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Employment

2022 – ···· ◇ Assistant Professor NCSU
2020 – 2021 ◇ NSF Postdoctoral Research Fellow Cornell University
2018 – 2020 ◇ Postdoctoral Researcher USDA-ARS, Ithaca, NY

Education

2018 ◇ PhD, Plant Breeding and Plant Genetics University of Wisconsin – Madison
 ◇ MS, Biometry University of Wisconsin – Madison
2012 ◇ BS, Plant Sciences Cornell University
 ◇ BS, Communications Cornell University

Publications

* equal contribution; ‡ undergraduate; § corresponding author

- Kick, D. R., Wallace, J. G., Schnable, J. C., Kolkman, J. M., Alaca, B., Beissinger, T. M., ... **Gage, J. L.** et al. (2023). Yield prediction through integration of genetic, environment, and management data through deep learning. *G3: Genes, Genomes, Genetics*, 13(4), jkadoo6.
- Lima, D. C., Aviles, A. C., Alpers, R. T., McFarland, B. A., Kaeppler, S., Ertl, D., ... Beissinger, T. et al. (2023). 2018–2019 field seasons of the maize genomes to fields (g2f) g x e project. *BMC Genomic Data*, 24(1), 1–4.
- **Gage, J. L.**§, Mali, S., McLoughlin, F., Khaipho-Burch, M., Monier, B., Bailey-Serres, J., ... Buckler, E. S. (2022). Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance. *Proceedings of the National Academy of Sciences*, 119(14), e2112516119.
🔗 doi:10.1073/pnas.2112516119
- Feldmann, M. J., **Gage, J. L.**, Turner-Hissong, S. D., & Ubbens, J. R. (2021). Images carried before the fire: The power, promise, and responsibility of latent phenotyping in plants. *The Plant Phenome Journal*, 4(1), e20023. 🔗 doi:https://doi.org/10.1002/ppj2.20023
- Franco, J. A. V.* , **Gage, J. L.*** , Johnson, L. C., Bradbury, P., Miller, Z. R., Buckler, E. S., & Romay, M. C. (2020). A maize practical haplotype graph leverages diverse NAM assemblies. *bioRxiv*.
🔗 doi:https://doi.org/10.1101/2020.08.31.268425
- **Gage, J. L.**§, Monier, B., Giri, A., & Buckler, E. S.§. (2020). Ten years of the maize nested association mapping population: Impact, limitations, and future directions. *The Plant Cell*, 32(7), 2083–2093.
🔗 doi:https://doi.org/10.1105/tpc.19.00951
- McFarland, B. A., AlKhalifah, N., Bohn, M., Bubert, J., Buckler, E. S., Ciampitti, I., ... Falcon, C. M. et al. (2020). Maize genomes to fields (G2F): 2014–2017 field seasons: Genotype, phenotype, climatic, soil, and inbred ear image datasets. *BMC research notes*, 13(1), 1–6.
🔗 doi:https://doi.org/10.1186/s13104-020-4922-8

- **Gage, J. L.**[§], Richards, E.[‡], Lepak, N., Kaczmar, N., Soman, C., Chowdhary, G., ... Buckler, E. S. (2019). In-field whole-plant maize architecture characterized by subcanopy rovers and latent space phenotyping. *The Plant Phenome Journal*, 2(1). doi:https://doi.org/10.2135/tppj2019.07.0011
- **Gage, J. L.**, Vaillancourt, B., Hamilton, J. P., Manrique-Carpintero, N. C., Gustafson, T. J., Barry, K., ... Kaeppler, S. M. et al. (2019). Multiple maize reference genomes impact the identification of variants by genome-wide association study in a diverse inbred panel. *The Plant Genome*. doi:https://doi.org/10.3835/plantgenome2018.09.0069
- Marand, A. P., Jansky, S. H., **Gage, J. L.**, Hamernik, A. J., de Leon, N., & Jiang, J. (2019). Residual heterozygosity and epistatic interactions underlie the complex genetic architecture of yield in diploid potato. *Genetics*, 212(1), 317–332. doi:https://doi.org/10.1534/genetics.119.302036
- Mazaheri, M., Heckwolf, M., Vaillancourt, B., **Gage, J. L.**, Burdo, B., Heckwolf, S., ... Kono, T. J. et al. (2019). Genome-wide association analysis of stalk biomass and anatomical traits in maize. *BMC plant biology*, 19(1), 1–17. doi:https://doi.org/10.1186/s12870-019-1653-x
- **Gage, J. L.**, De Leon, N., & Clayton, M. K. (2018). Comparing genome-wide association study results from different measurements of an underlying phenotype. *G3: Genes, Genomes, Genetics*, 8(11), 3715–3722. doi:https://doi.org/10.1534/g3.118.200700
- **Gage, J. L.**, White, M. R., Edwards, J. W., Kaeppler, S., & De Leon, N. (2018). Selection signatures underlying dramatic male inflorescence transformation during modern hybrid maize breeding. *Genetics*, 210(3), 1125–1138. doi:https://doi.org/10.1534/genetics.118.301487
- **Gage, J. L.**, Jarquin, D., Romay, C., Lorenz, A., Buckler, E. S., Kaeppler, S., ... Edwards, J. et al. (2017). The effect of artificial selection on phenotypic plasticity in maize. *Nature communications*, 8(1), 1–11. doi:https://doi.org/10.1038/s41467-017-01450-2
- **Gage, J. L.**, Miller, N. D., Spalding, E. P., Kaeppler, S. M., & de Leon, N. (2017). TIPS: A system for automated image-based phenotyping of maize tassels. *Plant Methods*, 13(1), 1–12. doi:https://doi.org/10.1186/s13007-017-0172-8
- Spindel, J., Wright, M., Chen, C., Cobb, J., **Gage, J. L.**[‡], Harrington, S., ... McCouch, S. (2013). Bridging the genotyping gap: Using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theoretical and applied genetics*, 126(11), 2699–2716. doi:https://doi.org/10.1007/s00122-013-2166-x

Talks

Invited

- 2022
 - ◇ “Gene regulation and GxE.” NCSU Genetics and Genomics Academy annual retreat.
 - ◇ “Genomewide Regulation of Gene Expression, and Effects on Phenotype, in Maize.” NCSU Plant and Microbial Biology Seminar Series.
- 2020
 - ◇ “In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping.” The Plant Phenome Journal Webinar Series. <https://youtu.be/d0Luqs660dM>
- 2019
 - ◇ “Improving crop measurement with rovers.” Wegmans Organic Summit. Canandaigua, NY.
 - ◇ “In-field whole plant maize architecture characterized by Latent Space Phenotyping.” Cornell Institute for Digital Agriculture Symposium. Ithaca, NY.
 - ◇ “In-field whole plant architecture characterized by scalable, affordable robots.” Corn Breeding Research Meeting. St. Louis, MO.
- 2018
 - ◇ “TIPS: A System for Automated Image-Based Phenotyping of Maize Tassels.” CyVerse - Software, Tools, and Services for Data-Driven Discovery Workshop, Plant and Animal Genome XXVI Conference. San Diego, CA.

Talks (continued)

Contributed

- 2022 ◇ "Natural, allelic variation in maize diel transcription patterns impacts phenotypes." Zeavolution online seminar series.
- 2017 ◇ "Mapping variants associated with phenotypic stability in maize." Gordon Research Seminar. Galveston, TX.
- 2016 ◇ "Genomic Prediction Within and Between Subpopulations of the USA National Maize Inbred Collection." Corn Breeding Research Meeting. Jacksonville, FL.
- 2015 ◇ "Genome-Wide Association Analysis of Tassel Size and Branch Number in the Wisconsin Diverse Association Panel." Corn Breeding Research Meeting, St. Charles, IL.

Mentoring and Teaching

Total (current) mentees: 1 (1) graduate; 2 (1) undergraduates; 1 (1) postdoc

Teaching: North Carolina State University

- 2023 ◇ Crop and Soil Sciences 590 – Sequence Analysis for Plant Genomics

Teaching Assistant: University of Wisconsin – Madison

- 2017 ◇ Agronomy 772 – Advanced Applications in ANOVA
 - ◇ Agronomy 811 – Biometric Procedures in Plant Breeding
- 2016 ◇ Agronomy 875 – Selection Theory for Quantitative Traits in Plants
- 2015 ◇ Agronomy 811 – Biometric Procedures in Plant Breeding

Service

Outreach

- 2020-
 - ◇ Engaged with grade school science classes on Skype-a-Scientist
 - 2019 ◇ Showcased robotic phenotyping on local news WSYR (<https://youtu.be/o6vKLVMBv14>).
 - ◇ Guest lecturer in undergraduate Digital Agriculture class.

Statistical Consultant

- 2018 ◇ Statistical Consulting Lab at the University of Wisconsin – Madison

Community Involvement

- 2023 ◇ Organized INTRINSyC, a weekly plant science seminar series
 - ◇ Organizer, Maize Genomes to Fields prediction contest
- 2022 - ◇ Mentor, Maize Genetics Cooperative Mentoring Program
 - 2021 ◇ Maize Genetics Meeting Steering Committee
 - 2019 ◇ Discussion Leader for Gordon Research Seminar in Quantitative Genetics and Genomics

Peer Review

Reviewed for Nature Biotechnology, The Plant Cell, New Phytologist, Heredity, The Plant Genome, Crop Science, Theoretical and Applied Genetics, PLoS One, Plant Biotechnology, Plant Direct, Field Crops Research, Agronomy, BioEnergy Research, Molecular Genetics and Genomics.

Awards & Achievements

Funded Awards

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|------|---|-------------|
| 2022 | ◇ USDA DSFAS-CIN: Integrating multiscale remote sensing data for enhancing data-driven predictive analytics in crop breeding and management (Co-PI) | \$1,000,000 |
| 2019 | ◇ NSF Postdoctoral Research Fellowship in Biology (PI) | \$231,000 |

Achievements

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| 2017 | ◇ Selected to talk at the Gordon Research Seminar in Quantitative Genetics and Genomics | |
| | ◇ G.O. Mott Meritorious Graduate Student Award | |
| 2016 | ◇ G.O. Mott Meritorious Graduate Student Award | |
| 2015 | ◇ Larry Darrah Award for Best Student Research Presentation | |
| | ◇ Vice President, Plant Sciences Graduate Student Council, University of Wisconsin | |
| 2012 | ◇ Intern at DuPont Pioneer, Johnston IA | |
| 2009-2011 | ◇ Dean's List – Cornell University | |
| 2008 | ◇ Perialis Prize for Persuasive Oratory | |