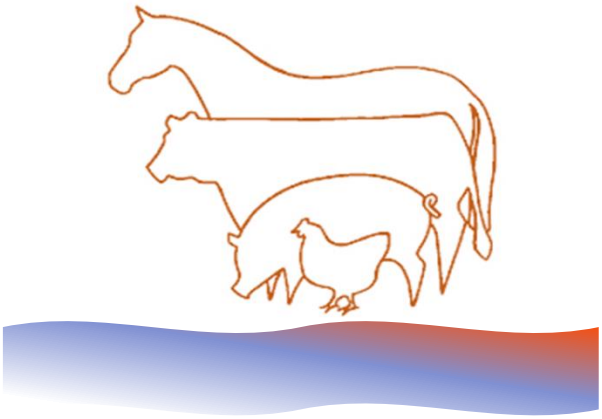
PROCEEDINGS OF THE SECOND UF-FAMU ANIMAL SCIENCES SYMPOSIUM

St. Augustine Hotel and Suites
St. Augustine, Florida

October 21 & 22, 2016



UF/IFAS-FAMU
Animal Sciences Symposium

WELCOME

Welcome to the second UF-FAMU Animal Sciences symposium. This symposium was organized to build camaraderie, to share science and to foster collaboration in our research efforts. The program contains a mixture of student presentations of proposed, ongoing and completed research. The presentations will be given by UF graduate students and FAMU students who interned at UF last summer. Friday evening will include a group photo session, a wine and cheese and poster session, and a keynote presentation by our distinguished speaker, Dr. Dwain Johnson, an Emeritus Professor of the UF Animal Sciences Department. On Saturday, we will have the opportunity to listen to more stimulating research presentations. Please take this time to learn about other research activities in our departments and to relax and enjoy the company of friends and colleagues.

Raluca Mateescu, on behalf of the Symposium Committee

ACKNOWLEDGMENTS

The faculty and students of UF and FAMU thank the following for their support of the Second Animal Sciences Symposium

Dr. Jacqueline K. Burns, Dean for Research and Director of the Florida Agricultural Experiment Station, IFAS, University of Florida

Dr. Robert Taylor, Dean and Director, College of Agriculture and Food Sciences, Florida A&M University

Dr. Geoff Dahl, Chair, Department of Animal Sciences, IFAS, UF

Dr. Peter Hansen, Distinguished Professor, Department of Animal Sciences, IFAS, UF

L.E. "Red" Larson Endowment

Animal Sciences Symposium Committee

Raluca Mateescu, Chair

Sally Williams

Albert De Vries

Nicolas DiLorenzo

Christopher Mortensen

Corwin Nelson

Renee Parks-James

Special thanks to Sally Williams and Renee Parks for the meals and beverages

2016 ANIMAL SCIENCES KEYNOTE SPEAKER

Dr. Dwain Johnson is a native of Abilene, Texas where his family is involved in a cattle, wheat and hay farming operation. He obtained a B.S. at Texas A&M University in Animal Science and a M. S. degree from Oklahoma State University in Food Science. He returned to Texas A&M University for a Ph.D. in Meat Science and Muscle Biology. In 1984, he joined the faculty of the Department of Animal Science at the University of Florida as an Assistant Professor. Currently he is Professor Emeritus of the Animal Sciences Department and serving on the Board of Directors of the Florida Beef Council.

The research program he and his students were involved in focused on ante mortem and postmortem factors influencing animal composition and meat palatability and he has produced more than 250 publications with more than 90 being in refereed scientific journals. In 2002, Dwain and his collaborators conducted a series of research projects aimed at identifying undervalued portions of the beef carcass. In the largest study of its kind, he evaluated more than 5,600 muscles for flavor and tenderness. The crown jewel of his research findings has received national notoriety and is named the "Flat-Iron" steak. Today, the Flat-Iron steak is the nation's fifth best-selling beef item. Recent figures show Flat-Iron steak sales now top 90 million pounds per year, compared to only half that number in 2006. In fact, the Flat-Iron steak outsells T-bone and porterhouse steaks combined in U.S. food service establishments. As a result of his outstanding contributions to the beef industry, Dwain received the Florida Cattlemen's Association "Researcher of the Year" award in 2003. In 2004, he and his co-workers received the International Meat Secretariat Prize for Meat Science and Technology in Winnipeg, Canada, for their significant contributions to the field of meat science. This marked the first time U.S. researchers had received this recognition since the inception of the award in 2000. More recently, he was selected as the 2009 Advanced Degree Alumnus of Distinction at Oklahoma State University and was the 2016 AMSA distinguished research award winner.

SECOND ANIMAL SCIENCES SYMPOSIUM
St. Augustine Hotel and Suites, St. Augustine, Florida

October 21 and 22, 2016

Program

FRIDAY, OCTOBER 21, 2016

12:30 **Welcome.** Dr. Raluca Mateescu, Graduate Coordinator, Department of Animal Sciences, UF/IFAS

12:40 **Collaborative opportunities.** Dr. John Davis, Associate Dean for Research and Associate Director of the Florida Agricultural Experiment Station, UF/IFAS

12:55 **Program.** Dr. Sally Williams, Department of Animal Sciences, UF/IFAS

1:00 **Session 1.** Chair: Lesley Blakely

1:00 Abstract #1: Anastasia Meredith, FAMU intern (Nelson)
1:08 Abstract #2: Therus Brown, FAMU intern (Laporta)
1:15 Abstract #3: Anil Sigdel (Peñagaricano)
1:30 Abstract #4: Bianca Libanori Artiaga (Driver)
1:45 Abstract #5: Tayler L Hansen (Warren)
2:00 Abstract #6: Carlos Martinez (Elzo)
2:15 Abstract #7: Darren D Henry (DiLorenzo)

2:30 **Break**

2:45 **Session 2.** Chair: Carlos Martinez

2:45 Abstract #8: Joel Leal (Mateescu)
3:00 Abstract #9: Kelsey C Horvath (Miller-Cushon)
3:15 Abstract #10: Laura Patterson Rosa (Brooks)
3:30 Abstract #11: Fernanda C Ferreira (De Vries)
3:45 Abstract #12: Lin Teng (Jeong)
4:00 Abstract #13: Marcos Zenobi (Staples)

4:15 **Break**

4:30 **Session 3.** Chair: Rachel Piersanti

4:30 Abstract #14: Katelyn Palermo (Brooks)
4:45 Abstract #15: Mesfin M Gobena (Mateescu)
5:00 Abstract #16: Pornpamol Pattamanont (De Vries)
5:15 Abstract #17: Achilles Vieira-Neto (Santos)

5:30 **Keynote: Collaboration.** Dr. Dwain Johnson, Professor Emeritus, Department of Animal Sciences, UF/IFAS

6:00 **Group picture**

6:15 **Session 4 (Posters) and Reception**

1. Abstract #18: Natalie Cleghorn (Nelson)
2. Abstract #19: Alexandra Swets (Wohlgemuth)
3. Abstract #20: Victoria Roe (Mateescu)
4. Abstract #21: Victoria Robbins (Warren)
5. Abstract #22: Shelby Wright (T. Scheffler)
6. Abstract #23: Pedro LP Fontes (Lamb)
7. Abstract #24: Ana Maria Mesa (Mortensen)
8. Abstract #25: Bahroz Muhammed Ahmed (Dahl)
9. Abstract #26: Leigh Ann Skurupey (Warren)
10. Abstract #27: Shinyoung Lee (Jeong)
11. Abstract #28: Jillian M Bobel (Warren)

7:15 **Dinner**

Late **BYOB party**

SATURDAY, OCTOBER 22, 2016

7:00 **Breakfast** (hotel)

7:55 **Program.** Dr. Corwin Nelson, Department of Animal Sciences, UF/IFAS

8:00 **Session 5.** Chair: Fernanda Ferreira

8:00 Abstract #29: Yi Han (Peñagaricano)
8:15 Abstract #30: Tessa M Schulmeister (DiLorenzo)
8:30 Abstract #31: Thiago F Fabris (Dahl)
8:45 Abstract #32: Rachel L Piersanti (Bromfield)
9:00 Abstract #33: Zhengxin Ma (Jeong)
9:15 Abstract #34: Juliana Ranches (Arthington)
9:30 Abstract #35: Leslie Blakely (Nelson)
9:45 Abstract #36: Yun Jiang (Adesogan)

10:00 **Session 6 (Posters) and Break**

1. Abstract #37: Charlotte Mason (T. Scheffler)
2. Abstract #38: Chengcheng Li (Wohlgemuth)
3. Abstract #39: Danielle Arnold (Mortensen)
4. Abstract #40: Francine Messias Ciriaco (DiLorenzo)
5. Abstract #41: Heather Hamblen (Mateescu)
6. Abstract #42: Mariana Garcia-Ascolani (DiLorenzo)
7. Abstract #43: Nicola Oosthuizen (Lamb)
8. Abstract #44: Zaira M Estrada Reyes (Mateescu)
9. Abstract #45: Carolina Collazos (Laporta)
10. Abstract #46: Mercedes F Kweh (Nelson)

11:00 **Session 7.** Chair: Achilles Vieira-Neto

11:00 Abstract #47: Samantha L Lewis (Brooks)
11:15 Abstract #48: Andres AP Cervantes (Adesogan)
11:30 Abstract #49: Junyi Tao (Hackmann)
11:45 Abstract #50: Ashenafi Beyi (De Vries)
12:00 Abstract #51: Carla D Sanford (Lamb)
12:15 Abstract #52: Clarissa Harris (Williams)

12:30 **Closing remarks.** Dr. Corwin Nelson, Department of Animal Sciences, UF/IFAS

Effects of dietary 25-hydroxyvitamin D_3 on leukocyte responses to lipopolysaccharide

Anastasia Meredith[1], Michael Poindexter[2], Mercedes Kweh[2], Natalie Cleghorn[2] and Corwin Nelson*[2]

[1]College of Food and Agricultural Sciences, Florida A&M University, Tallahassee
[2]Department of Animal Sciences, University of Florida, Gainesville

Bovine monocytes and neutrophils convert the 25-hydroxyvitamin D_3 metabolite to the active hormone, 1,25-dihydroxyvitamin D_3 in response to pathogen-associated molecules such as lipopolysaccharide (LPS). The objective of this experiment was to determine the effects of dietary 25-hydroxyvitamin D_3 on whole-blood responses to *ex vivo* LPS stimulation. This experiment was performed as part of a research trial that investigated the effects of dietary 25-hydroxyvitamin D_3 versus vitamin D_3 on vitamin D metabolism, mammary immunity, and resistance to mastitis of dairy cows. Sixty mid-lactation Holstein cows were individually fed a total mixed ration with a daily top-dress supplement that contained 1 or 3 mg of vitamin D_3 or 1 or 3 mg of 25-hydroxyvitamin D_3. Peripheral blood was collected into heparin tubes on 0 and 14 d of the trial. An aliquot of blood (0.5 mL) was mixed with an equal volume of RPMI 1640 cell culture media along with 0 or 100 ng/mL of LPS and cultured for 6 h at 37°C. Leukocyte RNA was extracted and cDNA generated for qPCR analysis of the vitamin D 1α-hydroxylase gene (*CYP27B1,* converts 25-hydroxyvitamin D to 1,25-dihydroxyvitamin D) and the inducible nitric oxide synthase gene (*iNOS*). LPS stimulation increased *CYP27B1* and *iNOS* expression ($P < 0.001$), but dietary treatment did not have an effect on *CYP27B1* and *iNOS* expression ($P > 0.1$) at 14 d. In conclusion, dietary 25-hydroxyvitamin D_3 treatment did not have an effect on the acute response of whole-blood leukocytes to LPS stimulation as measured by *CYP27B1* and *iNOS* gene expression.

Abstract #2

Effect of timing of heat stress during the dry period on milk yield and composition

T. Brown, T. F. Fabris, B. M. Dado, A. L. Skibiel, F. N. Corra, G. E. Dahl, and J. Laporta*

Department of Animal Sciences, University of Florida, Gainesville, FL, USA

Heat stress during the dry period (**DP**) impairs milk yield in the subsequent lactation. Objectives were to examine whether maternal exposure to heat stress during *early* or *late* DP *vs*. the entire DP affects milk yield and components during the subsequent lactation. Holstein cows were enrolled into four groups: heat stressed (**HT**, access to shade, *n*=13) or cooled (**CL**, access to shade, fans and soakers, *n*=13) during the entire DP; CL during the first 3 weeks of DP then switched to HT until calving (**CxH**, *n*=8) or HT during the first 3 weeks of DP then switched to CL until calving (**HxC**, *n*=8). After calving, all cows were managed similarly. Milk samples were collected at calving (d 0, colostrum), d1, d2, d7, and d14 (relative to calving) and analyzed for fat, protein, lactose, and solids non-fat (**SNF**) by spectrometry (Bentley 2000). Colostrum and milk volume were also recorded. Data was analyzed by ANOVA with d as repeated measures (SAS). Colostrum and milk yield were affected by DP treatment. Heat stress cows produced 6.5 kg less colostrum at d0 compared to CL cows (9.6 *vs* 16.2±4 kg, *P*=0.02), but colostrum yield for HxC and CxH cows (average 13±2 kg) was not different from HT or CL cows. Heat stress cows produced 5.6 kg less milk from d1 to d14 compared to CL, HxC, and CxH cows (27 ± 1.9 kg, average of three groups; *P*<0.06). There was no effect of treatment on protein, lactose and SNF. In all treatments, milk protein % and SNF were higher in colostrum and decreased gradually overtime (12.5-3.2±0.3% protein and 16.9-8.6±0.5 SNF for d0 to d14, respectively; *P*<0.001). Milk lactose % was lower in colostrum and gradually increased over time (3.1-4.6±0.06% d0 to d14; *P*<0.001). Milk fat % increased from d0 to d2 (3.7-5.3±0.3%) and remained stable thereafter for CL and HT cows, however, HxC and CxH cows had higher milk fat%, particularly on d7 (6.3±0.5%) compared to HT and CL cows. Preliminary data indicates that switching the HT and CL management between the early and late DP might benefit cow's subsequent milk production.

Abstract #3

Genome-wide association study for health traits in US Holstein cattle

A. Sigdel[1], C. Kuen Mak[2], R. Abdollahi-Arpanahi[3], K. Galvão[1], and F. Peñagarican*[1]

[1]University of Florida, [2]National Taiwan University, [3]University of Tehran

Health traits are of economic importance in dairy cattle. However, genetic improvement of health traits has not received enough consideration in dairy cattle breeding. The objective of this study was to perform a genome-wide association study (GWAS) for Clinical Mastitis (CM), Metritis (MET) and Ketosis (KET) in Holstein cattle. The analysis included health data records of 14,047 cows, and single nucleotide polymorphisms (SNPs) data on 6059 cows and 1204 sires. Single-step genomic-BLUP methodology was utilized to perform GWAS using a threshold model. The model included year-season and parity as fixed effects and animal and permanent environmental as random effects. The association analyses identified several regions in the bovine genome strongly associated with these three relevant post-partum diseases. For instance, genomic regions on BTA1, BTA6, and BTA28 were strongly associated with CM. These regions harbor many genes, including *ALOX5*, *CXCL13*, *GC*, *NPFFR2*, and *SEPT11*, that are directly involved in the inflammation process. Furthermore, strong association signals for MET were found on BTA14 and BTA15. These regions harbor genes such as *KLF10, GSDMC*, and *RRM2B*, which are involved in cellular stress and inflammation. For KET, this study identified regions on *BTA6*, *BTA8*, *BTA14* and *BTA16* that explained a large proportion of the genetic variance (between 0.70 and 1.23 %). Interestingly, the region on BTA14 contains the genes *TSTA3* and *PYCRL* that are related to the fructose-mannose metabolism. Overall, this study contributes to the identification of genetic variants underlying health traits thereby providing an opportunity for selection and permanent improvement of these relevant phenotypes.

Abstract #4

Therapeutic activation of NKT cells in pigs infected with influenza improves disease outcome and reduces virus shedding

B. L. Artiaga[1#], G. Yang[1#], T. E. Hutchinson[2], J. C. Loeb[3], J. A. Richt[4], J. A. Lednicky[3], S. Salek-Ardakani[2] and J. P. Driver[1]*

[1]Dept. of Animal Sciences, University of Florida, Gainesville, FL; [2]Dept. of Pathology, Immunology, and Laboratory Medicine, University of Florida, Gainesville, FL; [3]Dept. of Environmental and Global Health, University of Florida, Gainesville, FL; [4]College of Veterinary Medicine, Kansas State University, Manhattan, KS.

Swine influenza A viruses (IAV) are a major cause of acute respiratory disease that often leads to secondary bacterial infections and results in substantial costs for the pig industry. Currently, there are no available anti-viral therapies for infected pigs, which is greatly needed for limiting IAV transmission and production losses. Invariant natural killer T (NKT) cells are a lymphocyte population capable of potently stimulating innate and adaptive immune responses against numerous infectious diseases. Here we tested the anti-influenza efficacy of the NKT cell superagonist, α-galactosylceramide (αGC), which stimulates a wide array of anti-viral immune responses. Piglets (n=3) were challenged with A/California/04/2009 (CA04) H1N1 IAV and immediately administered αGC (100μg/kg) intranasally (IN αGC/CA04) or intramuscularly (IM αGC/CA04). Another group of virus-infected pigs were administered media via the intranasal route (Mock/CA04). Two additional piglets were mock infected and treated (Mock/Mock). We show that intranasal but not systemic administration of αGC dramatically ameliorated disease symptoms and resulted in the restoration of weight gain to the level of uninfected pigs. Correspondingly, viral titers in the upper-and lower-respiratory tract were reduced only in piglets that had received intranasal αGC. Lung pathology induced by virus persistence was largely prevented when NKT-cells were targeted via the respiratory route. These results suggest activation of NKT cells within the airway has potential to inhibit the replication of IAVs in swine and limit the impact for swine producers.

[#]These authors contributed equally to this study.

Maturity of bermudagrass hay affects digestibility by horses

T. L. Hansen, E. C. Chizek, O. K. Zugay, and L. K. Warren*

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Bermudagrass (*Cynodon dactylon*) hay is one of the most common preserved forages fed in the southeast United States. Bermudagrass, a C4 plant, has greater fiber concentrations than C3 plants. This study evaluated equine digestibility of Coastal bermudagrass hays differing in maturity. We hypothesized DM digestibility (DMD) would be reduced in bermudagrass diets compared to C3 legume and grass hays. Five dietary treatments (alfalfa hay, ALF; orchardgrass hay, ORCH; early maturity bermudagrass hay 4 wk regrowth, EARLY-BG; mid-maturity bermudagrass hay 5-6 wk regrowth, MID-BG; late maturity bermudagrass hay 8 wk regrowth, LATE-BG) were evaluated in a 5x5 Latin square design experiment with mature geldings (n = 5, BW = 552 ± 14 kg, mean ± SEM). Hay was fed at 1.62 ± 0.02% BW (DM basis). A 7-d dietary adaptation was imposed followed by a 3-d total fecal collection. A 2% subsample of daily fecal excretion was saved for DM, NDF, and ADF analyses. Data were analyzed as Latin square design using a generalized linear model and means separated by Sheffe's method (SAS, v. 9.3). Diets differed in DMD (Table, $P < 0.001$). Dry matter digestibility was greatest for ALF and least for MID-BG and LATE-BG diets ($P < 0.05$). Fiber digestibility differed by diet ($P < 0.001$) with NDFD and ADFD greater ($P < 0.05$) for ALF, ORCH, and EARLY-BG compared to MID-BG and LATE-BG diets. Despite similar fiber concentrations among the bermudagrass hays, digestibility of EARLY-BG was comparable to C3 forages. These results indicate fiber composition in bermudagrass changes with maturity, reducing forage digestibility.

Table. Hay digestibility by horses (n = 5).

	ALF	ORCH	EARLY-BG	MID-BG	LATE-BG	SEM	*P* <
DMD, %	62.1[a]	51.2[b]	47.2[b]	36.0[c]	36.8[c]	2.1	0.001
NDFD, %	43.1[a]	42.4[a]	46.2[a]	31.1[b]	31.8[b]	1.7	0.001
ADFD, %	40.2[a]	39.8[a]	39.8[a]	23.9[b]	24.3[b]	1.9	0.001

[abc]$P < 0.05$

Abstract #6

New statistical methods to account for correlated marker effects in genome-wide prediction through Gaussian concentration graph models: Bayesian and Frequentist formulations

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In genome-wide prediction, it is typically assumed that marker allele substitution effects are independent; however, in quantitative and statistical genetics it is well known that nature points to correlated effects. Graphical models are a useful and flexible tool for covariance estimation in high dimensional settings, which is a problem of contemporary interest in statistics. In particular, under Gaussian concentration graph models (GCGM), a set of random variables is assumed to be Markov with respect to an undirected graph G. In this study, the theory of GCGM was adapted to genome-wide prediction resulting in the development of new Bayesian (Bayes G and Bayes G-D) and frequentist (GML-BLUP) methods to predict breeding values. Several approaches to build the graph G using domain-specific knowledge were proposed. Furthermore, two propositions and a corollary establishing conditions for the induced graph to be decomposable were proven. These methods were implemented in small simulated datasets involving scenarios where partial correlations among allele substitution effects were expected to arise from different causes. Some improvements in correlations between phenotypes and predicted breeding values and accuracies of predicted breeding values were observed. An extension to accommodate multiallelic loci was described along with some possible refinements involving the incorporation of more flexible priors in the Bayesian approach. Models proposed here permit accounting for partially correlated marker effects and incorporating biological information in the prediction process through its use when constructing graph G. Furthermore, these models are more flexible and general than other models accounting for correlated marker effects that have been proposed previously because they have the ability to consider partial correlation structures arising from factors different from spatial correlation.

Effects of bismuth subsalicylate and calcium-ammonium nitrate on in vitro fermentation of bahiagrass hay with supplemental molasses

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A randomized complete block design was used to determine the effects of increasing amounts of bismuth subsalicylate (**BSS**) and calcium-ammonium nitrate (**CAN**) on in vitro fermentation of bahiagrass hay (*Paspalum notatum*). Serum bottles (125-mL) containing 100 mL of a 4:1 buffer:ruminal fluid inoculum and 0.7 g of an 80:20 bahiagrass hay:molasses substrate (DM basis) were incubated for 48 h. Three d (block) of incubation were performed. Treatments were arranged as a 4 × 3 factorial with 4 concentrations of BSS (0.00, 0.33, 0.66 and 1.00% of diet DM) and 3 concentrations of CAN (0.0, 1.2 and 2.4% of diet DM). Treatments were made isonitrogenous with urea. In vitro OM digestibility (**IVOMD**) was determined in a separate set of tubes. Gas production and IVOMD were linearly decreased ($P \leq 0.001$) as CAN and BSS increased. Ammonia-N was linearly decreased ($P = 0.001$) as CAN increased. Methane production (mmol/g substrate fermented) was linearly reduced ($P < 0.001$) as CAN and BSS increased. Both CAN ($P = 0.012$) and BSS ($P < 0.001$) reduced H_2S production, with 0.33% BSS reducing production by 61% compared with 0.00%. There was no effect ($P > 0.05$) of CAN on concentrations or molar proportions of any VFA analyzed. As BSS increased, concentration of acetate ($P = 0.002$), propionate ($P = 0.007$), and total VFA ($P = 0.003$) decreased linearly. Including BSS at 0.66% and 1.00% of the diet DM had negative effects on in vitro fermentation of bahiagrass hay. However, when BSS was included at 0.33%, A:P was decreased and total VFA concentrations were unaffected. Nitrate inclusion reduces methane production without negatively affecting fermentation. A combination of BSS and CAN may favorably affect ruminal fermentation while decreasing methane emissions.

Association of SNPs and haplotypes in µ-calpain and calpastatin genes with Warner-Braztler Shear Force in a crossbred Brahman-Angus population

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Tenderness results from proteolysis of key structural muscle sarcomere proteins, and is modulated by the calpain-calpastatin system. A total of 581 crossbreed Angus-Brahman steers with average slaughter weight of 537.94±55.31 kg at 17.31±1.23 months were used in this study. One steak of 2.54 cm of *Longissimus dorsi* aged for 14 days was used for Warner-Bratzler Shear Force (WBSF). Genotypes for 37 SNPs in µ-calpain and calpastatin genes from 250K Bovine SNP BeadChip were used. An association test was performed with each polymorphic SNP and haplotypes based on linkage disequilibrium (LD) analysis. One LD block was predicted in µ-calpain; for calpastatin three LD blocks were predicted. The third block is located in the seven final exons of calpastatin, including the 3'UTR. Only one individual SNP in calpastatin, ARSUSMARC116 was associated with WBSF. Similarly, the LD block 3, harboring ARSUSMARC116, was significantly associated with WBSF. The CG-CG diplotype (4.82±0.16 kg) was different from TA-CG (4.40±0.08 kg), and both of them were different from TA-TA (4.21±0.05 kg) and TG-CG (3.85±0.23 kg). A bioinformatic analysis of all reported SNPs in the associated block was performed. JAVA was used in the screening, substitutions, transcription and translation of sequences. From 6,787 SNPs located in calpastatin, only 786 SNPs located in the third block were included in this analysis. The wild DNA sequence was analyzed with MATCHTM in order to predict Transcription Binding Sites (TBS). The motives of those TBS were analyzed in each DNA sequence with JAVA and compared with the wild type prediction. Each mRNA sequence was analyzed with RNAFold for prediction of ΔG and folding. A protein analysis was performed with Swiss Model server and Compute PI/MW tool. Twelve SNPs were found to modify TBS and 8 SNPs were found to change the ΔG value and mRNA folding. At protein level, 13 SNPs were able to change the value of isoelectric point, 4 SNPs can modify structure, surface and electrostatic field of this protein.

Abstract #9

The effect of feeding enrichment during the milk-feeding stage on cognition in dairy calves

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The objective of this study was to evaluate the effects of simple nutritional enrichments on cognitive development in dairy calves. Individually-housed Holstein heifer calves were assigned to conventional management (C; n=10), with access to milk (6 L/d) via bucket and grain concentrate, or enriched feeding (E; n=10), with access to milk via teat, chopped hay, and concentrate. At week 5, calves were tested in a T-maze with a reward (0.2 L milk) to assess initial spatial learning, reversal learning where the reward location was changed, and response to novelty (a ball was placed in the maze). Calves received five sessions/d for 5 days or until criteria (moving directly to correct side in 3 consecutive sessions) was reached. Time to complete test, movement in maze, and kicks were recorded from video. Behavioral data were analyzed separately by stage in a general linear mixed model with session as a repeated measure. Sessions required to meet criteria were analyzed using the Wilcoxon signed rank test. The number of sessions required to meet criteria was similar between calves in initial learning (P=0.12) and reversal learning (*P*=0.20). However, in initial learning E calves took longer to complete the task in early sessions (treatment by session interaction; P=0.02), due to increased time spent on the correct side of maze before obtaining the reward (26.72 vs. 7.48 s; SE=3.4; *P*=0.005). In reversal learning, E calves completed the task faster (19.84 vs 27.22 s; SE=2.10; *P*=0.03), and C calves spent 1.5x longer on the incorrect side of the maze than E calves (*P*=0.04). The C calves kicked more frequently in both learning tasks (P < 0.04). In the novel object session, E calves found the reward faster (6.11 vs 20.6 s; SE=4.06; *P*=0.01), whereas C calves spent longer in the middle where the novel object was located (2.08 vs 13.4s; SE=5.33; *P*=0.04). These results suggest that providing simple feeding enrichments during the milk feeding stage may alter calf cognition and influence responses to environmental changes.

Abstract #10

Chronic Idiopathic Anhidrosis in the American Quarter Horse

Laura Patterson Rosa[1], Samantha A. Brooks*[1]

[1]Department of Animal Sciences, University of Florida, Gainesville, FL, USA

Chronic Idiopathic Anhidrosis (CIA) in horses is a condition characterized by a persistent reduction or complete lack of sweat. In order to dissipate excess body heat, the horse relies predominantly on evaporation of sweat from the skin surface. Horses in hot, tropical climates are typically at higher risks of developing CIA, yet this condition is now reported in non-tropical regions, especially temperate climates with the sudden onset of hot and humid summers. CIA affects 25% of racehorses training in Florida and perhaps thousands of Quarter Horses worldwide. Clinical signs include hyperthermia, tachypnea, reduced appetite, decreased water intake, alopecia and depression. CIA cases necessitate intensive medical management and restricted physical activity, and many affected horses never regain the ability to sweat and require retirement from breeding or competition. With no known cure or effective medical treatment, anhidrotic horses can suffer severe consequences, including multiple organ failure in response to hyperthermia and death. A recent epidemiological study conducted in Florida revealed that diagnosis of CIA was associated with breed, use, birth place, and most importantly, family history. Horses with a family history of CIA are 21.67 times more likely to develop the condition, supporting the hypothesis that genetics is contributing to development of CIA. Our research investigates CIA as a current source of suffering in the horse and a growing threat to the industry as global warming raises ambient temperatures. To identify genetics loci contributing to CIA we will pursue a Genome Wide Association (GWA) study and sample collection of 192 cases/controls is currently undergoing with support from the AQHA Foundation. We will also utilize a candidate gene approach utilizing one whole genome sequence of a severe CIA case. Although CIA is clearly a multifactorial condition and likely results from the action of several genes, our genomic approaches will provide information on genetic factors underlying this condition and the first clues as to the etiology of this frustrating disease.

Abstract #11

Measuring seasonality in conception rate in dairy herds using trigonometric functions

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Quantification of seasonal variation in herd performance contributes to management planning and decision making. Trigonometric functions are often used in models to describe seasonality. Our objective was to explore trigonometric models to describe and measure seasonality of conception rate (pregnancies/insemination, **CR**) in Florida dairy herds. Data consisted of lactation records from USDA of 47 Florida herds enrolled in the DHI program in 2010 with at least 50 cows. The CR was fit by 3 trigonometric models consisting of an increasing complex combination of sine (sin) and cosine (cos) functions of day of the year with different frequencies (harmonics), cow days in milk (**DIM**) and DIM^2. The individual cow was considered a random effect. Model fitting and model selection was done with the SAS proc glimmix. The models converged for 43 (91%) farms. The average R^2 for the three models were 0.57, 0.63 and 0.70, respectively. Due to the small difference in the sum of residuals and fewer parameters, model 2 was chosen. Seasonality was calculated per farm as the difference (amplitude) and the ratio between the maximum and minimum (min/max rate) values of CR as predicted by the model. Pearson and Spearman correlations for amplitude and mix/max ratios were -0.69 and -0.70, respectively. Farms were classified according to their amount of seasonality (Table 1). The average CR predicted by model 2 was 0.35. The average of the highest CR was 0.54 and 33% of the values were observed in March. The average of the lowest CR was 0.15 and 35% of the values were observed in August. Average CR increased with greater seasonality. The trigonometric functions appear useful to describe the seasonality in CR, but harmonic terms have to be added in order to capture the trends on different farms.

Table 1. Number and percentage of farms in each category of seasonality according to the amplitude and min/max ratio of CR, average highest and lowest CR and average CR for Florida farms in 2010

	Amplitude				Min/max ratio			
Seasonality	#farms	Average highest and lowest CR		Average CR	#farms	Average highest and lowest CR		Average CR
<0.2	1 (2%)	0.50	0.32	0.33	18 (41%)	0.56	0.06	0.31
0.2 – 0.29	10 (23%)	0.43	0.17	0.31	6 (14%)	0.48	0.13	0.30
0.3 – 0.39	12 (28%)	0.50	0.16	0.31	10 (23%)	0.51	0.17	0.35
0.4 – 0.59	17 (40%)	0.59	0.11	0.35	9 (21%)	0.50	0.23	0.39
>0.6	3 (7%)	0.80	0.36	0.36	0	-	-	-

Abstract #12

Comparative genomics of *Escherichia coli* O157:H7 from super-shedder and low-shedder cattle

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Shiga toxin-producing *Escherichia coli* (STEC) O157:H7 is a foodborne pathogen causing illness and threatens public health globally. STEC O157:H7 predominantly colonizes the terminal recto-anal junction of cattle, which are the major asymptomatic reservoir of this pathogen. Cattle shedding STEC O157:H7 of more than 10^4 CFU/g of feces are called super-shedders. Twelve *E. coli* O157:H7 strains from super-shedding and low-shedding cattle were isolated from a farm in North Florida. All isolates showed the same pulsed-field gel electrophoresis (PFGE) pattern and produced Shiga toxin. Whole genome sequencing (WGS) was conducted to identify the genetic features related to the super-shedding phenotype using the Illunima MiSeq. The results of WGS showed that the genome size ranged from 5,289,880 to 5,501,890 bps, containing 5213 to 5562 coding sequences. A plasmid, pO157, was identified in all of the strains. Comparative analysis showed similar genome features among the strains, including genome architecture, phage numbers and contents, and virulence factors. Phylogenetic analysis using genomewide single nucleotide polymorphisms (SNPs) showed strains mixed randomly without specific clustering based on super-shedding phenotype. Taken together, our findings suggest that bacterial factors may not determine the STEC O157:H7 super-shedders but animal and/or environmental factors may play key roles.

Feeding of increasing amounts of ruminally-protected choline (RPC) on development of fatty liver in nonlactating, multiparous Holstein cows

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Seventyseven pregnant, nonlactating multiparous Holstein cows were block by BCS and assigned to the study starting at dry off (65 ± 10 days prior to expected calving date). Dietary treatments were 0, 30, 60, 90, and 120 g/day of ReaShure (Balchem Inc.). For the first 5 days cows were fed in ad libitum amounts diets formulated to meet nutrient requirements for maintenance and pregnancy (NRC, 2001). From days 6 to 14, cows were restricted to 36% of their energy/protein but mineral and vitamins requirement for pregnancy and maintenance in order to create a negative energy state forcing cows to mobilize adipose tissue which eventually cause accumulating of triacylglycerides (TAG). The ReaShure treatments were top-dressed on the daily ration since cows were on trial. Smartamine was added to the top dressing during the period of restricted feeding to provide the same amount of daily methionine intake as consumed during the period of ad libitum feeding. At d 14 a fat challenge was done by feeding Energy Booster Mag (454 g) mixed with corn and dried molasses and fed at 1900 h. Blood samples were taken at before, 5 h and every 2 h after the fat challenge for 26 h. Liver tissue was collected for biopsy at 5 and 14 d whereas blood samples on d 5, 10 and 14. Data were analyzed using the MIXED procedure of SAS. Contrasts of interest were: linear, quadratic, cubic, and control vs. RPC. No differences among treatments on BW, BCS, DMI, energy balance, nonesterified fatty acid (NEFA) glucose, and β-hydroxybutyrate (BHBA) concentration were observed either at the ad libitum nor restricted periods ($P > 0.05$). However, by supplementing RPC glycogen (% wet tissue) increased linearly ($P = 0.02$). During the restricted period, even with a methionine sufficient diets, TAG and glycogen content differ among treatments (linear, $P < 0.01$; 0 vs. rest, $P = 0.02$, respectively). Interesting, RPC increased blood TAG (22%) (Quad, $P = 0.09$; 0 vs. rest, $P = 0.01$) during the fat challenge. These results show that that RPC, but not methionine reduce the liver TAG under negative energy state. Also, effect of RPC in ruminates is not limited to the liver, as it was showed for the first time that RPC increased fat absorption.

Abstract #14

Evaluating functional impacts of copy number variations in an equid specific sweat protein

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In all mammals cooling mechanisms are vital to thermoregulation and survival. Equids, and higher primate species uniquely evolved to produce sweat as a primary means of cooling, and thus the inability to sweat can lead to poor-performance, dangerous hyperthermia and death in these species. Latherin, a surfactant protein is uniquely utilized by equids. The primary secreted protein in sweat is thought to increase pelt wetting and aid in evaporative cooling. Encoded by the gene *LATH*, the locus is homologous to human Bactericidal Permeability-Increasing Protein Family A Member 4 (*BPIFA4*). A previous study observed a polymorphic copy number variant (CNV) encompassing the *LATH* gene region of the domesticated horse and varying in copy number among horses of diverse breeds. Although underappreciated as a source of phenotypic variation, CNVs are repeated sections of DNA that occur naturally during recombination and replication and may account for much of the structural polymorphism observed in mammals. We hypothesize that *LATH* CNVs among the extant living equid species may be a result of adaptive evolution for survival, and subsequently positively selected in domesticated horse breeds valued for athletic ability. To fully understand the impact of this structural polymorphism, we propose a precise re-assembly and annotation of the *LATH* gene region of multiple equid species domesticated breeds. We will then utilize digital PCR to assess CNV polymorphisms within and across these populations. Future work regarding the *LATH* gene region will include identification of subjects with extreme CNV gains or losses and quantification of the amount of *LATH* protein produced in sweat samples, which will be performed by western blot. Through our experimentation, we will bring novel information to both the equine and genetic communities regarding the importance of CNVs to phenotypic traits; our research will elucidate new insight into equine thermoregulation, as it is a vital part of homeostasis for athletic animals.

Abstract #15

Predicting breed composition in an Angus-Brahman crossbred population using genomic data

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Pedigree information has been used conventionally to estimate breed composition. However, these estimates begin to lose accuracy beyond F1 generations due to Mendelian sampling during crossing over. It has been suggested that breed composition or ancestry information derived from genomic data can be more accurate than data based on pedigree information. It can also be especially useful when pedigree information is missing or incomplete. The goal of this study was to examine the feasibility and accuracy of using genotype data to estimate breed composition and subsequently identify the minimum number of markers needed to determine breed composition with adequate accuracy. A total of 782 cattle consisting of purebred Angus, purebred Brahman and crossbreeds across the spectrum were used. DNA was extracted from blood or semen samples and genotyped with the Illumina Bovine 250k SNP chip (GGP F250). After filtering for minor allele frequency (>0.1) and call rate (>0.1), 96671 SNP remained and were used in subsequent analysis. Breed membership and level of admixture were estimated using Bayesian model based clustering implemented by the software STRUCTURE. Principal component analysis was performed in order to find major axes of variation that efficiently capture population structure. The first principal component (PC1) had strong correlation with pedigree-based breed composition (0.96) and level of admixture inferred by Bayesian model based clustering (>0.99). Genome wide association was performed with PC1 as a response variable, and SNP were ranked based on the strength of their association with PC1. Based on ranking, 20 subsets of SNP were selected starting from the top 5 and increasing the number by 5 up to 100. For each subset of SNP, a 5-fold cross validation was used to assess the accuracy of prediction. The dataset was randomly divided into 5 groups and a linear regression model was trained on 4 groups and tested on the 5^{th} group. Accuracy of prediction was measured by correlating the resulting breed composition with the composition known from pedigree. The results show that few SNP can be used to predict breed proportion, and accuracies > 0.9 can be reached with 25 SNP. This indicates a small number of DNA markers can be used to accurately predict breed proportion which would reduce genotyping cost. The methods described here can also be generalized to infer level of admixture in animals with potential ancestry from more than two breeds.

Abstract #16

Modeling change in milk production in the subsequence lactation from varying dry period lengths

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Our interest is in determining the economically optimal dry period length (**DPL**) for individual cows under various herd constraints such as limited parlor capacity. The DPL affects milk production in the subsequence lactation, but functions that describe change in milk yield as a result of a continuous change in DPL are not available. The objective of this ongoing study is to develop a model from the literatures that predicts the effect of DPL on the change of milk production in the subsequence lactation. Two observational studies were reviewed and use for model fitting. The first study used Jersey cows in USA. Data was collected from January 1997 to November 2004. The total number of cows was 73,797. The DPL was classified into 13 categories (0 to 20 d, 21 to 30 d, 31 to 40 d, 41 to 45 d, 46 to 50 d, 51 to 55 d, 56 to 60 d, 61 to 65 d, 66 to 70 d, 71 to 80 d, 81 to 90 d, 91 to 110 d, and 111 to 130 d). The loss of milk production in the subsequent lactation was in a range from 1,150 to 38 kg. The second study used Holstein cows in Iran. Data was collected from January 2000 to December 2009. The total number of cows was 65,971. The DPL was classified into 7 categories (0 to 35 d, 36 to 50 d, 51 to 60 d, 61 to 70 d, 71 to 85 d, 86 to 110 d, and 111 to 160 d). The loss of milk production in the subsequent lactation was in the range from 1,485 to 43 kg. The shortest DPL were associated with the greatest losses. A standard Wood's lactation curve was created which represented daily milk yield in the subsequent lactation with a previous 60 days DPL. Milk loss from varying DPL was modeled as a multiplier of the Wood's curve using the Goalseek function in Excel. Next, second polynomial regression equations were used to fit the association between the multiplier and DPL. The equations were created separately for these 2 studies and also between primiparous and multiparous cows in each study. Multipliers varied from 0.81 to 1.01. Primiparous cows had smaller multipliers for the short DPL categories compared to multiparous cows. Polynomial regression equations had R-square from 0.92 to 1. In conclusion, limited data are available to model the association between DPL and milk loss in the subsequent lactation. Modeling multipliers with the Wood's lactation curve is a reasonable and straightforward method to model change in milk production in the subsequence lactation from varying DPL.

Use of 1α,25-dihydroxyvitamin D_3 (calcitriol) to maintain postpartum blood calcium and improve immune function in dairy cows

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Objectives were to determine the effects of an injectable formulation of 1α,25-dihydroxyvitamin D_3 on mineral metabolism and measures of immune function in postpartum Holstein cows. Multiparous cows were assigned randomly to receive only vehicle (control, n = 25) or 300 μg of 1α,25-dihydroxyvitamin D_3 (Calcitriol, n = 25) subcutaneously within the first 6 h after calving. Blood was sampled before treatment and 12 h later, and then until 15 DIM and analyzed for concentrations of ionized Ca (iCa), total Ca (tCa), Mg (tMg), and P (tP), metabolites and hormones. Neutrophil function was evaluated in the first week postpartum. Calcitriol administration increased concentrations of 1α,25-dihydroxyvitamin D_3 in plasma within 12 h of application, which returned to baseline within 5 d. Blood concentrations of iCa and plasma tCa increased 24 h after treatment with Calcitriol. Concentrations of iCa, tCa, and tP remained elevated in cows treated with Calcitriol until 3, 5 and 7 DIM, respectively, compared with control cows, whereas concentration of tMg was less in Calcitriol than control cows until 3 DIM. Concentration of PTH decreased in Calcitriol compared with control cows. Calcitriol treatment tended to increase plasma concentration of BHBA. Calcitriol improved neutrophil function compared with control cows. The percentage of neutrophils in blood with oxidative burst activity, mean fluorescence intensity (MFI) for oxidative burst, and MFI for phagocytosis were all greater for Calcitriol than control cows. Administration of 300 μg of calcitriol at calving was safe and effective in increasing blood concentration of iCa and plasma concentrations of calcitriol, tCa, and tP for the first few days after treatment, and improved measures of innate immune function in early lactation Holstein cows.

Abstract #18

Effect of supplemental vitamin D on serum 25-hydroxyvitamin D concentrations of dairy cows

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Dairy cows are commonly supplemented with vitamin D_3 to compensate for the lack of endogenous vitamin D synthesis. The dose response relationship between supplemental vitamin D and serum 25-hydroxyvitamin D [25(OH)D)], the marker of vitamin D status, has not been established for mature cows. The NRC recommendation is 21,000 IU/d for lactating dairy cows, but dairy producers often supplement cows with 30,000 to 50,000 IU/d. We supplemented lactating Holstein cows with 20,000, 40,000, and 60,000 IU of vitamin D_3/d (n = 8/group) and measured serum 25(OH)D at 0 and 21 d of feeding vitamin D_3. Cows were housed in a freestall barn and fed a total mixed ration individually in Calan gates with vitamin D_3 supplied as a top-dress. Serum 25(OH)D was 71.7, 68.2, and 70.9 ng/mL (SE = 4.2 ng/mL) at 0 d. At 21 d, there was an effect of vitamin D_3 dose on serum 25(OH)D ($P < 0.05$) where serum 25(OH)D was 69.3, 73.3 and 75.8 ng/mL (SE = 2.1 ng/mL) for cows fed 20,000, 40,000 and 60,000 IU of vitamin D_3/d, respectively. In conclusion, our data suggest there is a dose response relationship between supplemental vitamin D_3, at rates between 20,000 to 60,000 IU/d, and serum 25(OH)D for dairy cows.

Impact of late gestation heat stress on mitochondrial function in neonatal heart and liver

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With rising temperatures more and more animals are at risk of being exposed to high ambient temperatures outside their thermal comfort zone for longer periods of time, especially in the southeastern US, resulting in reduced feed intake, and altered whole animal metabolism. In addition, chronic maternal heat stress (**CM-HS**) experienced *in utero* has been related to decreased embryo weight, increased in embryo mortality, and compromised postnatal whole body metabolism and growth. However, little is known about the impact of CH-HS on function of the mitochondria in the fetus, particularly in vital organs such as heart and liver. The objective of this study is to examine the effects of CH-HS in dairy cows during late gestation on mitochondrial (**mt**) function in heart and liver of newborn calves. We hypothesized that exposure to *late* gestation chronic HS will have little impact on mt activity in heart and liver, due, at least in part, to adaptive cellular mechanisms such as elevated expression of heat shock proteins (HSPs). To test our hypothesis, we assessed mt function by measuring activity of the mt enzymes citrate synthase (**CS**; marker of mt content), and cytochrome *c* oxidase (**COX**; marker of mt respiratory function). Heart and liver samples were collected at the UF Dairy Unit from neonatal bull calves born to dry cows that were evaporatively cooled (**CL**) or not cooled (**HT**) during the last 45 days of gestation. We found that activity of neither CS nor COX differed between treatment groups in both liver and heart (Liver: CS: 177±10 and 162±8 nmol/min/mg prot in CL and HT, resp.; COX: 309±20 and 322±7 nmol/min/mg prot in CL and HT, resp.. Heart: CS: 1.2±0.1 and 1.2±0.04 µmol/min/mg prot in CL and HT, resp.; COX: 1.2±0.03 and 1.2±0.05 µmol/min/mg prot in CL and HT, resp.). Our data suggest that *late* gestation HS did not alter mt content and function in these tissues in neonatal calves. Next, we will measure in heart and liver samples activity of the mt enzyme hydroxyacyl-coenzyme A dehydrogenase as a marker for mt fatty acid oxidation, as well as expression of HSPs using immunoblot.

Abstract #20

Genetic Markers in the Calpastatin Gene Associated with Beef Tenderness

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Genetic markers or SNPs (single nucleotide polymorphisms), are small fragments of DNA with a known location on a chromosome. These SNPs are associated with a specific gene or trait such as carcass quality and final cut characteristics, as well as tenderness, juiciness, and flavor. This is important because if a set of SNPs that affect carcass properties and palatability traits can be identified, they can be used to identify genetically superior bulls early in life for breeding or can be used to predict desirability for marketing purposes leading to higher and more consistent beef quality. For this study, 502 animals from the UF Angus-Brahman multibreed herd were used to investigate the role of a SNP in calpastatin gene in beef tenderness. DNA was extracted from blood using DNeasy Blood & Tissue Kit (Qiagen). A real-time PCR and high resolution melt curve analysis was performed for one SNP in the calpastatin gene. All three genotypes (GG, GC and CC) were observed in this population, however, the frequency of the GG genotype was very low (0.01). An association analysis was performed to determine if the SNP had an effect on beef tenderness measured by Warner-Bratzler shear force. It was found that the CAST1 SNP was not significant across genotypes. However, it was found that there was a trend for the Warner-Bratzler shear force to be higher (tougher meat) in animals with higher Brahman percentage. This is consistent with previous studies that showed Angus beef tends to be more tender than Brahman beef. Based on the findings of the present study, further investigations are needed either using other polymorphisms in these genes or with larger sample size for the GG genotype.

Abstract #21

Influence of oat beta-glucan on postprandial glycemic and insulinemic responses in horses

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Consumption of the soluble fiber beta-glucan (BG) in oats has been shown to improve management of blood sugar in diabetic humans. We hypothesized a diet rich in oat BG would reduce the magnitude of glucose and insulin produced in response to starch or sugar intake by horses. Mature Quarter Horses (n=8; 569 ± 2 kg) were fed 4 concentrates over 4, 22-d periods in a replicated 4 x 4 Latin square design. Concentrates differed in amount and source of BG: cracked corn (low BG control), standard feed oats (moderate BG), a high-BG oat variety (high BG), or corn top-dressed with a concentrated oat BG powder (high BG). High BG diets provided 170 mg BG/kg BW. All diets were isocaloric. Horses also had unlimited access to pasture and were fed a vitamin/mineral supplement. Glycemic and insulinemic responses were evaluated after an 8-h fast on d 21 in response to their assigned treatment diet, with meal size standardized to provide 0.8 g NSC/kg BW (an amount equal to the habitual meal size for both oat diets, but lowered meal size for diets containing corn); and again on d 22 in response to an oral dose of sugar (corn syrup, 0.15 mL/kg BW). At the completion of each 22-d period, horses underwent a 13-d dietary washout followed by reallocation of treatments. Time to consume the meal differed between diets ($P<0.0001$), averaging 13.4 and 7.5 min for diets containing oats and corn, respectively. Insulin response to a meal was affected by diet ($P<0.0001$), time ($P<0.0001$) and diet*time ($P<0.0001$), where serum insulin was higher and remained elevated longer in response to meals containing oats compared to corn. In response to the oral sugar test, insulin was affected by time ($P<0.0001$) and diet*time ($P=0.027$), with lower insulin in the 2 diets containing high BG compared to corn and standard oats. Diet did not affect glycemic responses. Results of the meal test likely reflect differences in foregut starch availability between oats and corn. However, responses to the oral sugar test suggest that habituation to diets containing higher BG may reduce insulin response.

Abstract #22

Relating Muscle Fiber Morphometrics and Protein Degradation to Meat Quality in a Multibreed Herd

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Brahman and Brahman-influenced cattle provide integral adaptations that benefit the cattle herd in the sub-tropical United States; however, they tend to exhibit less desirable carcass and palatability traits. When compared to Angus, Brahman are lower marbling, less tender, and have more connective tissue. The objective of this study was to determine influence of Brahman genetics on muscle metabolic phenotype and postmortem proteolysis. Cattle used in this study represent a continuous spectrum of Angus-Brahman genetic variation and were divided into six breed groups for analysis: Angus; ¾ Angus, ¼ Brahman; Brangus; ½ Angus, ½ Brahman; ¼ Angus, ¾ Brahman; and Brahman. Steers (n=6 per breed group) were harvested and samples from *longissimus lumborum* were collected at 1.5 h, 24 h, and 14 d postmortem. Western blotting and agarose gels were used to assess proteolysis during the 14 d aging period, and immunohistochemistry and enzyme activity were used to assess muscle fiber contractile and metabolic phenotype. Tenderness was determined objectively by Warner-Bratzler shear force. Data were analyzed using the linear fit model procedure in SAS-JMP Pro 11. As the percentage of Brahman genetics increased, WBSF increased ($R^2 = 0.28$, $P = 0.0009$). The degree of μ-calpain autolysis decreased as the percentage of Brahman increased ($R^2 = 0.24$, $P = 0.0025$). Degradation of troponin-T ($R^2 = 0.16$, $P = 0.0141$), desmin ($R^2 = 0.19$, $P = 0.0077$), titin ($R^2 = 0.20$, $P = 0.0059$) and nebulin ($R^2 = 0.11$, $P = 0.0614$) at 24 h decreased as the percentage of Brahman increased. Brahman genetics influenced oxidative capacity ($R^2 = 0.20$, $P = 0.0056$); citrate synthase activity increased as Brahman percentage increased. The cross-sectional area of type IIx fibers increased as Brahman influence increased ($R^2 = 0.32$, $P = 0.0004$). Brahman influenced cattle produced tougher steaks, evidenced by higher WBSF and decreased protein degradation. Brahman genetics also impacts muscle fiber size and metabolic properties.

Fetal versus maternal contributions of *Bos indicus* and *Bos taurus* genetics to early embryo development and offspring performance

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To determine how the maternal genotype, fetal genotype, and diet restriction influences early embryonic development in *Bos indicus* and *Bos taurus* cattle, a total of 186 cows were used in a 2x2x2 factorial experiment. Fifty-one donor cows (n = 24 Brangus and 27 Angus) were superovulated and AI with sex-sorted semen from the same breed, and total of 135 transferable embryos were produced. Reciprocal embryo transfer was performed to recipients (n = 65 Brangus and 70 Angus) that were synchronized to be at d 7 post-estrus at the time of embryo transfer. Recipient cows were housed in the University of Florida Feed Efficiency Facility, equipped with a GrowSafe System (GrowSafe System Ltd., Airdrie, AB, Canada). A feeding scheme was superimposed onto the recipient cows from 14 d before embryo transfer until 91 d of gestation, where cows were randomly assigned to a diet that met daily energy and protein requirements (100%) or a diet that restricted intake of nutrients to 70% of energy and protein requirements (NRC, 2000). Individual feed intake was recorded throughout the feeding period. Transrectal ultrasonography was completed with an Ibex portable ultrasound equipped with a linear 8-5 MHz multi-frequency transducer (E.I. Medical Imaging, Loveland, CO, USA). Fetal crown to rump (CRL) and crown to nose length (CNL) were measured weekly from d 28 to 91. Blood samples were harvested at d 18 and 21 post estrus to access peripheral blood leukocytes (PBL) interferon stimulated genes (ISG) mRNA expression. Blood samples were also harvested weekly from d 35 to 91 to evaluate plasma concentrations of progesterone (P4) and pregnancy-specific protein B (PSPB). All pregnant cows will be followed until parturition and the effects of treatments on offspring performance will accessed. Liver and muscle samples will be collected from all offspring at birth and weaning to evaluate mRNA expression of target genes related to production traits. Offspring will also be submitted to a feed efficiency evaluation at the Feed Efficiency Facility, where individual residual feed intake will be measured. The data from the experiment have not been analyzed yet.

Abstract #24

Effect of exercise on reproductive traits in cycling gilts

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Previous research has demonstrated that exercise can alter reproductive performance in the mare. Using the pig (n = 18) as a model, our objectives were to evaluate the effects of daily exercise on ovarian structures in cycling gilts (mean age = 225 d). All animals were treated orally with a synthetic progestin, and subsequently injected with a gonadotropin to synchronize their estrous cycles. Gilts were then trained to follow a target and run voluntarily along a 80 m track, and then subsequently randomly assigned to either the exercise or control group. Once synchronized, exercised pigs were worked twice daily during the last 10 days of their estrous cycle and covered on average a distance of 0.5 km/day at a 6.0 km/hour speed average. Rectal temperatures increased from a mean of 38.5° C at rest to a mean of 38.8° C immediately after exercise ($P<0.05$). Respiration rates also increased from a mean of 30.8 to 59.7 breathes per minute ($P<0.05$), respectively. Cortisol was measured in saliva at three time points during the exercising period; the day before the exercise protocol started (m1), then five days (m2) and 9 days (m3) after exercise initiation. All saliva collections were performed 20 min after the onset of exercise protocol and at the same time of day for non-exercised gilts. For the exercised pigs cortisol concentration were highest on the m3 collection (4.66±0.48 pg/mL), and subsequently higher on m1 (4.09±0.55 pg/mL; $P < 0.05$), compared to m2 (2.9±0.54 pg/mL). When treatment groups were compared, m2 and m3 exercised gilts had higher cortisol levels than control. Gilts were slaughtered and reproductive organs were collected and examined immediately. No differences were found amongst treatments in the total number of follicles, corpus hemorragicum, or corpus luteum. When classified by size, exercised gilts had more medium ($P < 0.01$) and small sized follicles than control ($P = 0.02$). Control gilts had a higher quantity of large follicles than exercised gilts ($P = 0.04$). There were no differences when the cumulus oocyte complex was classified by quality amongst groups. These data indicate that exercising pigs is associated with a stress response that can influence ovarian follicle development.

Abstract #25

Maternal heat stress reduces body and organ growth in calves: relationship to immune tissue development

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Maternal heat stress (HT) not only reduces fetal growth but also influences postnatal performance and immune function of the offspring. The objective was to evaluate the effect of in utero HT on overall fetal growth and organ development, particularly those associated with immune function. Dams were dried off 45 d before expected calving and randomly assigned to one of two treatments: HT or cooling (CL). During the dry period, all cows were housed under shade, where the pen for CL cows was equipped with active cooling including water soakers and fans whereas the pen for HT cows had no soakers and fans. Based on rectal temperature (RT) and respiration rate (RR), heat stress was severe. Average RT in HT cows was 39.3 ^{o}C compared with 38.9 ^{o}C for CL cows, and HT cows had 66.7 breath/min respiration rate and 43.2 for CL cows. Bull calves (n=30) were sacrificed at birth without colostrum feeding (5/trt) and 1 and 2 day of age (DOA, following colostrum feeding, 5/trt). Pooled colostrum (3.8 L) was fed within 4 h after birth to bulls slaughtered on 1 and 2 DOA. After slaughter, the small intestine dissected into duodenal, jejunal and ileal segments, and tissue samples from each section were fixed in 4% neutral formalin and then transferred to 70 % ethanol for immunohistochemistry. Bull birth weight from HT dams was lower than bulls from CL dams (HT: 39.3; CL: 43.8 SEM = 1.1 kg; $P < 0.01$). The thymus, spleen, and heart weight of HT bulls was lower compared with the CL bulls (Thymus, HT: 107.7; CL: 138.0, SEM = 14.4 g; $P = 0.02$; Spleen, HT: 75.5; CL: 93.7, SEM = 6.9 g; $P < 0.01$; Heart, HT: 292.4; CL: 329.4, SEM = 19.6 g; $P = 0.03$). The liver weight of HT bulls tended to be lower compared with the CL bulls (HT: 811.4; CL: 914.0, SEM = 70.4 g; $P = 0.09$). We conclude that the acute difference in heat strain on HT and CL cows during the dry period has significant impact on general fetal growth and on immune tissue development, which may be associated with reduced immune function in early life.

Abstract #26

Determining water soluble phosphorus in equine manure through sequential water extractions

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Application of manure to soils affects soil phosphorus (P) solubility and can lead to unintentional movement of water-soluble P (WSP) from manure to off-farm locations, increasing risk for ground and surface water contamination. Most methods for measuring WSP in feces employ a single water extraction. However, a single extraction may not adequately represent potential P losses from manure. We hypothesized that multiple, sequential extractions would result in progressively greater P removal from feces. Five successive water extractions were performed on 28 equine fecal samples. Feces were dried, ground, and a 1:20 w/v slurry of feces and nanopure water was created in a 50-mL conical tube. Samples were shaken for either 20 or 60 min to determine if agitation time influenced P extraction. Samples were centrifuged at 1250 x *g* for 20 min and supernatant was removed for P analysis. This process was repeated and each subsequent extraction was performed on the fecal residue remaining in the tube after bringing to the original 50-mL volume. Supernatant from all 5 washes was passed through a 0.45-µm filter and analyzed for P concentration using the molybdate blue colorimetric method. Total P content was determined on the original fecal samples after ashing and acid digestion. Quantity of WSP extracted in each wash and the WSP recovered as a percent of total P were compared with mixed model ANOVA with repeated measures. Agitation time (20 vs 60 min) had no effect on WSP extraction. The first water extraction captured the largest fraction (39.7 ± 1.0%) of the total P in the sample ($P<.0001$). Each subsequent water extraction captured progressively less total P ($P<0.001$), with 21.6, 11.4, 6.7 and 4.5% of additional total P recovered from extractions 2-5, respectively. After the 5th wash, a total of 82.4 ± 1.0% of the total P had been extracted from the feces. Although a single water extraction likely captures the most mobile P fraction in feces, results indicate that repeated exposure to water continues to solubilize P in feces. Use of multiple, sequential water extractions may better reflect potential for P losses from manure wet climates.

Abstract #27

Isolation and characterization of ESBL-producing *E.coli* isolated on commercial farms

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The prevalence of extended-spectrum beta-lactamase (ESBL)-producing bacteria is increasing rapidly, which is considered as a global concern. ESBL-producing bacteria are resistant to penicillins and most of third-generation cephalosporins. In this study, we isolated ESBL-producing *Escherichia coli* on 10 different commercial farms in North Florida. Cattle feces and environment samples, including soil, forage, and water, were plated on McConkey agar containing the antibiotic cefotaxime, commonly used to select ESBLs due to its strong bactericidal effect. In total, we isolated 62 ESBL-producing *E. coli* strains. All isolates carried a CTX-M gene, which confers resistance to the antibiotic cefotaxime. Antibiotic resistance profiles were evaluated by the antibiotic susceptibility test (AST) against 13 different antibiotics. All strains showed multi-drug resistance against 4 to 13 antibiotics. The whole genomes of 62 ESBL-producing *E.coli* were sequenced to analyze genetic features. We identified 15 different multi-locus sequence types (MLST), including sequencing type 10 involved in the human outbreaks. According to the farm locations, sample types, and sequence types, we selected 23 representative isolates to compare virulence genes and antibiotic resistance genes. All isolates encoded numerous virulence and antibiotic resistance genes with high diversity. Phylogenetic trees were generated to identify genomic relatedness among isolates. Most of the isolates were clustered based on the farm locations. Most importantly, the farm isolates were clustered with clinical human pathogens, indicating that transmission of ESBLs between human clinics and animal farms occurs.

Abstract #28

Use of a head elevation and nasopharyngeal flush model for short term immune distress in horses

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Prolonged head elevation has previously been used to induce bacterial and cytological changes in the upper and lower respiratory tract. Transtracheal washes or bronchoalveolar lavages are standard methods used to characterize cytology and diagnose respiratory disease. We hypothesized that prolonged head elevation would induce upper respiratory immune distress and that nasopharyngeal flushes (NPF) would offer a less invasive alternative to classify this response. Twelve mature horses (mean ± SEM, 552 ± 10 kg) were tethered with halter and lead in a standard head-tying position for 12 h. While tied, horses had free-choice access to Coastal bermudagrass hay and were offered water every 2 h. Each horse underwent head elevation on 4 occasions over the course of 5 mo. Each head-tie bout was separated by 30 d. NPF and whole blood samples were obtained before head elevation, immediately after, and 12, 24, and 72 h post-head elevation. NPF samples were obtained by passing a sterile urethral catheter through the nasal cavity into the pharyngeal region. Sterile PBS was pushed through the catheter and drainage was caught using a novel funnel collection cup system. Captured flush from both nostrils was combined, filtered and centrifuged in preparation for analysis of cellular populations by flow cytometry. Data were compared using mixed model ANOVA with repeated measures. The head elevation procedure was well tolerated by horses and induced reproducible upper respiratory distress as noted by mild coughing, increased nasal drainage and elevated mucus content in flush samples. Leukocytosis occurred in whole blood and NPF samples following head elevation ($P<.05$), which is consistent with diagnostic findings of horses with upper respiratory disease. Most horses recovered from this stressor in 3 d. This model for upper respiratory distress proved useful as a short term stressor with no long term symptoms. Further, NPF is less invasive and requires less sedation than other respiratory sampling techniques, which can allow more frequent sampling to track the progression of upper airway distress.

Abstract #29

Unravelling the genomic architecture of bull fertility in Holstein cattle

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Fertility is considered an important economic trait in dairy cattle. Most studies have investigated cow fertility while bull fertility has received much less consideration. The main objective of this study was to perform a comprehensive genomic analysis in order to unravel the genomic architecture underlying sire fertility in Holstein dairy cattle. The analysis included the application of alternative genome-wide association mapping approaches and the subsequent use of diverse gene set enrichment tools. The association analyses identified at least eight genomic regions strongly associated with bull fertility. Most of these regions harbor genes, such as *KAT8*, *CKB*, *TDRD9* and *IGF1R*, with functions related to sperm biology, including sperm development, motility and sperm-egg interaction. Moreover, the gene set analyses revealed many significant functional terms, including fertilization, sperm motility, calcium channel regulation, and SNARE proteins. Most of these terms are directly implicated in sperm physiology and male fertility. This study contributes to the identification of genetic variants and biological processes underlying sire fertility. These findings can provide opportunities for improving bull fertility via marker-assisted selection.

Effects of feeding green chopped winter forages on digestibility, ruminal fermentation and blood parameters in beef steers

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An experiment was conducted over 2 consecutive winters to evaluate the effects of feeding green chopped winter forages on digestibility and ruminal fermentation parameters in beef steers. Each yr, 9 ruminally cannulated Angus crossbred steers (yr 1: 359 ± 79 kg; yr 2: 481 ± 105 kg) received fresh chopped forage ad libitum, from pastures planted with one of the following mixtures, each combined with Prine annual ryegrass (*Lolium multiflorum* Lam.): 1) FL401 cereal rye (*Secale cereale* L.) (RYE); 2) Horizon 201 oats (*Avena sativa* L.) (OAT); 3) Trical 342 triticale (*X Triticosecale* spp.)(TRIT). Intake was measured using GrowSafe, and orts were discarded prior to feeding. After a 14 d adaptation, feed and fecal samples were collected twice daily for 4 d, to determine apparent total tract nutrient digestibility using iNDF as a marker. Blood and ruminal fluid samples were collected every 3 h during a 24 h period, to analyze BUN and glucose in the plasma, as well as NH_3-N, pH, and VFA concentrations in ruminal fluid. Data were analyzed as a generalized randomized block design with repeated measures. Treatments did not affect ($P > 0.05$) intake of DM, OM, CP, NDF, or ADF; however, apparent total tract digestibility of DM, OM, CP, NDF, and ADF was greater ($P < 0.05$) for OAT and TRIT, when compared with RYE. Steers fed OAT had greater concentrations of plasma glucose ($P < 0.05$) compared with TRIT and RYE. An effect of sampling time ($P < 0.01$) was observed for ruminal pH. Steers fed RYE had greater ($P < 0.05$) concentrations of NH_3-N, BUN, and the least concentrations of total VFA ($P < 0.05$). Molar proportion of acetate, BCVFA and A:P were greater ($P < 0.05$) for RYE when compared with OAT and TRIT. OAT and TRIT resulted in greater digestibility of nutrients, ruminal fermentation and blood parameters that are conducive to enhanced growth performance when compared with RYE.

Abstract #31

EFFECT OF OMNIGEN-AF® AND HEAT STRESS DURING THE DRY PERIOD ON SUBSEQUENT PERFORMANCE OF COWS

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Heat stress in dairy cows during the dry period impairs milk production in the next lactation. Feeding OmniGen-AF® (OG) to lactating cows during heat stress increases dry matter intake (DMI), lowers respiration rate (RR) and rectal temperature (RT), but effects in dry cows are not known. We hypothesized that OG supplementation before, during and after the dry period (approximately 160 days) would overcome the effects of heat stress and improve performance. Treatment groups were: heat stress (HT, only shade, n=17), heat stress with OmniGen-AF® (HTOG, 56 g/d, n=19), cooling (CL, shade, fans and sprinklers, n=16), and cooling with OmniGen-AF® (CLOG, n=11). Cows were randomly assigned to treatments based on previous mature equivalent milk production. Cows were dried off 45 d before expected calving and after parturition; cows were kept under the same cooling system and management, until 60 DIM. Cooling cows during the dry period reduced RT (CL vs. HT; 38.8 vs 39.0, $P < 0.01$) and RR (CL vs. HT; 44 vs. 73, $P < 0.01$). RR was also decreased by OG supplementation (OG vs. Non-OG; 56 vs. 61, $P < 0.01$). There was an interaction between OG supplementation and HT ($P < 0.1$); HTOG cows had lower RT compared to HT cows. During the dry-period, OG reduced DMI relative to non-OG cows ($P < 0.1$). Calf birth weight was greater in calves from CL cows (CL vs. HT, $P <0.01$). In cows, no differences in hematocrit, total protein and BCS among treatments were detected. Cows on CLOG had higher BW (kg) at parturition (CLOG, 794.9; CL, 746.8; HTOG, 762.9; HT, 720). Gestation length was approximately 4 d longer for CL cows compared with HT cows ($P < 0.01$). Cows on CLOG, CL and HTOG treatments produced more milk (5.2±1.9, 4.8±1.6 and 4.6±1.4 kg/d, respectively) than HT cows (35.9±1.5 kg/d). Body weight after parturition and DMI were evaluated up to 60 DIM and averaged DMI 19.4±0.7 kg/d, with no differences observed among treatments. These results confirm that exposure of dry cows to heat stress negatively impacts milk production in the subsequent lactation. Active cooling of dry cows and OG supplementation can reduce the negative effects of heat stress in the dry period.

Abstract #32

Accumulation of inflammatory cytokines alters oocyte and follicular development

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The follicular environment of the growing oocyte is critical to the developmental competence of subsequent embryos. Many cytokines involved in inflammation and immunity are also critical regulators of oocyte maturation and follicular development. Postpartum bacterial uterine infection affects 40% of dairy cattle, resulting in localized inflammation and subsequent infertility after the resolution of disease. Cows with active uterine infection accumulate the pathogen associated molecule lipopolysaccharide (LPS) in the follicular fluid of the dominant follicle. Subsequently granulosa cells exert an innate immune response to LPS by producing proinflammatory cytokines similar to hematopoietic cells during infection. In addition, LPS perturbs oocyte maturation following in vitro exposure. We hypothesize that exposure of cumulus oocyte complexes (COCs) to the proinflammatory cytokine TNFα during maturation will alter oocyte competence and the microenvironment of the follicle. Ovaries were acquired from a local abattoir and COCs were obtained from follicles less than 8mm in diameter. Cumulus oocyte complexes underwent in vitro maturation for 24 hours in the presence of 0, 1, 10 or 100 ng/ml of recombinant bovine TNFα and gonadotropins. Following 24 hours of maturation cumulus oocyte complex expansion was recorded and IL-6 accumulation measured by ELISA. Spontaneous COC expansion was prevented in the presence of increasing concentrations of TNFα when compared with the vehicle treated controls (24%, 26% and 14% reduction, respectively). While not statistically significant a 42% increase in IL-6 accumulation was observed in supernatants following maturation of COCs in the presence of 1 ng/ml of TNFα compared to vehicle treated controls. This observed TNFα induced IL-6 accumulation may have a negative biological impact on the developmental environment of the oocyte. While TNFα is involved in the physiological balance between cell survival and apoptosis, inappropriate induction by pathogen associated molecules like LPS may perturb this balance and negatively affect steroid production, oocyte competence and ultimately contribute to infertility in dairy cattle following uterine infection.

Comprehensive *In vitro and In vivo* Evaluation of Chitosan Nanoparticles for Risk Assessments with Intestinal Epithelial Cells and *Caenorhabditis elegans*

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A natural antimicrobial agent, chitosan nanoparticles (CN), has previously demonstrated broad-spectrum antimicrobial activity. CN have many potential applications in the food industry and offers an alternative to traditional antibiotics. However, it has not been determined whether CN may cause adverse side effects in humans and animals. The purpose of this study was to evaluate the toxicity of CN toward intestinal epithelial cells, Caco-2 cells, and an animal model, *C. elegans*. Four types of CN were prepared by cross-linking of chitosan. Two crosslinkers, sodium sulfate (SS) and tripolyphosphate (TPP), and two types of chitosan, low and high molecular weight (Mw), were used to generate CN. Caco-2 cells were treated with 0.1, 0.2 or 0.4% CN for 24 h. The morphological change of the cells was checked immediately following treatment. Cellular membrane damage was assessed by lactate dehydrogenase (LDH) assay. In addition, the four types of CN from 0.1 to 0.4% were administered to *C. elegans* for survival assay. The viability of *C. elegans* was monitored for 22 d. No change in cell viability was observed in Caco-2 cells treated with up to 0.2% of CN compared to the control. In LDH assay, SS CN showed higher toxicity compared with TPP CN. In addition, we observed toxicity of CN in the animal model. In the *C. elegans* survival assay, CN generated with TPP showed lower toxicity compared to the ones generated with SS. This data demonstrates that CN are not toxic toward Caco-2 cells, but are toxic in the animal model. These results will help with future development of animal models for the risk assessment of newly developed agents, especially nanomaterials.

Abstract #34

Effects of Se-fortified Hay Feeding During the Periparturient Period on Measures of Se Status in Cows and Calves

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This study evaluated the effect of supplemental Se source during prepartum, on Se status of cows and calves. 27 mature cows were randomly assigned to 3 treatments; no Se (Control; n = 6), Na selenite (n = 9) or High-Se hay (n = 12). Cows assigned to the Na selenite and High-Se hay treatments were provided 2.5 mg of supplemental Se daily. High-Se hay was created by biofortification of 'Jiggs' bermudagrass (Cynodon dactylon L.) hayfields, trough foliar application of Na selenate 8 weeks prior of harvest. Selenium concentration of hay harvested from Na selenate-treated fields was greater ($P < 0.001$) than fields without Na selenate treatment (10.8 vs. 0.1 mg Se/kg DM). Cows were moved into individual feeding areas at an estimated 30 d prior to calving (actual days on treatment = 29.07, 32.60, and 23.83 for high-Se hay, Na selenite, and Control treatments, respectively; SEM = 6.45). Cows calving sooner than 10 d on treatment were removed from the study, resulting in an unequal number of cows enrolled among treatments. Initial cow Se status was determined by blood and liver samples collected on d 0 (study enrollment). Placenta was collected at calving for determination of Se concentration of cotyledons. Four days after calving, blood and liver samples were collected from both cows and calves for determination of Se status. Initial liver Se concentrations were used as a covariate for analyses. Selenium-supplemented cows had greater ($P < 0.0001$) liver Se concentrations on d 4 after calving compared to Control and cows provided supplemental Se via High-Se hay tended ($P = 0.11$) to have greater liver Se concentrations compared to cows provided Na selenite (0.60, 1.22, and 1.13 mg/kg DM for Control, High-Se hay, and Na selenite, respectively; SEM = 0.057). Similarly, Se-supplemented cows had greater ($P = 0.03$) cotyledon Se concentrations at calving compared to Control, but source of Se did not differ ($P = 0.16$; 0.68, 0.88 and 0.79 mg/kg DM for Control, High-Se hay, and Na selenite, respectively; P=0.03; SEM=0.056). Calf liver Se concentrations did not differ ($P \geq 0.58$) among treatments (1.17, 1.27 and 1.21 mg/kg DM for High-Se hay, Na selenite, and Control, respectively). These data imply that Se biofortification of hayfields can increase Se status of periparturient cows.

Abstract #35

Effects of supplementing pasteurized waste milk with vitamins A, D and E on fat-soluble vitamin status, growth, and health of calves

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The objective of this study was to determine the effects of a milk supplement, MILKADE® (Stuart Products, Inc.), on growth, health and fat-soluble vitamin status of calves fed pasteurized whole milk. The MILKADE supplement contained 50,000 international units (IU) vitamin A as retinyl-palmitate, 50,000 IU vitamin D_3, and 500 IU vitamin E as *RRR-α-tocopherol* per milliliter of product. Forty Holstein calves (19 bulls, 21 heifers) were enrolled at birth and assigned to either control (n = 18, no supplement), 0.25 mL MILKADE (0.25ADE, n = 12), or 0.5 mL MILKADE (0.5ADE, n = 10) treatments. Calves were provided 2.85 L of pasteurized waste milk twice per day and the supplement was added individually to the calves' milk at the morning feeding. Responses to treatments were analyzed as repeated measures. Serum retinol concentrations averaged near 400 ng/mL during the trial and were not different ($P > 0.45$) between treatment groups. In contrast, control calves were vitamin D deficient throughout the trial with average 25-hydroxyvitamin D (25(OH)D concentrations <10 ng/mL of serum. 25(OH)D concentrations of 0.25ADE and 0.5ADE calves peaked 90 and 150 ng/mL of serum, respectively, after 3 weeks ($P < 0.001$). Similarly, serum α-tocopherol concentrations of control calves remained below 1.5 μg/mL throughout the trial but reached approximately 4.5 μg/mL of serum for both 0.25ADE and 0.5ADE groups after 5 weeks ($P < 0.05$). There was a treatment effect on overall body weight through the first 3 weeks of age ($P = 0.004$) such that 0.25ADE and 0.5ADE calves weighed less than control calves (49.3 kg and 46.4 kg vs 52.1 kg, $P = 0.013$ and $P < 0.001$, respectively) at 3 weeks of age. However, there was no difference in BW of heifers at week 6 of the trial ($P = 0.171$). There was no difference in feed intake or fecal and respiratory scores between groups ($P > 0.05$). In conclusion, calves fed pasteurized whole milk are deficient in vitamins D and E. Daily intakes for vitamins A and E were within ranges determined optimal for calves. The high serum 25(OH)D of the supplemented calves indicates vitamin D intakes above 10,000 IU/d are perhaps excessive for neonatal calves.

Correlation between the Abundance of Ruminal Bacteria with Milk Production and Total Tract Digestibility of Dairy Cows Fed Live and Killed Yeast

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The change in abundance and diversity of ruminal bacterial group reflects the shift in metabolic process in the rumen, which can affect animal performance. The objective of this study was to compare the abundance of different ruminal bacteria with the total tract nutrient digestibility and milk production of dairy cows fed diets supplemented with live or killed *Saccharomyces cerevisiae.* Four ruminally-cannulated lactating cows (284 $\pm$ 18 DIM) were assigned to 4 treatments arranged in a 4 x 4 Latin square design with four, 21-day periods. Cows were fed a non-acidotic total mixed ration (46.8% corn silage, 8.5% wet brewers grain and 44.7% concentrate, DM basis). The diet was supplemented with no yeast (CON) or with a low dose of live yeast (5.7×10^7 cfu/day; LLY), a high dose of live yeast (6.0×10^8 cfu/day; HLY), or a high dose of killed yeast (6.0×10^8 cfu/day before heating at 80^{o}C; HDY). Ruminal fluid sample was collected 0, 2, 4, 6, 8 and 10 h after the morning feeding on d 21 and strained through cheese cloth to separate solid and liquid fractions. Microbial diversity was examined by Illumina MiSeq sequencing of the V4 region of the 16S rRNA gene. Data were analyzed using R (R Core Team, 2013). In ruminal solid fraction, *Fibrobacter* showed positive correlation (r = 0.60, $P < 0.05$) with milk fat concentration. Also, Unknown genus in Lachnospiraceae, RFP12 were negatively ($P < 0.05$) correlated with NDF digestibility (r = -0.52 and -0.56, respectively). An unknown genus in Paraprevotellaceae is negatively ($P < 0.05$) correlated with milk fat and protein content (r = -0.56 and -0.52, respectively) and NDF digestibility (r = -0.65). An unknown genus in Clostridiaceae is negatively correlated with CP digestibility (r = -0.59, $P < 0.05$). In the liquid fraction, *Prevotella* was negatively correlated with DMI, milk protein and fat content (r = -0.64, -0.59 and -0.53, respectively, $P < 0.05$). Unknown genus in Succinivibrionaceae and Ruminococcaceae showed positive ($P < 0.05$) correlation with ADF digestibility (r = 0.63) and milk yield (r = 0.49), respectively. Unknown genera in Lachnospiraceae was negatively correlated with DM digestibility (r = -0.56, $P < 0.05$). In conclusion, this study revealed several uncultured or unknown ruminal bacteria that are important candidates for future studies because of their correlation with one or more indices of dairy cow performance.

Abstract #37

β-adrenergic agonist mediated changes in muscle growth and energy metabolism in AMPKγ3^{R200Q} pigs

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The β-adrenergic agonist Ractopamine (RAC) repartitions nutrients from adipose to skeletal muscle and enhances muscle accretion in a fast-fiber type specific manner. In contrast, muscles from pigs with a mutation in the key energy sensor, AMP-activated protein kinase (AMPK), exhibit a slower, more oxidative phenotype and elevated glycogen. Our objective was to utilize RAC and AMPK-mutated pigs to investigate the cellular signaling pathways regulating growth, energy metabolism, and meat quality. At approximately 90 kg, wild type and AMPKγ3^{R200Q} barrows were assigned to control diet or diet supplemented with RAC (9 ppm; Elanco Animal Health) for 28 d. Pigs were harvested and muscle was collected from the longissimus lumborum (LL) immediately after exsanguination (t=0 min) and at 1, 2 and 24 h; deep (red) and superficial (white) portions of the semitendinosus (STR and STW respectively) were collected at 15 min. Glycogen content and parameters of glycogen metabolism were analyzed. Regardless of RAC or muscle, AMPKγ3^{R200Q} increased glycogen (P<0.001) and glycolytic potential (P<0.001) compared to wild type. There was an interaction between genotype and RAC in the LL (P<0.04); RAC decreased glycogen in AMPK but not wild type. In STR, AMPKγ3^{R200Q} decreased AMPK content, whereas RAC increased AMPK protein (P<0.02). AMPKγ3^{R200Q} increased phosophorylated (Ser473) and total AKT protein in LL, STR and STW (P<0.01), although pAkt/total was not different. Content of UDP-glucose pyrophosphorylase (UGP2), an enzyme involved in glycogen synthesis, was higher in AMPKγ3^{R200Q} muscle; RAC also increased UGP2 (P<0.01). These results indicate that AMPK and RAC influence glycogen storage and muscle metabolism, which may ultimately impact capacity for muscle growth. Additional analyses will be conducted to assess protein synthesis signaling pathways and muscle contractile and metabolic phenotype.

Abstract #38

Impaired autophagosome formation and autophagy in skeletal muscle of aged American Quarter Horses

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In our previous study, we found that mitochondrial (mt) function decreased with age in equine skeletal muscle. One underlying cause for the age-related mt dysfunction could be an impairment of mt quality control mechanisms. Mitochondrial turnover by biogenesis and selective degradation of damaged mitochondria (autophagy) are two prominent quality control mechanisms that have been described. The objective of this study was to investigate mechanisms underlying the age-related decline in mt function in equine skeletal muscle by analyzing mRNA and protein level of factors involved in mt biogenesis (PGC-1α, Tfam, NRF-1) and autophagic activity (LC3, LAMP-2, SQSTM/p62). Muscle biopsies of the *gluteus* and *triceps* muscles were collected from young (1.8±0.1 y; n=24) and aged (20±5 y; n=12) American Quarter Horses, subsequently frozen in liquid nitrogen and stored at -80°C until further analysis using qRT-PCR and Western Blot. The mRNA level of the master regulator PGC-1α and its downstream target Tfam were decreased with age in *triceps* muscle ($P<0.05$ for both). In either muscle, mRNA level of NRF-1, ND1, COX1, and COX2 did not differ between young and old horses. However, consistent with decreased mt biogenesis suggested by decreased mRNA level of PGC-1α and Tfam, protein expression of citrate synthase (a marker of mt content) was decreased in aged *triceps* muscle ($P<0.05$). Age was associated with an increased mRNA expression of the autophagy marker LC3 in *gluteus* muscle ($P<0.001$), but had no effect on mRNA expression of the lysosomal membrane marker LAMP-2. The accumulation of the autophagosome cargo protein SQSTM/p62 was observed in both *gluteus* and *triceps* muscle ($P<0.05$ for both). Moreover, the increased SQSTM/p62 level in *triceps* muscle was accompanied by decreased protein levels of Atg5 ($P<0.05$) and the autophagosome-bound form of LC3 (LC3-II; $P<0.05$), suggesting impaired autophagosome formation and processing in aged skeletal muscle. Taken together, our data suggest that mitochondrial biogenesis and autophagic turnover were impacted by age in equine *triceps* muscle.

Assessing the molecular phylogeny, evolution and conservation of male gametes across the Afrotheria Taxa

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Sperm undergo intense and varied selections to ensure they are fertilization-competent. Our goal is to analyze sperm characteristics across taxa to investigate differences in spermatozoa between two related species. This study will compare sperm cell characteristics between the Asian elephant and the Florida manatee from the Afrotheria taxa, which are both threatened with extinction. Insight gained is expected to help lead to advanced sperm protocols and techniques for preservation of these gametes in these threatened species. The use of assisted reproductive techniques (ART) can be used to help increase the reproduction rates in these species and preserve genetic diversity. Our first objective will be to compare basic sperm parameters and morphology between manatees and elephants using computer assisted sperm analysis (CASA) and Diff-Quik staining. Our second objective will be to investigate the lipidomics of the sperm cell of elephants and manatees prior to, and after the cryopreservation process of semen through liquid chromatography–mass spectrometry (LC-MS) and nuclear magnetic resonance (NMR). Our central hypotheses are evolutionary conservation of sperm characteristics, such as sperm morphology and lipidomics, will be observed across Afrotheria taxonomy. Furthermore, we predict detrimental changes to the sperm lipidome will be observed after the cryopreservation process in both species. Semen samples will be collected from ten elephants from the Center for Elephant Conservation in Polk City, FL and 4 Manatees; 1 from Puerto Rico and 3 from Mexico. Basic sperm parameters and the lipidome will be assessed on fresh (raw), extended, and thawed samples after cryopreservation for within species and across species comparisons. Data from this study is expected to offer insight into the evolution of male gametes from this taxa and has potential to provide important insight into the cryopreservation process. These data are expected to provide a foundation for further research on optimizing cryopreservation protocols. Ultimately, we will provide new perspectives on which male spermatozoa traits have been conserved across the Afrotheria taxonomy.

Ruminal in situ degradability and in vitro organic matter digestibility of peanut hulls under different incubation times with calcium oxide

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Two experiments were conducted to evaluate the effects of calcium oxide (CaO) and different DM contents on ruminal in situ degradability and on in vitro OM digestibility (IVOMD) of peanut hulls (PH). In Exp. 1, PH were incubated in duplicate (2 consecutive years) in 20-L buckets following the treatments: 1) as is; 2) 50% DM for 7 d; 3) 50% DM for 14 d; 4) 50% DM + 5% CaO for 7 d; and 5) 50% DM + 5% CaO for 14 d. After 7 or 14 d of incubation, buckets contents were dried and ground to pass a 4-mm screen. Ruminal in situ degradability of DM, OM, NDF, and ADF of PH, either treated or not with CaO was determined by incubating nylon bags for 24, 48, and 72 h in duplicate, in 9 ruminally cannulated steers consuming bahiagrass hay. In Exp. 2 PH were incubated in 20-L buckets (2/treatment) following the treatments: 1) 70% DM; 2) 70% DM + 5% CaO; 3) 50% DM; 4) 50% DM + 5% CaO. Buckets were opened after 3, 6, 9, 12, and 15 d of incubation when a representative sample was collected, dried, ground (2 mm) and incubated for 48 h to determine IVOMD. For Exp. 1 data were analyzed as a randomized complete block design, using bucket as the experimental unit. The model included the fixed effect of treatment and random effect of year. For Exp. 2 data were analyzed as a completely randomized design with repeated measures and the model included the fixed effects of DM content, CaO, incubation days, and their interactions. For Exp. 1, at all ruminal incubation time points, no differences ($P > 0.05$) were observed on in situ degradability of DM, OM, NDF, and ADF. For Exp. 2, no effect of DM content ($P = 0.64$), CaO ($P = 0.27$) or their interaction ($P = 0.33$) were observed; however, there was a CaO × day of incubation interaction ($P = 0.07$) where, when CaO was added, IVOMD was greatest at 6 d of incubation and, up to 15 d of incubation, it decreased significantly. We conclude that treating peanut hulls with CaO was not effective at improving in situ ruminal degradability of nutrients. Moreover, regardless of moisture content, when peanut hulls were treated with CaO and incubated for more than 6 d, IVOMD was affected negatively.

Abstract #41

Genetics of thermotolerance in Brangus heifers – the role of sweating rate and coat score

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Cattle raised in tropical and subtropical environments are exposed to harsh environmental conditions. Heat stress can drastically limit the production efficiency of cattle raised under these conditions. With the forecasted global climate change, heat stress will increasingly impact beef cattle production around the world. Thermotolerance, the ability to maintain optimal growth, feed intake, and reproduction in the presence of heat stress, varies among individual animals and breeds. The overall goal of this study is to identify genetic markers associated with thermal tolerance, thus allowing genetic selection for improved thermotolerance in cattle herds exposed to high temperatures. Interactions of beef cattle with their thermal environment begins at the skin–hair coat interface. A temperature gradient is formed between the hair-coat surface and the skin when an animal is exposed to environmental heat making the hair coat a factor that can affect the rate of heat dispersion. The length of the hair coat affects conductive, convective and evaporative loss of heat from the skin. The color of the hair coat affects absorption of solar radiation. Sweating is one of the primary autonomic responses exhibited by cattle under heat stress. It allows heat loss through evaporation of water from the skin (sweating). When air temperatures are between 10° and 20°C, perspiration is responsible for 20 to 30% of total heat loss, but when temperatures exceed 30°C, it becomes the dominant mode of heat loss, accounting for approximately 85% of total heat loss, with the rest due to respiratory evaporation. The study was conducted with a total of 724 two-year old Brangus heifers. Each animal was assigned a coat score of 1-4 based on a visual assessment of the length and thickness of the hair coat. Coat scores are as follows: (1) excessively smooth, (2) fairly smooth, (3) long coat, and (4) wooly coat. Hair coat color was also recorded. In addition, hair samples were collected by pulling a small section of hair off the back. Hair length and thickness will be measured using computer software. Perspiration rate was measured using a Vapometer (Delphin Tech. Ltd., Kuopio, Finland), which is a digital moisture sensor that calculates water lost through the skin. Additionally, vaginal temperature was measured every five minutes for five days by I-button data loggers attached to a blank CIDR. A blood sample was collected from each heifer, which will be used for DNA extraction and genotyping. Data on weight, and temperament of each heifer was also recorded. Additionally, breeding records will be collected after artificial insemination. Environmental variables such as humidity and temperature in the sun and shade was also collected through the course of the experiment with the use of HOBO data loggers.

Abstract #42

Effect of Fermenten on nitrogen metabolism and ruminal fermentation profile of Angus crossbred steers

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Our objective was to assess the effect of two inclusion rates of Fermenten (FER, Church & Dwight Co., Inc., Princeton, NJ) on ruminal fermentation profile, BUN and nutrient apparent total tract digestibility of Angus crossbred steers. Eight steers, fitted with ruminal cannulas, were randomly assigned to a switchback design. Steers were fed a basal diet (92% TMR) and two different top-dressed premixes (8% TMR): soybean hulls and FER (4% inclusion rate of FER in TMR, 4% FER), or soybean meal and CGF (0% inclusion rate of FER in TMR, CTL). Diets were isoenergetic (69% TDN) and similar in RDP content (6.5% of DM), and were individually fed at 2.8% of BW. Individual intake was recorded using the GrowSafe System. Samples of ruminal fluid and blood were collected for 24 h, before feeding (0 h) and every 3 h, to determine ruminal pH, NH_3-N and VFA concentrations, and serum levels of BUN. Apparent total tract digestibility of nutrients was measured using indigestible NDF (iNDF) as an internal marker. Data were analyzed using the MIXED Procedure of SAS using steer as the experimental unit. Ruminal pH, VFA and NH_3-N concentrations and BUN were analyzed as repeated measures using the MIXED procedure of SAS. A treatment × time interaction tended to be significant for ruminal pH ($P = 0.09$). Steers in the 4% FER treatment had increased butyrate concentration ($P = 0.01$) and a tendency for lower acetate concentration ($P = 0.06$). Steers receiving 4% FER had decreased intake of all nutrients ($P < 0.05$), as well as a decreased DMI as %BW ($P = 0.03$). Apparent total tract nutrient digestibility was similar between treatments ($P > 0.05$), except for CP, which was greater for 4% FER treatment ($P = 0.012$). Decreased intake may hinder possible effects of FER on ruminal fermentation parameters, N metabolism, and nutrient digestibility.

Abstract #43

Administration of high concentrate Lutalyse in replacement beef heifers and the effects on estrus response and pregnancy rates

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To evaluate the effects of high concentrate Lutalyse (PG; Lutalyse, dinoprost tromethamine, Zoetis Animal Health) compared with conventional Lutalyse, 841 crossbred, beef heifers were enrolled in the study at 8 locations over the period of April 1 to July 15. Herd size ranged from 50 to 224 heifers. All heifers were exposed to the 7-day CO-Synch + CIDR protocol. Briefly, on d -7 heifers received a received 100 µg of GnRH (Factrel, gonadorelin hydrochloride, Zoetis Animal Health), a controlled internal drug releasing (CIDR) insert containing 1.38 g of progesterone (Pfizer Animal Health, New York, NY) for 7 d, PGF2α (PG; Lutalyse, dinoprost tromethamine, Zoetis Animal Health) at CIDR insert removal, and followed 54 h later by a second injection of GnRH and fixed-time AI (TAI). On day 0, at CIDR removal, within location, all eligible heifers randomly received one of two PGF treatments: 1) CONTROL (n = 417); heifers received a conventional 25 mg (5 mL) PG dose, administered i.m.; or 2) HiCON (n = 424); heifers received a high concentrated dose 12.5 mg (2 mL) PG dose, administered s.c. Estrus alert patches were placed on all heifers on d 0 and evaluated for estrual activity prior to TAI. Pregnancy was diagnosed by transrectal ultrasonography between 35 and 55 d after AI to determine the presence of a viable embryo, thereby assessing AI pregnancy rates. The percentage of heifers exhibiting estrus between CIDR removal and TAI differed ($P < 0.001$) among locations and ranged from 35% to 65%. The percentage of heifers exhibiting estrus between d 0 (CIDR removal) and TAI did not differ between CONTROL and HiCON treatments. In addition, although pregnancy rates differed ($P < 0.014$) among locations, pregnancy rates were similar between treatments.

The role of MHC Class II DRA gene in resistance of sheep and goats to *Haemonchus contortus*

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The immune mechanisms of resistance acquisition by sheep and goats to gastrointestinal nematodes are still unclear. Both innate and adaptive responses protect the host from *Haemonchus contortus* infections. In this context, the major histocompatibility complex (MHC) represents one of the most polymorphic protein-encoding loci associated with the peptide-antigen binding in small ruminants and vertebrates. The need to respond to pathogens such as gastrointestinal nematodes that evade immune responses led to high allelic diversity observed at ovine MHC loci. The ovine MHC Class II DR Alpha (DRA) locus plays a central role in the immune system by presenting peptides derived from extracellular proteins and is considered less polymorphic. Thus, only three allele sequences have been reported in sheep with few non-synonymous substitutions. In order to identify substitutions associated with the control of nematode populations within the host, the detection of single nucleotide polymorphisms (SNPs) in the OLA-DRA20 gene was performed in sheep and goats experimentally infected with *H. contortus*. Animals from 3 different breeds of sheep and goats were used for the study during three years of evaluation. Animals were dewormed with levamisole (12.5 mg/kg of live weight) and albendazole (10 mg/kg of live weight). Each experimental animal was infected with 10,000 L3 of *H. contortus* per kg of body weight per oral route and fecal samples were obtained to determine fecal egg count. Blood samples were collected to evaluate blood package cell volume (PCV) and to isolate DNA using DNeasy Blood & Tissue Kit (Qiagen). One SNP in the OLA-DRA20 gene segregating in this population was analyzed using High Resolution Melting assays and three genotypes were observed (AA, GA, GG). A GLM was fitted with MPCV, DMI, ADG, specie, year, breed and genotype as predictors and a mean of FEC as the response variable. According to the results, the best significant predictors were Genotype, Breed (Species), Specie and Year ($p < 0.05$). In conclusion, the polymorphism in the OLA-DRA20 gene could have an important role in the immune mechanisms against *H. contortus* infections in sheep and goats.

Abstract #45

Effects of the level and duration of dietary cation-anion difference in prepartum diets on calf growth, immunity and mineral metabolism

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There is limited information on how the metabolic acidosis caused by feeding acidogenic salts to dairy cows prepartum impact the growing calf in-utero and postnatally. Objectives were to evaluate measures of innate immunity, mineral metabolism and growth of calves born from cows fed different negative dietary cation-anion difference (**-DCAD**) diets prepartum. The experimental design was a randomized block design with a 2x2 factorial arrangement of *two levels* of -DCAD: -70 (**HI**) or -180 (**LO**) mEq/kg; and *two feeding durations:* 21d (short, **S**) or 42d (long, **L**) prepartum. Body weight was recorded at birth and weaning (d42). Blood was collected on d 0, 1, 2 and 3 after birth to measure ionized calcium (**iCa**) and pH. Hematological analyses were performed on d0, 1, 2, 3, 21 and 42. Data was analyzed by ANOVA, with d as repeated measures (SAS). At birth heifers born from L dams tended to weigh less compared with heifers from S dams (39.8 vs. 43.4 kg±0.87, P=0.07), and this effect was mainly caused by shorter gestation length for L compared with S cows (274 vs. 277 d±0.7, P=0.02). However, calves born to L dams had greater ADG compared with calves from S dams (0.86 vs. 0.75 kg/day±0.06, P=0.04). Calves born to LO dams had increased iCa concentrations from d0 to 3 (1.28 to 1.34±0.016 mM) compared to calves born to HI dams. Total calcium was not affected by dietary treatments but it gradually increased during the first 3 d of life and then decreased on d21 and 42 (3.03 and 2.87 mM, P<0.01). At birth, calves from HI dams had lower blood pH compared with calves from LO dams (7.28 and 7.33±0.015, respectively; P=0.04). Blood concentrations of leukocytes was less in the first days of life (8.47 K/uL±0.63) compared with d21 and 42 (11.7±0.61 K/uL), but there was no difference between treatments. Neutrophil counts and serum immunoglobulin G titers, did not differ between treatments or across d after birth. Extending the duration or exacerbating the level of maternal DCAD diets prepartum might impact the offspring's growth and mineral metabolism postnatally.

Abstract #46

Cytokine driven monocyte differentiation influences the vitamin D pathway-induced antimicrobial response

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Vitamin D deficiency is prevalent in some cattle populations and may be a contributing factor in incidence of infectious diseases of cattle. Toll-like receptor signaling activates the vitamin D pathway in bovine monocytes with up-regulation of *CYP27B1* and suppression of *CYP24A1* genes, resulting in increased production of the bioactive 1,25-dihydroxyvitamin D_3. The 1,25-dihydroxyvitamin D_3 subsequently up-regulates expression of inducible nitric oxide synthase (*iNOS*) and β-defensin genes. However, the effects of host cytokines on activation of the vitamin D pathway and vitamin D-mediated host-defense responses of bovine monocytes were unknown. Therefore, the objective of this study was to investigate the effects of immunostimulatory cytokines on vitamin D signaling in bovine monocytes. Peripheral blood monocytes were cultured for 12 h with colony-stimulating factor 2 (CSF2; 0, 0.1,1 & 10 ng/mL), interferon gamma (IFN-□ 0, 0.1, 1 & 10 ng/mL) or interleukin 4 (IL4; 0, 5, 50 & 500 ng/mL) in combination with 25-hydroxyvitamin D_3 (25D; 0 and 75 ng/mL). Responses of the vitamin D pathway, *iNOS* and β-defensin gene expression were evaluated by qPCR. CSF2, IFN-□□and IL-4 increased *CYP27B1* and decreased *CYP24A1* gene expression, indicating that each cytokine serves to activate the vitamin D pathway. CSF2 and IFN-□□stimulated *iNOS* expression, which was further increased with the addition of $25D_3$. In contrast, IL4 drastically decreased *iNOS* gene expression in the absence or presence of $25D_3$. In the absence of cytokine stimulation, $25D_3$ treatment increased β-defensin expression, however, CSF2, IFN-□□and IL4 decreased β-defensin expression relative to non-stimulated cultures. In conclusion, CSF2, IFN-□□and IL4 activate the vitamin D pathway in bovine monocytes, but have differential effects on vitamin D-mediated induction of *iNOS* and β-defensin expression. Our results indicate that both vitamin D and immunostimulatory cytokines influence host-defense responses of bovine monocytes, and that vitamin D deficiency may compromise disease resistance of cattle.

Abstract #47

Phenotyping Equine Metabolic Syndrome in Arabian horses in Florida

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Equine Metabolic Syndrome is signaled by obesity and hyperinsulinemia and often leads to secondary laminitis. Identifying the EMS phenotype is difficult yet crucial to diagnosis and prevention. We collected phenotype data from Arabian horses over age 10, residing in Florida with a history of obesity and EMS as well as healthy controls. Endocrine (leptin, ACTH, insulin), lipids, and glucose testing was completed via blood collected intravenously from each horse (n=64), and body measures used to create a neck circumference/height (NC/H) and heart girth circumference/height (HG/H) ratios for obesity estimates. Henneke Body Condition Scores assigned to each horse by owners and an average score from 3 researchers (AVG BCS), were compared. On average, owner assigned BCS was 0.958 points lower than scores assigned by researchers to the same animal, indicating that owners tend to underestimate obesity in their animals. To create an overall score of obesity we performed a Principle Component Analysis (PCA) followed by factor rotation on nine variables: Age, NC/H, HG/H, AVG BCS, ACTH, leptin, glucose:insulin ratio, triglycerides, and cholesterol. Factor 1 positively associated with measures of obesity, while, Factor 2 captured variation in age, ACTH, and cholesterol, three indicators of Pituitary Pars Intermedia Dysfunction, a condition distinct from EMS, but often found among older horses. We conclude that owners may benefit from use of the objective HG/H and NC/H measures in assessing obesity in their animals, as opposed to the qualitative BCS. Also, when diagnosing EMS, multiple factors should be evaluated including endocrine and lipid testing along with body measurements to decipher if a horse is affected by EMS, PPID or a combination of both. The Factor scores calculated here could be applied clinically to objectively diagnose EMS in the context of the spectrum of symptoms associated with the condition.

Functional characterization of bacterial expansin that synergistically increased hydrolysis of cellulose by cellulase

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The objective of this study was to examine if bacterial expansin (BsEXLX1) isolated from *Bacillus subtillis* could synergistically improve cellulose degradation mediated by purified cellulase and exogenous fibrolytic enzymes (EFE). Experiment 1 and 2 examined if BsEXLX1 in combination with cellulase from *Trichoderma reesei* would synergistically improve purified cellulose hydrolysis at different pH (3, 4, 4.8, 5, 6, 7, 8 and 9) and temperature (30, 35, 40 and 50 °C) levels, respectively. Experiment 3 evaluated the efficacy of BsEXLX1 in improving cellulose hydrolysis mediated by EFE (combination of cellulase and xylanase) at rumen conditions (pH 6 and 39 °C) in three independent runs. Treatments for Experiment 1 and 2 included 1) Control, 2) cellulase (20 µg /g substrate), and 3) cellulase (20 µg /g substrate) + BsEXLX1 (100 µg/g substrate) while treatments for Experiment 3 included 1) Control, 2) EFE (-233 µg /g substrate), and 3) EFE (233 µg /g substrate) + BsEXLX1 (100 µg/g substrate). Carboxymethyl cellulose was used as substrate (20 mg/g) for Experiment 1 and 2 while corn silage (100 mg) and bermudagrass silage (100 mg) was used as substrate for Experiment 3. Sugar released was measured as mg/ g of substrate after 12 h incubation. Data were analysed using the GLM procedure of R. Bacterial expansins in combination with cellulases synergistically increased ($P < 0.05$) cellulose hydrolysis at pH 4, 4.8, 5, and 6 by 31, 14, 43, and 44%, respectively. Similarly, cellulose hydrolysis was increased by 8, 45, 8, and 7% at 30, 35, 40 and 50 °C, respectively. The combination of EFE and BsEXLX1 at rumen conditions synergistically increased sugar release by 24 and 14 % ($P < 0.05$) compared to EFE using corn silage and bermudagrass silage, respectively. Bacterial expansin could be potentially used as feed additive to improve animal performance or nutritive value of silages.

Use of a fluorescent glucose analog (2-NBDG) to identify uncultured rumen bacteria that use glucose

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Most rumen bacteria are uncultured, making their niche in the rumen difficult to identify. Fluorescent substrates could potentially identify the substrates preferences and niche of these uncultured bacteria, but uptake of these substrates by rumen bacteria has not been evaluated. Our objective was to determine if a fluorescent substrate analog of glucose (2-NBDG) would be taken up by cultured and mixed rumen bacteria. When we incubated cultured species of rumen bacteria in 2-NBDG (0 to 100 μM) and monitored uptake with fluorimetry, we could detect uptake by the five of the twelve glucose-utilizing species tested. Across these five strains, V_{max} (maximal velocity of transport) was 3.19 (0.98 SEM) nmol mg protein^{-1} min^{-1} and K_m (Michaelis constant) was 1.24 (0.41 SEM) μM. These five species possessed the same type of glucose transporter (mannose phosphotransferase system [PTS]), and experiments with genetic mutants confirmed that this transporter was responsible for 2-NBDG uptake. When we incubated mixed rumen bacteria prepared from rumen fluid with 2-NBDG, we could detect uptake with fluorimetry, but V_{max} (0.180 [0.05 SEM] nmol mg protein^{-1} min^{-1}) was relatively low and K_m (6.37 [4.86 SEM] μM) was relatively high compared to the pure cultures. Uptake could also be detected by flow cytometry, with 18.5% of cells positive. Ongoing work is attempting to 1) separate 2-NBDG positive cells by cell sorting and them with DNA sequencing and 2) develop new analogs to target glucose-utilizing bacteria that do not take up 2-NBDG. In sum, 2-NBDG is taken up by some rumen bacteria that use glucose (those with a mannose PTS), and in combination with other fluorescent glucose analogs, could be used to identify uncultured rumen bacteria that use glucose.

Prediction of dairy cow retention pay-offs with K-Nearest Neighbors methods

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A dairy cow retention pay-off (RPO) is the value of keeping a cow in the herd until the optimal time of her replacement compared to immediate replacement with a heifer. Ranking cows by RPO aids culling decisions. Herd specific input variables such as heifer price affect the RPO. The RPO of all cows in a herd are traditionally calculated by stochastic dynamic programming models. Practical implementation of the software remains difficult. Alternatively, a large data set of pre-calculated RPO might be useful if it can predict the RPO for cows in new herds with sufficient accuracy. Objective was to investigate the K-Nearest Neighbor (**KNN**) method to predict RPO for new herds. Given a set of herd input variables, 2304 RPO are calculated for non-pregnant cows varying by parity (12), month in milk (24), and relative level of milk yield (8) with a stochastic dynamic programming model. We calculated the RPO for 500 sets of input variables which varied randomly by herd inputs heifer price, calf price, and body weight price (n=1,152,000 RPO). The mean of actual RPO in the 500 sets was $71 (min -$492, max $4,017). The data were divided into a training collection (450 sets) and a test collection (50 sets), all with known RPO. The KNN method calculates similarity by (weighted) Euclidian distance between the herd inputs in the test collection and the herd inputs in the 450 sets in the training collection and selects those k=5 training herd sets with the best similarity (the 5 nearest neighbors). The RPO for each test set were predicted by 3 variants of KNN: simple average of 5 RPO (**KNNs**), average of 5 RPO weighted by simple Euclidean distances (**KNNw**), and simple average of 5 RPO from training sets selected after weighing Euclidean distances by linear regression F-values of the 3 predictors (**KNNf**). Performances of each method were assessed by calculating similarity measures of the 2304 RPO in the test set and the equivalent predicted RPO: standard deviation (**SD**), root mean square error (**RMSE**), relative absolute error (**RAE**), and minimum and maximum prediction errors. Results are shown in Table 1. The KNNf method had the best results. Although average prediction errors were sufficiently small, some large prediction errors remained. Further improvements in the method are possible.

Table 1. Performance results of 50 test sets with the 3 K-Nearest Neighbors methods

Criteria	KNNs			KNNw			KNNf		
	Min	Mean	Max	Min	Mean	Max	Min	Mean	Max
SD	1.75	12.47	34.99	1.08	10.55	33.34	0.85	9.66	27.37
RMSE	2.14	15.22	42.29	1.37	12.88	40.24	0.86	12.03	36.90
RAE	0.36%	2.96%	11.49%	0.27%	2.50%	9.84%	0.13%	2.35%	7.75%
Min err	-213	-37	4	-180	-31	3	-131	-25	7
Max err	-8	29	132	-7	26	129	-5	27	157

Abstract #51

Florida Heifer Development Program: An extension project for educating producers and the development of beef heifers in the North Florida region

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The Florida Heifer Development Program is a new extension program with the purpose of engaging beef cattle producers in the learning of reproductive management and replacement heifer development strategies. The program will facilitate replacement heifer development while providing the producer data to assess potential lifetime productivity of individual heifers. Research-based data in the field of beef nutrition and reproductive physiology will be utilized to develop heifers consigned by producers from the North Florida region. Heifers will be required to weigh 1.75 lb per day of age, being a minimum of 535 lb at time of delivery to the NFREC Beef Unit. Registered, purebred or commercial bred heifers are eligible, but must be 10 to 14 months of age upon arrival. The nutrition portion of the program includes incorporating pasture grazing, free choice hay, and a supplement ration formulated for a target gain between 1.50 and 2.25 lb per day. Heifers will be enrolled in a fixed-time artificial insemination protocol and then be exposed to natural service for a minimum of 45 days following AI. Pregnancy diagnosis will be confirmed by ultrasonography within 120 days from time of breeding. Producers will be able to assess the individual heifers and evaluate potential as replacement females by evaluating additional development parameters made available through the program: frame score, pelvic area, reproductive tract score, pre-breeding cyclicity, adequate growth, and the ability to conceive and maintain pregnancy. At conclusion, producers will be surveyed to assess the overall perceived benefit of the program to track producer adoption of the recommended management practices enlisted in Florida Heifer Development Program. The end goal is to yield pregnant heifers and to assist beef cattle producers in the region as a means of increasing their positive impact on the beef industry.

Abstract #52

The Antimicrobial Effects of Buffered Vinegar and Lauric Acid against Salmonella spp. on Commercial Broiler Poultry

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Food safety is an ongoing struggle and studies have proven that poultry is the leading commodity that is responsible for many foodborne outbreaks. To reassure human health and reduce economics losses, numerous studies have tested a wide variety of approaches to sanitize meat and poultry products after harvesting. These methods include but are not limited to cold and hot water rinses, steam pasteurization or steam vacuum treatment, trimming, a variety of chemical rinses including chlorine or chlorine dioxide, ozonated or electrolyzed water, trisodium phosphate, or acidified calcium sulfate, organic acid rinses (eg., lactic, acetic) with or without surfactants, and gamma irradiation or electron beam irradiation. The experimental approach in this study included the evaluation of a buffered dried vinegar ingredient and a lauric acid rinse for controlling *Salmonella* spp. in retail poultry. The antimicrobial effects of buffered dried vinegar and lauric acid were investigated *in vitro*. Salmonella spp. was inoculated into the dried vinegar solutions (0% positive control, 0% negative control, 5, 6, 7, 8, 9, and 10%) and lauric acid solutions (0% positive control, 0% negative control, 0.25, 0.5, and 1.0%). The treatments were analyzed for bacterial total plate count, and *Salmonella*. The results revealed that buffered vinegar (10%) ($p \leq 0.05$) 1.45 log reduction, and lauric acid (1.0%) ($p \leq 0.05$) 1.96 log reduction, had the largest reduction of *Salmonella*. Lauric acid (1.0%) ($p \leq 0.05$) 1.16 log reduction, had the largest reduction of total plate count bacteria and there was no significant difference among the buffered vinegar solutions.

Abstract #53

Pre-weaning injections of bovine somatotropin enhanced puberty attainment of bos indicus-influenced beef heifers

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A 2-yr study evaluated the effects of three pre-weaning 14-d apart injections of bovine somatotropin (bST) on growth and puberty of beef heifers. On d 0 of each yr, Angus × Brangus heifers (n = 15 heifers/treatment/yr; BW = 153 ± 21 kg; age = 135 ± 12 d) were stratified by BW and age, and randomly assigned to receive s.c. injections of saline (**SAL**; 5 mL; 0.9% saline) or half-dose of **bST** (250 mg of sometribove zinc; Posilac, Elanco, Greenfield, IN) on d 0, 14 and 28. Cow-calf pairs were allocated to 4 bahiagrass (*Paspalum notatum*) pastures (7-8 pairs/pasture/yr) from d 0 until weaning (d 127). Unshrunk BW and blood samples were collected on d 0, 14, 28 and 127. From d 127 to 346, heifers were pooled by treatment and allocated to bahiagrass pastures (1 pasture/treatment/yr) and fed blackstrap molasses-based concentrate at 1.1% BW (DM basis). Unshrunk post-weaning BW was obtained every 28 d, and blood samples every 9-10 d to determine plasma progesterone (P4) concentrations. Heifers were considered pubertal when 2 consecutive plasma samples had P4 ≥ 1.5 ng/mL. Each group of heifers was placed with 1 Brangus bull from d 282 to 346. Effects of treatment × yr and treatment × yr × time were not detected for any variable measured in the study ($P \geq 0.11$). During pre-weaning phase, bST heifers had greater mean plasma IGF-1 concentrations (115 vs. 102 ± 3.8 ng/mL; $P = 0.02$) and ADG from d 0 to 42 (1.17 vs. 1.06 ± 0.035 kg/d; $P = 0.01$), but tended to have less ADG from d 42 to 127 than SAL heifers (0.77 vs. 0.84 ± 0.029 kg/d; $P \geq 0.06$). Hence, BW at weaning did not differ between bST and SAL heifers (267 vs. 270 ± 1.70 kg, respectively; $P = 0.58$). During post-weaning phase, bST heifers had similar ADG from d 127 to 347 (0.17 vs. 0.12 ± 0.07 kg/d; $P = 0.11$), BW and age at puberty (290 vs. 291 ± 6.9 kg and 395 vs. 419 ± 14 d, respectively; $P \geq 0.15$), but greater puberty achievement at start of breeding season (63 vs. 44 ± 7.9%; $P = 0.02$) than SAL heifers. Hence, three half-dose injections of bST administered to suckling beef heifers at 14-d intervals may be a feasible management practice to enhance puberty attainment at the start of the breeding season.

Abstract #54

Modeling ammonia emission rate from horses fed different concentrations of dietary crude protein

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Evaluating the impact of animal agriculture on air quality has been the focus of recent research. Ammonia (NH_3) volatilization occurs when excess CP is fed and excreted as urinary nitrogen. Information regarding NH_3 emission from equine facilities is limited, and effects of dietary CP intake on NH_3 emission have not been investigated. Nine mature (562 ± 13.1 kg) geldings were used in a 3 X 3 Latin square design to determine the effects of dietary CP concentration on NH_3 losses from horses fed an all forage diet. We hypothesized that increasing dietary CP would increase NH_3 emission rate. Three diets were formulated using bahiagrass and bermudagrass hays fed at 3 different CP concentrations: LOW-CP, MED-CP, and HIGH-CP (10.6, 11.5, and 12%, respectively). Study periods consisted of an 11 d diet adaptation phase, followed by a 3-d total collection of urine. Samples were pooled within a period by diet (n=3) and mixed with either wheat straw or wood shavings. Ammonia emission of these samples were measured using a 12-vessel emission system with a constant airflow rate at 20^{o}C over a 7 d period. Concentration of NH_3 in each vessel was measured using a photoacoustic multi-gas analyzer. Temperature, airflow rate and NH_3 concentration in each vessel were used to calculate NH_3 emission rate (ER). Data were analyzed as a Latin square using the Mixed Model procedure with repeated measures (JMP Pro v. 11). Concentration and ER data were log transformed. Vessel NH_3 concentrations were different across diets ($P < 0.05$), ranging from 51.8 ppm (LOW-CP) to 87 ppm (HIGH-CP), and bedding types ($P < 0.01$) with straw being higher than shavings (97 vs. 73.5 ppm, respectively). Cumulative urinary NH_3 ER also differed across diets ($P < 0.01$) ranging from 4.9 g/m^2 to 8.2 g/m^2 and bedding types ($P < 0.01$), with straw being higher than shavings (11.1 vs. 6.9 g/m^2, respectively). The results confirm that high crude protein intake and wheat straw bedding increases NH_3 ER from equine urine.

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