Editorial: Rhizosphere microbiome special issue

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The rhizosphere is the narrow zone surrounding plant roots which provides a niche for interactions between roots, soil components and microorganisms, and is one of the most dynamic interfaces on Earth. The rhizosphere is a conceptual zone of soil influenced by a root; the zone is smallest for phosphate, greater for nitrate, and even greater for water, and thus is conceptually highly significant, but physically ill-defined, unlike the rhizosheath (Lambers 2022). The rhizosphere or rhizosheath hosts complex microbial communities, referred to as the rhizosphere microbiome, which plays critical roles in nutrient cycling, organic

matter decomposition, plant productivity, plant stress tolerance and even human health. The interactions between plants, microorganisms and soils has been considered as a common phenomenon in the rhizosphere environment, and mainly involve three aspects: (1) plants may selectively stimulate microorganisms with traits that are beneficial to plant growth and health; (2) soils may directly or indirectly modulate the rhizosphere microbial communities and functions; (3) the rhizosphere microbiome may provide positive feedback on plant growth and stress tolerance by nutrient cycling and synthesis of phytohormones. With the development of “omics” and culture techniques, we are now able to better understand the composition and function of the microbiome, and the interactions between microbes and plant roots in the rhizosphere.

This special issue on Rhizosphere Microbiome focuses on various aspects of the rhizosphere microbiome, including microbial community composition and diversity, microbial biogeochemical cycling, and the interactions between plants and microbes. The call for papers was widely acknowledged within the community, reflected by 12 research papers now published in this Special Issue.

Six of the research papers focused on the impact of agricultural management practices on rhizosphere microbiomes in field experiments, greenhouse experiments or laboratory culture experiments. In field experiments, Li et al. (2022a) found that plastic film mulch (PFM) changed the composition,

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assembly, and co-occurrence patterns of maize root-associated microbiomes, and recruited specific taxa potentially beneficial to plant growth, while Wu et al. (2022) found that peat-vermiculite enhanced microbiota-driven soil fertility and crop productivity. In a short-term greenhouse experiment, Obermeier et al. (2022) observed changes of soil-rhizosphere microbiota after organic amendment application. In laboratory culture experiments, Li et al. (2022b) found that lime application changed the microbial composition and potential functions, which eventually resulted in the improvement of soybean plant growth, while Wang et al. (2022) found that organic matter input increased the microbial diversity and network interactions in the *Populus* rhizosphere. Zhang et al. (2022a) studied the composition of the microbial community over four consecutive plant cycles (generations), using mRNA sequencing of the microbial communities in the rhizosphere of *Jacobaea vulgaris*.

Two of the research papers examined the relationships between rhizosphere microbes and biogeochemical cycling, one in a natural ecosystem and one in a farmland. In a natural ecosystem, Yang et al. (2022) investigated how ectomycorrhizal and arbuscular mycorrhizal associations affect the rhizosphere soil nutrient economy in karst forests soils. In farmland, Liu et al. (2022) evaluated the interactive effects of elevated CO₂ and warming on the rhizosphere microbial community and its relationship with soil N₂O emission in a Chinese wheat field.

Three of the papers investigated the effects of plants on the rhizosphere microbiome. Chen et al. (2022) found that rice genotypes enriched specific bacterial communities to inhabit the rhizosphere at both the taxonomic and functional levels. Shi et al. (2021) demonstrated that *Artemisia annua* assembled the specific root-associated microbial communities with increased abundance of plant-growth-promoting microorganisms and built inter-kingdom co-occurrence networks, which might be beneficial for the fitness of plants in natural environments. In a greenhouse pot experiment, Zhang et al. (2022b) found that the intraspecific plant interaction affects arbuscular mycorrhizal fungal species richness. Lu et al. (2022) found that roots and the microbiome jointly drive the distributions of 17 phytohormones in the plant-soil continuum in a phytohormone-specific manner.

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