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## **MICROBIAL COMMUNITY STRUCTURE ASSOCIATED WITH RICE ROOTS IN CONTRASTING RICE AGROSYSTEMS IN WESTERN BURKINA FASO**

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### **Text**

Plants recruit soil microorganisms to provide various functions or protection against pathogens. Crop plants and their associated microbial communities are therefore increasingly studied together. However, the mechanisms that control the assembly of the root-associated microbiome remain difficult to disentangle, especially in rice ecosystems, which are poorly studied. Here, we compare the assembly of rice root-associated microbiota sampled from 19 smallholder fields in the irrigated and rainfed lowlands of Burkina Faso. Using a 16S rRNA gene amplicon and ITS metabarcoding approach, we show that the rice production system is a major factor in the structure of the microbiome in addition to the expected structure by root compartments (root vs. rhizosphere) and geographic areas. In irrigated systems, we found greater diversity of rhizosphere prokaryotic communities and more complex co-occurrence networks, compared to rainfed lowlands, while fungal communities showed an opposite pattern. The main taxa were different between the two systems, and indicator species were identified: mostly within Bacillaceae in the rainfed lowlands, and within Burkholderiaceae and Moraxellaceae in the irrigated areas. Finally, a higher abundance in rainfed lowlands was found for mycorrhizal fungi. Our results highlight profound differences in the microbiome induced by contrasting rice production systems that should therefore be considered for microbial engineering applications.

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## **TOWARDS A MORE SUSTAINABLE CONTROL OF ALMOND WOOD DISEASES**

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### **Text**

Almond is one the most important nut crops worldwide. The implementation of new management techniques such as high-density cultivation, prune intensification, drip irrigation and fertilization, mechanical harvest, use of more productive varieties, and the cultivation in agronomically and environmentally more favorable cropping areas, has increased the