Intersectionalities Between the Phyllosphere, Phosphorus and our Communities

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Introduction

The threat that unsustainable nutrient management poses to ecological biodiversity is of great concern not only to food producers, but also communities because of food insecurity and the loss of natural resources. It is only by focusing on shifts in the phyllosphere microbiome and contextualizing those effects within the horticultural sector can we begin to identify the obstacles and opportunities present in nutrient management, cycling and distribution systems within and outside farmlands. Several projects focused on the importance of social and ecological diversity as well as different aspects of nutrient cycling. Biodiversity was explored through the scope of crop management, waste cycling, the roles of bacteria and fungi in the phyllosphere microbiome, soil sampling and the laboratory analysis of nutrients present in the rhizosphere. The aim of these projects is to highlight the roles of community engagement and science communication to food production, as well as the invaluable benefits of collaborating with local farms.

Methods

- Inoculation of *Pseudomonas fluorescens* (PF) and *Saccharomyces cerevisiae* (SC) extracellular vesicles (EVs)
- 16s rRNA/ITS genome sequencing of microbes found on surface of *Arabidopsis thaliana* leaves (Illumina MiSeq platform)
- Soil and water sampling from Ore Knob and Robeson County areas
- Community Outreach
- Collaboration with local farms

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Results

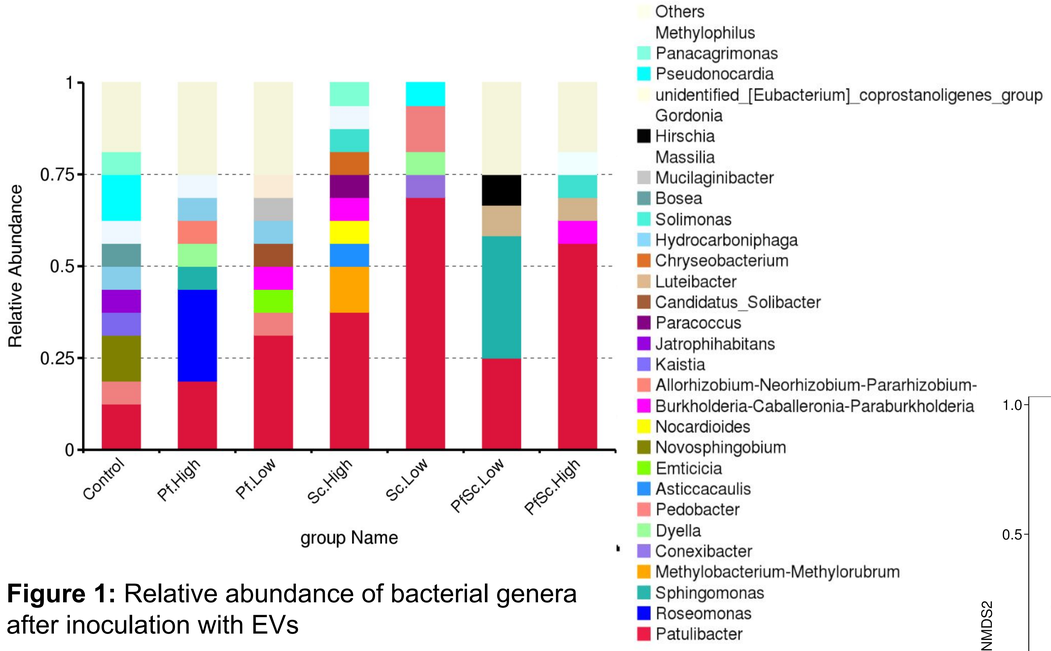

Figure 1: Relative abundance of bacterial genera after inoculation with EVs

Figure 3: Soil sampling in Robeson County (Lumbee Tribe Territory)

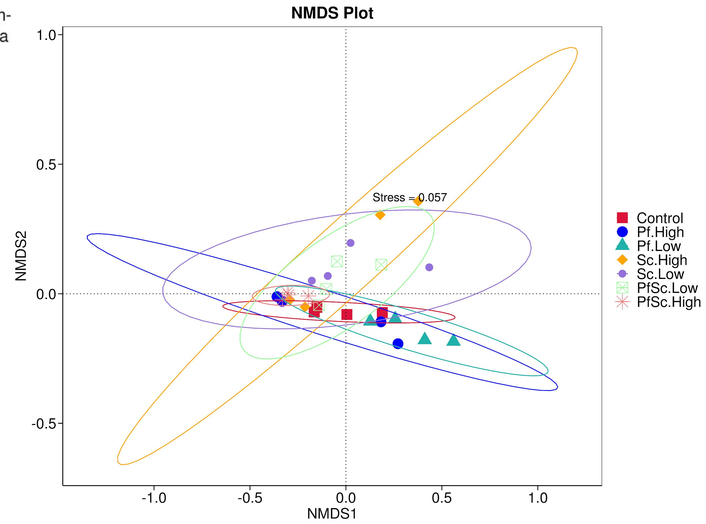

Figure 2: Ordination plot for predicted bacterial association across all treatments

The application of PF and SC EVs resulted in an abundance of Proteobacteria and Actinobacteria, respectively. Bacterial genera, *Patulibacter* exert a significant (at $p < 0.05$) dominance across most treatments and is only outcompeted by species in the genera of *Sphingomonas*. In fungal communities, the application of PF and SC EVs resulted in an abundance of fungal species from the genera *Cytobasidium* and *Russula,* respectively. Nevertheless, none of the fungal OTUs identified assert a significant dominance over treatments, indicating an antagonistic role behind PF colonization, bacterial defense mechanisms and decreased symbiosis with fungi. These results reflect the roles of bacteria in the breakdown and decomposition of compounds in compost as well as the contrast between plant defense mechanisms in nutrient-rich, loamy soils of the High Country and adverse conditions like the arid soils of Robeson County.

Discussion

Bacterial and fungal communities share similarities with PFAM and TIGRFAM groups associated with nutrient uptake (P), biofilm formation, antimicrobial and antifungal agents, as well as other mechanisms for bacterial and fungal succession. This is consistent with experiences in the LLC garden with nutrient cycling and sampling results from Ore Knob and Robeson County sites, which present conditions that are favorable for bacterial and fungal colonization. Both sites have hosted effects from plant growth promoters as a result of their conservation practices. Through the continuation of outreach, our communities can begin to uncover the connections between the phosphorus in our soils and the phyllosphere.

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