

Soil Microbiomes: Pivotal Agents of Sustainable Agriculture under Intensive Farming in Bangladesh

Protima Rani Sarker ^a,

^aDivision of Soil Science, Regional Agricultural Research Station, Bangladesh Agricultural Research Institute, Jamalpur-2000, Bangladesh.

Abstract

The soil microbiomes, comprising diverse bacteria, fungi, archaea, and other microorganisms, forms the foundation of soil health and ecosystem functionality. This review explores the structural and functional aspects of soil microbial communities, including their composition, spatial organization, and interactions, as well as the environmental and anthropogenic factors that shape them. The soil microbiome plays pivotal roles in nutrient cycling, soil structure formation, plant growth promotion, stress mitigation, and greenhouse gas regulation, directly influencing soil organic carbon (SOC) dynamics and overall soil fertility. Microbial activities also contribute to climate change mitigation and support sustainable agricultural practices. In Bangladesh, intensive farming practices have significantly altered microbial community composition and functions, posing challenges to soil health and productivity. Strategies such as organic amendments, crop diversification, reduced chemical inputs, and bioinoculant applications are crucial to restoring microbial health in these systems. Understanding the intricate links between soil microbiome structure, function, and agricultural management is essential for promoting sustainable and resilient farming systems under intensive cultivation.

Keywords: Soil; microbiomes; sustainable; agriculture; intensive; farming.

*Corresponding author

Dr. Protima Rani Sarker, Bangladesh Agricultural Research Institute; e-mail: protimasarker90@gmail.com

1. Introduction

Soil is full of tiny living organisms that help keep it healthy and supports plant growth. It harbors a vast, living community of microorganisms whose collective activities sustain soil fertility, plant health, and ecosystem resilience (Timmis and Ramos, 2021). The soil microbiome, including bacteria, fungi, archaea, and protists, is central to fertility, nutrient cycling, and climate-smart agriculture. It drives critical processes such as nutrient cycling (nitrogen, phosphorus, carbon), organic matter decomposition, soil aggregation, water retention, and suppression of plant pathogens (Hartmann and Six, 2023).

In Bangladesh intensive farming system is increasingly popular. Farming systems that maximize productivity per unit of land using high inputs of labor, capital, and technology-such as machinery, chemical fertilizers, and pesticides is called intensive farming. The goal is to achieve high yields of crops or livestock from a small area, often for commercial sale, as opposed to subsistence farming which focuses on self-sufficiency and these type of farming is termed as intensive farming (Pretty and Bharucha, 2014). This is especially timely because intensive farming practices- including heavy use of chemical fertilizers, repeated tillage, monoculture cropping, and over-exploitation of land-are increasingly common (Sharma *et al.* 2023). Such practices often disrupt the balance and functions of microbial communities, which can degrade soil structure, reduce fertility, and weaken resilience to environmental stresses (Ortega *et al.* 2024).

In such conditions the soil microbiome offers a promising pathway toward sustainable agriculture: by promoting beneficial microbes e.g., plant-growth promoting rhizobacteria, mycorrhizal fungi, adopting organic amendments, reducing chemical inputs, and integrating microbiome-aware management (Wang *et al.* 2025). These approaches can enhance nutrient uptake, improve soil health, support crop yield stability, and reduce environmental impacts- all of which are vital for long-term food security and ecological sustainability in Bangladesh. As pressures on Bangladesh's agricultural lands

intensify - from population growth, increased cropping intensity, climate change, and land degradation-understanding and managing soil microbiomes becomes not just scientifically interesting, but practically urgent. Research into soil microbiome dynamics under intensive farming thus holds major potential to transform farming practices, rehabilitate degraded soils, and contribute to resilient agro-ecosystems.

2. Structures of the Soil Microbiome

2.1 Composition of the Soil Microbiome

The soil microbiome comprises one of the most important and complex components of all terrestrial ecosystems as it harbors millions of microbes including bacteria, fungi, archaea, viruses, and protozoa. Bacteria are single-celled microorganisms that can reach billions per gram of soil, but their populations can rapidly rise or fall with changes in the soil environment. Modern molecular techniques now allow scientists to identify and study many bacteria that cannot be cultured in the laboratory. e.g., Proteobacteria, Actinobacteria, Firmicutes (Young *et al.* 2013). Fungi can thrive in a wide range of environments because of their high adaptability (Islam *et al.* 2017). They release various extracellular enzymes that break down organic matter into CO₂, biomass, and organic acids, helping decompose soil components and maintain nutrient balance (Žifčáková *et al.* 2016). e.g., Ascomycota, Basidiomycota and AMF. Archaea account for roughly 0.5% to over 10% of soil prokaryotes, with populations reaching 10⁷–10⁸ cells per gram of soil (Mende *et al.* 2013). They contribute significantly to soil nutrient cycling, particularly through carbon, nitrogen, and sulfur transformations, such as methanogenesis in paddy soils and nitrification by specific archaeal groups. Soil contains 10⁷–10⁹ viruses per gram, yet their interactions with plants and soil vectors are still poorly understood (Andika *et al.* 2016). These viruses play an important role in shaping microbial community dynamics. Protozoa are among the least explored soil protists, with approximately 10³–10⁵ cells per gram of soil.

2.2 Spatial Structure

The spatial structure of soil microbial communities varies greatly across different zones and depths. Microbial abundance and activity typically decline with increasing soil depth from 0 to 100 cm due to reduced organic inputs and oxygen availability (Fierer *et al.* 2003). Strong contrasts also exist between the rhizosphere-rich in root exudates-and bulk soil, where nutrients are more limited (Philippot *et al.* 2013). Additionally, localized hotspots such as the rhizosphere, detritusphere, drilosphere (earthworm burrows), and other biopores support intense microbial activity, making them key centers of organic matter decomposition and nutrient cycling within soil ecosystems (Kooch and Kuzyakov, 2024).

2.3 Factors Shaping Microbiome Structure

Soil microbiome structure is shaped by multiple interacting environmental and management factors. Among these, soil pH is recognized as the strongest global determinant of microbial community composition (Fierer & Jackson, 2006). Soil texture and mineralogy-such as clay-rich versus sandy soils-affect habitat stability and nutrient retention. Organic matter availability and root-derived carbon inputs strongly influence microbial growth and diversity (Yang *et al.* 2023). Moisture and oxygen levels also play critical roles, especially in paddy soils where alternating aerobic-anaerobic conditions structure microbial niches (Khoshru *et al.* 2023). Land-use practices, including tillage, fertilizer inputs, and biochar application, further modify microbial communities by altering physical and chemical soil conditions (Lehmann *et al.* 2011). Finally, climate factors such as temperature and rainfall patterns affect microbial activity and biogeographical distributions (Brockett *et al.* 2012).

2.4 Microbial Interactions

Microbial interactions play a central role in shaping soil community structure and ecosystem functioning. These interactions range from competition for nutrients and space to mutualistic and commensal relationships that enhance survival and resource use (Sarsan *et al.* 2022). Fungi-bacteria interactions further influence decomposition, nutrient cycling, and soil aggregation (Zhang *et al.* 2022). Plant-microbe symbioses, such as rhizobia-legume nitrogen fixation and mycorrhizal associations, are key drivers of plant productivity and soil nutrient dynamics (Chauhan *et al.* 2023). At

the community scale, microbial networks formed through co-occurrence and co-exclusion patterns reveal complex ecological relationships that govern soil stability and resilience (Karimi *et al.* 2012).

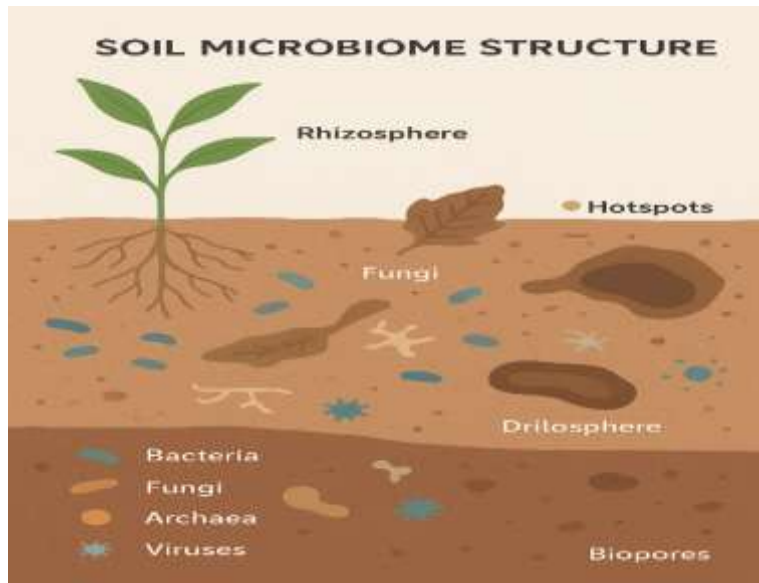


Fig.2 Soil microbiome structure showing rhizosphere, microbial groups, and hotspots.

3. Functions of the Soil Microbiome

3.1 Nutrient Cycling

Soil microbiomes are fundamental drivers of soil nutrient cycling, regulating the transformation, availability, and storage of essential elements. Soil microbiomes drive nutrient cycling by decomposing organic matter and transforming key elements such as carbon, nitrogen, phosphorus, and sulfur into forms that plants can use. Through processes like mineralization, nitrogen fixation, and sulfur and phosphorus transformation, microbes regulate nutrient availability and contribute to soil organic carbon formation (Prasad *et al.* 2020). These interactions maintain soil fertility, support plant productivity, and stabilize ecosystem functioning.

3.2 Soil Structure Formation

Soil microorganisms play a vital role in soil structure formation by producing extracellular polysaccharides (EPS) that act as binding agents, helping soil particles stick together. Their activity enhances aggregate stability and promotes microaggregate formation, which improves soil porosity, water retention, and resistance to erosion (Costa *et al.* 2018). Additionally, fungal hyphal networks serve as structural scaffolds, physically binding soil particles and reinforcing soil architecture, thereby maintaining soil health and fertility.

3.3 Plant Growth Promotion

Soil microbiomes promote plant growth through multiple mechanisms, including the production of siderophores that enhance iron availability and the secretion of phytohormones such as IAA, cytokinins, and gibberellins that stimulate root and shoot development (Pattnaik *et al.* 2021). They also suppress plant diseases by outcompeting pathogens or producing antimicrobial compounds, and improve nutrient availability through phosphate-solubilizing bacteria (PSB), potassium-solubilizing bacteria (KSB), and arbuscular mycorrhizal fungi (AMF), thereby supporting healthier and more productive plants (Sharma *et al.* 2025).

3.4 Stress Mitigation

Soil microbiomes help plants mitigate environmental stresses by enhancing drought tolerance through the production of osmolytes and improving salinity stress resilience via ion homeostasis and compatible solutes (Ma *et al.* 2020). They also contribute to metal detoxification by transforming or immobilizing toxic metals and assist plants in surviving flooding or anoxic conditions, particularly in paddy fields, by facilitating anaerobic nutrient cycling and producing stress-alleviating metabolites (Phurailatpam *et al.* 2022).

3.5 Greenhouse Gas Regulation

Soil microbiomes regulate greenhouse gas emissions by controlling the production and consumption of gases such as methane, with methanogens producing CH₄ under anaerobic conditions and methanotrophs oxidizing it to CO₂ (Meetei *et al.* 2024). They also influence N₂O emissions through the activity of nitrifiers and denitrifiers and drive CO₂ fluxes via the decomposition of organic matter, thereby playing a key role in ecosystem carbon and nitrogen balance (Butterbach-Bahl *et al.* 2013).

4. Microbial influence on nutrient cycling and SOC formation

Microorganisms play a crucial role in nutrient cycling and soil organic carbon (SOC) formation by mediating the decomposition, transformation, and stabilization of organic materials in soils under intensive farming. In the carbon cycle, soil microbes decompose plant residues, releasing CO₂ through respiration while converting part of the carbon into microbial biomass. Upon microbial death, necromass binds to soil minerals, forming a stable SOC pool that contributes to long-term carbon sequestration (Schimel & Schaeffer, 2012). In the nitrogen cycle, microbes regulate nitrogen availability through three main processes: nitrogen-fixing bacteria convert atmospheric N₂ into ammonia; nitrifying bacteria and ammonia-oxidizing archaea transform ammonia to nitrate; and denitrifying microbes reduce nitrate back to N₂ or N₂O, returning it to the atmosphere (Kuypers *et al.* 2018). These processes influence both soil fertility and carbon-nitrogen interactions that shape SOC dynamics. For phosphorus and sulfur cycling, microorganisms mineralize organic P and S into plant-available forms and solubilize insoluble phosphates, releasing organic acids and enzymes that enhance nutrient uptake (Richardson *et al.* 2011). In sulfur cycling, microbes oxidize sulfide and elemental sulfur to sulfate and reduce sulfate to sulfide under anaerobic conditions, controlling sulfur mobility and availability.

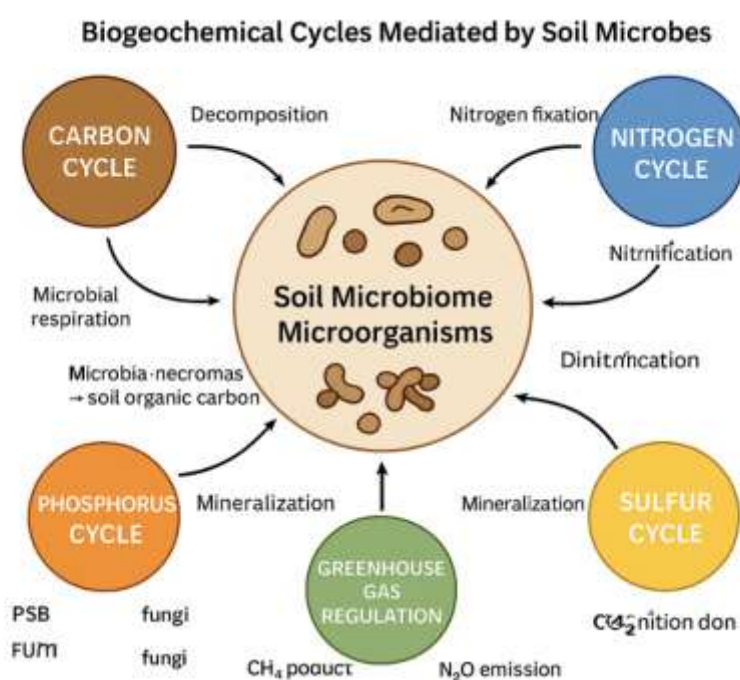


Fig. 3. Biogeochemical cycles mediated by soil Microbiomes

Overall, microbial activities drive nutrient release, SOC stabilization, and soil fertility, supporting plant growth and maintaining ecosystem biogeochemistry even under the pressures of intensive farming. These processes are vital for sustaining productivity and soil health in Bangladesh's high-input agricultural systems (Wen *et al.* 2025).

5. Soil Microbiome in Soil Health

The soil microbiome is a critical determinant of soil health, influencing both its physical structure and biological functioning. Soil microorganisms produce extracellular polysaccharides and other biofilms that enhance soil aggregation, porosity, and water retention, which are essential for maintaining soil fertility and resilience (Ali *et al.* 2024). Beneficial microbes, including plant-growth-promoting bacteria and fungi, also suppress soil-borne pathogens through mechanisms such as competitive exclusion, production of antimicrobial compounds, and induction of systemic resistance in plants (Mende *et al.* 2011). Furthermore, microbial biomass and community diversity serve as sensitive indicators of soil quality, reflecting the biological integrity of soils subjected to intensive cropping or degradation (Nannipieri *et al.* 2017). In the context of Bangladesh's high-input agricultural systems, maintaining a diverse and active soil microbiome is essential for sustaining productivity, nutrient cycling, and ecosystem resilience.

6. Microbial Functions in Climate Change

Soil microorganisms play a critical role in regulating greenhouse gas (GHG) emissions from agricultural ecosystems, including CO₂, N₂O, and CH₄ fluxes from rice paddies and croplands (Gupta *et al.* 2021). Climate variability, such as increased flooding, droughts, and temperature fluctuations, significantly affects microbial activity, organic matter decomposition, and nutrient turnover, altering soil fertility and ecosystem functioning (Singh *et al.* 2022). In Bangladesh, where agriculture is highly vulnerable to climate extremes, managing microbial processes—through practices like biofertilizer application, organic amendments, and conservation agriculture—can enhance nutrient cycling, improve soil resilience, and support climate-smart agriculture (Sharma *et al.* 2023). Understanding microbial responses to climate change is therefore essential for mitigating environmental impacts and sustaining crop productivity in intensively farmed landscapes.

7. Microbial Contribution to Sustainable Agriculture

Microorganisms play a pivotal role in promoting sustainable agriculture by enhancing nutrient availability, improving soil health, and reducing reliance on chemical inputs. The use of biofertilizers, such as *Rhizobium*, *Azotobacter*, phosphate-solubilizing bacteria, and *Trichoderma*, can increase nutrient uptake and crop productivity while minimizing environmental impacts associated with synthetic fertilizers (Bashan *et al.* 2014). Similarly, microbial-based soil amendments, including compost and vermicompost, stimulate soil microbial activity, improve soil structure, and enhance nutrient cycling, particularly for nitrogen, phosphorus, and carbon (Singh *et al.* 2022). Integrating these microbial technologies with conservation agriculture practices—such as reduced tillage, crop rotation, and organic amendments—further enhances soil resilience, water-use efficiency, and the long-term sustainability of intensive farming systems in Bangladesh (Pretty & Bharucha, 2014). Collectively, leveraging the soil microbiome offers a promising strategy to achieve productive, resilient, and environmentally sustainable agroecosystems.

8. Impacts of Intensive Farming on Microbial Communities in Bangladesh

Intensive farming practices in Bangladesh, characterized by heavy reliance on chemical fertilizers, pesticides, and monoculture cropping, have profound effects on soil microbial communities. These practices reduce microbial diversity, disrupt nutrient cycling, and impair soil ecosystem functions (Geisseler *et al.* 2016). Conventional tillage further exacerbates the loss of soil organic matter, leading to a decline in microbial biomass and weakening soil carbon sequestration (Naresh *et al.* 2017). Moreover, high cropping intensity, such as continuous rice–rice or rice–vegetable rotations, often creates nutrient imbalances and environmental stresses that reduce the abundance and activity of beneficial microbial functional groups, including nitrogen-fixing bacteria and phosphate-solubilizing microorganisms (Sharma *et al.* 2023). Collectively, these factors compromise soil health and long-term agricultural sustainability, highlighting the need for management strategies that preserve microbial diversity and function.

9. Strategies to Restore Microbial Health in Intensive Farming

Restoring and maintaining soil microbial health is essential for sustaining productivity in intensive farming systems. The adoption of organic amendments, such as compost, manure, and biochar, enhances soil organic carbon content and stimulates microbial activity, improving nutrient cycling and soil structure (Rahman *et al.* 2019). Practices such as crop diversification, legume inclusion, and reduced tillage promote microbial diversity and support functional groups critical for nutrient transformation and soil resilience (Zou *et al.* 2024). Integrated nutrient management (INM), which combines judicious use of chemical fertilizers with microbial biofertilizers, ensures balanced soil fertility while maintaining beneficial microbial communities (Wei *et al.* 2024). Additionally, the application of microbial inoculants and native microbial consortia, adapted to local Bangladeshi agro-ecosystems, can enhance plant growth, suppress soil-borne pathogens, and strengthen ecosystem services, providing a practical strategy for sustainable agriculture under intensive cultivation.

10. Conclusion

The soil microbiome forms the foundation of soil health, driving essential processes such as nutrient cycling, organic matter decomposition, and carbon sequestration. The structure and diversity of microbial communities determine key ecosystem functions, including soil fertility, disease suppression, and resilience to environmental stresses, particularly under intensive farming systems in Bangladesh. Understanding the complex links between microbial composition, soil function, and agricultural management is crucial for sustainable agriculture, enhancing crop productivity while mitigating greenhouse gas emissions. Leveraging microbial communities through biofertilizers, organic amendments, and conservation practices offers a viable strategy for soil restoration, ecosystem resilience, and long-term agricultural sustainability.

References

- Ali, N., Abbas, S.A.A.A., Sharif, L., Shafiq, M., Kamran, Z., Haseeb, M. and Shahid, M.A., 2024. Microbial extracellular polymeric substance and impacts on soil aggregation. In *Bacterial secondary metabolites* (pp. 221-237). Elsevier. <https://doi.org/10.1016/B978-0-323-95251-4.00021-1>
- Andika, I.B., Kondo, H. and Sun, L., 2016. Interplays between soil-borne plant viruses and RNA silencing-mediated antiviral defense in roots. *Frontiers in Microbiology*, 7, p.1458. <https://doi.org/10.3389/fmicb.2016.01458>
- Bashan, Y., de-Bashan, L.E., Prabhu, S.R. and Hernandez, J.P., 2014. Advances in plant growth-promoting bacterial inoculant technology: formulations and practical perspectives (1998–2013). *Plant and soil*, 378(1), pp.1-33. <https://doi.org/10.1007/s11104-013-1956-x>
- Brockett, B.F., Prescott, C.E. and Grayston, S.J., 2012. Soil moisture is the major factor influencing microbial community structure and enzyme activities across seven biogeoclimatic zones in western Canada. *Soil biology and biochemistry*, 44(1), pp.9-20. <https://doi.org/10.1016/j.soilbio.2011.09.003>
- Butterbach-Bahl, K., Baggs, E.M., Dannenmann, M., Kiese, R. and Zechmeister-Boltenstern, S., 2013. Nitrous oxide emissions from soils: how well do we understand the processes and their controls?. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 368(1621), p.20130122. <https://doi.org/10.1098/rstb.2013.0122>
- Chauhan, P., Sharma, N., Tapwal, A., Kumar, A., Verma, G.S., Meena, M., Seth, C.S. and Swapnil, P., 2023. Soil microbiome: diversity, benefits and interactions with plants. *Sustainability*, 15(19), p.14643. <https://doi.org/10.3390/su151914643>
- Costa, O.Y., Raaijmakers, J.M. and Kuramae, E.E., 2018. Microbial extracellular polymeric substances: ecological function and impact on soil aggregation. *Frontiers in microbiology*, 9, p.1636. <https://doi.org/10.3389/fmicb.2018.01636>
- Dubey, A., Malla, M.A., Khan, F., Chowdhary, K., Yadav, S., Kumar, A., Sharma, S., Khare, P.K. and Khan, M.L., 2019. Soil microbiome: a key player for conservation of soil health under changing climate. *Biodiversity and Conservation*, 28(8), pp.2405-2429. <https://doi.org/10.1007/s10531-019-01760-5>
- Fierer, N. and Jackson, R.B., 2006. The diversity and biogeography of soil bacterial communities. *Proceedings of the National Academy of Sciences*, 103(3), pp.626-631. <https://doi.org/10.1073/pnas.0507535103>

- Fierer, N., Schimel, J.P. and Holden, P.A., 2003. Variations in microbial community composition through two soil depth profiles. *Soil Biology and Biochemistry*, 35(1), pp.167-176. [https://doi.org/10.1016/S0038-0717\(02\)00251-1](https://doi.org/10.1016/S0038-0717(02)00251-1)
- Geisseler, D., Lazicki, P.A. and Scow, K.M., 2016. Mineral nitrogen input decreases microbial biomass in soils under grasslands but not annual crops. *Applied Soil Ecology*, 106, pp.1-10. <https://doi.org/10.1016/j.apsoil.2016.04.015>
- Gupta, K., Kumar, R., Baruah, K.K., Hazarika, S., Karmakar, S. and Bordoloi, N., 2021. Greenhouse gas emission from rice fields: a review from Indian context. *Environmental Science and Pollution Research*, 28(24), pp.30551-30572. <https://doi.org/10.1007/s11356-021-13935-1>
- Hartmann, M. and Six, J., 2023. Soil structure and microbiome functions in agroecosystems. *Nature Reviews Earth & Environment*, 4(1), pp.4-18. <https://doi.org/10.1038/s43017-022-00366-w>
- Islam, W. and Ahmed, M., 2017. Identification of different fungi associated with grain discoloration complex disease of rice and management of infested grains through fungicides. *Int. J. Sci. Res. Agric. Sci*, 4(2), pp.30-35.
- Karimi, B., Maron, P.A., Chemidlin-Prevost Boure, N., Bernard, N., Gilbert, D. and Ranjard, L., 2017. Microbial diversity and ecological networks as indicators of environmental quality. *Environmental Chemistry Letters*, 15(2), pp.265-281. <https://doi.org/10.1007/s10311-017-0614-6>
- Khoshru, B., Khoshmanzar, E., Lajayer, B.A. and Ghorbanpour, M., 2023. Soil moisture-mediated changes in microorganism biomass and bioavailability of nutrients in paddy soil. In *Plant Stress Mitigators* (pp. 479-494). Academic Press. <https://doi.org/10.1016/B978-0-323-89871-3.00005-7>
- Kooch, Y. and Kuzyakov, Y., 2024. Earthworm Effects on Microbial and Enzyme Activities in Soil. In *Earthworms and Ecological Processes* (pp. 357-372). Cham: Springer Nature Switzerland. https://doi.org/10.1007/978-3-031-64510-5_13
- Kuypers, M.M., Marchant, H.K. and Kartal, B., 2018. The microbial nitrogen-cycling network. *Nature Reviews Microbiology*, 16(5), pp.263-276.
- Lehmann, J., Rillig, M.C., Thies, J., Masiello, C.A., Hockaday, W.C. and Crowley, D., 2011. Biochar effects on soil biota—a review. *Soil biology and biochemistry*, 43(9), pp.1812-1836. <https://doi.org/10.1016/j.soilbio.2011.04.022>
- Ma, Y., Dias, M.C. and Freitas, H., 2020. Drought and salinity stress responses and microbe-induced tolerance in plants. *Frontiers in plant science*, 11, p.591911. <https://doi.org/10.3389/fpls.2020.591911>
- Meetei, T.T., Singh, N.S., Devi, Y.B. and Bokado, K., 2024. Diversity of Greenhouse Gas Producing and Mitigating Microbes in Soil. In *Greenhouse Gas Regulating Microorganisms in Soil Ecosystems: Perspectives for Climate Smart Agriculture* (pp. 201-217). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-031-70569-4_12
- Mende, D.R., Sunagawa, S., Zeller, G. and Bork, P., 2013. Accurate and universal delineation of prokaryotic species. *Nature methods*, 10(9), pp.881-884. <https://doi.org/10.1038/nmeth.2575>
- Nannipieri, P., Ascher, J., Ceccherini, M., Landi, L., Pietramellara, G. and Renella, G., 2017. Microbial diversity and soil functions. *European journal of soil science*, 68(1), pp.12-26. https://doi.org/10.1111/ejss.4_12398
- Naresh, R.K., Timsina, J., Bhaskar, S., Gupta, R.K., Singh, A.K., Dhaliwal, S.S., Rathore, R.S., Kumar, V., Singh, P., Singh, S.P. and Tyagi, S., 2017. Effects of tillage, residue and nutrient management on soil organic carbon dynamics and its fractions, soil aggregate stability and soil carbon sequestration: A review. *EC Nutrition*, 12(2), pp.53-80.
- Ortega, R., Miralles, I., Domene, M.A., Meca, D. and Del Moral, F., 2024. Ecological practices increase soil fertility and microbial diversity under intensive farming. *Science of The Total Environment*, 954, p.176777. <https://doi.org/10.1016/j.scitotenv.2024.176777>**
- Pattnaik, S., Mohapatra, B. and Gupta, A., 2021. Plant growth-promoting microbe mediated uptake of essential nutrients (Fe, P, K) for crop stress management: Microbe–soil–plant continuum. *Frontiers in Agronomy*, 3, p.689972. <https://doi.org/10.3389/fagro.2021.689972>
- Philippot, L., Spor, A., Hénault, C., Bru, D., Bizouard, F., Jones, C.M., Sarr, A. and Maron, P.A., 2013. Loss in microbial diversity affects nitrogen cycling in soil. *The ISME journal*, 7(8), pp.1609-1619. <https://doi.org/10.1038/ismej.2013.34>
- Phurailatpam, L., Dalal, V.K., Singh, N. and Mishra, S., 2022. Heavy metal stress alleviation through omics analysis of soil and plant microbiome. *Frontiers in Sustainable Food Systems*, 5, p.817932. <https://doi.org/10.3389/fsufs.2021.817932>
- Prasad, S., Malav, L.C., Choudhary, J., Kannojiya, S., Kundu, M., Kumar, S. and Yadav, A.N., 2020. Soil microbiomes for healthy nutrient recycling. In *Current trends in microbial biotechnology for sustainable agriculture* (pp. 1-21). Singapore: Springer Singapore. https://doi.org/10.1007/978-981-15-6949-4_1
- Prasad, S., Malav, L.C., Choudhary, J., Kannojiya, S., Kundu, M., Kumar, S. and Yadav, A.N., 2020. Soil microbiomes for healthy nutrient recycling. In *Current trends in microbial biotechnology for sustainable agriculture* (pp. 1-21). Singapore: Springer Singapore. https://doi.org/10.1007/978-981-15-6949-4_1

- Pretty, J. and Bharucha, Z.P., 2014. Sustainable intensification in agricultural systems. *Annals of botany*, 114(8), pp.1571-1596. <https://doi.org/10.1093/aob/mcu205>
- Pretty, J. and Bharucha, Z.P., 2014. Sustainable intensification in agricultural systems. *Annals of botany*, 114(8), pp.1571-1596. <https://doi.org/10.1093/aob/mcu205>
- Rahman, G.M., Rahman, M.M., Alam, M.S., Kamal, M.Z., Mashuk, H.A., Datta, R. and Meena, R.S., 2019. Biochar and organic amendments for sustainable soil carbon and soil health. In *Carbon and nitrogen cycling in soil* (pp. 45-85). Singapore: Springer Singapore. https://doi.org/10.1007/978-981-13-7264-3_3

References

- Richardson, A.E., Lynch, J.P., Ryan, P.R., Delhaize, E., Smith, F.A., Smith, S.E., Harvey, P.R., Ryan, M.H., Veneklaas, E.J., Lambers, H. and Oberson, A., 2011. Plant and microbial strategies to improve the phosphorus efficiency of agriculture. *Plant and soil*, 349(1), pp.121-156. <https://doi.org/10.1007/s11104-011-0950-4>
- Sarsan, S., Pandiyan, A., Rodhe, A.V. and Jagavati, S., 2022. Synergistic interactions among microbial communities. In *Microbes in microbial communities: Ecological and applied perspectives* (pp. 1-37). Singapore: Springer Singapore. https://doi.org/10.1007/978-981-16-5617-0_1
- Schimel, J.P. and Schaeffer, S.M., 2012. Microbial control over carbon cycling in soil. *Frontiers in microbiology*, 3, p.348. <https://doi.org/10.3389/fmicb.2012.00348>
- Sharma, P., Kaushal, S., Tandon, R., Goel, S. and Baishya, R., 2025. Plant growth promoting bacteria and arbuscular mycorrhizal fungi induced salinity tolerance in *Withania somnifera* (L.) Dunal. *Journal of Plant Growth Regulation*, pp.1-21. <https://doi.org/10.1007/s00344-025-11672-0>
- Sharma, U.C., Datta, M. and Sharma, V., 2023. Land use and management. In *Soils in the Hindu Kush Himalayas: Management for Agricultural Land Use* (pp. 295-462). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-031-11458-8_7
- Singh, P., Sharma, A. and Dhankhar, J., 2022. Climate change and soil fertility. In *Plant Stress Mitigators: Action and Application* (pp. 25-59). Singapore: Springer Nature Singapore. https://doi.org/10.1007/978-981-16-7759-5_3
- Timmis, K. and Ramos, J.L., 2021. The soil crisis: the need to treat as a global health problem and the pivotal role of microbes in prophylaxis and therapy. *Microbial Biotechnology*, 14(3), pp.769-797. <https://doi.org/10.1111/1751-7915.13771>
- Wang, L., Guo, S., Zhang, J., Field, K.J., Baquerizo, M.D., de Souza, T.A., Lee, S.J., Hijri, M., Shang, X., Sun, D. and Cao, H., 2025. Arbuscular mycorrhizal networks—a climate-smart blueprint for agriculture. *Plant Communications*, 6(11).
- Wei, X., Xie, B., Wan, C., Song, R., Zhong, W., Xin, S. and Song, K., 2024. Enhancing soil health and plant growth through microbial fertilizers: Mechanisms, benefits, and sustainable agricultural practices. *Agronomy*, 14(3), p.609. <https://doi.org/10.3390/agronomy14030609>
- Wen, Y., Liu, X., Yang, N., Li, Y. and Zhang, J., 2025. The Contribution of Microbial-and Plant-Derived Carbon to Soil Organic Carbon Fractions and Stability Under Manure Application Combined with Straw Incorporation. *Agronomy*, 15(6), p.1424. <https://doi.org/10.3390/agronomy15061424>
- Young, S., Juhl, A. and O'Mullan, G.D., 2013. Antibiotic-resistant bacteria in the Hudson River Estuary linked to wet weather sewage contamination. *Journal of water and health*, 11(2), pp.297-310. <https://doi.org/10.2166/wh.2013.131>
- Zhang, S., Hu, W., Xu, Y., Zhong, H., Kong, Z. and Wu, L., 2022. Linking bacterial and fungal assemblages to soil nutrient cycling within different aggregate sizes in agroecosystem. *Frontiers in Microbiology*, 13, p.1038536. <https://doi.org/10.3389/fmicb.2022.1038536>
- Žifčáková, L., 2017. Molecular biology and ecology of microbial decomposition of plant-derived biopolymers in forest ecosystems. <http://hdl.handle.net/20.500.11956/16935>
- Zou, Y., Liu, Z., Chen, Y., Wang, Y. and Feng, S., 2024. Crop rotation and diversification in China: Enhancing sustainable agriculture and resilience. *Agriculture*, 14(9), p.1465. <https://doi.org/10.3390/agriculture14091465>