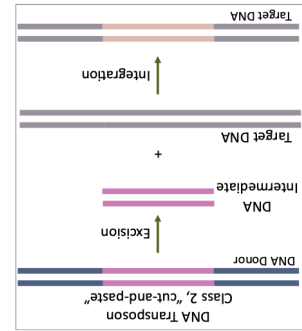
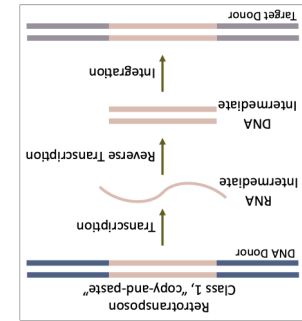
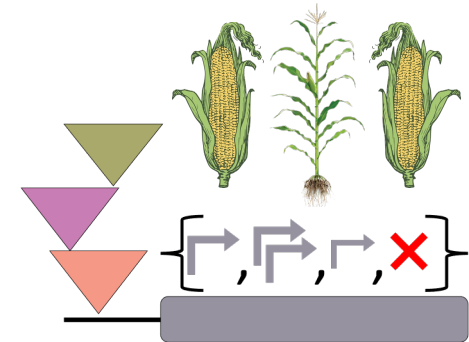


Transposable elements (TEs), or "jumping genes," are repetitive mobile genetic sequences that can alter their host's genome & phenotypes.

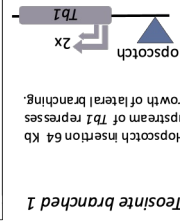
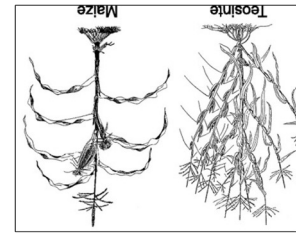
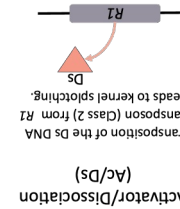


Limited contribution of transposable elements to regulatory adaptation in maize inbreds and hybrids



Poster: **PE0378**
Plant & Animal Genome
Conference 2023
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?



Graduating
summer/fall 2023

Contact me:



mbb262@cornell.edu



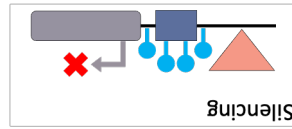
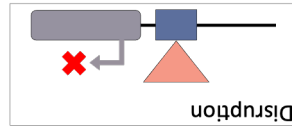
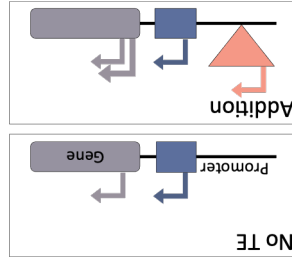
@MerKhaiBurch



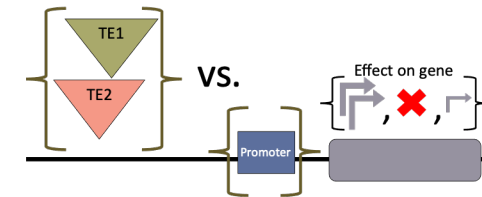
Check out my Google
Scholar profile!

Unfold this zine for
my resume!

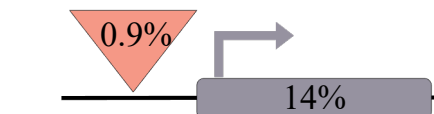
This regulatory grammar can be provided through multiple methods.



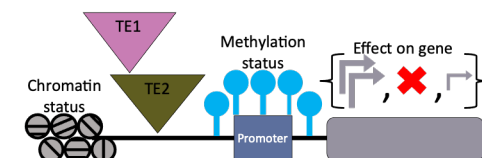
Key Takeaways



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



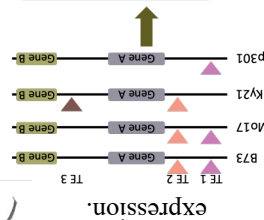
In those 34% of genes, 11,811 (0.9%) TE insertions impact 5,418 (14%) genes.



Future work includes characterizing the regulatory landscape surrounding TEs and their associated genes.

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

	Hp301	Ky21	Mo17	B73
Hp301	1.0	0.0	0.3	0.5
Ky21	0.0	1.0	0.7	0.0
Mo17	0.3	0.7	1.0	0.9
B73	0.5	0.0	0.9	1.0

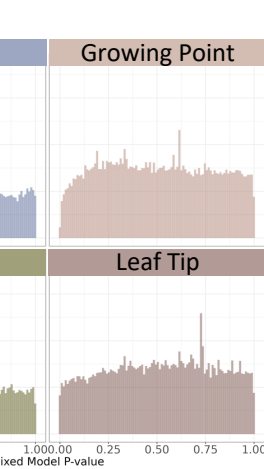


Collected and sequenced 372 inbred and hybrid maize samples and measured gene expression.

Generated a table of when TE insertions were either present or absent across our diverse maize lines.

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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EDUCATION

Fall 2023

Cornell University, NY

*Doctor of Philosophy,
Plant Genetics, minor Genomics*

May 2018

South Dakota State University, SD

*Master of Science,
Biological Sciences*

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

Genome Alignment

Cloud Based Computing (Google
Colab, HPC services)

Microsoft Office

CAREER OBJECTIVE

I am an geneticist with a broad range of experiences in quantitative genetics, classical transmission genetics, molecular biology, plant breeding, and bioinformatics using the model organism *Zea mays*. I am interested in designing and implementing models to understand the genetic basis and regulation of complex quantitative traits.

PROFESSIONAL EXPERIENCE

August 2018–Present

Ph.D. Student

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
- Using association mapping I curated and mapped 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.
- Used mixed linear models to understand the impact of transposable elements on gene expression across 372 maize inbreds and hybrids.

HONORS AND AWARDS

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

*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 Romy, M., & Buckler, E. S. (2022). Elucidating the patterns of pleiotropy and its biological relevance in maize. In bioRxiv (p. 2022.07.20.500810).

Maharjan, 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 (Teb1). 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.