**Termination Report**

**Project or Activity Number**: S-1064

**Title:** Genetic improvement of adaptation and reproduction to enhance sustainability of cow-calf production in the Southern United States

**Period Covered:**  05-2018 through 05-2019 (annual)  09-2015 through 09-2019 (termination)

**Date of This Report:**  March 27, 2020

**Annual Meeting Dates:** May 21 – 24, 2019

**Participants:**

| Name | Institution | Email |
|------|-------------|-------|
| David Riley | TAMU | david-riley@tamu.edu |
| Rhonda Vann | Mississippi State, MAFES | rvanntx@gmail.com |
| Bob Godfrey | Univ Virgin Islands | rgodfre@uvi.edu |
| Jeremy Powell | Univ of Arkansas | jerpow@uark.edu |
| Trent Smith | Mississippi State | ts289@ads.msstate.edu |
| Bryan Kutz | Univ of Arkansas | bkutz@uark.edu |
| Joe West | Univ of Georgia | joewest@uga.edu |
| Jim Sanders | TAMU | j-sanders@tamu.edu |
| Raluca Mateescu | University of Florida | raluca@ufl.edu |
| Romdhane Rekaya | University of Georgia | rrekaya@uga.edu |

**Brief summary of minutes of annual meeting:**  Individual station progress was reported for current objectives.  Proposed project objectives were discussed relative to the pending (at that time) review.  Opportunities for identifying other contributing stations were discussed.

## 2019

**Accomplishments:**

**Objective 1: Estimate genetic variation associated with animal health using classical animal breeding and genomic techniques to facilitate sustainable beef cattle production systems.**

**EYES**

- Added ~200 new images (*Bos indicus* crosses) at McGregor, Menard

- Totals of images for GWAS: ~1700 Bos indicus, ~1150 Bos taurus, ~500 Hereford
- Repeated images from TX, KS herds ~ 800 cows

- Summer intern to focus on documentation of scleral pigmentation changes and lesions and analyses.

- 3-dimensional camera initial data collected on calves approximately 9 months of age (quite difficult) and on skulls (super easy).  Methodology collaborator developed to quantify antler characterization in deer.  Developing a pre-picture scoring assessment for calves.

**UDDERS**

- 4 years of repeated udder and teat scores at 4 Texas research units for whiteface cows; 3 years of Brahman at 2 locations
- Now have ~800 cows with records
- Collecting on all cows (*Bos indicus* crosses) at College Station.
- Lots of data, minimal time to devote to analysis.
- Brahman study with UF records also would be great.
- An Angus-based fall calving cowherd (n ≈ 200) was observed and udder scores were recorded at weaning.

**FEET**

- An Angus-based fall calving cowherd (n ≈ 200) was observed and hoof scores were recorded at weaning.  Cows were evaluated on a scale from 1 to 9 for claw set and foot angle according to the American Angus Association

**Objective 2:  Meta-analyses of economically important traits of cow productivity and fertility to assess breed and production system combinations**

- M.S. student Carlos Peña is analyzing calving rate, calving interval, calf weight weaned per cow exposed and cow longevity for Brown Loam cows (~1200).  Effects of interest:  % Brahman (2 categories: 0 to 25%; 26 to 60%.   This should permit combination with other units' records.

- M.S. student Kyle Wilson will evaluate runs of homozygosity in 4 generations of genomics populations and train for two weeks at UGA this summer.

## Objective 3:  Documentation of genetic components pertaining to heat tolerance adaptive traits in sustainable beef cattle production systems.

- Collection of phenotypic data from the UF multibreed Angus-Brahman (MAB) and Brahman herds (health, survival, fertility, growth, ultrasound, carcass, meat palatability), and eight Florida Brahman herds (fertility, growth, ultrasound, and carcass).  Number of animals with records = 17,239. (M. Elzo)

- Collection of tissue samples from calves, sires, and dams from UF MAB, UF Brahman, and Florida Brahman breeders (n = 7,778). (M. Elzo)
- Statewide Brahman and Brahman-Angus tissue sample (blood, ear-notches, semen) and DNA repository housed at the Animal Science Department of the University of Florida (UF MAB, UF Brahman, Florida Brahman herds). (M. Elzo)

- Statewide Brahman and Brahman-Angus database: phenotypes, pedigree, genotypes (GeneSeek GGP250k).  Phenotypic and pedigree data came from UF, Florida Brahman breeders, and ABBA (American Brahman Breeders Association).  Number of animals with one or more phenotypic records = 17,239 (10,137 Brahman and 7,092 Angus and Brahman-Angus crossbreds).  Number of animals in the pedigree file = 25,379 (17,601 Brahman and 7,778 Angus and Brahman-Angus crossbreds).  Number of animals with genotypes = 3,429 GGP250k. (M. Elzo)

- Genomic-polygenic and polygenic predictions for twenty growth, fertility, ultrasound, carcass, and tenderness traits in the statewide multibreed Brahman-Angus multibreed population.  Number of evaluated animals = 25,379. (M. Elzo)

- FORTRAN and SAS software for editing of phenotypes, genotypes, and pedigree data, and construction of input files for imputation and genetic evaluations using genomic-polygenic and polygenic models.

- GWAS and gene enrichment analysis reveal membrane anchoring and structural proteins associated with meat quality in beef (R. Mateescu).

- RNA-seq analysis identifies genes and pathways related to cytoskeletal structure and proliferation for meat quality in beef (R. Mateescu)

- Collection of phenotypic data describing thermal tolerance in *Bos Indicus* influenced populations and characterization of the genetic component underlying these traits. (R. Mateescu)

- Collected another year of monthly shedding scores on about 60 Angus cows
- Scored quantity only on *Bos indicus* cross cows (all McGregor almost monthly) because most don't strongly exhibit a growth/shedding pattern like Angus.

## Objective 4:  Investigation of early cow-life performance (first four parities) affecting lifetime production in Brahman and Brahman-Angus cows.

- Records from McGregor for approximately 60 Brahman cows.
- Records from Overton for approximately 200 Brahman cows.
- We are expanding the Brahman herd at McGregor and are making reciprocal cross $F_1$ calves.
- An Angus-based commercial beef cattle herd ((n ≈ 200/yr) in Arkansas was observed from 2012 through 2018. Once monthly from March until July, at approximately 28-day intervals, mature cows and replacement heifers were evaluated for shedding on a scale from 1 to 5.

## Impact Statements:

- The successful completion of the 2nd genomic-polygenic evaluation of animals in the Florida Multibreed Angus-Brahman population for twenty growth, fertility, ultrasound, carcass, and tenderness traits showed the feasibility of developing a statewide genetic evaluation system for sub-tropically adapted animals based on phenotypic, pedigree, and genotypic data from experimental and private herds. This system required the development of a statewide database (phenotypes, pedigree, genotypes) and a tissue sample and DNA repository. The feasibility of extending this system to the US Southern Region merits to be explored.

- A structural model with carcass quality as an independent latent variable and meat quality as a dependent latent variable was able to satisfy the variance-covariance structure present in the sample data. Carcass quality was measured by QG, FOR and MARB, and meat quality was measured by JC, TD and CT. The GWAS analysis allowed the discrimination between genomic regions with effect on carcass quality and meat quality independently, but also made possible to uncover genomic regions responsible for the genetic correlation between these latent phenotypes.

- Expression of a number of cytoskeletal proteins and transmembrane anchoring molecules was identified in the expression and DE analysis in the present population and these proteins can have a direct effect on tenderness and marbling. Cytoskeletal proteins and transmembrane anchoring molecules can influence meat quality by allowing cytoskeletal filament interaction with myocyte and organelle membranes, contributing to cytoskeletal structure, microtubule network stability, and cellular architecture maintenance during the postmortem. Some of these cytoskeletal and transmembrane proteins can modulate cell proliferation. Several pathways related to structural proteins and energy metabolism were identified as enriched showing that these kinds of genes are overrepresented and are crucial for meat quality in the present population.

- The proportion of phenotypic variance explained by SNP genotypes was medium-high for all traits describing the thermotolerance varying from 0.194 for PC2 to 0.285 for PC1, indicating a good predictive power for all these traits. Estimates of heritability for hair diameter, undercoat length, topcoat length, body temperature under low THI conditions and body temperature under high THI conditions were 0.50, 0.67, 0.42, 0.32, and 0.26, respectively. The genetic parameters estimated in this study indicate a large, exploitable genetic variance which can be selected upon to improve tolerance in cattle.

- Additive genetic variance for intramuscular fat in Hereford cattle changes by longitude and latitude coordinates and will result in different EPDs for sires.

- High percentage *Bos indicus* cows do not grow and shed winter coat in the same pattern-based manner of Angus.  Consequently, it may be more appropriate to evaluate those in terms of quantity: e.g, 1 = minimum quantity and 5 = maximum quantity.

- Udder and teat quality are among the most important functional traits of beef females. Unsound udders and teats are associated with reduced productive life and inferior calf performance, and poor udder and teat conformation is a major reason why cows are culled from the breeding herd. Understanding the implications of theses scores could improve the culling process and improve production efficiency.

- Sound feet are important components in cattle production systems and can influence nutritional aspects of cattle. Hoof soundness have been reported to have effects on breeding and reproductive success and both body weight and body composition. Implementing these scores can aid in selecting for more sound cows.

- Hair shedding scores, although subjective, are well within the reach of both commercial and seedstock breeders.  By using these scores and understanding their implications in cattle production will aid them in the match of genetic resource to production resources.  This could easily increase current overall production.

## Publications:

Coleman, S.W., C.C. Chase, Jr., W.A. Phillips, and D.G. Riley.  2018.  Feed efficiency of tropically adapted cattle when fed in winter or spring in a temperate location.  J. Anim. Sci.  96:2438–2452.  doi: 10.1093/jas/sky138.

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver.  2019.  The Florida Brahman Genomic Selection Project: April 2019 Genomic EBV.  The Florida Cattleman & Livestock Journal (Submitted).

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver.  2019.  FY2019 FCEF Report 2 of the Florida Brahman Genomics Project. Univ. Florida, Gainesville, pages 1-11.

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver.  2019.  The Florida Brahman Genomic Selection Project: January 2019 Genomic EBV.  The Florida Cattleman & Livestock Journal 83(7):56-59.

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver.  2019.  FY2019 FCEF Report 2 of the Florida Brahman Genomics Project.  University of Florida, Gainesville, FL, p 1-8.

Fan, P., C. D. Nelson, J. D. Driver, M. A. Elzo, F. Peñagaricano, and K. C. Jeong.  2019.  The Bovine Meconium microbiota varies with birthweight and its effects on the gut microbiota establishment during early life.  ASM Microbe, San Francisco, CA, June 20-24, 2019. (Submitted)

Fan, P., C. D. Nelson, J. D. Driver, M. A. Elzo, and K. C. Jeong.  2019.  Understanding the role of host genetics on gut microbiota through life by using the Angus-Brahman multibreed herd. 17th Annual Anim. Mol. Cell Biol. Res. Symp., Cocoa Beach, FL, April 12-13-2019.

Fan, P.[*], C. D. Nelson, J. D. Driver, M. A. Elzo, and K. C. Jeong. 2019. Animal breed composition influences the gut microbiota structure and antibiotic resistome in an Angus-Brahman multibreed herd. Front. Microb. (Submitted)

Fan, P.[*], L. Teng, C. Nelson, J. D. Driver, M. A. Elzo, and K. C. Jeong. 2019. Animal breed composition shapes the gut microbiota, and its effects on the host metabolic and immunological status. eLife J. (Submitted)

Hawryluk, B., P. M. Ramos, D. D. Johnson, M. A. Elzo, C. C. Carr, and T. L. Scheffler.  2019.  Comparing heat shock proteins in Angus and Brahman cattle and their effect on tenderness.  Recip. Meat Conf. Amer. Meat Sci. Assoc., Fort Collins, CO, June 23-26, 2019. (Submitted)

Leal, J., M. A. Elzo, and R. M. Mateescu.  2019.  Differential gene expression and eQTL analysis in skeletal muscle related to meat quality of beef. Genetics Seminar, Dept. Anim. Sci. Univ. Florida, Gainesville, January 22, 2019.

Leal, J., M. A. Elzo, and R. M. Mateescu.  2019.  Identification of trait-associated genes related to meat quality using an RNA-seqanalysis approach.  PE0366 27th Plant and Animal Genome Conference, San Diego, CA, January 12-16, 2019.

Leal J. D.[*], M. A. Elzo, D. D. Johnson, H. Hamblen, and R. G. Mateescu.  2019.  RNA-seq analysis identifies cytoskeletal structural genes and pathways for meat quality in beef.  BMC Genomics (Submitted).

Leal J. D.[*], M. A. Elzo, D. D. Johnson, H. Hamblen, and R. G. Mateescu.  2019.  Genome wide association and gene enrichment analysis reveal anchoring and structural proteins associated with meat quality in beef.  BMC Genomics 20:151.

Littlejohn*, B.P., D.G. Riley, T.H. Welsh, Jr., R.D. Randel, S.T. Willard, and R.C. Vann.  2018.  Use of random regression to estimate genetic parameters of temperament across an age continuum in a crossbred cattle population.  J. Anim. Sci.  96:2607–2621.  doi:  10.1093/jas/sky180.

Littlejohn, B.P., D.M. Price, D.A. Neuendorff, J.A. Carroll, R.C. Vann, P.K. Riggs, D.G. Riley, C.R. Long, T.H. Welsh, Jr., and R.D. Randel.  2018.  Prenatal stress alters genome-wide DNA methylation in suckling Brahman bull calves.  J. Anim. Sci.  96:5075–5099.  doi:  10.1093/jas/sky350.

Langdon*, J.M. II, J.S. Delgadillo, A.D. Herring, H. Blackburn, S.E. Speidel, S. Sanders, and D.G. Riley.  2018.  Genetic-environment considerations for heritability estimation and genetic evaluation in American Hereford cattle.  Proc. 64th Annual Texas A&M Beef Cattle Short Course.  Pages E-11 to E-24.

Muntean*, C.T., A.D. Herring, D.G. Riley, C.A. Gill, J.E. Sawyer, and J.O. Sanders.  2018.  Evaluation of F1 cows sired by Brahman, Boran, and Tuli bulls for reproductive, maternal, and cow longevity traits.  J. Anim. Sci.  96:2545–2552.  doi:10.1093/jas/sky169.

Sarlo Davila, K. M. [*], H. Hamblen, P. J. Hansen, S. Dikmen, M. A. Elzo, P. A. Oltenacu, and R. G. Mateescu. 2019. Genetic parameters for hair characteristics and core body temperature in a multibreed Brahman-Angus herd. J. Anim. Sci. (Submitted)

## Presentations/Abstracts:

C. L. McGuire, J. G. Powell, R. N. Cauble, B. R. Kutz, K. S. Anschutz, T. D. Lester, and W. A. Gragg. 2019. Foot Scoring Effects on Cow and Calf Performance at Breeding, and Weaning. American Society of Animal Science Southern Section Meeting. Oklahoma City, OK.

Dikmen S., K.M. Sarlo Davila, E.E. Rodriguez, H.Hamblen, P.J. Hansen and R.G. Mateescu. 2019. Genetics of thermotolerance. Brahman Field Day. Gainesville, FL. Poster.

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver. 2019. The Florida Brahman Genomic Selection Project: April 2019 Genomic EBV. Univ. Florida, Gainesville, April 26, 2019.

E. N. Davis, **R. N. Cauble**, J. G. Powell, T. D. Lester, W. A. Gragg, B. R. Kutz, and C. F. Rosenkrans. 2019. Relationships among Circulating Prolactin Concentrations, Hair Coat Score, and Weights of Grazing Cows. American Society of Animal Science Southern Section Meeting. Oklahoma City, OK.

Fan, P., C. D. Nelson, J. D. Driver, M. A. Elzo, and K. C. Jeong. 2019. The Bovine Meconium microbiota varies with birthweight and its effects on the gut microbiota establishment during early life. ASM Microbe, San Francisco, CA, June 20-24, 2019 (Submitted).

Fan, P., C. D. Nelson, J. D. Driver, M. A. Elzo, and K. C. Jeong. 2019. Understanding the role of host genetics on gut microbiota through life by using the Angus-Brahman multibreed herd. 17th Annual Anim. Mol. Cell Biol. Res. Symp., Cocoa Beach, FL, April 12-13-2019.

Leal, J., M. A. Elzo, and R. M. Mateescu. 2019. Differential gene expression and eQTL analysis in skeletal muscle related to meat quality of beef. Genetics Seminar, Dept. Anim. Sci. Univ. Florida, Gainesville, January 22, 2019.

Leal, J., M. A. Elzo, and R. M. Mateescu. 2019. Identification of trait-associated genes related to meat quality using an RNA-seq analysis approach. PE0366 27th Plant and Animal Genome Conference, San Diego, CA, January 12-16, 2019.

Riley, D.G., and N. Rebollar Villalba. 2018. La metilación de los ADN es otra dimensión del control genética: ¿Será la oportunidad para usar en el mejoramiento de ganado Brahman? Memorias XIX World Brahman Congress

Riley, D.G., and N. Rebollar Villalba. 2018. Nuevos avances en la investigación y el desarrollo de la raza Brahman en E.E.U.U. Memorias XIX World Brahman Congress

R. N. Cauble, J. G. Powell, B. R. Kutz, K. S. Anschutz, T. D. Lester, and W. A. Gragg. 2019.
Winter Hair Coat Shedding Effects on Pre-Breeding, Weaning, and Calf Performance of Fall Calving Beef Cows. American Society of Animal Science Southern Section Meeting. Oklahoma City, OK.

Sarlo Davila K. M., H. Hamblen, P.J. Hansen, S. Dikmen, M.A. Elzo, P.A. Oltenacu, R.G. Mateescu. (2018). Genetic parameters for hair characteristics and vaginal temperature in a mulitbreed Brahman-Angus herd under hot humid conditions. 4th Annual Animal Science Symposium. St. Augustine, FL. Oral Presentation.

Sarlo Davila K. M., H. Hamblen, P.J. Hansen, S. Dikmen, M.A. Elzo, P.A. Oltenacu, R.G. Mateescu. (2018) Effect of hair characteristics on vaginal temperature under hot and humid conditions in an Angus-Brahman multibreed herd. 2018 American Association of Animal Science Annual Meeting. Vancouver, Canada. Poster.

RESOLUTIONS
S-1064 Technical Committee
Raymond, MS
May 22-24, 2019

Whereas the S-1064 Technical Committee is committed to improving beef cattle production systems in the southern region and other regions of the United States.

And whereas the S-1064 Technical Committee is improved by exchange of research findings and approaches at different institutions and locations as well as observing different beef cattle production systems.

Therefore, be it resolved that the S-1064 Technical Committee expresses its gratitude to Dr. Rhonda Vann at the Brown Loam Research Station for planning and coordinating its 2019 annual meeting in Raymond, MS and for coordinating tours of the research cattle herds at the Brown Loam Research Station and privately owned cattle herds belonging to Greg Lott (Remington-Lott Farms), Bill and Nancy Howard (Sedgewood Plantation) and Shep and Tracey Batson (Rocking B Cattle) and Bill and Yvonne Woods (Woodstone Angus Ranch).

Be it also resolved that the S-1064 Technical Committee expresses appreciation to Dr. Sherry Surrette for her welcoming comments and Dr. Wes Burger and MAFES for sponsorship of this meeting.

Be it also resolved that the S-1064 Technical Committee extends its thanks to Dr. Joe West for his oversight, leadership, and friendship as administrative advisor of the project.


Respectfully submitted 5/23/19

David Riley

Trent Smith

**Impact statements**

## Objective 1.

Because of the low correlation of tick load between cows and calves, and within calves, it may be difficult to select for the trait of tick resistance.  One hypothesis is that the frequent dipping schedule (4-6 wk intervals) is suppressing any innate tick resistance of the cattle.  Calves raised on forage in the tropics will have different growth traits that can be influenced by gender and year.


The tick load scoring system has been incorporated into data collection as part of the routine management of the herd.  The low correlation of tick load between cows and calves, and even within calves, and the frequent dipping schedule may limit the amount of progress that can be made when selecting for the trait of tick resistance.

Knowledge of the effect of gender on growth traits of calves raised on a forage based system in the tropics can be used to assist producers when managing and selecting animals.

 Because of the low correlation of tick load between cows and calves, and within calves, it may be difficult to select for the trait of tick resistance.  One hypothesis is that the frequent dipping schedule (4-6 wk intervals) is suppressing any innate tick resistance of the cattle.  The tick load scoring system has been incorporated into data collection as part of the routine management of the herd.  The low correlation of tick load between cows and calves, and even within calves, and the frequent dipping schedule may limit the amount of progress that can be made when selecting for the trait of tick resistance.


Hereford cattle have substantially less eye pigmentation, and less scleral pigmentation than Hereford-*Bos taurus* or Hereford-*Bos indicus* (including Braford) crosses.

Hereford and Hereford-*Bos indicus* crossbred cows had higher lesion occurrence than Hereford-*Bos taurus* crossbred cows.

Preliminary mean and variability of udder pigmentation, measured as a subjective 0 (no pigmentation) to 5 (complete pigmentation) was established with Hereford-*Bos indicus* and Hereford-*Bos taurus* cows: mean = 1.7 to 2.4 with SD = 1.4 to 1.8.

Approximately the same distribution of udder score and teat score (both defined by Beef Improvement Federation Guidelines) means for cow age categories were observed in Hereford-*Bos indicus* and Hereford-*Bos taurus* cows at the time of calving, mid-lactation, and one week after weaning of calves (7

mo age).  Those scores for Brahman cows at the time of calving were similar with a similar age distribution.

Udder and teat scores at calving and weaning were moderately correlated with weaning weight (–0.35 to -0.3), indicating that smaller udders and teats and less pendulous udders were associated with higher weaning weights.

Udder and teat quality are among the most important functional traits of beef females. Unsound udders and teats are associated with reduced productive life and inferior calf performance, and poor udder and teat conformation is a major reason why cows are culled from the breeding herd.  Understanding the implications of theses scores could improve the culling process and improve production efficiency.

Determining resistance and/or resilience to horn flies would be helpful in both organic production systems and unconventional production systems that desire to reduce pesticide use or that have issues with pesticide resistance. Additional cooperator herds willing to forego chemical treatment of their herds will be identified.

These data indicate that udder suspension and teat size scores differ with age and that udder suspension does have an effect on adjusted 205-day weight.

Udder score means by Brahman fraction at calving, 6 months, and weaning indicated that cows with higher Brahman percentages tended to have poor udders.  A similar trend existed for teat score means at calving (cows with higher Brahman percentages had better teats); a slightly negative trend towards Brahman occurred at 6 months and at weaning.  Conversely, udder and teat score means at calving, 6 months, and weaning showed consistent downward trends as cows aged, thus younger cows tended to have better udders and teats than older cows at all lactation stages.


## Objective 2

University of Virgin Islands: Knowledge of the effect of gender on growth traits of calves raised on a forage-based system in the tropics can be used to assist producers when managing and selecting animals.  Calves raised on forage in the tropics will have different growth traits that can be influenced by gender.

The similarity between genomic-polygenic and genomic predictions for reproductive, pre and postweaning growth direct, preweaning growth maternal, postweaning ultrasound, and carcass traits indicated that genomic information added little information to genetic predictions for these traits.

The large variability among genomic-polygenic and genomic EBV among animals of each 32nds Brahman fraction indicated that selecting animals in this multibreed Angus-Brahman herd could be accomplished using a common set of objectives across all Angus-Brahman breed compositions.

Genome-wide association analysis with the GGPHD150k chip from GeneSeek indicated several genomic regions associated with tenderness and the predictive analysis suggested the possibility of developing a more precise system to assess tenderness and improve consumer expectations.

In spite of the high autozygosity, inbreeding depression is limited which could be due to incomplete reporting or/and population adaptation to ancient inbreeding

Recent inbreeding negative effects could be attenuated by making use of the variation in genomic inbreeding

The level of autozygosity and its effects on performance varies across chromosomes indicating that inbreeding will have different effects for different traits.

Large amounts of variation exist within water intake in beef steers.  Preliminary analyses of the SNP data on groups 1-5 indicate that WI is moderately heritable.  Future analyses include generation of genetic correlations between WI and other economically important production traits as well as preliminary genome-wide association analyses.  As all groups are completed, we will augment currently analyses to ensure that values do not change substantially as new records are added to the analysis/population.

## Objective 3

Hair shedding scores, although subjective, are well within the reach of both commercial and seedstock breeders.  Using these scores and understanding their implications in cattle production will aid in the match of genetic resources to production resources.  This could easily increase current production by 10%.

Hair shedding scores could be taken in May of each year by beef producers in the southeastern U. S. and used to select animals that would be more adaptable to their environment.

Water intake research can help producers better manage water resource during drought and may enable selection for increased water efficiency to conserve on-farm water resources.  Large amounts of variation exist within water intake in beef steers.  The first genotypes will be available in summer 2016, which will allow the first analysis of the heritability of water intake in beef cattle.

Previous work has suggested a relationship between early shedding of the winter hair coat by the dam and an increase in weight of the weaned calf. Selection of cows that are more adapted to their environment can be profitable. Hair shedding could be an important trait to consider in selection and its potential relationship to other economic important traits..

Scleral lesions were the most frequently observed in all breed types.

Age of cow only appeared to be primarily influential for Angus cow coat scores in transition seasons (spring and fall).

In these data, month of first shedding (MFS) score influenced cow BW prebreeding, adjusted calf birth weight, and adjusted calf weaning weight. Shedding of the winter hair coat was not noted to also affect pregnancy status.

Heritabilities for all different vaginal temperature measures were low or medium and ranged from 0.11 to 0.27. The lowest heritability estimate was for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively). Coat score and temperament influenced vaginal temperature responses to heat stress in Brangus heifers. Vaginal temperature increased as THI increases, with a one-hour lag time in the animal's response. Temperament was important for both sweating rate and vaginal temperatures, with calm cattle having lower sweating rates and maintaining lower body temperatures, suggesting that heifers with a calmer demeanor respond better in hot conditions.

## Objective 4

The successful completion of the first genomic-polygenic evaluation of animals in the Florida Multibreed Angus-Brahman population for twenty growth, fertility, ultrasound, carcass, and tenderness traits showed the feasibility of developing a statewide genetic evaluation system for sub-tropically adapted animals based on phenotypic, pedigree, and genotypic data from experimental and private herds.  This system required the development of a statewide database (phenotypes, pedigree, genotypes) and a tissue sample and DNA repository.  The feasibility of extending this system to the US Southern Region should be explored.

Proteolysis and tenderization in Angus, Brahman and Brangus is related to pH decline and calpain-1 autolysis. Longissimus from Brahman exhibited slower rate of pH decline that coincided with slower tenderization, evidenced by reduced calpain-1 autolysis at 24h postmortem and less troponin-T degradation. The slower rate of acidification in Brahman indicated that ATP levels were maintained longer, prolonging calcium uptake by the sarcoplasmic reticulum and mitochondria, thereby delaying calpain activation and tenderization.

Structural equation analysis and genome wide association for growth, carcass quality and meat quality in an Angus-Brahman multibreed population indicated that three biological mechanisms could explain the association of identified genes with latent constructs for carcass and meat quality: postmortem proteolysis of structural proteins and cellular compartmentalization, cellular proliferation and differentiation of adipocytes, and fat deposition.

Meconium microbiota was associated with fetal development, establishment of postnatal gut microbiota, and subsequent animal growth. Meconium from the low birthweight group tended to have higher microbial richness compared to meconium from the high birthweight group, including pathogens such as *Pseudomonas*, *Legionella*, and *Actinobacillus*. Microbes likely colonize the fetus in its early stages influencing fetal development and affecting the establishment of gastrointestinal tract microbiota pre and postnatally.

## Publications

Arthington, J.D., D.G. Riley, and J. Vendramini.  2015.  Helping Angus cattle adapt to subtropical climate.
Feedstuffs September 21, 12, 15.

Coleman, S.W., C.C. Chase, Jr., D.G. Riley, and M.J. Williams.  2017.  Influence of cow breed type, age and
previous lactation status on cow height, calf growth, and patterns of body weight, condition,
and blood metabolites for cows grazing bahiagrass pastures.  J. Anim. Sci.  95:139–153.

Dias, M.M., A. Cánovas, C. Mantilla-Rojas, D.G. Riley, P. Luna-Nevárez, S.J. Coleman, S.E. Speidel, R.M.
Enns, A. Islas-Trejo, J.F. Medrano, S.S. Moore, M.R.S. Fortes, L.T. Nguyen, B. Venus, I.S.D.P. Diaz,
F.R.P. Sousa, L.F.S. Fonseca, F. Baldi, L.G. Albuquerque, M.G. Thomas, and H.N. Oliveira.  2017.
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**Authorization: _____**

       **Joe W. West**

       **Administrative Advisor**