



THE DEEP CONNECTION BETWEEN SOIL MICROBES AND TREES: DNA METABARCODING AND REFORESTATION

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Forest restoration can be better facilitated by considering the diversity and biomass of soil microbiomes.

Tropical deforestation has contributed to the atmospheric rise in greenhouse gas levels, negative impacts on nutrient cycles, and declines in biodiversity. While forest restoration schemes are being implemented, the success of such efforts needs to be better evaluated. Our study demonstrates that soil microbial communities can guide the selection of key tree species important for local forest restoration processes and, ultimately, the global recovery of tropical forests.

Tropical forests only comprise 7–10% of the Earth's land surface but contain 20% of the planet's carbon within the first three metres of soil. They also exchange more carbon dioxide (CO₂) with the atmosphere than any other terrestrial ecosystem. Such characteristics make tropical areas critical for terrestrial primary productivity and global nutrient cycling. Yet, these important ecosystems are continually under threat from human-driven land-use practices.

Deforestation activities across the tropics contribute to the increase of atmospheric CO₂ at levels comparable to fossil fuels¹. If tropical deforestation were a country, it would be the third largest contributor of CO₂ emissions (behind China and the United States), producing more than the European Union². One of the main contributing factors, often ignored, is the large release of CO₂ from the soil when forests are clear-cut; this occurs due to alterations in the respiration maintenance processes of soil microbes that result in a rapid release of the massive stock of soil carbon that has accumulated over time. Moreover, the soil in areas facing extraction-based land-use strategies have been so degraded that the capacity to recover and sustain biological productivity, and to capture and store carbon is significantly reduced.

To remediate these consequences, restoration attempts have been implemented throughout the tropics. However, the success of these efforts is largely

Aerial view of Laguna del Lagarto Lodge and primary forest, Costa Rica
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explored by studying charismatic organisms, such as birds, or by assessing plant biomass, with substantially less focus on soil dynamics. As soil microbes are key components in biogeochemical and nutrient cycling processes, it is thought that certain tree species and their affiliated soil microorganisms may help to serve as a principal pathway to ameliorate degraded soils. Many tropical trees can convert or ‘fix’ atmospheric nitrogen (N_2) into ammonium through specialized root microbial symbionts. This conversion is critical to the growth and development of plants and soil microbes, yet the influence that N-fixing trees can have on the soil organisms in their immediate vicinity is still unclear.



2-year old logging road amongst Costa Rican primary forest with no re-growth due to soil degradation and compaction.
PHOTO CREDIT: Katie McGee

The use of DNA-based identification techniques has significantly advanced research on soil microbial communities. Since the 1980s, popular methods have involved Terminal Restriction Fragment Length Polymorphism techniques and Sanger sequencing. However, all of these methods are time consuming, costly, and involve laborious processes. The more recent development of DNA metabarcoding has allowed us to rapidly and comprehensively characterize soil biotic communities.

DNA metabarcoding is a method that combines traditional marker gene surveys – targeting particular organisms using standardized PCR primers for specific gene regions – with next-generation sequencing. By comparing obtained DNA sequences to a standard reference library of known organisms, taxa present in an environmental sample such as soil can be identified with high confidence. This allows us to address ecological questions linked to environmental impact and biomonitoring in a more efficient manner.

Using DNA metabarcoding, our study investigated individual plant effects of the soil collected around two types of trees, *Pentaclethra maculosa* (Gavilán;

nitrogen-fixing) and *Dipteryx panamensis* (Almendro; non-nitrogen-fixing), in Costa Rica’s northern region. We wanted to examine differences in the soil bacterial and fungal community composition.

We found that each plant species contained a unique soil microbial community, and that the nitrogen-fixing tree, *Pentaclethra*, supported soil microbes and microbial biomass at levels similar to those measured in primary forests. This indicates their importance for the recovery of soils to a pre-disturbed state. In comparison to the non-N-fixer *Dipteryx*, *Pentaclethra* stimulates a soil microbial community that is more efficient in storing soil carbon into biomass, as opposed to carbon loss via aforementioned respiration maintenance processes. These effects appeared to be associated with the amount of soil ammonium that the *Pentaclethra*-soil is able to provide to the surrounding soil.

Our results indicate the importance of this N-fixing tree in building back up carbon storage as biomass in the soil as well as promoting plant and soil microbial growth. As such, we suggest the use of *Pentaclethra* and its associated soil microbiome as an important ecosystem restoration tool in facilitating early regeneration of secondary forests.

Our method of using soil microbes, characterized by DNA metabarcoding, is a novel approach that can be applied globally to guide regeneration efforts that most effectively improve the quality and fertility of degraded soils as well as inform restoration ecology and the policy surrounding it.

References:

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