

Transposable element-derived genotypic variation is likely associated with diverse root responses to nitrogen stress

Stephanie P. Klein and Sarah N. Anderson

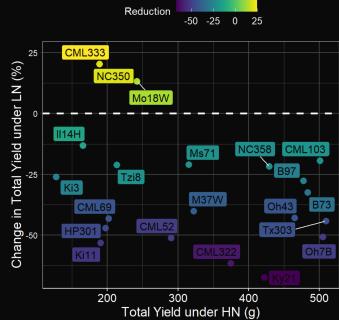
Department of Genetics, Developmental and Cell Biology, Iowa State University

The NAM founders are variably sensitive to nitrogen stress with respect to yield

B73 and 23 NAM parents were grown under high (HN) and low N (LN) conditions in a split-plot design ($n=2$).

In October, cobs from each plant were collected, dried, shelled, and weighed as the total yield (g). M162W and P39 have been omitted. The relative change in total yield (%) was calculated for each genotype as:

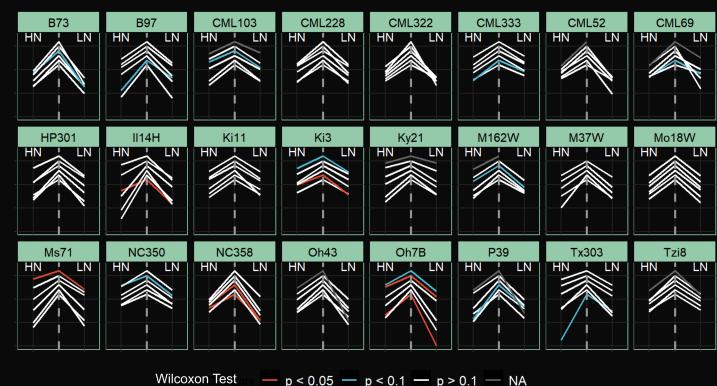
$$100 \times \frac{(LN - HN)}{HN}$$



From all phenotyping efforts, B73 was found to have steep-angled roots and to be non-responsive to N-stress. In contrast, Oh7B contained shallow-angled roots and was N-responsive.

Root growth angle in the NAM founders is diverse and variably responsive to low nitrogen

Prior to anthesis, root crowns were harvested using shovelingomics and imaged to measure root growth angle at each crown root whorl. Wilcoxon tests determined significant differences in root growth angle under HN and LN.



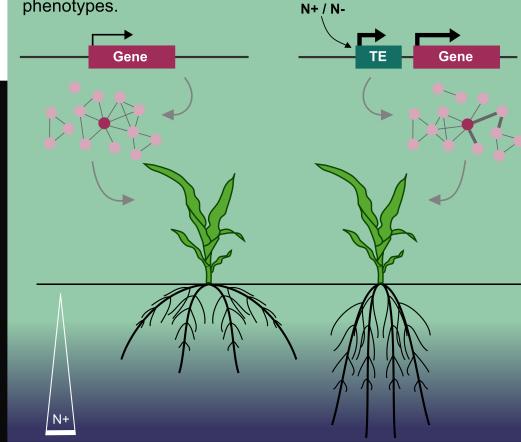
Wilcoxon Test: — p < 0.05 — p < 0.1 — p > 0.1 — NA

Background:

- Transposable element (TE) content is variable across maize genotypes.¹
- TEs are stress-responsive,² modulate the activity of nearby genes,³ and alter transcriptional networks.⁴

Hypothesis:

TEs are responsive to nitrogen (N) stress and may modulate transcriptional networks and induce downstream changes in root phenotypes.



Quantifying TE presence/absence variation in the NAM founders

① Project TE coordinates from B73v4 to B73v5

Using CrossMap, approximately 95.5% of TEs were lifted over successfully.



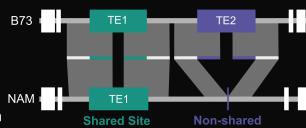
② Extract flank sequences surrounding each TE from B73v5 genome

We collected DNA sequences of 400 bp left and right flanks centered on the start and end coordinates of each TE from the B73v5 genome.

③ Map flank sequences to each NAM genome to identify shared TEs using BWA-MEM

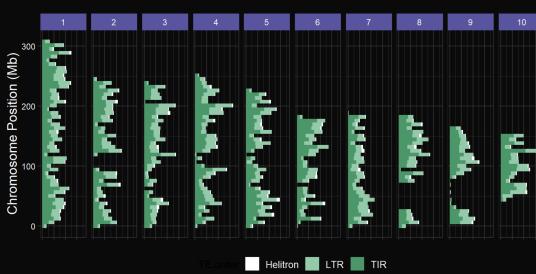
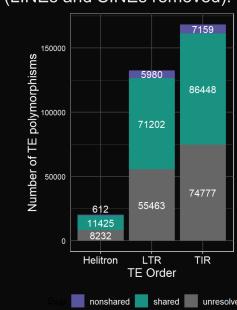
TEs were defined as **shared site defined** when at least one flank aligned in the search window with at least 90% sequence identity over 90% of the flank length.

TEs were defined as **non-shared site defined** when both flank tags mapped uniquely to the search window but were soft-clipped to the sequence outside the TE insertion.



In **Oh7B**, 52.6% of TEs are shared while 4.3% are non-shared (LINEs and SINEs removed).

The 13.8k non-shared sites are widely distributed, indicating widespread novel TE insertions in B73 relative to Oh7B.



Key References:

- Anderson et al. (2019) Transposable elements contribute to dynamic genome content in maize, *Plant Journal*; Liang et al. (2021) Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize, *Plant Phys*;
- Noshay et al. (2021) Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons, *Genetics*; Lisch (2013) How important are transposons for plant evolution?, *Nat. Rev. Genet*.

IOWA STATE UNIVERSITY



National Institute of Food and Agriculture
U.S. DEPARTMENT OF AGRICULTURE

Stephanie P. Klein
spklein@iastate.edu
@spklein2

