan, and 3.51 Mcal/kg ME. All detailed procedure was identical to Exp. 1. Pigs fed a diet with 5% FSBM had a greater ($P < 0.05$) ADG and gain/feed than pigs with 0% FSBM when lactose contents were the same among the treatments. Pigs with 10% FSBM had the same ADG and gain/feed to those with 0% FSBM and 10% FSBM. Diarrhea scores were the same ($P > 0.05$) among the treatments. Fermented soybean meal can be used up to 10% in a nursery diet successfully replacing the use of dried skim milk when the lactose contents were matched.

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Key Words: Fermented Soybean Meal, Dried Skim Milk, Nursery Pigs

180 Comparative efficacy of plant and animal protein sources on the growth performance, nutrient digestibility and intestinal morphology of the early-weaned pigs. J. H. Yun, I. K. Kwon, J. D. Lohakare, W. T. Cho, and B. J. Chae*, *Kangwon National University*, *Chunchon, Kangwondo, Korea*.

The present study was conducted to evaluate and compare the effects of various animal and plant protein sources on piglet's performance, digestibility of amino acids and gut morphology in the weaned pigs till 28 days after weaning. Two hundred seventy weaned pigs of 17 ± 3 days of age (Landrace × Yorkshire × Duroc) were allotted to five treatments with three replicates, comprising 18 pigs in each replicate. The plant protein sources used were soybean meal (SBM), fermented soy protein (FSP), rice protein concentrate (RPC); and animal protein sources tested were, whey protein concentrate (WPC) and fish meal (FM). Iso-proteinous (21%) diets were formulated and lysine (1.55%) content was same in all the diets. The level of each protein source added was 6% by replacing SBM to the same extent from the control diet containing 15% SBM. The ADG was higher ($P < 0.05$) in the groups fed animal proteins as compared with plant proteins at all the levels of measurement, except during 15-28 days. The highest ADG was noted in WPC and FM fed diets and lowest in SBM fed diet. The feed intake was higher in animal protein fed groups than plant proteins at all phases. The digestibilities of gross energy, dry matter and crude protein were higher in animal protein fed groups than to plant protein fed sources. The apparent ileal digestibilities of essential amino acids like Leu, Thr, and Met were significantly higher ($P < 0.05$) in animal proteins fed animals as compared with plant protein fed groups. But the apparent fecal digestibilities of essential amino acids like Arg and Ile were significantly higher ($P < 0.05$) in plant protein diets than animal protein sources. The villous structure studied by scanning electron microscope were prominent, straight finger-like, although shortened and densely located in FM fed group as compared with others. Overall, it could be concluded that animal protein sources in the present study showed better effects on growth performance, nutrient digestibility and gut morphology than plant protein sources.

Key Words: Plant Protein, Animal Protein, Pigs

181 Growth performance, gut health and digestive function in newly weaned pigs fed fermentable proteins and carbohydrates. E. A. Jeaurond* and C. F. M. deLange, *University of Guelph*, *Guelph, Ontario, Canada*.

Feeding fermentable carbohydrates (FC) may reduce the negative impact of enteric proteolytic fermentation in pigs. A total of 144 newly weaned pigs (6.23 kg BW; six pens per treatment; six pigs per pen) were used to determine the interactive effects of feeding fermentable protein (FP) and FC on growth performance, indicators of digestive function and intestinal health. Dietary treatments were: (1) basal diet (control), (2) control + 10% poultry meal (PM) as FP source, (3) control + 5% beet pulp (BP) as FC source and (4) control + PM and BP. Diets were formulated to be similar in digestible energy and digestible amino acid contents. In general, no interactive effects of FC and FP were observed ($P > 0.10$). During the 3-week post-weaning period, feeding FP reduced ADG (269 vs. 242g/d; SE, 7), while feeding FC increased ($P < 0.05$) ADG (243 vs. 269 g/d; SE, 7). Overall feed intake did not differ between treatments ($P > 0.10$). Based on PCR-DGGE, feeding FC and FP appeared to increase microbiota diversity in colon contents. On d 14 and 28 post-weaning, Clostridia sp. counts in colon contents, White Blood Cell counts and segmented blood Neutrophils were lowered ($P < 0.05$) by feeding FC, suggesting lower bacteriological stress. Blood urea nitrogen was increased by feeding FP (6.5 vs. 9.5 mg/dL; SE, 0.5), while ammonia concentration in colon contents was lowered ($P = 0.06$) by FC (193 vs. 154 ug/mL; SE, 14.2). Among biogenic amines, levels of tyramine (304 vs. 140 nmol/g DM; SE, 38) and spermidine (219 vs. 174 nmol/g DM; SE, 14) in colon contents were lowered by feeding FC ($P < 0.05$). Acetic, proprionic and butyric acid contents in colon contents were increased by feeding FC, while valeric acid content was decreased by feeding FP ($P < 0.05$). Feeding FC and FP had no effect ($P > 0.10$) on colon histology, pH of colon contents, fecal consistency score and organ weights. Results suggest that FP and FC have independent effects on newly weaned pigs, while effects appear to be partly related to changes in gut micro flora.

Key Words: Pig, Gut Function, Fermentration