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RECEIVED 24 August 2024
ACCEPTED 27 August 2024
PUBLISHED 06 September 2024

CITATION

Mitra D, Rodríguez-Seijo A, Adhikari P, Villalobos SdS, Panneerselvam P, Del Gallo M and Pellegrini M (2024) Editorial: Unearthing and harnessing the power of the soil microbiome and mycorrhizas to enhance plant nutrient utilization under climate stress. *Front. Soil Sci.* 4:1485795. doi: 10.3389/fsoil.2024.1485795

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Editorial: Unearthing and harnessing the power of the soil microbiome and mycorrhizas to enhance plant nutrient utilization under climate stress

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KEYWORDS

soil nutrient dynamics, PGPM-arbuscular mycorrhizal fungi interaction, microbial inoculants, stress management, plant growth promotion

Editorial on the Research Topic

Unearthing and harnessing the power of the soil microbiome and mycorrhizas to enhance plant nutrient utilization under climate stress

The population of the Earth, estimated at 7.86 billion currently, is projected to reach 9.8 billion by 2050 and 11.2 billion by 2100, according to the United Nations Department of Economic and Social Affairs (1). This growth is expected to increase the demand for agricultural land to achieve food security, however, the sustainability of agriculture continues to be hindered by its over-reliance on chemical fertilizers, pesticides, and herbicides, which can lead to severe negative environmental consequences, such as a decrease in soil organic matter and a reduction in soil microbial diversity, ultimately impacting the production of food. This problem is further compounded by climate change, soil health degradation, and a variety of biotic and abiotic stresses (2). Adapting the soil microbiome can lead to improvements in biotic and abiotic stress management, increased crop yields, optimized nutrient cycling, and enhanced natural resource utilization (3). Identifying and harnessing beneficial soil microorganisms is essential for sustainable agricultural production, especially given the challenges posed by biotic and abiotic stressors. Among the various potentially beneficial microorganisms, plant growth-promoting microbes (PGPM) and arbuscular mycorrhizal fungi (AMF) are often considered safe and environmentally friendly solutions for addressing a range of stressors (4). A better understanding of interaction and application of PGPM and AMF in agricultural systems can help to develop novel methods that enhance crop yield, soil health, and fertility (5).

In this Research Topic, the potential and prevalence findings was observed in the area of plant-soil-microbial interactions and these findings emphasize the primary factors involved in the biological, physical and chemical changes that occur in the rhizosphere, and the positive impact these changes may have on plant nutrient acquisition. Additionally, the study sheds light on how the soil microbiome and specific species can promote nutrient uptake, plant-growth and development, and alleviate climate stress. The study of [Wan et al.](#) found that soil microbial communities are vital for terrestrial ecosystem functions and indicate grassland health. It observed that drought stress significantly impacts bacterial and fungal diversity, with bacteria being more sensitive than fungi. This implies that bacterial community diversity or structure could indicate alpine grassland health status. The study identified soil moisture, plant diversity, and soil organic matter as the key factors influencing soil fungal & bacterial community and composition of functional potential. Importantly, microbial functional potential can be predicted through taxonomic profiles. This research elucidates the mechanisms behind microbial community composition and functional responses to climate change, specifically prolonged drought, in semiarid alpine grasslands. Similarly, the implications of drought brought on by the increase of groundwater depth on soil microbiota and multi-functionality remain unclear, hindering our comprehension of the sustainability of water-deficient ecosystems that heavily depend on ground-water resources. This research examined the effects of modified ground-water depths, induced by hydrological processes or anthropogenic activities, on rhizospheric microbiota and multi-functionality in a semi-arid area. The composition of soil microbiota was altered due to the rising ground-water depth, resulting in a decrease in the relative abundance of dominant phyla, such as Proteobacteria and Ascomycota ([Zhao et al.](#)). [Mukhongo et al.](#) conducted a study using morphotyping and enumeration to assess the composition and spore abundance of Arbuscular Mycorrhizal Fungi (AMF) in sweet potato cultivation areas in eastern Uganda. They identified six AMF genera: *Gigaspora*, *Entrophospora*, *Glomus*, *Archaeospora*, *Scutellospora*, and *Acaulospora*. The study found that soil parameters impacted AMF spore abundance differently across genera, with pH, N, SOC (soil organic carbon), Na, silt, and Mg, having the most significant effects. The predominant AMF species, *Glomus* and *Acaulospora*, have potential for local bio-inoculant production. [Huang et al.](#) investigated microbial diversity and its relationship with soil properties and enzyme activities along an elevational gradient in Southwest China. While specific soil properties varied significantly among sites on the elevational gradient, overall soil chemistry was not clearly differentiated by elevation. Conversely, bacterial and fungal communities differed significantly on the elevation gradient. Fungal diversity exhibited an N-shaped pattern, while bacterial diversity decreased with elevation. Microbial abundance peaked at 1,800 m, but only bacterial variations correlated with soil pH. Soil enzyme activities were elevation-dependent and linked to specific microbes: Acidobacteria and Planctomycetaceae bacteria were associated with catalase and ACP (extracellular acid phosphatase) changes, respectively. Fungi were mainly associated with β -glucosidase, sucrose, and urease changes. Herpotrichiellaceae positively

correlated with β -glucosidase and sucrose, and Sebacinaceae with urease. [Li et al.](#) identified Actinobacteriota, Chloroflexi, Firmicutes, Acidobacteriota and Proteobacteria as the dominant bacteria in non-organic, organic, and intercropping soil groups, with variations in their relative abundance. Acidobacteria bacterium particularly increased in the organic and intercropping soils. [Venice et al.](#) examined a mature silver fir stand affected by windstorm-induced uprooting and compared it to a nearby undamaged area. The site, impacted by root rot agents *A. ostoyae* and *H. abietinum*, showed that these agents were not the sole cause of damage. The study found that tree uprooting increased alpha diversity, primarily due to wood-decay fungi, likely resulting from the rise in dead plant material. Additionally, certain mycorrhizal taxa responded to plant succession, marked by increased grasses and shifts in plant symbionts. According to [Li et al.](#), intricate decomposition pathways within soil micro-food webs play a crucial role in facilitating the cycling of soil organic carbon and nutrients, ultimately impacting the productivity, quality, and sustainability of soil systems. [Ducousso-Détrez et al.](#) highlighted P insufficiency in croplands, even in regions using P fertilizers, prompting interest in microorganisms that convert unavailable P into plant-accessible forms. *Bacillus* and *Pseudomonas*, the most common genera identified, are promising candidates for biofertilizers, potentially forming bioinoculant consortia to improve P nutrition and growth in soils rich in reactive P. Another finding by [Liu et al.](#) showed that the soil samples from Fujian Province and Xinjiang Autonomous Region exhibited a rich fungal diversity, comprising thirty-one classes, two hundred families, eleven fungal phyla, eighty-six orders, three hundred eighty-eight genera, and five hundred fifteen species. These samples revealed dominant fungal phyla that play crucial roles in energy cycling and organic matter degradation, such as *Agaricomycetes*, *Leotiomycetes*, *Sordariomycetes*, and *Archaeosporomycetes*. [Ji et al.](#) reported that the influence of halotolerant nitrogen-fixing bacteria (HNFB) on AMF community in the rhizosphere of apple plants is affected by soil nitrogen levels. It was found that the inoculation of HNFB resulted in an increase in microbial biomass and the relative abundance of beta-glucosidase-related genes. According to research by [An et al.](#), Astragalus-cultivated soils exhibit an enhanced presence of AMF. The study identified a total of seventy-four OTUs and classified them into a single phylum, Glomeromycota; 1 class, Glomeromycetes; 4 orders; 4 families; and 6 genera. [Liu et al.](#) examined the impact of exogenous organic acid composite biological substrates on bacterial community structures in beach soils. Their findings showed that these substrates did not significantly alter bacterial alpha diversity ($p \geq 0.05$). Nonetheless, the fulvic acid composite pine needle treatment slightly increased alpha index values relative to the control. [Ng et al.](#) demonstrated that PGPR and elevated CO_2 (eCO_2) enhance plant yield and quality *via* interactions with rhizosphere microorganisms. For *Pseudostellaria heterophylla*, PGPR (*Bacillus subtilis* and *Pseudomonas fluorescens*) under 1000 ppm eCO_2 positively influenced the plant and its rhizosphere microbes. This resulted in a 38% increase in yield and a 253% higher in the accumulation of active ingredient polysaccharides in the tuber.

Finally, we believe that this Research Topic on “Unearthing and Harnessing the Power of the Soil Microbiome and Mycorrhizas to Enhance Plant Nutrient Utilization under Climate Stress” will offer valuable insights into the latest developments and advantages of soil microorganism application to attain sustainable agricultural production, as well as the utilization of microbial inoculants to boost crop yields while conserving soil health.

Author contributions

DM: Conceptualization, Supervision, Writing – original draft, Writing – review & editing. MP: Supervision, Writing – original draft, Writing – review & editing. AR-S: Project administration, Supervision, Writing – original draft, Writing – review & editing. PA: Conceptualization, Writing – original draft, Writing – review & editing. SS: Conceptualization, Supervision, Writing – original draft, Writing – review & editing. PP: Conceptualization, Supervision, Writing – original draft, Writing – review & editing.

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MG: Conceptualization, Supervision, Writing – original draft, Writing – review & editing.

Conflict of interest

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