Plant–Microbe Interactions: Mechanisms, Applications, and Future Directions

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Abstract
Plant–microbe interactions (PMIs) are fundamental to plant health and ecosystem functioning. Plants host complex microbial communities across the rhizosphere, endosphere, and phyllo sphere that affect nutrient acquisition, stress tolerance, and immunity [1–3]. Recent advances in omics, synthetic community studies, and imaging have accelerated our mechanistic understanding and translation into agriculture [4–6]. This review synthesizes current knowledge of PMI mechanisms, microbial community assembly, immune responses, and applications in biocontrol, biofertilization, and phytoremediation. We highlight key technologies (metagenomics, metabolomics, genome editing) and propose research priorities for predictive microbiome engineering [7,8].

Keywords: plant–microbe interactions; rhizosphere; microbiome; biocontrol; omics; sustainable agriculture

1. Introduction
The plant halobiont concept recognizes plants and their associated microbiota as an integrated unit influencing health and productivity [1]. Early research focused on pathogenic and mutualistic symbioses (e.g., rhizobia, mycorrhizae) [9], but metagenomic approaches have revealed a diverse microbiome that mediates plant responses to biotic and abiotic stress [2,10]. Understanding and managing PMIs can reduce fertilizer and pesticide use, supporting sustainable agriculture [3,5].

2. Types of plant–microbe interactions
PMIs encompass mutualism, commensalism, and pathogenicity [11]. Beneficial microbes such as Rhizobium and arbuscular mycorrhizal fungi enhance nutrient uptake [12,13], while PGPRs like Pseudomonas fluorescens promote growth and immunity [14]. Conversely, pathogens manipulate plant signaling to facilitate colonization [15]. Microbe–microbe interactions (competition, syntropy, antibiosis) shape community stability and host outcomes [16].

3. Mechanisms underpinning PMIs
Plants secrete exudates containing sugars, amino acids, and secondary metabolites that recruit beneficial microbes [17,18]. Microbial signals such as lipo-chit oligosaccharides and VOCs reciprocally affect plant development [19,20]. Microbes influence hormone homeostasis—producing auxins, cytokinin, and ACC deaminase—to enhance growth under stress [21].

Plant immune receptors detect MAMPs and trigger PTI and ISR responses [22,23]. Beneficial microbes can induce ISR through jasmone and ethylene pathways, strengthening defenses against pathogens [24].

4. Microbiome assembly and stability
Microbiome assembly is determined by host genotype, soil type, and management practices [25]. Priority effects and keystone taxa strongly influence stability and function [26]. Network analyses have identified core and accessory taxa essential for resilience [27].

5. Technological advances
Omics approaches—metagenomics, met transcriptomics, metabolomics—reveal active metabolic processes during PMIs [4,28]. Spatial imaging and single-cell methods localize microbial activity within roots [29]. Synthetic communities (SynComs) enable reproducible, mechanistic studies [30]. CRISPR tools and metabolic modeling facilitate microbial engineering for targeted benefits [31].

6. Applications
Microbial inoculants serve as biofertilizers (N-fixers, phosphate-solubilizers) [32], biocontrol agents [33], and stress mitigators under drought or salinity [34]. Microbiome engineering aims to create predictable synthetic consortia adapted to host genotype and soil [35].Plant–microbe partnerships are also crucial in phytoremediation, enhancing pollutant degradation and metal sequestration [36].

7. Challenges
Field reproducibility remains a key limitation due to context dependency [37]. Cultivation bottlenecks and ecological risks constrain application [38]. Future efforts should integrate predictive modeling and trait-based microbe selection [39].

8. Future directions

Emerging priorities include:

Predictive Phyto biome ecology integrating omics and AI [40] Trait-based microbial discovery emphasizing metabolite function over taxonomy [41] Host breeding for beneficial microbiomes [42] Field-scale testing and regulatory harmonization [43]

9. Conclusion

PMIs are central to sustainable crop production. Integrating ecological, molecular, and computational approaches will enable rational microbiome design. Future progress depends on linking lab discoveries with real-world agricultural systems through predictive, field-validated frameworks.

References

1. Berg G, et al. The plant microbiome explored: implications for experimental botany. J Exp Bot. 2020;71(6):1789–1795.
2. Mendes R, et al. The rhizosphere microbiome: significance of plant–microbe interactions for plant growth and health. FEMS Microbiol Rev. 2013;37(5):634–663.
3. Compant S, et al. Use of plant growth-promoting bacteria for biocontrol of plant diseases: principles, mechanisms, and prospects. Soil Biol Biochem. 2019; 133:1–14.
4. Jacoby RP, et al. The role of soil microorganisms in plant mineral nutrition—current knowledge and future directions. Soil Biol Biochem. 2017; 115:54–67.
5. Bakker PAHM, et al. Microbe-assisted crop production: recent advances and future prospects. Microbe Biotechnology. 2020;13(5):1346–1352.
6. Oyserman BO, et al. Predicting microbiome function: from genes to ecosystems. Trends Microbiol. 2018;26(7):531–543.
7. Busby PE, et al. Research priorities for harnessing plant microbiomes in sustainable agriculture. PLoS Biol. 2017;15(3): e2001793.
8. de Souza RSC, et al. Unlocking the potential of plant growth-promoting rhizobacteria in agriculture: challenges and opportunities. Appl Soil Ecol. 2020; 150:103478.
9. Oldroyd GED, et al. Signaling in symbiotic and pathogenic plant–microbe interactions. Science. 2021;372(6539): eaba0191.
10. Sasse J, et al. Root exudates shape the root microbiome. Trends Plant Sci. 2018;23(1):25–41.
11. Babalola OO. Beneficial bacteria of agricultural importance. Biotechnol Lett. 2010;32(11):1559–1570.
12. Pozo MJ, Azcón-Aguilar C. Unraveling mycorrhiza-induced resistance. Curr Opin Plant Biol. 2007;10(4):393–398.
13. Smith SE, Read DJ. Mycorrhizal Symbiosis, 3rd ed. Academic Press; 2008.
14. Lugtenberg B, Kamilova F. Plant-growth-promoting rhizobacteria. Annu Rev Microbiol. 2009; 63:541–556.
15. Toruño TY, et al. The plant–pathogen interface: molecular cross-talk between host and pathogen. Annu Rev Phytopathol. 2016; 54:419–441.
16. Durán P, et al. Harnessing plant microbiome interactions for biocontrol: a new framework. Trends Plant Sci. 2018;23(4):342–352.
17. Badri DV, Vivanco JM. Regulation and function of root exudates. Plant Cell Environ. 2009;32(6):666–681.
18. Canarini A, et al. Root exudation of primary metabolites: mechanisms and functions. New Phytol. 2019;223(1):17–40.
19. Tsiknia M, et al. Chemical communication in plant–microbe interactions. Rhizosphere. 2021; 19:100400.
20. Fincheira P, Quiroz A. Microbial volatile organic compounds in the rhizosphere: perspectives and challenges. Plant Soil. 2018;432(1):31–48.
21. Glick BR. Plant growth-promoting bacteria: mechanisms and applications. Scientific. 2012; 2012:963401.
22. Dodds PN, Rathjen JP. Plant immunity: towards an integrated view of plant–pathogen interactions. Nat Rev Genet. 2010;11(8):539–548.
23. Pieterse CMJ, et al. Induced systemic resistance by beneficial microbes. Annu Rev Phytopathol. 2014; 52:347–375.
24. Choudhary DK, et al. Role of PGPR in sustainable agriculture: a review. Eur J Soil Biol. 2011;47(2):85–92.
25. Walters WA, et al. Influence of soil properties and plant genotype on the root microbiome. ISME J. 2018;12(1):1–13.
26. Banerjee S, et al. Keystone taxa in the soil microbiome: an ecological concept. FEMS Microbiol Rev. 2018;42(5):507–523.
27. Toju H, et al. Core microbiomes across plant species. Nat Commun. 2018; 9:2204.
28. Hacquard S, et al. Microbial hubs in plant microbiomes. Nat Rev Microbiol. 2017;15(12):761–773.
29. Bulgarelli D, et al. Structure and function of the bacterial root microbiota. Annu Rev Plant Biol. 2013; 64:807–838.
30. Niu B, et al. Simplified and representative bacterial community of maize roots. Proc Natl Acad Sci USA. 2017;114(12): E2450–E2459.
31. Ravanbakhsh M, et al. Synthetic biology for microbiome engineering. Trends Biotechnol. 2022;40(9):1019–1031.
32. Vessey JK. Plant growth-promoting rhizobacteria as biofertilizers. Plant Soil. 2003; 255:571–586.
33. Raaijmakers JM, et al. Microbial antagonists and biocontrol of soilborne pathogens. Trends Microbiol. 2009;17(8):423–433.

34. Timmusk S, et al. Drought-tolerance engineering via rhizobacteria. Front Microbiol. 2014; 5:36.
35. Herrera Paredes S, et al. Design of synthetic bacterial communities for predictable plant phenotypes. PLoS Biol. 2018;16(2):e2003962.
36. Mishra AK, et al. Molecular insights into plant–microbe interactions for sustainable remediation. Environ Res. 2021; 199:111260.
37. Kaminsky LM, et al. Challenges in plant–microbiome research. Soil Biol Biochem. 2019; 131:255–262.
38. Verbruggen E, et al. Ecological risks of microbial inoculants in agriculture. Biol Fertil Soils. 2021; 57:439–453.
39. Trivedi P, et al. Microbiome interactions shape plant health. Nature Rev Microbiol. 2020; 18:607–621.
40. Toju H, et al. Predictive microbiome ecology for sustainable agriculture. Curr Opin Microbiol. 2021; 61:76–83.
41. Marco DE, et al. Trait-based microbial ecology. Trends Ecol Evol. 2022;37(5):412–425.
42. Walters KE, et al. Breeding for plant traits that shape beneficial microbiomes. Trends Plant Sci. 2023;28(3):312–325.
43. Sessitsch A, et al. Regulation and future prospects for microbial inoculants. Microbe Biotechnology. 2019;12(6):1322 export this as a. dox