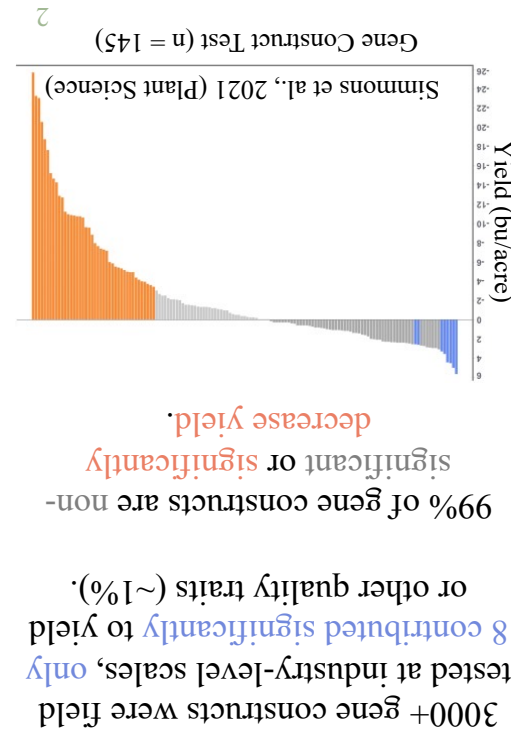


The perils and promise of single-gene solutions to crop yield: extraordinary claims require extraordinary evidence



Poster: **P209**
Maize Genetics Conference
Merritt Khaipho-Burch



Have any questions, suggestions, or available positions?
Unfold this zine for my resume!



Graduating
December 2023

Contact me:

mbb262@cornell.edu

[@MerKhaiBurch](https://twitter.com/MerKhaiBurch)

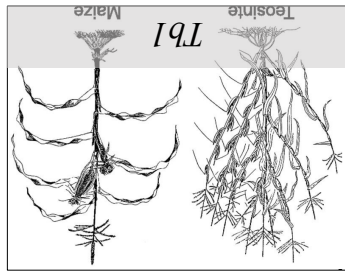
Check out my website!



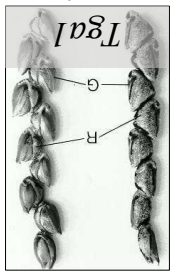
Check out my other posters:
P221: Modeling TE effects on gene expression.
P114: Developing a seed dispersal game.



Limited env. adaptation



Improving harvestability



Processing & consumption



Response to synthetic fertilizers

We **suggest approaches** for researchers and reviewers to use when evaluating the impact of single genes on crop yield:

- Robustly measure crop-relevant plot-wide yield, not plant-level yield.
- Define a significant minimum yield advantage target to justify further testing. Yield increases of 1-5% are strong candidates.
- Create field designs that pay attention to inter-plant competition and GxE.
- Use elite germplasm.
- Prioritize genes that evolution may have missed or whose variation has been exhausted within elite germplasm.
- Develop collaborations and use public sector frameworks such as the Genome to Fields Initiative to test changes at scale.



Plant breeding programs can deliver robust yield increases using **genomic prediction and selection**.



Figure modified from Jesse Poland

Merritt Khaipho-Burch

Ph.D. Candidate



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EDUCATION

Aug 2018 - Fall 2023 (expected)
Cornell University, NY
*Doctor of Philosophy,
Plant Genetics, minor Genomics*

Aug 2016 - May 2018
South Dakota State University, SD
*Advisor: Donald Auger
Master of Science,
Biological Sciences*

Aug 2012 - May 2016
University of Hawaii at Hilo, HI
*Bachelor of Science,
Biology (Cell and Molecular Track)*

RELEVANT SKILLS

R/RStudio

Association Analyses

Genomic Prediction & Selection

RNAseq Data Analysis

Cloud Based Computing (Google
Colab, HPC services)

Microsoft Office

PROFESSIONAL EXPERIENCE

Ph.D. Candidate

Buckler Lab, Cornell University, Ithaca, NY

- Topics: Elucidating the patterns of pleiotropy and its biological relevance in maize AND Regulatory adaptation of transposable elements and their effect on gene expression in maize and the Andropogoneae.
- Curated and built association models to map 120,549 traits across two diverse maize populations to uncover the patterns of pleiotropy and created multiple machine learning models (random forest, gradient boosting) to describe how these pleiotropic loci were biologically regulated.
- Developed mixed linear and gradient boosting models to understand the impact of TEs on gene expression across 372 maize inbreds and hybrids.

SELECT LEADERSHIP ROLES (3 of 8)

2022-2023 – **Co-chair** of the Synapsis Professional Development Committee.
2020-2021 – **President** of Synapsis, the academic and social organization of the faculty, graduate students, and alumni of the Section of Plant Breeding and Genetics at Cornell University.
2019-2020 – **Committee Chair** for 9th Annual Cornell University Graduate Student Plant Breeding Symposium titled “Bringing Back Biodiversity” held Virtually. Sponsored by Corteva Agriscience.

SELECT HONORS AND AWARDS (3 of 7)

2022 – **USDA NIFA Predoctoral Fellowship** for “Regulatory Adaptation Of Transposable Elements And Their Effect On Gene Expression In Maize And The Andropogoneae”. Total amount: **\$180,000**.
2022 – **David L. Call Award** from the American Indian and Indigenous Studies Program. Given to one Indigenous graduate or professional student per year who displays outstanding leadership, service, and commitment in pursuit of a graduate degree.
2021 – **Best PhD Poster Video** at the 6th International Conference of Quantitative Genetics.

SELECT PUBLICATIONS (5 of 8)

*Corresponding author, **Joint Corresponding

Khaipho-Burch, M.**, Cooper, M., Crossa, J., de Leon N., Lewis, R., McCouch, S., Murray, S., Rabbi, I., Ronald, P., Ross-Ibarra, J., Weigel, D., Yan, J., Buckler, E. S.** (2022). *The perils and promise of single-gene solutions to crop yield: extraordinary claims require extraordinary evidence*. Submitted.

Khaipho-Burch, M.*, Ferebee, T., Giri, A., Ramstein, G., Monier, B., Yi, E., Cinta Romay, M., & Buckler, E. S. (2022). *Elucidating the patterns of pleiotropy and its biological relevance in maize*. In bioRxiv (p. 2022.07.20.500810).

Maharajan, N., **Khaipho-Burch, M.****, Awale, P., Gyawali, A., Shrestha, V., Wu, Y., & Auger, D. L. (2022). *Genomic mapping of the modifiers of teosinte crossing barrier 1 (Tcb1)*. In bioRxiv (p. 2022.07.18.500501).

Gage JL, Mali S, McLoughlin F, **Khaipho-Burch M**, Monier B, Bailey-Serres J, et al. *Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance*. Proc Natl Acad Sci U S A. 2022;119: e2112516119.
Washburn JD, **Burch MB**, Franco JAV. *Predictive breeding for maize: Making use of molecular phenotypes, machine learning, and physiological crop models*. Crop Sci. 2020;60: 622–638.