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# Editorial: Rhizosphere conversation among the plant-plant microbiome-soil under consecutive monoculture regimes

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## Editorial on the Research Topic

[Rhizosphere conversation among the plant-plant microbiome-soil under consecutive monoculture regimes](#)

Intensive agricultural and horticultural cultivation, including consecutively growing the same crop in the same fields, has been contributing to meet the increasing food demands of a rapid growing human population (Diaz-Ambrona and Maletta, 2014). However, intensive consecutive monoculture results in replant disease/soil sickness, which causes serious plant diseases and subsequent declines in the quality and quantity of crop products (Xiong et al., 2017; Winkelmann et al., 2019; Wu and Lin, 2020; Zhou and Wu, 2021). The current knowledge suggests that the factors underlying replant disease may be associated with soil nutrient imbalance (Huang et al., 2013), accumulation of root exudate autotoxicity (Zhang et al., 2019; Busnena et al., 2021), and changes in the rhizosphere microbial community (Li et al., 2014; Wu et al., 2019; Balbín-Suárez et al., 2021). Yet, we still know little about the mechanisms behind the negative effects of consecutive monoculture regimes on plants, which might hinder the key to develop strategies to alleviate replant disease.

Healthy plants are colonized by a rich diversity of microbes (i.e., bacteria, fungi, protists, and viruses), forming complex microbial consortia that impact plant growth and health. Increasing evidence is showing that the accumulation of soil-borne pathogens (e.g., *Fusarium*, *Pythium*, *Alternaria*, *Ralstonia*,

members of *Nectriaceae*) at the expense of plant-beneficial microbes (e.g., *Pseudomonas*, *Bacillus*, *Paenibacillus*) might be a major driving factor of replanting disease (Lareen et al., 2016; Xiong et al., 2017; Yim et al., 2017; Popp et al., 2020; Wu and Lin, 2020). For example, the consecutive monoculture regimes significantly increased the abundance of potential pathogenic *Ralstonia* sp. and *Fusarium oxysporum* in the plant leaf and root of *Radix pseudostellariae* (Wu et al., 2022b), increased the diversity of soil-borne plant viruses in the rhizosphere of *R. pseudostellariae* (Wu et al., 2022a), and caused the strong accumulation of plant parasites, plant pathogens, and parasites while significantly reducing the relative abundance of bacteria-feeders nematodes and omnivores (Wu et al., 2021). The interactions between plant, soil, and microorganisms within the soil food-web play a crucial role in creating the conditions that cause the negative effects due to consecutive monoculture. Previous research mainly focused on changes in the soil microbial community structure and composition under consecutive monoculture conditions (Wu et al., 2021), while the effects of intensive monoculture on the overall plant and soil microbiome, in combination with the role determined by root exudates, received little attention.

As a response to the importance of plant-plant microbiome-soil interactions in replant disease, we proposed the Research Topic “Rhizosphere conversation among the Plant-Plant Microbiome-Soil under Consecutive Monoculture Regimes.” In this Research Topic, we have collected six original research and one review articles that contribute on expanding our knowledge about the rhizosphere ecological processes under consecutive monoculture regimes. In their review, Somera and Mazzola comprehensively focused on the multiple factors that contribute to generate an apple replant disease-suppressive soil microbiome and highlighted the importance of considering host genetic factors. Reim et al. contributed to the understanding of apple plant response to replant disease by comparing the transcriptome of two apple genotypes differing in susceptibility in conducive and sterilized soil. Yuan et al. showed that the plant *Pseudostellaria heterophylla* is able to recruit plant-beneficial microbes against the pathogen *Fusarium oxysporum* under continuous monocropping regime. Cui et al. found a more pronounced effect driven by continuous cropping of sugar beet on the fungal than on the bacterial communities inhabiting different plant compartments (bulk soil, rhizosphere soil, and beetroot). Pang et al. suggested that the sugarcane-peanut intercropping pattern could potentially improve soil nutrients, cane agronomic parameters, peanut yield, and bacteria diversity in sugarcane root systems compared to the monoculture farming system. Similarly, Bai et al. found that intercropping walnut and tea positively impacted the soil's nutritional conditions and helped in enriching soil with beneficial bacterial and fungal taxa, suggesting that

intercropping was able to alleviate the replant disease by altering the plant-associated microbial communities. He et al. studied the response mechanism of alien invasive and the native plants to acid rain by analyzing plant phenotypic characteristics, soil physicochemical properties, and rhizosphere microbial communities.

Overall, the papers in this Research Topic focus on plant health and reveal the responses of soil physicochemical properties, plant characteristics and soil microbial community to environmental conditions generated by consecutive monoculture regimes. Plant health is intimately influenced by the plant associated microbiome, a complex assembly of organisms that changes dramatically throughout plant development (Xiong et al., 2020). The recruitment of microorganisms in the rhizosphere occurs *via* root exudates directed from plants to microorganisms, and subsequent interactions between microorganisms and between microorganisms and the host plant (Doornbos et al., 2012; Sasse et al., 2018; Balbín-Suárez et al., 2021). Previous studies showed the rhizosphere protists within the microbiome to be key determinants of plant health (Geisen et al., 2018; Xiong et al., 2020) and the plant microbiome and that they are able to alter plant metabolic functions and enhance the disease resistance to pathogens (Chaudhry et al., 2021). Moreover, soil-borne plant viruses can potentially infect plants through mechanical friction, nematode vectors and fungal vectors (Reavy et al., 2014; Wu et al., 2022a). While the study of the consequences of plant-microbiome-environment interactions is attracting a wide interest, we are only at the beginning of understanding the mechanisms that regulate the plant responses to their own interactions with the community of microorganisms they co-inhabited as well as higher order soil organisms. We are optimistic that soon we will be able to combine the power of sequencing technologies, high-throughput phenotyping, high-performance computing, and big data approaches coupled to machine learning to understand the rules that regulate plant-microbiome interactions, and how to exploit them to support a sustainable agriculture.

## Author contributions

HW drafted the editorial. All authors contributed to editorial revision and approved the final paper.

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