Lihe Liu **June 2023**

Contact Information

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Research Interests

My research interest lies in the field of computational biology and bioinformatics. Specifically, multi-omics data integration. Currently, I am working on the evaluation of the effects of prenatal nutritional factors on the offspring epigenome and transcriptome. I also have interest in software development.

Education

University of Wisconsin-Madison, Madison, Wisconsin USA

Ph.D., Animal Sciences, 09/2020 - 08/2023 (Expected)

- Advisor: Dr. Francisco Peñagaricano

M.S., Computer Sciences, 09/2021 - 05/2023

University of Florida, Gainesville, Florida USA

M.S., Animal Sciences, 08/2018 - 08/2020

- Thesis: Deciphering Complex Biological Processes Using Gene Coexpression Networks
- Committee: Dr. Francisco Peñagaricano, Dr. Samantha Brooks and Dr. Matias Kirst

Huazhong Agricultural University, Wuhan, P.R. China

B.S., Animal Sciences, 09/2014 - 07/2018

- Joint program (50 credits for B.S.) at China Agricultural University, Beijing P.R. China
- Study abroad (18 credits for B.S.) at University of Florida, FL USA

Work Experience

Department of Animal and Dairy Sciences
University of Wisconsin-Madison, Madison, Wisconsin USA

- Graduate Research Assistant **09/2020 - Present**

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

- Graduate Research Assistant **09/2018 - 08/2020**
- Graduate Teaching Assistant **Fall 2019**

Peer Reviewed Journal Articles

2023

8. R Amorín*, **L Liu***, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2023) **Maternal diet induces persistent DNA methylation changes in the muscle of beef calves.** *Sci Rep.* 13, 1587. doi: 10.1038/s41598-023-28896-3

2022

7. CM Sheftel, **L Liu**, SL Field, SR Weaver, CM Vezina, F Peñagaricano and LL Hernandez(2022) Impact of Fluoxetine Treatment and Folic Acid Supplementation on the Mammary Gland Transcriptome During Peak Lactation. *Front Pharmacol.* 13:828735. doi: 10.3389/fphar.2022.828735

2021

6. **L Liu**, R Amorín, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2021) Maternal methionine supplementation during gestation alters alternative splicing and DNA methylation in bovine skeletal muscle. *BMC Genomics*. 22, 780. doi: 10.1186/s12864-021-08065-4
5. MA Mezera, W Li, **L Liu**, R Meidan, F Peñagaricano, MC Wiltbank (2021) Effect of natural pre-luteolytic prostaglandin F2α pulses on the bovine luteal transcriptome during spontaneous luteal regression. *Biology of Reproduction* . 105 (4), 1016-1029. doi: 10.1093/biolre/ioab123
4. SL Field, MG Marrero, **L Liu**, F Peñagaricano, J Laporta (2021) Histological and transcriptomic analysis of adipose and muscle of dairy calves supplemented with 5-hydroxytryptophan. *Scientific reports*. 11.1: 1-10. doi: 10.1038/s41598-021-88443-w

2020

3. **L Liu**, R Amorín, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2020) Differential network analysis of bovine muscle reveals changes in gene coexpression patterns in response to changes in maternal nutrition. *BMC genomics*. 21.1: 1-12. doi: 10.1186/s12864-020-07068-x
2. H Louvandini, PS Corrêa, R Amorín, **L Liu**, EH Ieda, CR Jimenez, SM Tsai, CM McManus, F Peñagaricano (2020) Gestational and lactational exposure to gossypol alters the testis transcriptome. *BMC genomics*. 21(1), 1-11. doi: 10.1186/s12864-020-6487-2
1. A Sigdel, **L Liu**, R Abdollahi-Arpanahi, I Aguilar, F Peñagaricano (2020) Genetic dissection of reproductive performance of dairy cows under heat stress. *Animal Genetics*. 51(4), 511-520. doi: 10.1111/age.12943

Software Development

R package

- EnrichKit - R /Web: performs over-representation test in multiple biological pathway databases.

Honors/Awards

2022 • ***Neal A. Jorgensen* Genome Travel Awards** | PAG Conference 30 (San Diego)

2019 • ***Top-up Award*** | University of Florida, ANS Department

2017 • ***Study Abroad Scholarship*** | China Scholarship Council (CSC)

2016 • ***National Scholarship of P.R.China (Undergraduate)*** | Ministry of Education

2014-2015 • ***Outstanding Undergraduate Award*** | Huazhong Agricultural University, China

Technical Skills

Bioinformatics & Data Analysis • RNA-seq, WGB-Seq, Bioconductor, Tidyverse, Pandas/NumPy/SciPy, scikit-learn, TensorFlow

Programming Languages • Python, Java, R, Shell (Bash), SQL (MySQL), C++, JavaScript/HTML/CSS, MATLAB

Framework • Django, Spring Boot, ReactJS, NodeJS, JUnit, CUDA, OpenMP

Developer Tool • Git, Docker, Conda, Nextflow, Slurm, GCP, AWS (EC2, RDS, S3), Elasticsearch, Jira