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EDITED AND REVIEWED BY
Sören Thiele-Bruhn,
University of Trier, Germany

*CORRESPONDENCE
Zhikun Chen,
✉ zhikunchen@ams.xab.ac.cn

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Editorial: Soil carbon sequestration and microbial energy metabolism

Guanghua Jing, Ning Zhao and Zhikun Chen*

Shaanxi Key Laboratory of Qinling Ecological Security, Xi'an Botanical Garden of Shaanxi Province (Institute of Botany Shaanxi Province), Xi'an, China

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Editorial on the Research Topic

Soil carbon sequestration and microbial energy metabolism

Introduction

Soil microorganisms, as central drivers of soil organic carbon (SOC) dynamics, play a critical role in biogeochemical cycles (Ma et al., 2024; King and Sokol, 2025). Over the past few decades, extensive research has been conducted on the effects of microbial community structure, functional traits, and metabolism on soil carbon sequestration under specific climatic and edaphic conditions (Zhang et al., 2024; Fu et al., 2025). In recent years, microbial carbon use efficiency (CUE) has been increasingly adopted as a key parameter in carbon cycle models to quantify carbon cycling processes (Cotrufo et al., 2013; Domeignoz-Horta et al., 2020). These processes largely depend on the solubility and decomposability of organic compounds. Moreover, microorganisms utilize organic carbon primarily as an energy source for cell maintenance, growth, and the recycling of organic compounds and nutrients recycling (Liang et al., 2017). Consequently, soil carbon sequestration is governed not only by the chemical structure of organic matter but also by microbial energy acquisition and allocation strategies. Nevertheless, the mechanistic link between microbial carbon utilization and energy transformation remains poorly understood. Therefore, the Research Topic “Soil Carbon Sequestration and Microbial Energy Metabolism” has been organized.

Interest in this research topic mainly encompassed: 1) new insights into the dynamics and threshold responses of soil carbon pools under environmental gradients and disturbances; 2) novel perspectives on the divergent pathways and ecological regulation of the microbial carbon pump; 3) recent advances in understanding how energy metabolism governs carbon stabilization; 4) the development of predictive models for carbon pool stability based on microbial functional traits; 5) innovative strategies to enhance soil carbon sequestration among plants, microbial functionality, and soil minerals; 6) emerging technologies for monitoring and manipulating the microbial energy-carbon sequestration. Thirteen articles were published in this Research Topic, highlighting key progress in the field.

Soil-plant interactions

The interplay between plants, soil, and microbes is crucial for carbon flow and stabilization

Andargie et al. (2025) adopted moist heat treatment (MHT) to establish a dysbiotic gradient in the soil microbiome, thereby systematically varying microbial abundance. This approach analyzed how microbial abundance and community dynamics influence plant phenotype and gene expression. The study integrated phenotypic and transcriptomic profiling of cucumber (*Cucumis sativus* L.) and quantified the rhizosphere microbiome shifts. The findings highlight the modulation of initial microbial abundance as a critical strategy for remodeling the rhizosphere, improving bioinoculant performance, and eliciting beneficial plant transcriptomic responses.

Deng et al. (2024) collected 0–20 cm soil from three Chinese fir plantations and separated it via wet-sieving into large macro-aggregates (>2 mm), macro-aggregates (0.25–2 mm), and micro-aggregates (<0.25 mm). The Biolog Eco microplate method was employed to determine associated microbial metabolic activities, functional diversity, and carbon source utilization characteristics. The study found that micro-aggregates consistently exhibited the highest levels of microbial metabolic activity and microbial diversity in all Chinese fir plantations. The findings highlighted that the functional attributes of soil microbial communities were influenced by both planting regime (mixed cultivation) and aggregate size, largely through their effects on soil nutrient dynamics.

Wang T. et al. (2024) explored the impact of the different duration (3, 6, and 10 years) of grape cultivation on soil organic carbon, physicochemical properties, enzyme activities, microbial communities, and carbon cycle pathways in both rhizosphere and bulk soils. Long-term grape cultivation reduced soil microbial diversity in bulk soil, likely due to diminished ecological niches and elevated salinity. In bulk soil, soil enzymes increased soil organic matter accumulation through litter decomposition. In contrast, in the rhizosphere, fungi appear to play a dominant role in SOM, potentially via fine-root decomposition and mycelial production. These findings provide insights of the mechanisms of soil organic carbon accumulation under long-term grape culture and support grape cultivation as a viable strategy for restoring degraded desert ecosystems.

Yang et al. (2025) collected tobacco rhizosphere soils from non-continuous cropping, continuous cropping for 5 years, and continuous cropping for 10 years, to analyze the effects of long-term continuous cropping on nutrients, enzyme activities, microbial community structure, and function. The study emphasized soil carbon and iron as key drivers in structuring the microbial community within the tobacco rhizosphere. The results provide theoretical support for modifying the rhizosphere microbial environment through nutrient regulation.

Effects of agricultural practices and fertilizer application

Management practices significantly influence microbial communities and carbon dynamics

Jindo et al. (2024) assessed the impact of different agronomic practices on soil properties, microbial communities, and SOC levels in semi-arid Moroccan wheat fields. Soil microbial biomass, as assessed by phospholipid fatty acids analysis, was positively correlated with SOC content. These findings highlight that following as a viable strategy to sustain SOC stocks can mitigate negative effects of biophysical constraints on agricultural productivity in the semi-arid agroecosystems of Northwest Africa.

Kong et al. (2024) investigated the dynamics and driving factors of soil microbial carbon metabolic activity and functional diversity at different maize growth stages following plastic film mulching by the Biolog EcoPlate technique. Plastic film mulching significantly enhanced soil microbial carbon metabolic activity and functional diversity at the seedling and maturity stages, but decreased soil carbon metabolic capacity at flowering stage. The results highlights that supplementing soil carbon sources should be considered after continuous film mulching to sustain or enhance farmland productivity and soil quality.

Mei et al. quantified the microbial contribution to SOC in citrus orchards of different ages by analyzing key biomarkers (amino sugars, glomalin) and carbon fractions (particulate organic carbon, POC; mineral-bound organic carbon, MAOC) in the 0–20 cm soil layer. The results revealed that microbial-derived carbon pools showed a progressive and significant decline over the orchard chronosequence ($P < 0.05$). However, microbial residue carbon remained a primary source of organic carbon, with its contribution depending on the age of the orchard. These results provide theoretical understanding of cultivation-induced SOC dynamics and offer practical guidance for mitigating soil degradation in perennial cropping systems.

Ye et al. (2025) demonstrated the response of alpine grassland C dynamics to N addition through a meta-analysis of 57 peer-reviewed studies (794 observations). Short-term N addition (≤ 5 years; ≤ 30 kg N ha⁻¹ yr⁻¹) enhanced SOC through increased plant biomass and microbial C sequestration. In contrast, long-term N additions promote C loss, driven by progressive soil acidification and a critical microbial community shift, -particularly a decreased fungal-to-bacterial ratio. The study showed that N addition rates should not exceed 10 kg N ha⁻¹ yr⁻¹ to sustain alpine ecosystem functions. The findings highlight that future research should prioritize the interactions among historical N deposition, soil acidification, and microbial functional shifts in high-altitude regions.

Cai et al. (2024) conducted a three-year field experiment to evaluate the differential effects of microbial inoculants and organic fertilizers on the accumulation of microbial-derived carbon within distinct soil aggregate fractions. The interactive effects of the two fertilizers had significant impacts on the accumulation of microbial residual carbon. *Azotobacter chroococcum* fertilizer was more

efficient than *Bacillus mucilaginosus* fertilizer in enhancing microbial residue accumulation. These findings imply distinct underlying processes for the accumulation of bacterial and fungal microbial residue carbon in bamboo forest soils following amendment with microbial versus organic fertilizers.

Response to multifaceted environmental stressors

Multifaceted environmental stressors directly affect SOC sequestration and microbial metabolic function

Qu and Hai (2025) explored the implications of soil-specific enzyme activity for soil microbial necromass carbon (NC) and SOC accumulation through sand dune fixation (mobile, semi-mobile, semi-fixed, and fixed). The study showed that dune fixation significantly increased soil-specific enzyme activity per unit of soil organic carbon (SOCE) or microbial biomass carbon (MBCE). These results indicate that SOCE and MBCE dynamics serve as promising proxy indicators and should be incorporated into assessment frameworks for monitoring microbial necromass and SOC sequestration in sandy land restoration.

Doherty et al. (2025) conducted a laboratory soil mixing experiment to simulate the thaw-induced blending of active layer and permafrost soils. The study aimed to quantify the effects of different mixing ratios on microbial community structure, heterotrophic respiration, and substrate utilization patterns. Soil mixing increased carbon substrate utilization compared to permafrost. Equal-ratio blends enhanced microbial diversity and produced communities similar to the active layer. Experimentally mixed soils diverged from the natural transition zone communities.

Wang Z. et al. (2024) used Biolog ECO-plates and enzyme stoichiometry to evaluate the impact of exogenous copper addition on microbial metabolic profiles and nutrient limitations in *Panax notoginseng* soils. CUE was primarily regulated by microbial biomass carbon (MBC), available phosphorus (AP), the soil C:P ratio, and leucine aminopeptidase (LAP) activity. This suggests that soils under *P. notoginseng* cultivation can maintain microbial functionality and alleviate nutrient limitations under moderate copper stress.

Tang et al. (2024) synthesized how abiotic (e.g., temperature, moisture, pH, nutrient availability, substrate quality) and biotic (e.g., microbial community composition and diversity) factors regulate CUE. The study also called for further investigation into the combined effects of multi-nutrient additions and the interactions between biotic and abiotic factors on CUE.

The aim of this Research Topic is to explore new perspectives for the regulation of microorganisms on carbon turnover processes through dimensions such as functional genes, metabolic efficiency, and ecological strategies. All results above in this Research Topic will

provide good insights to reveal the role of microbial community on soil carbon stability under specific climatic and edaphic conditions. However, the research on microbial energy metabolism is still insufficient. In the future, we should continue to focus on soil carbon sequestration regulated by microbial energy metabolism in response to climate change and anthropogenic activities, providing theoretical support and practical guidance for soil carbon management.

Author contributions

GJ: Writing – original draft, Writing – review and editing. NZ: Writing – review and editing. ZC: Writing – original draft, Writing – review and editing.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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