



# MONITORING THE MICROBIAL DIVERSITY AND FUNCTIONAL ACTIVITIES IN RESPONSE TO LAND-USE CHANGES AND DEFORESTATION UNDER SOYBEAN AND SUGARCANE CULTIVATIONS

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## SCIENCE QUESTIONS AND OBJECTIVES

One assumption often made is that biodiversity loss is happening more rapidly in the tropics due to agricultural activities. The processes of land conversion and agricultural intensification are one of the most significant causes of biodiversity loss, with consequent negative effects both on the environment and on the sustainability of agricultural production. The consequent reduction in the diversity of the soil community, including cases of species extinction, may cause a catastrophic loss in function, reducing the ability of ecosystems to withstand periods of stress and leading to undesirable environmental effects. Scientists have begun to quantify the causal relationships between (i) the composition, diversity and abundance of soil organisms, (ii) sustained soil fertility and associated crop production, and, (iii) environmental effects including soil erosion, greenhouse gas emissions and soil carbon sequestration. Consequently, actions that directly target the conservation of components of the microbiological diversity will have environmental benefits at ecosystem, landscape and global scales.

Our purpose is to integrate data from soil chemistry and microbiology, molecular biology and bioinformatics in an effort to detect, quantify and correlate the microbial processes involved in the C and N biogeochemical turnover in soybean and sugarcane cultivations, under natural areas (forest) and two agricultural system – conventional and sustainable agriculture (minimum tillage and mulching practices). Using three estimators of diversity (rarefaction, Chao1, ACE), it is proposed a high throughput DNA pyrosequencing and statistical inference to assess bacterial and *Archaea* diversity and quantify the functional genes associated to the microbial

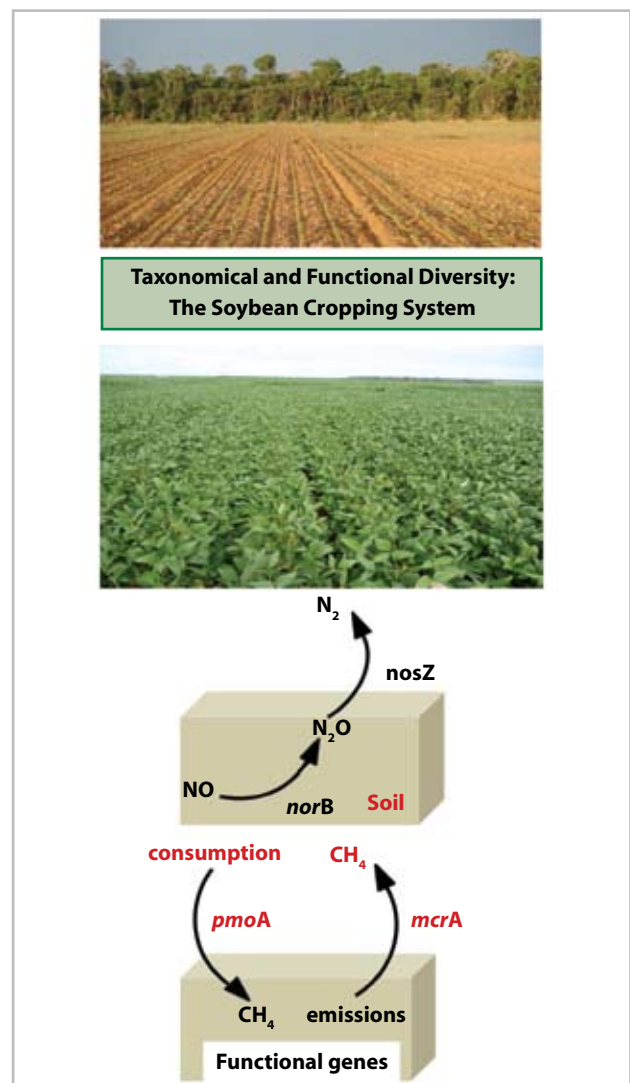


Figure 1. Functional genes of the microbial C and N cycles involved in the greenhouse gas emissions from the cropping systems

turnover in soils under different land use systems and greenhouse gas (GHG) emissions.



## CURRENT RESULTS AND PERSPECTIVES

Field and greenhouse (mesocosms) studies using biochemical and molecular tools were developed with the aim of evaluating the impacts of the greenhouse gas emissions/sequestration due to land-use under soybean and sugarcane. We are monitoring 10 different sampling sites under soybean cultivation, the adjacent forests and recent deforestation areas in Mato Grosso and Mato Grosso do Sul and three different sugarcane cultivation system and their adjacent forest areas in São Paulo state.

We found significant differences between the soybean arable fields and adjacent forests regarding to community size of *Acidobacteria* in soil. The highest number of total bacterial 16S rRNA gene copies was detected in the soils taken from longer soybean cultivation past histories. Relative abundances of *Acidobacteria* and *Verrucomicrobia* were lower in soils under recent deforestation history. To validate these results, clone libraries were constructed using two different new specific-primers designed for *Verrucomicrobia* based on sequences previously recovered from tropical soils. Culturability and molecular detection of hitherto-uncultured bacteria from soil were studied from arable field samples collected from different chronosequences of soybean croppings. Bacterial cultivations were undertaken under a similar belowground hypoxic environment of 2% O<sub>2</sub> and 93% N<sub>2</sub> atmosphere with elevated concentration of CO<sub>2</sub> (5%).

Soils from six areas occurring in Southeast Amazonian comprising adjacent forest, deforested field, a 7-year cultivation soybean crop field and pasture of Mato Grosso were collected for profiling the microbial community structures using T-RFLP, a cultivation-independent molecular technique. Redundancy Analysis (RDA) showed differences among the environments, distinguishing the samples according to the land-uses. These analyses also correlated the microbial structures to the soil attributes revealing that those related to soil acidity, as pH, potassium, H+Al, displayed a significant correlation with bacterial and archaeal community structure variance. For bacterial community, the richness of Operational Taxonomic Units (OTUs) did not show significant differences among the sites. On the other hand, the archaeal communities showed sharp decreases in richness from forest to soybean crop and pasture as well.

These data reveal that land-use changes clearly alter the community structure and abundance of bacterial and archaeal domains in soils. Therefore, the molecular determination of temporal and spatial variations in the microbial community structures and functional genes associated to GHG consumption/ emission can be used as additional data when monitored at ground surface or in the rhizosphere of the plant crops.

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