Editorial

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Microbes as a gift from God

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The unseen wonders, microbes are tiny creatures that are not visible to the naked eye. Microorganisms are ubiquitous in nature and known to exist everywhere from the equator to poles, deserts to the deep sea, rocks, geysers, and even in extreme hot and cold conditions. Microbes are unicellular or multicellular organisms and belong to three domains, i.e. archaea, bacteria, and eukarya. These tiny creatures are truly a gift from God as they play several roles for the environment and every creature of the earth, such as humans, plants, and animals, without (gnotobiotic condition) which the quality and quantity of life will drastically reduce. Microbes maintain the biogeological cycles in the environment and on the other hand, they maintain the soil fertility. In plants, beneficial microbes help in growth promotion as well as protecting them from pathogens and fulfilling nutritional requirements, whereas in humans and animals, they maintain cognitive functions. Their important role played in nature has attracted the attention of scientists over the past many decades. Microorganisms have been studied via culturable and unculturable (metagenomics) techniques.

The beneficial microbes are the gift from God. They play a diverse and important role for bioeconomy, environment and human systems. (Fig. 1). Humans have evolved together with the beneficial microbes that inhabit animal bodies and create complex, niche–habitat- specific, ecosystems relentlessly adapted to changing host physiology. Oral sites harbor a particular diversity of microbial communities, similar in complexity to the microbial communities of the gut, and tend to be pre-dominated by different species of *Streptococcus*. Microbiomes colonizing the skin depend on the skin properties and are predominantly *Staphylococcus*, *Propionibacterium*, and *Corynebacterium* [3]. Another important niche for bacteria is human milk. Human milk is known to consist of a diversity of microbial communities. Most of the microorganisms isolated from milk belong to *Staphylococcus* sp., *Streptococcus* sp., *Lactobacillus* sp., and *Bifidobacterium* sp., where the latter two genera have a long history of their use as probiotics [4]. Studies have shown the role of microbes presents in human milk in the infant's gut. The bacterial communities are known to reduce the incidence and severity of infections in the breastfed infant by diverse mechanisms, including the production of antimicrobial compounds, competitive exclusion and increasing production of mucine, and reducing, intestinal permeability thereby improving the intestinal barrier functions [5].

Plants have a plethora of microbes, which they recruit from their surrounding environment, especially from the soil. They are known to harbor microbes in the diverse parts of the plant, including the surface of above-ground (phyllosphere/ epiphytic), below-ground parts (rhizosphere), and interior tissues (endophytic). The root microbiome is generally derived from the surrounding, which may transfer from one part to another via a vertical route (Fig. 2). Generally, microbes interact with plants, because of nutrients and shelter as plant, secretes an extensive variety of useful organic compounds such as sugars, natural acids, & vitamins. These organic compounds are utilized by microbes as supplements. In return, microbes also benefit the plants by releasing miniature molecules, phyto-hormones, and volatile compounds that straightforwardly or in a roundabout way immunize the plant and enhance plant growth and development. Diverse microbial communities belonging to all three domains (archaea, bacteria, and eukarya)

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have been reported from the diverse parts of plants [6, 7] (Fig. 1).

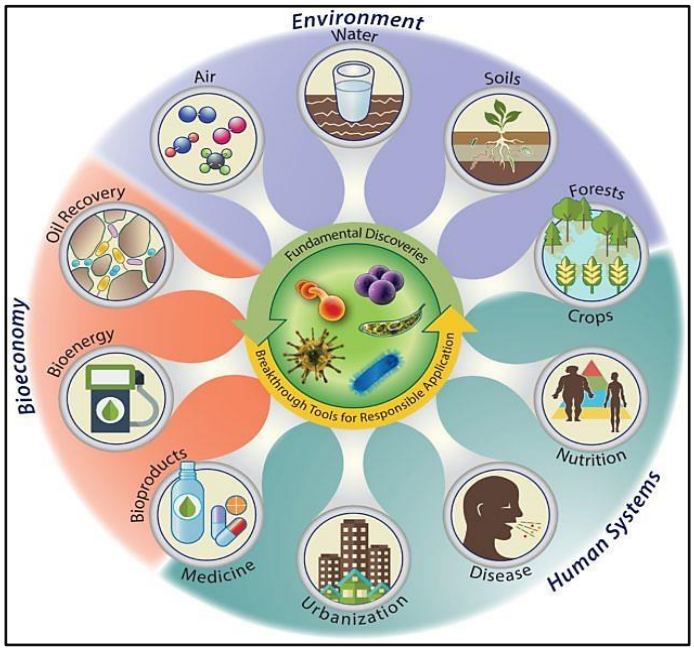

Fig. 1: The potential impacts of a unified microbiomes initiative to understand and responsibly harness the activities of microbial communities (Credit: Diana Swantek, Berkeley Lab).

The phyllosphere or the aerial plant surface is one of the compartments of the plants in which diverse groups of microbes reside. The phyllosphere or epiphytic microbiomes are known to harbor different microbes such as bacteria, viruses, filamentous fungi, yeast, algae, and occasionally nematodes and protozoa. At phylum level bacterial communities mainly belong to the Actinomycetota, Bacillota, Bacteroidetes, and Pseudomonadota. The members of Alphaproteo bacteria and Gammaproteo bacteria are the most dominant. At the genus level, the studies have suggested that the most dominant genera are *Arthrobacter bacillus*, *Methylobacterium*, *Massilia*, *Pseudomonas*, and *Pantoea* [9]. Talking about another compartment of the plants, the endosphere also harbors a diverse group of microbes. In this compartment, the microbes reside inside the host plant including internal tissues of the roots, stem, leaves, and seeds. These types of microbes residue inside the plant without causing any harm. The microbial community inside the plants is predominantly composed of the bacterial phyla Proteo-bacteria, Actinobacteria, Bacteriodetes, and Firmicutes followed by the fungal phyla Ascomycota and Basidiomycota [7]. On the other hand, rhizospheric microbes, i.e. microbes living in the soil associated with roots, enclose the microbial world. Phyla *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* are the major phyla of the rhizospheric microbiomes [10].

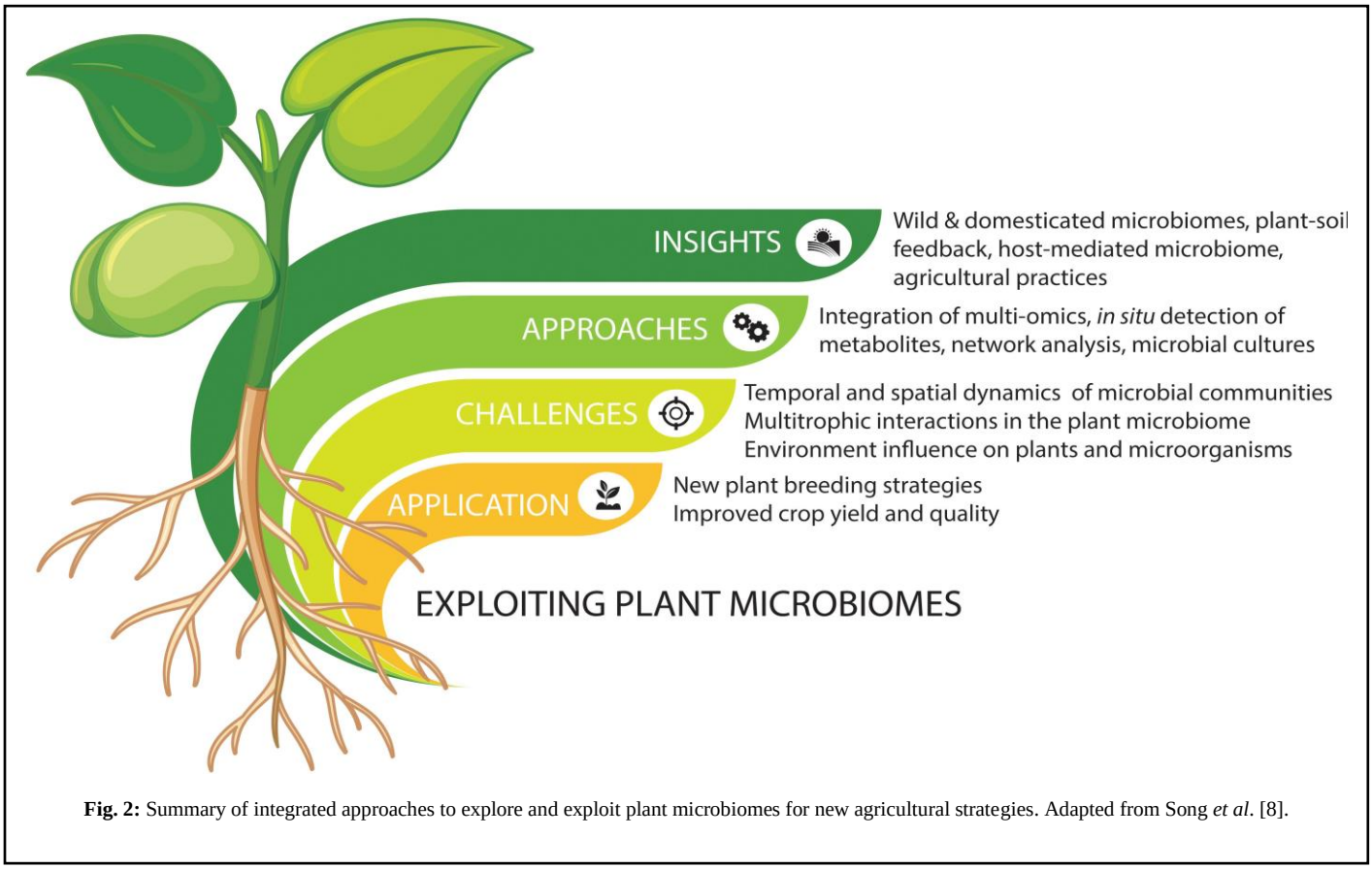

Fig. 2: Summary of integrated approaches to explore and exploit plant microbiomes for new agricultural strategies. Adapted from Song *et al*. [8].

All these diverse microbial communities associated with the plants have been recognized to have various applications in the different sectors including agriculture, environment, as well as industries. In the agriculture sector, plant microbiomes could be used as bioinoculants, biofertilizers and biopesticides, which are among the best applications of these microbes as there is an urgent need for a sustainable approach. Phytomicrobiome promotes plant growth through various mechanisms (direct and indirect). The microbes promoting plant growth via direct mechanisms such as biological N2-fixation, minerals (P, K, Zn, and Se) solubilization, production of Fe-chelators. Plant growth regulators (auxin, gibberellins, and cytokinin) are often known as biofertilizers [11]. On the other hand, microbes indirectly promote plant growth through mechanisms like the production of ammonia, hydrogen cyanide, siderophores, and 1-aminocyclopropane-1-carboxylic acid (ACC) that act as biopesticides. Microbes also help in alleviating biotic and abiotic stress [12].

Apart from the agricultural and environmental applications of plant microbiomes, they also has industrial applications. Phytomicrobiomes, especially endophytic microbes, are known to produce several bioactive secondary metabolites and enzymes with have a wide range of applications in the industries like food, pharmaceuticals, detergents, and biorefineries [13]. In a study, *Huperzia serrata* fungal endophyte *Penicillium spinulosum* was reported to release anti-acetylcholinesterase secondary metabolites, which could be used as a drug for the treatment of Alzheimer's disease [14]. In another report, PGP rhizobacterium, *Paenibacillus polymyxa* is reported for degradation of lignocellulose biomass as well as production of biofuel [15].

Soil is a dynamic, living matrix that forms an essential part of the diverse terrestrial ecosystems. It is a critical resource for agricultural production, food security, and maintenance of most life processes. Soil is considered a storehouse of microbial activity [16]. There is an estimation that one gram of typical soil contains around 90–100 million bacteria and about 2×10^5 fungi, with the majority of these organisms being located around the roots of plants [17]. These microbes either have a beneficial, neutral, or harmful relationship with the plants. Beneficial microbes that promote the growth and development of plants are plant growth-promoting (PGP) microbes. Microbes drive numerous processes needed for robust plant growth and health. Harnessing microbial functions is the key to productive and sustainable food production. Soil microbiomes are among the most important components of the ecosystem with the potential to enhance soil efficiency and plant growth. Plants require at least 16 macro- and micro-nutrients for their growth and yield.

The deficiency of any of the nutrients in soil adversely affects plant performance and leads to the high demand for chemical fertilizers, which are undoubtedly necessary for the healthy growth of plants but at the same time harmful to the environment as well as, living beings. The use of beneficial soil microbes to increase the bioavailability of nutrients is an effectual, cost-effective, and economical approach for reducing the use of chemical fertilizers and a healthy environment. Soil microbiomes play a key role in stimulating the growth of plants through the production of phytohormones, inhibiting the activity of the plant pathogens, improving the soil structure, and bioaccumulation or microbial leaching of inorganics. Further, microbial communities are known to be effective in bioremediation of polluted soils [18]. Soil microbiomes are thus an effective alternative for a clean and green environment.

Air microbiomes are the microbial flora of aerosols. They consists of a combination of viable and non-viable microbes including archaea, bacteria, fungi, and viruses. The microbes present in the air resemble the soil microbes, especially, bacteria and fungi. The microbiome of air is dominated by the *Bacillus* and *Micrococcus* genera especially from the stratosphere. The air microbiome plays a significant role in the meteorological processes including atmospheric chemistry, air quality, cloud formation, and precipitation [19]. Microbial communities dominate all inland water habitats and the appropriate functioning of an aquatic ecosystem is supported by the rich microbial diversity depending upon the nutrients and prevailing environmental conditions. Microbial diversity in freshwaters is known to comprise the culturable bacterial group, viz., Actinobacteria, Bacteroidetes, Firmicutes, α, β, and γ-Proteobacteria as well as archaea [20]. Fungi also form an important component of aquatic microbial communities through their diversity and functional roles remain poorly characterized. Currently, 3000–4000 fungal species have been classified as aquatic fungi even though global fungal diversity ranges from 0.5 to 10^6 species [21]. Most aquatic fungi have been known to belong to Ascomycetes and Chytridiomycetes, while Basidiomycetes have been reported comparatively less from this ecosystem [22]. The microbial communities in the marine environment have received growing attention as the sources of bioactive compounds and have great potential to increase the number of marine natural products in clinical trials [23].

In conclusion, the tiny and ubiquitous creatures as gifts from God, are playing a diverse and important role in nature, without which the life quality and quantity will be reduced. Beneficial microbes have been well recognized for their applications in agriculture, industry, and environment sectors, which sustain life. After a long period of research on microbes to date not

even 2% of microbial diversity and their roles have been explored, so, the study on microbial species should be continued for diversity and applications.

CONFLICTS OF INTEREST

Author declares that there are no conflicts of interest.

REFERENCES

1. Ursell LK, Metcalf JL, Parfrey LW, and Knight R. Defining the human microbiome. Nutr Rev 2012; 70:S38-S44. https://doi.org/10.1111/j.1753-4887.2012.00493.x
2. Mackie RI, Sghir A, and Gaskins HR. Developmental microbial ecology of the neonatal gastrointestinal tract. Am J Clin Nutr 1999; 69:1035s-1045s. https://doi.org/10.1093/ajcn/69.5.1035s
3. Grice EA, Kong HH, Conlan S, Deming CB, Davis J, Young AC, et al. Topographical and temporal diversity of the human skin microbiome. Science 2009; 324:1190-1192.
4. Gomez-Gallego C, Garcia-Mantrana I, Salminen S, and Collado MC. The human milk microbiome and factors influencing its composition and activity. Semin Fetal Neonatal Med. 2016. 21:400-405. https://doi.org/10.1016/j.siny.2016.05.003
5. Yadav AN, Kour D, and Yadav N. Beneficial microorganisms for healthy soils, healthy plants, and healthy humans. J Appl Biol Biotechnol 2023; 11:i-v. https://doi.org/10.7324/JABB.2023. 148173
6. Verma P, Yadav AN, Khannam KS, Kumar S, Saxena AK, and Suman A. Molecular diversity and multifarious plant growth promoting attributes of Bacilli associated with wheat (*Triticum aestivum* L.) rhizosphere from six diverse agro-ecological zones of India. J Basic Microbiol 2016; 56:44-58. https://doi.org/10.1002/ jobm.201500459
7. Rana KL, Kour D, Kaur T, Devi R, Yadav AN, Yadav N, et al. Endophytic microbes: biodiversity, plant growth-promoting mechanisms and potential applications for agricultural sustainability. Antonie van Leeuwenhoek 2020; 113:1075-1107. https://doi.org/10.1007/s10482-020-01429-y
8. Song C, Zhu F, Carrión VJ, and Cordovez V. Beyond plant microbiome composition: Exploiting microbial functions and plant traits via integrated approaches. Front Bioeng Biotechnol 2020; 8:896. https://doi.org/10.3389/fbioe.2020.00896
9. Yadav AN, Kumar V, Dhaliwal HS, Prasad R, and Saxena AK. Microbiome in Crops: Diversity, Distribution, and Potential Role in Crop Improvement, in Crop improvement through microbial Biotechnology. 2018, Elsevier: Amsterdam. p. 305-332. https://doi.org/10.1016/B978-0-444-63987-5.00015-3
10. Kour D, Rana KL, Yadav N, Yadav AN, Kumar A, Meena VS, et al., Rhizospheric Microbiomes: Biodiversity, Mechanisms of Plant Growth Promotion, and Biotechnological Applications for Sustainable Agriculture. In: Plant Growth Promoting Rhizobacteria for Agricultural Sustainability: From Theory to Practices 2019, Springer Singapore: Singapore. p. 19-65. https://doi.org/10.1007/978-981-13-7553-8_2
11. Kour D, Rana KL, Yadav AN, Yadav N, Kumar M, Kumar V, et al. Microbial biofertilizers: Bioresources and eco-friendly technologies for agricultural and environmental sustainability. Biocatal Agric Biotechnol 2020; 23:101487. https://doi.org/ 10.1016/j.bcab.2019.101487
12. Kaur T, Devi R, Kour D, Yadav A, Yadav AN, Dikilitas M, et al. Plant growth promoting soil microbiomes and their potential implications for agricultural and environmental sustainability. Biologia 2021; 76:2687–2709. https://doi.org/10.1007/s11756-021-00806-w
13. Yadav AN, Kour D, Kaur T, Devi R, Yadav A, Dikilitas M, et al. Biodiversity, and biotechnological contribution of beneficial soil microbiomes for nutrient cycling, plant growth improvement, and nutrient uptake. Biocatal Agric Biotechnol 2021; 33:102009. https://doi.org/10.1016/j.bcab.2021.102009
14. Wang Z, Ma Z, Wang L, Tang C, Hu Z, Chou G, et al. Active anti-acetylcholinesterase component of secondary metabolites produced by the endophytic fungi of *Huperzia serrata*. Elect J Biotechnol 2015; 18:399-405. https://doi.org/10.1016/j.ejbt. 2015.08.005
15. Weselowski B, Nathoo N, Eastman AW, MacDonald J, and Yuan Z-C. Isolation, identification and characterization of *Paenibacillus polymyxa* CR1 with potentials for biopesticide, biofertilization, biomass degradation and biofuel production. BMC Microbiol 2016; 16:244. https://doi.org/10.1186/s12866-016-0860-y
16. Devi R, Kaur T, Kour D, Yadav A, Yadav AN, Suman A, et al. Minerals solubilizing and mobilizing microbiomes: A sustainable approach for managing minerals' deficiency in agricultural soil. J Appl Microbiol 2022; 133: 1245–1272. https://doi.org/10.1111/ jam.15627
17. Glick BR. Soil microbes and sustainable agriculture. Pedosphere 2018; 28:167-169. https://doi.org/10.1016/S1002-0160(15)60020-7
18. Kumar A, Yadav AN, Mondal R, Kour D, Subrahmanyam G, Shabnam AA, et al. Myco-remediation: A mechanistic understanding of contaminants alleviation from natural environment and future prospect. Chemosphere 2021; 284:131325. https://doi.org/10.1016/j.chemosphere.2021.131325
19. Tignat-Perrier R, Dommergue A, Vogel TM, and Larose C. Microbial Ecology of the Planetary Boundary Layer. Atmosphere 2020; 11:1296. https://doi.org/10.3390/atmos11121296
20. Yadav AN, Yadav N, Kour D, Kumar A, Yadav K, Kumar A, et al., Bacterial community composition in lakes, In: Freshwater Microbiology. 2019, Academic Press. pp. 1-71. https://doi.org/10.1016/B978-0-12-817495-1.00001-3
21. Grossart H-P and Rojas-Jimenez K. Aquatic fungi: targeting the forgotten in microbial ecology. Curr Opin Microbiol 2016; 31:140-145. https://doi.org/10.1016/j.mib.2016.03.016
22. Shearer CA, Descals E, Kohlmeyer B, Kohlmeyer J, Marvanová L, Padgett D, et al. Fungal biodiversity in aquatic habitats. Biodiver Conser 2007; 16:49-67. https://doi.org/10.1007/s10531-006-9120-z
23. Waters AL, Hill RT, Place AR, and Hamann MT. The expanding role of marine microbes in pharmaceutical development. Curr Opin Biotechnol 2010; 21:780-786. https://doi.org/10.1016/j.copbio.2010.09.013

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