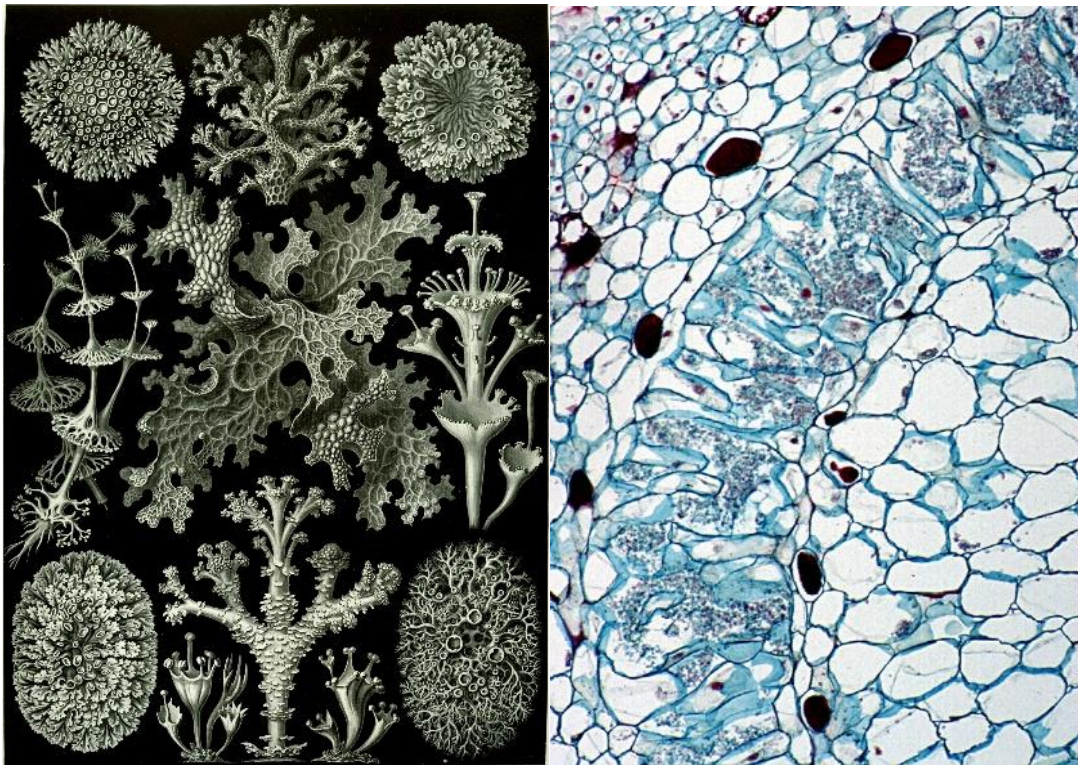




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Development of a multigenic metabarcoding of prokaryotic microbiota: application to Bacteria and Archaea of agronomical interest encountered in the rice rhizosphere of Camargue

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It is our hypothesis that 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 the rhizosphere and in the endosphere as endophytes. These microbial communities affect the fitness of both the hosts and the microbes and further play important roles in C and N cycles. Much less is known about the role played (if any) by archaea within both the plant rhizosphere and endosphere. Interestingly, a recent study has revealed a relatively high archaeal concentration in internal plant tissues (Müller *et al.*, 2015). The objective of our study is to develop a multigenic metabarcoding approach to accurately describe the biodiversity of relevant microbial 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, etc.) that are likely to enhance archaeal growth. We will retain universal prokaryotic primers and archaeal specific primers within the 16S rRNA gene, two housekeeping genes, *gyrB* (encoding the β subunit of the DNA gyrase) and *rpoB* (encoding the β subunit of the RNA polymerase) for bacteria, and the thermosome TF55 gene (encoding a type II chaperonin) for archaea. Primers evaluation will be conducted on mock cultures and by sampling rice plants during both rice paddies flooding and drying periods. This study is likely to be a first step towards better understanding the dynamics of Camargue rice paddies microbial communities in relation with abiotic constraints.

References

Müller H, Berg C, Landa BB, Auerbach A, Moissl-Eichinger C, Berg G. 2015. Plant genotype-specific archaeal and bacterial endophytes but similar *Bacillus* antagonists colonize Mediterranean olive trees. *Front. Microbiol.* 6:138.

Keywords

Prokaryotic microbiota, multigenic metabarcoding, rice paddies