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Eco-Evolutionary Characterization of Microbial Communities in Rice Ecosystems

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Plant-associated microbial communities influence the fitness of hosts by the mitigation of abiotic and biotic stresses, the supply of nutrients essential for hosts, growth promotion, and the involvement in normal development. In the present study, we investigated microbial communities in paddy soil, rice plant, and rice seeds to unveil the complex relationship among plant, microbiota, and environment. Firstly, we discovered a comprehensive blueprint of the bacterial, archaeal, and fungal communities in rice paddy soils with differing soil types and chemical properties. We revealed that the compositional changes of microbial communities by soil nutrients were governed by microbial trophic lifestyles. Secondly, we examined the dynamics of microbial communities from developing rice seedlings. Niche differentiation between above- and belowground compartments leads to compositional differences in endophytic bacterial and fungal communities originating from seeds. Longitudinal tracking of the composition of microbial communities revealed that bacterial and fungal communities originating from seeds persist in the leaf, stem, and root endospheres throughout the life cycle. Finally, we explored evolutionary relationship between rice and its associated microbial communities. We found that speciation of *Oryza* spp. and domestication significantly affect seed microbial communities. In particular, the composition of bacterial community was relatively conserved whereas fungal membership was dramatically changed following the domestication. Taken together, our study will provide eco-evolutionary insights into understanding plants and their associated microbial communities as the starting point of the holobiont of plants, microbial communities, and surrounding environments.