(P≥0.05) by CP level were detected. After 7 d of RAC withdrawal, ADG was depressed (P≤0.01) compared to CON pigs (0.650 vs 0.836 kg/day, respectively). However, no differences (P≥0.05) were detected at any time during RAC withdrawal for ADFI, F:G back fat or loin depth, as RAC pigs equal CON pigs' growth performance after day 7. The drop in ADG (after 7d) that resulted from RAC withdrawal, denied the advantages of RAC use, this should be considered in use–rest–use programs to establish a resting period no longer than 7 days.

Key Words: Ractopamine, Withdrawal, Finishing Pigs

Nonruminant Nutrition: Understanding Protein Synthesis and Degradation and Their Pathway Regulations

630 Postnatal ontogeny of skeletal muscle protein synthesis in pigs. T. A. Davis*, A. Suryawan, R. A. Orellana, and M. L. Fiorotto, *USDA/ARS Children's Nutrition Research Center, Baylor College of Medicine*, *Houston, TX*.

The neonatal period is characterized by rapid growth and elevated rates of synthesis and accretion of skeletal muscle proteins. The fractional rate of muscle protein synthesis is very high at birth and declines rapidly with development. The elevated capacity for muscle protein synthesis in the neonatal pig is driven by the high ribosome content and, together with an increased efficiency of the translation process, promotes accelerated protein synthesis rates. Feeding profoundly stimulates muscle protein synthesis in neonatal pigs and the response decreases with age. The feeding-induced stimulation of muscle protein synthesis is modulated by an enhanced sensitivity to the post-prandial rise in insulin and amino acids. The developmental decline in the response to insulin and amino acids parallels a marked fall in the feeding-induced activation of translation initiation factors that regulate the binding of mRNA to the 40S ribosomal complex. The abundance and activation of many known positive regulators of the nutrient- and insulin-signaling pathways that are involved in translation initiation are high and that for many negative regulators are low in skeletal muscle of younger pigs. Thus, the activation and/or abundance of the positive regulators, insulin receptor, insulin receptor-substrate-1, phosphoinositide-3 kinase, phosphoinositide-dependent kinase-1, protein kinase B, mammalian target of rapamycin, raptor, ribosomal protein S6 kinase-1, eukaryotic initiation factor (eIF) 4E-binding protein 1, and eIF4E associated with eIF4G are greater in 7- than in 26-day-old pigs. The activation of negative regulators, protein tyrosine phosphatase-1B, PTEN, protein phosphatase 2A, and tuberous sclerosis complex 1/2 are lower in 7- than in 26-day-old pigs. The developmental changes in the abundance and activation of these signaling components likely contribute to the high rate of protein synthesis and rapid gain in skeletal muscle mass in neonates. (NIH AR44474, USDA NRI 2005-35206-15273, USDA CRIS 58-6250-6-001)

Key Words: Swine, Protein Synthesis, Muscle

631 Measuring in vivo intracellular protein degradation rates in animal systems. W. G. Bergen*, *Auburn University*, *Auburn, AL*.

Whole body protein degradation, synthesis and accretion have been determined in animals utilizing isotopic tracers and urinary excretion of irreversible skeletal muscle metabolic end-products combined with various techniques to estimate changes in body protein content. Method refinements have centered on improvements of whole body isotope-kinetic approaches and explorations of tissue specific protein turnover of liver, small intestines and skeletal muscle proteins or specifically myofibrillar, sarcoplasmic, and connective tissue protein fractions of skeletal muscles. Utilizing contemporary GC-MS technology and isotopic infusion strategies, direct measurement of fractional protein synthesis (FSR) with stable isotopes of branched chain amino acids coupled with tissue amino acid specific activity values based on keto leucine or keto valine has emerged as the most robust technique to measure FSR in various tissues in animals and humans. Direct measures of whole body protein degradation or fractional breakdown rate (FBR) based on skeletal muscle irreversible metabolite excretion, such as 3- methyl histidine (3MH), in pigs has severe limitations. Some workers have addressed direct measures of skeletal muscle protein breakdown in pigs utilizing 3MH with compartmental kinetic models, but regrettably such procedures have not widely utilized. Contrariwise, the urinary 3MH excretion method has some merit in ruminants. Our understanding of the mechanisms and regulation of protein synthesis and protein breakdown has advanced to a point where it may be possible to use surrogates/markers to provide directional data, either enhanced or attenuated, for FSR and FBR. Rates of expression or activation status of regulatory transcription factors, initiation factors or signal pathway components, such as mTOR, eIF-4 and PKB, and abundance of mRNA for components of the intracellular proteolytic pathways may be exploited to study relative rates of FSR, FBR, muscle growth and metabolic efficiency in food producing animals.

Key Words: Protein Turnover, Isotope Kinetics, Proteasome

632 The non-lysosomal Ca^{2+}-dependent protein degradation pathway: The calpains, proteasome, and myofibrillar protein turnover. D. E. Goll*, G. Neti, S. W. Mares, and V. F. Thompson, *University of Arizona*, *Tucson*.

It is now clear that proteins in cells turnover metabolically, that the rate of this turnover can vary widely in response to physiological demand, and that turnover of proteins assembled in intracellular structures requires first disassembly of the proteins from the structure followed by their degradation. The proteasome is the major mediator of intracellular protein degradation, but the proteasome cannot degrade proteins assembled in intracellular structures, and the mechanism by which proteins are disassembled before their degradation remains unknown for most structures. It is also unclear how myofibrillar proteins, which must be assembled in myofibrils to be functionally contractile, are removed from this structure before degradation. It was proposed over 30 years ago that the calpains may initiate myofibrillar protein turnover by removing an outer layer of filaments from myofibrils, and that the calpain-removed proteins are then degraded by intercellular proteases, predominantly the proteasome. Studies have reported that striated muscle contains a group of myofilaments, ~ 10-15% of total myofibrillar protein, that can be released from myofibrils by triturating in the presence of ATP. These easily releasable myofilaments (ERMs)

are postulated to be intermediates in myofibrillar turnover. It is unclear whether ERMs are indeed a subset of myofilaments on the surface of myofibrils or whether they are simply removed by shearing during trituration and more filaments can be removed by repeated trituration. We have found that ERMs can be prepared from either rat or bovine muscle; that the yield is less than previously reported (0.5-0.8 % of myofibrillar protein); that once removed, repeated trituration does not yield more ERMs; and that ERMs can not be obtained from thoroughly washed myofibrils where presumably the ERMs have already been removed. Hence, ERMs seem to be a real subset of filaments. Mild treatment with calpain increases the yield of ERMs by 2 to 2.5-fold, so the calpains can release ERMs as proposed over 30 years ago. Supported by NRI, NIH, MDA.

Key Words: Calpain, Proteasome, Myofibrillar Protein

633 The mTOR-signaling pathway in regulating metabolism and growth. X. Yang*, C. Yang, A. Farberman, C. F. M. de Lange, J. France, and M. Z. Fan, *University of Guelph*, *Guelph, Ontario, Canada*.

The mammalian target of rapamycin (mTOR) plays key roles in cell growth and the cell cycle and acts as a central regulator of protein synthesis and ribosome biogenesis at transcriptional and translational levels. mTOR senses and integrates signals from mitogens and nutrients. Ribosomal protein S6 protein kinase S6K1 and eukaryotic initiation factor 4E binding protein 4E-BP1 are currently the two best-known downstream effectors of mTOR signaling. Interactions of mTOR with raptor or rictor result in two types of mTOR complexes with the former being the primary controller of cell growth and the latter mediating effects that are insensitive to rapamycin such as cytoskeletal organization. Upstream elements of mTOR signaling include Ras-homolog enriched in brain (Rheb), and tuberous sclerosis complex 1 and 2 (TSC1/2) with TSC2 as the linker between PI3K/Akt or Ras/Raf/MEK/ERK pathways and the mTOR pathway. AMP activated kinase (AMPK), an important cellular energy sensor, can work with mTOR signalling to maintain cellular energy homeostasis. Nutrients and hormonal factors can differentially mediate metabolism and cellular growth via the mTOR pathway with effectors specific to organ or tissue types involved.

Key Words: Growth, Metabolism, Mammalian Target of Rapamycin (mTOR)

Physiology & Endocrinology - Livestock and Poultry: Endocrinology

634 Relationship between leptin and carcass quality and yield grade in a population of Certified Angus Beef–type cattle. D. L. McNamara*[1], T. B. Schmidt[3], E. L. Walker[4], M. M. Rolf[1], A. N. Brauch[1], W. Pittroff[2], and D. H. Keisler[1], [1]*University of Missouri*, *Columbia*, [2]*University of California*, *Davis*, [3]*Mississippi State University*, *Starkville*, [4]*Missouri State University*, *Springfield*.

Leptin is a protein hormone secreted by adipocytes. Serum concentrations of leptin increase with adiposity in various species, including beef cattle. In this investigation, we utilized a relatively uniform population of cattle — i.e. those destined for a Certified Angus Beef–type market, to determine the relationship between serum concentrations of leptin and phenotypic variables associated with carcass quality. This work differs from our prior investigations in which we utilized a non–uniform and random population of cattle from a commercial slaughter facility. Our hypothesis was that serum concentrations of leptin would be higher in heifers than steers and that serum concentrations of leptin would be an accurate, positive indicator of carcass quality and yield grades in a Certified Angus Beef–type population of cattle. In the current investigation blood samples were collected at slaughter and analyzed for serum concentrations of leptin from 2,815 black slaughter steers and heifers. The PROC GLM method of SAS was used with leptin as the dependent variable and all carcass merit variables analyzed as independent variables within the model. Any independent variables that were not significant within the model were removed from the final analysis. We observed that leptin levels were significantly greater in heifers than steers (25.12 vs 20.94 ng/ml, respectively; $P < 0.0001$). Independent of gender however, leptin concentration at the time of slaughter was a significant predicative indicator of the carcass quality grades: select, low choice, upper two-thirds choice, high choice, and prime (20.60, 22.16, 23.38, and 25.99 ng/ml, respectively; $P < 0.006$). Likewise, USDA Yield grades were resolvable by leptin levels at Yield grades 2, 3, and 4 (20.95, 23.32, and 25.74, respectively; $P < 0.001$), but incapable of resolving Yield grade 4 vs. 5 cattle — a threshold point (yield grade >3) at which carcasses typically begin to be discounted for excessive fat. We suggest that these data provide evidence that serum concentrations of leptin are indicative of the greater fat mass across gender and carcass merit.

Key Words: Leptin, Adipose, Carcass

635 Variation in maintenance energy requirements of gestating beef cows and relationships with calf performance and plasma IGF-I. M. J. Prado-Cooper*, N. M. Long, R. P. Wettemann, G. W. Horn, L. J. Spicer, and C. R. Krehbiel, *Oklahoma Agricultural Experiment Station*.

Variation in maintenance energy requirements (MR) was determined in spring-calving Angus × Hereford cows during gestation in each of two years (yr 1, n = 27; yr 2, n = 32). A second objective was to determine if MR were related to plasma concentrations of IGF-I and postnatal calf growth. Nonlactating cows (4 to 7 yr of age) with a BCS of 5.0 ± 0.2, and BW of 582 ± 37 kg, in the second to third trimester of gestation, were individually fed a complete diet in amounts to meet predicted MR (Model 1, NRC 2000). After 2 wk, daily feed intake was adjusted each 7 d until constant BW was achieved. Regression analysis was used to determine constant BW. Final BCS averaged 5.0 ± 0.2 (yr 1) and 4.6 ± 0.4 (yr 2). Daily MR averaged 0.0892 (yr 1) and 0.0930 (yr 2) (Mcal/$BW_{kg}^{.75}$). Cows were classified based on MR as low (> 0.5 SD less than mean, L), moderate (± 0.5 SD of mean, M) or high (> 0.5 SD more than mean, H). The greatest differences in MR for all cows were 29% (yr 1) and 24% (yr 2). ADG and IGF-I were