Microbial signatures of tropical tees across a land use gradient and implications for function

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Introduction

Above and below ground components of ecological communities interact to determine an ecosystem’s biodiversity and function. Plant species shape their environment both directly and indirectly through leaf litter quality and species-specific processes, which create changes in soil chemical ratios (C: N: P), microbial biomass, and pH.

Human land use legacies also affect species composition and structure, and human disturbance produces forests with different species compositions at local scales. It is vitally important to understand the link between human land use and the microbial communities associated with specific species to create predictive frameworks for rapidly changing tropical ecosystems.

Our research evaluated the effects of two distinct tree species, *Casearia arborea* (Salicaceae) and *Dacryodes excelsa* (Burseraceae), on soil microbial communities in the Luquillo forest dynamics plot of the El Yunque National Forest in Puerto Rico. We examined how the scale each species’ “zone of influence” changed with human land use history, and the implications of predicted species-specific microbial signatures on nutrient cycling. Specifically, we tested the hypothesis that the microbial zone of influence for individual tree species would be more pronounced in areas that had not experienced intensive land use within the past 75 years.

Materials and Methods

DNA from all soil samples was extracted and sequenced using the Illumina HiSeq platform. DNA extracts are currently being analyzed on the GeoChip platform, which contains approximately 82,000 probes covering 141,995 coding sequences from 410 functional gene families related to nutrient cycling. Soil pH is also being measured for all samples.

Results

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Conclusions and Implications

- Unique microbial and fungal signatures were detected for both tree species, which could be due to differences in species traits and impacts on soil chemistry.
- The differences in community similarity from the base of the tree to the end of the transect was higher in the regenerative forests, showing that microbial signatures decreased in strength in the regenerating forest. This may be due to changes in soil chemistry and nutrient availability, creating an environment that deters highly sensitive fungal communities.
- GeoChip data will allow us to detect microbial functional genes that are important to biochemical, ecological, and environmental processes and whether or not the observed compositional changes in the microbial signatures correspond to changes in ecosystem functions.
- Soil pH governs the availability of many essential nutrients and the abundance of soil microorganisms. The pH data, which are being collecting now, will allow us to detect correlations with host species, land use type, and fungal composition.