Conversion of a tropical forest to agriculture – Effects on the diversity of soil microbial communities as revealed by a DNA metabarcoding approach

Place of work/: [Plant Functional Genomics Unit, FCUL]

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It is estimated that 25% of all biodiversity lives in the soil. Soil microorganisms contribute to a number of life-support functions, including maintaining of soil fertility essential for the production of food for human consumption. However, together with climate change, the increasing intensification of agriculture jeopardizes the functionality of soils, contributing to their degradation. Several studies point to a generalized loss of soil biodiversity with the intensification of agriculture, due to the use of methods such as tilling, use of chemical fertilizers and pesticides. Land-use change, specifically deforestation, is one of the most important drivers of change in soil biodiversity. However, its impact on soil microbial communities is still largely unknown. Increasing the knowledge on how microbial soil communities change following land conversion to agriculture can provide valuable information for soil management and assessment of the impact of deforestation of vulnerable ecosystems.

This study aims to evaluate how the conversion of a tropical native forest into a field for agricultural production impacts the taxonomic, phylogenetic, and functional diversity of the soil microbial community. The soils being analyzed were collected in Guiné-Bissau, at 3 locations with different land uses: a primary forest, an annual crop field (peanut) and a perennial crop field (cashew), during the wet and dry season. Specifically, we want to test how the soil microbiome responds to changes in land use, as well as to seasonal changes, on each soil type. To achieve this, we will use a DNA metabarcoding analyses targeting bacterial 16S rRNA and fungal ITS regions. Datasets from Illumina sequencing will be processed, clustered and annotated using software tools, such as QIIME [1], MicrobiomeAnalyst [2] or mothur [3]. Taxonomic identity will be performed searching against the SILVA database for prokaryotic operational taxonomic units (OTUs) and the

UNITE database for fungal OTUs. The FUNguild tool [4] will be used for functional assignment (e.g., saprotrophs, pathogens, and symbionts) of the fungal OTUs. Diversity estimates (OTU richness, Michaelis-Menten fit, Chao1, Shannon, Simpson) and rarefaction curves will be calculated, and statistical methods will be used to support any findings. The work benefits from an ongoing project with the Guinean Institutions financed by the FAO (Food and Agriculture Organization) of the United Nations and will increase soil biodiversity knowledge in this understudied region of the world.

[1] Caporaso J.G. et al. QIIME allows analysis of high-throughput community sequencing data. Nat. Methods 7, 335–336 (2010).

[2] Dhariwal A. MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. Nucleic Acids Research, 45, (2017).

[3] Schloss P.D. et al. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl. Environ. Microbiol., 75, 7537–7541 (2009).

[4] Nguyen, N. H. et al. FUNGuild: an open annotation tool for parsing fungal community datasets by ecological guild. Fungal Ecol. 20, 241–248 (2016)

"Students selected for this project, after thesis registration, are eligible to apply to the BioISI Junior Programme (supporting 8 students with a 6-month Scholarship(BII), being the selection criterium the academic merit of the candidates."