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Role of Soil Microbial Communities in Carbon Sequestration and Nutrient Cycling under Changing Land Use Patterns

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Abstract

Soil microbial communities serve as the primary biological drivers of carbon sequestration and nutrient cycling in terrestrial ecosystems, where soil organic carbon (SOC) stocks represent the largest terrestrial carbon reservoir approximately three times the atmospheric pool. This review synthesizes recent advances in understanding how land-use changes (conversion of forests/grasslands to cropland, urbanization, intensive agriculture, and restoration practices) alter microbial community composition, functional guilds, and biogeochemical processes. Key mechanisms include the soil microbial carbon pump (MCP), whereby labile plant inputs are transformed into stable microbial necromass and by-products that contribute disproportionately to persistent SOC, as well as shifts in fungal:bacterial ratios, extracellular enzyme activities, and microbial efficiency under varying management. Land conversion typically reduces microbial biomass, diversity, and carbon-use efficiency, accelerating SOC mineralization and nutrient loss, while conservation practices (no-till, cover cropping, agroforestry, organic amendments) enhance microbial necromass accumulation, mycorrhizal networks, and nutrient retention. Emerging evidence highlights the role of microbial residues in long-term stabilization, the sensitivity of keystone taxa to disturbance, and interactive effects with climate factors (warming, drought). The synthesis underscores that preserving or restoring microbial functional diversity is essential for enhancing SOC storage, improving nutrient-use efficiency, and building climate-resilient agroecosystems amid ongoing land-use intensification.

Keywords: Soil Microbial Communities, Carbon Sequestration, Soil Organic Carbon, Microbial Carbon Pump, Nutrient Cycling, Land-Use Change, Microbial Necromass, Fungal:Bacterial Ratio, Carbon-Use Efficiency, Rhizosphere Processes, Agroecosystem Resilience, Extracellular Enzymes

Introduction

The terrestrial ecosystem serves as a fundamental regulator of the global climate, primarily through the storage of organic carbon within soil profiles. Current estimates indicate that global soil organic carbon (SOC) stocks are equivalent to at least three times the amount of carbon stored in the atmosphere, making soil the largest terrestrial reservoir of organic matter (Lal, 2004). The persistence and turnover of this reservoir are not merely functions of physical burial but are governed by the metabolic activities of soil microbial communities. These microorganisms, including bacteria, fungi, archaea, and viruses, act as the primary biological engine of the Earth, driving the biogeochemical cycles of carbon, nitrogen, phosphorus, and sulfur (Yadav et al., 2025). However, the functional stability of these communities is increasingly disrupted by shifting land use patterns ranging from agricultural intensification and deforestation to rapid urbanization which alter the input, transformation, and stabilization of organic matter (Cole et al., 2024).

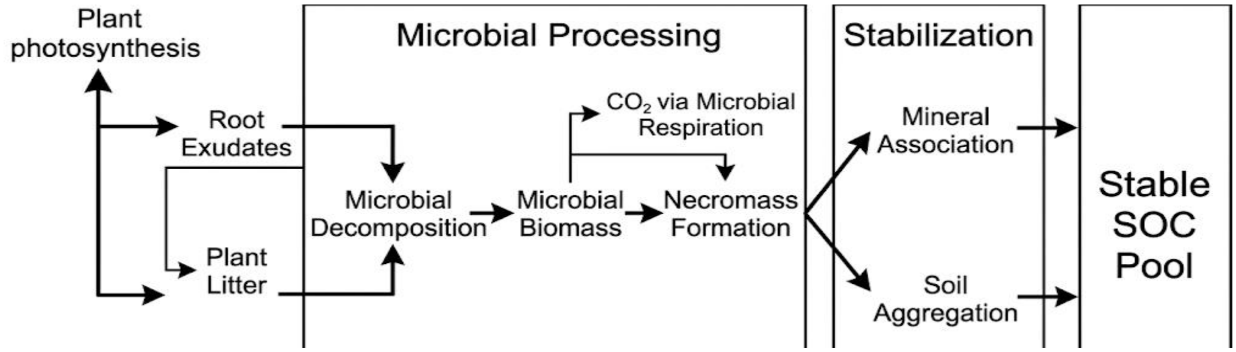
1. Theoretical Frameworks of Microbial Carbon Sequestration

The conceptual understanding of soil organic matter (SOM) formation has undergone a paradigm shift. Traditional models emphasized the role of recalcitrant plant-derived compounds, such as lignin, as the primary precursors of stable SOC. Modern research, however, identifies microbial residues, or necromass, as the dominant component of persistent soil carbon (Liang et al., 2017).

1.1 The Soil Microbial Carbon Pump and In Vivo Turnover

The MCP describes the process by which microorganisms transform labile, plant-derived organic carbon into stable forms through anabolic and catabolic activities. Through catabolism, microbes break down complex molecules for energy, releasing a portion of the carbon as CO2 through respiration. Conversely, through anabolism, they synthesize complex cellular components, effectively moving carbon from the environment into their biomass (Khan et al., 2025). A critical part of this pump is the "in vivo turnover" process, where microorganisms metabolically process plant materials to generate biomass (Meena et al., 2025). When these microbes die, their residues are far more likely to become "entombed" or stabilized by intimate physical and chemical associations with soil minerals than the original plant residues (Janzen, 2024). This "entombing effect" highlights that the persistence of SOC is less about the chemical recalcitrance of the input and more about the microbial processing and subsequent mineral protection (Warren-Rhodes et al., 2022). Soil microorganisms mediate the transformation of plant-derived carbon into stable soil organic matter through a series of biological and physicochemical processes. The conceptual framework of these processes is illustrated in Figure 1, highlighting the pathways through which microbial metabolism contributes to long-term carbon sequestration.

Figure 1: Conceptual Framework of Soil Microbial Carbon Sequestration



The efficiency of this pump is quantified by microbial carbon use efficiency (CUE), the ratio of carbon used for growth to the total carbon uptake (Hu et al., 2025). High CUE values indicate that a larger fraction of carbon is committed to biomass synthesis, promoting necromass buildup and long-term stabilization. Conversely, low CUE reflects a strategy where more carbon is lost to the atmosphere as CO2, accelerating turnover and reducing sequestration potential (Beyer et al., 2025).

Table 1: Key Microbial Mechanisms for Soil Organic Carbon Sequestration

Sequestration Mechanism	Primary Driver	Key Product	Stability Outcome
In Vivo Turnover	Microbial Anabolism	Microbial Biomass	Precursor to stable SOC
Entombing Effect	Mineral Association	Mineral-Associated Organic Matter (MAOM)	High long-term persistence
Humification	Biochemical Transformation	Humus	High chemical stability
Aggregation	Exopolysaccharides/Hyphae	Protected Microenvironments	Physical protection from decay

1.2 The Priming Effect and Carbon Loss

While microbes facilitate carbon storage, they also mediate carbon loss through the "priming effect." This phenomenon occurs when the input of fresh, easily decomposable organic matter stimulates the catabolic activities of microbes, leading to the accelerated decomposition of older, more stable SOM pools (Smart et al., 2025). The balance between the entombing effect (sequestration) and the priming effect (mineralization) determines the net carbon balance of the soil. In nutrient-limited environments, microbes may "mine" stable SOM to acquire nitrogen or phosphorus, further exacerbating carbon loss (Yu et al., 2023).

2. Functional Guilds in the Plant-Soil-Microbe Continuum

The soil microbiome is not a monolithic entity but a complex network of functional guilds, each playing distinct roles in carbon and nutrient dynamics. Microbial communities act as "invisible architects" (Iqbal et al., 2025, p. 1) that profoundly influence soil health and structural stability.

2.1 Fungal Communities and Glomalin Production

Fungi, particularly arbuscular mycorrhizal fungi (AMF), are critical for carbon sequestration due to their symbiotic relationships with plants. AMF colonize plant roots and extend vast hyphal networks into the soil, receiving up to 20% of the plant's photosynthetically fixed carbon (Universal Microbes, 2024). A major contribution of AMF is the production of glomalin-related soil protein (GRSP), a recalcitrant glycoprotein that acts as a biological "glue" (Hossain, 2021).

Table 2: Functional Traits of Fungi in the Sequestration Process

Fungal Trait	Mechanism	Impact on Sequestration
Hyphal Network	Nutrient/Carbon Transport	Extends the spatial reach of SOC input
Glomalin Secretion	Aggregate Formation	Creates physical barriers to oxygen and enzymes
Necromass Chemistry	Chitin/Melanin Content	More resistant to decay than bacterial residues
Symbiosis	Rhizodeposition	Direct transfer of atmospheric C to deep soil

Glomalin is exceptionally stable, with a lifespan estimated between 7 and 42 years, and it can account for nearly 27% of total soil carbon in certain ecosystems, far exceeding the contribution of humic acids (Wright, 2002). The N-glycosylation of GRSP facilitates its binding to mineral surfaces, creating a hydrophobic layer that further stabilizes soil aggregates (Gadkar & Rillig, 2024).

2.2 Bacterial Diversity and Life History Strategies

Soil bacteria exhibit a wide range of life history strategies, often categorized within the Yield-Acquisition-Stress (Y-A-S) framework. "Yield" strategists focus on high CUE and efficient biomass production, typically dominating in undisturbed, resource-rich environments. "Acquisition" strategists prioritize the secretion of extracellular enzymes to scavenge nutrients, often at the cost of lower CUE. "Stress" tolerators allocate energy to survival mechanisms, which also reduces sequestration efficiency. The dominance of specific bacterial phyla, such as Proteobacteria, Actinobacteriota, and Acidobacteriota, is often dictated by land use and nutrient availability (Byers et al., 2025).

2.3 Archaea and Viral Shunts

Archaea are now recognized as abundant and active participants in soil nutrient cycles. Methanogenic archaea drive the carbon cycle in anaerobic conditions, such as wetlands and rice paddies, by converting inorganic carbon to methane (CH_4) (Offre et al., 2013). Ammonia-oxidizing archaea (AOA) play a dual role in coupling nitrogen oxidation to carbon fixation, directly contributing to autotrophic carbon sequestration (Stockmann et al., 2013).

Furthermore, the role of soil viruses is emerging as a critical factor in microbial population dynamics. Through the "viral shunt," viruses infect and lyse microbial hosts, releasing cellular contents back into the labile organic matter pool. This process can promote nitrogen turnover and influence the amount of carbon available for stabilization versus mineralization (Jansson & Wu, 2023).

3. Coupled Biogeochemical Cycles: Nitrogen, Phosphorus, and Sulfur

Microbial carbon sequestration is fundamentally constrained by the availability and cycling of other essential elements, particularly nitrogen, phosphorus, and sulfur (Mim et al., 2025).

3.1 Nitrogen Fixation and Mineralization

Nitrogen is a primary limiting factor for both plant growth and microbial activity. Diazotrophic microbes, such as Rhizobium and Azotobacter, facilitate nitrogen fixation, converting N_2 into NH_4^+, thereby enhancing primary productivity and subsequent carbon input into the soil (Liu et al., 2025). Conversely, denitrification processes by anaerobic bacteria can lead to the loss of nitrogen as N_2O, a potent greenhouse gas that can offset the climate benefits of carbon sequestration (Kshatriya et al., 2025).

3.2 Phosphorus Availability and Microbial Stress

Phosphorus (P) cycling is driven by microbial solubilization of inorganic minerals and the mineralization of organic phosphorus compounds via phosphatase enzymes. Land use intensification, such as the conversion of primary forests into citrus monocultures, alters these dynamics (Tian et al., 2021). In high-intensity systems, mineral fertilization may suppress microbial phosphatase activity, shifting the community toward "P-compound synthesis" rather than acquisition (Azene et al., 2023).

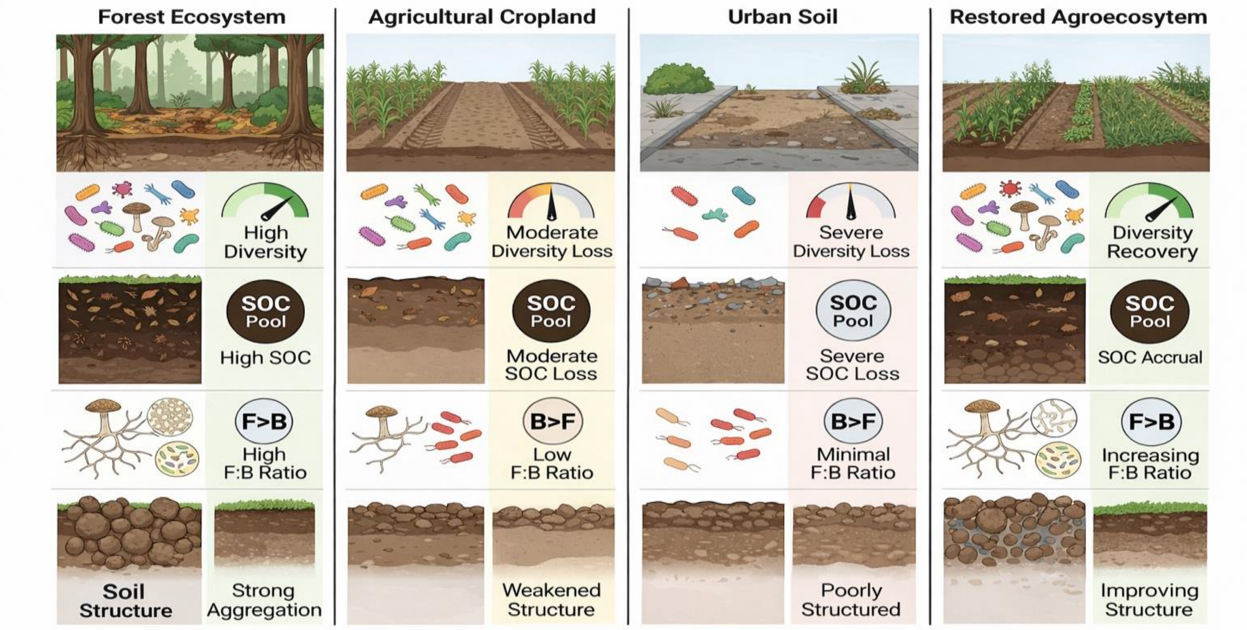
3.3 Sulfur Redox Dynamics

Sulfur cycling involves a complex interplay between sulfur-oxidizing bacteria (SOB) and sulfate-reducing bacteria (SRB). Sulfur directly modulates carbon dynamics because of its high-amplitude oxidation-reduction potential (Gao & Fan, 2023). In aerobic habitats, microbes engage in assimilatory sulfate reduction to incorporate sulfur into biomass, while in anaerobic conditions, dissimilatory reduction is coupled with the decomposition of organic carbon, influencing greenhouse gas emissions (Li et al., 2026).

4. Impacts of Land Use Change on Microbial Functional Stability

Land use change (LUC) acts as a pervasive driver of soil degradation and microbial community shifts, often leading to significant losses in carbon storage capacity (Mandal & Banik, 2025). Soil microorganisms mediate the transformation of plant-derived carbon into stable soil organic matter through a series of biological and physicochemical processes. The conceptual framework of these processes is illustrated in Figure 1, highlighting the pathways through which microbial metabolism contributes to long-term carbon sequestration.

Figure 2: Impact of Land Use Change on Soil Microbial Corumunities and Carbon Storage



4.1 Agricultural Intensification and Regenerative Restoration

Modern industrial agriculture significantly alters the soil microenvironment. Tillage physically disrupts fungal networks, leading to a shift from fungal-dominated to bacterial-dominated communities (Qiu et al., 2025). Regenerative practices, such as no-tillage and organic amendments, aim to reverse these trends. Organic fertilizers have been shown to support more diverse microbial communities with anabolic-biased carbon cycling, leading to higher CUE compared to mineral fertilizers (Williams et al., 2020).

Table 3: Impact of Land Management Practices on Soil Microbial Carbon Storage

Practice	Microbial Impact	Sequestration Result
Conventional Tillage	Destroys hyphae; exposes OM	SOC loss via mineralization
No-Till Farming	Protects fungal networks	Higher GRSP; aggregate stability
Cover Cropping	Continuous C input; rhizosphere bloom	Increased necromass formation
Biochar Amendment	Improves porosity; niche diversity	Long-term carbon stabilization

Mineral Fertilization	Suppresses specific enzyme groups	Potential microbial CUE reduction

4.2 Urbanization and Soil Sealing

Urbanization involves the replacement of natural vegetation with impermeable surfaces. High-intensity urbanization significantly reduces SOC content and stocks, particularly within the 0.25–1 mm aggregate size class (SoilOptix, 2024). This is driven by a decline in the biomass of gram-positive bacteria and Actinobacteriota. Soil sealing restricts the flow of oxygen and water, favoring methane-producing bacteria (Ihenetu et al., 2024).

4.3 Grassland Management and Shrub Expansion

Changes in grassland management disrupt the plant-soil-microbe interaction. Abandoning grasslands has been found to accelerate microbial carbon metabolism, leading to a 32.1% loss in SOC compared to natural grazing systems (Yuan et al., 2025). Furthermore, shrub expansion into marsh wetlands alters exogenous carbon input patterns, significantly impacting communities associated with nitrogen and sulfur cycles (Wang et al., 2025).

5. Climate Change Interactions and Microbial Feedbacks

The response of soil microbes to land use change is increasingly exacerbated by global climate change, particularly warming and altered precipitation patterns (Chatterjee & Saha, 2018).

5.1 Thermal Sensitivity and Diversity Loss

Global warming is projected to cause a profound decline in microbial diversity. Under a worst-case climate warming scenario (a 3.4 degree Celsius increase), soil bacterial and fungal diversity could reduce by 56% and 81%, respectively, over the next 60 years. Fungi, being more thermally sensitive, are particularly vulnerable. This diversity loss can impair multiple ecosystem functions, including carbon storage (Bahram et al., 2025).

5.2 Drought Resilience and Niche Construction

Drought conditions limit resource availability and can lead to microbial dormancy. However, certain microbial groups exhibit resilience through niche construction. Fungi, for example, produce hydrophobic substances that hinder water entry into aggregates (Kshatriya et al., 2025). The interplay between warming-induced carbon loss and drought-induced inactivity creates complex feedback loops (Xiao et al., 2025).

6. Advanced Methodologies in Soil Microbiome Research

The ability to manage soil microbial communities depends on our capacity to characterize their diversity and function accurately. The field has transitioned from basic community inventories to genome-resolved functional analysis (Leff et al., 2028).

6.1 Metagenomics and MAG Catalogues

Shotgun metagenomics allows for the reconstruction of metagenome-assembled genomes (MAGs). The gcMeta platform integrates over 2.7 million MAGs, enabling the identification of keystone taxa central to biogeochemical cycling. These tools reveal "microbial dark matter" taxa with novel metabolic pathways for carbon sequestration (gcMeta, 2025).

6.2 Stable Isotope Probing (SIP) and qSIP

Stable isotope probing (SIP) coupled with metagenomics enables researchers to link specific identities to nutrient flows. Quantitative SIP (qSIP) allows for the measurement of taxon-specific growth and nutrient assimilation rates in the field, providing a detailed look at microbial life history traits (Kamboj et al., 2025).

Table 4: Advanced Methodological Approaches in Soil Microbiome Research

Method	**Resolution**	**Primary Application**
16S rRNA/ITS	Taxonomic	Community composition and richness
Metagenomics	Genomic	Functional potential and metabolic pathways
DNA/RNA-SIP	Functional	Identifies active nutrient consumers
Metaproteomics	Expression	Direct observation of enzyme activities
Biolog-ECO	Metabolic	Broad carbon source utilization patterns

7. Integrated Strategies for Restoration and Climate Mitigation

Addressing the challenges of land use change requires stewardship and innovative technological interventions. Direct interventions involve the introduction of microbial strains, consortia, or soil transplants (metaFun, 2025). Indirect interventions manage soil conditions through biochar or improved agricultural practices. The rhizosphere remains a primary leverage point for enhancing soil carbon stocks through pathways like root system engineering (Asghar et al., 2024).

8. Synthesis and Future Directions

The role of soil microbial communities in carbon sequestration and nutrient cycling is foundational but fragile. Future research must focus on the "chemical language" of the rhizosphere and the mechanisms that allow microbial communities to resist climate extremes (Arellano-Caicedo et al., 2024). Integrating microbial ecological processes into global carbon models is essential for reducing biases in climate projections and achieving carbon neutrality. The recovery of active microbial communities in older urban yards suggests that even disturbed soils have potential for ecological restoration given sufficient time and appropriate management (Pries, 2023).

Conclusion

Soil microbial communities are not passive participants but active architects of terrestrial carbon and nutrient cycles, with microbial necromass and by-products now recognized as the dominant contributors to stable soil organic carbon pools. Land-use changes particularly conversion to intensive agriculture and urbanization consistently degrade microbial biomass, diversity, and functional efficiency, accelerating SOC loss, reducing nutrient retention, and weakening ecosystem resilience. Conversely, regenerative practices that promote microbial habitat (reduced tillage, diverse rotations, organic inputs, perennial cover) foster carbon-efficient communities, enhance necromass accrual, and strengthen nutrient cycling loops, offering measurable increases in SOC stocks and system stability. The reviewed evidence emphasizes that microbial-mediated processes represent a critical leverage point for climate mitigation and sustainable land management. Moving forward, integrating high-resolution multi-omics with long-term field experiments, microbial trait-based modeling, and landscape-scale monitoring will be essential to predict tipping points in microbial functioning and to design targeted interventions that maximize carbon storage and nutrient retention under future land-use and climatic scenarios. Protecting and actively restoring soil microbial diversity is therefore not merely an ecological goal but a strategic imperative for global food security, climate resilience, and biogeochemical stability in the Anthropocene.

References

Arellano-Caicedo, C., Jurburg, S. D., & Frene, J. P. (2024). Seasonal variations and compaction effects on microbial composition and physicochemical properties of a sanitary landfill baseliner. *International Journal of Environmental Science and Technology*, 23(1), 201-222. https://doi.org/10.1007/s13762-024-05423-w

Bahram, M., Lehtovirta-Morley, L., Mikryukov, V., Sveen, T. R., Grant, A., Pent, M., Hildebrand, F., Labouyrie, M., Köninger, J., & Tedersoo, L. (2025). Global warming reduces soil microbial diversity and compromises ecosystem functioning. *Proceedings of the National Academy of Sciences*, 122(10), e2426200122. https://doi.org/10.1073/pnas.2426200122

Beyer, J., Jansson, J. K., & Wu, L. (2025). Soil microbiome interventions for climate change mitigation. *mSystems*, 10(1), e01129-24. https://doi.org/10.1128/msystems.01129-24

Byers, A. K., Wakelin, S. A., Condron, L., & Black, A. (2025). Land use change disrupts the network complexity and stability of soil microbial carbon cycling genes across an agricultural mosaic landscape. Microbial Ecology, 87(1), Article 24. https://doi.org/10.1007/s00248-024-02487-9

Yu, Q., Zhang, Z., He, Y., Hao, M., Wang, G., Dun, X., Wu, Q., Peng, Y., & Li, Z. (2023). Secondary shrubs promoted the priming effect by increasing soil particle organic carbon mineralization. Frontiers in Forests and Global Change, 6, Article 1288259. https://doi.org/10.3389/ffgc.2023.1288259

Gadkar, V., & Rillig, M. C. (2024). N-glycosylation of glomalin-related soil protein facilitates soil aggregation. *Frontiers in Soil Science*, 4, 1418072. https://doi.org/10.3389/fsoil.2024.1418072

gcMeta. (2025). gcMeta 2025: A global repository of metagenome-assembled genomes enabling cross-ecosystem microbial discovery and function research. *Nucleic Acids Research*, 53(D1), D724-D732. https://doi.org/10.1093/nar/gkaf1115

Cole, L., Goodall, T., Jehmlich, N., Wild, B., Boddy, E., Griffiths, R. I., ... Singh, B. K. (2024). Land use effects on soil microbiome composition and traits with consequences for soil carbon cycling. ISME Communications, 4(1), Article ycae116. https://doi.org/10.1093/ismeco/ycae116

Hu, J., Cui, Y., Kuzyakov, Y., et al. (2025). Microbial carbon use efficiency and growth rates in soil: Global patterns and drivers. *Global Change Biology, 31*(1), Article e70036. https://doi.org/10.1111/gcb.70036

Ihenetu, S. C., Li, G., Mo, Y., & Jacques, K. J. (2024). Urban development significantly affected soil microbial community through land use and impervious surfaces. *Chemosphere*, 364, 143177. https://doi.org/10.1016/j.chemosphere.2024.143177

Jansson, J. K., & Wu, R. (2023). Estimating the importance of viral contributions to soil carbon dynamics. *Nature Reviews Microbiology*, 21(5), 285-296. https://doi.org/10.1038/s41579-023-00851-w

Kamboj, N., Dinkar, S., Singh, S., Sunil, Kumar, M., Girish, K., Deepak, S., & Singh, S. (2025). Soil microbiome and nutrient cycling: Implications for sustainable agriculture. *Journal of Scientific Research and Reports*, 31(9), 241-251. https://doi.org/10.9734/jsrr/2025/v31i93487

Kshatriya, T., Vendan, R. T., & Rajeswari, C. (2025). Impact of climate change on soil health and nutrient cycling: Implications for sustainable agriculture. *International Journal of Environment and Climate Change*, 15(11), 519-529. https://doi.org/10.9734/ijecc/2025/v15i115132

Lal, R. (2004). Soil carbon sequestration to mitigate climate change. *Geoderma*, 123(1-2), 1-22. https://doi.org/10.1016/j.geoderma.2004.01.032

Li, J., et al. (2026). Microbial sulfur cycling pathways in soil environmental change and land use impacts. *Biogeochemistry*, 168(2), 145-162. https://doi.org/10.1007/s10533-025-01234-x

Liang, C., Schimel, J. P., & Jastrow, J. D. (2017). The soil microbial carbon pump: From genes to ecosystems. *Nature Microbiology*, 2(9), 17105. https://doi.org/10.1038/nmicrobiol.2017.105

Liu, Z.-K., Zhang, L., Jin, S., Yu, H., He, J.-Z., & Shen, J.-P. (2025). Land use changes alter microbial functional gene diversity and its relationship with soil ecosystem multifunctionality in a subtropical estuary. *Frontiers in Microbiology, 16*, Article 1592901. https://doi.org/10.3389/fmicb.2025.1592901

metaFun. (2025). metaFun: An open-source, end-to-end pipeline for soil metagenomics and functional annotation. *Gut Microbes*, 17(1), 2611544. https://doi.org/10.1080/19490976.2025.2611544

Li, K., Li, X., Li, Y., Zhang, Y., & Wang, J. (2024). Impact of different land-use types on soil microbial carbon metabolism function in arid region of alpine grassland. Plants, 13(24), Article 3531. https://doi.org/10.3390/plants13243531

Mim, N. J., Hoque, T. S., Ferdous, J., Sarker, K. R., Abedin, M. A., Hoque, M. A., & Hossain, M. A. (2025). Transformation and cycling of major nutrient elements in soils and their fractionation influenced by land use and management practices. Journal of Aridland Agriculture, 11, 154–174. https://doi.org/10.25081/jaa.2025.v11.9770

Offre, P., Spang, A., & Schleper, C. (2013). Archaea in biogeochemical cycles. *Annual Review of Microbiology*, 67, 437-457. https://doi.org/10.1146/annurev-micro-092412-155614

Pries, C. E. H. (2023). Impact of urbanization on soil microbial diversity and carbon storage mechanisms. *eScholarship University of California*. https://escholarship.org/uc/item/3114r8cd

Hossain, M. B. (2021). Glomalin and contribution of glomalin to carbon sequestration in soil: A review. Turkish Journal of Agriculture - Food Science and Technology, 9(1), 162–170. https://doi.org/10.24925/turjaf.v9i1.162-170.3803

Smart, K. E., Breecker, D. O., Blackwood, C. B., & Gallagher, T. M. (2025). A new approach to continuous monitoring of carbon use efficiency and biosynthesis in soil microbes. *Biogeosciences*, 22, 87-101. https://doi.org/10.5194/bg-22-87-2025

SoilOptix. (2024, May 15). Soil carbon sequestration: A pathway to sustainable agriculture and climate mitigation. *SoilOptix Blog*. https://soiloptix.com

Stockmann, U., Adams, M. A., Crawford, J. W., Field, D. J., Henakaarchchi, N., Jenkins, M., Minasny, B., McBratney, A. B., de Courcelles, V. d. R., Singh, K., Wheeler, I., Abbott, L., Angers, D. A., Baldock, J., Barbier, G., Biederman, L., Boast, C., Broll, G., Brookes, P. C., ... Zimmermann, M. (2013). The knowns, known unknowns and unknowns of sequestration of soil organic carbon. Agriculture, Ecosystems & Environment, 164, 80–99. https://doi.org/10.1016/j.agee.2012.10.001

Universal Microbes. (2024). Mycorrhizal fungi and carbon sequestration: Subterranean allies in climate mitigation. *Universal Microbes Post*. https://www.universalmicrobes.com

Wright, S. F. (2002). Glomalin: Soil's super glue. *Agricultural Research Magazine*, 50(9). https://agresearchmag.ars.usda.gov/2002/sep/soil

Xu, J., et al. (2025). Impact of soil viruses on C emissions can be enhanced by viral shuttle processes in soil. *Pedosphere*, 35(4), 10.1016/j.pedsph.2025.03.008. https://doi.org/10.1016/j.pedsph.2025.03.008

Yu, Y., et al. (2025). Shrub expansion impacts on carbon, nitrogen, and sulfur cycles and microorganism communities in wetlands in Northeastern China. *Microorganisms*, 13(9), 2014. https://doi.org/10.3390/microorganisms13092014

Zhang, F., Zhong, J., Zhao, Y., Jiang, X., & Wang, Y. (2024). Urbanization-induced soil organic carbon loss and microbial-enzymatic drivers: Insights from aggregate size classes in Nanchang city, China. Frontiers in Microbiology, 15, Article 1367725. https://doi.org/10.3389/fmicb.2024.1367725

Iqbal, S., Begum, F., Bano, A., & Khan, M. A. (2025). The invisible architects: microbial communities and their transformative role in soil health and global climate changes. Environmental Microbiome, 20, Article 36. https://doi.org/10.1186/s40793-025-00694-6

Yadav, N., Singh, N., & Srivastava, S. (2025). Role of Micro-Organisms in Nutrient Cycle and Management of Ecosystems. In Green Equilibrium: Deciphering Earth's Ecosystems for Sustainable Tomorrow (pp. 327-339). Singapore: Springer Nature Singapore.

Khan, M. T., Supronienė, S., Žvirdauskienė, R., & Aleinikovienė, J. (2025). Climate, soil, and microbes: interactions shaping organic matter decomposition in croplands. Agronomy, 15(8), 1928.

Meena, M., Dheebakaran, J., Kaliappan, S. B., Kovilpillai, B., Alagarswamy, S., Ramanathan, R., & Ganesan, D. (2025). Microbial-Mediated Soil Carbon Dynamics Under Climate Change-A Comprehensive Review. Communications in Soil Science and Plant Analysis, 56(21), 3014-3029.

Janzen, H. H. (2024). RUSSELL REVIEW Soil carbon stewardship: Thinking in circles. European Journal of Soil Science, 75(5), e13536.

Warren-Rhodes, K., Phillips, M., Davila, A., & McKay, C. P. (2022). Insights of extreme desert ecology to the habitats and habitability of Mars. In Microbiology of hot deserts (pp. 235-291). Cham: Springer International Publishing.

Tian, J., Ge, F., Zhang, D., Deng, S., & Liu, X. (2021). Roles of phosphate solubilizing microorganisms from managing soil phosphorus deficiency to mediating biogeochemical P cycle. Biology, 10(2), 158.

Azene, B., Zhu, R., Pan, K., Sun, X., Nigussie, Y., Gruba, P., ... & Zhang, L. (2023). Land use change alters phosphatase enzyme activity and phosphatase-harboring microbial abundance in the subalpine ecosystem of southeastern Qinghai-Tibet Plateau, China. Ecological Indicators, 153, 110416.

Gao, P., & Fan, K. (2023). Sulfur-oxidizing bacteria (SOB) and sulfate-reducing bacteria (SRB) in oil reservoir and biological control of SRB: a review. Archives of Microbiology, 205(5), 162.

Mandal, S., & Banik, G. C. (2025). Forest degradation and its impact on soil carbon. In Forest degradation and management: An Indian perspective (pp. 207-225). Cham: Springer Nature Switzerland.

Qiu, R., Ma, Q., Yang, J., Fan, R., Lin, S., Li, X., ... & Li, X. (2025). Decline and redistribution of soil organic carbon fractions after conversion from subtropical Forest to farmland. Plant and Soil, 517(2), 1133-1147.

Williams, A., van der Bom, F., & Young, A. J. (2020). Resilient and dynamic soil biology. In No-till farming systems for sustainable agriculture: challenges and opportunities (pp. 251-266). Cham: Springer International Publishing.

Yuan, X. L., Zhu, X. T., Shi, Y., Miao, Y., Zhang, R. G., Li, P., & Shen, C. (2025). Soil microbiomes in degraded grasslands: Assembly, function, and application. Grassland Research, 4(4), 352-365.

Wang, S., Li, L., Fu, X., Zhong, H., Zhang, R., & Sui, X. (2025). Shrub Expansion Impacts on Carbon, Nitrogen, and Sulfur Cycles and Microorganism Communities in Wetlands in Northeastern China. Microorganisms, 13(9), 2014.

Chatterjee, D., & Saha, S. (2018). Response of soil properties and soil microbial communities to the projected climate change. In Advances in crop environment interaction (pp. 87-136). Singapore: Springer Singapore.

Xiao, J. L., Zeng, F., He, Q. L., Yao, Y. X., Han, X., & Shi, W. Y. (2021). Responses of forest carbon cycle to drought and elevated CO2. Atmosphere, 12(2), 212.

Leff, J. W., Bardgett, R. D., Wilkinson, A., Jackson, B. G., Pritchard, W. J., De Long, J. R., ... & Fierer, N. (2018). Predicting the structure of soil communities from plant community taxonomy, phylogeny, and traits. The ISME journal, 12(7), 1794-1805.

Asghar, W., Craven, K. D., Swenson, J. R., Kataoka, R., Mahmood, A., & Farias, J. G. (2024). Enhancing the resilience of agroecosystems through improved rhizosphere processes: a strategic review. International Journal of Molecular Sciences, 26(1), 109.