536 Thinking outside the box: Linkages with agencies and educational opportunities for undergraduates and graduate students. M. A. Ottinger*, *University of Maryland*, *College Park*.

The range of career paths and training requirements has become increasingly complex in the animal sciences. As a result, our students often spend most of their time in the classroom and some highly motivated students seek experience at veterinary clinics to meet the criteria for acceptance to professional school. Experiential learning and internships provide opportunities for broadening the experiences of our students outside the classroom. Internships in agriculture related organizations, which may be involved in research, policy, or many other potential activities provide wonderful opportunities for our students to deepen their understanding of the demands of various careers. At the University of Maryland, our students can work with numerous federal and state agencies, other universities, and private corporations. Working relationships with these entities may be on many levels, including MOUs, centers, adjunct faculty, or informal collaborations. Student internships may be for academic credit, as volunteer or paid positions. It is critical that these experiences have some type of structure to ensure high quality and commitment by student and the agency mentor. The types of positions and several methods for structuring this program will be discussed, including establishing MOUs and consideration of appropriate work demands and deliverables from the student. These partnerships with scientists and professionals in regional federal and state agencies can provide benefits for our students, including extending their technical capabilities and providing experience in a range of potential career choices. These experiences will encourage our young scientists to become enthusiastic contributors to agricultural sciences and energize them in interesting career paths in global agricultural programs. Furthermore, networking with our international collaborators will keep us on the cutting edge of international advances in agriculture and in affiliated disciplines.

Key Words: Experiential Learning Opportunities, MOUs with Agencies, Internships and Academic Credit for Student Interns

537 Animal sciences curricula: Future directions. T. Field*, *Colorado State University*, *Fort Collins*.

The fortunate reality of offering a futuristic perspective is that we are rarely held to account for our predictions. Nonetheless, our profession and our students will be faced with one certainty - change. Demand for food, fiber, and other products originating from livestock and poultry will increase on a global scale. Concurrently, consumers will demand higher value, more convenience, better food safety, environmental compatability, and evidence of excellent animal husbandry in our production practices. The opportunities for graduates of animal, dairy, and poultry science programs will continue to diversify as will the availability of enhanced tools and technologies that can be applied in the industry. Practioners of our craft in the future will have to successfully merge biological, financial, public policy, marketing, and human resources skills to be successful in the future. While technical training will continue to be an important focus of our teaching efforts, our students will not be well prepared for the challenges that will confront them unless they receive an education that is also broad in scope - particularly at the bachelors and masters levels. Curriculum design must also accomodate training that moves students beyond disciplines and into the realm of systems thinking and multi-disciplinary problem solving. Effective curricula will contain significant experiential learning opportunities, case-based course design, and international study. The challenge of the future will be to find the optimal balance of rigor, depth, breadth, and customization in the development of a course of study.

Key Words: Future, Curricula, Students

Growth and Development - Livestock and Poultry II

538 Ontogenic expression of microRNA in bovine mammary gland. A. V. Capuco*[1], L. L. Coutinho[2], C. M. Evock-Clover[1], A. Minuti[3], T. S. Sonstegard[1], Y. R. Boisclair[4], M. E. Van Amburgh[4], G. Bertoni[3], and L. K. L.K. Matukumalli[1], [1]*Bovine Functional Genomics Laboratory, USDA-ARS*, *Beltsville, MD*, [2]*University of Sao Paulo-ESALQ*, *Piracicaba, SP, Brazil*, [3]*Institute of Zootechnics, Catholic University*, *Piacenza, Italy*, [4]*Cornell University*, *Ithaca, NY*.

MicroRNAs (miR) are small RNA molecules (~22 nucleotides) that are important regulators of numerous biological processes, including organ and tissue morphogenesis and function. In this capacity, most miR inhibit protein synthesis by binding to the 3′-untranslated region of targeted mRNA species. Hundreds of genes can be regulated in this fashion. The objective of this experiment was to evaluate expression of miR in mammary tissue from Holstein cows at different developmental and functional stages. Tissues were obtained from: prepubertal heifers (6 mo) that were (1) intact, (2) ovariectomized, (3) intact + estrogen, (4) ovariectomized + estrogen; (5) from primiparous cows, 100-250 d of gestation; (6) from lactating cows, 14 d lactation; (7) from cows during the dry period, 40 d dry and 20 d prepartum. Total RNA was extracted from three or four animals at each stage and pooled to determine patterns of miR expression by hybridization to a microarray containing modified RNA targets complementary to all known mirR. Expression of miR such as miR-221 and miR-127 appeared to be differentially expressed prepubertally. Expression of miR-615 was enhanced by estrogen treatment and miR-29a by ovariectomy. During first gestation, expression of miR-20a was increased. During lactation, miR were typically expressed at low levels, but there was increased expression of a limited number of miR, including miR-326 and miR-350. During the dry period, there was increased expression of miR-542-5p and miR-690. We subjected individual RNA samples to quantitative RT-PCR and confirmed patterns of expression revealed by microarray in 4 of 5 genes tested. Our quantitative RT-PCR results confirmed the utility of evaluating miR expression by microarray and suggested that miR function as regulators of mammary gland development and function.

Key Words: Regulatory RNA, Gene Expression, Lactation

539 Growth hormone stimulates growth hormone receptor expression through STAT5-activation of growth hormone receptor 1A promoter in the bovine liver. H. Jiang*, Y. Wang, M. Wu, and R. Torres-Diaz, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The objective of this study was to determine whether and how growth hormone (GH) regulates hepatic expression of GH receptor (GHR) mRNA and protein in cattle. Ribonuclease protection assays revealed that injection of recombinant bovine GH in a slow-release formula increased both hepatic GHR and insulin-like growth factor I (IGF-I) mRNAs one week after initiation of treatment. The increases in GHR and IGF-I mRNAs were highly correlated. Western blot analysis showed that the injection also increased GHR protein level in the liver. In cattle and several other mammals, hepatic GHR mRNA is expressed as variants that differ in the 5′-untranslated region, due to use of different promoters in transcription and/or alternative splicing. We found that GH injection increased the expression of the liver-specific GHR mRNA variant 1A (GHR1A), without affecting GHR1B and GHR1C mRNAs, the other two major GHR mRNA variants in the bovine liver. Transient transfection analyses of a 2.7 kb GHR1A promoter in reconstituted GH-responsive cells showed that GH could robustly activate reporter gene expression from this promoter, suggesting that GH augmentation of GHR1A mRNA expression in the liver is at least partially mediated at the transcriptional level. Further transfection analyses of serially 5′-truncated fragments of this GHR1A promoter narrowed the GH-responsive sequence element down to a 210 bp region that contained a putative signal transducer and activator of transcription 5 (STAT5) binding site. Electrophoretic mobility shift assays demonstrated that this putative STAT5 binding site was able to bind to STAT5b protein. In transfection assays, deletion of this putative STAT5 binding site abolished most of the GH response of the GHR1A promoter. These observations together suggest that GH stimulates the expression of one GHR mRNA variant, GHR1A, through binding STAT5 to its promoter, thereby increasing GHR protein expression in the bovine liver.

Key Words: Cattle, Growth Hormone Receptor, Liver

540 Temporal longissimus muscle gene expression profiles due to plane of dietary energy in early-weaned Angus steers. D. E. Graugnard*, S. L. Rodriguez-Zas, D. B. Faulkner, L. L. Berger, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana*.

Energy-dense nutrients might trigger long-term genomic adaptations of economic importance in skeletal muscle of young steer calves. Objectives were to evaluate temporal gene expression profiles in longissimus muscle (LM) of early-weaned (~140 d age) Angus steers (n = 6/diet) fed a high-grain (HiE, NE = 1.43 Mcal/kg) or high-byproduct (HiF, NE = 1.19 Mcal/kg) diet for 120 d, at which point all steers were switched to a common feedlot diet until slaughter. LM biopsies for transcript profiling and blood for metabolite analyses were collected at 0, 60, and 120 d of feeding. BW, ADG, back fat (d 60 and 120), and marbling scores (d 60 and 120) also were measured. A 13,257 bovine oligonucleotide (70-mers) array was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human, mouse, and bovine UniGene databases, the human genome, and the cattle TIGR database. Cy3- and Cy5-labelled cDNA from LM and a reference standard were used for hybridizations. Feeding HiE vs. HiF resulted in greater (time × diet $P < 0.05$) temporal blood glucose concentrations (88 vs. 80 mg/dL on d 120), whereas HiF increased (time × treatment $P = 0.06$) blood β-hydroxybutyrate (BHBA) concentration (0.48 vs. 0.36 mmol/L on d 120) to a greater extent than HiE. ADG over the 120 d tended ($P = 0.08$) to be greater with HiE (3.6 vs. 3.4 kg/d). ANOVA (FDR $P = 0.10$) identified 504, 67, and 141 differentially expressed genes due to time, diet, and diet × time, respectively. Genes associated with aspects of metabolism (e.g. protein or fatty acid synthesis), development, and signal transduction activity predominated among those affected by time × treatment. Results suggest that high plane of dietary energy during the early growth phase might improve efficiency of gain at least in part through the provision of a specific pattern of nutrients (e.g. glucose vs. BHBA) to skeletal muscle, which can in turn directly or indirectly promote genome-wide alterations in gene expression affecting tissue growth and development.

Key Words: Genomics, Growth, Energy

541 Creation of a gene atlas in cattle using sequence-based transcriptional profiling. T. S. Sonstegard*[1], J. W. Keele[2], G. P. Harhay[2], T. P. L. Smith[2], L. K. Matukumalli[1,3], G. Liu[1], C. P. Van Tassell[1], and L. J. Alexander[4], [1]*USDA, ARS, Beltsville Agricultural Research Center*, *Beltsville, MD*, [2]*USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*, [3]*George Mason University*, *Fairfax, VA*, [4]*USDA, ARS, Livestock and Range Research Laboratory*, *Miles City, MT*.

Numerous opportunities to advance the understanding of how heritable variation affects economically important traits are being provided through resources generated from the Bovine Genome Sequencing project. Success in these investigations relies upon the depth in which the sequence assembly is annotated. In humans and biomedical model species, extensive annotation to identify genes and report relative levels of expression in various tissues has been accomplished by creation of Gene Atlas databases that provide researchers instant access to the expression profile of a gene under study. Similarly, we are constructing a Bovine Gene Atlas database that will house transcript profiles from 100 different bovine tissues collected from major organ systems. RNA was extracted using tissues derived from the genome sequencing cow and her offspring. Transcript profiles were captured using a digital, sequence-based approach known as Sequence-By-Synthesis from a Clonal Single Molecule Array. Yield of 20 bp cDNA sequence tags exceeded more than 5 million counts per sample. The more than 500 million tags were grouped according to tissue of origin, sequence similarity and genome map position in order to assign gene identities and account for potential sequencing errors. To test the correlation between the sequence tag data and a known pathway for synthesis of 3, 16 or 17-Glucuronide, tag counts for gene members of this pathway were compared between adult testes, two stages of uterus development, muscle, and placentome. Tag count analysis revealed this metabolic pathway is greater than 50 fold more active in ovary and uterus versus testes, placentome, and muscle. We conclude relative levels of expression for nearly all genes, even those for rare and species-specific transcripts, can be accurately determined. Such a framework of expression data will allow determination of regional transcriptional control, tissue phylogeny and interconnected gene networks. This Gene Atlas will be provided as a query-based resource to other researchers through a Web accessible database.

Key Words: Cattle, Gene Expression, Transcription

542 Effect of an enhanced-growth feeding program on gastrointestinal tract and spleen development. M. Terré*[1], M. Devant[1], A. Aris[1], and A. Bach[1,2], [1]*IRTA-Unitat de Remugants*, *Barcelona, Spain*, [2]*ICREA*, *Barcelona, Spain*.

Eighteen Holstein male calves (4.4 ± 1.85 d old) were arranged in 2 groups to study the effect of an enhanced-growth (EF) and conventional feeding program (CF) on gastrointestinal tract (GIT) and spleen development. Calves were fed a milk replacer (21% CP, 19.2% fat) at increasing rates during 4 d until reaching 4 l/d at 12.5% DM. Calves on CF received 4 l/d at 12.5% DM until weaning, and EF calves were fed 4 l/d at 15% DM from 5-11 d, 4 l/d at 18% DM from 12-18, 6 l/d at 18% DM from 19-38 d, and 3 l/d at 18% from 39-45 d. Calf starter was offered ad libitum until the end of the study (54 d). Individual calf starter consumption and BW were recorded. Half of the calves of each treatment were euthanized at 4 wk of study, and the rest at 54 d. Then, the spleen was dissected and weighed. Each anatomical part of the GIT was separated, weighed, emptied, weighed again, and pH of the contents of each GIT segment measured. Calves on EF grew faster ($P < 0.05$) than CF calves (0.82 vs 0.50 ± 0.089 kg/d, respectively). Starter intake was greater ($P < 0.05$) in CF than EF calves from 30 to 33 d, but lower ($P < 0.05$) from 48 to 54 d. Calves on CF had a greater ($P < 0.05$) rumen pH at 4-wk and 7-wk sacrifices (5.47 ± 0.056) and a lower abomasum pH ($P < 0.05$) at 4-wk sacrifice (3.01 ± 0.362) than EF calves (5.26 ± 0.056 and 5.04 ± 0.362, respectively). The spleen weight of EF calves was greater ($P < 0.05$) than that of CF calves (0.32 vs 0.24 ± 0.022 kg, respectively), but when expressed as a percentage of BW there were no differences between treatments. Abomasum weight expressed as a percentage of total GIT weight was greater ($P < 0.05$) in CF than in EF calves (11.0 vs 8.8 ± 0.54, respectively), but jejunum-ileum weight expressed as a percentage of GIT was greater ($P < 0.01$) in EF than in CF calves (50.4 vs 46.7 ± 0.98, respectively). Although EF calves grew faster, abomasum weight decreased and jejunum-ileum weight increased as a percentage of GIT when raising calves on an enhanced-growth feeding program.

Key Words: Calves, Enhanced-Growth, Gastrointestinal Tract

Animal Behavior & Well-Being - Livestock and Poultry: New Methodologies Symposium

543 Utilizing neural network analysis in animal behavior studies. W. B. Roush*, *USDA-ARS Poultry Research Unit*, *Mississippi State, MS*.

The objective of this presentation is to introduce the concept of artificial neural networks (ANN) and the related technologies of fuzzy logic (FL) and genetic algorithms (GA) to the analysis of animal behavioral responses. These technologies have been developed in the areas of Artificial Intelligence and Artificial Life for the study of Complex Systems. ANN were inspired by the biological neuron with inputs, a processing unit, and output(s). The concept for ANN is very similar to the concept of regression analysis. A fundamental difference is that regression analysis is philosophically linear; whereas, ANN are nonlinear. Most biological responses are nonlinear in nature and therefore a nonlinear analytical technique like ANN can more accurately and precisely be used to analyze the data. An example is the analysis of the effect of stressors (e.g., debeaking, coccidiosis, electrical shock, ammonia, heat stress, and noise) on the live gain response of birds. FL and GA are related computer techniques that can be used for analysis and optimization. FL can represent imprecise concepts such as hot, cold, heavy, light, comfort, and stress. The technique has been applied to the problem of defining stress of caged laying hens based on a FL representation of mortality, corticosterone level and egg production. Fuzzy Cognitive Maps (FCM), based on the principles of FL, can be used to define social conditions as defined by interactive matrices. An example is the structuring of a virtual world involving the interaction between sharks, fish and dolphins. GA optimize by evolving the inputs of a formula (e.g. ANN) into an optimal solution. Artificial intelligence and Artificial Life techniques such as ANN, FL and GA promise to provide powerful tools for the analysis of animal behavior studies.

Key Words: Behavior, Artificial Neural Network, Fuzzy Logic

544 Identification of QTL affecting disposition in *Bos indicus* influenced cattle. C. A. Gill*, C. R. Boldt, C. A. Abbey, M. A. Wegenhoft, D. K. Lunt, J. E. Sawyer, A. D. Herring, and J. O. Sanders, *Texas A&M University*, *College Station*.

Disposition was measured in 2 resource populations: 614 progeny from 40 *Bos indicus* (Brahman or Nellore) x Angus reciprocal backcross families and 3 F_2 families (Angleton herd); and, 465 progeny from 17 Nellore x Angus F_2 families and paternal half-sib families produced by natural service (McGregor herd). In the Angleton study, disposition scores were taken twice (weaning and slaughter) using a 1 to 5 scale. In the McGregor study, overall disposition and 4 component traits of behavior (aggressiveness, nervousness, flightiness, and gregarious) were measured 1 mo after weaning by a panel of 4 evaluators using a 1 to 9 scale. Steer progeny were scored again about 1 wk prior to slaughter by a single evaluator and overall disposition was scored prior to slaughter. The MIXED procedure of SAS was used to analyze disposition with fixed factors of sire, family nested within sire, birth year-season combination and sex x family within sire interaction, plus sequence within pen within birth year-season combination for the McGregor study. Mendelian and partially imprinted QTL for overall disposition were detected following interval mapping by linear regression under a line-cross model using residuals from the Angleton study. Three QTL on BTA 5, 17 and 25 affecting disposition at weaning and 2 QTL on BTA 1 and 18 affecting disposition prior to slaughter were estimated to have additive effects. Three QTL on BTA 4, 9 and 25 affecting disposition prior to slaughter were estimated to have dominance effects. A QTL affecting disposition at weaning on BTA13 was estimated to be partially maternally imprinted, while a QTL on BTA8 affecting disposition prior to slaughter was estimated to be partially paternally imprinted, and a QTL on BTA16 was estimated to be partially maternally imprinted. Only the QTL on BTA25 appeared to affect both weaning and final disposition. We have begun to characterize candidate genes for these QTL. We expect to validate these QTL in the McGregor study and to identify QTL for the 4 component traits of behavior.

Key Words: Disposition, Bovine, QTL