Taking a Closer Look at Bacterial & Fungal Interactions in Soil Using Imaging

Demosthenes Morales, III,^{1,2*} (<u>dmorales@lanl.gov</u>), Geoffrey House,² Julia Kelliher,² Jim Werner,¹ and **Patrick Chain**²

¹Center of Integrated Nanotechnologies, Los Alamos National Laboratory; Los Alamos, NM ²Biosecurity and Public Health, Los Alamos National Laboratory, Los Alamos, NM

https://genomicscience.energy.gov/research/sfas/lanlbfi.shtml

Project Goals: This project intends to inform the use of soil microbiomes to address DOE priorities in overcoming energy and environmental challenges. We are focusing on understanding the role of bacterial:fungal interactions in ecosystem development by connecting microbial diversity to actionable phenotypic responses. To do so, genomic and metagenomic sequencing of soil microbes will be combined with advanced imaging techniques and metabolomics to determine a mechanistic route in which these organisms associate to augment soil fertility and plant growth.

There is a great complexity of conditions affecting soil that have no absolute value, making it difficult to generate models predicting states for optimal plant growth. One such factor is the soil microbiome which has long been recognized to be important for nutrient solubilization and transfer required for plant development, but difficulties in characterizing microbial composition and function has made studying their influence quite elusive. Recent ease in accessibility to whole genome sequencing and advances in multi-omics analyses has improved the ability to quantitate plant and soil microbe relationships. Here we will take a quantitative look at how bacteria directly alter the genetic profile of a single fungal cell in a spatial dependent manner as a result of bacterial-fungal interactions using single molecule fluorescence in situ hybridization (smFISH). By determining how the intimate relationships between bacteria and fungi influence soil conditions we might better predict how microbial structure ultimately affects the quality of plant life.

This SFA is supported under the Computational Biosciences Program of the Office of Biological and Environmental Research in the DOE Office of Science.