848 Effect of sulphite salts on the aerobic stability and intake levels of whole crop wheat by grazing of dairy cattle. J. K. Margerison*[1] and R. R. Edwards[2], [1]*Massey University*, *Palmerston North, New Zealand*, [2]*University of Plymouth*, *Plymouth, UK*.

Two experiments were completed to measure the effect sulphite salts on the aerobic stability and intake levels of whole crop wheat (WSW) offered to grazing dairy cattle. In experiment 1: 40 cows (60 days postpartum), were allocated into matched pairs according to milk yield and composition: 20 received WSW with no additive (NoSS), 20 received WSW with added sulphite salts (SS) for 42 days, with a 28 day measurement period using pre-treatment milk yield and composition as covariates. In experiment 2: 1.5 kg of WSW from each treatment in experiment 1 was used for laboratory aerobic stability studies and plate yeast culture. WSW intake levels (kg DM/d) were significantly lower in SS 6.9, NoSS 5.9 (SE 0.19), grazing time (min/d) SS - 263.5, NoSS 296.0 (SE 6.911), ruminating time (min /d), SS 546.6, NoSS 530.8, 3.353 was significantly greater with NoSS. Diet had no significant effect on milk yield (kg/d), SS 33.3, NoSS 32.9, (SE 0.52), milk fat (g/kg), SS 40.5, NoSS 42.1, 0.07 or protein (g/kg), SS 33.6, NoSS 33.6 (SE 0.03) content. Mean live weight (kg) was significantly greater in SS cows, SS 666.81, NoSS 660.14 (0.823). Time to peak temperature (h), SS 128.64, NoSS 82.89 (SE 1.547), maximum temperature (°C), SS 6.76, NoSS 10.90 (0.372) heat generated (°C), SS 39744.0, NoSS 54938.0 (1171.00) and yeast numbers (NoSS 4.951, NSS 4.156 (SE 0.62) log cfu/ml) were greater with NoSS. In conclusion, silage quality, live weight gain and aerobic stability of WCW was increased by the addition of sulphite salts, but had no significant effect on milk yield.

Key Words: Aerobic Stability, Whole Crop, Wheat

Growth and Development - Livestock and Poultry: Transcriptional Factors and Cell Mechanisms for Regulation of Growth and Development with Application to Animal Agriculture

849 Defining the transcriptional signature of skeletal muscle stem cells. Z. Yablonka-Reuveni*, I. Kirillova, G. Shefer, K. Rider, R. Almuly, A. Vine, B. Kwiatkowski, and K. Day, *University of Washington*.

Skeletal muscle myofibers are supplied with new nuclei by satellite cells, myogenic progenitors located between the plasma membrane and the basal lamina of the myofiber. During postnatal growth, satellite cells proliferate and contribute myoblasts that fuse with the enlarging myofibers. In mature muscles, satellite cells are mitotically quiescent, but they can enter the cell cycle and produce myoblasts in response to stimuli generated by muscle damage. Quiescent satellite cells commonly express the paired-homeobox transcription factor Pax7, while their proliferating progeny co-express Pax7 and the muscle-specific transcription factor MyoD. Upregulation of FGFR4, along with the induction of the muscle-specific transcription factor myogenin and a concomitant decline in Pax7, marks the transition of satellite cell progeny into the differentiation phase. These cells rapidly withdraw from the cell cycle, terminally differentiate and fuse into myotubes. We identified expression of green fluorescent protein (GFP) driven by regulatory elements of the nestin gene within satellite cells of different muscles in mice. This GFP expression establishes a novel means for characterizing satellite cells in their niche. Sorted GFP+ cells exclusively acquired a myogenic fate, even when supplemented with media supporting non-myogenic development. Common and unique gene expression patterns were identified in satellite cells from different muscle groups. GFP+ sorted cells from hindlimb, diaphragm and extraocular muscles expressed relatively high levels of Pax7 and Myf5. Only the diaphragm cells exhibited a distinctly greater expression of Pax3. GFP expression declined following satellite cell activation and was reacquired in late stage myogenic cultures by non-proliferating Pax7+ progeny. The dynamics of this expression pattern reflect the cycle of satellite cell self-renewal. The nestin-GFP model reveals unique transcriptional activity within quiescent satellite cells and permits novel insight into the heterogeneity of their molecular signatures. Supported by USDA and NIH.

Key Words: Satellite Cells, Pax7, Skeletal Muscle

850 The role of microRNAs in muscle development. T. P. L. Smith*[1], T. G. McDaneld[1], M. E. Doumit[2], L. K. Matukumalli[3], T. S. Sonstegard[3], L. L. Coutinho[4], and R. T. Wiedmann[1], [1]*USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*, [2]*Michigan State University*, *East Lansing*, [3]*USDA, ARS, Bovine Functional Genomics Laboratory*, *Beltsville, MD*, [4]*University of Sao Paulo*, *Brazil*.

The genomes of multicellular eukaryotic organisms encode numerous non-coding RNA (ncRNA) species with a variety of known functions, as well as many whose functions are currently unknown. One class of ncRNA genes produce transcripts that are processed by specific cellular machinery to result in small ~18-22 nucleotide-long micro-RNAs (miRs) that provide a targeting mechanism to direct RNA-protein complexes (RISC) to cognate mRNAs. Association of the RISC complex with mRNA has been shown to control gene expression by inhibiting translation or targeting messenger RNA for degradation. The data on miR expression and activity suggests that a major role for this level of regulation is to provide a mechanism for switching the physiological state of the cell in a rapid fashion, as a single miR may have numerous target genes and may act more rapidly than transcriptional control by silencing mRNA already present in the cell. Tissue-specific miRs have been implicated in control of development, homeostasis, and immune response. Studies in mouse myoblast cell lines have defined significant responses of miR populations during differentiation. Our studies of miR profiles in porcine and bovine satellite cell and fetal muscle samples demonstrate marked similarity, but also significant differences, to the murine system. In addition, miR profiles in fast-growing neonatal muscle and fully mature muscle indicate potential roles for regulation of gene expression throughout the life cycle. Analysis of mRNA coexpression through these developmental stages of muscle growth and maturity begins to provide a picture of the interplay between protein-coding gene expression and regulation at the post-transcriptional level via miRs. The data suggest potentially critical roles for miRs in the switch from proliferation to differentiation, in regulating muscle growth in early life, and in maintaining tissue homeostasis in mature muscle.

Key Words: Muscle Development, Non-coding RNA, Gene Regulation

851 Cellular and molecular regulation of muscle growth and development in meat animals. W. R. Dayton*, M. E. White, and M. R. Hathaway, *University of Minnesota*, *St Paul*.

Insulin-like growth factor (IGF)-I and IGF binding proteins (IGFBP) play a significant role in mediating the actions of myostatin, TGF- β and anabolic steroids on muscle cells at the cellular and molecular level. Both myostatin and TGF-β suppress proliferation in porcine embryonic myogenic cell (PEMC) cultures. Treatment with myostatin or TGF-β also increases production and secretion of IGFBP-3 and IGFBP-5 by PEMC cultures. Immunoneutralization of IGFBP-3 and IGFBP-5 in the culture media of TGF-β or myostatin-treated PEMC cultures returns proliferation rate to 90% of levels observed in control cultures that were not treated with myostatin or TGF-β. Consequently, it appears that IGFBP-3 and IGFBP-5 play a crucial role in mediating the proliferation-suppressing actions of myostatin and TGF-β in PEMC cultures. Furthermore, the mechanisms by which IGFBP-3 and IGFBP-5 facilitate the proliferation-suppressing activity of myostatin and TGF-β appear to be IGF-independent and do not involve reduced phosphorylation of Smad2 or Smad3 by the TGF-β or myostatin receptors. The IGF/IGFBP system also plays a significant role in mediating the muscle-growth-enhancing actions of anabolic steroids. Steers implanted with a combined trenbolone acetate/estradiol (TBA/E) implant have increased circulating IGF-I levels and increased IGF-I mRNA levels in muscle tissue. Treatment of cultured bovine satellite cells (BSC) with E or trenbolone (TB) results in increased levels of IGF-I mRNA in these cells. Additionally, treatment of cultured BSC with either TB or E results in increased proliferation rate. Although, these data suggest that TBA/E-induced increases in muscle IGF-I levels may mediate the enhanced muscle growth observed in feedlot steers implanted with these steroids, studies utilizing the IGF-I receptor blocker JB1 indicate that the proliferation-promoting effects of TB and E in BSC cultures may not result solely from increased IGF-I levels.

Key Words: Muscle, Myostatin, Anabolic Steroid

852 Application of cellular mechanisms to growth and development of food producing animals. B. J. Johnson*, *Kansas State University*, *Manhattan*.

Postnatal skeletal muscle growth is a result of hypertrophy of existing skeletal muscle fibers in food producing animals. Accumulation of additional nuclei, as a source of DNA, to the multinucleated skeletal muscle fiber aids in fiber hypertrophy during periods of rapid skeletal muscle growth. Muscle satellite cells are recognized as the source of nuclei to support muscle hypertrophy. Exogenous growth enhancing compounds have been used to modulate growth rate and efficiency in meat animals for over a half century. In cattle, these compounds enhance efficiency of growth by preferentially stimulating skeletal muscle growth compared to adipose tissue. There are two main classes of compounds approved for use in cattle in the United States: anabolic steroids and β-adrenergic agonists (β-AA). Administration of both trenbolone acetate (TBA) and estradiol (E) as implants increased carcass protein accumulation 8 to 10% in yearling steers. Muscle satellite cells isolated from steers implanted with TBA/E had a shorter lag phase in culture compared to satellite cells isolated from control steers. Collectively, these data indicate that activation, increased proliferation, and subsequent fusion of satellite cells in muscles of implanted cattle may be an important mechanism by which anabolic steroids enhance muscle hypertrophy. Oral administration of β-AA to ruminants does not alter DNA accumulation in skeletal muscle over a typical feeding period. The enhanced muscle hypertrophy observed due to β-AA feeding occurs by direct, receptor-mediated changes in protein synthesis and degradation rates of skeletal muscle tissue. Often, the muscle is unable to sustain this level of hypertrophy due to no additional accumulation of nuclei to support the increased protein accretion. Proper timing of anabolic steroid administration when coupled with β-AA feeding could result in a synergistic response in skeletal muscle growth due to the effects of anabolic steroids at increasing satellite cell activity which then can support the rapid hypertrophic changes of the muscle fiber when exposed to β-AA.

Key Words: Anabolic Steroid, β-Adrenergic Agonist, Skeletal Muscle

International Animal Agriculture - Livestock and Poultry: Global Livestock and Poultry Issues

853 Factors affecting milk price and revenues of dairy farms in the central region of Thailand. J. A. Rhone*[1], R Ward[1], S Koonawootrittriron[2], and M. A. Elzo[1], [1]*Univeristy of Florida*, *Gainesville*, [2]*Kasetsart University*, *Bangkok, Thailand*.

Milk prices in Thailand are based on a base price set by the government as well as premiums and deductions, based on milk quality and components, given by dairy cooperatives. The objectives of this study were 1) to determine month and year, farm location, and farm size effects on milk price, and 2) to calculate farm milk revenues across time, farm location, and farm size. There were a total of 967,110 farm milk yield and 58,575 milk price records from 1034 farms collected from 2003 to 2006. Farm milk revenues were calculated as the product of farm milk yield and milk price. Milk price was analyzed using a linear model. Fixed effects were 1) pricing system (1 = price based on milk fat and bacterial score, and 2 = price based on milk fat, bacterial score, and bulk tank somatic cell count, 2) interaction of pricing system by month nested within year, 3) interaction of pricing system by farm size (number of cows milked per day); small: < 10 cows; medium: 10 to 19 cows; and large: > 20 cows, and farm location (4 districts: Kaeng Khoi, Muaklek, Pak Chong, and Wang Muang). All fixed effects were important ($P < 0.05$) sources of variation for milk price. Milk prices in system 1 were higher (11.54 vs. 11.71 Thai bhat, $P < 0.05$) than in system 2. Under pricing system 1, large farms had the lowest milk price ($P < 0.05$) in all districts except Kaeng Khoi. Under pricing system 2, small farms had higher ($P < 0.05$) milk prices than medium and large farms across all districts. Farms in Kaeng Khoi had the least loss of revenue due to milk price, whereas farms in Wang Muang had the greatest. Higher bacterial scores and (or) bulk tank somatic cell counts in large and medium farms made them lose more revenue than small farms. Improvements in farm management and sanitary conditions would need to be implemented if milk revenues are to be increased.

Key Words: Milk Price, Milk Revenue, Thailand