



INTERNATIONAL PHYTOBIOMES CONFERENCE 2018

4-6 DECEMBER

LE CORUM
MONTPELLIER
FRANCE

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Development of a multigenic metabarcoding protocol for deciphering the diversity of *Archaea*

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Soil and plant microbiota are playing an eminent role in shaping both natural ecosystems and agricultural production systems. It is now widely admitted that bacterial communities show a great diversity in both the plant rhizosphere and the plant endosphere. These microbial communities affect the fitness of the hosts and further play important roles in C and N cycles. While bacterial communities have been widely studied, much less is known about archaeal communities and the role they play within the rhizosphere and the endosphere. The objective of our study was to develop a multigenic metabarcoding approach to accurately describe the diversity of archaeal communities interacting with rice paddies in the Rhône delta region. This pilot agro-ecosystem was selected because it is annually subjected to several abiotic stresses (water stress associated to rice paddies flooding, soil salinity, high production of methane, etc.) that are likely to enhance archaeal growth. We used archaeal specific primers within the universal 16S rRNA gene and the *mcrA* gene (encoding the methyl-coenzyme M reductase subunit A of methanogens). An evaluation of the efficiency of the primers was carried out on mock cultures and plant samples. Two rice-compartments during both rice paddies flooding and drying periods were collected and analyzed. This study is likely to be a first step towards better describing rice-associated archaeal communities and understanding the dynamics of these communities in relation with abiotic constraints of rice paddies in Camargue.

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Exploring within-host diversity of plant viruses in rice agrosystems using two high-throughput sequencing strategies

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The virome is an essential component of the phytobiome as viruses correspond to the most abundant and diverse biological entity in Nature and interact with all living organisms. The recent advances in high-throughput sequencing (HTS) has proven efficient for characterizing within-host diversity of several viruses, which has shed light on the influence of this diversity on the global fitness and virulence of viruses. We here aimed at evaluating the impact of rice management on the within-host diversity of Rice yellow mottle virus (RYMV) in order to optimize the cultural practices and to limit the burden of Rice yellow mottle disease in Africa.

We worked on rice plants collected from traditional and intensive rice fields in East Africa, which is the center of origin of Rice yellow mottle virus. Interestingly, several strains with contrasted pathogenic and epidemiological parameters co-exist in this region and recombination between strains were identified recently. We selected twelve RYMV symptomatic samples from fields managed under different types of practices that were analyzed using two HTS strategies: a metagenomics-based approach and a RYMV specific sequencing approach.

Combining both strategies, we tested if the RYMV was associated with other viral species in rice, and if some cases of co-infections between RYMV strains occurred. Both approaches indicate a significant within-host RYMV diversity, which allows us to perceive the diversification processes of RYMV strains at the field scale. The detection of recombinants and the comparison of the within-host genetic diversity depending on the cultivation practices are underway.