

Ziliang Luo

Department of Genetics, University of Georgia, Athens, GA

kennyluo4@gmail.com

352-281-7270

www.ziliangluo.com

Education

2017 – 2021	Ph.D.	Agronomy	University of Florida
2010 – 2014	B.S.	Plant Science and Technology	Huazhong Agricultural University

Research & Work Experience

2022 – present, Postdoctoral fellow, Department of Genetics, University of Georgia.
Studying plant cis-regulatory elements biology using single-cell and spatial omics approaches. Supervisor: Dr. Bob Schmitz

2021 – 2022, Postdoctoral fellow, Department of Agronomy, University of Florida.
Investigating the genes controlling peanut nodule symbiosis and sugarcane orange rust resistance using single-cell and spatial transcriptomics. Supervisor: Dr. Jianping Wang

2017 – 2021, Graduate Research Assistant, Department of Agronomy, University of Florida.
Studying the genetic and epigenetic control of peanut (*Arachis hypogaea*) nodulation at the infection stage by RNA-seq, whole genome bisulfite sequencing and CRISPR/Cas9. Supervisor: Dr. Jianping Wang

2015 – 2016, Data analyst, Shanghai OE Biotech. Co., Ltd.
Conducting microarray and RNA-seq gene expression analysis; Screening candidate genes by clinical survival analysis and gene expression analysis using the Cancer Genome Atlas database.

2014 – 2015, Research Assistant, National Key Laboratory of Crop Genetic Improvement.
Field management and phenotyping; Phenotype data and QTL analysis of rapeseed (*Brassica napus*) yield-related traits. Supervisor: Dr. Jun Zou and Dr. Jinling Meng

Publications

* indicates co-first author.

Bang, S., Zhang, X., Gregory, J., **Luo, Z.**, Chen, Z., Minow, M.A., Galli, M., Gallavotti, A. and Schmitz, R.J., 2025. WUSCHEL-dependent chromatin regulation in maize inflorescence development at single-cell resolution. *Genome biology*, 26(1), p.329.

Yan, H., Mendieta, J.P., Zhang, X., **Luo, Z.**, Marand, A.P., Liang, Y., Minow, M.A., Zhong, Y., Jin, Y., Jang, H. and Li, X., 2025. A single-cell rice atlas integrates multi-species data to reveal cis-regulatory evolution. *Nature Plants*, pp.1-22.

Jin, Y., Yan, H., Zhu, X., Yang, Y., Jia, J., Sun, M., Najeeb, A., Luo, J., Wang, X., He, M. and Xu, B., **Luo, Z.**, Huang, L. 2025. Single-cell transcriptomes reveal spatiotemporal heat stress response in pearl millet leaves. *New Phytologist*.

Luo, Z. and Schmitz, R.J., 2025. Protocol for preparing fresh frozen soybean tissues for spatial transcriptomics. *STAR protocols*, 6(2), p.103790.

- Marand, A.P., Jiang, L., Gomez-Cano, F., Minow, M.A., Zhang, X., Mendieta, J.P., **Luo, Z.**, Bang, S., Yan, H., Meyer, C. and Schlegel, L., 2025. The genetic architecture of cell type-specific cis regulation in maize. *Science*, 388(6744), p.eads6601.
- Zhang, X. *, **Luo, Z.** *, Marand, A.P. *, Yan, H., Jang, H., Bang, S., Mendieta, J.P., Minow, M.A. and Schmitz, R.J., 2025. A spatially resolved multi-omic single-cell atlas of soybean development. *Cell*, 188(2), pp.550-567.
- Zhou, Y., Mihail, E.S., **Luo, Z.**, Sood, S., Islam, M.S. and Wang, J., 2025. Exploring Morphological, Transcriptomic, and Metabolomic Differences Between Two Sister Lines with Contrasting Resistance to Orange Rust Disease in Sugarcane. *International Journal of Molecular Sciences*, 26(8), p.3490.
- Jin, Y., Yan, H., Zhu, X., Yang, Y., Jia, J., Sun, M., Najeeb, A., Luo, J., Wang, X., He, M., Xu, B., Li, X., **Luo, Z.**, Mao, C. and Huang, L., 2025. Single - cell transcriptomes reveal spatiotemporal heat stress response in pearl millet leaves. *New Phytologist*.
- Zhang, Y., Jang, H., **Luo, Z.**, Dong, Y., Xu, Y., Kantamneni, Y. and Schmitz, R.J., 2024. Dynamic evolution of the heterochromatin sensing histone demethylase IBM1. *Plos Genetics*, 20(7), p.e1011358.
- Peng, G., Liu, M., **Luo, Z.**, Deng, S., Wang, Q., Wang, M., Chen, H., Xiao, Y., Zhang, Y. & Hong, H. (2024). An E3 ubiquitin ligase CSIT2 controls critical sterility-inducing temperature of thermo-sensitive genic male sterile rice. *New Phytologist*,
- Yan, H., Mendieta, J. P., Zhang, X., Marand, A. P., Liang, Y., **Luo, Z.**, Roule, T., Wagner, D., Tu, X. & Wang, Y. (2024). Evolution of cell-type-specific accessible chromatin regions and the cis-regulatory elements that drive lineage-specific innovation. *BioRxiv*, 2024.2001.2008.574753,
- Liu, H., Lin, X., Li, X., **Luo, Z.**, Lu, X., You, Q., Yang, X., Xu, C., Liu, X. & Liu, J. (2023). Haplotype variations of sucrose phosphate synthase B gene among sugarcane accessions with different sucrose content. *BMC genomics*, 24, 1-12,
- Peng, G., Liu, M., Zhu, L., Luo, W., Wang, Q., Wang, M., Chen, H., **Luo, Z.**, Xiao, Y. & Zhang, Y. (2023). The E3 ubiquitin ligase CSIT1 regulates critical sterility-inducing temperature by ribosome-associated quality control to safeguard two-line hybrid breeding in rice. *Molecular plant*, 16, 1695-1709,
- Zhao, Z., Wang, Y., Peng, Z., **Luo, Z.**, Zhao, M. & Wang, J. (2023). Allelic expression of AhNSP2-B07 due to parent of origin affects peanut nodulation. *Frontiers in plant science*, 14, 1193465,
- Wang, M. et al. (2022). Methylesterification of cell-wall pectin controls the diurnal flower-opening times in rice. *Molecular plant*, 15, 956-972,
- Peng, Z., Chen, H., Tan, L., Shu, H., Varshney, R. K., Zhou, Z., Zhao, Z., **Luo, Z.**, Chitikineni, A. & Wang, L. (2021). Natural polymorphisms in a pair of NSP2 homoeologs can cause loss of nodulation in peanut. *Journal of Experimental Botany*, 72, 1104-1118,
- Zhao, Y., Feng, M., Paudel, D., Islam, T., Momotaz, A., **Luo, Z.**, Zhao, Z., Wei, N., Li, S. & Xia, Q. (2021). Advances in Genomics Approaches Shed Light on Crop Domestication. *Plants*, 10, 1571,
- Luo, Z.** *, Cui, R. *, Chavarro, C., Tseng, Y.-C., Zhou, H., Peng, Z., Chu, Y., Yang, X., Lopez, Y. & Tillman, B. (2020). Mapping quantitative trait loci (QTLs) and estimating the epistasis

- controlling stem rot resistance in cultivated peanut (*Arachis hypogaea*). *Theoretical and Applied Genetics*, 133, 1201-1212,
- Peng, Z., Paudel, D., Wang, L., **Luo, Z.**, You, Q. & Wang, J. (2020). Methods for Target Enrichment Sequencing via Probe Capture in Legumes. *Legume Genomics*. Humana, New York, NY.
- Shu, H., **Luo, Z.**, Peng, Z. & Wang, J. (2020). The application of CRISPR/Cas9 in hairy roots to explore the functions of AhNFR1 and AhNFR5 genes during peanut nodulation. *BMC plant biology*, 20, 1-15,
- Yang, X., **Luo, Z.**, Todd, J., Sood, S. & Wang, J. (2020). Genome-wide association study of multiple yield traits in a diversity panel of polyploid sugarcane (*Saccharum* spp.). *The Plant Genome*, 13, e20006,
- You, Q., Sood, S., **Luo, Z.**, Liu, H., Islam, M. S., Zhang, M. & Wang, J. (2020). Identifying genomic regions controlling ratoon stunting disease resistance in sugarcane (*Saccharum* spp.) clonal F1 population. *The Crop Journal*,
- Weijian, Z. et al. (2019). The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. *Nature genetics*, 51, 865–876,
- Yang, X., Song, J., Todd, J., Peng, Z., Paudel, D., **Luo, Z.**, Ma, X., You, Q., Hanson, E. & Zhao, Z. (2019a). Target enrichment sequencing of 307 germplasm accessions identified ancestry of ancient and modern hybrids and signatures of adaptation and selection in sugarcane (*Saccharum* spp.), a ‘sweet’ crop with ‘bitter’ genomes. *Plant biotechnology journal*, 17, 488-498,
- Yang, X., Sood, S., **Luo, Z.**, Todd, J. & Wang, J. (2019b). Genome-wide association studies identified resistance loci to orange rust and yellow leaf virus diseases in sugarcane (*Saccharum* spp.). *Phytopathology*, 109, 623-631,
- Yang, X., Todd, J., Arundale, R., Binder, J. B., **Luo, Z.**, Islam, M. S., Sood, S. & Wang, J. (2019c). Identifying loci controlling fiber composition in polyploid sugarcane (*Saccharum* spp.) through genome-wide association study. *Industrial Crops and Products*, 130, 598-605,
- You, Q., Yang, X., Peng, Z., Islam, M. S., Sood, S., **Luo, Z.**, Comstock, J., Xu, L. & Wang, J. (2019). Development of an Axiom Sugarcane100K SNP array for genetic map construction and QTL identification. *Theoretical and Applied Genetics*, 132, 2829-2845,
- Luo, Z.** *, Wang, M. *, Long, Y., Huang, Y., Shi, L., Zhang, C., Liu, X., Fitt, B. D., Xiang, J. & Mason, A. S. (2017). Incorporating pleiotropic quantitative trait loci in dissection of complex traits: seed yield in rapeseed as an example. *Theoretical and Applied Genetics*, 130, 1569-1585,
- Wang, X., Long, Y., Wang, N., Zou, J., Ding, G., Broadley, M. R., White, P. J., Yuan, P., Zhang, Q. & **Luo, Z.** (2017). Breeding histories and selection criteria for oilseed rape in Europe and China identified by genome wide pedigree dissection. *Scientific Reports*, 7, 1-11,
- Zhang, Y., Thomas, C. L., Xiang, J., Long, Y., Wang, X., Zou, J., **Luo, Z.**, Ding, G., Cai, H. & Graham, N. S. (2016). QTL meta-analysis of root traits in *Brassica napus* under contrasting phosphorus supply in two growth systems. *Scientific Reports*, 6, 1-12,
- Zou, J., Raman, H., Guo, S., Hu, D., Wei, Z., **Luo, Z.**, Long, Y., Shi, W., Fu, Z. & Du, D. (2014). Constructing a dense genetic linkage map and mapping QTL for the traits of flower development in *Brassica carinata*. *Theoretical and Applied Genetics*, 127, 1593-1605

Research Presentations

Oral presentations

- 2026 *Adapting a high-resolution, cost-efficient spatial platform for plant research*, Workshop on spatial omics in plants, Kanagawa, Japan
- 2024 *The spatially resolved multi-omic single-cell atlas of soybean*, Informatics Interest Group seminar, Minnesota Supercomputing Institute, University of Minnesota
- 2022 *Identifying sugarcane orange rust resistance genes by single-cell and spatial transcriptomics*, The American Society of Sugarcane Technologists (ASSCT) Annual Meeting, ASSCT
- 2020 *Mapping QTL controlling white mold resistance in peanut (Arachis Hypogaea)*, Agronomy Annual Symposium, University of Florida
- 2019 *Molecular and epigenetic controls of peanut (Arachis hypogaea L.) nodulation at early infection stage*, Agronomy Annual Symposium, University of Florida
- 2019 *Utilize symbiosis to improve agricultural sustainability*, Three Minute Thesis (3MT) presentation, University of Florida

Poster presentations

- 2025 *Adapting high-res and low-cost spatial omics for plant research*, Plant Center Retreat, University of Georgia
- 2025 *Spatially resolved chromatin profiling for plant tissues using spatial ATAC-seq*, Single-Cell Approaches in Plant Biology, Gordon Research Conference
- 2025 *Enhancing the understanding of soybean biology through spatial transcriptomics*, Soy 2025, University of Wisconsin - Madison
- 2024 *Constructing spatial transcriptome atlas of poplar*, Plant Center Retreat, University of Georgia
- 2024 *Single-cell and spatial regulatory maps of poplar*, Genomic Science Program, U.S. Department of Energy.
- 2023 *The spatial-temporal transcriptome of soybean seed development*, Plant Genomes, Systems Biology & Engineering, Cold Spring Harbor Laboratory
- 2023 *The spatial-temporal transcriptome of soybean seed development*, Single-Cell Approaches in Plant Biology, Gordon Research Conference
- 2022 *Using spatial transcriptomics to reveal the responsive genes in sugarcane infected by orange rust disease*, Florida Genetics Symposium, University of Florida
- 2021 *Identifying genomic regions and evaluating the epistasis controlling stem rot resistance in cultivated peanut (Arachis hypogaea)*, American Peanut Research & Education Society Annual Meeting
- 2020 *Host gene expression and epigenetic regulation in peanut (Arachis hypogaea) in response to rhizobial early infection*, American Peanut Research & Education Society Annual Meeting
- 2020 *Host gene expression and epigenetic regulation in peanut (Arachis hypogaea) in response to rhizobial early infection*, Plant Biology 2020 Worldwide Summit, American Society of Plant Biologists.

2018 *Mapping QTL Controlling White Mold Resistance in Peanut (Arachis Hypogaea)*, Florida Genetics Symposium, University of Florida.

Awards & Grants

2025 Plant Center Retreat poster presentation award (2st place), University of Georgia,
2024 Plant Center Retreat poster presentation award (1st place), University of Georgia
2020 CALS Outstanding Achievement Awards, University of Florida
2020 Agronomy Graduate Student Association Awards (3rd place), Agronomy Annual Symposium, University of Florida
2019 Travel Award, Summer Institute in Statistical Genetics, University of Washington
2017 - 2019 Grinter Fellowship, University of Florida
2014 Merit Student Award, Huazhong Agricultural University
2012 Academic Progress Award, Huazhong Agricultural University
2011 Students Research Funding, Huazhong Agricultural University, project: Transferring clubroot resistance from radish to oilseed rape using new-type *Brassica napus*

Teaching and Mentorship

Teaching Assistant

2020 Spring, Plant Chromosomes and Genomics (Graduate), University of Florida
2018 - 2020 Summer, Genetics (Undergraduate), University of Florida
2013 Fall, Seed Industrialization and Technology (Undergraduate), Huazhong Agricultural University

Co-instructor

2021 Summer, Genetics (Undergraduate), University of Florida

Undergraduate students mentored

Sebastian Mihail, University of Florida, Project: CRISPR/Cas9 gene editing in peanut hairy root
Camila Sanchez, University of Florida, Project: CRISPR/Cas9 gene editing in peanut hairy root
Lindsay Dobrie, University of Florida, Project: Transcriptome analysis on peanut root nodulation

Services

Reviewer for Scholarly Journals

BMC plant biology, Frontiers in plant science, Scientific Reports, Plants journal, Genes journal

University of Florida

Treasurer of Agronomy Graduate Student Association, University of Florida: 2018-2019

Certificates

Data Analysis with Python, Coursera, 2020

Summer Institute in Statistical Genetics: Integrative Genomics and Pathway & Network Analysis for Omics Data, University of Washington, 2019

Python for Genomic Data Science, Coursera, 2018

Biology Meets Programming: Bioinformatics for Beginners, Coursera, 2018