



Manipulating Plant Microbiomes for Sustainable Management of Plant Diseases

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Introduction

Plant diseases remain a major constraint to crop production and are responsible for considerable losses in agricultural systems. Conventional disease management has largely depended on resistant cultivars, chemical pesticides and cultural practices. Although these approaches remain important, repeated and intensive use of chemical pesticides can contribute to environmental contamination, disruption of non-target microorganisms and development of resistant pathogen populations. These limitations have increased interest in biological and ecological approaches that use naturally occurring interactions between plants and microorganisms for disease management. Plants are colonized by diverse microbial communities in the rhizosphere, phyllosphere and endosphere. Collectively, these microorganisms constitute the plant microbiome and influence nutrient acquisition, growth, stress tolerance and plant immunity (Trivedi *et al.*, 2020). Beneficial bacteria and fungi can also restrict pathogen establishment through competition, antibiosis, parasitism and induction of plant defence responses. Consequently, manipulation of plant-associated microbial communities is increasingly being considered as a complementary approach to conventional plant disease management.

The rhizosphere is particularly important because root exudates provide carbon compounds and other metabolites that influence microbial recruitment and community assembly. Plants can select particular microorganisms from the surrounding soil, while the associated microbes can influence plant metabolism and defence. Under pathogen attack, plants may alter their exudation patterns and recruit beneficial microorganisms, a phenomenon often described as a “cry-for-help” response (Andargie *et al.*, 2023). Understanding these interactions provides a basis for developing disease-suppressive microbiomes rather than relying solely on individual microbial antagonists. Recent



advances in metagenomics, metabolomics, high-throughput sequencing and microbial ecology have made it possible to examine plant-associated microbial communities at greater depth. These technologies are providing new opportunities to identify microorganisms and microbial functions associated with disease suppression and to develop strategies for deliberately modifying microbiome composition and activity (Compant *et al.*, 2025).

Plant Microbiome and Disease Suppression

Disease suppression by plant-associated microorganisms can occur through direct and indirect mechanisms. Direct suppression involves competition for nutrients and space, production of antimicrobial compounds, secretion of hydrolytic enzymes and parasitism of pathogens. Beneficial bacteria belonging to groups such as *Bacillus*, *Pseudomonas* and *Streptomyces*, together with antagonistic fungi, have been widely investigated for their ability to restrict plant pathogens. Competition for nutrients is particularly important in the rhizosphere. Beneficial microorganisms can rapidly colonize root surfaces and consume nutrients required by pathogens. Siderophore production is another important mechanism because microorganisms can bind iron and reduce its availability to competing pathogens. Some beneficial bacteria also produce antibiotics and other secondary metabolites that directly inhibit pathogen growth (Andargie *et al.*, 2023).

Indirect disease suppression occurs through stimulation of plant defence. Beneficial microorganisms can activate induced systemic resistance (ISR), priming plants to respond more rapidly to pathogen invasion. This process involves complex interactions among microbial signals and plant hormones, particularly jasmonic acid and ethylene, although salicylic acid-related pathways may also contribute depending on the host–microbe interaction (Trivedi *et al.*, 2020).

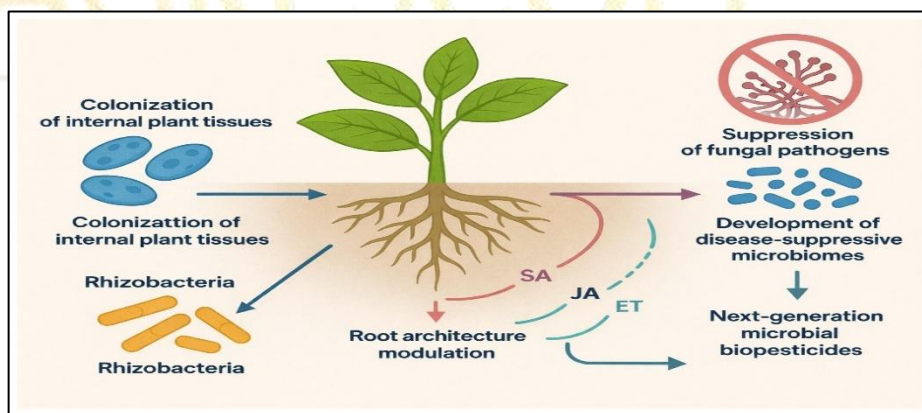


Figure:-Mechanistic role of endophytes and rhizobacteria in plant defence, microbiome assembly and suppression of fungal pathogens. Adapted from Danesh *et al.* (2026).



An important characteristic of microbiome-mediated resistance is that disease suppression does not necessarily depend on one microbial species. A diverse microbial community may provide several complementary functions, including nutrient competition, antimicrobial production, immune stimulation and ecological exclusion of pathogens. Therefore, maintaining a functionally active microbial community may be more reliable than introducing a single microbial antagonist.

Factors Affecting Microbiome Assembly and Disease Suppression

The composition of the plant microbiome is influenced by both biotic and abiotic factors. Plant genotype, developmental stage, root exudates, soil type, pH, nutrient availability, temperature, moisture and agricultural practices can all influence microbial community assembly. Because these factors interact, changing one component does not necessarily result in predictable changes in microbiome function (Andargie *et al.*, 2023). Root exudates are particularly important in shaping the rhizosphere microbiome. Plants release sugars, amino acids, organic acids, phenolics and other compounds into the surrounding soil. These substances provide nutrients for microorganisms and can influence the recruitment of particular microbial groups. During pathogen infection, changes in root metabolism and exudation may favour microorganisms capable of contributing to disease suppression.

Soil properties also strongly influence microbiome-mediated disease management. Soil pH and nutrient availability can affect microbial diversity and the abundance of beneficial microorganisms. Organic amendments, compost, crop rotation, cover crops and reduced tillage can modify soil microbial communities and may increase disease suppressiveness (Chen *et al.*, 2023). The concept of disease-suppressive soil provides an important example of natural microbiome-mediated disease control. In suppressive soils, pathogens may fail to establish, remain at low population densities or cause less severe disease. Suppression may result from the combined activity of many microorganisms or from specific microbial groups with strong antagonistic activity against particular pathogens (Andargie *et al.*, 2023).

Strategies for Manipulating Plant Microbiomes

Manipulation of the plant microbiome can be achieved through several approaches. The simplest strategies involve modification of agricultural practices to favour beneficial microorganisms. Crop rotation, cover cropping, organic amendments and appropriate nutrient management can influence



microbial community composition and improve soil health. Such approaches do not necessarily introduce new microorganisms but modify the environment in a way that favours naturally occurring beneficial populations (Chen *et al.*, 2023). A second approach involves the application of microbial inoculants. Beneficial bacteria, fungi and mycorrhizal microorganisms can be introduced to seeds, roots, soil or plant surfaces. These inoculants may improve plant growth and reduce disease through direct antagonism or stimulation of plant defence. However, their performance can vary under field conditions because introduced microorganisms must compete with established native communities and adapt to environmental conditions.

The limitations of single-strain inoculants have encouraged research into synthetic microbial communities (SynComs). SynComs consist of selected microbial strains combined to perform complementary functions. Rather than depending on one microorganism, a SynCom can potentially combine pathogen antagonism, root colonization, nutrient acquisition and immune stimulation. Recent research has shown increasing interest in rationally designed microbial communities for crop protection (Panchal *et al.*, 2026). Microbiome manipulation can also involve enrichment of naturally occurring beneficial microorganisms. Plants or soils with disease-suppressive characteristics can serve as sources of beneficial microbial communities. These communities may be transferred or enriched in disease-conducive soils. Such approaches aim to restore microbial functions rather than simply adding individual antagonists.

Modern sequencing technologies provide another opportunity for microbiome manipulation. Metagenomic and metatranscriptomic analyses can identify microbial taxa and functions associated with disease suppression. Metabolomic studies can further identify compounds involved in communication among plants, beneficial microorganisms and pathogens. Integrating these datasets may help identify microbial combinations that are more stable and effective under field conditions (Compant *et al.*, 2025).

Microbiome Engineering and Sustainable Disease Management

The concept of microbiome engineering extends beyond simple microbial inoculation. It involves deliberate modification of microbial communities to obtain specific functions, such as pathogen suppression or enhanced plant immunity. Recent work has proposed the use of ecological principles, microbial interaction networks and computational approaches to design more effective microbial communities (Panchal *et al.*, 2026). One major advantage of microbiome-based disease



management is that it can operate through several mechanisms simultaneously. A disease-suppressive community may restrict pathogen growth through competition while also stimulating plant defence. Such multifunctionality may reduce the likelihood that pathogens overcome the control mechanism compared with approaches based on a single mode of action.

However, successful microbiome engineering remains challenging. Introduced microorganisms may fail to establish because of competition with native microbes or unsuitable environmental conditions. Microbial communities can also change with crop genotype, soil characteristics and climate. Compant *et al.* (2025) emphasized that inconsistent performance under field conditions remains one of the major limitations to the wider application of plant microbiome technologies. Therefore, future microbiome-based disease management should focus on function rather than microbial composition alone. The presence of a particular bacterial or fungal taxon does not necessarily guarantee disease suppression. More attention should be given to microbial genes, metabolites, ecological interactions and functional traits responsible for disease reduction.

Future Perspectives

Future research should combine microbiome science with plant pathology, molecular biology, soil science and bioinformatics. High-throughput sequencing can identify microorganisms associated with healthy and diseased plants, while metabolomics and transcriptomics can help determine how these microorganisms influence plant defence and pathogen behaviour. Synthetic microbial communities represent an important direction because they allow researchers to select microorganisms with complementary functions. Recent research has reported the potential of SynComs for crop protection in several crops, including tomato, rice, wheat and maize (Panchal *et al.*, 2026). Nevertheless, their stability and effectiveness under different field environments need further evaluation.

Climate variability should also be considered during microbiome development. Temperature, drought and excessive moisture can influence microbial colonization and activity. A microbial consortium that performs well under controlled conditions may not show the same performance in agricultural soils. Therefore, field validation under different soil and climatic conditions is essential. Another important area is integration of microbiome manipulation with conventional integrated disease management. Microbiome-based approaches should not necessarily replace resistant cultivars, cultural practices or chemical protection. Instead, they can be incorporated with



these methods to reduce disease pressure and potentially decrease dependence on chemical pesticides.

Conclusion

Plant microbiomes represent an important and relatively new resource for sustainable plant disease management. Beneficial microorganisms can suppress pathogens through competition, antimicrobial activity, nutrient limitation and stimulation of plant defence. Manipulation of microbial communities through agronomic practices, microbial inoculants, enrichment of beneficial populations and synthetic microbial communities provides several opportunities for improving crop health. The development of reliable microbiome-based technologies will require a better understanding of microbial community assembly, host–microbe communication and interactions among beneficial microorganisms and pathogens. Recent advances in sequencing, metabolomics, computational biology and synthetic community design are providing tools to move from empirical microbial applications towards more targeted microbiome manipulation. For practical disease management, the most promising approach is likely to involve integration of microbiome manipulation with host resistance, biological control and appropriate agronomic practices. Such an integrated strategy can improve disease suppression while supporting soil health and reducing dependence on chemical inputs. Continued field-based research will be essential for translating microbiome research into consistent and economically viable disease-management technologies.

References

1. Andargie, Y.E., Lee, G.D., Jeong, M., Tagele, S.B. & Shin, J.H. (2023). Deciphering key factors in pathogen-suppressive microbiome assembly in the rhizosphere. *Frontiers in Plant Science*, 14, 1301698. <https://doi.org/10.3389/fpls.2023.1301698>.
2. Chen, W., Modi, D. & Picot, A. (2023). Soil and phytomicrobiome for plant disease suppression and management under climate change: A review. *Plants*, 12, 2736. <https://doi.org/10.3390/plants12142736>.
3. Compant, S., Cassan, F., Kostić, T., Johnson, L., Brader, G., Trognitz, F. & Sessitsch, A. (2025). Harnessing the plant microbiome for sustainable crop production. *Nature Reviews Microbiology*, 23, 9–23. <https://doi.org/10.1038/s41579-024-01079-1>.



4. Panchal, K.P., Sudhir, A. & Prajapati, A.S. (2026). Engineering the plant microbiome: Synthetic community approaches to enhance crop protection. *Frontiers in Plant Science*, 16, 1705289. <https://doi.org/10.3389/fpls.2025.1705289>.
5. Trivedi, P., Leach, J.E., Tringe, S.G., Sa, T. & Singh, B.K. (2020). Plant–microbiome interactions: From community assembly to plant health. *Nature Reviews Microbiology*, 18, 607–621. <https://doi.org/10.1038/s41579-020-0412-1>.

