

# Chronic Nutrient Enrichment Alters the Soil Microbiome in a Coastal Plain Wetland



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## Background

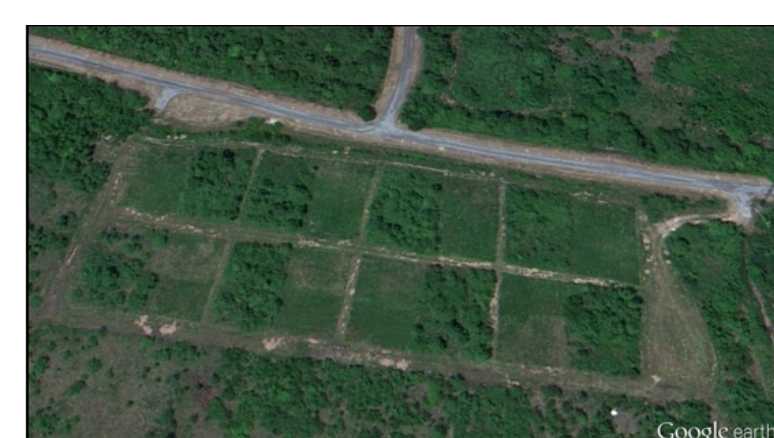
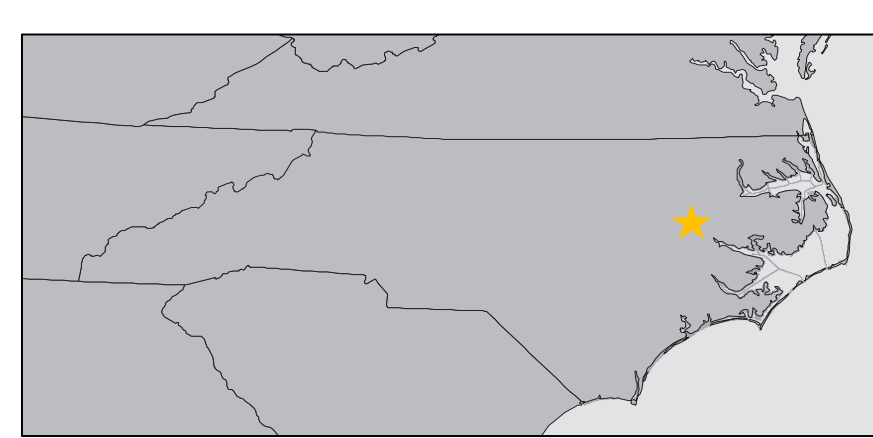
- Human activities (e.g., industrial agriculture, fossil fuel combustion) have caused an imbalance to global nutrient cycles.
- Beneficial plant-microbe relationships aid in plant health by suppressing diseases, improving nutrient uptake, and increasing plant richness.
- Increased nutrient enrichment of low nutrient ecosystems could disrupt beneficial plant-microbe interactions.
- Changes in plant-microbe interactions could alter functional traits in soil microbes and modify plant communities.

**QUESTION:** How has chronic nutrient enrichment of a low nutrient wetland altered plant-microbe relationships and antibiotic resistance of culturable soil microbiome?

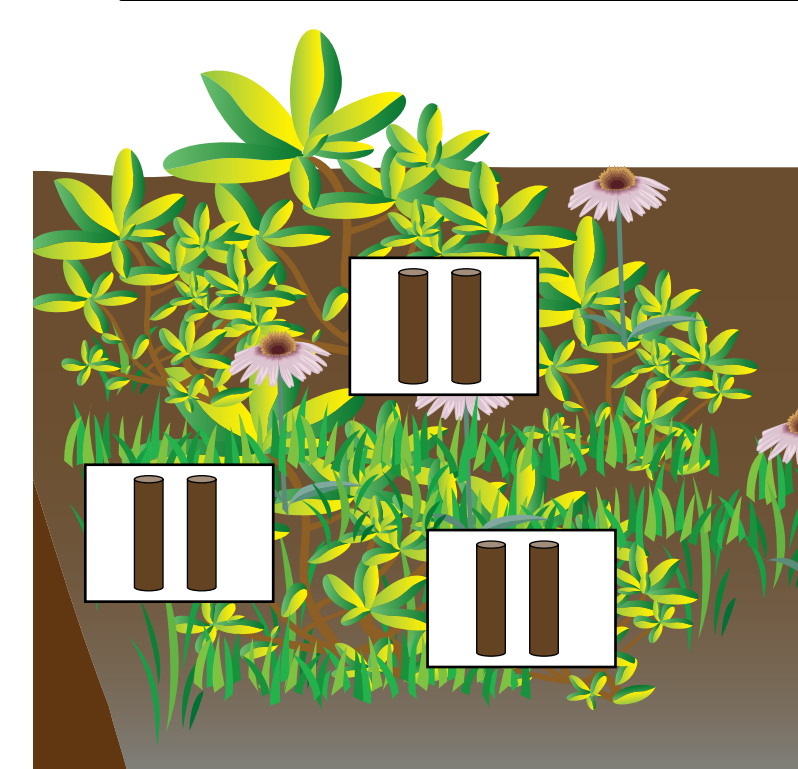
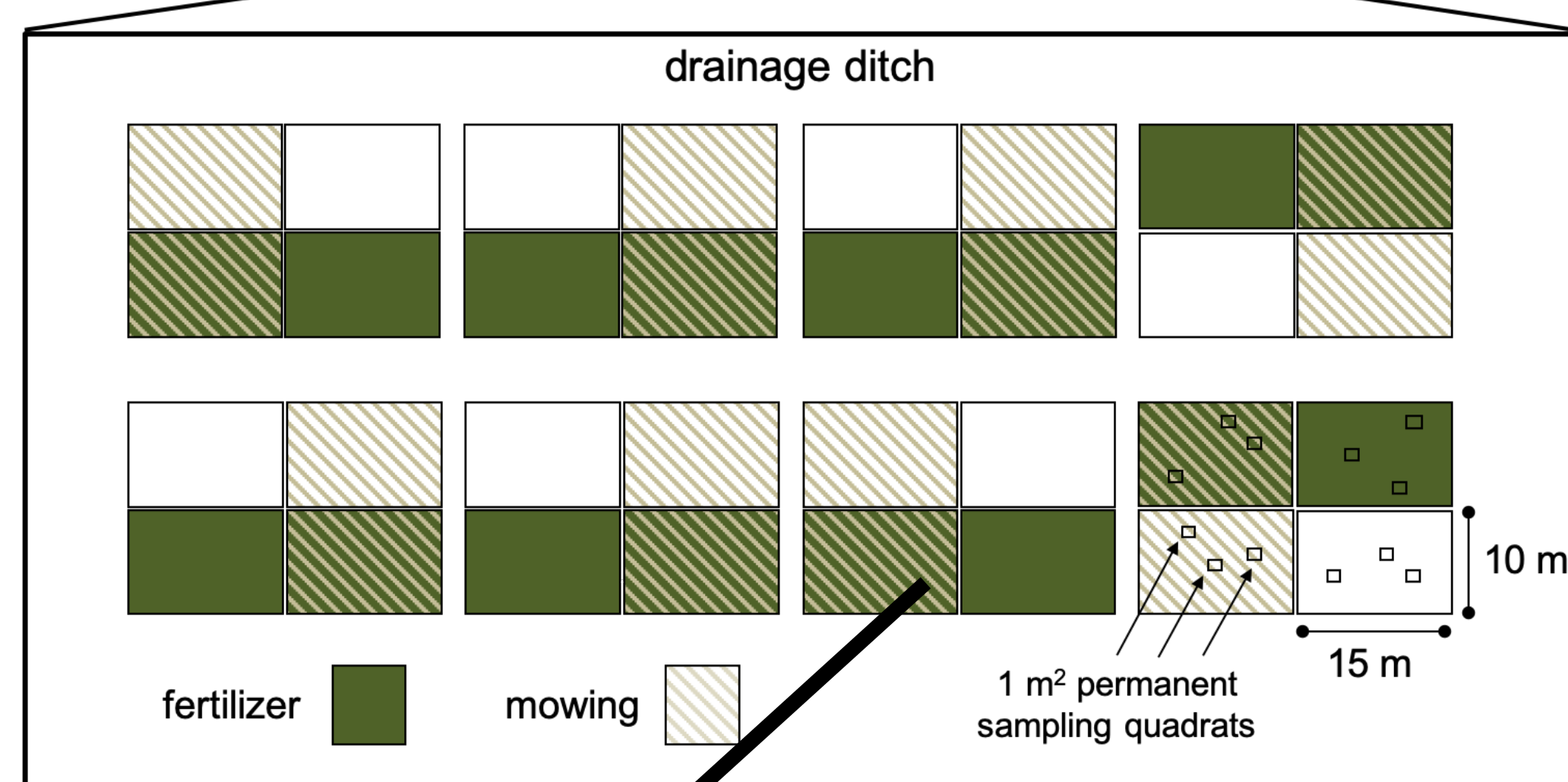
**HYPOTHESIS:** Long term nutrient enrichment will cause plant-microbe interactions to become more competitive than mutualistic.

## Field Experimental Design

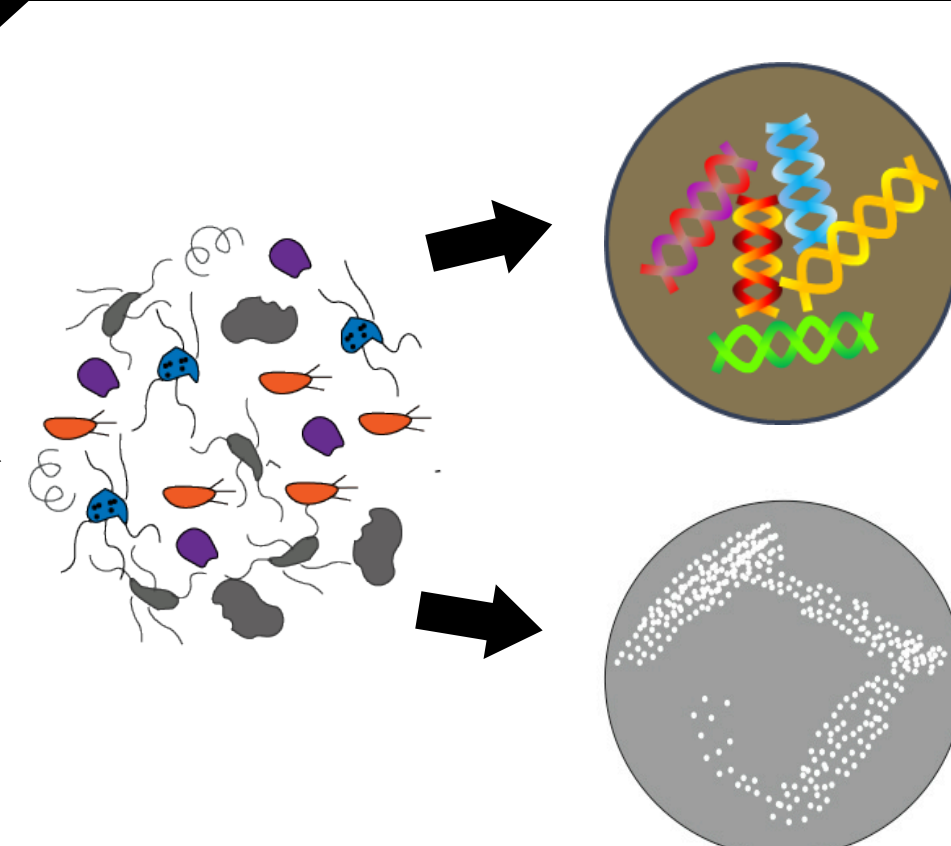
ECU's West Research Campus: Long-term fertilization experiment (est. 2003)



**Sample Collected 2018 and 2019:**  
Treatment (4 replicate blocks)  
Mowed-Unfertilized, mowed-fertilized  
1x yearly, mowing & raking  
3x yearly NPK (10-10-10)



6 soil cores (12 cm depth, 1.9 cm dia.) combined



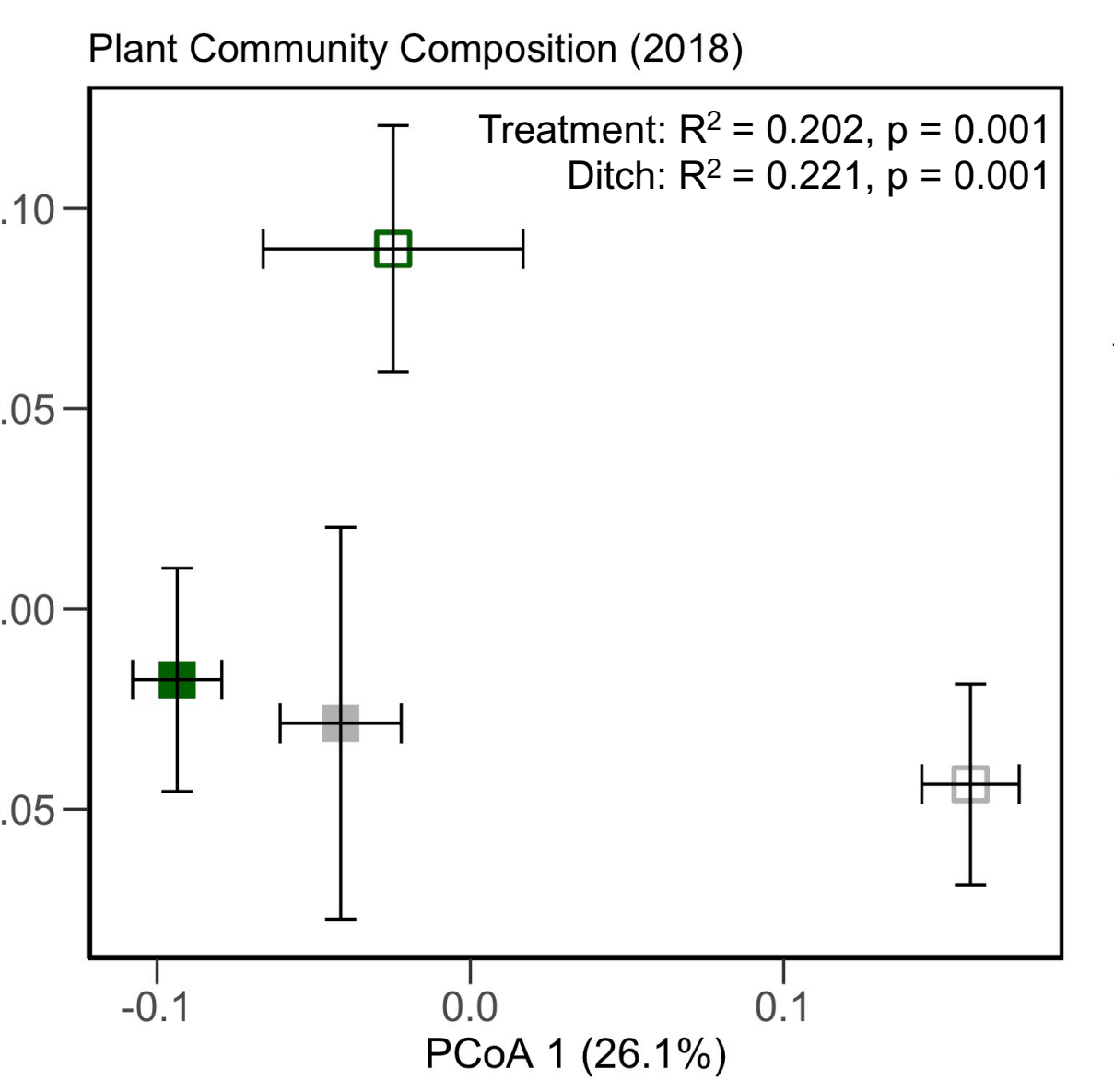
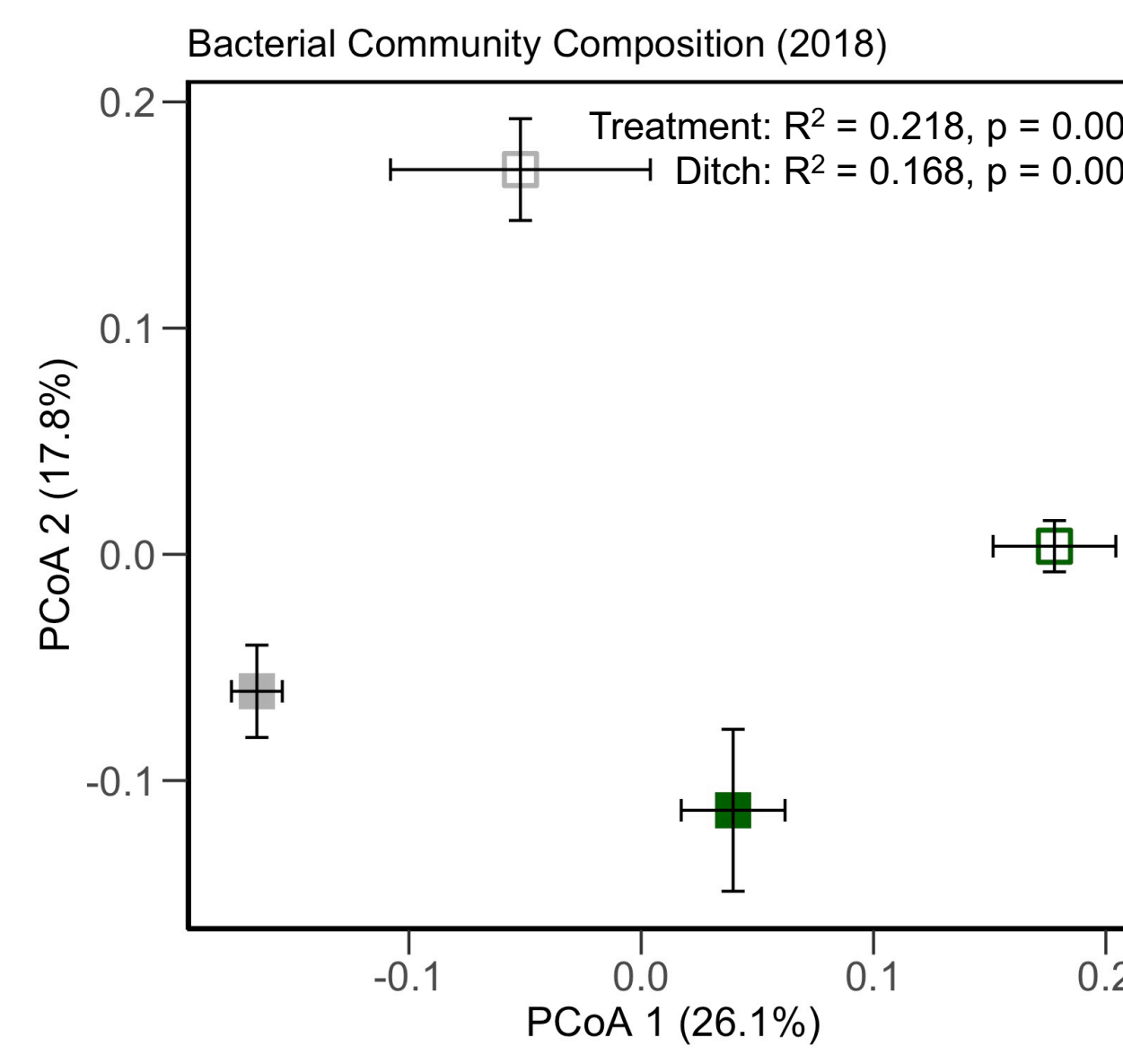
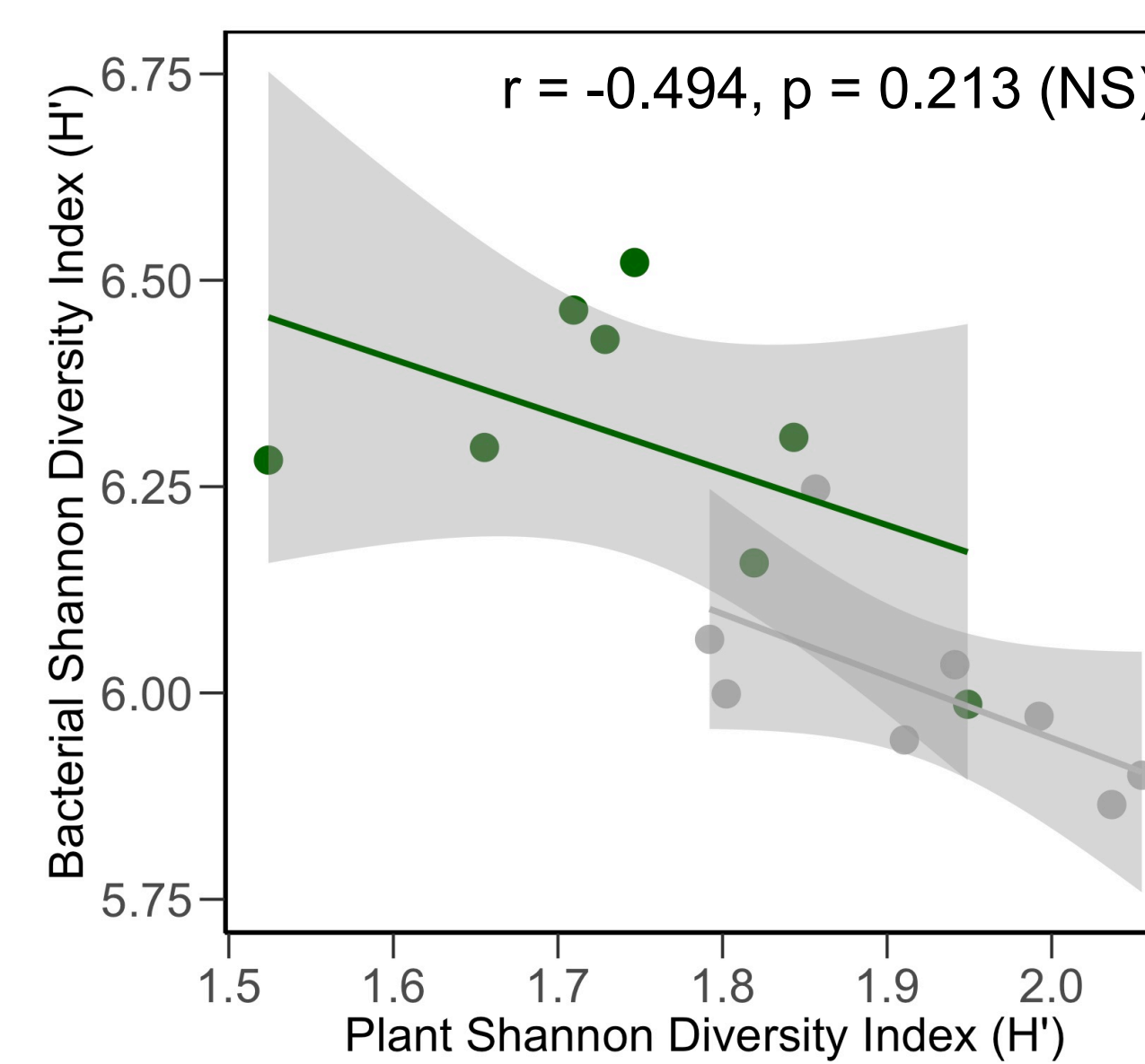
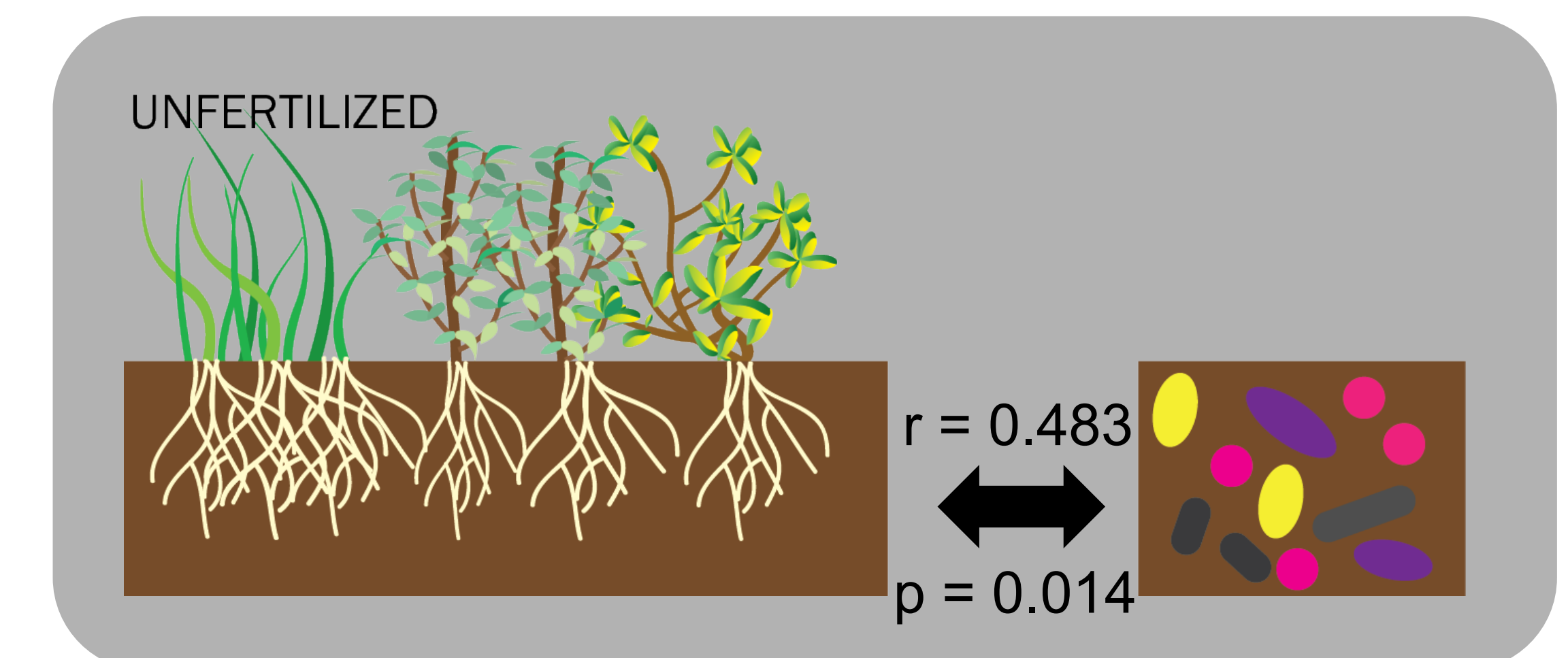
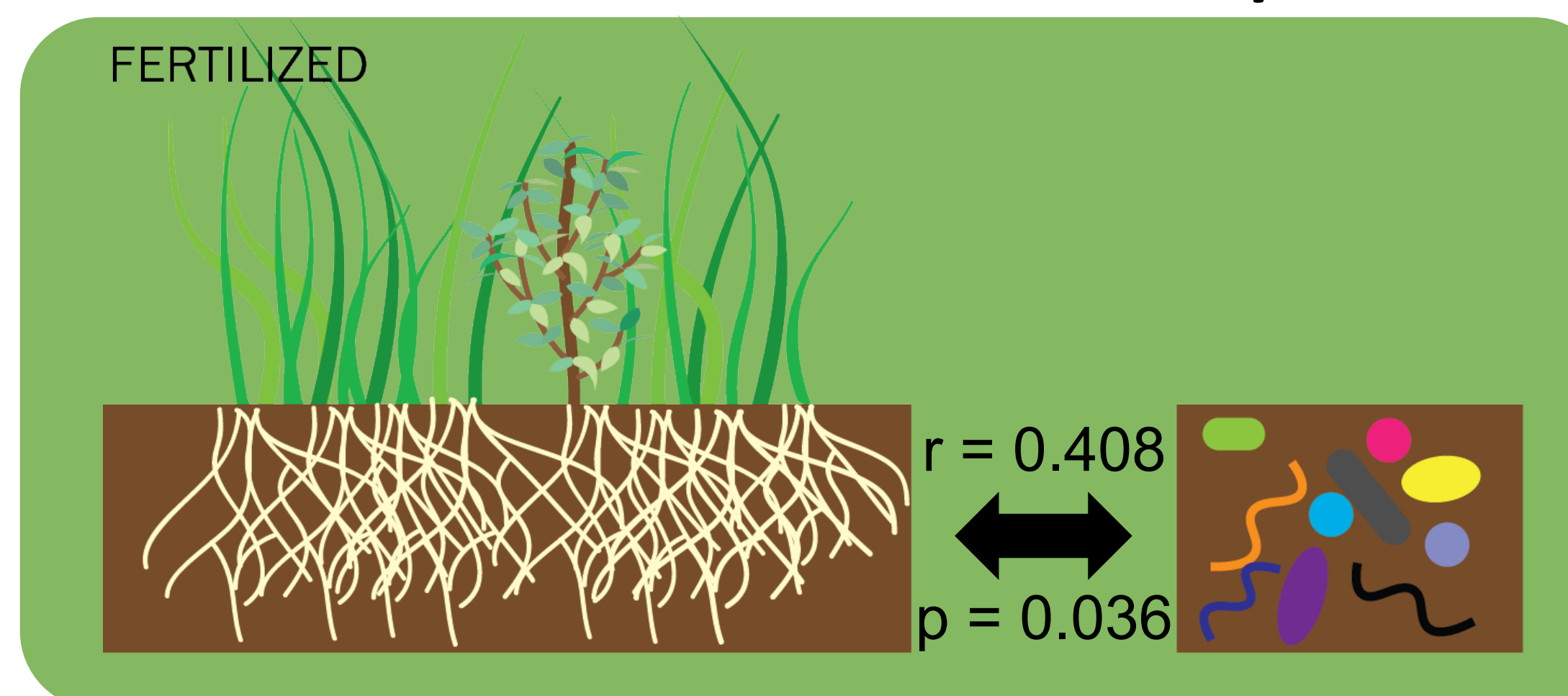
Targeted Illumina sequencing of 16S rRNA gene

Sanger sequencing of 16S rRNA gene and antibiotic resistance

## Nutrient enrichment decreases plant-microbe associations and alters community composition of soil microbiomes

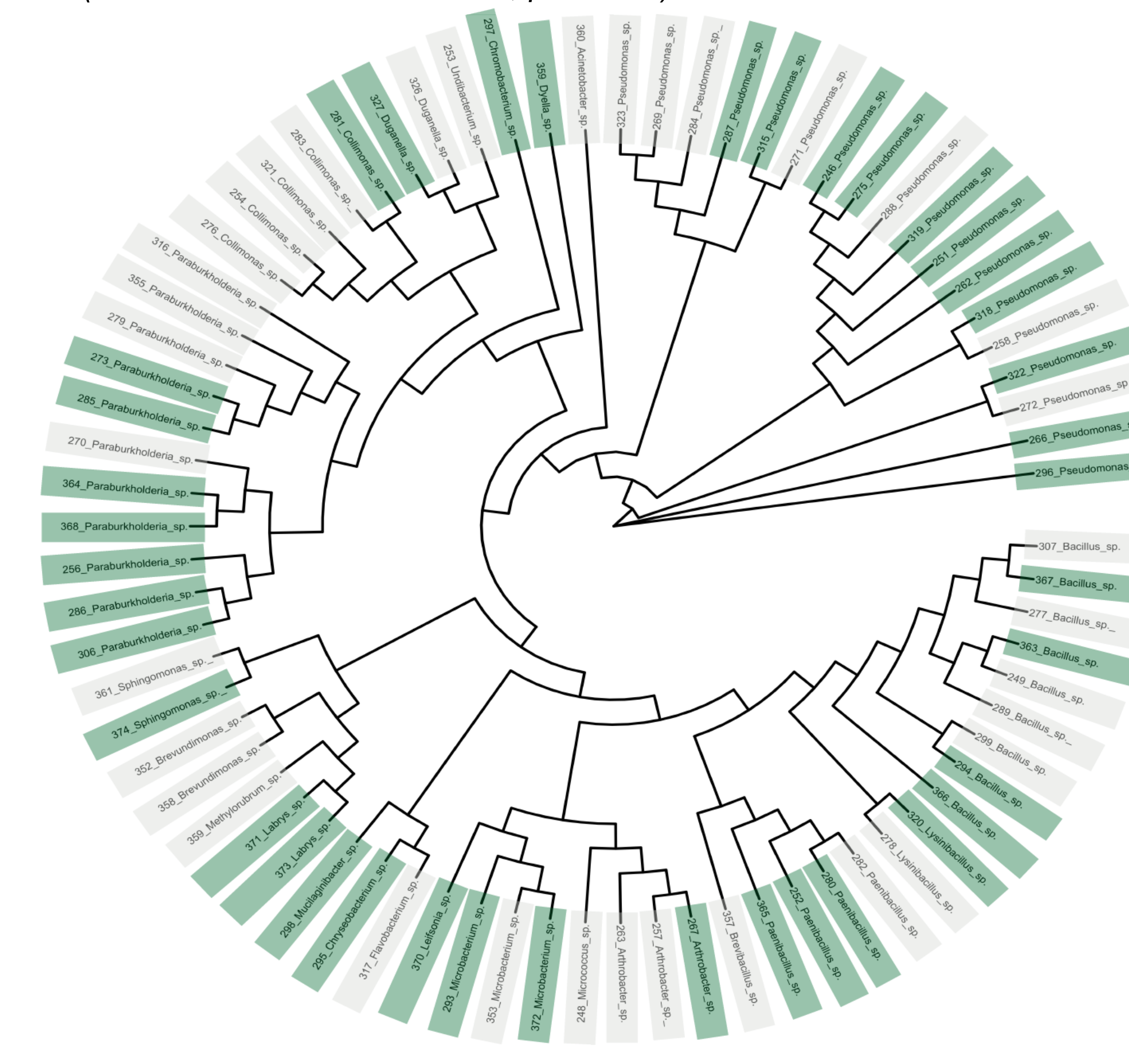
### Results

Excessive nutrient enrichment modifies the soil microbiome weakens plant-microbe interactions.



Plant and bacterial diversity (Pearson correlation  $r = -0.641$ ,  $p = 0.087$ )

Plant and bacterial community matrix comparison (Mantel  $r$ ):  
mowed/unfertilized: Mantel  $r = 0.483$ ,  $p = 0.014$ ; mowed/fertilized: Mantel  $r = 0.408$ ,  $p = 0.036$



There is overlap in the identity of cultured bacterial representatives, but community composition of fertilized plots is different than unfertilized plots. This could support a difference in microbial function.

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