Poster #1-43

A Synthetic Community Approach to Understanding Root-Bacterial Interactions During Drought in *Clusia pratensis*

Kristine Grace Cabugao[1,2,3*], Alyssa Carrell[2,3], David J. Weston[2,3], and Richard J. Norby[1,2,3]

[1] University of Tennessee, Knoxville, TN;
[2] Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN;
[3] Climate Change Science Institute, Oak Ridge National Laboratory, Oak Ridge, TN

Contact: kcabugao@vols.utk.edu

BER Program: TES
Project: NGEE–Tropics
Project Website: https://ngee-tropics.lbl.gov/

Models increasingly predict a rise in the severity and duration of drought events, which threaten tropical forests and the role they play in global cycles. Roots serve as the interface between plant and soil, but roots also host a rich and diverse microbial community, which contain functional traits that complement root nutrient and water uptake. Efforts to untangle the interactions between roots and microbial communities and relate them to plant fitness have been hampered by the inherent complexity in natural ecosystems. Thus, we designed synthetic microbial communities to study how combinations of microbial functions may affect root traits in drought conditions and what this might mean for tropical forests in a changing world.

Our synthetic communities consist of bacterial isolates collected from Luquillo Experimental Forest in Puerto Rico. Approximately 100 bacterial isolates were screened for the highest activities in four functions considered beneficial to plant growth: phosphatase activity, phosphorus solubilization, indole-3-acetic acid (IAA) production, and drought tolerance. We created four different communities of bacterial isolates and inoculated them onto Clusia pratensis, a tropical tree species ($n = 10$ plants for each constructed community). Drought conditions were imposed on half the plants for 2 months in a randomized block design and bi-weekly measurements of gas exchange were taken along with leaf samples for physiology assays and soil samples for microbial DNA extraction and analysis. Roots were harvested at the end of 2 months for biomass, phosphatase activity, length, and diameter.

The drought treatment predictably drove the largest differences between plants regardless of the inoculated constructed community. Leaf assays of membrane damage (lipid peroxidation) and stress (proline concentration) show a strong divergence mid-way through the drought trial ($p< 0.001$), indicating strong drought stress in droughted plants. However, there was no effect of microbial community composition on leaf stress response. Biomass was significantly higher in watered plants ($p < 0.001$), but not between microbial communities. Drought plants inoculated with drought tolerant and IAA producing isolates had 36% higher root biomass relative to drought plants grown in sterilized soil (control). Similarly, drought plants inoculated with high phosphatase and P solubilizing isolates showed 55% higher root biomass when compared to the control. These results suggest that microbial communities benefit plants through influencing root growth and nutrient acquisition, which may extend drought tolerance. Next steps include measuring root traits and sequencing the soil collected throughout the trial in order to determine how our synthetic communities changed throughout the trial and whether those changes can be matched to leaf and root physiological status.