



## **Effect of crop rotation and straw application on microbial communities in paddy soil**

Claudia Knief, Sarah Maarastawi, and Katharina Frindte  
INRES, University of Bonn, Bonn, Germany (knief@uni-bonn.de)

The composition and activity of microbial communities in soils is controlled by various factors. We evaluated the influence of two agricultural management practices, crop rotation and straw application, on the soil and maize rhizosphere microbiota upon cultivation in rice field soils. The two management practices are considered to lead to more sustainable rice production by reducing methane emissions, water loss and carbon leaching. Fields subjected to rice-maize, maize-maize and rice-rice rotation were included in the study. We analyzed the microbial responses to these management practices in comparison to factors that are known to influence soil and rhizosphere communities, i.e. field location and time. Responses in the composition of the bacterial and fungal community were analyzed by 16S rRNA gene and ITS based amplicon sequencing, respectively. The soil and rhizosphere microbial communities were most strongly influenced by field location, followed by crop rotation and rice straw application. The strength of the response to the treatments differed for fungal and bacterial communities. To assess the impact of straw application on soil and rhizosphere microorganisms more specifically, we applied <sup>13</sup>C-labeled rice straw and analyzed labelled microorganisms using the DNA-SIP approach. We compared the straw degrading bacterial and fungal communities in the soil over time and to those in the rhizosphere. This revealed a temporal dynamic in the soil and a overlap between straw degrading microorganisms in the rhizosphere and bulk soil, suggesting that different groups of microorganisms in the rhizosphere profit from different carbon sources. Taken together, our results demonstrate that agricultural management practices influence the composition and activity of the soil and rhizosphere inhabiting microbiota.