Investigating nitrogen-related genes with a diverse maize x teosinte introgression population

Hannah D. Pil[1,2], Nirwan Tandukar[1,2], Fausto Rodríguez Zapata[1], Lauren Insko[1], Zehta Glover[1,2], Carolina Escalona Weldt[1], Ruthie Stokes[1], Katelyn Fritz[3], Cinta Romay[4,5], Allison C. Barnes[1,6], Joseph L. Gage[3], Edward S. Buckler[4,5,7], Ruairidh Sawers[8], James B. Holland[3,6], José de Jesús Sánchez González[9], Rubén Rellán Álvarez[1]

[1] Department of Molecular and Structural Biochemistry, North Carolina State University, Raleigh, NC, USA.
[2] Genetics and Genomics, North Carolina State University, Raleigh, NC, USA.
[3] Department of Crop and Soil Sciences, North Carolina State University, Raleigh, NC, USA.
[4] Institute for Genomic Diversity, Cornell University, Ithaca, NY, USA.
[5] Section of Plant Breeding and Genetics, Cornell University, Ithaca, NY USA.
[6] USDA-ARS, Plant Science Research Unit, Raleigh, NC, USA.
[7] USDA-ARS, Robert W. Holley Center for Agriculture and Health, Ithaca, NY, USA.
[8] Department of Plant Science, Pennsylvania State University, State College, PA, USA.
[9] Universidad de Guadalajara, Centro Universitario de Ciencias Biológicas y Agropecuarias, Zapopan, Jalisco, Mexico.

Teosinte, the wild ancestor of maize, harbors a rich reservoir of interesting traits that have been largely diminished during maize domestication. Recognizing the potential of these unknown alleles, here, we present a method for investigating candidate genes using a new teosinte introgression population. Its donor lines consist of 81 georeferenced teosinte accessions from different species of the Zea genus, including *Zea mays* ssp. *parviglumis*, ssp. *huehuetenangensis*, ssp. *mexicana*, *Zea diploperennis*, and *Zea luxurians*, with around 2100 total derived lines. Evaluating the impact of teosinte alleles on agronomic traits is inherently difficult due to the differences in photoperiod and growth habitat of maize. This population, “BZea,” addresses this challenge by creating BC2S3s with B73, creating derived lines with 12.5% of the original teosinte donors. Introgression into B73 allows for the evaluation of teosinte alleles in a maize background in temperate conditions. To characterize this population, we conducted whole genome sequencing of 1400 of these derived lines with an average sequencing depth of 0.8x. We are using this germplasm to answer diverse experimental questions by generating allelic series for candidate genes related to maize nitrogen dynamics. By selecting lines that carry teosinte introgressions for these specific loci, we can investigate sequence-level variation of alleles from diverse teosinte accessions. We also have georeferenced environmental data for each of the original parent lines. This allows us to explore whether particular sequence variants for candidate nitrogen genes are tied to different soil nitrogen levels. Overall, this strategy allows us to discover wild alleles that can carry valuable adaptive value tied to soil nitrogen availability.