



Review Paper

Soil Microbial Diversity and It's Technology to Promote Sustainable Agroecosystem

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Abstract

Soil is home to a vast array of microorganisms that are essential to ecosystem multifunctionality (EMF), which includes climate regulation, organic matter breakdown, and nutrient cycling. This literature review summarizes the state of knowledge regarding how soil microbial diversity affects agricultural ecosystem services and functions, emphasizing important processes including phosphorus solubilization, nitrogen fixation, and nutrient mobilization. It describes the ideas of functional redundancy and niche complementarity, which help ecosystems remain stable and resilient in the face of environmental stress. In addition, it also examined the anthropogenic forces that affect soil microbial communities, such as pollution and land-use change. This article describes the biotic and abiotic drivers of microbial diversity. The promise of methodological advancements like machine learning, stable isotope probing, and omics technologies to expand the understanding of soil microbial ecology is investigated. To maximize microbial potential for environmental resilience and sustainable development, we provide the review of promoting new emerging technology for microbial diversity identification and policy integration. Overall, this article shows the importance of preserving and managing soil microbial diversity to promote sustainable agriculture, enhance soil health, and reduce the effects of climate change.

Keywords

Climate change; Eco-system multifunctionality; Microbial diversity; Sustainability

1. INTRODUCTION

The term “microbial diversity” refers to the variety of bacterial and fungal species within microbial communities; genetic diversity, which is the quantity and distribution of genetic information within microbial species; and ecological diversity, which is the variation in community structure, complexity of interactions, number of trophic levels, and number of guild (Nannipieri et al., 2017). The soil microbiome, one of the planet’s most varied and vital ecosystems, is the base of terrestrial life. Soil microorganisms, which include bacteria, fungi, archaea, protists, and viruses, are responsible for a variety of life-sustaining functions, including carbon sequestration and nutrient cycling (Bardgett et al., 2008). Soil microorganisms are invisible, but they control more than 90% of biogeochemical processes; therefore, their biodiversity is essential to the health of the planet (Wall et al., 2015). It is anticipated that agriculturally significant microorganisms will be crucial in several strategies to produce a profitable and healthy crop, such as integrated nutrient management and disease and insect control to reduce the use of agrochemicals without sacrificing agronomic output. These helpful microorganisms appear to have every possibility to offer a different way to

mitigate the negative impacts of certain aspects of conventional agriculture that are widely used (Gupta et al., 2022). The structure of the soil microbial community has been discovered to be affected by agricultural practices such as conventional tillage, the use of agrochemicals, crop rotation, composting, etc.

As a result, any decline in microbial diversity caused by global environmental changes like land use, nitrogen enrichment, and climate change will control microorganisms’ ability to support a variety of above- and below-ground ecosystem services (Jing et al., 2015). This makes it more difficult to develop sustainable management and conservation strategies and to predict how microbes multifunctionality will change facing continuous global environmental change (Delgado-Baquerizo et al., 2016). Previous study showed that biogeochemical cycling in agricultural land was impacted by diversity loss which caused significant danger to soils (Philippot et al., 2013). Therefore, the objective of this article is to explore how microbial diversity supports agricultural ecosystems for sustainability and long-term production and to highlight gaps and recommend measures to improve microbial functioning.

2. COMPOSITION OF SOIL MICROBIAL DIVERSITY

The origin, characteristics, and the makeup of inorganic and organic components in soils have a significant impact on the composition of microbial population quantitatively and qualitatively (Balasubramanian, 2017). Soil microorganisms are primarily categorized as bacteria, fungi, actinomycetes, algae, and protozoa under various size of micro and macro fauna. Most soil microorganisms make up less than 0.4 to 0.5% (w/w) of the total soil mass. However, they have a significant influence on the processes and characteristics of the soil. Algae, cyanobacteria, fungi, bacteria, yeasts, and actinomycetes are among the soil microorganisms. Most of them can break down nearly every type of natural substance. A significant portion of the world's terrestrial biodiversity is made up of soil organisms (Chakraborty, 2022).

3. FACTORS CONTROLLING SOIL MICROBIAL DIVERSITY

3.1 Abiotic Factors

The non-living elements that affect the makeup and quantity of microorganisms in the soil are referred to as abiotic drivers of microbial diversity. Temperature, pH, salinity, soil moisture, and nutrient availability are some of these variables. Changes in soil physical and chemical properties can have an indirect impact on the variety of microorganisms, but have a direct impact on microbial growth and survival. The α -diversity of both bacteria and fungi is significantly shaped by the abiotic soil properties. An important abiotic factor controlling bacterial α -diversity is the level of soil pH. The level of acidity and alkalinity has a direct impact on cytoplasmic homeostasis (Krulwich et al., 2011), soil phosphorus and nitrogen availability, and different symbiotic strategies for plant nutrient acquisition throughout the pH gradient (Hong et al., 2022). Soil pH has a significant effect on bacterial richness and variety. However, because of the detrimental indirect effect through interactions with vegetation diversity, aboveground biomass, and soil organic matter (SOM), the overall effect of pH on fungal α -diversity is negligible (Bahram et al., 2018).

3.2 Biotic factors

Plant diversity, litter quality, and interactions within the soil microbial community are examples of biotic factors that control soil microbial diversity. Microbes' access to resources can be influenced by plant diversity, which can increase diversity and niche divergence. Plant functional groups determine the quality of the litter, which affects the makeup of the microbial population and the decomposition processes. Microbial α -diversity is also strongly influenced by biotic variables, particularly for fungi and aboveground biomass (Kinsbergen et al., 2025). There was positive connection between diversity and functions of soil microorganisms, highlighting the potential of replacing mineral fertilizers with organic amendments to preserve microbial diversity,

enhance soil microbial functions and increase crop yields (Shu et al., 2022).

3.3 Anthropogenic Factors

Global soil microbial communities have been impacted by a range of environmental stressors caused by human activity, such as chemical pollution and climate change. Numerous environmental stressors influenced by human disturbances significantly affect microbial populations in various environments. Studies have calculated the effects of a single stressor in detail, but limited information available on how microbial communities react to several environmental stressors at once. Several stresses were responsible for the competitive and cooperative behaviors among microorganisms (Wu et al., 2024). Concern over whether and how various anthropogenic pressures endanger microbial populations has been grown, given the significance of soil microorganisms in supporting ecological activities (Ban et al., 2022).

4. BENEFITS OF SOIL MICROBES

Microbes in the soil serve as ecosystem engineers mediating critical processes in both natural and managed systems. Different microbial communities, such as bacteria, fungi, archaea, protozoans, and nematodes are generally found in soil. These populations are vital to sustainable agriculture and enhance the processes that support plant health, soil fertility, and ecosystem resilience. Soil microbes have potential roles through enhancing the processes of nitrogen fixation, phosphate solubilization, the synthesis of chemicals that promote growth, nutrient uptake, soil structure stabilization, and the detoxification of toxic substances. All these processes improve the growth of plants (Kiprotich et al., 2025).

4.1 Nutrient Cycling

Numerous ecosystem processes related to production of inorganic nitrogen, nitrogen cycling, carbon cycling and numerous other ecosystem attributes and services are significantly controlled by the actions of microbes and their interactions (Philippot et al., 2024). In addition to having a major impact on soil-plant-microbe interactions, soil microbes are also crucial for preserving the quality of the soil. Nutrient cycling is the most significant of these interactions. Soil biota regulates root growth, flow, and nutrient storage in a healthy soil-plant system. Effective rhizospheric bacteria may even filter fertilizers before the crop or plant uses them (Dubey et al., 2016).

4.2 Organic Matter Decomposition

The breakdown of organic matter is mostly regulated by soil microbes. Heterotrophic microflora and microfauna, which include bacteria, fungi, actinomycetes, and protozoa, are responsible for decomposition. Heterotrophs get their energy and carbon for growth only from organic materials, unlike autotrophic organisms that can make their own food

from basic chemicals (Khatoon et al., 2017). Fungal hyphal networks bind plant roots and soil aggregates create stable soil structures. Soil organic matter acts as a substrate and supports microbial activity, number and growth [35]. Adsorption of microbial metabolites and organic matter decomposition products on mineral surfaces are likely to be involved in aggregate formation. Under field conditions the effect of organic matter on aggregate stability or aggregate-size distribution may be masked by multiple factors, such as climatic conditions, soil texture, type of clay, the dynamics of soil moistures and organic matter content [37].

4.3 Nitrogen Fixation

As the building block of key biological components, including proteins, DNA, and RNA, nitrogen is a necessary element for life. Nitrogen fixation is the process of transforming atmospheric nitrogen into a form that is useful to life, such as ammonia. As the main agents of nitrogen fixation, microorganisms—especially bacteria and archaea—are essential to this process, maintaining the health and productivity of ecosystems (Andrianantoandro et al., 2006). Prokaryotic microorganisms, which can be divided into two groups according to their ecological roles and symbiotic relationships, are principally responsible for nitrogen fixation: These comprise some cyanobacteria like *Anabaena* and *Nostoc*, as well as bacteria like *Azotobacter* and *Clostridium*. In soils, water, and other habitats, these microbes fix nitrogen on their own.

4.4 Phosphorus Solubilization

Phosphorus significantly controls crop productivity and plant growth. Available phosphorus in the forms of HPO_4 and H_2PO_4 is the two main forms of phosphorus that plants can absorb and use directly. Currently, about 400-1000 mg/kg of total phosphorus are found in soils globally, of which only 1.00-2.50% is plant-accessible. This has a significant impact on plant growth and agricultural productivity, leading to a high level of total phosphorus in soils and a shortage of available phosphorus. Phosphorus-solubilizing bacteria (PSB) can significantly increase the uptake and utilization of phosphorus by plants (Pan and Cai, 2023). The genes for phosphorus solubilization in microbes include glucose dehydrogenase (gcd) and pyrroloquinoline quinone (pqq) are crucial to enhance the activity of PSB (Rawat et al., 2021).

4.5 Soil Health

Land degradation lowers the functions of soil to promote soil health and sustainability to support crop production. The roles of soil microbes to better soil health are also controlled by soil hydrology. The dynamics of soil water significantly influences the population and activity of soil microbes to improve the properties of physical, chemical and

biological of soil. Studies indicate that soil microorganisms have the potential to restore soil functions ecologically (Coban et al., 2022). Mycorrhizal fungi and some Actinomycetes are considered helpful microbes which develop symbiotic associations with plant roots, enhancing nutrient and water intake and providing defense against soil-borne infections. Soil fungi and bacteria are also crucial for the process of organic matter decomposition, pathogen inhibition, nitrogen cycling, and soil structure formation. For instance, Firmicutes phylum contains *Bacillus subtilis* (bacteria) that can produce organic acids, *Bacillomycin*, and antibiotic proteins which can prevent the growth and spread of infections (Zhang et al., 2022).

4.6 Land Restoration

It has been suggested that microbial communities can be used to improve the process of recovery of the degraded ecosystems, in addition to serve as a gauge of ecosystem health at any restoration level. Previous studies demonstrate that soil microbial community has potential to restore soil functions physically, chemically and biologically (Coban et al., 2022). Community manipulation shows promise in increasing the rate of recovery of degraded systems, whereas community measurement displays the state of the system with respect to restoration targets and the efficacy of management measures (Harris, 2009).

4.7 Climate Change Mitigation

It is evident that certain soil bacteria have the capacity to affect the sequestration and retention of soil carbon, and that inoculation of soil systems can be used to foster and leverage this capacity.

Soil microorganisms influence the dynamics of major greenhouse gases such as carbon dioxide and methane and nitrous oxide for either produced or consumed. Soil properties such as total porosity, moisture content and fertility level control whether soil microbe communities in the environment contribute to greenhouse gas emission sources or sinks. The greenhouse gas emission control is performed by soil microbes which exists in soil systems to establish if the soil will affect climate change or not (Mason et al., 2023). Soil microbes can mitigate climate change by driving carbon sequestration, converting atmospheric carbon dioxide into stable soil organic carbon. They also regulate greenhouse gas emissions by managing nitrogen and methane cycles. They also improve ecosystem resilience through soil structure stabilization and plant health enhancement (Tiedje et al., 2022).

5. BIODIVERSITY-FUNCTION RELATIONSHIPS

Soil microorganisms' biodiversity-function represents how the microbial community's diversity controls the ecosystem processes (Trivedi et al., 2016). It promotes the functions of healthy ecosystem, although the degree of the associa-

tion varies according to management techniques, functional traits, and environmental context (Khattoon et al., 2017).

5.1 Niche Complementarity

Understanding the intricate relationships between bacteria and fungi that control carbon (C) and nutrient fluxes, as well as the structure, composition, and activities of microbial communities in soil, is essential to understand the biogeochemical cycles. The primary determinant of adaptation and niche divergence between these two major microbial species in soil is competition for resources, among other interactions. This is because energy and carbon constraints on microbial development are the norm rather than the exception. The carbon and energy requirements of the two main kingdoms in soil, fungi, and bacteria are reviewed here, along with how their struggle for these and other resources leads to niche divergence and the effects of global change on this competition (Wang and Kuzyakov, 2024). According to the normalized microbial utilization preference, fungi are 1.1-4.1 times more efficient at using complex compounds as substrates than bacteria, which are 1.4-5 times more efficient at absorbing simple organic molecules (Wang and Kuzyakov, 2024).

5.2 Functional Redundancy of Microbes

Amazing taxonomic diversity is frequently seen in microbial communities raising the issue of the mechanisms that allow species to coexist and how this diversity controls the functions of microbial affects community. However, the notion that species should occupy discrete metabolic niches is contradicted by the fact that multiple coexisting, but taxonomically distinct bacteria can encode the same energy-yielding metabolic activities (Wohl et al., 2004). Through facilitation, higher beginning species richness sustains higher species richness over time. This taxonomic variability of soil microbes is often attributed to ecological drift between similar microbes. These patterns, which link the roles of function, functional redundancy, and taxonomy in microbial systems, are unavoidable emergent characteristics of open microbial systems that are primarily caused by biotic interactions as well as environmental and spatial processes. They are not likely to be the consequence of ecological drift (Louca et al., 2018). For instance, 0.5% of the functional genes were associated with carbon-degrading functions, but over 21% of the genes were related to stress, and 15% of the genes were related to carbon cycling on average across all bacterial networks (Wohl et al., 2004).

6. DYNAMICS OF MICROBIAL DIVERSITY

6.1 Spatial and Temporal Scales of Microbial Diversity

Microbial populations significantly impact plant-livestock disease, the biogeochemical cycle, farming system and bioremediation. It has been challenging to identify the ecological mechanisms that govern the formation of microbial communities and to distinguish the various effects of these

mechanisms. Different processes predominate at different dimensions, and a more precise, understandable, and practical understanding of microbial community construction can be produced by explicitly considering geographical, temporal, and phylogenetic grains and extents—the two components of scale (Ladau and Eloe-Fadrosh, 2019). In order to identify diversity hotspots and deserts, finding the linking to the environmental conditions and test theories about dispersion restriction or the random nature of community formation is crucial to comprehend how microbial communities differ at various spatial scales (Gonzalez et al., 2012). Like spatial studies, temporal studies can determine the relative contributions of various processes, such as stochastic processes and priority effects, to community structure, as well as correlations with environmental factors that impact the microbial communities (Balser and Firestone, 2005).

7. METHODOLOGIES TO IDENTIFY SOIL MICROBES

7.1 Culture-dependent Method for Microbial Diversity Analysis

The study of soil microbial community has historically used culturing methods by utilizing a range of culture media intended to optimize the recovery of various microbial species. This is particularly accepted for research on soil health. In many instances, these methods have identified a variety of microorganisms linked to different aspects of soil quality, such as organic matter decomposition or mineralization and the plant disease suppression. It has been estimated that less than 0.1% of the microorganisms found in common farming land are culturable using existing culture medium formulations, despite recent efforts to develop better culture media to optimize the recovery of various microbial groups from soils. This is based on comparisons between recovered colony-forming units and direct microscopic counts of microorganisms in soil samples (Atlas, 1998).

7.2 Culture-independent Method for Microbial Analysis

Soil microbial ecologists are increasingly using culture-independent community analysis techniques by considering the intrinsic limitations of culture-based approaches. The composition of communities can be observed using culture-independent approaches based on either sophisticated fluorescence microscopy techniques or the extraction, measurement, and identification of chemicals from soil that are unique to certain microorganisms or microbial groups. Phospholipid fatty acids and nucleic acids are useful substances for these kinds of investigations (van Elsas et al., 2006), whereas the microscopic methods entail either the hybridization of fluorescently labeled nucleic acid probes with total RNA recovered from soils or hybridizations with cells in situ (Hill et al., 2000).

7.3 Advanced Techniques for Microbial Diversity Identification

7.3.1 Omics Techniques and Stable Isotope Probing

The limitations of traditional methods like PCR-based approaches and culture make soil microbiology an especially difficult field. A useful method for getting over these challenges and illuminating the dynamic character of the microbial communities in soil is metagenomics (Garg et al., 2024). Targeted metagenomics, which uses techniques like high-throughput sequencing and stable-isotope probing, is essential for analyzing specific microbial taxa and genes in complex ecosystems. One method for identifying the microorganisms in environmental samples that employ a certain growth substrate is called stable isotope probing, or SIP. To identify active microorganisms, the technique uses a substrate that is greatly enriched in a stable isotope, like ^{13}C , and selectively recovers and analyzes isotope-enriched cellular components. stable isotope probing (SIP) links identity to function by monitoring the transport of carbon from plants to microbial groups (Dumont and Murrell, 2005).

7.3.2 Machine Learning

The goal of machine learning (ML), a unique subfield of artificial intelligence (AI), is to identify patterns in vast amounts of diverse data. It was first proposed by Arthur Samuel (Bell Labs, IBM, Stanford) in 1959 (McCarthy and Feigenbaum, 1991). The basic principle is to use algorithms to parse the data, evaluate the patterns in the data automatically, and then utilize these patterns to generate predictions and decisions on real-world events (Jordan and Mitchell, 2015). The primary accomplishments in the evolution of microbial community research toward computational biology are now classification and prediction (Jiang et al., 2022). Algorithms use microbiological data to predict EMF; however, there are still issues in translating lab results to field circumstances (Wagg et al., 2019).

8. CHALLENGES

8.1 Knowledge Gaps

Microbial communities, which collectively make up microbial dark matter, contain billions of new species and genes, as well as innumerable spatiotemporal dynamic patterns. There is still much to learn about these communities (Zha et al., 2022). The most prevalent and varied cellular life forms on Earth are microbes, which occupy a variety of environmental niches. We have just scratched the surface of this enigmatic microbial world, though, as over 99% of bacterial and archaeal species have not been acquired in pure culture. The vast diversity of uncultivated microorganisms that microbiologists can only investigate through cultivation-independent methods is known as Microbial Dark Matter (MDM) (Jiao et al., 2021).

8.2 Ethical and Practical Barriers

Concerns regarding unforeseen ecological consequences are raised by the bioengineering of microbes for carbon capture (Jansson et al., 2023). Deliberately altering and transferring specially generated gene assemblies through sophisticated methods has caused ongoing controversy throughout the world. In addition to the advantages and benefits of these fields, it is necessary to express ethical concerns about informed consent, confidentiality, research subjects, equal access to research benefits, mortality, and benefits to the individual hired for research, such as liability, insurance, and intellectual property rights (Munshi and Sharma, 2018).

9. FUTURE DEVELOPMENTS

9.1 Emerging Technologies for Future

Numerous genetic circuits and metabolic pathways have been programmed in individual cells through the development of genetic components and devices based on transcriptional, translational, and post-translational modules. A novel area of synthetic biology is the extension of engineering skills from single-cell behaviors to multicellular microbial consortia. The use of synthetic microbial consortia for distributed bio-computations, the generation of chemicals and bioenergy, human health and medicine, and ecosystems. A comprehensive understanding of naturally occurring microbial consortia and the logical engineering of these complex consortia for new applications will be made possible by the synergistic development of systems and synthetic biology (Song et al., 2014).

9.2 Policy and Management

Achieving sustainable development and biodiversity protection requires incorporating soil biodiversity into global frameworks such as the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) and the UN Sustainable Development Goals (SDGs). This integration encourages more efficient and comprehensive land management techniques while acknowledging the critical role that soil biodiversity plays in sustaining ecosystem services and human well-being. One useful tool for determining and analyzing the state of soil health would be a consistent system for evaluating soil health (Amgain et al., 2022). These measurable characteristics of soil, which comprise its physical, chemical, and biological aspects, are sometimes referred to as soil health indicators. Cost-effectiveness, the impact of land management techniques on soil characteristics, and the connection between soil functions and agricultural productivity are all requirements for the chosen soil health indicators (Nunes et al., 2021).

10. CONCLUSIONS

A fundamental element of agricultural ecosystems, soil microbial diversity powers vital processes that sustain life on Earth. The importance of soil microbes in ecosystem

multifunctionality (EMF), which includes nitrogen fixation, organic matter breakdown, nutrient cycling, and climate regulation, is highlighted in this review. All of these emphasize the foundation of soil ecosystem function and agricultural sustainability is microbial diversity.

The understanding of mechanisms that connect microbial diversity to EMF is still limited despite their enormous ecological impact. This is because biodiversity research has traditionally focused on plants and animals. The interaction between niche complementarity and microbial functional redundancy demonstrates how resilient and adaptable these communities are to changing environmental circumstances. Soil microbial communities are shaped by a variety of biotic (such as plant diversity and microbial interactions) and abiotic (such as pH and temperature) factors. However, microbial diversity and the stability of ecosystem services are under threat from human-induced stressors such as pollution, climate change, and changes in land use. Our understanding of microbial roles is being improved by cutting-edge technologies like metagenomics, stable isotope probing, and machine learning; yet there are still ethical and practical obstacles to using this knowledge for ecological restoration and climate change mitigation. However, there are still a lot of unanswered questions, particularly regarding context-specific biodiversity-function correlations and microbial dark matter.

In the future, it will be crucial to embrace recent biotechnologies and incorporate soil biodiversity into international policy frameworks. In addition to being essential to environmental sustainability, understanding and utilizing the power of microbiological life beneath our feet is also critical to human culture's ability to adapt to a changing global environment.

REFERENCES

- Amgain, N. R., N. Xu, A. Rabbany, Y. Fan, and J. H. Bhadha (2022). Developing Soil Health Scoring Indices Based on a Comprehensive Database under Different Land Management Practices in Florida. *Agrosystems, Geosciences & Environment*, **5**; e20304
- Andrianantoandro, E., S. Basu, D. K. Karig, and R. Weiss (2006). Synthetic Biology: New Engineering Rules for an Emerging Discipline. *Molecular Systems Biology*, **2**; 2006–0028
- Atlas, R. M. (1998). *Microbial Ecology: Fundamentals and Applications*. Pearson Education India
- Bahram, M., F. Hildebrand, K. S. Forslund, et al. (2018). Structure and Function of the Global Topsoil Microbiome. *Nature*, **560**; 233–237
- Balasubramanian, A. (2017). Soil Microorganisms. University of Mysore, pp. 5–22
- Balser, T. C. and M. K. Firestone (2005). Linking Microbial Community Composition and Soil Processes in a California Annual Grassland and Mixed-Conifer Forest. *Biogeochemistry*, **73**; 395–415
- Ban, Z., X. Hu, and J. Li (2022). Tipping Points of Marine Phytoplankton to Multiple Environmental Stressors. *Nature Climate Change*, **12**; 1045–1051
- Bardgett, R. D., C. Freeman, and N. J. Ostle (2008). Microbial Contributions to Climate Change through Carbon Cycle Feedbacks. *The ISME Journal*, **2**; 805–814
- Chakraborty, S. (2022). Types of Microorganisms in Soil. *Emerging Trends in Agriculture Sciences*, **1**
- Coban, O., G. B. Deyn, and M. van der Ploeg (2022). Soil Microbiota as Game-Changers in Restoration of Degraded Lands. *Science*, **375**; abe0725
- Delgado-Baquerizo, M., F. T. Maestre, P. B. Reich, T. C. Jeffries, J. J. Gaitan, D. Encinar, M. Berdugo, C. D. Campbell, and B. K. Singh (2016). Microbial Diversity Drives Multifunctionality in Terrestrial Ecosystems. *Nature Communications*, **7**; 10541
- Dubey, G., B. Kollah, V. K. Gour, A. K. Shukla, and S. R. Mohanty (2016). Diversity of Bacteria and Archaea in the Rhizosphere of Bioenergy Crop *Jatropha curcas*. *3 Biotech*, **6**; 1–10
- Dumont, M. G. and J. C. Murrell (2005). Stable Isotope Probing—Linking Microbial Identity to Function. *Nature Reviews Microbiology*, **3**; 499–504
- Garg, D., N. Patel, A. Rawat, and A. S. Rosado (2024). Cutting Edge Tools in the Field of Soil Microbiology. *Current Research in Microbial Sciences*; 100226
- Gonzalez, A., A. King, M. S. Robeson II, S. Song, A. Shade, J. L. Metcalf, and R. Knight (2012). Characterizing Microbial Communities Through Space and Time. *Current Opinion in Biotechnology*, **23**; 431–436
- Gupta, A., U. B. Singh, P. K. Sahu, S. Paul, A. Kumar, D. Malviya, S. S. Singh, P. Kuppasamy, P. Singh, D. Paul, J. P. Rai, H. V. Singh, M. C. Manna, T. C. Crusberg, A. Kumar, and A. K. Saxena (2022). Linking Soil Microbial Diversity to Modern Agriculture Practices: A Review. *International Journal of Environmental Research and Public Health*, **19**; 3141
- Harris, J. (2009). Soil Microbial Communities and Restoration Ecology: Facilitators or Followers? *Science*, **325**; 573–574
- Hill, G. T., N. A. Mitkowski, L. Aldrich-Wolfe, L. R. Emele, D. D. Jurkonie, A. Ficke, S. Maldonado-Ramirez, S. T. Lynch, and E. B. Nelson (2000). Methods for Assessing the Composition and Diversity of Soil Microbial Communities. *Applied Soil Ecology*, **15**; 25–36
- Hong, P., B. Schmid, F. De Laender, N. Eisenhauer, X. Zhang, H. Chen, D. Craven, H. J. De Boeck, Y. Hautier, O. L. Petchey, P. B. Reich, B. Steudel, M. Striebel, M. P. Thakur, and S. Wang (2022). Biodiversity Promotes Ecosystem Functioning Despite Environmental Change. *Ecology Letters*, **25**; 555–569
- Jansson, J. K., R. McClure, and R. G. Egbert (2023). Soil Microbiome Engineering for Sustainability in a Changing

- Environment. *Nature Biotechnology*, **41**; 1716–1728
- Jiang, Y., J. Luo, D. Huang, Y. Liu, and D.-D. Li (2022). Machine Learning Advances in Microbiology: A Review of Methods and Applications. *Frontiers in Microbiology*, **13**; 925454
- Jiao, J.-Y., L. Liu, Z.-S. Hua, B.-Z. Fang, E.-M. Zhou, N. Salam, B. P. Hedlund, and W.-J. Li (2021). Microbial Dark Matter Coming to Light: Challenges and Opportunities. *National Science Review*, **8**; nwaa280
- Jing, X., N. J. Sanders, Y. Shi, H. Chu, A. T. Classen, K. Zhao, L. Chen, Y. Shi, Y. Jiang, and J.-S. He (2015). The Links Between Ecosystem Multifunctionality and Above- and Belowground Biodiversity Are Mediated by Climate. *Nature Communications*, **6**; 8159
- Jordan, M. I. and T. M. Mitchell (2015). Machine Learning: Trends, Perspectives, and Prospects. *Science*, **349**; 255–260
- Khatoon, H., P. Solanki, M. Narayan, L. Tewari, and J. P. Rai (2017). Role of Microbes in Organic Carbon Decomposition and Maintenance of Soil Ecosystem. *International Journal of Chemical Studies*, **5**; 1648–1656
- Kinsbergen, D. T., A. M. Kooijman, E. Morriën, K. English, and J. G. Oostermeijer (2025). Abiotic and Biotic Drivers of Soil Microbial Diversity in an Intensively Grazed Natural Ecosystem. *npj Biodiversity*, **4**; 10
- Kiprotich, K., E. Muema, C. Wekesa, T. Ndombi, J. Muoma, D. Omayio, D. Ochieno, H. Motsi, S. Mncedi, and J. Tarus (2025). Unveiling the Roles, Mechanisms and Prospects of Soil Microbial Communities in Sustainable Agriculture. *Discover Soil*, **2**; 10
- Krulwich, T. A., G. Sachs, and E. Padan (2011). Molecular Aspects of Bacterial pH Sensing and Homeostasis. *Nature Reviews Microbiology*, **9**; 330–343
- Ladau, J. and E. A. Elloe-Fadrosh (2019). Spatial, Temporal, and Phylogenetic Scales of Microbial Ecology. *Trends in Microbiology*, **27**; 662–669
- Louca, S., M. F. Polz, F. Mazel, M. B. Albright, J. A. Huber, M. I. O'Connor, M. Ackermann, A. S. Hahn, D. S. Srivastava, S. A. Crowe, M. Doebeli, and L. W. Parfrey (2018). Function and Functional Redundancy in Microbial Systems. *Nature Ecology & Evolution*, **2**; 936–943
- Mason, A. R., M. J. Salomon, A. J. Lowe, and T. R. Cavagnaro (2023). Microbial Solutions to Soil Carbon Sequestration. *Journal of Cleaner Production*, **417**; 137993
- McCarthy, J. and E. A. Feigenbaum (1991). *Arthur L. Samuel: Pioneer in Machine Learning*. SAGE Publications, London
- Munshi, A. and V. Sharma (2018). Safety and Ethics in Biotechnology and Bioengineering: What to Follow and What Not To. In *Omics Technologies and Bio-Engineering*. Elsevier, pages 577–590
- Nannipieri, P., J. Ascher, M. Ceccherini, L. Landi, G. Pietramellara, and G. Renella (2017). Microbial Diversity and Soil Functions. *European Journal of Soil Science*, **68**; 12–26
- Nunes, M. R., K. S. Veum, P. A. Parker, S. H. Holan, D. L. Karlen, J. P. Amsili, H. M. van Es, S. A. Wills, C. A. Seybold, and T. B. Moorman (2021). The Soil Health Assessment Protocol and Evaluation Applied to Soil Organic Carbon. *Soil Science Society of America Journal*, **85**; 1196–1213
- Pan, L. and B. Cai (2023). Phosphate-Solubilizing Bacteria: Advances in Their Physiology, Molecular Mechanisms and Microbial Community Effects. *Microorganisms*, **11**; 2904
- Philippot, L., C. Chenu, A. Kappler, M. C. Rillig, and N. Fierer (2024). The Interplay Between Microbial Communities and Soil Properties. *Nature Reviews Microbiology*, **22**; 226–239
- Philippot, L., A. Spor, C. Hénault, D. Bru, F. Bizouard, C. M. Jones, A. Sarr, and P.-A. Maron (2013). Loss in Microbial Diversity Affects Nitrogen Cycling in Soil. *The ISME Journal*, **7**; 1609–1619
- Rawat, P., S. Das, D. Shankhdhar, and S. C. Shankhdhar (2021). Phosphate-Solubilizing Microorganisms: Mechanism and Their Role in Phosphate Solubilization and Uptake. *Journal of Soil Science and Plant Nutrition*, **21**; 49–68
- Shu, X., J. He, Z. Zhou, L. Xia, Y. Hu, Y. Zhang, G. Zhang, and C. Wang (2022). Organic Amendments Enhance Soil Microbial Diversity, Microbial Functionality and Crop Yields: A Meta-analysis. *Science of the Total Environment*, **829**; 154627
- Song, H., M.-Z. Ding, X.-Q. Jia, Q. Ma, and Y.-J. Yuan (2014). Synthetic Microbial Consortia: From Systematic Analysis to Construction and Applications. *Chemical Society Reviews*, **43**; 6954–6981
- Tiedje, J. M., M. A. Bruns, A. Casadevall, C. S. Criddle, E. Elloe-Fadrosh, D. M. Karl, K. Nguyen, N. K. Nguyen, and J. Zhou (2022). Microbes and Climate Change: A Research Prospectus for the Future. *MBio*, **13**; e00800–22
- Trivedi, P., M. Delgado-Baquerizo, C. Trivedi, H. Hu, I. C. Anderson, T. C. Jeffries, J. Zhou, and B. K. Singh (2016). Microbial Regulation of the Soil Carbon Cycle: Evidence from Gene–Enzyme Relationships. *The ISME Journal*, **10**; 2593–2604
- van Elsas, J. D., J. T. Trevors, J. K. Jansson, and P. Nannipieri (2006). *Modern Soil Microbiology*. CRC Press
- Wagg, C., K. Schlaeppli, S. Banerjee, E. E. Kuramae, and M. G. A. van der Heijden (2019). Fungal–Bacterial Diversity and Microbiome Complexity Predict Ecosystem Functioning. *Nature Communications*, **10**; 4841
- Wall, D. H., U. N. Nielsen, and J. Six (2015). Soil Biodiversity and Human Health. *Nature*, **528**; 69–76
- Wang, C. and Y. Kuzyakov (2024). Mechanisms and Implications of Bacterial–Fungal Competition for Soil Resources. *The ISME Journal*, **18**; wrae073
- Wohl, D. L., S. Arora, and J. R. Gladstone (2004). Functional Redundancy Supports Biodiversity and Ecosystem Function in a Closed and Constant Environment. *Ecology*, **85**; 1534–1540
- Wu, M., S. Xie, J. Zang, Y. Sun, S. Xu, S. Li, and J. Wang

- (2024). Multiple Anthropogenic Environmental Stressors Structure Soil Bacterial Diversity and Community Network. *Soil Biology and Biochemistry*, **198**; 109560
- Zha, Y., H. Chong, P. Yang, and K. Ning (2022). Microbial Dark Matter: From Discovery to Applications. *Genomics, Proteomics & Bioinformatics*, **20**; 867–881
- Zhang, Z., Y. Wang, S. Wang, L. Zhao, B. Zhang, W. Jia, Z. Zhai, L. Zhao, and Y. Li (2022). Effects of Antibacterial Peptide-Producing *Bacillus subtilis*, Gallic Acid, and Cellulase on Fermentation Quality and Bacterial Community of Whole-Plant Corn Silage. *Frontiers in Microbiology*, **13**; 1028001