Integrating soil microbiome insights into crop breeding for enhanced INTEGRATINGstress resilience: A Systematic Review

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ABSTRACT

Soil microbiomes play a critical role in enhancing crop resilience by regulating nutrient cycling, suppressing pathogens, and mediating plant responses to environmental stress. Despite this, conventional crop breeding programmes have largely prioritized plant genetic traits while overlooking the functional contributions of plant-associated microbial communities. In the context of escalating climate change–induced stresses, including drought, salinity, and soil degradation, integrating soil microbiome knowledge into crop breeding represents a promising strategy for sustainable agricultural development. This systematic review synthesizes recent advances in microbiome-assisted breeding, with emphasis on microbial mechanisms underlying plant stress tolerance, approaches for selecting microbiome-compatible crop genotypes, and challenges associated with field-level implementation. A total of 103 peer-reviewed studies were analyzed, highlighting key microbial interactions involving plant growth–promoting rhizobacteria, arbuscular mycorrhizal fungi, and microbe-induced systemic resistance that collectively enhance plant resilience. The review further examines the application of advanced tools such as metagenomics, synthetic microbial consortia, and genome-wide association studies in breeding programmes aimed at optimizing plant–microbiome interactions. Despite significant progress, factors such as environmental variability, competition with native soil microbiota, and regulatory constraints continue to limit large-scale adoption. Addressing these challenges through integrated research efforts and supportive policy frameworks is essential for realizing the full

potential of microbiome-assisted breeding in developing climate-resilient crops and ensuring sustainable food production.

Keywords: Soil microbiome; Plant–microbe interactions; Stress resilience; Microbiome-assisted breeding; Sustainable agriculture

INTRODUCTION

Soil microbiomes play a pivotal role in shaping plant health and productivity by influencing nutrient cycling, disease suppression, and adaptation to stress (Naitam *et al*., 2021). These microbial communities form complex interactions with plants, enhancing root function, promoting growth, and protecting the plants against pathogens (Hassan and Nawchoo, 2022). However, as climate change and environmental stressors such as drought, salinity, and soil degradation continue to threaten global food security, there is an urgent need for innovative strategies to improve crop resilience (Zenda *et al*., 2021).

One promising approach is the integration of soil microbiome insights into crop breeding, leveraging beneficial microbial interactions to enhance plant tolerance to biotic and abiotic stresses (Gonzalez-Guzman *et al*., 2022). Traditional breeding techniques have primarily focused on genetic traits within plants, often overlooking the crucial role of the plant-associated microbiome (Nerva *et al*., 2022). However, recent advancements in metagenomics, microbiome engineering, and systems biology have uncovered the intricate ways in which soil microorganisms contribute to plant adaptation and survival under stress conditions (Meier *et al*., 2021). By incorporating these insights into breeding programmes, scientists can develop crops with enhanced stress resilience, improved nutrient uptake, and sustainable productivity in changing environments (Hafeez *et al*., 2023).

Despite growing research in this area, a comprehensive synthesis linking soil microbiomes to crop breeding remains limited (Huang *et al*., 2022). While numerous studies have explored specific plant-microbe interactions, there remains a gap in translating this knowledge into practical breeding strategies (Yang *et al*., 2021). This review aims to bridge that gap by analyzing recent literature on soil

2

microbiome-assisted crop resilience, discussing the mechanisms underlying plant-microbe interactions, and highlighting potential applications in modern breeding programmes.

This paper is structured as follows: Section 2 outlines the methodology used for literature selection and analysis; Section 3 explores key microbial mechanisms that enhance plant stress tolerance; Section 4 discusses breeding strategies incorporating microbiome insights; and Section 5 identifies future research directions in this field.

METHODOLOGY

2.1 Review Design and Reporting Standard

This study was conducted as a systematic literature review following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines. The PRISMA framework was adopted to ensure transparency, reproducibility, and methodological rigor in the identification, screening, eligibility assessment, and inclusion of relevant studies.

2.2 Literature Search Strategy

A comprehensive literature search was conducted on 17 February 2025 across multiple electronic databases to capture peer-reviewed studies relevant to soil microbiomes and crop breeding for stress resilience. The databases searched included:

- Scopus
- Web of Science (Core Collection)
- Google Scholar (accessed via *Publish or Perish* software, version 8.)

The inclusion of multiple databases was intended to minimize database bias and maximize coverage of relevant literature. Google Scholar was used as a supplementary source to capture additional studies not indexed in Scopus or Web of Science.

The search employed Boolean operators and the following query string:

("soil microbiome" OR "rhizosphere microbiota" OR "plant microbiome") AND ("crop breeding" OR "plant breeding" OR "genetic improvement") AND ("stress resilience" OR "abiotic stress tolerance" OR "biotic stress tolerance")

Search results were restricted to articles published between 2020 and 2024 to ensure inclusion of recent advances in microbiome-assisted breeding.

2.3 Study Identification

The initial database search yielded a total of 200 records. All retrieved records were exported into reference management software, where duplicates were identified and removed.

- Records identified through database searching: 200
- Duplicate records removed: 32
- Records remaining after duplicate removal: 168

2.4 Screening Process

Titles and abstracts of the remaining records were screened independently to assess relevance to the research objective.

Studies were excluded at this stage if they:

- Did not address soil or plant-associated microbiomes
- Were unrelated to crop breeding or stress resilience
- Focused solely on animal, human, or aquatic microbiomes

Following title and abstract screening:

- Records excluded: 63
- Records retained for full-text assessment: 105

2.5 Eligibility Criteria and Full-Text Assessment

Inclusion Criteria

Studies were included if they met all of the following conditions:

- Published in peer-reviewed journals
- Written in English
- Directly addressed soil or plant-associated microbiomes
- Examined crop stress resilience (biotic and/or abiotic)
- Provided insights relevant to crop breeding, genetic improvement, or microbiome-assisted selection

Exclusion Criteria

Studies were excluded if they:

- Were conference abstracts, editorials, opinion pieces, or book reviews
- Focused on non-agricultural systems
- Lacked clear relevance to crop improvement or breeding strategies

4

After full-text assessment:

- Full-text articles excluded: **2** (due to insufficient relevance)
- Final studies included in the review: 103

2.6 Quality Assessment

To ensure methodological robustness, all included studies were subjected to a qualitative quality assessment based on adapted criteria from established systematic review guidelines. Each study was evaluated for:

- Clarity of objectives
- Appropriateness of experimental or analytical design
- Relevance of microbiome–plant interactions to stress resilience
- Strength of evidence linking microbiomes to breeding or crop improvement

Only studies meeting minimum quality thresholds were retained for synthesis.

2.7 Data Extraction

From the final set of **103 studies**, relevant data were systematically extracted using a standardized data extraction form. Extracted information included:

- Crop species and stress type (drought, salinity, heat, pathogens, etc.)
- Microbial groups involved (e.g., PGPR, AMF, endophytes)
- Mechanisms of stress tolerance (nutrient mobilization, phytohormone regulation, induced systemic resistance)
- Breeding strategies and genetic approaches (GWAS, QTL mapping, genotypic selection)
- Reported limitations and field-level challenges

2.8 Data Synthesis and Analysis

A qualitative thematic synthesis approach was adopted due to heterogeneity in experimental designs and outcome measures across studies. The extracted data were categorized into three major thematic areas:

1. Microbial mechanisms contributing to plant stress tolerance
2. Microbiome-assisted crop breeding strategies
3. Challenges, limitations, and future research directions

Trends in publication frequency and research focus were also analyzed descriptively to identify emerging patterns in microbiome-assisted breeding research.
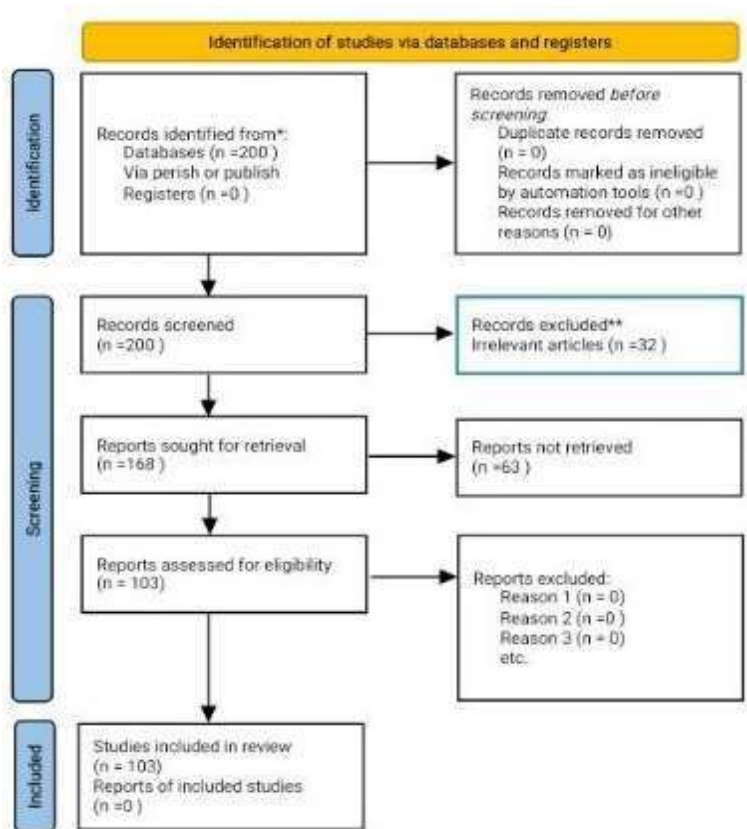
2.9 PRISMA Flow Diagram

The study selection process is summarized using a PRISMA 2020 flow diagram (Figure 1), detailing the number of records identified, screened, assessed for eligibility, and included in the final synthesis.

Figure 1: Prisma Flow diagram

RESULTS

3.1 Study Selection

The systematic literature search and selection process followed the PRISMA 2020 framework. A total of 200 records were initially identified across Scopus, Web of Science, and Google Scholar. After the removal of 32 duplicate records, 168 studies were screened based on titles and abstracts.

Following this screening, 63 studies were excluded due to irrelevance to soil microbiomes, crop breeding, or stress resilience.

Full-text assessment was conducted for 105 articles, of which 2 studies were excluded for insufficient relevance to microbiome-assisted crop improvement. Consequently, 103 peer-reviewed studies met the eligibility criteria and were included in the qualitative synthesis.

3.2 Characteristics of Included Studies

The 103 included studies, published between 2020 and 2024, covered a wide range of crops, stress conditions, microbial taxa, and breeding approaches. The studies predominantly focused on staple crops such as maize, wheat, rice, and legumes, with stress factors including drought, salinity, heat stress, nutrient deficiency, and pathogen pressure.

Based on their primary research focus, the studies were categorized into three thematic groups (Table 3.1):

- Microbial mechanisms enhancing plant stress tolerance
- Microbiome-assisted crop breeding strategies
- Challenges, sustainability considerations, and emerging approaches

Table 3.1: Distribution of Research Themes

Study Category	Number of Studies	Percentage (%)
Microbial mechanisms for stress tolerance	43	41.7
Microbiome-assisted breeding strategies	30	29.1
Challenges, sustainability, and emerging approaches	30	29.1
Total	103	100

Analysis:

Most studies (41.7%) focused on elucidating microbial mechanisms underlying plant stress tolerance, while fewer studies directly

addressed the integration of microbiome insights into breeding programs. This imbalance highlights a persistent gap between mechanistic understanding and applied breeding implementation.

3.4 Microbial Mechanisms Contributing to Plant Stress Tolerance

Across the reviewed literature, soil and plant-associated microbiomes were consistently shown to enhance plant resilience through three dominant mechanisms:

3.4.1 Nutrient Mobilization and Symbiotic Associations

Plant growth-promoting rhizobacteria (PGPR), including *Pseudomonas*, *Bacillus*, and *Azospirillum* species, enhanced nitrogen fixation, phosphorus solubilization, and potassium mobilization under stress conditions. Arbuscular mycorrhizal fungi (AMF) improved phosphorus uptake, root hydraulic conductivity, and soil aggregation, thereby mitigating drought and nutrient stress (Hirayama and Mochida, 2022; Iqbal *et al*., 2023).

3.4.2 Phytohormone Modulation and Stress Signaling

Several studies reported microbial regulation of plant hormones such as auxins, cytokinins, gibberellins, and abscisic acid (ABA). These hormonal adjustments promoted adaptive root architecture, improved stomatal regulation, and enhanced water-use efficiency under drought and salinity stress (Gogolev et al., 2021; Favela et al., 2021).

3.4.3 Induced Systemic Resistance and Antioxidant Activity

Microbial taxa such as *Trichoderma* and *Streptomyces* activate induced systemic resistance (ISR), leading to enhanced pathogen defense. Additionally, microbial inoculation increased antioxidant enzyme activities (superoxide dismutase, catalase, and peroxidase), reducing oxidative damage under heat and drought stress (Wolfgang *et al*., 2023; Yang *et al*., 2021).

3.5 Microbiome-Assisted Crop Breeding Strategies

3.5.1 Selection of Microbiome-Compatible Genotypes

Several studies demonstrated that certain crop genotypes possess an inherent ability to recruit beneficial microbial communities (Huang *et al*., 2022). Genome-wide

8

association studies (GWAS) identified microbiome-associated quantitative trait loci (QTLs), providing a genetic basis for incorporating microbiome traits into breeding programs (Meier *et al*., 2021).

3.5.2 Synthetic Microbial Consortia (SynComs)

The use of synthetic microbial consortia emerged as a promising approach to enhance stress tolerance. AMF-based and multi-strain bacterial consortia significantly improved nutrient uptake, root biomass, and yield stability under stress conditions.

3.5.3 Integration of Multi-Omics Approaches

Metagenomics, transcriptomics, and metabolomics were increasingly applied to characterize functional plant–microbe interactions. These approaches enabled precision identification of beneficial microbial taxa and informed breeding strategies aimed at sustaining favorable microbiome associations.

3.6 Challenges Limiting Large-Scale Implementation

Despite encouraging findings, several constraints were consistently reported:

Challenge	Description
Microbial instability	Inconsistent colonization across environments
Competition with native microbiota	Reduced the establishment of introduced microbes
Environmental variability	Influence of soil type, climate, and management
Regulatory barriers	Lack of standardized approval frameworks
Knowledge gaps	Limited understanding of the genetic control of microbial recruitment

DISCUSSION

The integration of soil microbiome insights into crop breeding represents a promising strategy for enhancing plant stress resilience in the context of climate change, soil degradation, and increasing global food demand. Findings from this systematic review demonstrate that soil and plant-associated microbial communities consistently contribute to improved plant performance under stress conditions through multiple, interacting mechanisms. Importantly, the reviewed evidence highlights that while microbial functions are well characterized, their systematic incorporation into breeding programmes remains limited, underscoring a critical translational gap.

5.1 Microbial Mechanisms Underpinning Plant Stress Tolerance

The findings of this systematic review provide strong evidence that soil and plant-associated microbiomes play a fundamental role in enhancing crop tolerance to a wide range of biotic and abiotic stresses. Across diverse cropping systems and environmental conditions, microbial communities were consistently shown to modulate plant physiological, biochemical, and molecular responses in ways that improve stress resilience. These effects are particularly relevant in the context of climate change, where increased frequency of drought, salinity, heat stress, and nutrient depletion poses significant threats to global food security.

One of the most extensively documented mechanisms through which microbes enhance plant stress tolerance is nutrient mobilization. Nitrogen-fixing bacteria such as *Rhizobium* and *Azospirillum* were frequently reported to increase nitrogen availability, particularly in leguminous crops, thereby supporting plant growth under nutrient-limited conditions. Similarly, phosphate-solubilizing bacteria, including *Pseudomonas* and *Bacillus* species, were shown to enhance phosphorus uptake by converting insoluble soil phosphorus into bioavailable forms (Hassan and Nawchoo, 2022). These microbial processes are especially critical in degraded or low-fertility soils, where chemical fertilizer inputs are often insufficient or unsustainable.

Arbuscular mycorrhizal fungi (AMF) emerged as another key microbial group contributing to stress tolerance. Numerous studies reported that AMF colonization

improved root surface area, water absorption, and nutrient uptake, particularly under drought and salinity stress (Zenda et al., 2021). In addition to their nutritional benefits, AMF enhance soil structure through hyphal networks that improve soil aggregation, thereby increasing water retention and reducing erosion. These multifunctional roles position AMF as vital components of sustainable stress mitigation strategies in agriculture.

Beyond nutrient dynamics, microbial modulation of phytohormones represents a critical adaptive pathway. Several studies documented the ability of plant growth-promoting rhizobacteria (PGPR) to synthesize or regulate hormones such as auxins, cytokinins, gibberellins, and abscisic acid. These hormonal interactions influence root architecture, stomatal conductance, and shoot growth, enabling plants to optimize resource acquisition under stress conditions. For instance, increased auxin production promotes lateral root formation, enhancing access to water and nutrients, while abscisic acid regulation contributes to stomatal closure and improved water-use efficiency during drought.

Another important but often underemphasized mechanism is the production of microbial exopolysaccharides (EPS). PGPR strains such as *Pseudomonas fluorescens* and *Bacillus subtilis* produce EPS that improve soil aggregation and create protective biofilms around roots. These structures help retain moisture in the rhizosphere, reduce osmotic stress, and protect plant roots from desiccation. Such microbial traits are particularly valuable in arid and semi-arid agroecosystems.

Microbe-induced systemic resistance (ISR) also plays a central role in plant defense against pathogens and environmental stressors. The reviewed studies consistently showed that microbial taxa such as *Trichoderma* and *Streptomyces* activate plant defense signaling pathways, leading to the accumulation of defensive secondary metabolites and enhanced resistance to diseases (Chandra et al., 2020). Importantly, ISR does not impose the same metabolic costs as constitutive defense activation, making it an efficient and sustainable mechanism for stress mitigation.

In addition, microbial enhancement of antioxidant defense systems was frequently reported. Increased activity of enzymes such as superoxide dismutase, catalase, and peroxidase helps plants mitigate oxidative damage caused by drought, heat, and salinity

stress (Hafeez et al., 2023). Collectively, these findings demonstrate that microbial mechanisms operate at multiple biological levels, reinforcing the concept that soil microbiomes are integral to plant stress resilience rather than passive environmental components.

5.2 Implications for Microbiome-Assisted Crop Breeding

While the role of soil microbes in enhancing plant stress tolerance is increasingly well documented, the translation of this knowledge into crop breeding programmes remains a developing frontier. The evidence synthesized in this review strongly suggests that microbiome compatibility should be considered alongside traditional genetic traits in modern breeding strategies. Conventional breeding has largely prioritized yield, disease resistance, and agronomic performance, often neglecting plant traits that influence microbial recruitment and interaction (Nerva et al., 2022).

Several studies included in this review demonstrated that plant genotypes differ significantly in their ability to recruit and sustain beneficial microbial communities. Such genotype-specific microbiome assembly has been observed in crops such as maize, wheat, and rice, with direct implications for nutrient uptake efficiency and stress tolerance (Huang et al., 2022). These findings indicate that microbial responsiveness is, at least in part, genetically controlled, providing opportunities for breeders to select varieties that foster advantageous plant–microbe associations.

Microbiome-assisted breeding strategies encompass a range of approaches, including selection of microbiome-compatible genotypes, deployment of microbial inoculants, and the development of synthetic microbial consortia (SynComs). Among these, SynComs have gained increasing attention due to their ability to provide consistent functional benefits by combining multiple microbial strains with complementary traits. Studies evaluating SynComs reported substantial improvements in phosphorus acquisition, root biomass, and drought tolerance in cereal crops, highlighting their potential as scalable stress mitigation tools (Gonzalez-Guzman et al., 2022).

Advances in multi-omics technologies have further expanded the potential for integrating microbiome insights into breeding programmes. Metagenomics,

12

transcriptomics, proteomics, and metabolomics enable detailed characterization of microbial community structure and function, as well as their interactions with host plants. These tools facilitate the identification of microbial taxa and metabolic pathways associated with desirable plant traits, thereby informing precision breeding strategies (Meier et al., 2021).

Genome-wide association studies (GWAS) represent a particularly promising avenue for microbiome-assisted breeding. By linking plant genetic loci to microbiome composition and function, GWAS enables the identification of quantitative trait loci (QTLs) associated with microbial recruitment and activity. Such insights allow breeders to incorporate microbiome-related traits into selection indices, bridging the gap between plant genetics and soil microbiome ecology (Yang et al., 2021).

Despite these advances, the practical integration of microbiome-assisted breeding remains limited. Most studies to date have been conducted under controlled conditions, with relatively few long-term field evaluations. Moreover, breeding programmes rarely include microbiome traits as formal selection criteria, reflecting

both technical challenges and a lack of standardized methodologies. Addressing these limitations will require interdisciplinary collaboration among plant breeders, microbiologists, soil scientists, and agronomists.

Overall, the evidence indicates that microbiome-assisted breeding has the potential to complement conventional genetic improvement by enhancing stress resilience, reducing dependence on chemical inputs, and improving sustainability. However, realizing this potential will require a paradigm shift in breeding objectives to explicitly account for the plant–soil–microbiome continuum.

5.3 Challenges, Limitations, and Future Research Directions

Despite the considerable promise of microbiome-assisted breeding, this review identifies several challenges that currently limit its widespread adoption in agricultural systems. One of the most significant barriers is the variability of microbial establishment and performance across different environments. Soil microbiomes are highly dynamic and are influenced by soil type, pH, moisture, temperature, cropping history, and management practices. As a result,

13

microbial inoculants that perform well under controlled conditions may exhibit inconsistent effects under field conditions.

Competition with native soil microbiota further complicates the effectiveness of introduced microbial strains. Indigenous microbial communities are often well adapted to local soil environments and can outcompete introduced inoculants, reducing their persistence and functional impact. Several studies emphasized the importance of understanding microbial community interactions and ecological compatibility to improve inoculant success (Timaeus et al., 2021). This highlights the need for ecological approaches that prioritize microbial consortia adapted to specific agroecosystems rather than universal solutions.

Regulatory and commercialization barriers also pose major challenges. The absence of standardized regulatory frameworks for microbial products creates uncertainty for manufacturers, researchers, and farmers. In many regions, microbial inoculants are regulated inconsistently or lack clear approval pathways, limiting their adoption at scale (Yang et al., 2021). Establishing robust regulatory guidelines that ensure product efficacy, safety, and quality is essential for

fostering trust and facilitating commercialization.

Another critical limitation is the incomplete understanding of plant–microbe genetic interactions. While evidence suggests that modern breeding practices may have inadvertently reduced beneficial plant–microbiome associations, the genetic basis of this phenomenon remains poorly understood (Maheshwari et al., 2021). Further research is needed to identify plant traits that promote microbial recruitment and to determine how these traits can be reintroduced or enhanced through breeding.

Future research should therefore focus on developing microbial formulations with improved environmental stability and host specificity. Greater emphasis should be placed on long-term field trials that evaluate microbiome-assisted breeding outcomes under realistic agricultural conditions. Integrating microbiome data into genomic selection frameworks and breeding pipelines will also be crucial for translating experimental findings into practical applications.

In addition, exploring plant–microbe coevolution may provide valuable insights into sustainable crop improvement.

Understanding how plants and microbes have co-adapted over evolutionary timescales could inform breeding strategies that restore beneficial interactions disrupted by intensive agriculture. Ultimately,

CONCLUSION

This systematic review demonstrates that integrating soil microbiome knowledge into crop breeding represents a critical advancement in the pursuit of sustainable and climate-resilient agriculture. Across diverse crops and stress conditions, beneficial soil microorganisms consistently enhance nutrient acquisition, improve tolerance to abiotic and biotic stresses, and strengthen plant defense responses through mechanisms such as phytohormone regulation, nutrient mobilization, induced systemic resistance, and antioxidant activation. These findings reinforce the concept that soil microbiomes are not passive components of the agroecosystem but active drivers of plant performance and resilience.

The evidence further indicates that microbiome-assisted breeding offers a viable complement to conventional genetic improvement strategies. By selecting microbiome-compatible genotypes and leveraging advances in multi-omics

overcoming these challenges will be essential for establishing microbiome-assisted breeding as a mainstream approach to sustainable crop production.

technologies and genome-wide association studies, breeding programmes can move beyond a plant-centric paradigm toward a holistic plant–soil–microbiome framework. Such an approach has the potential to enhance crop productivity while reducing dependence on synthetic inputs, thereby contributing to environmentally sustainable agricultural systems.

Despite its promise, the widespread adoption of microbiome-assisted breeding remains constrained by ecological variability, limited field-scale validation, incomplete understanding of plant–microbe genetic interactions, and insufficient regulatory frameworks for microbial products. Addressing these challenges will require interdisciplinary collaboration, long-term field studies, and the development of standardized guidelines to support microbial inoculant deployment and commercialization.

In the context of escalating climate change, soil degradation, and global food demand, harnessing plant–microbiome interactions

represents a strategic and sustainable pathway for future crop improvement. Continued investment in microbiome research and its integration into breeding pipelines will be essential for building resilient agroecosystems capable of supporting long-term food security and ecosystem health.

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