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Phosphorous Fertilization Rates and Rhizolocales Drive Fungal and Bacterial Rhizocommunity Structures in Romaine Lettuce Grown in Pahokee Muck

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Abstract

Florida is the third leading producer of lettuce in the USA. Most production takes place in Pahokee Muck in the Everglades Agriculture Area (EAA). Phosphorus is an essential macronutrient for production and is typically sourced from mines that have negative environmental impacts. The role of microbes in nutrient acquisition and growth support in crops has become apparent. It is important to investigate how different phosphorous-amendment rates, cultivars, and environmental factors affect microbial rhizocommunities, so that these systems may be better managed. Two romaine cultivars were grown in the EAA across two seasons with conventional, half, and no-phosphorous fertilization, for 16s and ITS rRNA sequencing at harvest. Fungal and bacterial communities were assessed for differences in composition, diversity, and other metrics. SparCC Network models were constructed and analyzed. *Alternaria* and *Curvularia* were identified as fungal network drivers in the full fertilization groups but not the other fertilization groups. Field season (trial) and rhizolocale were found to be primary drivers of diversity differences between samples. Across trials and rhizolocales and in order of relative abundance, Proteobacteria, Bacteroidota, Acidobacteria, Chloroflexi, and Firmicutes were the dominant bacterial Phyla, and Ascomycota, Unresolved-Fungi, Basidiomycota, Mortierellomycota, and Rozellomycota were the dominant fungal Phyla. DESEQ2 models identified microbes differentially abundant between HalfP and the other P-rates; and between all treatment groups in the fungal dataset. Although year and plot/location have contributed to the fungal and bacterial community compositions/structures, significant impacts of fertilization rate on both bacterial and fungal communities in the rhizosphere and rhizoplane were observed.