

# MicAgroRice

## Microbiome for AgroEcology in Rice

### ABSTRACT

It is well known that soil microbial communities influence plant growth, health and resource use efficiency, especially the subset that is recruited by plants to form the root microbiome. Recent advances in next-generation sequencing have allowed unprecedented studies of soil and plant microbial communities at the plant, field and metaanalysis levels. Moreover, specific software packages that predicts the functional capabilities of microbial communities based on 16S rRNA datasets make possible inferring the microbial functions operating in the holobiont. For last five years the numerous studies on the effects of agricultural practices such as fertilization regime on the presence or absence of pathogens and beneficial microbes and its potential optimization to contribute to sustainable intensification of agriculture have been published. However, these data seems still difficult to be integrated by the agronomists in their analyses aiming to understand and model how agroecological practices affect the performance of cropping systems. In this interdisciplinary project we propose to 1) assess the effect of agroecological practices on rice plants (holobionte), by carrying out on-farm trials, 2) learn how the information from microbiome analysis can be integrated and used to document the outcome of potential agroecological practices, and systemic agronomy, and 3) determine the constraints and levers for the adoption of practices identified as beneficial for the plant and its environment. To this purpose, intensive field work will be conducted in rice fields being chosen for their contrasting cultural practices. Sampling of plants at two growth stages will be performed in order to provide the material for root microbiome analysis and detailed plant phenotype characterization on one hand, and on other hand, to provide the agronomic data (at rice maturity) on the rice yield and plant nutrition. The microbiome analyse will trace the changes in prokaryotic (bacteria & archaeae) and eukaryotic (protists, fungi, streptophyta, and metazoan) communities and inferred functions in rice roots cultivated different field condition. Obtained results will be analysed to investigate the agroecological significance of the rice root microbiome diversity and function change resulting from different agro-ecological practices in Sudano-Sahelian area of Burkina Faso. Through this multi-disciplinary approach combining analysis of agroecological practices yield estimation with and microbiome molecular characterisation we aim to learn how the microbiome diversity and its functions could be analysed at the agroecological scale to contribute in the sustainable crop production, in order to develop a common approach combining fundamental sciences and agronomy for an integrative study of agroecological intensification.

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**Project leader's institution :** IRD

**Project leader's RU :** IPME-PHIM

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