

# Maize microbiome-associated phenotypes: a promising solution for mitigating soil nitrogen loss

Our overall objective is to determine how recruitment of microbial communities in the maize rhizosphere can be managed in ways that lead to N retention at the ecosystem level. Can we achieve synergy between N fixation (generating ammonium), BNI (inhibiting nitrification, the transformation of ammonium to nitrate), potentially reducing fertilizer N input requirements for productive agroecosystems?

## INTRODUCTION

- Excessive synthetic nitrogen (N) inputs to attain higher productivity can magnify N losses through several pathways, including leaching and gaseous forms, which has consequences for both climate and future food security of increasing population (1). Retaining soil N calls for better understanding of the soil microbiome, particularly N cycling groups and their functions.
- Specific maize genotypes have displayed promising microbial-associated phenotypes for biological nitrification inhibition (BNI), which could potentially reduce leaching losses. Moreover, application of N-fixing bacterial products can provide supplemental N for the maize utilization.
- Synergy between BNI and diazotrophs can present a sustainable pathway to improve retention of nitrogen in the system.

1. Yan et al., 2020 <https://doi.org/10.1111/gcb.14908>

## MATERIALS AND METHODS

- Fertility Management:** Urea was applied pre-plant broadcast with light incorporation at rates of 0, 30, and 60 lbs N acre<sup>-1</sup>. Across N rates, plots were either left untreated as a control or treated with a N-fixing bacteria (*Klebsiella variicola*) in-furrow at planting at a product rate of 0.1 gallon acre<sup>-1</sup>.
- Cultural Practices:** Either B73 maize inbred or a B73 near-isogenic line (NIL) with BNI was planted at a target population of 19,000 plants acre<sup>-1</sup>.
- Experimental Design:** Experimental units were plots, four rows wide, 20 inch row spacing, and 17.5 feet long, arranged in a randomized complete block design with four replications.
- Analyses:** DNA amplicons analysed by QIIME2 pipeline, and R toolkit was used for the downstream analyses.

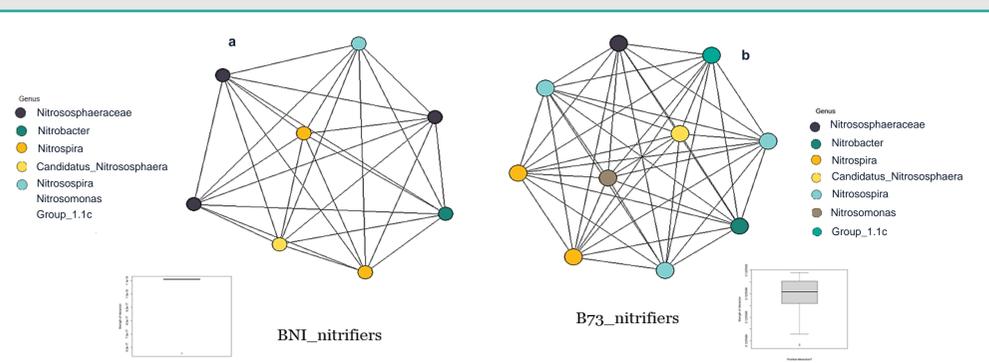


Fig 3 a-b Shifts in pattern of taxon co-existence among the BNI NIL (a) and B73 (b) nitrifiers

- Shifts in overall pattern of taxon co-existence** among the BNI NIL and B73 nitrifiers suggested that the BNI trait reduces interactions among nitrifier taxa (Fig 3).
- Nitrification potential was reduced** by the BNI phenotype, particularly in presence of the N-fixing inoculant, supporting a promising role for BNI in N retention (Fig 4).

## CONCLUSIONS

Together, the consortium of host-dependent microbiome-associated phenotypes defines the activity of specific N cycling microbes which supports soil N retention. Agroecosystem management along with maize breeding plan altered this consortium and their functions. As revealed before (2) host-microbiome interactions can further be used to shape rhizosphere microbiome as the extended phenotypes of maize through which nutrient retention, reduction of GHG production, and soil health and productivity can be achieved.

2. Favela et al., 2021 <https://doi.org/10.1038/s41396-021-00923-z>

## RESULTS AND DISCUSSION

- The assembly of N cycling microbial community** was distinct among growth stages of B73 and BNI NIL and in plots treated by 60 lbs acre<sup>-1</sup> synthetic N fertilizer specifically (Fig 1).

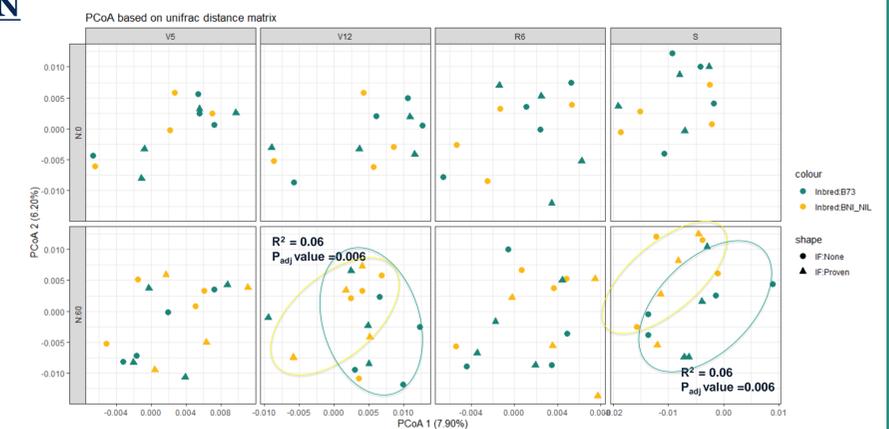


Fig 1 PCoA plots based on Bray-Curtis distance matrix to show the variation of community assemblages between B73 and a BNI NIL among growth stages and fertility management. PERMANOVA results are shown on significant plots. Maize vegetative stages V5 & V12, reproductive stage (R), and Senescence stage (s).

- To evaluate the mechanism behind the microbiome-associated phenotype of BNI maize**, the differential abundance of N cycling microbial functional groups (nitrifiers, denitrifiers, and diazotrophs) was assessed in fertilized and inoculated treatments (Fig. 2). The relative abundance of these groups was not reduced in the BNI maize rhizosphere, suggesting that the reduction of nitrification shown in Fig. 4 is achieved through modulating nitrifier activity rather than relative abundance.

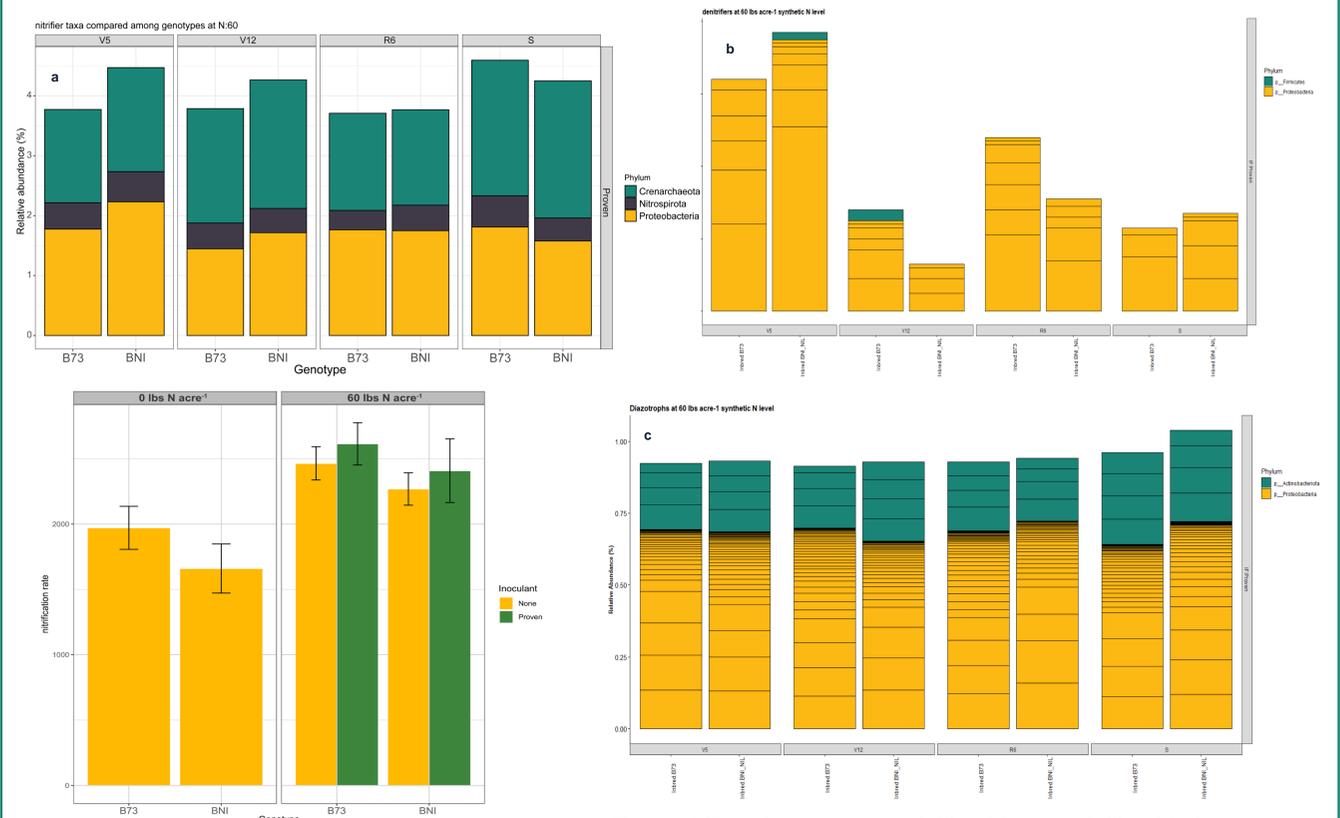


Fig 4 Nitrification potential of B73 vs BNI genotypes under fertility management with N-fixing bacteria (*Klebsiella variicola*) and 60 lbs acre<sup>-1</sup> synthetic N amendment.

Fig 2 a-c Differential abundance of nitrifiers (a), and denitrifiers (b) diazotrophs genes under fertility management with N-fixing bacteria (*Klebsiella variicola*) and 60 lbs acre<sup>-1</sup> synthetic N amendment in rhizosphere of both genotypes to evaluate their synergistical function for reducing N loss.