

Wellison Jarles da Silva Diniz, Ph.D.

North Dakota State University
Department of Animal Sciences
P.O. Box 6050, Dept. 7630
Fargo, ND 58108-6050

w.dasilvadiniz@ndsu.edu
Phone: (+1) 701 541 1997
ORCID <https://goo.gl/zSsREs>

SUMMARY

- Molecular geneticist and bioinformatics expert with 5+ years of experience in functional genomics and HPC for data analysis
- Interdisciplinary collaborator with an approach to handle research challenges with an optimal outcome
- Expertise to work with genomic and systems biology data analyses

EDUCATION

2015-10 – 2019-10	Ph.D. in Evolutionary Genetics and Molecular Biology Federal University of São Carlos, SP, Brazil
2013-09 – 2015-08	M.Sc. in Evolutionary Genetics and Molecular Biology Federal University of São Carlos, SP, Brazil
2008-03 – 2012-06	Bachelor in Animal Sciences (husbandry) Federal Rural University of Pernambuco, Garanhuns, Brazil

TECHNIQUES/SKILLS

Data Analysis

- Unix and R programming and high-performance computing
- Genomics, transcriptomics, metabolomics, and epigenomics
- Systems biology data integration and functional genomics

Molecular Biology

- PCR, qPCR, electrophoresis, RNA-Seq, RRBS methylation

Management

- Trained students in RNA-seq data analyses (1) and molecular biology techniques (5)

Written and oral communication

- Proficient in both spoken and written English
- Published 20 peer-reviewed papers, and 9 conference abstracts
- Presented in 4 international conferences

RESEARCH / WORK EXPERIENCE

	North Dakota State University. Postdoctoral Researcher Fellow. Department of Animal Sciences
	Genomics and Bioinformatics
2020-01 – present	<ul style="list-style-type: none">▪ Analyzing the effects of pre- and perinatal maternal nutrition on fetal developmental programming in beef cattle based on genomic analyses▪ Transcriptomic analyses of placentogenesis in ewe
	Brazilian Agricultural Corporation. Ph.D. Student Researcher Department of Research and Development
	Genomics and Bioinformatics
2015-09 – 2019-10	<ul style="list-style-type: none">▪ Analyzed and interpreted genome-wide SNP array, RNA-seq, and RRBS methylation data using Unix/linux and R▪ Identified different epigenetic markers between efficient and inefficient animals by using R to analyze liver methylation▪ Measured significant genome-wide miRNA and mRNA transcriptional differences in bovine muscle▪ Trained master students in mRNA data analyses

Molecular Biology

- Elucidated the genetic basis underlying feed efficiency, mineral content, and meat quality traits in cattle by applying qPCR and PCR analyses
- Characterized mRNA and miRNA genome-wide profile by sampling liver and muscle tissues

2018-03 – 2019-02 Technical University of Denmark-DTU. **Guest Ph.D. Researcher**
Department of Mathematics and Computer Science

Systems Biology and Data analysis

- Developed and implemented bioinformatic approaches to identify miRNA-mRNA regulatory networks
- Screened public databases to identify miRNA gene targets
- Collaborated in metabolomics data analysis and network construction associated to feed efficiency in pigs

2013-09 – 2015-08 Brazilian Agricultural Corporation. **M.Sc. Student Researcher**
Department of Research and Development

Genomics and Bioinformatics

- Analyzed muscle transcriptomics data to identify differentially expressed genes underlying muscle mineral composition in cattle

AWARDS

2014. Best Poster in the X Genetics Winter School

São Paulo State University, UNESP/FCAV, Jaboticabal, SP, BR

2013. Best Alumni award in Animal Sciences Bachelor

Federal Rural University of Pernambuco, Campus Garanhuns, PE, BR

2013. Honorable mention for the best poster – Improvement genetics and reproduction

Northeastern Conference in Animal Production. Fortaleza, CE, BR

SHORT COURSES

2019 **Systems Biology and Gene Networks Inference: Application to Livestock Breeding and Genetics**

University of São Paulo- ESALQ, Piracicaba, Brazil. 35 hrs

2018 **Introduction to Scientific Python**

Computer Science Retreat, Malmö, Sweden. 08 hrs

2018 **Methods for Analyzing Complex Traits GWAS data**

Aarhus University, Aarhus, Denmark. 08 hrs

2018 **XI Summer School in Bioinformatics**

University of São Paulo, Ribeirão Preto, BR. 80 hrs

2016 **Data Analysis in SAS**

São Paulo State University, Jaboticabal, BR. 42 hrs

2015 **RNA-Seq Data Analysis**

Brazilian Agricultural Research Corporation, Piracicaba, BR. 24 hrs

2015 **Gene network with AWM/PCIT and Cytoscape**

Brazilian Agricultural Research Corporation, São Carlos, BR. 24 hrs

TEACHING

12- 2017 – 12 -2017 **Invited lecturer:** "RNA-Sequencing: Exploring new frontiers in animal genetics". Master students in Evolutionary Genetics and Molecular Biology. Prof. Dr. Luciana Regitano. Federal University of São Carlos

Course: Genetics and Animal Breeding

Teaching assistant

10-2016 – 02-2017 Undergraduate Biotechnology course under the guidance of Dr. Marcos R. Chiaratti. Federal University of São Carlos. **Course:** Animal Biotechnology.

03-2016 – 09-2016 **Teaching assistant**

PEER REVIEWER



2020	Animal Production Science
	BMC Genomics
	Heredity
	Scientific Reports
2019	Journal of Animal Feed Science and Technology
	Journal of Agricultural and Food Chemistry

PUBLICATIONS

1. **Diniz WJS**, Banerjee P, Mazzone G, et al. Interplay among miR-29 family, mineral metabolism, and gene regulation in Nelore muscle. **Molecular Genetics and Genomics**. Doi: 10.1007/s00438-020-01683-9.
2. De Souza MM, Zerlotini A, [...], **Diniz WJS**, et al. Allele-specific expression is widespread in *Bos indicus* muscle and affects meat quality candidate genes. **Scientific Reports**. Doi: 10.1038/s41598-020-67089-0.
3. Afonso J, Fortes MSR, Reverter A, **Diniz WJS**, et al.. Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. **Scientific Reports**. Doi: 10.1038/s41598-020-65454-7.
4. Carmelo VA, Banerjee P, **Diniz WJS**, et al. Blood metabolites associated with feed efficiency and related-traits in Duroc and Landrace. **Scientific Reports**. 2020. Doi: 10.1038/s41598-019-57182-4.
5. Lima AO, Koltjes JE, **Diniz WJS**, et al. Potential biomarkers for feed efficiency-related traits in Nelore cattle identified by co-expression network and integrative genomics analyses. **Frontiers in Genetics**. Doi:10.3389/fgene.2020.00189.
6. **Diniz WJS**, da Rosa KO, Tizioto PC, Mourão GB, de Oliveira PSN, Regitano LCA. *FABP1* and *SLC2A5* expression levels affect feed efficiency-related traits. **AgriGene**. 2019. Doi: 10.1016/j.aggene.2019.100100.
7. **Diniz WJS**, Banerjee P, Regitano LCA. Cross-talk between mineral metabolism and meat quality: a systems biology overview. **Physiological Genomics**. 2019. Doi: 10.1152/physiolgenomics.00072.2019.
8. **Diniz WJS**, Mazzone G, Coutinho LL, et al. Detection of co-expressed pathway modules associated with mineral concentration and meat quality in Nelore cattle. **Frontiers in Genetics**. 2019. Doi:10.3389/fgene. 2019.00210.
9. De Oliveira PSN, Coutinho LL, [...] **Diniz WJS**, et al. MiRNA-mRNA co-expression reveals potential regulatory roles of miRNAs in fatty acid composition in skeletal muscle. **Frontiers in Genetics**. 2019. Doi: 10.3389/fgene.2019.00651.
10. Afonso J, Coutinho LL, [...], **Diniz WJS**, et al. Muscle transcriptome analysis reveals genes and metabolic pathways related to mineral concentration in *Bos indicus*. **Scientific Reports**. 2019. Doi: 10.1038/s41598-019-49089-x.
11. **Diniz WJS**, Rosa KO, Coutinho LL, et al. *KCNJ11* gene expression is associated to feed consumption and growth traits in Nelore beef cattle. **Agri Gene**. 2018. Doi: 10.1016/j.aggene.2018.05.004.
12. De Oliveira PSN, Coutinho LL, [...], **Diniz WJS**, et al. An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. **Scientific Reports**. 2018. Doi: 10.1038/s41598-018-35315-5.
13. De Souza MM, Zerlotini A, [...], **Diniz WJS**, et al. A comprehensive manually-curated compendium of bovine transcription factors. **Scientific Reports**. 2018. Doi: 10.1038/s41598-018-32146-2.
14. **Diniz WJS**, Canduri F. Bioinformatics: an overview and its applications. **Genetics and Molecular Research**. 2017. Doi: 10.4238/gmr16019645.
15. **Diniz WJS**, Vilaça LF, Melo TF, et al. Polymorphisms within the 3'UTR region of *SLC11A1* gene in Holstein and Girolando dairy herds. **Medicina Veterinária (UFRPE)**. 2017. Doi: 10.26605/medvet-n1-1626.

-
16. **Diniz WJS**, Coutinho LL, Tizioto PC, et al. Iron content affects lipogenic gene expression in the muscle of Nelore beef cattle. **Plos One**. 2016. Doi: 10.1371/journal.pone.0161160.
 17. Tizioto PC, Coutinho LL, [...] **Diniz WJS**, et al. Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. **Scientific Reports**. 2016. Doi: 10.1038/srep39493.
 18. De Souza MM, Niciura SCM, [...], **Diniz WJS**, et al. Allele- and parent-of-origin-specific effects on expression of the KCNJ11 gene: A candidate for meat tenderness in cattle. **Genetics and Molecular Research**. 2016. Doi: 10.4238/gmr.15038549.
 19. De Oliveira PSN, Tizioto PC, [...], **Diniz WJS**, et al. A single nucleotide polymorphism in NEUROD1 is associated with production traits in Nelore beef cattle. **Genetics and Molecular Research**. 2016. Doi:10.4238/gmr.15028161.
 20. Vilaça LF, **Diniz WJS**, Melo TF, et al. BoLA-DRB3 gene polymorphisms in 5/8 Girolando and Holstein dairy cattle herds in the Pernambuco State. **Arch. Zootec**. 2016. Doi: 10.21071/az.v65i249.435.
-

PUBLICATIONS

Under Review

1. **Diniz WJS**, Crouse MS, Cushman RA, et al. Multi-tissue regulatory network uncovers maternal nutrition effects in developmental programming of beef cattle. **Scientific Reports**.
-

CONFERENCE PROCEEDINGS

-
1. **Diniz WJS**, Dorsam ST, Vasquez-Hidalgo VA, et al. Genome-wide expression profile of trophoblastic cells during late pregnancy in ewes. In: **2020 ASAS-CSAS-WSASAS Virtual Annual Meeting and Trade Show**. 2020. USA.
 2. **Diniz WJS**, Crouse MS, Caton JS, et al. Maternal energy restriction in early gestation affects MYOG network topology of bovine skeletal muscle. In: **2020 ASAS-CSAS-WSASAS Virtual Annual Meeting and Trade Show**. 2020. USA.
 3. **Diniz WJS**, Banerjee P, Mazzoni G, et al. Interplay among miRNA, gene expression, and mineral metabolism in Nelore cattle. In: **37th International Society for Animal Genetics**, 2019, Lleida, Spain.
 4. **Diniz WJS**, Banerjee P, Mazzoni G, et al. Network analysis uncovers the interplay among miRNA, mRNA and iron concentration in Nelore muscle. In: **70th Annual Meeting of the European Federation of Animal Science**, 2019, Ghent.
 5. **Diniz WJS**, Cesar ASM, Coutinho LL, Kadarmideen HN, Regitano LCA. Mineral content and immune system association revealed by Nelore muscle gene co-expression network. In: **69th Annual Meeting of the European Federation of Animal Science**, 2018, Dubrovnik.
 6. de Souza MM, [...], **Diniz WJS**, et al. Genome-wide distribution of allele-specific expression in Nelore steers muscle. In: **World Congress on Genetics Applied to Livestock Production**, 2018, New Zealand.
 7. Afonso J, [...], **Diniz WJS**, Lima AO, et al. Genetic factors related to mineral concentration in Nelore cattle unveiled by transcriptome analysis. In: **7th International Symposium on Animal Functional Genomics**, 2018 Adelaide, Australia.
 8. de Souza MM, [...], **Diniz WJS**, et al. In silico identification of putative cis-eQTLs affecting allelic expression. In: **7th International Symposium on Animal Functional Genomics**, 2018 Adelaide, Australia.
 9. **Diniz WJS**, Cesar ASM, Geistlinger L, et al. Co-expression network analysis identifies genes associated with meat tenderness. In: **International Society for Animal Genetics**, 2017, Dublin.
-