Final Technical Report FCEB Project #29

Improving the accuracy of genomic selection for carcass and meat quality Year 3

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SPECIFIC AIMS

The *long-term* goal is to provide the Florida cattle industry with genomic tools needed to implement an effective genomic selection and management program aimed at improving carcass traits (marbling) and meat quality (tenderness) in Brahman and Brahman influenced cattle. A genomic selection program has been initiated to improve three target traits: tenderness, marbling, and reproductive tract score. Current accuracies for genomic EPDs in this program, in particular for the young and unproven males and females, are extremely low. For this program to succeed and ensure genetic improvement for tenderness and marbling, it is imperative to increase the number of animals with these traits recorded in our database. The number of purebred Brahman available is minimal and the use of crossbred animals with accurate phenotypes and genotypes is a well-known method for increasing accuracy of genomic evaluations. Development of these genomic selection and management tools will contribute to a sustainable and profitable future for the Florida beef industry.

Specific objectives:

- Measure carcass and meat quality traits on a new set of 120 Brahman crossbred steers. This will increase our database to approximately 1,320 animals with meat quality records. Growth records are already available on the entire population. Increasing the number of animals with carcass and in particular meat quality records is imperative for an accurate estimation of genetic merit.
- 2) Conduct the annual genomic evaluations for tenderness, marbling, reproductive tract score and other reproduction, growth, ultrasound, and carcass traits. Calculate the change in the mean EPD values (i.e., genetic trends) for sires, dams, and calves over years to assess the effectiveness of the selection and mating program in the UF Brahman and Multibreed populations.

This proposal addresses the "Animal Genetics - Improving the Brahman breed to optimize commercial cow/calf production" research priority. Genomic selection programs that incorporate a large number of genetic markers can result in a 32% improvement in accuracy compared to parental average breeding values. However, for multi-breed beef cattle, which constitute a large proportion of the beef population, in particular commercial herds, genomic selection is still in the development stage. Also, when breed-specific markers are used in a different breed or crossbred populations, the genetic correlation between the trait of interest and the genomically-enhanced EPD clusters around zero indicating that the usefulness of these markers for selection is mostly limited to the breed used for their discovery and validation. It is therefore imperative that these genomic tools are developed in the populations targeted for improvement to be effective.

SIGNIFICANCE

This proposal will benefit the Florida Beef Cattle Industry by developing the resources needed to develop genomic selection and management tools for Brahman and Brahman influenced cattle. Brahman is a key component of the crossbred beef production system in Florida. Brahman brings great adaptability to Brahman-Bos taurus crossbred cattle permitting them to endure adverse hot and humid conditions. Brahman cattle are frequently criticized for a perceived lack of meat tenderness and marbling and their lower fertility relative to other breeds and crossbred cattle. However, recent research on the multibreed herd at University of Florida revealed that there is a high level of variation in tenderness across all quality grades. Furthermore, we showed that Brahman animals exhibit a range of EPD for fertility, growth, ultrasound, and carcass traits comparable to that of Angus, Brangus, and Brahman x Angus crossbreds.

Because the beef industry is currently using the USDA grading system to determine premium and discounts, Brahman and Brahman influenced cattle are routinely penalized for relatively low marbling score. About 30% to 40% of the variation in tenderness is due to genetics. Recent developments in genomics paves the way for making significant improvement in tenderness via genomic selection and offer opportunities for marketing of cattle on the basis of tenderness. Genetic markers discovered in other populations (Angus) are not informative in Brahman influenced populations. To adopt this technology, producers need population/breed specific information on the value of genetic testing and our project will provide this information for Brahman influenced cattle.

APPROACH

This proposal will build on the historical database developed at UF which includes the Brahman and the Multibreed Herds. A multitude of growth, carcass, reproduction, meat quality traits have been recorded and a large number of animals have been genotyped over the years. This allowed the initiation of a genomic selection program in these populations with the goal of improving tenderness, marbling, and reproductive tract score. However, the number of animals with carcass and meat quality data remains small which translates into low accuracy for genomic EPDs for these traits. Addition of new animals with phenotypes and genotypes is essential for increasing these accuracies. Price of genotyping these animals is included in a separate proposal.

 Record carcass ultrasound, carcass and meat quality traits for a new set of 150 crossbred steers. This will increase our database to 1,320 animals with carcass records and 1,250 animals with meat quality records. Growth records are already available on the entire population. Increasing the number of animals with carcass and in particular meat quality records is imperative for increasing the accuracy of the genomic evaluation.

Cattle were implanted with Revalor XS (Merck & Co., Inc., Kenilworth, NJ) and fed a standard feedlot diet consisting of corn, protein, vitamins, and minerals until they reached a common physiological endpoint, with the goal of 1.27 cm of subcutaneous fat over the back. Cattle will be harvested under USDA-FSIS inspection. Hot carcass weight (HCW) will be recorded immediately following harvest. Carcasses will be ribbed between the 12th and 13th rib at 48 hours postmortem and carcass traits will be recorded. Marbling score, lean maturity, and skeletal maturity will be

recorded according to USDA standards and used to calculate overall maturity and USDA quality grade using an industry standard method (Hale et al., 2006). Fat over the ribeye (FOE; cm) and ribeye area (REA; cm²) will be measured. Yield grade (YG) will be calculated using the industry standard formula: YG = 2.5 + 2.5(FOE) + 0.2(KPH) + 0.0038(HCW) – 0.32(REA).

One 2.54 cm thick steak from the *longissimus lumborum*, posterior to the 12th rib will be obtained from each carcass and kept on ice until returning to the University of Florida Meat Processing Center (Gainesville, FL, United States). Steaks will be trimmed of external fat then placed in heat shrink vacuum pack bags (B2570; Cryovac, Duncan, SC), and vacuum sealed with a Multivac C500 (Multivac Inc., Kansas City, MO). Steaks will be aged for 14 days at 4°C then placed in a freezer at -20°C for storage.

Tenderness will be measured by WBSF on steaks from 150 Brahman influenced steers according to the American Meat Science Association Sensory Guidelines. Frozen steaks will be allowed to thaw at 4°C for 24 hours, cooked to an internal temperature of 71°C in an open-hearth grill and cooled at 4°C for 18 to 24 hours. From each steak, six cores with a 1.27-cm diameter and parallel to the muscle fiber will be sheared with a Warner-Bratzler head attached to an Instron Universal Testing Machine (model 3343; Instron Corporation, Canton, MA). The Warner-Bratzler head will move at a cross head speed of 200 mm/min. The average peak load (kg) of six cores from the same animal will be calculated and subsequently analyzed.

2) Conduct the annual genomic evaluations for tenderness, marbling, reproductive tract score and other reproduction, growth, ultrasound, and carcass traits.

The genomic evaluation program will compute an annual genomic EPD using the unified approach developed by Ignacy Misztal and collaborators at the University of Georgia. This method yields the best possible accuracy for genomic EPD because it utilizes all available phenotypic, pedigree, and genotypic records. We will continue to compute genomic EPD and accuracy information for tenderness, marbling, reproductive tract score, and other reproductive, growth, ultrasound, and carcass traits from all animals in the UF herds.

Sires and dams in the UF Brahman and Multibreed herd will be selected based on their EPD for tenderness, marbling, reproductive tract score, and other relevant reproduction, growth, ultrasound, and carcass traits. Selection will be followed by assortative mating (i.e., high EPD sires to high-EPD dams) to increase the likelihood of obtaining progeny with higher EPD for these traits. This selection and mating strategy will effectively create three groups of Brahman cattle in the UF Brahman herd: a group with emphasis on tenderness (tenderness line), a group with emphasis on marbling (marbling line), and a group with emphasis on reproductive tract score (fertility line).

This is a long-term project whose impact on the UF Brahman and Multibreed populations will be assessed only after a number of years of consistent selection and assortative mating for these traits. Thus, this selection program would need to be continued for at least three generations of selection (9 to 10 years). Changes in the mean EPD values (i.e., genetic trends) for sires, dams,

and calves over years will be used to assess the effectiveness of the selection and mating program. Yearly evaluation of genetic trends will also allow making timely modifications to within-herd and across-herd selection objectives and mating plans.

ANTICIPATED OUTCOMES AND POTENTIAL BENEFITS

Beef quality and consumer satisfaction are important to the beef industry. Cattle buyers are demanding more uniform and consistent cattle, typically in large quantities, and consumers are demanding higher quality beef. Beef quality contributes to consumers' decision to purchase beef. An improvement of beef quality can increase demand, benefiting both producers and consumers.

Genomic technologies offer the opportunity to change the economic position of the beef industry through improved demand for beef products. Simulation studies on selection strategies to improve meat tenderness through selection of bulls or bulls and replacement females with desirable genomically-enhanced EPDs for Warner-Bratzler shear force revealed a potential mechanism to create a positive shift in beef demand. The shift in demand caused by improvement in tenderness, a trait where no direct pricing mechanism exists, results in consumers rewarding beef value chain participants with high prices for 'higher valued' products (Weaber and Lusk, 2007).

The value of using genetic markers or genomic selection for practical application mainly depends on accuracies of genomic breeding values (GEBV). Selection programs that incorporate a large number of markers covering the whole genome in genomic selection that has been reported to result in a 32% improvement in accuracy compared to parental average breeding values, have drawn the attention of both beef researchers and producers. However, it is imperative for these genomic tools to be developed in the populations targeted for improvement. The proposal outlined here was designed for this purpose.

The PI and co-PIs on this proposal take active roles in advocating for animal agriculture in general and educate the producers on the use of new genomic technologies available. Different venues will be used to publicize the work funded through this proposal and the importance of using genomic information in commercial herds. These venues will include: articles in the Florida Cattlemen & Livestock Journal, Gulf Coast Cattlemen, presentations during the Beef Improvement Federation (BIF) Convention, Cattle Industry Convention & NCBA Trade Show, different Field Days (e.g.: International Brangus Breeders Association, Adams Ranch Annual Field Day), national and international conferences, symposiums, meetings, and interviews with different TV and radio and printed press outlets.

ESTIMATED PROJECT FUNDING

Cost		
Tissue collection/DNA \$600		
Genotyping \$5,040		
Ultrasound \$1,440		
Meat Analysis Carcass \$6,600		
Animal Per diem (\$1.9/head/day; 4d) \$941		
6-mo support for one graduate student	6-mo support for one graduate student	
(stipend + fringe benefits)		
on Remission 6-mo, UF rate of \$17,346/Year \$8,673	Tuition	
Total Direct Cost\$37,269		
UF Indirect cost (12%) \$4,472		
Total \$41,741		

BUDGET JUSTIFICATION

Tissue collection and DNA extraction: \$600

Funding at \$5/sample is requested for materials to collect blood samples, and reagents to extract DNA from 120 steers.

High-density Genotypes, SkimSeek: \$5,040

We have budgeted \$42 per DNA sample for 120 head of steers to be genotyped with the high density SkimSeek product through Neogene (GeneSeek). This will provide detailed genotypes at the sequence level (millions of SNPs or genetic markers).

Carcass Ultrasound: \$1,440

Funding is requested for performing carcass ultrasound on 120 steers, at \$12/head.

Carcass and Meat quality: \$6,600

Funding is requested for collecting carcass data (HCW, REA, FOR, MARB), a steak and measuring meat quality traits (tenderness and palatability) on 120 steers, at \$55/head.

Animal Per Diem: \$941

Per Diem of \$1.96/head/day for 120 head of steers for 4 days is requested. Handling the animals is required for collection of blood samples.

Graduate Student: \$22,648

Support for 6 months of graduate student support to be involved in this project is requested. Tuition Remission for University of Florida for FY 2024 is \$17,346. The graduate student will be directly involved in all research aspects of the project, including data analysis for the annual genomic evaluation.

Indirect Costs: \$4,472

UF indirect rate of 12% of total direct costs.

RALUCA G. MATEESCU

Professor - Quantitative Genetics and Genomics, Dept. of Animal Sciences, UF

EDUCATION:

- Ph.D. May 2004 Animal Breeding & Genetics, Cornell University, Ithaca, NY
- M.S. May 2001 Animal Science, Cornell University, Ithaca, NY
- B.S. June 1997 Molecular Biology and Genetics, Bucharest University, Romania

PROFESSIONAL EXPERIENCE:

2019 - present Professor & Graduate Programs Director, Dept. of Animal Science, Univ. of Florida

2014 – 2019 Associate Professor & Graduate Programs Director, Dept. of Animal Science, University of Florida

- 2012 2014 Associate Professor, Dept. of Animal Science, Oklahoma State University
- 2006–2012 Assistant Professor, Dept. of Animal Science Oklahoma State University
- 2004–2006 Postdoctoral Associate, Cornell University, College of Veterinary Med.
- 1999 –2004 Graduate Research Assistant, Dept. of Animal Science, Cornell University

HONORS AND AWARDS:

- UF/IFAS Diversity Difference Maker Award, 2022
- University Term Professorship award, University of Florida, 2018-2021
- New Teacher Award, Gamma Sigma Delta, April 2012
- Recipient of National Wool Growers Memorial Fellowship, July 2003

PROFESSIONAL ACTIVITIES:

- · Editorial Advisory Board, CABI Agriculture and Bioscience, 2020 present
- Member, Beef Species Program Committee for ASAS. 2020-2023
- Member, Small Ruminant Program Committee for ASAS. 2020-2024
- Reviewer, Genomic Evaluation Configuration, American Brahman Breeders Association. June-July 2019
- Panel Member USDA-NIFA Tools and Resources for Animal Breed., Genet. & Genomics, Dec 2018
- Invited speaker, 7th International Symposium on Animal Functional Genomics, Adelaide, AU, Nov 2018.
- Invited speaker and co-chair "*Precision Livestock Farming in nutrition, genetics, and in physiology*" 69th Annual Meeting of the European Federation of Animal Science (EAAP), Dubrovnik, Croatia, Aug 2018.
- Chair/moderator of the "Molecular Genetics" section during the *World Congress on Genetics Applied to Livestock Production*. Auckland, NZ, Feb 2018.
- Member of the organizing committee, The Livestock High-Throughput Phenotyping and Big Data Analytics Meeting, November 13-14, 2017, Beltsville, MD.
- International Technical Consultant for the "*National Bovine Genome Center*" under National Bureau of Animal Genetic Resources Karnal, Indian Council of Agricultural Research, India. Oct. 2017 present.
- Member S-1064 Multistate Research Project: Genetic improvement of adaptation and reproduction to enhance sustainability of cow-calf production in the Southern US. Since Aug 2016
- Member, Beef Improvement Federation, 2016 present
- Panel Member, USDA-AFRI-NIFA, "1890 Institution Teaching, Research and Extension Capacity Building Grants", September 12-16, 2016
- Member, Breeding and Genetics Program, Am. Soc. of Animal Science's Southern Section, 2015 2019
- External reviewer for Alberta Livestock and Meat Agency, April 2015
- Panel Member USDA-NIFA Tools and Resources for Animal Breeding, Genetics and Genomics, Sept 14
- Reviewer 2013 OSU Planning Grants for Establishing Creative Interdisciplinary Programs
- · Journal of Animal Science Editorial Board Animal Genetics section, December, 2013-present
- Mentor, Women's Mentorship Program, Office of Multicultural Affairs within the Division of Institutional Diversity, Oklahoma State University. September 2011 – 2014.
- External Expert Reviewer for "Linear Models in Animal Breeding" course, online graduate curriculum in animal breeding and genetics funded through a USDA-NIFA Higher Education Challenge Grant, July 13

- Panel Member USDA-NIFA Tools and Resources for Animal Breeding, Genetics and Genomics, May 13
- External reviewer Louisiana Board of Regents' Pilot Funding for New Research (Pfund) program. Nov 09
- Member NCERA-214 Multistate Research Proj. Increased Efficiency of Sheep Production. 2009 present
- Organizer of the Cattle/Sheep Workshop, Plant and Animal Genome Mtg. Jan. 10-14, 2009
- The Porcine Reproductive and Respiratory Syndrome Coordinated Agricultural Project (PRRS CAP) Panel – Grant Reviewer. November 11, 2008
- Member of research team National Beef Cattle Evaluation Consortium. Since Aug. 2007.
- Member of NCERA-190 Multistate Research Project: Increased Efficiency of Sheep Production. 2007-09
- Member of the National Animal Genome Research Program (NRSP-8). Since Aug. 2006.
 - **PUBLICATIONS:** <u>Selected</u> Refereed Journal Articles. (*Graduate Student, ^FPostoctoral Fellow)
 - ^GRodriguez E.E, H. Hamblen, S. Flowers, J.D. Leal-Gutiérrez, C. Carr, T. Scheffler, and <u>R.G. Mateescu.</u> 2023. Carcass and Meat quality in Brangus Steers. *Translational Animal Science*. 7, 1-6
 - ^gDavidson, B.D., Sarlo Davila, K.M., **Mateescu, R.G.**, Dahl, G.E., and Laporta, J. 2022. Effect of in utero exposure to hyperthermia on postnatal hair length, skin morphology, and thermoregulatory responses. *J Dairy Sci* 105, 8898–8910. doi: 10.3168/jds.2022-22202.
 - ^FRezende F.M., ^{*}E. Rodriguez, ^FJ.D. Leal-Gutiérrez, M.A. Elzo, D.D. Johnson, C. Carr and <u>R.G. Mateescu.</u> 2021. Genomic approaches reveal pleiotropic effects in crossbred beef cattle. *FrontGenetics*.
 - ^{*}Leal-Gutiérrez J.D., M.A. Elzo, C. Carr, and **R.G. Mateescu.** 2020. RNA-seq analysis identifies cytoskeletal structural genes and pathways for meat quality in beef. *PLOS One*. 15(11): e0240895.
 - ^{*}Leal-Gutiérrez J.D., ^{*}F.M.Rezende, J.M Reecy, L.M. Krammer, F. Peñagaricano and <u>**R.G. Mateescu.**</u> 2020. Whole genome sequence data provides novel insights into the genetic architecture of meat quality traits in beef. *Frontiers in Genetics*.
 - ^GSarlo Davila K.M., A. Howell, A. Nunez, A. Orelien, V. Roe, ^{*}E. Rodriguez, ^FS. Dikmen, and <u>**R.G.**</u> <u>**Mateescu**</u>. 2020. Genome-wide association study identifies variants associated with hair length in Brangus cattle. *Animal Genetics*.
 - Mateescu R.G., ^{*}K.M. Sarlo Davila, ^FS. Dikmen, ^{*}E. Rodriguez, and P.A. Oltenacu. 2020. The effect of Brahman genes on body temperature plasticity of heifers on pasture under heat stress. *J. Anim. Sci.*.
 - *Leal J.D., M.A. Elzo, and **<u>R.G. Mateescu.</u>** 2020. Identification of eQTLs and sQTLs associated with meat quality in beef. *BMC Genomics.* 21:104.
 - *Leal J.D. and **<u>R.G. Mateescu.</u>** Genetic basis of improving the palatability of beef cattle: Current insights. Invited Review. *Food Biotechnology*.
 - ^{*}Leal J.D., Elzo, M.A., Johnson D.D., ^GHamblen H., and <u>**R.G. Mateescu.**</u> 2018 Genome wide association and gene enrichment analysis reveal membrane anchoring and structural proteins associated with meat quality in beef. *BMC Genomics.* 20(1):151
 - ^{*}Leal J.D., Rezende F.M., Elzo, M.A., Johnson D.D., Peñagaricano F. and <u>**R.G. Mateescu.**</u> 2018. Structural equation modeling and whole-genome scans uncover chromosome regions and enriched pathways for carcass and meat quality in beef. *Frontiers in Genetics*. 9:532.
 - *Flowers S., *H. Hamblen, *J.D. Leal, M.A. Elzo, D.D. Johnson and <u>R.G. Mateescu</u>. 2018. Fatty acid, mineral content and palatability of beef from a multibreed Angus-Brahman population. *J. Anim. Sci.*
 - *Hamblen H., A. Zolini, P.J. Hansen, P.A. Oltenacu, and <u>R.G. Mateescu</u>. 2018. Thermoregulatory response of Brangus heifers to naturally occurring heat exposure on pasture. J. Anim. Sci. 96:3131-37
 - Dikmen S., R.G. Mateescu, M.A. Elzo, and P.J. Hansen. 2018. Determination of the optimum contribution of Brahman genetics in an Angus-Brahman multibreed herd for regulation of body temperature during hot weather. J. Anim. Sci. 96:2175–2183.
 - ^{*}Gobena M., M.A. Elzo and <u>**R.G. Mateescu.**</u> 2018. Population structure and genomic breed composition in an Angus-Brahman crossbred cattle population. *Frontiers in Genetics*. 9:90-100
 - ^{*}Leal J.D., M.A. Elzo, D.D. Johnson and <u>**R.G. Mateescu**</u>. 2018. Effect of micro-calpain and calpastatin SNPs and haplotypes on Warner-Braztler shear force in a crossbred Brahman-Angus population. *Frontiers in Genetics*. 9:56-65
 - Elzo M.A., R. G. Mateescu, D.D. Johnson, T.L. Scheffler, J.M. Scheffler, C. Carr, D.O. Rae, J.G. Wasdin, M.D. Driver and J.D. Driver. 2017. Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes. *Livestock Science*. 202:58

PERSONAL INFORMATION

Office Addre	ss: University of Florida 2250 Shealy Dr. Gainesville, FL 32608	Home Address:	444 S.W. Wacahoota Rd. Micanopy, FL 32667 Cell: 352-213-4911
	<u>enadean @ un.edu</u>		<u>cenadean @gman.com</u>
EDUCATIO	<u>DN</u>		
Doctor of Phi	losophy		May 2006
Major: A	nimal Science Emphasis: Meat Scien	ce	
Universit	y of Missouri, Columbia, MO		
Master of Science			August 2004
Major: A	nimal Science Emphasis: Meat Scien	ce	
Oklahom	a State University, Stillwater, OK		
Bachelor of S	cience		May 2001
Major: A	nimal Science		
Oklahom	a State University, Stillwater, OK		
EMPLOYN	IENT		
Date	Position		Location
Currently	Professor and State Extension Spec	cialist	U. of Florida, Gainesville
2013-2022	Associate Professor and State Exte	nsion Specialist	U. of Florida, Gainesville

CURRENT ACADEMIC APPOINTMENT

70% Cooperative Extension Education/30% Undergraduate & Graduate Teaching

Assistant Professor and State Extension Specialist

EXTENSION PROGRAM

2007-2013

My position as Florida Meat Extension Specialist includes developing and implementing extension education to 1) ensure the safety and wholesomeness of meat; and, 2) improve the production, utilization, value, and sustainability of meat. Additionally, I develop and administer 3) youth programming in meat-animal agriculture, to develop responsible and productive youth to secure the future of our industry. The majority of educational effort has been toward developing educational programming materials and delivering presentations and training sessions at regional, state, and county meetings. I divide my time equally between these three major focus areas:

U. of Florida. Gainesville

Since promotion in 2013, I and/or my team of UF meat science staff, faculty members and graduate students have led 196 in-person trainings throughout Florida to over 17,100 Floridians. These programs have resulted in over 2,900 in-person contact hours per year

TEACHING PROGRAM

Since promotion in 2013, I have taught more than 1,600 Gators primarily in five undergraduate classes, ANS2002 The Meat We Eat, ANS3613L Live Animal and Carcass Evaluation, ANS4623C Pork Production, ANS3636C Meats, and ANS6932 HACCP Systems. My 30% teaching appointment includes regularly instructing these courses and coordinating the Intercollegiate Meat Judging Team and the Intercollegiate Livestock Judging Team as well as coaching the Intercollegiate Meat Animal Evaluation Team. Additionally, since 2007, I have chaired or co-chaired 12 master's graduates.

PRESENTATIONS

Since 2007, I have been an invited speaker for 4 international meetings, 10 national meetings, and 42 regional or state meetings.

FUNDING

Since 2007, I have been awarded grants and contracts toward our research and extension program exceeding \$426,000. Additionally, I have facilitated gathering monetary donations exceeding \$402,000.

PROFESSIONAL MEMBERSHIP

American Meat Science Association (AMSA) Member, 2001-present Intercollegiate Meat Judging Coaches Association (IMCA) Member, 2001-present American Society of Animal Science, (ASAS) Member, 2001-present National Cattlemen's Beef Association (NCBA) Member, 2012-present Southeastern Meat Association (SEMA) Academic Member, 2008-present Florida Cattlemen's Association (FCA) Member, 2008-present Florida Farm Bureau Federation Member, 2008-present

Professional Leadership

Member of LEAD IFAS Cohort 12, 2020

Member of UF Animal Sciences Department Chair Search committee, 2019 Board of Directors for the American Meat Science Association, 2017-2020 Chair of search committee for Meat Scientist Faculty Position, 2017 Chair of UF Animal Sciences Department Beef Committee, 2016-2022 American Meat Science Association Meat Lexicon Committee Member, 2016-present Invited member of National Pork Board Pork Quality Focus Team, 2016-present American Meat Science Association Pork 101 Committee Chairman, 2009-present Intercollegiate Meat Judging Coaches Association President, 2009-2010 Intercollegiate Meat Judging Coaches Association Executive Committee, 2013-2015 American Meat Science Association Extension Committee, 2007-present

PUBLICATIONS

Since 2006, I have authored or co-authored 31 peer-reviewed journal articles and an additional 59 extension documents and 54 research abstracts.

Fernanda Marcondes de Rezende, PhD

Assistant Professor of Statistical Genetics and Genomics Department of Animal Sciences, University of Florida (352) 294-6988, frezende@ufl.edu

Education

Ph.D.	May 2012	Animal Science, University of Sao Paulo, Brazil
M.S.	March 2009	Animal Science, University of Sao Paulo, Brazil
B.S.	July 2005	Animal Science, University of Sao Paulo, Brazil

Professional Experience

2021- present	Assistant Professor, University of Florida
2020-2021	Postdoctoral Associate, University of Florida
2019	Visiting Research Scientist, AgriBio Centre for AgriBioscience, Australia
2017-2020	Postdoctoral Researcher, University of Florida
2015-2020	Associate Professor, Federal University of Uberlandia, Brazil
2012-2015	Assistant Professor, Federal University of Uberlandia, Brazil
2007-2012	Graduate Research Assistant, University of Sao Paulo, Brazil

Honors and Awards

2022	Nominated and selected for the 2021 UF/IFAS High Impact Research Publ			
	representing the Animal Science Department			
2015-2016	Honored as Outstanding Teacher by the 1 st , 2 nd and 3 rd classes on Biotechnology			
	at Institute of Biotechnology, Federal University of Uberlandia, Brazil			
2017	Nominated for the Excellence in scientific research award, National Council for			
	Scientific and Technological Development "CNPq", Brazil			
2017-2018	Honored as Outstanding Teacher by the 74 th , 75 th , 76 th and 77 th classes of			
	Veterinary Medicine, Federal University of Uberlandia, Brazil			

Professional Society Membership

International Society for Animal Genetics American Dairy Science Association American Society of Animal Science Florida Cattlemen's Association

Refereed Publications (2018-present)

Lopes, F., Rosa, G., Pinedo, P., Santos, J. E. P., Chebel, R. C., Galvao, K. N., Schuenemann, G. M., Bicalho, R. C., Gilbert, R. O., Rodriguez-Zas, S. L., Seabury, C. M., **Rezende, F. M.**, Thatcher, W. (2022) Investigating functional relationships among health and fertility traits in dairy cows. Livestock Science, 266, 105122.

Dauria, B., Sigdel, A., Petrini, J., Bóscollo, P., Pilonetto, F., Salvian, M., **Rezende, F. M.**, Pedrosa, V. B., Machado, P., Coutinho, L. L., Bittar, C. M., Wiggans, G., Mourao, G. B. (2022). Assessing milk fatty acids as a biomarker of heat stress in a Brazilian Holstein population. *Journal of Dairy Science*, 105(4), 3296-3305.

Fernandes, A. C., Silva, V. H., Goes, C. P., Moreira, G. C. M., Godoy, T. F., Ibelli, A. M. G., Peixoto, J. O., Cantão, M. E., Ledur, M. C., **Rezende, F. M.** & Coutinho, L. L. (2021) Genome-wide detection of CNVs and their association with performance traits in broilers. *BMC Genomics*, 22, 354.

Rezende, F. M., Rodriguez, E., Leal-Gutiérrez, J. D., Elzo, M. A., Johnson, D., Carr, C. & Mateescu, R. G. (2021) Genomic approaches reveal pleiotropic effects in crossbred beef cattle. *Frontiers in Genetics*, 12, 627055.

Bonin, M. N., Pedrosa, V. B., Silva, S. L., Bünger, L., Ross, D., Gomes, R. C., Santana, M. H. A., Cucco, D. C., **Rezende, F. M.**, Ítavo, L. C. V., Novais, F. J., Pereira, M. W. F., Oliveira, E. C. M. & Ferraz, J. B. S. (2021) Genetic parameters associated with meat quality of Nellore cattle at different anatomical points of longissimus: Brazilian standards. *Meat Science*, 171, 108281.

Rezende, F. M., Haile-Mariam, M., Pryce, J. E. & Peñagaricano, F. (2020) Across-country genomic prediction of bull fertility in Jersey dairy cattle. *Journal of Dairy Science*, 103(12), 11618-11627.

Leal-Gutiérrez, J. D., **Rezende, F. M.**, Reece, J. M., Kramer, L. M., Peñagaricano, F. & Mateescu, R. G. (2020) Whole genome sequence data provides novel insights into the genetic architecture of meat quality traits in beef. *Frontiers in Genetics*, 11, 538640.

Pacheco, H. A., **Rezende, F. M.** & Peñagaricano, F. (2020) Gene mapping and genomic prediction of bull fertility using sex chromosome markers. *Journal of Dairy Science*, 103(4), 3304-3311.

Bonin, M. N., Silva, S. L., Bünger, L., Ross, D., Feijó, G. L. D., Gomes, R. C., Rennó, F. P., Santana, M. H. A., **Rezende, F. M.**, Ítavo, L. C. V., Novais, F. J., Surita, L. M. A., Bonin, M. N., Pereira, M. W. F. & Ferraz, J. B. S. (2020) Predicting the shear value and intramuscular fat in meat from Nellore cattle using Vis-NIR spectroscopy. *Meat Science*, 163, 108077.

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SPONSOR:

FL CATTLE ENHANCEMENT BOARD P.O. Box 421929 Kissimmee FL 34742-1929 United States Invoice Date: Invoice Period: Principal Investigator: Award Begin Date: Award End Date: 08/15/2024 05/01/2024 - 07/31/2024 Mateescu,Raluca 10/30/2023 07/31/2024

UF FEIN:

59-6002052

Sponsor Award ID:	29
Award Title:	Improving the accuracy of genomic selection for
	carcass and meat quality
Award Amount:	\$41,741.00

Invoice #	1000130489
UF Award #	AWD15789
Primary Project #	P0324557
Primary Department:	60090000
Current Invoice Amount:	\$31,701.26

Description	Current	Cumulative
Personnel - Salary Personnel - Fringe Benefits Tuition Contractual Services Animal	\$16,900.03 \$808.45 \$0.00 \$7,346.70 \$3,249.77	\$21,305.66 \$1,328.30 \$4,038.57 \$7,346.70 \$3,249.77
Direct Cost	\$28,304.95	\$37,269.00
Facilities and Administrative Costs	\$3,396.31	\$4,472.00
Total	\$31,701.26	\$ <mark>41,741.00</mark>

For billing questions, please call 352.392.1235 Torres,Kannika S <u>kannika@ufl.edu</u> Please reference the UF Award Number and Invoice Number in all correspondence

By signing this report, I certify to the best of my knowledge and belief that the report is true, complete, and accurate, and the expenditures, disbursements and cash receipts are for the purposes and objectives set forth in the terms and conditions of the federal award. I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil, or administrative penalties for fraud, false statements, false claims or otherwise. (U.S Code Title 18, Section 1001 and Title 31, Sections 3729-3730 and 3801-3812).

Outstanding Balance: \$31,701.26 Note: Outstanding balance includes current invoice amount

Cumulative Invoices:

Payments Received:

Payment History

\$41,741.00

\$10,039.74

Certifying Official

Kanníka Torres

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Project ID	Deptid	Department Name	Current	Cumulative
P0324557	60090000	AG-ANIMAL SCIENCES	\$31,701.26	\$41,741.00