



OPEN ACCESS

EDITED AND REVIEWED BY
Jesús Navas-Castillo,
La Mayora Experimental Station (CSIC), Spain

*CORRESPONDENCE
Manoj Kumar Solanki
✉ mkswings321@gmail.com

SPECIALTY SECTION
This article was submitted to
Microbe and Virus Interactions with Plants,
a section of the journal
Frontiers in Microbiology

RECEIVED 20 December 2022
ACCEPTED 29 December 2022
PUBLISHED 11 January 2023

CITATION
Solanki MK, Mandal A, Medeiros FHVD and
Awasthi MK (2023) Editorial: Emerging frontiers
of microbial functions in sustainable
agriculture. *Front. Microbiol.* 13:1128267.
doi: 10.3389/fmicb.2022.1128267

COPYRIGHT
© 2023 Solanki, Mandal, Medeiros and Awasthi.
This is an open-access article distributed under
the terms of the [Creative Commons Attribution
License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution or
reproduction in other forums is permitted,
provided the original author(s) and the
copyright owner(s) are credited and that the
original publication in this journal is cited, in
accordance with accepted academic practice.
No use, distribution or reproduction is
permitted which does not comply with these
terms.

Editorial: Emerging frontiers of microbial functions in sustainable agriculture

Manoj Kumar Solanki^{1*}, Asit Mandal²,
Flavio Henrique Vasconcelos De Medeiros³ and
Mukesh Kumar Awasthi⁴

¹Plant Cytogenetics and Molecular Biology Group, Faculty of Natural Sciences, Institute of Biology, Biotechnology and Environmental Protection, University of Silesia, Katowice, Poland, ²Indian Institute of Soil Science, Indian Council of Agricultural Research, Bhopal, India, ³Plant Pathology Department, Universidade Federal de Lavras, Lavras, Brazil, ⁴College of Natural Resources and Environment, Northwest A&F University, Xianyang, China

KEYWORDS

plant microbiome, microbial symbiosis, mineral solubilizers, composting, fruit microbiome

Editorial on the Research Topic

Emerging frontiers of microbial functions in sustainable agriculture

Introduction

Climate change scenarios have significantly impacted food production, crop, and soil quality. Many developed countries are using microbes as an alternative to chemical fertilizers. Microbes play a pivotal role in soil fertility through the nutrient cycling process (Patil and Solanki, 2016; Kumari et al., 2020). Different kinds of microbes associated with soil and plants are involved in many fundamental processes, such as biological nitrogen fixation, biotic and abiotic stress regulation, and plant growth promotion (Verma et al., 2020; Mandal et al., 2023). Microbial diversity and function are regulated through the host type, age, ecosystem, climatic condition, and geographical location. The Research Topic “Emerging Frontiers of Microbial Functions in Sustainable Agriculture” is in the “Microbe and Virus Interactions with Plants” section in the journal Frontiers in Microbiology. We present a summary of 12 published original research papers.

Plant microbiome diversity and function

Microbial symbiosis helps plants draw minerals, which boost their growth and defense, through chelation and mineralization. These potential microbiomes can be utilized as bioinoculants to sustain crop production. The structures of plant-associated communities are strongly impacted by soil texture, geography, and agrochemicals, including mineral fertilizers, intercropping systems, developmental stages, and crop rotation (Habig and Swanepoel, 2015; Galazka et al., 2018; Dastogeer et al., 2020; Mandal et al., 2020; Solanki et al., 2020). Kim et al. discussed the decrease of N-cycling communities, such as nifH, archaeal amoA, and nirS, and the increase of bacterial amoA with N fertilization. The report concludes that soil acidification and high nutrient availability disrupt soil N-cycling communities in the cover cropping of corn monocultures. However, cover cropping has a limited impact after 2 years, and long-term applications may cause significant modifications in the microbial communities. On the other

hand, Zheng et al. emphasized the importance of tree ages and soil texture in bacterial diversity and composition. *Proteobacteria*, *Acidobacteria*, and *Actinobacteria* were the dominant bacterial taxa in pomelo tree soil. Soil properties, such as pH and phosphorus availability, play important roles in shifts in bacterial communities. Bacterial genera *Sinomonas* and *Streptacidiphilus* were found to be unique in red soil, while *Actinoallomurus* and *Microbacterium* were found in paddy soil. The microbial co-occurrence network showed that old trees (20 and 30 years) have more complex networks and are more stable than young trees. Li et al. showed that phytase-producing *Pseudomonas* spp. is predominantly found in the alpine grassland of the Qinghai-Tibetan Plateau. These bacteria can promote the growth of *Lolium perenne* L and show multiple plant growth-promoting traits, such as P solubilization, plant production, nitrogen fixation, 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase activity, and antimicrobial activity. Nong et al. described *Burkholderia* sp. strain GXS16, a diazotrophic bacteria colonization response in sugarcane roots. Bacterial colonization enhances antioxidants, such as H₂O₂ and malondialdehyde. Differentially expressed genes linked to ethylene pathways were much more highly expressed than those linked to abscisic acid and gibberellin.

Microbes and agricultural practices

Plant rhizosphere and endosphere-associated microbes are strongly involved in nutrition transport and plant growth development (Solanki et al., 2019). Organic manure positively influences microbial functions and improves soil nutrient availability and uptake by plants (Alori et al., 2017; Jiao et al., 2019). Zhao et al. revealed that cattle manure improves oat plant root length and surface. Bacterial genera *Pseudoxanthomonas*, *Pseudomonas*, and *Sphingomonas*, and the fungal phylum Ascomycota, were positively related to oat biomass and nutrient accumulation during cattle manure application. Results revealed that Basidiomycota is more abundant in cattle manure deposition treatment than the control. Moreover, cattle manure disrupts the growth of pathotrophs, such as the fungal genera *Alternaria* and *Fusarium*, and encourages the development of saprotrophic and symbiotrophic fungi.

Soil health restoration through different kinds of microbes is an ecological process (Solanki et al., 2019; Solanki et al., 2021), and soil health monitoring through microbial activity and response plays an essential role in all restoration processes. Bhaduri et al. discussed the major strategies that can help restore and maintain ecosystem stability. Various bio-indicators, such as microbial biomass, enzymes, genetic markers, metabolites, and microbial communities, could be used to identify soil health in the presence of different pollutant-contaminated soil samples. Next, Choudhary et al. reported that soil properties and fungal communities play a significant role in climate-smart agricultural (CSA) practices. The fungal taxon Ascomycota was found to be abundant in rice-based CSA scenarios. Additionally, higher levels of soil organic carbon and nitrogen were found in CSA scenarios, improving crop yield.

Microbes and plants: Biotic and abiotic stresses

Biotic and abiotic factors are considerable limitations in sustainable agriculture production. In recent years, drought stress has

become a major issue for agriculture sectors in developing countries (Yandigeri et al., 2012; Wang et al., 2018). Morales-Quintana et al. showed that the fungal endophytes *Penicillium brevicompactum* and *P. chrysogenum*, isolated from Antarctic vascular plants, provoke drought stress regulation in strawberry plants. These endophytes enhance photosynthetic activity, antioxidants, and proline content and reduce lipid peroxidation, which helps plants regulate drought stress. These symbiotic fungi can also be used as an eco-friendly strategy to cope with drought in other crops. Palmieri et al. revealed that patulin biosynthesis by *Penicillium expansum* strongly correlates with extracellular pH in wounded apples. The pH modulation by *Papiliotrema terrestris* LS28 is vital for reducing the amount of patulin. Jia et al. delved into the microbial diversity associated with healthy and wilted *Paeonia suffruticosa* rhizosphere soil. Fungal genera *Fusarium*, *Cylindrocarpon*, and *Neocosmospora* were directly associated with plant yield reduction and disease incidence. Bacterial and fungal networks were more complex in diseased plants than in healthy ones. The bacterial network significantly impacted the diseased plants that provide a comfortable environment in which the fungal group can grow efficiently. Dastogeer et al. showed that the microbiomes of leaf and grain tissues are altered significantly at the *Magnaporthe oryzae* infection site. The bacterial genus *Rhizobium* increased, whereas the fungal genera *Tylospora*, *Clohesyomyces*, and *Penicillium* declined in the symptomatic leaf and grain tissues. The microbial network identified several direct interactions between *Magnaporthe oryzae* and other microbes. A higher percentage of soil bacteria was tracked from healthy root samples.

Fruit-associated microbiome

Microbial communities are associated with fruit surfaces and internal tissues and are impacted by the host's age, evolution, and diversity. The fruit carposphere harbors a wide diversity of microbes (Droby and Wisniewski, 2018). In this regard, Zhimo et al. identified 15 bacterial and 35 fungal core taxa that are abundant at different stages of the apple carposphere of three cultivars that grow in the same environmental conditions. This study represents the strong microbial cross-domain associations, uncovers potential microbe-microbe correlations in the apple carposphere and provides essential information regarding microbial recruitment in the fruit carposphere and its influence over time.

Conclusion

The non-judicial use of agrochemicals, including fertilizers, and mismanagement of natural soil and water resources greatly impact soil microbial community function, which may result in barren or unproductive soil in the long term. Moreover, soil degradation through the depletion of soil carbon is a critical factor for judging soil carrying capacity and its future utility. In this regard, it is highly pertinent that plant rhizosphere microbes and their symbiotic associations or endophytes play an optimistic candidature, and that their proper use sustains the utility of the soil in the long term.

Perspectives

- Microbial resources and their significance for maintaining soil ecosystems has been highly recognized in recent decades.

However, microbial performance varies greatly depending on the various biotic and abiotic factors that are directly linked with the agroecological conditions.

- Nutrient cycling, restoration of pollutant-contaminated soil, and protection of soil and plant diversity are only possible by the virtue of symbiotic association among microbes in plants and soil.
- Soil health represents the accumulation of healthy soil biota or biodiversity over a period of time or through the proper management of soil biotic components.
- Bridging multiple technologies to better understand the microbial relationships in plant growth and soil productivity. Here, several molecular approaches are applied to extract the insight information. However, research and obstacles run parallel with each other, and advanced technologies may help unlock the secret information in the future.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Funding

AM was thankful to the Science and Engineering Research Board (SERB)-DST (Grant No. ECR/2017/002121).

References

- Alori, E. T., Glick, B. R., and Babalola, O. O. (2017). Microbial phosphorus solubilization and its potential for use in sustainable agriculture. *Front. Microbiol.* 8, 971. doi: 10.3389/fmicb.2017.00971
- Dastogeer, K. M. G., Tumpa, F. H., Sultana, A., Akter, M. A., and Chakraborty, A. (2020). Plant microbiome—an account of the factors that shape community composition and diversity. *Curr. Plant Biol.* 23, 100161. doi: 10.1016/J.CPB.2020.100161
- Droby, S., and Wisniewski, M. (2018). The fruit microbiome: a new frontier for postharvest biocontrol and postharvest biology. *Postharvest Biol. Technol.* 140, 107–112. doi: 10.1016/J.POSTHARVBIO.2018.03.004
- Galazka, A., Grzadziel, J., Galazka, R., Ukalska-Jaruga, A., Strzelecka, J., and Smreczak, B. (2018). Genetic and functional diversity of bacterial microbiome in soils with long term impacts of petroleum hydrocarbons. *Front. Microbiol.* 9, 1923. doi: 10.3389/FMICB.2018.01923
- Habig, J., and Swanepoel, C. (2015). Effects of conservation agriculture and fertilization on soil microbial diversity and activity. *Environments* 2, 358–384. doi: 10.3390/environments2030358
- Jiao, S., Xu, Y., Zhang, J., and Lu, Y. (2019). Environmental filtering drives distinct continental atlases of soil archaea between dryland and wetland agricultural ecosystems. *Microbiome* 7, 1–13. doi: 10.1186/S40168-019-0630-9
- Kumari, B., Mani, M., Solanki, A. C., Solanki, M. K., Hora, A., and Mallick, M. A. (2020). “Phytobiome engineering and its impact on next-generation agriculture,” in *Phytobiomes: Current Insights and Future Vistas*, eds M. K. Solanki, P. L. Kashyap, and B. Kumari (Singapore: Springer), 381–403.
- Mandal, A., Sarkar, B., Mandal, S., Vithanage, M., Patra, A. K., and Manna, M. C. (2020). “Impact of agrochemicals on soil health,” in *Agrochemicals Detection, Treatment and Remediation (Butterworth-Heinemann)*, ed M. N. V Prasad (London: Academic Press), 161–187.
- Mandal, A., Thakur, J. K., Sarkar, A., Saha, M., Solanki, M. K., Rudrashetti, A. P., et al. (2023). “Efficacy of microbial endophytes in bioremediation: current research and future

FM was thankful for the productivity scholarship grant CNPq 3172266/2021-7.

Acknowledgments

We deeply thank all the authors and reviewers who have significantly contributed to this Research Topic.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

outlook,” in *Microbial Endophytes and Plant Growth*, eds M. K. Solanki, Y. M. Kumar, B. P. Singh, and V. K. Gupta (London: Academic Press), 283–295.

Patil, H. J., and Solanki, M. K. (2016). “Microbial inoculant: Modern era of fertilizers and pesticides,” in *Microbial Inoculants in Sustainable Agricultural Productivity: Vol. 1: Research Perspectives*, eds D. Singh, H. Singh, and R. Prabha (New Delhi: Springer), 319–343. doi: 10.1007/978-81-322-2647-5_19

Solanki, M. K., Kashyap, P. L., Kumari, B., Ansari, R. A., Sumbul, A., Rizvi, R., et al. (2021). “Mycorrhizal fungi and its importance in plant health amelioration,” in *Microbiomes and Plant Health*, eds M. K. Solanki, P. L. Kashyap, R. A. Ansari, and B. Kumari (London: Academic Press), 205–223.

Solanki, M. K., Wang, F.-Y., Wang, Z., Li, C.-N., Lan, T.-J., Singh, R. K., et al. (2019). Rhizospheric and endospheric diazotrophs mediated soil fertility intensification in sugarcane-legume intercropping systems. *J. Soils Sediments* 19, 1911–1927. doi: 10.1007/s11368-018-2156-3

Solanki, M. K., Wang, Z., Wang, F.-Y., Li, C.-N., Gupta, C. L., Singh, R. K., et al. (2020). Assessment of diazotrophic proteobacteria in sugarcane rhizosphere when intercropped with legumes (peanut and soybean) in the field. *Front. Microbiol.* 11, 1814. doi: 10.3389/fmicb.2020.01814

Verma, P., Solanki, A. C., Solanki, M. K., and Kumari, B. (2020). “Linkages of microbial plant growth promoters toward profitable farming,” in *Phytobiomes: Current Insights and Future Vistas*, eds M. K. Solanki, P. L. Kashyap, and B. Kumari (Singapore: Springer), 163–190.

Wang, Z., Solanki, M. K., Yu, Z.-X., Yang, L.-T., An, Q.-L., Dong, D.-F., et al. (2018). Draft genome analysis offers insights into the mechanism by which *Streptomyces chartreusis* WZS021 increases drought tolerance in sugarcane. *Front. Microbiol.* 9, 3262. doi: 10.3389/fmicb.2018.03262

Yandigeri, M. S., Meena, K. K., Singh, D., Malviya, N., Singh, D. P., Solanki, M. K., et al. (2012). Drought-tolerant endophytic actinobacteria promote growth of wheat (*Triticum aestivum*) under water stress conditions. *Plant Growth Regul.* 68, 411–420. doi: 10.1007/s10725-012-9730-2