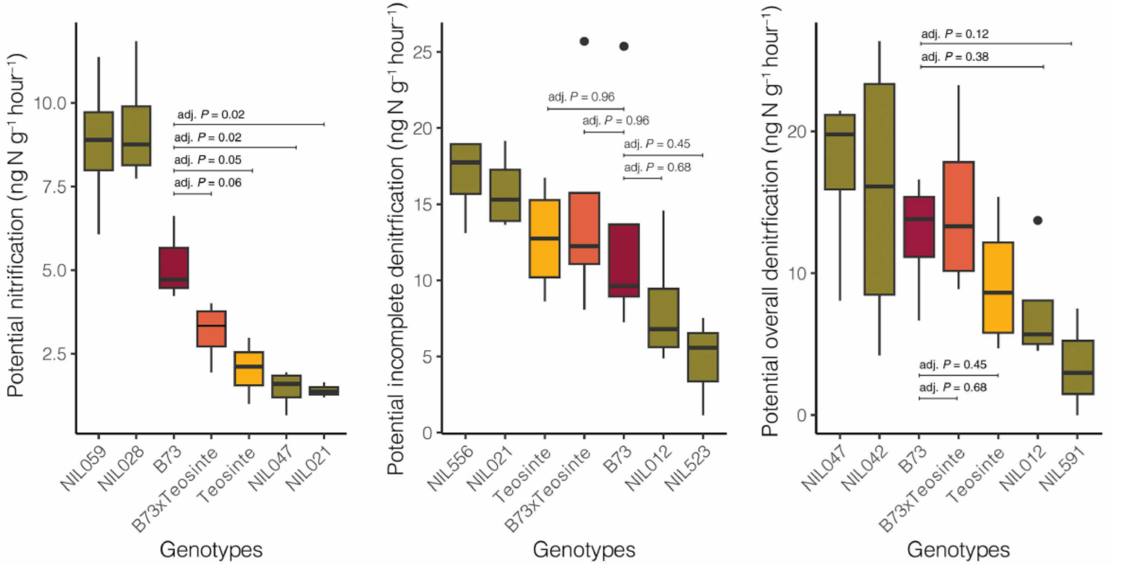
# Lost and Found: Rediscovering Microbiome-Associated Phenotypes that Reshape Agricultural Sustainability

## Background/Objective

Microbial processes contribute to nitrogen (N) loss in agroecosystems by altering soil N mobility and reactivity. Plant phenotypes such as biological inhibition of nitrification (BNI) and denitrification (BDI) can suppress these microbial activities resulting in reduced N loss and improved N uptake. However, the most robust BNI and BDI activities have been found in wild crop relatives. This work explores the potential to harvest genetic variation from teosinte, the wild relative of maize, to improve maize N sustainability.

## Approach

A panel of 41 maize-teosinte near isogenic lines (NILs), along with maize (B73) and teosinte (PI384071) parents and their F1 hybrid were grown in a common field in Urbana, IL. The rhizosphere microbiome was characterized, including key N cycling functional genes. Rhizosphere soils were assayed for nitrification and denitrification potential. Static chamber $N_2O$ fluxes were measured for B73, the F1 hybrid, and PI384071.



**Comparison of functional assays for nitrification potential (left) incomplete denitrification potential (center) and overall denitrification (right) between NILs.**

## Results

Introgressions from teosinte into B73 altered plant-microbiome interactions and significantly suppressed nitrification and denitrification, reducing N loss. Introgressions explained 13% of the variation in rhizosphere prokaryote communities and 12% of rhizosphere fungal communities. Microbiome assemblage behaved as a heritable trait with B73 and teosinte having distinct microbiomes and their F1 hybrid having an intermediate assemblage.

## Significance/Impacts

These findings offer a path toward resilient N management in maize agriculture by leveraging microbial ecology, and demonstrate the potential for crop genetic control over microbiome processes in the rhizosphere in this model crop and other bioenergy crops.

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