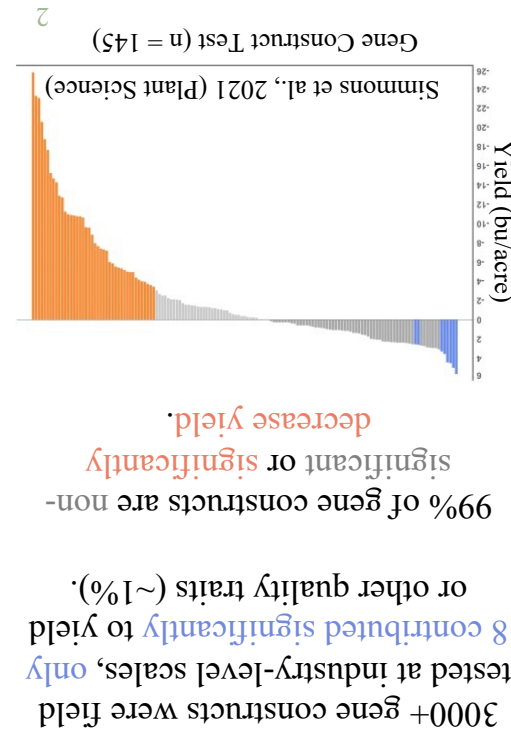


The perils and promise of single-gene solutions to crop yield: extraordinary claims require extraordinary evidence



NAPB 2023
Merritt Khaipho-Burch



Have any questions or suggestions?

Learn more about me and my work by unfolding this zine for my resume!

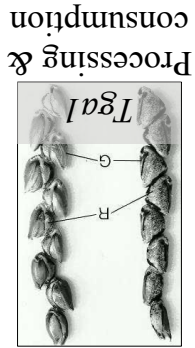
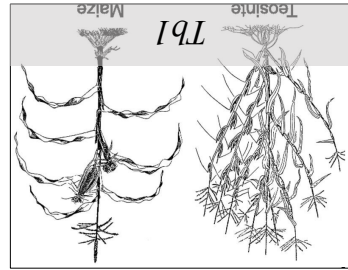
Contact me:

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@MerKhaiBurch

Check out my website!



Many single genes have worked well for adaptation or yield stabilization.

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 plot 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.



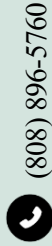
Plant breeding programs can deliver robust intrinsic yield increases using **genomic prediction and selection**.



Figure modified from Jesse Poland

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Ph.D. Candidate



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[MerKhaiBurch.github.io](https://github.com/MerKhaiBurch)

EDUCATION

Aug 2018 – May 2024 (expected)

Cornell University, NY

Advisor: Edward Buckler

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 5)

2022-2023 – **Co-chair** of the Synapsis Professional Development Committee.

2020-2021 – **President** of Synapsis, the academic and social organization of the Section of Plant Breeding and Genetics at Cornell University.

2019-2020 – **Committee Chair** for virtual 9th Annual Cornell University Graduate Student Plant Breeding Symposium titled “Bringing Back Biodiversity.”

SELECT HONORS AND AWARDS (4 of 7)

2023 – **Barbara McClintock Award** from the Cornell School of Integrated Plant Science. This award honours senior graduate students demonstrating exceptional academic, research, teaching, and outreach achievements and potential to continue an outstanding career in the plant sciences.

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)

Khaipho-Burch, M.**, Cooper, 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*. Under revision in Nature.

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*. *PLoS Genetics*, 19(3), e1010664.

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.