

Signatures of Local Nitrogen Adaptation in the *Brachypodium distachyon* Root Microbiome

Background/Objective

Plant microbiomes impact their fitness, but microbiome contributions to plant adaptation remain unclear. Plant recruitment of its microbiome can be both highly variable and genetically determined. We investigated the adaptive benefit of plant microbiome recruitment, testing the hypothesis that genotypic variation in the rhizosphere microbiome is partially due to adaptive variation, contributing to the local adaptation of *Brachypodium distachyon* to its historic nitrogen (N) environment.

Approach

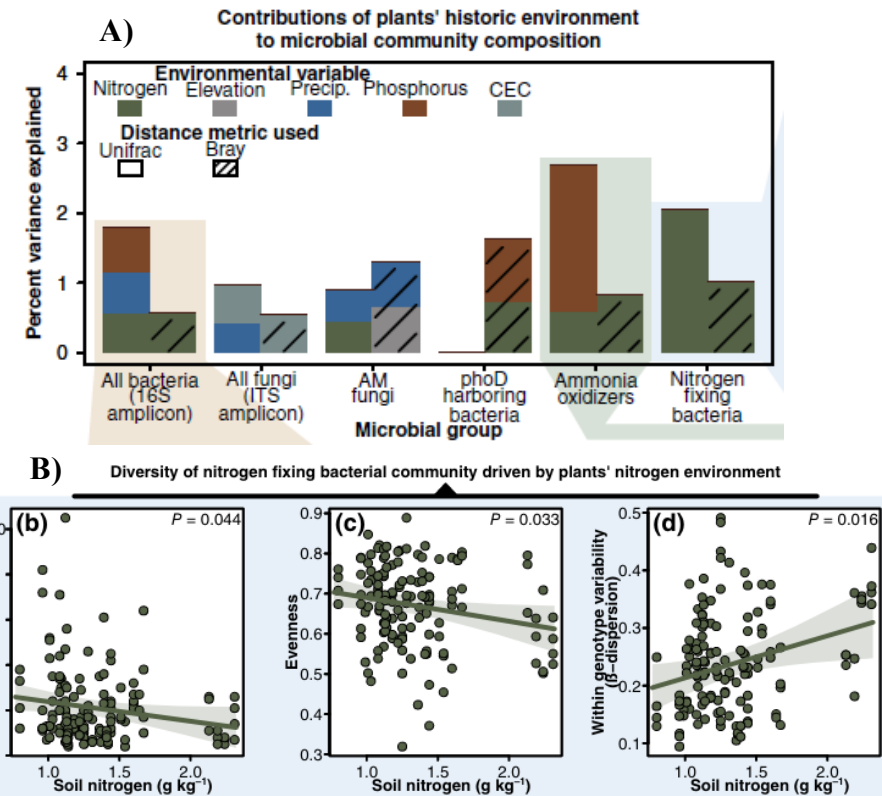
We characterized rhizosphere communities across a genotypic panel of *Brachypodium distachyon* (N =40) in a common garden experiment. We linked microbial communities to their host genotype's historic environment (particularly historical N context), identifying signatures of selection on plant-microbiome recruitment.

Results

Plant-microbiome composition was significantly correlated with host genotype historic environment, with enrichment of microbial traits aligned to local resource conditions. For example, genotypes from low-N environments recruited communities enriched in N acquisition traits.

Significance/Impacts

This study provides evidence that local adaptation in plants may be partially mediated by recruitment of beneficial microbiomes and that plant adaptation may be an emergent property of host-microbe interactions where evolutionary response favors traits that promote recruitment of locally beneficial microbiomes.



A) Significant drivers of *B. distachyon* microbiome structure, specifically the plant's historical environment as predictor variables. B) Diversity of nitrogen-fixing taxa within the rhizosphere is significantly influence by native nitrogen environment. Microbiome data characterized using 16S rRNA and functional gene Illumina amplicon sequencing