2018 PROCEEDINGS OF THE FOURTH UF/IFAS ANIMAL SCIENCES SYMPOSIUM

Courtyard by Marriott St. Augustine Beach
605 A1A Beach Blvd.
St. Augustine, FL 32080

Thursday, November 1st

&

Friday, November 2nd

UF/IFAS ANIMAL SCIENCES

4th Graduate Symposium

WELCOME

Welcome to the fourth UF-IFAS 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 undergraduate students who interned at UF last summer. Thursday evening will include a group photo, wine and cheese reception, a poster session, and a keynote presentation by our distinguished speaker, Dr. Fred Owens, Professor Emeritus of Animal Science, Oklahoma State University. On Friday, we will have the opportunity to listen to more stimulating research presentations and a poster session. Please take this time to learn about other research activities in our department 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 IFAS thank the following for their support of the Fourth Animal Sciences Symposium:

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

Dr. Charles Staples, Interim Chair, Department of Animal Sciences, UF/IFAS

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

L.E. “Red” Larson Endowment

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Pornpamol Pattamanont
Xiaxioa Dai
Jason Rizo

2018 ANIMAL SCIENCES KEYNOTE SPEAKER

Dr. Fred Owens

Born in Wisconsin, Dr. Owens grew up on a beef and swine farm near River Falls. Dr. Owens received his B.S. in animal science and his PhD in ruminant nutrition from the University of Minnesota under the guidance of noted beef cattle nutritionists Dick Goodrich and Jay Meiske. In 1968 he joined the faculty at the University of Illinois where he started his research program on chemical and physical factors regulating synthesis of microbial protein in the rumen. While there, he received the Midwestern Section of ASAS Outstanding Young Scientist Award for Research.

In 1974, Dr. Owens moved to the Animal Science department at Oklahoma State University where he continued his basic ruminant nutrition research program. He worked closely with Dr. Don Gill and many graduate students and post-doctoral fellows on feedlot nutrition. He also taught courses in beef cattle nutrition, fat and carbohydrate metabolism, rumenology, and vitamins and minerals. He developed widely recognized research programs on protein nutrition, feed intake control, grain processing, rumen function, and feed additives. While at OSU, Dr. Owens served as the Ruminant Nutrition Section Editor for the Journal of Animal Science and later as its Editor-in-Chief. He also served on the National Research Council committees that compiled the 1984 Nutrient Requirements of Beef Cattle that is still used by a few traditional nutritionists and the 1985 NRC publication on Nitrogen Metabolism of Ruminants. In 1986, he received the American Feed Industry Association award for research in animal nutrition, and he served as President of the American Society of Animal Science (ASAS) in 1992-93. In 1995 he was named a Fellow of the ASAS and in 1996 received the Morrison Award, which is the highest honor given by ASAS, and in 2010, the Plains Nutrition Council presented Dr. Owens with its Professional Excellence Award.

Dr. Owens has authored or co-authored over 200 referred journal papers including significant review papers on grain processing, acidosis, starch digestion, growth and development, carcass traits, and nitrogen metabolism. Dr. Owens helped organize and edited symposia on Beef Cattle Feed Intake, Protein Nutrition, Grain Processing, and Growth Promoting Implants, each composed of chapters written by invited scientists from around the world. At OSU, he was named the Sarkeys Distinguished Professor in Animal Sciences and Regents Professor, and at his first retirement in 1998 was named Professor Emeritus.

After 24 years at OSU, Dr. Owens began a new career as a Senior Research Nutritionist at DuPont Pioneer Hi-Bred and moved with his family to Iowa. For 18 years at Pioneer, he was involved with developing, testing, and evaluating cereal crops, oilseeds, ensiled feeds, and forage additives that can improve nutrient availability and quality of milk and meat produced by ruminants. In 2016, Dr. Owens retired from Pioneer and moved back to Wisconsin to be near his boyhood home. Since that time, he has worked as a ruminant nutrition consultant in the U.S. and internationally.

4TH UF/IFAS ANIMAL SCIENCES SYMPOSIUM

Courtyard by Marriott
Flagler Rooms A and B
St. Augustine Beach, St. Augustine, Florida
November 1st and November 2nd

Program

THURSDAY, NOVEMBER 1, 2018

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

12:40 **Program.** Faculty, UF/IFAS, Department of Animal Sciences

12:45 **Session 1.** Chairs: Pornpamol Pattamanont and Joel Gutierrez

12:45 Abstract #16: Juliana Ranches (Arthington)
1:00 Abstract #17: Peixin Fan (Jeong)
1:15 Abstract #18: William Ortiz (Bromfield)
1:30 Abstract #19: Teri Williams (Nelson)
1:45 Abstract #20: Bethany Dado-Senn (Laporta)
2:00 Abstract #21: Marcela Marrero-Pérez (Laporta)

2:15 **Break**

2:30 **Session 2.** Chairs: Teri Williams and Marcela Marrero-Pérez

2:30 Abstract #22: Lorrayny Galoro da Silva (Faciola)
2:45 Abstract #23: Joel Leal Gutierrez (Mateescu)
3:00 Abstract #24: Clarissa Harris (Williams)
3:15 Abstract #25: Juan Bollatti (Staples)

3:30 **Break - pick-up room key from Symposium registration table**

3:45 **Collaborative opportunities.** Dr. John Davis, Associate Dean for Research and Associate Director of the Florida Agricultural Experiment Station, UF/IFAS

4:00 **Session 3.** Chairs: Lorrayny Galoro da Silva and Juan Bollatti

4:00 Abstract #26: Cierra Miller, Summer Intern (Laporta)
4:08 Abstract #27: Hannah Hillard, Summer Intern (Brooks)
4:15 Abstract #28: Elizabeth Palmer (Moriel)
4:30 Abstract #29: Zaira Estrada Reyes (Mateescu)
4:45 Abstract #30: Xiaoxia Dai (Faciola)

5:00 **Break**

5:15 **Keynote Speaker:** Dr. Fredric N.Owens

6:00 **Group picture**

6:15 **Session 4. Posters and Reception**

Abstract #1: Sarah Flowers (Mateescu)
Abstract #2: Daianna Torres Astacio, Summer Intern (Ferraretto)
Abstract #3: Jose Arce Cordero (Faciola)
Abstract #4: Pornpamol Pattamanont (De Vries)
Abstract #5: Hugo Monteiro (Faciola)
Abstract #6: Carla Dean Sanford (DiLorenzo)
Abstract #7: Shinyoung Lee (Jeong)

7:00 **Dinner**

FRIDAY, NOVEMBER 2, 2018

7:15 **Breakfast**

7:55 **Program.** Faculty UF/IFAS, Department of Animal Sciences

8:00 **Session 5.** Chairs: Tayler Hansen and Benjamin Saylor

8:00 Abstract #31: Lin Teng (Jeong)
8:15 Abstract #32: Gleise Da Silva (DiLorenzo)
8:30 Abstract #33: Michael Schmitt (De Vries)
8:45 Abstract #34: Lautaro Rostoll Cangiano (DiLorenzo)
9:00 Abstract #35: Kaitlyn Sarlo Davila (Mateescu)
9:15 Abstract #36: Rocio Amorín (Peñagaricano)
9:30 Abstract #37: Ana Caroline Cerqueira de Melo Vasco (Wickens)
9:45 Abstract #38: Adeoye Oyebade (Vyas)

10:00 **Session 6. Posters and Refreshments**

Abstract #08: Alexa Chiroussot (Mateescu)
Abstract #09: Cody McCary (Ferraretto)
Abstract #10: Virginia Neves Brandao (Faciola)
Abstract #11: Ariane Pereira de Sousa (Wohlgemuth)
Abstract #12: Emmanuel Duvalsaint (Vyas)
Abstract #13: Isabella Pachota, Undergraduate (Brooks)
Abstract #14: Taylor Langford (J. Scheffler)
Abstract #15: Federico Podversich (DiLorenzo)

10:45 **Session 7.** Chairs: Xiaoxia Dai and Virginia Neves Brandao

10:45 Abstract #39: Tayler Hansen (Warren)
11:00 Abstract #40: Kelsey Horvath (Miller-Cushon)
11:15 Abstract #41: Benjamin Saylor (Ferraretto)
11:30 Abstract #42: Ali Husnain (Santos)
11:45 Abstract #43: Luara Canal (DiLorenzo)
12:00 Abstract #44: Laura Patterson-Rosa (Brooks)

12:15 **Closing remarks.** Dr. Raluca Mateescu, Graduate Coordinator, UF/IFAS, Department of Animal Sciences,

Abstract #1

Effect of Nutritional Information on Consumers' Willingness-to-Pay for Beef

Sarah Flowers[1], Brandon R. McFadden[2], Chad Carr[1], Raluca G. Mateescu[1,*]

[1]Animal Sciences Department, University of Florida, Gainesville
[2]Food and Resource Economics, University of Florida, Gainesville

Nutritional value impacts consumers' purchasing decisions of food products. Beef is a nutrient rich foodstuff excelling in protein, vitamins, and minerals. There is growing controversy regarding fat content of beef and its healthfulness in the diet. Although much of the fatty acid (FA) content in beef is considered "healthy," many consumers are confused about the different FA. The objective of this study was to determine consumers' knowledge of beef nutritional value and its importance in their purchasing decisions and willingness-to-pay (WTP). A national survey was administered online to over 1,000 respondents. The study asked respondents to choose between two steaks that varied in polyunsaturated and saturated FA levels, iron content, and price. Respondents were asked to categorize "Trans Fat," "Saturated Fat," "Monounsaturated Fat," and "Polyunsaturated Fat," as either "healthy" or "unhealthy." Respondents were asked these questions both before and after an educational excerpt was provided. A WTP taste panel auction was conducted to determine consumers' true WTP dollar value for a steak of improved nutritional value. The results from the survey indicate many consumers are confused about the differences in beef nutritional value, specifically FA content. Initially, only 66.40%, 69.05%, 79.14% and 79.24% of respondents correctly categorized the monounsaturated, polyunsaturated, saturated, and trans fat, respectively. However, a favorable shift occurred and more than 90% of respondents correctly categorized the FA once provided the educational excerpt. Moreover, after the educational excerpt, respondents were WTP a premium for a product of improved FA composition. However, in the WTP taste panel auction when participants had to put forth a monetary value, these premiums were reduced. Our results indicate that relaying healthfulness information to consumers is extremely important to their WTP for beef. These findings provide insight for beef promotion and marketing opportunities.

Abstract #2

Evaluation of washing method, grinding size, and determination of an indigestible fraction on in situ degradation of starch in mature corn grain

Daianna N. T. Astacio, Tatiane Fernandes[1,2], and Luiz F. Ferraretto*

[1]Department of Animal Sciences, University of Florida, Gainesville
[2]Department of Animal Sciences, University of Lavras, Brazil

This study aimed to determine: 1) the most adequate method to estimate the rapidly degradable fraction A; 2) a time-point to measure the indigestible fraction C; and 3) the feasibility of using less time-points to estimate starch fractional disappearance rate (**kd**) of mature corn grain ground through 4 grinding sizes (**GS**; 1, 2, 4, and 6-mm). Different methods were used to determine Fraction A: washing in a bucket or washing machine; rumen immersion plus bucket or washing machine; immersion in water for 30-min plus bucket or washing machine. Indigestible starch (fraction C) were determined through ruminal in situ incubations at 48, 72, 96, and 120 h. Kinetics of starch disappearance were performed at 0 (washing machine), 3, 6, 12, 18, 24, and 48 h. Two or 3-pools models were used and kd was calculated using the linear slope of the 'ln' of bag residues as a proportion of incubated samples over time. Then, effective ruminal disappearance (ERD) was calculated. Data were analyzed using PROC MIXED of SAS, method (either washing or model), GS, and their interaction were considered as fixed effect and cow, or run was considered as random. Fraction A was only affected by GS. Fraction C was greater at samples ground at 6-mm compared to other GS at 48, 72 or 96 h, but not at 120 h. Model affected only fraction B values. As GS increased it was observed greater fraction of B and C. However, kd and ERD were reduced. Samples incubated for 120 h emphasized the lack of a fraction C of starch. Rinsing using washing machine, and time points 0, 3, and 48 h using a 2-pool model are suggested to determine starch degradation kinetics under the conditions of the present study. Grinding size affected starch degradation kinetics, but not fraction A determination.

Abstract #3

Effect of calcium magnesium tetrahydroxide on ruminal pH in a dual-flow continuous culture system

J. A. Arce, H. Monteiro, V. Brandao, X. Dai, M. Nehme, S. Bennet, J. Vinyard, and A. P. Faciola*

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

Ruminal acidosis represents a major issue for modern cattle industry, and some mineral sources may act as potential buffers or neutralizers of ruminal acidity. Supplemental Mg is typically provided as MgO; however, other sources may successfully provide soluble Mg while having greater impact on ruminal pH. This experiment evaluated the effect of $CaMg(OH)_4$ on ruminal pH when fed as a source of Mg in dairy rations in a dual-flow continuous culture system. Experimental diets were formulated by using a common basal ration plus different mineral sources that were added to provide the same concentration of nutrients to all the treatments: 16% CP, 30% NDF, 1.69 MCal ENl/kg, and 0.22% Mg. Four treatments were defined as: 0%OH, 50%OH, 100%OH, and 0.5%Na. The first 3 represented the proportion of supplemental Mg requirement supplied by $CaMg(OH)_4$, and the fourth treatment was a positive control with MgO as the sole source of supplemental Mg plus 0.5% Na sesquicarbonate as a buffer. A 4x4 latin square design was used with 4 periods of 10 d each. Fermenters were fed daily 106 g DM divided in 2 equal meals at 0800 and 1800. On days 8 and 9 of each period, pH was measured at 0, 1, 2, 4, 6, 8, and 10 h post morning feeding. Data for pH kinetics were analyzed with MIXED procedure of SAS as repeated measures. Estimates of h below pH = 6 threshold (pHB6) and area under the pH curve (pHAUC = pH units/10h) were also calculated. Repeated measures analysis showed no differences between treatments (average pH = 6.23). However, pHB6 for 0%OH (3.75 h) was greater than pHB6 for the other 3 treatments which did not differ between each other averaging 1.5 h. Similarly, pHAUC for 0%OH (60.90) was smaller than pHAUC for both 50%OH (62.04) and 0.5%Na (61.98). Orthogonal contrasts indicated an alkaline effect of $CaMg(OH)_4$ supplementation by increasing pHAUC and decreasing pHB6 relative to 0%OH, being similar to the effect observed for 0.5%Na. Effects of $CaMg(OH)_4$ on further ruminal fermentation parameters are currently being analyzed.

Abstract #4

Effects of milk yield and dry period length on milk yield in the subsequent lactation

Pornpamol Pattamanont and Albert De Vries*

Department of Animal Sciences, University of Florida, Gainesville

Dry period length (days dry: **DD**) affects milk yield in the current and subsequent lactation (**SUBLAC**). Our first objective was to develop a milk loss function for the SUBLAC that depends on a continuous function of DD. Our second objective was to quantify the effect of milk yield in the current lactation, combined with DD, on milk loss in the SUBLAC. Milk test records of Holstein cows in parities 1 (current) and 2 (SUBLAC) were obtained from DHIA. The cleaning criteria were last day dry was in 2014 or 2015 and number of test days in parity 1 was at least 6. Gestation length was limited to between 270 and 290 d to have some assurance that a short DD was not the result of premature calving. Milk yield at the dry-off date (**YDO**) was estimated with a Wood's lactation curve. After data cleaning, records for 631,134 cows were available. All models included the independent continuous effects of age at first calving, gestation length, DIM at dry-off, and DIM at last test day in the SUBLAC, and the random effect of herd-year-season of dry-off. Measures of milk yield in the current lactation were cumulative milk yield to last test day before dry-off (**MILKLTDx**) and YDO. Dependent variable was milk yield lactation-to-date (**MILKLTDy**) in the SUBLAC. Milk loss for any DD was estimated as predicted MILKLTDy – predicted MILKLTDy at 60 DD. A model from the literature with MILKLTDx and 16 DD categories was used as a reference model. The same model but with a 4th degree polynomial function of DD had AIC and RMSE that were less than 0.01% smaller, suggesting a good fit. Adding YDO, YDO^2 and DD:YDO decreased the RMSE by 0.7%. For example, at 30 DD and 15 vs. 35 kg/d YDO, milk losses were 840 kg and 1,044 kg. Exclusion of milk yield measures increased the RMSE by 12.4%. In conclusion, MILKLTDx and YDO are relevant predictors of milk loss in the SUBLAC. Milk yield in the current lactation needs to be included in the calculation of milk loss to determine the economically optimal dry period length more accurately.

In vitro ruminal effects of probiotics containing different lactobacillus species in high starch dairy cow diets

H. F. Monteiro[1], J. Arce-Cordero[1], V. N. Brandao[1], A. L. J. Lelis[1], R. Restelatto[2], L. R. Lima[3], L. G. Silva[1], X. Dai[1], and A. P. Faciola[1,*]

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The objective of this study was to evaluate the effects of feeding different live probiotics as a mix of *Lactobacillus acidophilus* and *Propionibacterium freudenreichii* (MIX), or as pure *Lactobacillus plantarum*, at two different doses (PD1 and PD2), in a high starch dairy cow diet. We hypothesized that probiotics containing pure lactic-acid bacteria would improve ruminal fermentation, and would not negatively affect fermentation. Eight-1,830 mL dual-flow continuous culture fermenters were used in a 4 x 4 replicated Latin square design. A basal diet was formulated according to the NRC (2001) based on a cow producing 45 kg of milk/d, and contained 29.3% of starch (DM basis). A single probiotic was added to each basal diet in replacement of corn to compose their respective treatments. Therefore, treatments were: Control (basal diet only), MIX = 0.01% (% of diet DM), and PD1 = 0.05% and PD2 = 0.10% (% of diet DM). Mixed linear models were used to analyze the data, and means were compared using orthogonal contrasts. Probiotics did not affect true digestibility of nutrients, pH, and total VFA and lactic acid concentrations during fermentation. However, there was a trend for greater propionate concentration in PD1 compared to PD2 treatments ($P = 0.06$). Except for NH_3-N, which decreased in all probiotic treatments for both 24 hours pool ($P = 0.05$) and over the day concentrations ($P < 0.01$), the overall N metabolism were not affected by probiotic inclusion. Therefore, in this experiment, besides not having a negative effect on ruminal fermentation, probiotic containing lactic-acid bacteria had similar positive effects in the rumen.

Biweekly administration of recombinant bovine somatotropin during the first trimester of pregnancy failed to alter uterine hemodynamics in suckled beef cows

Carla Sanford[1], Megan Owen[2], Keelee McCarty[2], Luara Canal[1], Francine Ciriaco[1], Darren Henry[3], Tessa Schulmeister[1], Caleb Lemley[2], Nicolas DiLorenzo[1]*, and Cliff Lamb[4]

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[3]Department of Animal Science, Texas A&M University, College Station
[4]Department of Animal and Food Sciences, Texas Tech University, Lubbock

Our objective was to examine the effects of recombinant bovine somatotropin (bST) administration on uterine hemodynamics during gestation. Crossbred beef cows (n = 150) were stratified by breed, days postpartum, parity, estrous cyclicity status, and BCS before being assigned to either bi-weekly injections of bST (BST; 500 mg/14 d) at fixed-timed artificial insemination (TAI; d 0) until d 97 or no bST (CTL). Blood samples were collected biweekly until d 97 for analysis of plasma concentrations of IGF-1. Cow BW and BCS was recorded on d -10, 0, 13, 27, 41, 55, 69, 83, 97, 173, and 233. A subset of pregnant cows (BST, n = 24; CTL, n = 28) were selected for assessment of uterine arterial BF, pulsatility index, and resistance index of the uterine arteries via Doppler ultrasonography on d 97 and 233. Data were analyzed using PROC MIXED of SAS with repeated measures. The model included the fixed effects of treatment, parity and d, and the random effect of cow (treatment parity). No differences ($P < 0.10$) were detected for BW or BCS; however, plasma concentrations of IGF-1 were greater ($P < 0.001$) in BST-treated cows. No differences ($P > 0.10$) were detected for Doppler ultrasonography parameters. A treatment × d interaction ($P = 0.007$) was detected for maximal systolic velocity (Vmax), where no differences were observed on d 97; however, on d 233, Vmax was greater ($P < 0.001$) for BST-treated cows. Mean heart girth diameter, crown-to-rump length, and calf birth weight did not differ ($P > 0.10$). Bi-weekly bST administration increased plasma concentrations of IGF-1 but failed to alter uterine hemodynamics or calf size at birth.

Occurrence and Genomic Characteristics of Cefotaxime Resistant Bacteria in Wildlife

Shinyoung Lee[1,2], Raoul K. Boughton[3], and Kwangcheol Casey Jeong[1,2*]

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Wildlife are important but poorly-studied carriers and sources of antimicrobial resistance bacteria (ARB). Their behaviors can accelerate the dissemination of antibiotic resistance by interacting with livestock, humans, or the environment. However, the transmission of ARBs among livestock, wildlife, and environments is largely unknown. To understand ARB's transmission mechanisms, we characterized ARBs isolated from different niches. We isolated cefotaxime resistant bacteria and extended-spectrum β-lactamase (ESBL)-producing bacteria from cattle (n=48), feral swine (n=52), coyote (n=3), soil (n=6), and water (n=5). The prevalence of ESBL-producing bacteria in cattle, swine, coyote, soil, and water samples was 0.0%, 3.8%, 66.6%, 33.3%, and 20%, respectively. By whole genome sequencing and phylogenetic analysis, we found ESBL-producing *E. coli* from different sources were unlikely transmitted among each other as isolated ESBL-producing *E. coli* from different animals contained distinct genomes, with high number of single nucleotide polymorphisms (SNPs). In addition, plasmid types and ESBL genotypes from feral swine were different to coyote isolates, suggesting antimicrobial resistance against extended-spectrum β-lactams were not mediated by common plasmid. Potentially pathogenic *Pseudomonas* spp., which have diverse virulence factors including toxins and bacterial effector secretion systems, were identified from a coyote. Furthermore, ESBL-producing *E. coli* isolated from a feral swine and a coyote had same sequencing type 155 and 398 with human clinical strains, suggesting clinically relevant pathogens are prevalent in wildlife and they may transmit to livestock and humans.

Hair Phenotype Effect on Thermotolerance of Beef Cattle Evident on SNP in the Prolactin Gene

Alexa M. Chiroussot, Eduardo E. Rodriguez, Kaitlyn Sarlo-Davila and Raluca G. Mateescu*

Department of Animal Science, University of Florida, Gainesville, Fl, USA

Heat stress does not allow maximum genetic potential to be reached, however, some breeds are better suited for subtropical and tropical environments. The slick hair phenotype is known to have a positive impact, making beef cattle more resilient to harsh environmental conditions. Single nucleotide polymorphisms (SNPs) in the prolactin gene and its receptor were identified as associated with the slick phenotype. The SNPs in the prolactin gene are associated with thermoregulation and hair morphology which we know has a significant impact on beef cattle thermotolerance. Hair and blood samples were collected from 262 Brangus cattle from the Seminole Tribe herd in Okeechobee, FL. Each cow was given a coat score: excessively smooth (score 1, n=180), fairly smooth (score 2, n=79), long (score 3, n=2), woolly (score 4, n=1). Five short hairs and five long hairs from each cow were measured using the ImageJ software and the averages of the long and short hairs was subsequently used in the analysis. DNA was extracted from the blood samples and a Polymerase Chain Reaction (PCR) was run on each DNA sample to amplify the region of interest in the prolactin gene. A high resolution melt curve analysis was performed to genotype each cow as Wild Type (AA), Heterozygous (AB) or Homozygous (BB). A statistical analysis was carried out to identify a possible association between the hair length and prolactin genotypes. The SNP in the prolactin gene was significantly associated with the long hair phenotype ($p = 0.02$). LSMeans and standard errors for AA, AB, and BB were 16.46mm (0.375), 15.24mm (0.964), and 13.94mm (0.903) respectively. No significant association was found between the prolactin genotype and the short hair phenotype ($p > 0.05$).

Effect of particle size on in-situ ruminal digestibility of sorghum kernels

Cody L. McCary[1], Celso Heinzen[1], Evan C. Diepersloot[1], Daniella Heredia Castaneda[1], Eduardo M. Paula[1], Luiz F. Ferraretto[1]*

Department of Animal Science, University of Florida[1]

The objective of this study was to evaluate the effects of particle size on ruminal dry matter (DM) and starch digestibility in sorghum kernels. Twenty-five sorghum hybrids were grown at the University of Florida Plant Science Research and Education Unit (Citra, FL) and kernels were collected at various silage maturities. Kernel samples were combined into three 400g composites. Each composite was assigned to either intact, 2, or 4 pieces (1P, 2P, 4P) processing levels. Sorghum kernels were manually cut using X-Acto knives. After cutting, kernels were dried in a forced air oven at 60℃ for 48 hours. Thereafter, geometric mean particle size (GMPS) surface area, and particle size distribution were determined using a Ro-Tap Shaker with 9 sieves of varying nominal square apertures. Additionally, a ruminal in-situ digestion trial was performed, to determine ruminal DM and starch digestibility with 3 lactating Holstein cows at the University of Florida Dairy Research Unit (Gainesville, FL). Incubation times were 0, 6, 12, 48, 120 hours and treatments were triplicated within each cow. Polyester bags containing 5.00 ± 0.02 g of DM, yielding a ratio of sample mass per bag area of 16.6 mg/cm, were utilized to measure fraction A, fraction C, and to estimate the fractional disappearance rate (kd) of fraction B and the effective ruminal disappearance (ERD). Data were analyzed using PROC MIXED of SAS with the fixed effect of treatment and the random effect of cow. Particle separation results indicated a numerically successful reduction of GMPS (2152, 1696, and 1278 µm for 1P, 2P, and 4P, respectively). Reductions in GMPS led to increased ERD of DM (averaged 3.12, 17.8, and 23.9 % DM for 1P, 2P, 4P, respectively) and starch (averaged 15.2, 22.6, 39.7 % of starch for 1P, 2P, 4P, respectively). These results indicate more extensive processing of sorghum kernels improves ruminal DM and starch digestibility through the increase of surface area for microbial attachment and fermentation.

Abstract #10

How does ruminal fermentation affect energy supply? A meta-analytical approach using dual-flow continuous culture system as a model

Virginia Brandao[1] and A. Faciola[1*]

Department of Animal Sciences, University of Florida, Gainesville

Our objective was to evaluate how energy supply is affected by microbial fermentation using dual-flow continuous culture system as a model. A meta-analysis was performed using data from 75 studies. Data were analyzed using linear and non-linear models. Significance levels for fixed and random effects were $P \leq 0.05$. Independent variables were: dietary neutral detergent fiber (NDF) and crude protein (CP), and fermenter dry matter intake (DMI), and dependent variables were: total volatile fatty acids (VFA) concentration, molar proportions of acetate, propionate, and butyrate, true ruminal digestibility of organic matter (OM), CP, and NDF, ammonia nitrogen (NH_3-N) concentration, bacterial-N, dietary-N, and efficiency of microbial protein synthesis (EMPS). Digestibilities of OM, NDF, and CP decreased as fermenter DMI increased. Total VFA linearly increased as DMI increased; exponentially decreased as dietary NDF increased; and was quadratically associated with dietary CP. Total VFA concentration was maximized at 18% dietary CP. Acetate exponentially increased as dietary NDF increased. Propionate linearly increased and exponentially decreased as DMI and dietary NDF increased, respectively. Concentration of NH_3-N quadratically decreased as DMI increased. Bacterial-N and dietary-N increased as DMI increased. Flows of bacterial-N and dietary-N linearly decreased as dietary NDF increased, and dietary-N flow was maximized at 18% CP. EMPS linearly increased as dietary CP increased. Fermenter DMI was mostly associated with increases in energy supply due to greater substrate availability, resulting in increases in total VFA concentration and molar proportion of propionate. Dietary CP affected energy supply by increasing molar proportion of propionate and bacterial-N flow; however, it was positively associated with NH_3-N concentration. Overall, the analysis of this dataset demonstrates that the dual-flow continuous culture system can be a robust, and reliable model to evaluate ruminal fermentation.

Abstract #11

Effects of *in utero* heat stress on mitochondrial function in skeletal muscle of dairy cows

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Environmental heat stress (HS) throughout pregnancy can disturb growth and development of the fetus and impair metabolic regulation and mitochondrial function in postnatal life. The objective of this study was to evaluate the effects of early compared to late gestational HS on skeletal muscle (SKM) metabolic function in adult dairy cows with a focus on mitochondrial (mt) energy metabolism. SKM samples were collected from Holstein cows (F1) born to primiparous dams (F0) bred during the summer (summer-conceived, SC; n=15) or winter (winter-conceived, WC; n=11). F1 cows had been raised identically at the UF Dairy Unit, and biopsies were taken from the *gluteus medius* during early lactation. Lactation and growth measurements were recorded. Mitochondrial respiratory function of the samples was analyzed by high resolution respirometry (OROBOROS O2k, Innsbruck, Austria) using a standard substrate-uncoupler-inhibitor titration protocol to assess different respiratory states (LEAK, L; activated respiration with complex I, P_{CI}; and complex I and II substrates, $P_{CI+II;}$ and maximal respiratory capacity, E). Activity of mitochondrial enzymes (cytochrome C oxidase, citrate synthase and 3-Hydroxyacyl-CoA dehydrogenase) was assessed spectrophotometrically. We compared the two groups using One-Way ANOVA with posthoc analysis (SAS JMP Pro), with significance set at $p \leq 0.05$. No statistical difference was found for enzyme activity or growth parameters. Muscle mitochondria from SC cows tended to have a higher L (p=0.0361), P_{CI} (0.034), P_{CI+II} (p=0.0471) and E (p=0.069). LEAK respiration, which is not associated with ATP production, is oxygen flux compensating for proton and electron leak through the inner mt membrane, and can be associated with membrane composition. Our data suggest that HS during early gestation may affect the composition of the inner mt membrane in SKM, thereby changing bioenergetic efficiency.

Effects of supplementing incremental levels of rumen-protected lysine on lactation performance of dairy cows

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The objective of this study was to evaluate the effects of increasing amounts of N-acetyl L- lysine (NALL, CJ Cheiljdang, Seoul, South Korea) on the performance of lactating dairy cows fed corn silage-based diets. The ruminal escape rate, intestinal digestion coefficient, and lysine concentration of NALL were 29.2%, 91.5%, and 77.7 % respectively. Sixteen lactating multiparous (parity 2 to 3; 60-70 DIM) Holstein dairy cows were used in a 4×4 Latin square design. Diets were formulated using NDS Professional (R.U.M.&N, Reggio Emilia, Italy), a software based on the Cornell Net Carbohydrate and Protein System equations (CNCPS v.6.5) to supply adequate metabolizable energy but deficient in metabolizable lysine (-7 g/d) for dairy cows producing 42 kg/d of milk with 3.80% milk fat, and 3.20% milk protein. Cows were blocked by days in milk and assigned to one of four treatments: (1) **Control** diet (2) 40 g/d NALL **(Lys40)**, (3) 80 g/d NALL **(Lys80)**, and (4) 120 g/d NALL **(Lys120)**. Treatments were applied as top-dress once daily. Data were analyzed using GLIMMIX procedure of SAS (version 9.1). The statistical model included treatment, day and treatment × day interaction. Cow (square) and period (square) were used as random factors. Statistical differences were declared significant at $P \leq 0.05$ and tendencies at $0.05 < P \leq 0.10$. Dry matter intake (DMI) and milk yield tended to be greater with Lys80. No treatment differences were observed on milk protein, milk fat, and milk lactose. However, milk urea nitrogen (MUN) was greater with Lys120 compared with other treatments. In conclusion, NALL supplemented at 80 g/d has potential to improve DMI and milk yield. The efficacy of NALL in improving animal performance should be validated using long-term feeding trials.

Conformational Analysis of Quantitative Measurements in Stock-Type Horses

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Stock-type horses are used for a variety of riding disciplines. While they are primarily the preferred breed for ranch events and trail riding, they are known to compete and excel in disciplines such as pleasure, jumping, and racing. The demands of various disciplines lead to selection of unique conformational traits and therefore a visible variance of body types within the same breed. To understand this variance, we took 35 quantitative conformational measurements on 43 registered Stock-Type horses of 2 years of age. The UF Horse Breeding managers categorized these horses as pleasure, hunter, or ranch type. We performed quantitative facial, limb, and body measurements utilizing a standardized set of conformational landmarks to better determine the muscling and frame of each horse. All horses measured were registered stock-type horses bred in the UF equine sciences breeding program, born from 2012-2016, measured within one week of their second birthday to control for maturity. During measurement, the horse stood haltered on a level surface and allowed to assume a natural, relaxed position. Statistical analysis conducted in JMP v13 (SAS Institute Inc., 2007) determined height ranges from 55in to 64in (mean 58.5) and does not significantly vary based on the year. Yet, cannon lengths seem to be increasingly different per year ($p=0.0392$, ANOVA). There is a shift in height ($p=0.0483$, T-test) from 2014 to 2015. This may be due to a breeding practice more focused on pleasure and hunter type horses. We hypothesize that pleasure type horses will be of median height, build, and muscling with finer limbs. Hunter type horses will be finer muscled and taller with longer, finer limbs and ranch type horses will be shorter, stocky, and heavily muscled with the shortest limbs, comparatively. Data analysis is still ongoing. Future research will look into correlations between the hoof size, body structure, and health history, as previous work suggests that disproportionately small hooves can lead to lameness issues.

Abstract #14

The efficacy of Drying Contaminated Lean Ground Beef in Reducing Salmonella to Improve the Food Safety and Shelf Stability of Ethiopia's Domestic Meat Supply Chain.

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Market structure and inefficiencies in Ethiopia's livestock and meat industries present many food safety issues and contribute to low consumption of animal-sourced foods (ASFs). The use of dehydration to preserve meat would allow Ethiopian butchers the opportunity to improve food safety, shelf stability, and add value to left-over product. In the United States, illnesses due to *Salmonella* and *E. coli* O157:H7 from homemade jerky indicate improvements can still be made to the jerky drying process (USDA, 2016). Raisins have low water activity, acid pH, phenolic acids, and high osmolarity provide antimicrobial activities (Ziemke, 1980), are available in Ethiopia and may improve log reduction of key pathogens. The objective of this study is to develop a procedure for producing a dried beef jerky product, validated to control five Serotypes of *Salmonella enterica*, with the constraints of equipment and ingredients available in Ethiopia. Lean round cuts of beef (94% lean, 6% fat) with salt (2.5%) and Berbere (Ethiopian spice) (2%) were ground and mixed by hand. Pureed raisins were added at 0, 5, 10 and 15% of the overall weight and mixed until evenly distributed throughout product. The ground meat and raisin mixture was inoculated with 9.17 $\log_{10}$ CFU/g cocktail of five *S. enterica* serotypes (Saintpaul, Anatum, Typhimurium, Newport, Dublin), formed into strips and dehydrated using two BioChef® Arizona Sol 9-tray dehydrators to achieve an a_w of <0.7. Dried meat strips (25g) were stomached with 225mL of 0.1% Peptone. Serial dilutions were vortexed, mixed with Tryptic Soy Agar before being overlaid on XLT-4 agar plates and incubated for 18 hours before enumeration. There was a linear effect of raisin inclusion (P=0.0007) on lethality of *S. enterica*. Finished jerky containing 15% raisins had a greater reduction (P<.0001) of *S. enterica* at 5.41 CFU/g. versus the control at (4.44 CFU/g.). Drying ground beef in Ethiopia with additional interventions would be a cost-effective tool for butchers to reduce *S. enterica* loads and improve shelf stability, reduce waste, and increase access to ASFs.

Sorghum silage: Effects of different processing technologies on feed characteristics and animal response

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Sorghum bicolor is a noble crop known for its drought tolerance, soil plasticity, and resistance, and it has been used since ancient times in livestock and human feeding. Despite being a very important agronomic crop, there are certain challenges with the processing of the whole plant when harvested for silage. The breakage of sorghum grain is difficult, mostly because of its size and hardiness of the pericarp, which can impair ruminal microbial degradation and further enzymatic digestion in the small intestine, potentially reducing starch digestibility in the total tract. In the last decade a new silage processor named Shredlage was developed, originally to be used for corn silage to obtain larger theorical length of cut without compromising grain processing. Shredlage has been widely tested for whole plant corn silage, and significant improvements in the quality of the material were obtained compared to the conventional kernel processing. Reported improvements range from 64 to up 88% on in situ starch digestibility for corn silage processed with Shredlage. However, there is no information about Shredlage utilization in sorghum silage, which creates a research opportunity to assess the potential of this technology at improving whole plant digestibility. Therefore, we hypothesize that the use of the Shredlage processor may improve sorghum silage processing and nutrient digestibility. The objective of this project is to conduct a series of experiments to characterize sorghum silage processed by Shredlage vs. a conventional processor, on situ nutrient digestibility and performance of beef cattle. The results from this project would fill the gap of information available for sorghum silage, allowing a better understanding of the processing of sorghum grain, which in turn may promote a wider adoption of this crop in beef cattle production systems.

Low moisture, cooked molasses blocks for limit-creep: A method for supplementing trace minerals to pre-weaned beef calves

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Two studies were conducted at UF/IFAS, Range Cattle Research and Education Center to evaluate, (1) preferential intake of low moisture, cooked molasses blocks (LMB) differing in formulation only by source of Cu, Zn, and Mn, and (2) pre-weaning performance of calves consuming LMB with and without trace mineral fortification. In Exp. 1, 18 calves were placed in 6 bahiagrass paddocks (*Paspalum notatum*; n = 3 /paddock) for 6 wk. Calves were provided concentrate daily at 2% of BW in addition to simultaneous and continuous access to 3 separate LMB fortified with differing sources of Cu, Zn, and Mn (hydroxychloride, sulfate, or organic proteinate). Preferential intake was estimated by disappearance rate. Blocks formulated with hydroxychloride sources had the greatest disappearance when compared to sulfate ($P = 0.03$) and organic ($P = 0.005$) sources. There were no differences ($P = 0.58$) in disappearance rate between sulfate and organic sources (340, 277, and 254 g/calf daily for hydroxychloride, sulfate, and organic sources, respectively; SEM = 45.8). In Exp. 2, 24 cow-calf pairs were placed in 12 bahiagrass pastures (n = 2 /pasture). Calves were provided supplement in cow exclusion areas for 84 d. Treatments consisted of 2 LMB formulations; (1) no added minerals, Control, or (2) 550, 1,650, and 2,200 mg/kg of Cu, Zn, and Mn from hydroxychloride sources; Fortified. Intake was estimated by the disappearance of LMB. Intake was greater ($P < 0.05$) for Control vs. Fortified (395 vs 272 g/calf daily; SEM = 85.5). Despite differences in intake, calf ADG did not differ (0.88 and 0.88 kg/d for Control and Fortified, respectively; SEM = 0.111; $P = 0.97$). Liver biopsy samples were collected from calves at the end of study. Calves consuming Fortified LMB had greater ($P < 0.001$) liver Co, Cu, Mn, Se, and Zn concentrations compared to Control. Additionally, liver Se concentrations were in the deficiency range (< 0.60 mg/kg DM) for calves consuming Control, but not Fortified LMB (0.49 vs 1.19 mg/kg DM; SEM = 0.150). Weaned calves display a preference for consumption of LMB fortified with hydroxychloride vs. sulfate or organic sources of Cu, Zn, and Mn. Pre-weaning supplementation of mineral-fortified LMB is an efficient strategy to improve the trace mineral status of calves.

Development of gut microbiota through life in an Angus-Brahman multibreed herd

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Commensal bacteria in the intestinal tract provide energy for the host and inhibit pathogen colonization. In this study, we investigated the effects of age, host genetics, and environmental factors on the gut microbiota development in an Angus-Brahman multibreed (MAB) herd from birth through entire life. The MAB herd was kept on the pasture before weaning, and steers were transported to a feedlot after weaning, while heifers were still kept on the pasture. We collected fecal samples from 278 calves belonging to the herd at four time points (within 12 hours, 3, 12, and 18 months after birth), and analyzed their gut microbiota structure by using 16S rRNA gene sequencing. Gut microbiota structure was gradually changed, with increased bacterial richness and diversity until stabilized 12 months after birth. However, the gut microbiota was altered dramatically after calves were moved to the feedlot, with decreased bacterial richness and diversity. *Enterobacteriaceae* (50%) and *Clostridaceae* (18%) were most abundant bacterial families right after birth. *Ruminococcaceae* (24%) *and Bacteroidaceae* (13%) became predominant during growth on the pasture, while *Prevotellaceae* (14%) elevated to be the second most abundant family in calves kept in feedlot. The animal weight steadily increased after birth and the growth rate was accelerated in feedlot, which was associated with *Succinivibrionaceae* and *Spirochaetaceae* proportion. We identified relative abundance of numerous bacteria linearly correlated with breed composition during 3~18 months after birth. *Clostridium* showed constant negative correlations with Brahman proportion through life. Similar consistent negative correlations were observed between plasma IgG1 level and Brahman proportion. In conclusion, these results indicate the existence of associations between specific gut commensal bacteria and animal growth and immunity through life. Further studies are needed to uncover the underneath host-microbe interactions.

Effects of intrauterine infusion of seminal plasma at artificial insemination on fertility of lactating Holstein cows.

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An inflammatory response is induced in the reproductive tract by the deposition of semen during natural mating. It has been proposed that this response could facilitate establishment and maintenance of pregnancy by modifying the microenvironment of the reproductive tract. The best evidence for this idea comes from mice where females mated with males lacking seminal vesicles experience reduced conception rates, embryos with poor development to the blastocyst stage, low implantation rates, and offspring with altered postnatal phenotype. Here we hypothesized that intrauterine infusion of 0.5 mL of seminal plasma at the time of artificial insemination (AI) in first-service lactating Holstein cows will improve pregnancy rate per insemination. The experiment was conducted at a commercial dairy farm in north-central Florida during the winter (November to February); voluntary waiting period was 82 d. Cows were inseminated [multiparous cows (n = 1105), conventional semen; primiparous cows (n = 515), X-sorted semen] using the Double Ovsynch protocol. Cows were randomly assigned to receive intrauterine infusion of either 0.5 mL seminal plasma (prepared as a single pool from 44 bulls) or vehicle (saline) immediately after AI. Pregnancy diagnosis was performed at d 32 and d 60 after AI. Data were analyzed by the GLIMMIX procedure of SAS. Pregnancy rate per AI was affected by parity ($P = 0.0030$) and treatment ($P = 0.0586$) but not by the interaction. Least squares means for multiparous cows were 46.9 + 2.8% for vehicle and 45.6 + 2.6% for seminal plasma. Least squares means for primiparous cows were 42.4 + 3.9% for vehicle and 38.4 + 3.8% for seminal plasma. Results do not support a beneficial effect of seminal plasma on pregnancy rate per AI at first service. Further research to evaluate effects of seminal plasma on pregnancy loss and characteristics of the offspring is warranted. *Study supported by Select Sires.*

Abstract #19

Effects of dietary 25-hydroxyvitamin D on vitamin D metabolism and performance of dairy heifers

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Vitamin D plays a role in maintaining calcium and phosphorous homeostasis as well as activating innate immune defenses of cattle. The 25-hydroxyvitamin D metabolite is the precursor to the active vitamin D hormone, 1,25-dihydroxyvitamin D. Feeding 25-hydroxyvitamin D (HyD) is more effective in raising serum 25-hydroxyvitamin D concentrations in mature cows than feeding vitamin D. Effects of both short-term and long-term supplementation need to be tested to see if elevated serum 25-hydroxyvitamin D concentrations from feeding HyD would benefit physiological actions of vitamin D in the body. The effects of 25-hydroxyvitamin D availability on growth, health, and overall production of cattle are unknown. Therefore, the objective of this project is to test the use of dietary HyD on heifer growth, health and performance. One-hundred forty-three Holstein heifer calves were assigned to one of two treatments starting at one to two weeks of age. Control diets were formulated to provide vitamin D_3 at a rate of 1.5 μg/kg BW and HyD diets were supplemented with 1.5 μg/kg BW HyD. Calves were individually fed, either with an automated feeding system, or bucket fed. Calves were supplemented individually. Body weight and height of calves were recorded every seven days for four weeks and then weighed every 14 days. Serum 25(OH)D concentrations of HyD heifers were greater compared to CON (123 vs 44 +/- 6 ng/mL), $P < 0.001$. BW of HyD heifers was 4 kg greater at weaning compared to CON (81.5 vs 77.1 +/- 0.9 kg, $P = 0.02$). Hy D heifers were also heavier than CON at 4 Mo (125.4 vs. 121.7 +/- 0.9 kg; $P = 0.01$). Whither height of HyD heifers tended ($P = 0.06$) greater compared with CON. In conclusion, treating dairy heifers for up to four months with 25-hydroxyvitamin D increased weight gain.

Abstract #20

Effect of pre- and postnatal thermal environment on calf thermoregulation and growth

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Dairy calves exposed to prenatal heat stress experience compromised growth and immune competence compared to those provided prenatal heat abatement (e.g. maternal cooling). We hypothesize that heat stress abatement postnatally will promote dairy calf thermoregulation and improve growth, particularly if dairy calves were also exposed to heat stress abatement prenatally. Holstein calves born to heat-stressed (HT, shade) or cooled (CL, shade, fans and soakers) dams during late gestation (~46 d, temperature-humidity index (THI) ≥ 68) were randomly assigned to four pens and exposed to heat stress (HT, shade) or cooling (CL, shade and fans) for 21d (HTHT, HTCL, CLHT, and CLCL; n=6/treatment). Wind speed and THI were monitored daily. Skin temperature (ear), rectal temperature (RT), and respiration rate (RR) were recorded daily (7:00, AM; 13:00, AF; and 19:00, PM). BW was recorded twice weekly. THI was not different, while wind speed was higher in postnatal cooled vs. heat pens (3.80 vs. 0.25 m/s, $p<0.01$, respectively). Skin temperature was ~3˚C lower throughout the day in postnatal cooled compared to heat stress calves (i.e. AM: 29.4 vs. 32.9 ± 0.28 ˚C, $p<0.01$, respectively). RT did not differ between treatments in the AM and AF, but PM RT tended to be lower for postnatal cooled calves compared to heat stressed calves (39.23 vs. 39.33 ± 0.04 ˚C, $p=0.09$). RR was lower in calves under postnatal cooling compared to those heat stressed in the AM (39 vs. 46 ± 2 bpm, $p=0.03$) and PM (52 vs. 63 ± 3 bpm, $p<0.01$). In the AF, there was an interaction between pre- and postnatal treatments, whereby the HTHT calves had higher RR compared to other treatments (70 vs. 60, 52, and 61 ± 3 bpm for HTHT vs. CLCL, HTCL, and CLHT respectively). Average daily gain did not differ between treatments, and while there was a 2.3 kg difference in birthweight between prenatal treatments, this difference was not statistically significant. This preliminary data indicates that regardless of prenatal conditions, cooling calves postnatally for 21 d improves thermoregulation without affecting average daily gain.

Improving serotonin bioavailability alters serotonin receptor expression on peripheral blood leukocytes of Holstein dairy calves

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Serotonin (**5-HT**), a monoamine derived from L-tryptophan, is naturally produced by peripheral tissues and plays a role in several biological functions, including immunity. Here, we administered a serotonin precursor (5-hydroxy-L-tryptophan, **5-HTP**) or a serotonin reuptake inhibitor (fluoxetine, **FLX**) to modulate 5-HT bioavailability in dairy calves. Bull Holstein calves (21 ± 2 d old) were fed milk replacer (8 L/d) with either saline (**CON**, 8 mL/d, *n*=8), FLX (40 mg/d, *n*=8) or 5-HTP (90 mg/d, *n*=8) for 10 consecutive d in a complete randomized block design. Blood samples were collected at d-1 and daily (d1-10) to measure serotonin concentrations. Leukocytes were isolated from whole blood on d10 and evaluated for transcript abundance of fifteen serotonin receptors and five key enzymes involved in serotonin metabolism using the RT-qPCR Fluidigm Delta Gene assay. Complete blood hematology analysis was assessed on d-1 and 10. Data were analyzed using linear models in R. Blood 5-HT concentrations increased in calves fed 5-HTP starting on d2, and decreased in calves fed FLX starting on d6, compared to CON (6325, 2262 *vs* 3166 ± 710 ng/mL, respectively, treatment by day interaction; $P<0.001$). 5-HTP supplementation upregulated the gene expression of *5-HT1A, 1B, 1D, 1F, 3C, 4* and *MAOA* ($P<0.05$) and tended to upregulate *5-HT2B, 3B, 2C* and *MAOB* ($P<0.09$). FLX supplementation downregulated the gene expression of *5-HT2A* and *3C* ($P<0.05$), upregulated *MAOA* ($P=0.005$), and tended to upregulate *5-HT2C*, 4 and *MAOB* ($P<0.10$). On d10, calves fed 5-HTP or FLX had greater red blood cells counts compared to CON (7.0, 7.5 *vs* 6.3 ± 0.2 x $10^6/\mu L$, respectively; $P=0.02$ and tended to have more circulating neutrophils compared to CON (3.4 *vs* 2.8 ± 0.3 x $10^3/\mu L$, $P=0.06$). FLX fed calves had higher hemoglobin on d10 compared to CON (7.9 *vs* 7.3 ± 0.2 g/dl, $P=0.01$. Increasing 5-HT bioavailability impacts 5-HT receptor profiles on peripheral leukocytes and could potentially modulate the immune system of Holstein dairy calves.

Sodium propionate and sodium butyrate effects on HDACs activity, histone H3 acetylation, and inflammatory gene expression in bovine mammary epithelial cells

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The objective was to evaluate the role of sodium propionate (SP) and sodium butyrate (SB) as histone deacetylase (HDAC)-dependent regulators of inflammatory gene expression in bovine mammary epithelial cells (MAC-Ts). We postulated that SP and SB would inhibit HDAC activity and increase histone acetylation and consequently decrease inflammatory gene expression. For this study, MAC-Ts stimulated with lipopolysaccharide (LPS) were used as a model for bovine mammary inflammation. Cell lysates were incubated with SP or SB (0 to 5 m*M*) prior to HDAC substrates incubation and HDACs activity was determined. Next, cells were pretreated with SP or SB (0 to 3.0 m*M*) prior to LPS (1 µg/mL) stimulation and assessed for histone H3 acetylation. After, cells were pretreated with SP or SB (1m*M*) prior to LPS (1 µg/mL) stimulation. RNA was isolated for inflammatory gene expression evaluation by PCR array and quantitative real-time PCR. One-way ANOVA followed by Tukey post-hoc analysis was conducted and significance set at $P < 0.05$. SP and SB dose-dependently and selectively inhibited class I HDAC activity, which differed between short-chain fatty acids (SCFAs), where SB inhibited HDACs 2, 3, and 8, while SP inhibited HDACs 2 and 8. Histone H3 acetylation was dose-dependently increased by SCFAs. Similarly to the differential regulation of HDAC activity, SCFAs effected differently histone H3 acetylation. However, SP and SB did not decrease overall inflammatory gene expression. Under our conditions, findings suggested that in MAC-Ts, SP and SB regulate epigenetic markers on nucleosomal DNA in addition to regulation of inflammatory gene events independent of HDAC activity. Nevertheless, examination of SCFAs and/or HDACs inhibitors in bovine mammary gland are worth being further investigated to delineate the potential impact of HDAC inhibition and histones hyperacetylation on mammary gland tissue inflammation.

Identification of trait-associated genes related to meat quality using an RNA-seq analysis approach

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A total number of 120 steers born in 2013 and 2014 were analyzed. The animals belonged to the multibreed Angus-Brahman herd from the University of Florida and were classified into six different groups based on their expected Angus composition. Steers were harvested when their subcutaneous fat thickness over the ribeye reached 1.27 cm. Five grams of the *Longissimus* muscle was sampled after splitting the carcass and used for RNA extraction. After 48 hours postmortem, marbling was recorded in the ribeye muscle at the cut surface at the 12th/13th rib interface, and two 2.54 cm steaks from the *Longissimus dorsi* muscle were sampled from each animal, aged for 14 days at 1 to 4°C and cooked at an internal temperature of 71°C. The first steak was used to measure Warner Bratzler shear force (WBSF) and cooking loss, and the second steak was used to measure tenderness, juiciness and connective tissue by sensory panel. A principal component analysis for all recorded phenotypes was performed. The first three principal components were used to construct a meat quality index useful to rank each animal. Eighty animals were selected based on extreme meat quality index. After mRNA isolation and dscDNA synthesis, RNA-seq libraries were sequenced to generate 100 bp paired-end reads. Paired-end reads were mapped using Tophat and Bowtie2 against to the Btau_4.6.1 reference genome. Gene paired-end read counts for all annotated genes were determine using HTSeq including only uniquely mapped paired-end reads to known chromosomes. Robust regression was used for identifying trait-associated genes including the constructed meat quality index as phenotype. The association of gene counts was perform by gene accounting for breed group and year of birth. A total number of 148 genes were associated with the meat quality index (p value < 0.05). In the top twenty, multiple cytoskeletal and transmembrane proteins such as TMEM120B, TMEM186 and SYNJ2 were identified. Additionally, some transcription factors such as WDR77 and NFKB2 were uncovered.

Abstract #24

The Antimicrobial Effects of Lauric Arginate (LAE®) and Ethylenediamine Tetraacetic Acid (EDTA) against *Salmonella* Typhimurium on Skinless Ground Chicken Breast

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Antimicrobials are effective at reducing the risk of foodborne illness when treated during or after processing. Lauric arginate, LAE®, is an innovative and non-toxic food preservative with extremely high antimicrobial activity. Lauric arginate is an active ingredient in combating *Salmonella* and combining it with a novel antimicrobial could make it more effective. The experimental approach in this study evaluated the effects of LAE and EDTA against *Salmonella* Typhimurium on skinless, ground chicken breast. Except for the negative control, the ground chicken meat was inoculated with *Salmonella* Typhimurium (ATCC 13311) and treated with LAE and EDTA. The nine treatments for the chicken meat included no treatment (meat only negative control), meat plus inoculum (positive control), and meat plus inoculum plus 0.25% EDTA, 0.5% LAE, 1% LAE, 2% LAE, and LAE in combination with 0.25% EDTA. The ground chicken meat was packaged in sterile Whirl-Pak bags, stored at 3±1 C and analyzed on days 0, 1, 3, 5, and 7 for *Salmonella*, total psychrotrophs, and pH. The ground chicken meat treated with the combination of 1% and 2% LAE and EDTA resulted in a significant reduction ($P < 0.05$) in *Salmonella* Typhimurium on all days. There was also a significant reduction ($P < 0.05$) in psychrotrophs on day 3 with the LAE and EDTA combinations. The results indicate that adding the LAE and EDTA to the chicken will decrease the growth of *Salmonella* Typhimurium and psychrotrophs over seven days.

Timing of initiation and duration of feeding ruminally-protected choline (RPC) affects performance of lactating Holstein cows.

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The objective was to evaluate the timing of initiation and duration of feeding RPC (ReaShure, Balchem Corp., New Hampton, NY) on dairy cow performance. The experiment was divided into the following 2 periods of time: -21 to 21 DIM and 22 to 105 DIM with data from periods analyzed separately using repeated measures within the MIXED procedure of SAS. From -21 to 21 DIM, multiparous Holstein cows (n = 99) were top-dressed with 0 or 60 g/d of RPC (12.9 g/d choline ion). Starting at 22 DIM, cows were switched to the alternate diet (control to RPC or RPC to control) or maintained on the same diet (control to control or RPC to RPC) resulting in a 2 by 2 factorial arrangement of treatments. Methionine (Perdue Ag Solutions LLC, Salisbury, MD) was formulated to 2.9% of metabolizable protein (MP) in the prepartum diets and to 2.4% of MP in the postpartum (PP) diets. Feeding RPC did not affect prepartum DMI, BW, or BCS (means of 11.7 kg/d, 774 kg, and 3.46, respectively). During the first 21 d PP, RPC did not affect DMI (16.2 vs. 16.4 kg/d; $P = 0.72$) or milk yield (35.1 vs. 36.8 kg/d; $P = 0.13$) of control and RPC-fed cows, respectively. Milk fat % was greater for cows fed RPC (4.41 vs. 4.60%; $P = 0.05$). As a result, cows fed RPC produced more energy-corrected milk (ECM; 39.0 vs. 42.0 kg/d; $P = 0.04$) and feed efficiency (FE; ECM/DMI) was greater (2.44 vs. 2.64, $P = 0.01$). Extent of BW loss was greater by cows fed RPC (35.9 vs. 53 kg, $P < 0.01$). Between 22 and 105 DIM, yield of milk tended to be greater (44.8 vs. 46.8 kg/d; $P = 0.08$) and yield of ECM was greater (43.4 vs. 45.5 kg/d; $P = 0.06$) for cows fed RPC in transition ((control-control + control-RPC) vs. (RPC-control + RPC-RPC), respectively). Feed intake did not differ between treatment groups (23.5 vs. 23.3 kg/d), therefore FE was improved by feeding RPC during transition (1.81 vs. 1.92; $P = 0.01$). Concentration of milk fat (mean of 3.46%) and milk protein (mean of 2.85%) were unchanged by treatments. Initiation of feeding RPC at 22 DIM or extending RPC supplementation beyond 21 DIM did not improve milk yield; however, supplementation of RPC between 21 d prepartum and 21 d PP increased yield of ECM over 15 wk PP.

Abstract #26

Effect of pre- and postnatal thermal environment on calf blood hematology

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Passive and cell-mediated immune function of dairy calves is reduced by prenatal heat stress, resulting in increased susceptibility to diseases during their early postnatal life. The objective of this study was to assess whether providing heat stress abatement pre- and post-natally will improve blood hematology parameters. Holstein calves born to heat-stressed (HT, shade) or cooled (CL, shade, fans and soakers) dams during late gestation (~46 d, temperature-humidity index ≥ 68) were randomly assigned to four pens and exposed to heat stress (HT, shade) or cooling (CL, shade and fans) for 56 d (HTHT, HTCL, CLHT, and CLCL, n=6/group). Whole blood was collected from the jugular vein into vacutainer tubes containing K_2EDTA at birth at 1, 7, 14, 21, 28, 35, 42, 49 and 56 d of age and analyzed (within 2 h of collection) using the Idexx ProCyte Dx analyzer. Data were analyzed by PROC GLM and PROC MIXED (repeated measures) in SAS. Prenatal CL calves had higher red blood cell counts and tended to have higher hemoglobin postnatally, particularly on d 49 and 56, compared to prenatal HT calves (8.6 vs. $7.9 \pm 0.26 \times 10^6$/µL red blood cells; 11 vs 9.8 ± 0.4 g/dl hemoglobin, average d 49 and 56 for parental CL and prenatal HT; $p<0.07$). White blood cell counts were similar at birth, between treatments and across days ($p>0.18$). Neutrophil counts were similar at birth and tended to decrease overtime (6.6 to 4.6×10^3/µL on d7 and 56, respectively; $p=0.06$) but there were no significant effects of treatments or interactions. Lymphocyte counts were similar at birth, and tended to increase overtime (3.5 to 4.5×10^3/µL on d7 and 56, respectively; $p=0.06$). There was an interaction between pre and postnatal treatments, where CLCL calves tended to have higher lymphocyte counts compared to HTCL (4.9 vs 3.6 ± 0.45 10^3/µL; respectively; $p=0.10$). Our preliminary data indicates that prenatal cooling can modulate calf hematology parameters which might confer health benefits during the postnatal preweaning period.

Digital phenotyping for estimation of the breeding value of American Paint Horses

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In collaboration with the American Paint Horse Association (APHA), the UF Equine Genetics Lab analyzed registered horses based on phenotypes determined from photographs and provided genotypes for known spotting patterns . Currently, the APHA visually evaluates photographs to determine the horses registration type. A previous study in cattle, used photo analysis to link phenotypic white spotting patterns with KIT Locus (Reinsch, et al. 1999). We propose that digital photographic quantification of spotting pattern can serve as a more accurate tool for categorization of animals and estimation of breeding value for spotting patterns. Ideally, the APHA would use genetic testing, the most accurate assay method to differentiate horse patterns. To examine the phenotype of registered APHA horses, we analyzed digital photographs with the GIMP program. We used photographs sent to us by the APHA, cropped out the background and converted the image to black and white. Then, we highlighted the white spots on the edited imaged to match the original photograph. Here we will compare the percent of white spotting on each individual horse with their registered pattern and then relate these findings to known genotypes for each horse provided by the APHA. Currently, analysis on 212 samples is completed and double-checked with 417 photos waiting on verification by a second observer. Digital quantification of spotting patterns identified, in conjunction with our genotype database, has identified 59 horses inaccurately registered as "spotted" (no white spotting genes) as well as 86 horses with white spotting genes registered as solid. Accurate registration of horses within the APHA will improve the perceived "fairness" of the registration process, and inform responsible breeding practices to avoid the dangers of conceiving a lethal white foal, in which the foal dies in pain hours after birth. Furthermore, proper registration gives breeders increased accuracy in determining white spotting patterns in future foals, increasing the economic value of their foal crops.

Abstract #28

Timing of concentrate supplementation during late gestation impacts calf pre-weaning growth, but not reproductive performance of *Bos indicus*-influenced cows

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The objective of this study was to evaluate timing of dried distillers grains (DDG) supplementation during late gestation on the reproductive performance of *Bos indicus*-influenced cows and the impact on calf growth. Approximately 84 d prior to calving (d 0), 84 mature Brangus cows were stratified by BW and BCS (422 ± 42 kg; BCS = 5.0 ± 0.14) and assigned randomly to bahiagrass pastures (14 cows/pasture). Treatments were assigned randomly to pastures (2 pastures/treatment) and consisted of no prepartum supplementation (CON), 1 kg/d of DDG from d 0 to 84 (LATE84; 84 kg of DM/cow), or 2 kg/d of DDG from d 0 to 42 (LATE42; 84 kg of DM/cow). Weekly supplement amount was divided into 3 feeding events (Monday, Wednesday, and Friday). Cow BCS were collected on d 0, 45, 84 (calving), 140 (start of breeding season), and 224 (end of breeding season). Calf BW were collected at birth and d 346 (weaning). Reproductive and growth data were analyzed using the GlMMIX and MIXED procedures of SAS. Cow BCS did not differ ($P \geq 0.20$) from d 45 to 224 between LATE84 and LATE42 but were always greater ($P \leq 0.05$) than CON cows. Percentage of pregnant cows on d 283, calving date, and calf birth weight did not differ ($P \geq 0.19$) among treatments. LATE84 calves tended to have enhanced pre-weaning ADG ($P = 0.12$; 0.88, 0.83, and 0.82 ± 0.02 kg/d, respectively) and BW at weaning ($P = 0.10$; 263, 254, and 252 ± 4.4 kg, respectively), while pre-weaning ADG and calf weaning weight did not differ ($P \geq 0.58$) between CON and LATE42. Overall, timing of DDG supplementation during late-gestation did not influence cow reproductive performance. Nonetheless, calf weaning weight was improved when cows were supplemented DDG for the entire length of late-gestation compared to shorter or no prepartum supplementation.

Abstract #29

Signatures of Selection in lambs and kids bred for low fecal egg count during *Haemonchus contortus* exposure

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Host genetic variation for resistance to *Haemonchus contortus* allows selective breeding of animals for increased resistance. This positive selection increases the prevalence of particular alleles at different loci in the population and creates a unique genetic patterns in the DNA sequence. The aim of this study was to identify loci with divergent allelic frequencies using *F*st statistic in lines of sheep and goats selectively bred for low *Haemonchus contortus* fecal egg count (FEC). Three different breeds of lambs (Dorper, Katahdin and St. Croix) and kids (Boer, Kiko and Spanish) derived from resistant lines were used. One hundred and forty four lambs and kids, respectively, were genotyped using Capture-Seq for 100 genes related to the immune response during *H. contortus* infections. Genotypes were discarded if call rate was less than 95% and MAF<0.01. After quality control, 1,339 SNPs (sheep) and 1,020 SNPs (goats) were used for the analysis. Analysis of genetic differentiation using the *F*st statistic based on the pure drift model proposed by Nicholson et al. (2002) was performed in R software. For lamb populations, Dorper was used as the susceptible breed for sheep and Boer for goats. *F*st analysis was performed for all three sheep or goat breeds and between each susceptible vs resistant breed (Dorper vs Katahdin, Dorper vs St. Croix, and Boer vs Kiko, Boer vs Spanish). Our results for lamb populations showed regions associated with resistance to *H. contortus* within chromosome 1, 2, 3, 5, 7, 11, 12, 14, 19 and X. For kids, loci within chromosome 2, 3, 5, 11, 12, 14 and 26 were associated to low FEC. Interestingly, loci within ITGA4, NOS2, TGFB2, IL2RB2 genes were under selection in both species. In conclusion, SNPs within immune response genes related to *H. contortus* exposure are loci under selection for low FEC in sheep and goat populations. Results from this study support the hypothesis that resistance to gastrointestinal parasites is likely to be controlled by many loci.

Effects of lipopolysaccharide dosing on bacterial community composition and fermentation in a dual-flow continuous culture system

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The objectives of this study were to evaluate the effects of lipopolysaccharide (LPS) dosing on bacterial community composition (BCC) and fermentation. Diets were randomly assigned to 6 fermenters in a replicated 3 × 3 Latin square with three 11-d experimental periods that consisted of 7 d for diet adaptation and 4 d for sample collection. Treatments were control diet (CON), wheat and barley diet (WBD) to induce SARA, and control diet + LPS (LPSD). Fermenters were fed 72 g of DM/d. The WBD diet was achieved by replacing 40% of dry matter of the CON diet with 50% ground wheat and 50% ground barley. The LPS concentration in LPSD was 200,000 EU, which was similar to that observed in cows with SARA. The SARA inducing and LPS dosing started at d 8. The LPSD and CON maintained pH above 6 for the entire experimental period, and the WBD kept pH between 5.2 and 5.6 for 4 h/d, successfully inducing SARA. Digestibility of NDF and CP in LPSD were not different from WBD but tended to be lower than CON. LPS dosing had no effect on pool of VFA concentrations and profiles but decreased bacterial N; pattern changes of VFA and LPS in LPSD started to increase and be similar to WBD 6 h after LPS dosing. Pool of LPS concentration was around 11-fold higher in WBD and 4-fold higher in LPSD than CON. In the solid fraction, the BCC of LPSD was different from WBD and tended to be different from CON. In the liquid fraction, the BCC was different among treatments. The LPS dosing increased the relative abundance of *Succinimonas*, *Anaeroplasma*, *Succinivibrio*, *Succiniclasticum*, and *Ruminobacter*, which are main gram-negative bacteria related to starch digestion. Our results suggest that LPS dosing does not affect pH alone. However, LPS could drive the development of SARA by affecting bacteria and bacterial fermentation. For future studies, samples are suggested to be taken 6 h after LPS dosing in a dual- flow continuous culture system.

Comparative Genomics Reveals Clinically Relevant Extended spectrum β-lactamases (ESBL)-and AmpC β-lactamases (AmpC)-producing *Escherichia coli* from Beef Cattle

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ESBL- and AmpC-producing *Escherichia coli* have been rising concerns to public health, as they cause treatment failure of ampicillins and cephalosporins. Cattle are natural reservoirs of these pathogens. The objective of this study is identifying the pathogenicity, multidrug resistance, and clinical importance of these *E. coli* from bovine source by phenotypic characterization and whole genome sequencing. In this study, we collected fecal samples from the rectal anal junction of 1,535 beef cattle in two research farms in North and Central Florida. Among these samples, 42.6% (618/1,535) of the samples contained cefotaxime resistant bacteria (n=2,769), including CTX-M type ESBL-producing *E. coli* (n= 63) from 1.8% (28/1,535) samples and CMY-2 type AmpC-producing *E. coli* (n=117) detected in 5.73% (88/1,535) samples. Following whole genome sequencing of 36 isolates, phylogenetic analysis revealed that these isolates clustered into 10 clades with limited (0-30) single nucleotide polymorphisms (SNPs). We selected 11 representative isolates, based on the whole genome architectures to further characterize their virulence factor (VF) profiles and antimicrobial resistant gene profiles. CMY-2 and CTX-M genes were detected in the plasmids of bacteria, indicating plasmid transformation is a key mechanism to spread antimicrobial resistance. Comparative genomics revealed highly similar VF profiles among animal isolates and clinical isolates. We further confirmed a hyper-virulent strain JEONG5446 as it showed high expression level of Shiga toxin I, as well as high adhesion capability. In conclusion, these results underline the risk of ESBL- and AmpC-producing *E. coli* from beef cattle as human pathogens.

Supplementation with molasses and bypass methionine in beef cows during early gestation improved offspring postnatal growth performance and nutrient digestibility

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A completely randomized design experiment evaluated the postnatal growth and nutrient digestibility of beef calves whose dams were supplemented with bypass methionine or fishmeal in early gestation. From d -30 to 90, relative to start of the breeding season, Brangus × Angus lactating beef cows (n = 108) were provided 1 of 3 treatments: 1) Control (CON) limpograss hay (*Hemarthria altissima*) and molasses plus urea (22% CP, DM basis) at 1.7 kg DM/d, 2) Bypass protein (BPP), CON plus 300 g DM/d of fishmeal to meet metabolizable protein requirements (3.7 g of bypass methionine), or 3) Bypass methionine (BPM), CON plus 10 g DM/d of MetaSmart Liquid (3.7 g of bypass methionine). At weaning, steer calves born to supplemented cows (211.7 ± 28.3 kg of BW; 199 ± 8 d of age) were randomly allocated into 1 of 23 drylot pens (1 steer/pen; n = 8 CON, n = 7 BPP, and n = 8 BPM) and received a common 80:20 grain:roughage (*Cynodon dactylon L* hay.) diet at 2.2% of BW (DM basis) for 43 d. Effects of treatment were not detected for weaning weight ($P = 0.364$), however, BPP and BPM calves had greater ADG, G:F, and final BW compared with CON calves ($P \leq 0.04$). Calves born to BPP dams, had the least concentration of BUN ($P = 0.005$) and BPM calves had the least concentration of blood glucose ($P = 0.001$). Apparent total tract digestibility of DM, OM, and CP was not affected by treatment ($P \geq 0.52$); nevertheless, BPM calves tended to have greater digestibility of NDF and ADF ($P \geq 0.057$) compared with BPP calves, whereas CON calves were intermediate. In conclusion, supplementation with methionine in early gestation altered post weaning calf growth performance, and tended to increase fiber digestion during the growing phase.

Genetic predictions using financial investment analysis versus Lifetime Net Merit as measures of selection

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Current USDA selection indexes such as Lifetime Net Merit (NM$) estimate lifetime profit given a linear combination of 13 traits. In these indexes, every animal gets credit for 2.78 lactations of the traits expressed per lactation, independent of its productive life (PL). Selection among animals with different PL is an example of investment in mutually exclusive projects which have unequal duration. Such projects are best compared with the annualized net present value (ANPV) technique. Additionally, asset replacement theory dictates that as replacement animal's genetic superiority increases with each year, delaying their entry into the herd resulting from increased PL requires a penalty. Therefore, the objective was to develop two new selection indexes based on financial investment comparison techniques, where one contains the opportunity cost of delaying replacement (AVOC) and one does not (ANPV), then compare with NM$ for 1,500 marketed Holstein sires from the December 2017 genetic evaluation. Cash flows from each PTA trait were discounted for the value of time and combined for the expected number of lactations, which were adjusted to maintain a consistent cull rate at the herd level. The lowest Pearson correlation coefficient was 0.978 between AVOC and NM$, while the highest was 0.999 between ANPV and NM$. Although high correlations exist at the population level, the 95th and 5th percentile of changes of individual rank between AVOC and NM$ were +131 and -164, while ANPV and NM$ were +27 and -45, respectively. Sires with a combination of low lactation income and high PL resulted in a decrease of AVOC rank compared to NM$ rank that was greater than a sire with a combination of high lactation income and high PL. These results provide evidence that using classical investment analysis for genetic selection changes animal mating selections compared to the current method of NM$.

Abstract #34

Effect of olive bioactive extracts on immune response in lipopolysaccharide challenged heifers

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During infection, peripheral tissues spare fuels to support the immune response (IR). An excessive IR can hinder normal physiological function. Olive bioactive extracts (OBE) have anti-inflammatory activity, and it could modulate the IR. A randomized block design was used to evaluate the effects of feeding OBE on newly weaned Angus and Brangus heifers (210 ± 19 kg of BW) that where challenged i.v. with lipopolysaccharide (LPS; 0.10 μg/kg of BW). Animals were divided into 3 periods, and randomly assigned to 1 of 4 treatments (Trt): Negative control (receiving saline, CTL-); Positive control (receiving LPS, CTL+); low and high dose of OBE on the diet (receiving LPS, and OBE at 0.04% and 0.16% for OBE L and OBE H respectively). Animals were adapted for 21 days prior to the LPS challenge. Blood samples were collected right before the LPS challenge at h 0, and at h 1, 2, 4, and 8 after the challenge on d 0, and on d 10. Vaginal temperature was recorded using I buttons. Peripheral blood leukocyte cell counts (CC) and expression of cluster of differentiation CD11b, CD14 and CD62L proteins were measured by flow cytometry. Data were analyzed for fixed effect of Trt, and Trt × time. Orthogonal contrasts were performed comparing CTL+ vs. OBE, OBE L vs. OBE H, and CTL+ vs. CTL-. Significance declared at $P < 0.05$, and tendency at $P < 0.10$. Supplementation of OBE-H had a lowering effect on intravaginal temperature when compared to the non-supplemented ones, CTL+, between h 2 and 4, on d0 ($P < 0.05$). LPS exposure decreased lymphocytes, monocytes, and neutrophils CC ($P < 0.01$). Supplementation with OBE had a 61% recovery of lymphocyte CC compared with CTL+ ($P = 0.05$). Exposure to LPS increased the expression of monocyte CD14 ($P < 0.01$) and CD11b ($P \leq 0.01$). Supplementation of OBE ameliorated the increase on expression of CD14 and of CD11b on monocytes ($P < 0.01$). Supplementation of OBE ameliorated the immune response to LPS through downregulation of specific receptors associated with LPS recognition.

Abstract #35

Genetic parameters for hair characteristics and vaginal temperature in a multibreed Brahman-Angus herd under hot humid conditions.

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Thermal stress in hot humid conditions limits cattle production. The objectives for this study were to estimate genetic parameters for short hair length, average hair length, long hair length, vaginal temperature under low temperature humidity index (THI) conditions and vaginal temperature under high THI conditions. In 2017, vaginal temperature was measured every 5 minutes over a 5 day period using an iButton temperature measuring device implanted in a blank CIDR in 113 heifers from the University of Florida multibreed herd (ranging from 100% Angus to 100% Brahman). Ambient environmental conditions monitored using HOBO data loggers were used to calculate the THI. Hair samples were also collected from the heifers at the time of CIDR insertion and measured for length using ImageJ software. Restricted maximum likelihood procedures were used to estimate genetic and phenotypic covariances from multivariate animal models using the WOMBAT program. Estimates for heritability for short hair length, average hair length, long hair length, vaginal temperature under low THI conditions and vaginal temperature under high THI conditions were 0.50, 0.50, 0.50, 0.25 and 0.10, respectively. Genetic correlations were greater than 0.90 for all relationships among the three hair traits. Genetic correlation between the average hair measurements and vaginal temperatures under high THI and low THI were 0.16 and 0.17, respectively. The short and long hair measurements had similar genetic correlations with the temperature traits. The genetic correlation between vaginal temperature at low THI and high THI was found to be 0.68, indicating that genetic selection for vaginal temperature at either THI will also improve thermoregulation at the other THI despite the difference in estimated heritabilities.

Prenatal methionine supplementation alters splicing patterns in the muscle transcriptome

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Maternal nutrition can induce modifications in the epigenome of the fetus, such as changes in DNA methylation, which in turn can alter gene expression and impact future performance. Fetal DNA methylation is related to maternal nutrition through the one carbon cycle, which involves methionine. The repression of gene expression via hypermethylation of the promoter is well documented. Little is known, however, about the role of gene body methylation. Some studies have suggested that DNA methylation within the gene is associated with gene expression activation, while other studies have reported that it may be involved in post-transcriptional regulation, mainly through the alteration of splicing dynamics. We hypothesized that an increased dietary methionine in beef cows during early gestation would impact the fetal epigenome, thus affecting alternative splicing patterns. Muscle samples from 20 bull calves, 10 maternal control diet and 10 maternal methionine-rich diet, were collected at 1 month of age. Both whole-genome DNA methylation and gene expression were evaluated using next-generation sequencing methods. DNA methylation analysis revealed 96k differentially methylated cytosines located in gene bodies. In addition, a total of 516 genes, 285 transcripts, and 8249 exons showed differential expression between maternal diets. Interestingly, 82 non-differentially expressed genes ($p\text{-value} > 0.05$) showed differentially expressed transcripts ($p\text{-value} < 0.05$). Isoform switching was detected in only 3 out of the 82 genes, as a result of poor transcript annotation. Consequently, we assembled the muscle transcriptome for both maternal diets and found that methionine diet resulted in 2894 new splicing events. Notably, 1465 of these splicing events had differentially methylated cytosines in key regions. Overall, our findings provide evidence that changes in the epigenome may impact alternative splicing patterns.

Characterization of forage utilization and pasture management on Florida horse operations

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Forages are essential components of the diet of horses. Depending on the forage and management practices implemented, they can provide a significant source of nutrition. Forage utilization and approaches to managing pastures have not been well described for horse operations in Florida. Therefore, the aim of this study was to characterize forage utilization and management on horse properties in the state. An online survey was administered as a cross-sectional study targeting horse operation managers. From a total of 58 survey responses, 49 were small-scale operations (<10 horses). The recreational purpose was the primary function most reported (72%), followed by training and boarding (7% each), and others (14%). All operations were reported to have pasture available for horses, with 54% reporting horses were housed on pasture full-time (24 h/d) and 55% reporting use of rotational grazing management. Most respondents reported using a combination of hay and pasture (55%) as their primary source of forage (PSF), followed by pasture only (35%) and hay only (10%). Time horses spent on pasture was associated with PSF ($P<0.05$), where operations using full-time pasture access were associated with pasture as PSF, and limited pasture access (4 h/d) was associated with hay as PSF. When asked to describe the level of pasture management (PML) performed, 7% of respondents reported no pasture management, 10% pasture establishment only (e.g., soil preparation, forage planting), and 83% both pasture establishment and maintenance (e.g., mowing, harrowing, weed/pest control). An association between PSF and PML was observed ($P<0.05$), where a lower PML was linked with hay as PSF. Time horses spent on pasture and PML were the best predictors of the PSF ($P<0.05$). Compared to operations implementing both pasture establishment and maintenance practices, operations reporting no pasture management were less likely to utilize pasture only as PSF (OR=0.007, $P=0.002$), whereas pasture establishment only was equally likely to use pasture only (OR=0.39, $P=0.329$). Compared to full-time pasture access, operations reporting fixed-time access were less likely to use pasture only as PSF (OR=0.04, $P= 0.006$). Opportunities exist for improving the pasture management in horse operations in Florida.

Abstract #38

Screening of exogenous enzymes for *in* vitro ruminal degradation of dent corn

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The objective was to evaluate efficacy of exogenous enzymes and optimal dose rate for improving *in vitro* dry matter digestibility (IVDMD) and gas production, using dent corn (DC; 4mm ground) as substrate. Three *in vitro* experiments were conducted with 28 commercial enzymes, and each experiment included a Control group (with no enzyme), positive Control (Flaked corn - FC), and a negative Control (Flint corn). In experiment 1, 9 enzymes were evaluated at dose of 0.25mg/g DM. Substrates were incubated in an *in vitro* batch culture containing buffering medium and ruminal fluid at 39^{o}C. Gas production was measured at 3, 6, 9, and 12 h, while IVDMD and pH was measured after 12 h incubation. Nine enzymes were evaluated at doses 0.25, 0.75, and 1 mg/g DM in experiment 2 while 18 enzymes were evaluated at 0.25, 0.50, and 1.0 mg/g DM in experiment 3. The incubation conditions were similar to those described for experiment 1, except gas measurements were conducted after 2h, 5h, and 7h incubation. Data were analyzed using the GLIMMIX procedure of SAS, and differences were considered significant at $P \leq 0.05$. In experiment 1, 4 enzymes (22Amylex, 19NZ2443, 28AFU and 27TrGA) improved IVDMD relative to Control, while only 22Amylex showed improvement in IVDMD compared to FC. Gas production was greater at 9 and 12 h of incubation with 22Amylex. In experiment 2, 22Amylex increased IVDMD at a dose rate of 0.25mg/g while both 22Amylex and 23LAT improved IVDMD at 0.75 and 1mg/g DM. In experiment 3, 2 enzymes (22Amylex and 36C8955) showed greater IVDMD at 0.25, 0.50, and 1 mg/g DM while 1 (29PZNew) and 3 (5Trga, 27TrGA and 23LAT) additional enzymes showed greater IVDMD at dose 0.50 and 1mg/g DM, respectively. Gas production was greater with 22Amylex at 1 mg/g DM after 5 and 7h of incubation. In conclusion, *in vitro* screening of exogenous enzymes revealed potential candidates for improving IVDMD; however, future *in vivo* trials must validate their efficacy in improving animal performance.

Abstract #39

Soluble fiber in equine diets alters fecal characteristics

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Sources of soluble fiber are often added to equine diets to increase overall digestible energy concentration while maintaining gut health. Almond hulls are a 1.6 million ton annual byproduct of the almond industry but have received little attention for use in equine diets. The objective of this study was to compare fecal characteristics from horses fed almond hulls to other common ingredients. We hypothesized the inclusion of soluble fiber from almond hulls or beet pulp would reduce fecal output. Four mature Quarter Horse geldings were fed 4 dietary treatments at 1.69% BW (DM basis) consisting of either 93% orchardgrass hay (ORCH), 53% orchardgrass hay and 40% molassed sugar beet pulp (MSBP), 53% orchardgrass hay and 40% almond hulls (HULL), or 59% orchardgrass hay and 34% crimped oats (OATS) in a 4×4 Latin square design. Each diet was supplemented with a vitamin-mineral pellet to meet requirements. After a 10-day dietary adaptation, a 3-day total fecal collection was performed. Data were analyzed as a Latin square design using a mixed model with significant means separated by Scheffe's method. Horses defecated more frequently ($P < 0.05$) when fed ORCH (12.6 times/d) compared to other diets (8.8, SEM = 0.5). Individual defecation weight (as-excreted) was greater ($P < 0.05$) for horses fed HULL (1.72 kg) compared to other diets (1.54, SEM = 0.08), but daily fecal output tended to be greatest ($P \leq 0.1$) for ORCH (18.4, SEM = 0.82 kg). Fecal DM ranged 23.0 to 27.3% (SEM = 0.7%) and tended to differ ($P = 0.080$) between dietary treatments. Soluble fiber sources reduced fecal output to similar levels of a mixed hay and grain diet. These data indicate digestibility and bulking capacity of different types of fiber alter fecal characteristics in horses.

Abstract #40

The effect of hay and social housing during the milk-feeding stage on cognition of dairy calves

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Environmental complexity can affect cognitive development and increasing the complexity of dairy calf housing environments may enhance cognitive abilities. We hypothesized that supplemental feed and social housing would improve success in a cognitive task. Holstein heifer calves were randomly assigned at birth to 1 of 4 housing treatments differing in complexity: individual housing without (IC; n=8) or with hay (IH; n=8), or group housing (4 calves/pen) without (GC; n=5) or with hay (GH; n=6). All calves had access to grain and milk (8 L/d) via an artificial teat. At week 5 of age, calves were tested in a spatial discrimination task, conducted in a T-maze with a reward in one arm (0.2 L milk). After learning an initial reward location, calves were assessed in a reversal learning task, where the reward location was changed to the opposite arm. Calves received 5 sessions/d for 5 days until they met passing criteria (moving directly to reward in 3 consecutive sessions) or reached a maximum of 20 sessions. Session completion time and number of sessions to pass were analyzed in a generalized linear mixed model. Passing rate was compared between treatments using Fisher's exact test. Passing rate for the initial learning stage did not differ between treatments but housing complexity affected pass rate of the reversal learning stage (P=0.02), with more group-housed calves passing overall and IC having the lowest pass rate: IC: 33%, IH: 50%, GC: 100%, and GH: 100%. Calves provided hay ($P = 0.01$) and social housing ($P = 0.004$) also required fewer sessions to pass the reversal learning task (IC: 16.67, IH: 14.88, GC: 13.0, GH: 6.83 sessions; SE=2.2), and there was a tendency for a hay by social housing interaction (P=0.08) with GH calves requiring fewer sessions than others. These results suggest that both nutritional and social complexity may enhance early cognitive development, and possibly improve longer-term welfare, as behavioral flexibility improves the ability of the calf to navigate changing environments.

Abstract #41

Influence of length of storage and microbial inoculation on fermentation profile, N fractions, and ruminal in situ starch digestibility of whole-plant corn silage

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The objective of this study was to determine the effects of storage length and microbial inoculation with heterofermentative inoculants and homofermentative inoculants containing *Enterococcus faecium* on the fermentation profile, N fractions, and ruminal in situ starch digestibility (isSD) of whole-plant corn silage (WPCS). Whole-plant corn (33.3 ± 1.0 % DM) was ensiled in quintuplicate vacuum pouches untreated (CON) or after the following treatments: *Lactobacillus plantarum* at 1×10^5 and *E. faecium* at 5×10^4 cfu/g of fresh forage (LPEF); *L. buchneri* and *Lactococcus lactis* at 1.5×10^5 cfu/g (LBLL); and *E. faecium* at 1.5×10^5 cfu/g (EF). Silos were allowed to ferment for 0, 30, 60, 90 or 120 d. Data were analyzed as a 4 × 5 factorial design using PROC GLIMMIX in SAS. Silage pH was greater with LBLL compared to the other 3 treatments. Total acids were greatest with LPEF, intermediate with CON and LBLL, and lowest with EF. Ammonia-N (as % of CP) was greatest with CON, intermediate with LPEF and LBLL, and lowest with EF. Silage pH decreased linearly as storage length increased from 30 to 120 d. Ammonia-N increased linearly as storage length progressed. Concentrations of lactic acid were lower with LBLL compared to the other treatments at 30, 90, and 120 d. Acetic acid concentrations were similar between all treatments at 30 d but were greater for LBLL after 60 d. Soluble CP (as % of CP) was significantly higher with CON compared to the other treatments at d 30 and 90, but not different at d 60 and 120. Ruminal in situ starch digestibility was lower for CON compared to the other 3 treatments at d 60 and 90. However, at d 120, isSD was similar across all treatments. No benefits of inoculating *E. faecium* on starch digestibility were observed. As expected, LBLL increased concentrations of acetic acid.

Meta-analysis of the effects of prepartum dietary protein on performance of dairy cows

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The objectives were to use meta-analytic methods to determine the effects of changes in dietary content or degradability of protein (CP) fed prepartum on productive performance of dairy cows. The hypothesis was that the response to dietary CP prepartum would differ between nulliparous and parous cows, and yields of milk and milk components would be maximized at a greater dietary CP in nulliparous than parous cows. The literature was systematically reviewed, searching randomized experiments with transition dairy cows in which the prepartum dietary content or degradability of protein was manipulated. Twenty-seven experiments including 125 treatment means and 1,801 cows were included in the meta-analysis. Of those, 8 experiments with 27 treatment means reported responses for 510 nulliparous cows. Data collected included the ingredient composition of prepartum diets with respective chemical analyses reported, parity group prepartum, days on prepartum treatment, days of measurement postpartum, and means and respective measure of variance for dry matter intake (DMI), body weight, body condition, and yields of milk and milk components. Random effects meta-analyses were conducted weighting by the inverse of SEM squared to account for the precision of each experiment. Models include the effects of dietary CP content, net energy of lactation content of the diet, parity group prepartum, and covariates that showed significance in univariable analysis. Final models were selected based on parsimony and model fit. Responses to metabolizable protein (MP) were analyzed separately for nulliparous and parous cows because of the different ranges in estimated supplies. Increasing the prepartum dietary CP content from 12 to 15% increased the DM intake 0.5 kg/d during prepartum and 1.3 kg/d during postpartum periods in nulliparous. However, in parous cows, intake was influenced only in prepartum period and it was decreased by 0.1 kg/d with increasing prepartum dietary CP content. Increasing CP content prepartum resulted in quadratic increase for milk fat yield in both nulliparous and parous cows. However, quadratic response for milk protein yield was observed only in nulliparous and it was maximized at 14% CP in prepartum diet. Increasing the prepartum estimated supply of MP from 800 to 1,000 g/d resulted in increase of 1.7 kg/d of postpartum DM intake, 1.2 kg/d of milk yield and 1.5 kg/d of fat corrected milk yield in nulliparous cows. The quadratic response was observed for milk fat content and protein yield by increasing estimated supply of prepartum MP in nulliparous and it was maximized slightly above 1,000 g/d. The present meta-analysis demonstrated that increasing prepartum dietary CP content and MP supply benefit more nulliparous cow than parous cows and approximate upper limit for nulliparous is 1,100 g/d of MP supply.

Abstract #43

The relationship between feed efficiency and fertility in replacement beef heifers

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The objective of our study was to investigate the relationship between feed efficiency and fertility in growing heifers. One hundred and seventy-nine replacement beef heifers were enrolled. Heifers from 10 to 12 months of age entered the University of Florida Feed Efficiency Facility (FEF) and received a diet high in forage to reflect a pasture-based diet. While in the FEF, heifers were exposed to a 14-d adaptation period, followed by a 70-d data collection period that included data for residual feed intake (RFI) and feed to gain ratio. Weekly BW, BCS, and blood samples were collected. Attainment of puberty was determined by concentrations of progesterone. Antral follicle count was assessed in all heifers on the first day of the breeding season using transrectal ultrasonography. Conception and pregnancy rates were determined after transrectal ultrasonography evaluating the presence of a viable conceptus. Our data have revealed no differences in the mean age at puberty, pregnancy rates to AI and overall pregnancy, ADG, FTG, RFI among breeds. An effect was detected between breed and DMI, BCS and BW, where Braford heifers had a lower DMI, BW and BCS. Results indicated an effect of RFI group on ADG, FTG and DMI. Ranking heifers into RFI groups did not affect pregnancy rates, and initial or final BW and BCS. Results revealed that heifers in the Low RFI group attained puberty at a younger age than heifers in the high RFI group. Therefore, more efficient heifers attained puberty earlier compared to less efficient heifers.

Differential Gene Expression in Skin from Foals with Macrolide Induced Anhidrosis

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Hyperthermia is a common and occasionally fatal side-effect of treatment with macrolides, the antimicrobial class most commonly used for the treatment of foals with *Rhodococcus equi* pneumonia. In a previous study, macrolide-induced hyperthermia was shown to be caused by profound impairment of sweat responses (Stieler at al. 2015). To better understand these findings, we performed a genomics study evaluating differential gene expression in skin biopsies acquired from 6 foals before, during, and after treatment with the macrolide erythromycin (ERY). Quantitative sweat tests were used to show that sweating was suppressed during treatment but had recovered by the time of the last biopsy. RNA extraction was performed according to gold standard protocols, and sequencing of RNA was done by Illumina RNA-seq at the UF ICBR Sequencing Core. After read quality checking (FastQC and MultiQC), differential expression analysis was accomplished using the kallisto and sleuth tools. A WT model including day as variable and a 0.1 FDR was applied to the abundance of pseudo-aligned reads. There were highly significant effects of day on terbutaline (T) sweat responses ($P<0.0005$). Compared with baseline (pretreatment days 1, 2, 3) values, sweat weights in treated foals were significantly lower ($P <0.05$) on treatment days (4, 5, 8), and on post-treatment days 12 and 27, but were not significantly different on day 42. Between 47,253 and 995,557 reads per sample were successfully pseudoaligned. We tested 2197 loci for differential expression and detected 214 potential candidate genes (qval<0.05) up and down-regulated during ERY treatment. These pathways involve, and can be influenced by, the broad class of macrolide drugs. Analysis of additional pathways and genes is currently ongoing. These results will provide insight into gene function and pathways correlated to the thermoregulatory dysfunction seen with the use of macrolides.

TABLE OF CONTENTS

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