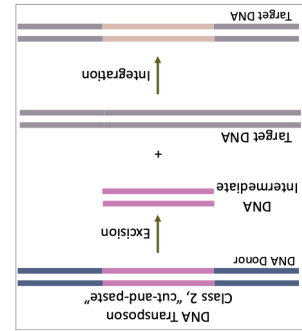
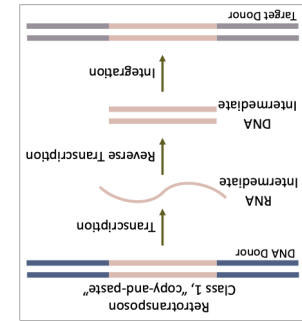
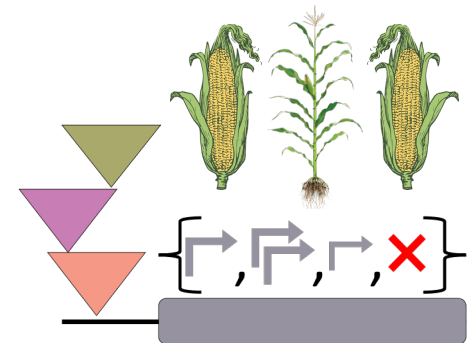


Transposable elements (TEs), or "jumping genes," are repetitive mobile genetic sequences that can alter their host's genome & phenotypes.



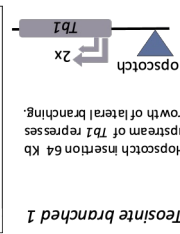
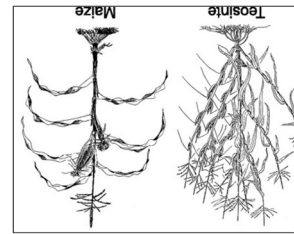
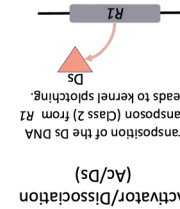
Limited contribution of transposable elements to regulatory adaptation in maize inbreds and hybrids



Poster: **P221**

Maize Genetics Conference
Merritt Khaipho-Burch

In maize, 85% of the genomic sequence is made up of TEs. TEs can alter kernel color and other phenotypes, but it's unclear how much they alter gene expression.



Have any questions, suggestions, or available positions?

Unfold this zine for my resume!



Graduating
December 2023

Contact me:



mbb262@cornell.edu



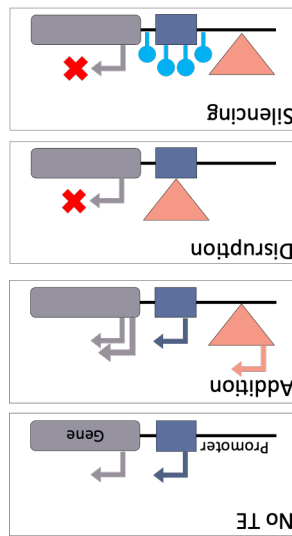
@MerKhaiBurch

Check out my website!



Check out my other posters:
P209: Developing yield testing guidelines.
P114: Developing a seed dispersal game.

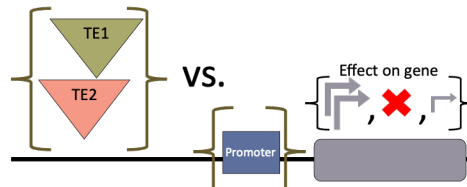
This regulatory grammar can be provided through multiple methods.



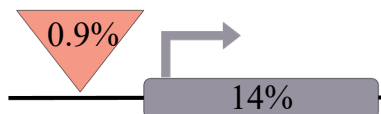
Hypothesis

Due to their abundance, transposable elements have become a source of gene regulatory grammar in maize that impacts RNA expression.

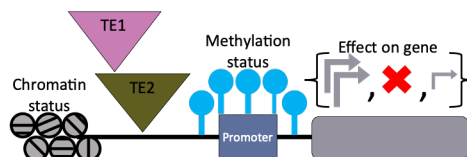
Key Takeaways



Due to high relatedness, we can only study TE effects in a small number of genes (34%).



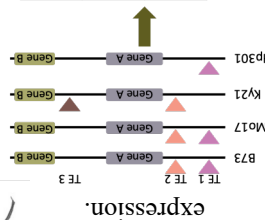
In those 34% of genes, 11,811 (0.9%) TE insertions impact 5,418 (14%) genes.



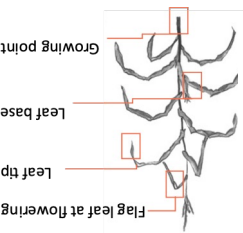
Future work includes building new models that incorporate the genomic landscape and TE features to explain gene expression.

Created a kinship matrix to determine how related our maize lines were.

	Hp301	Ky21	Mo17	B73
Hp301	1.0	0.0	0.0	0.0
Ky21	0.0	1.0	0.0	0.0
Mo17	0.0	0.0	1.0	0.0
B73	0.0	0.0	0.0	1.0



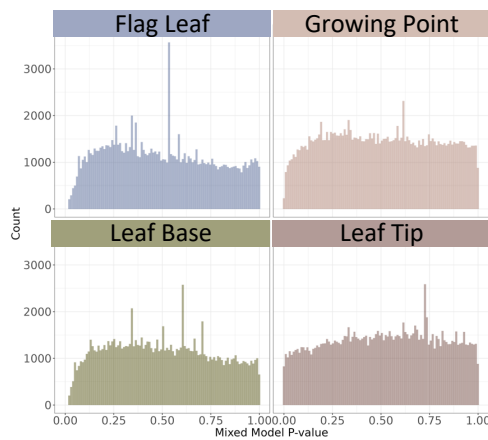
Collected and sequenced 372 inbred and hybrid maize samples and measured gene expression.



Methods

Our model

RNA Expression ~ TE Presence or Absence + Kinship



Our models suggest that only 0.9% of all TE insertions (11,811) significantly ($p < 0.05$) impact the expression of 14% of all maize genes (5,418).

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Ph.D. Candidate



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MerrittKhaiphoBurch

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.