



Diverse organic carbon activates soil microbiome functioning via niche modulation

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Considering the “One Health” framework, the soil microbial community is essential for plant, animal, and ultimately to human health (Banerjee and van der Heijden, 2023). Similar to the microbiome in human gut (Berendsen et al., 2012), the plant-associated microbiota drives key functions in agroecosystems, such as supporting nutrient uptake, suppressing plant pathogens, or improving host stress tolerance (Hartmann and Six, 2023). However, continuous monocropping run in intensified agroecosystems often leads to the loss of soil biodiversity, reduces resistance to plant pathogens, and ultimately causes the outbreak of soil-borne diseases (Tsiafouli et al., 2015; Raaijmakers and Mazzola, 2016). This represents a major threat to global food security and sustainable development in agriculture (Strange and Scott, 2005; Butler, 2013). Accordingly, soil microbiome engineering is widely recognized as a promising approach to promote plant health and agricultural sustainability (Raaijmakers and Mazzola, 2016; Hartman et al., 2018).

Introducing efficient probiotics is an essential way to manipulate soil microbiome. Significant progresses have been made in isolating from disease-suppressive soils key microbes (i.e., bacteria, fungi, protists, and phages) that contribute to plant health promotion (Mendes et al., 2011; Cha et al., 2016; Yuan et al., 2021; Guo et al., 2022; Yang et al., 2023). The inoculation of these isolates into diseased soils has been proven to be an effective strategy for suppressing plant diseases. For recent examples, Gu et al. (2022) explored and isolated five bacterial strains that shown to significantly suppress tomato bacterial wilt, when they were inoculated into soils. Tao et al. (2023) revealed that *Trichoderma* application significantly decreased banana *Fusarium* wilt disease incidence through modifying the composition and functioning of the resident soil fungal microbiome. Zhou et al. (2022) reported that the cross-kingdom synthetic microbiota was more effective than those of fungal or bacterial synthetic communities alone. Neverthe-

less, unsuccessful colonization of these inoculated agents in the soil or rhizosphere remains a limitation that needs to be further resolved.

Another strategy to harness soil microbiome is by promoting or even constructing suitable environments for the plant beneficial microbes. Some important environmental variables structuring soil microbial communities have been highlighted, such as pH, or organic carbon quality and quantity (Fierer, 2017). Since most microbes in the soil are starving, available organic resources derived from plant root exudates or from soil organic matter are effectively shaping soil microbial communities and functions (Zhalnina et al., 2018). Hence, in complement to provide suitable resources for plants, organic amendments are widely used in practice to modify soil microbial composition to control plant diseases (Roszkopf et al., 2020). In essence this approach is very similar to the dietotherapy dispensed in clinical practices (Patnode et al., 2019). Unfortunately, the disease suppression effects of organic amendments remains unpredictable (Berihu et al., 2023), highly variable from positive to negative (Bonanomi et al., 2018). Ideally, the application of pathogens-unfavorite and probiotics-favorite organic resources ought to be effective in suppressing plant pathogens and control diseases. However, the heterogeneity in plant-pathogen-soil systems makes the effects of these organic resources case-dependent, and it is difficult to propose specific organic resources consistently suppressing plant diseases in all cases.

Theoretically, different microbial species have differential resource preferences, and resource diversification can induce niche partitioning and establish a more diverse community (Furey and Tilman, 2021; Yu et al., 2021). Microbial communities with high diversity are supposed to have a greater ability to suppress plant pathogens and diseases. To test this hypothesis, Zhou et al. (2023) investigated the effects of the diversity of available organic resources on plant pathogen and disease suppression, and shed light on how high carbon resource diversity enhanced the certainty of successful suppression of plant pathogen and disease

control.

The authors first determined the organic resources utilization patterns of 8 residential bacterial strains and a well-studied tomato pathogen, *Ralstonia solanacearum*. These tested organic resources covered a range of carbohydrates (CAs), organic acids (OAs), and amino acids (AAs). Then, they assembled three kinds of SynCom by randomly selecting 4, 6, and 8 residential strains, and prepared organic resources mixtures with diversity gradient by randomly selecting 1–11 carbon sources from the three pools (CAs, OAs, and AAs). The pathogen was co-cultivated with these SynComs in microcosms supplied with these resources mixtures. As a result, the authors found that the pathogen inhibition rate increased significantly along with the increase in carbon diversity. Interestingly, the deviation of the pathogen inhibition rate decreased significantly meanwhile, indicating high carbon diversity increased the certainty of successful pathogen suppression. To further figure out how carbon diversity influenced pathogen suppression ability, the authors developed a three-dimensional evaluation system, involving average utilization intensity (AUI), Evenness_{strain}, and Evenness_{carbon}, to comprehensively assess the trophic network architecture between strains and carbon sources. Using this evaluation system, the authors found that carbon diversity positively influenced the Evenness_{strain}, representing the evenness of resource utilization ability among residential strains, and further determined the pathogen inhibition rate. This result indicated that high carbon diversity homogenized the resource utilization ability among residential members and activated them to participate in resource competition. Similarly, the authors reported that the incidence of tomato bacterial wilt disease significantly decreased when high diversity resources mixtures were added in a subsequent resident-controlled pot experiment.

Furthermore, while previous studies mostly described similar effects of carbon additions on niche partitioning, Zhou et al. (2023) confirmed their results in a soil experiment with *in vivo* microbiota. They show that high carbon diversity increased the evenness of bacteria, particularly abundant bacteria, and thus decreased tomato wilt disease incidence. The authors also reported that high carbon diversity enhanced the connections among abundant bacterial members, and upregulated plant immune system regulation-related microbial functions, which should also contribute to the disease suppression in addition to increase bacterial evenness.

Considering the crucial functions of soil microbes in agroecosystems, directed engineering of soil microbiome is essential for a sustainable agriculture (Hartmann and Six, 2023). Effective and reliable soil microbiome management strategies need to be explored to support plant health and productivity. Zhou and her colleagues (2023) demonstrated that increasing the diversity of available organic resources

can be an effective method for successful and consistent suppression of plant pathogens and diseases, and proposed a principle of how to develop organic resource-mediated disease management approaches. Yet, many issues regarding the relationships among organic resources, microbial compositions and functions remain, such as how to predict the resources preference of specific microbial agents under *in vivo* systems and how to precisely manipulate their functions with specific resources. The answers of these questions are supportive to developing an ecologically sustainable and plant-beneficial soil microbial environment, which paves the way for “smart farming.”

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