

Master Thesis at FiBL

Preliminary titel

"Soil nitrogen cycling and underlying microbial communities as influenced by organic and conventional farming systems in tropical soils"

Background

Closing nutrient cycles and maintaining biodiversity are among the greatest challenges for the development of sustainable agricultural systems. Nitrogen is one of the most important nutrients and it's availability often limits crops production. Nitrogen cycling is mainly governed by the vast diversity of soil microbes. Most processes hold agronomic or environmental relevance, such as provision of nutrients through nitrogen mineralization or the mitigation of greenhouse gases through N_2O reduction. Long term farming systems shape the diversity and functionality of soil microbes. Organic agricultural practice are widely discussed as environmental-friendly and viable alternatives to intensive agricultural practice. Yet, so far there is little knowledge how organic systems in the tropics shape soil microbial activity, diversity and soil nitrogen cycling processes.

The thesis will be elaborated in frame of a SNF funded project to characterize microbial community composition in tropical organic and conventional farming systems.

The main working place will be at FiBL in Frick (AG). The aims are (I) to quantify soils potential to perform nitrogen transforming processes using enzymatic assays and (2) to characterize the abundance and/or diversity of herein involved functional soil microbial communities.

The ideal candidate will have a basic knowledge of soil science and a great interest in agro-ecological systems. Basic laboratory experience and a high level of motivation are a prerequisite. Experience on statistical analysis via R and molecular biological methods are of advantage.

Methods

The methodological approach includes conduction of functional assays to quantify processes such as nitrogen mineralization and N_2O reduction. Furthermore, molecular biological techniques (e.g. DNA extraction, PCR) and bio-informatical analysis of next generation sequencing data will be part of the thesis.

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