



Microbiome-Assisted Breeding: Engineering the Holobiont in Horticultural Crops

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Abstract— Horticultural crop improvement is moving from a plant-centred model toward a soil-plant-microbiome framework in which host genotype, root-zone biology and the production environment are considered together. Microbiome-assisted breeding (MAB) aims to select plant genotypes that recruit, accommodate or respond to microbial communities capable of improving nutrient acquisition, soil fertility, disease suppression, abiotic-stress resilience, fruit quality and post-harvest performance. This review synthesizes the current basis of holobiont engineering with a primary focus on soil and plant-associated microbes of horticultural crops. The rhizosphere, rhizoplane, root endosphere, seed, flower and fruit compartments are considered as connected but functionally distinct microbial habitats. Important microbial groups include arbuscular mycorrhizal fungi, plant-growth-promoting rhizobacteria, diazotrophs, phosphate-solubilizing bacteria and fungi, actinobacteria, *Trichoderma*, endophytes, yeasts and defined synthetic communities. Recent literature highlights three developments: regulation of rhizosphere microbiomes by host traits and management, microbiome-interactive traits as potential breeding targets, and rhizosphere hybridization or microbiome engineering to build climate-smart and disease-suppressive soils. However, microbial abundance alone is not evidence of function, and inoculants frequently perform inconsistently when they cannot establish within a compatible native community. A practical MAB pipeline should combine host genotyping, soil physicochemical analysis, 16S/ITS or shotgun sequencing, culturomics, metabolomics, causal inoculation, synthetic-community testing and multi-environment validation. The review proposes priority research pathways for fruit, vegetable, spice, ornamental and underutilized crops and emphasizes that plant genotype × microbiome × soil management interactions must be measured explicitly. MAB should therefore complement—not replace—conventional breeding, crop management, conservation and farmer knowledge.

Keywords— holobiont; horticultural crops; soil microbiome; rhizosphere; plant-growth-promoting rhizobacteria; arbuscular mycorrhizal fungi; microbiome-assisted breeding; synthetic communities; climate-resilient horticulture.

I. INTRODUCTION

Horticultural crops are expected to produce high yield, nutritional quality, flavour, appearance and shelf life while facing heat, drought, salinity, soil degradation, emerging pathogens, declining biodiversity and restrictions on agrochemical use. Conventional breeding has delivered major gains, but it generally evaluates the plant phenotype while treating the microbial environment as background. That assumption is increasingly difficult to defend. Roots release carbon compounds, organic acids, amino acids, sugars and signalling molecules that structure the rhizosphere, while soil microorganisms transform nutrients, modify root development, antagonize pathogens and influence plant immunity. The plant is therefore not an isolated genetic entity but a host embedded in a dynamic soil-plant-microbe system [1], [2].

The term holobiont is useful as a systems concept when it describes the interacting host and its microbiota; it should not automatically be interpreted as a single evolutionary unit in every crop or environment. The phytomicrobiome concept places microbial partners at the centre of plant nutrition, resistance and environmental adaptation. Microbiome-assisted breeding extends this view by asking whether a plant genotype can recruit a stable, beneficial and context-compatible microbial community, and whether that host-microbe association remains useful across soils and seasons [3], [4].

Early proposals for microbiome selection suggested reciprocal soil transplantation, artificial ecosystem selection and co-propagation of beneficial microbiota. Recent frameworks have developed this idea toward measurable microbiome-interactive traits, climate-smart crops and plant-microbiome breeding roadmaps. The goal is not simply to add a commercial microbe to soil; it is to select host genotypes and microbial communities that work together under realistic management [5], [6].

This review synthesizes the current state of knowledge on MAB in horticulture, covering soil-plant-microbiome architecture, important microbial groups, mechanisms linking microbes to horticultural traits, breeding frameworks, crop-specific priorities, and challenges for implementation.

II. REVIEW METHODOLOGY

This narrative review was prepared to: (i) explain the soil-plant-microbiome basis of MAB; (ii) identify important microbial groups associated with horticultural crops; (iii) summarize mechanisms relevant to breeding; (iv) integrate recent literature on rhizosphere regulation, microbiome-interactive traits, rhizosphere hybridization and synthetic communities; and (v) propose a practical research pipeline for horticultural breeding programmes.

Literature was identified through targeted searches of journal pages, PubMed Central, publisher platforms and official journal websites using search terms including "microbiome-assisted breeding," "holobiont," "horticultural crops," "rhizosphere microbiome," "plant-growth-promoting rhizobacteria," "arbuscular mycorrhizal fungi," and "synthetic communities." Recent sources from 2024-2026 were prioritized where available, alongside foundational papers necessary to define the field. Species or strain associations are reported as candidate or documented examples only when supported by the cited source; no candidate taxon is presented as universally beneficial.

III. SOIL-PLANT-MICROBIOME ARCHITECTURE

3.1 Soil as the Microbial Reservoir

Soil provides the largest reservoir of microbial diversity available to roots. Its pH, texture, organic carbon, mineralogy, moisture, salinity, redox status, nutrient pools and management history filter which organisms can survive and interact. A plant does not recruit microbes from a neutral background: it recruits from a soil community already shaped by climate, crop rotation, compost, fertilizer, pesticide exposure and previous roots. Consequently, the same inoculant may succeed in one soil and fail in another [7], [8].

3.2 Root Zones as Selection Interfaces

The rhizosphere is soil influenced by the root; the rhizoplane is the root surface; and the endorhizosphere includes microbial habitats inside root tissues. Root exudates feed and select microbes, but plant uptake and microbial metabolism also change soil pH, nutrient availability, enzyme activity and carbon flow. The rhizosphere is thus a selection interface, a nutrient-processing zone and a microbial battlefield in which mutualists, commensals and pathogens compete [9], [10].

3.3 Above-Ground and Reproductive Compartments

Seed, flower, leaf and fruit microbiomes can affect seedling establishment, pollination, disease susceptibility, aroma, ripening and post-harvest decay. For perennial fruit crops, rootstock-scion combinations and plant age may be as important as cultivar identity. A useful breeding programme should therefore sample the entire crop life cycle instead of treating the rhizosphere as the only microbial compartment [11], [12].

TABLE 1
HORTICULTURAL HOLOBIONT COMPARTMENTS AND BREEDING-RELEVANT FUNCTIONS

Compartment	Main Environmental Filters	Breeding-Relevant Functions	Minimum Validation	Key Citations
Bulk soil	pH, texture, organic matter, moisture and management history	Microbial reservoir and soil-health baseline	Physicochemical profile plus community sequencing	[7], [9]
Rhizosphere	Root exudates, oxygen, pH and nutrient gradients	Nutrient mobilisation, disease suppression, stress buffering	Host genotype × soil × season comparison	[7], [10]
Rhizoplane	Root surface chemistry and attachment	Colonisation and microbial competition	Root-wash and microscopy-based confirmation	[11], [12]
Root endosphere	Plant immune filtering and tissue barriers	Systemic signalling and internal stress tolerance	Surface sterilization, re-isolation and tissue localization	[23], [24]
Seed and seedling	Maternal transmission, drying and storage	Early vigour and establishment	Seed-to-seedling tracking and transmission assay	[57], [58]
Fruit and flower	Sugars, acidity, cuticle, humidity and storage	Pollination, quality and post-harvest disease control	Controlled pollination, metabolomics and storage challenge	[23], [24]

3.4 The Holobiont as a Multi-Kingdom System

The horticultural holobiont is not limited to bacteria and fungi. Archaea contribute to ammonia oxidation, methanogenesis and nitrogen transformations; protists graze on bacteria and release mineral nutrients; bacteriophages regulate bacterial populations and horizontal gene transfer; oomycetes and other microbial eukaryotes include both pathogens and ecologically important decomposers. The relative importance of each group changes with crop, tissue, season, soil chemistry and management. A broad holobiont analysis should therefore combine bacterial, archaeal, fungal, oomycete, protist and viral measurements rather than defining the microbiome from a single marker alone [41]-[45].

3.5 Plant Genotype, Rootstock, Scion and Domestication

Host genetics influence the quantity and chemistry of rhizodeposition, root architecture, immune filtering, mucilage production and habitat structure. Rootstock-scion combinations add another layer of genetic control in perennial fruit crops because the rootstock shapes nutrient acquisition and the scion modifies carbon allocation and signalling. Domestication and intensive selection may reduce the ability of crops to recruit beneficial microbes that were present in wild relatives. Wild accessions,

landraces, heritage trees and underutilized horticultural species are therefore valuable reservoirs for discovering host traits that support resilient microbiomes [49]-[53].

3.6 Management as a Component of the Holobiont

Fertilizers, pesticides, irrigation, mulches, compost, cover crops, intercropping and tillage alter microbial recruitment and function. Chemical management may increase crop growth while simultaneously reducing network connectivity or weakening the relationship between microbial structure and plant performance. Organic amendments can supply carbon and stimulate microbial activity, but their effects depend on maturity, nutrient balance, salinity and the starting soil community. Microbiome-assisted breeding must therefore test genotypes under the management systems in which they will be deployed [54]-[58].

IV. IMPORTANT MICROBIAL GROUPS IN HORTICULTURAL CROPS

Microbial functions are often more stable and informative than taxonomic labels. A genus may contain strains with contrasting effects; therefore, every candidate should be resolved to strain or functional-gene level before deployment. The following groups represent the most important and frequently investigated soil and plant-associated partners in horticulture.

4.1 Bacterial Members of the Horticultural Holobiont

Frequently investigated bacterial genera include *Bacillus*, *Pseudomonas*, *Paenibacillus*, *Azospirillum*, *Azotobacter*, *Rhizobium*, *Bradyrhizobium*, *Herbaspirillum*, *Burkholderia*, *Paraburkholderia*, *Enterobacter*, *Serratia*, *Streptomyces*, *Micromonospora*, *Arthrobacter*, *Rhizobacter*, *Massilia*, *Sphingomonas*, *Flavobacterium*, *Lysobacter*, *Variovorax*, *Microbacterium*, *Devosia*, *Rhodococcus*, *Phyllobacterium*, *Methylobacterium*, *Acinetobacter*, *Chryseobacterium*, *Dyella* and *Comamonas*. Their possible functions include nitrogen fixation, phosphate and potassium solubilization, siderophore production, auxin modulation, ACC deaminase activity, volatile organic compounds, pathogen antagonism, biofilm formation and induced systemic resistance. Because some genera contain opportunistic or pathogenic strains, species- and strain-level identification is essential before field use [59]-[63].

4.2 Fungal Members of the Horticultural Holobiont

Important fungal partners include AMF such as *Rhizophagus*, *Funneliformis*, *Claroideoglomus*, *Gigaspora* and *Acaulospora*; beneficial filamentous fungi such as *Trichoderma*, *Penicillium*, *Talaromyces*, *Clonostachys* and selected dark septate endophytes; and yeasts that inhabit flowers, leaves and fruits. Fungal functions include mycorrhizal nutrient exchange, root exploration, mineral weathering, mycoparasitism, antibiosis, enzyme production, stress buffering and post-harvest biocontrol. Inoculation outcomes depend on propagule identity, soil P, host genotype, native fungal competition, water regime and compatibility with bacterial partners [64]-[68].

4.3 Archaea, Protists, Viruses and Oomycetes

Archaea and protists are underrepresented in horticultural microbiome datasets despite their potential importance. Ammonia-oxidizing archaea may contribute to nitrification, while protist grazing can regulate bacterial abundance and nutrient release. Bacteriophages can restructure bacterial networks and may be developed for targeted biological control, although their ecological persistence requires testing. Oomycetes include major pathogens such as *Phytophthora* and *Pythium*, but the broader eukaryotic soil community also includes predators and decomposers that affect disease expression. Future holobiont breeding should include these groups when they are mechanistically relevant to the target trait [69]-[73].

TABLE 2
IMPORTANT MICROBIAL GROUPS IN THE HORTICULTURAL HOLOBIONT

Microbial Group	Representative Taxa Frequently Investigated	Important Functions	Horticultural Examples / Breeding Use	Key Citations
Arbuscular mycorrhizal fungi (AMF)	<i>Rhizophagus irregularis</i> , <i>Funneliformis mosseae</i> , <i>Claroideoglomus</i> , <i>Gigaspora</i> , <i>Acaulospora</i>	Phosphorus and micronutrient uptake, water relations, soil aggregation and stress buffering	Citrus, grape, apple, banana, vegetables and ornamentals; select rootstocks for mycorrhizal responsiveness	[19]-[22], [64]
Plant-growth-promoting rhizobacteria	<i>Bacillus</i> , <i>Pseudomonas</i> , <i>Pae nibacillus</i> , <i>Paraburkholderia</i> , <i>Massilia</i>	IAA, siderophores, phosphate solubilization, volatiles, induced systemic resistance and pathogen antagonism	Tomato, pepper, papaya, citrus, grape and nursery crops; select genotypes with stable recruitment	[14]-[18]
Diazotrophs	<i>Azospirillum</i> , <i>Azotobacter</i> , <i>Herbaspirillum</i> , selected endophytes	Biological nitrogen input, root architecture and nitrogen-use efficiency	Fruit-tree nurseries, vegetables and low-input systems; breed for compatible exudation	[14], [16], [17]
Phosphate- and potassium-solubilizing microbes	<i>Bacillus</i> , <i>Pseudomonas</i> , <i>Aspergillus</i> , <i>Trichoderma</i> , <i>Talaromyces</i>	Organic-acid production, mineral weathering and nutrient release	Acid lime, mandarin, tomato, chilli and root crops; select under reduced P/K supply	[13], [15], [64]
Actinobacteria	<i>Streptomyces</i> , <i>Micromonospora</i> , <i>Actinoplanes</i>	Antibiotics, siderophores, enzymes, decomposition and disease suppression	Orchard soils and suppressive soils; include network connectivity and pathogen inhibition	[35], [36]
Beneficial filamentous fungi	<i>Trichoderma</i> , dark septate endophytes and selected saprotrophs	Mycoparasitism, root colonization, enzyme activity and stress protection	Banana, grape, vegetables and fruit nurseries; test compatibility with AMF and bacteria	[23], [24], [64]
Endophytic bacteria and fungi	<i>Bacillus</i> , <i>Pseudomonas</i> , <i>Burkholderia</i> , yeasts and fungal endophytes	Internal colonization, hormone modulation, systemic resistance and stress tolerance	Seed, root and shoot endospheres; select stable colonization and absence of virulence traits	[41]-[45]
Fruit- and flower-associated yeasts	Host- and environment-specific yeasts; strain-level identification required	Biocontrol, volatile production, aroma, fermentation and decay suppression	Grape, berries, tomato, apple and other fleshy fruits; breed surface chemistry and shelf life	[46], [47]
Defined synthetic communities	Complementary bacterial and fungal members selected by function	Reproducible testing of community function and host response	Research platform for MAB; evaluate establishment and stability in native soils	[12], [23], [24]

V. MECHANISMS LINKING MICROBES WITH HORTICULTURAL TRAITS

5.1 Nutrient Acquisition and Soil Fertility

Microbes improve nutrient supply through biological nitrogen fixation, phosphate solubilization, potassium release, siderophore-mediated iron acquisition, decomposition and enzyme activity. AMF extend the effective soil-exploration network beyond root hairs and can improve phosphorus and micronutrient acquisition. MAB should measure nutrient-use efficiency, isotope fluxes, root architecture and yield under reduced input rather than simply selecting plants with high microbial abundance [13], [14], [15].

5.2 Root Architecture and Carbon Allocation

Microbial auxins, cytokinins, volatile compounds and modulation of plant hormone signalling can affect root length, branching, root hairs and root-to-shoot allocation. Conversely, the plant controls microbial recruitment through exudates and mucilage. Root length, root biomass, exudate chemistry and rhizosphere community composition have been proposed as microbiome-interactive traits. These traits provide a measurable bridge between plant breeding and microbial ecology [16], [17].

5.3 Disease Suppression

Suppressive soils can limit pathogens through competition, antibiosis, parasitism, nutrient sequestration, spatial exclusion and induced systemic resistance. Banana disease-suppressive soils have been associated with bacterial families including Bacillaceae and Streptomycetaceae, and selected *Bacillus* strains have been investigated as biocontrol agents. In fruit crops, rhizosphere hybridization has been proposed as a way to combine microbial diversity from resilient tree systems to create climate-smart suppressive soils. These ideas require careful validation because transferring a community may also transfer pathogens, resistance genes or undesirable functions [18], [19], [20].

5.4 Abiotic-Stress Tolerance

Microbiomes can influence osmotic adjustment, antioxidant responses, ion homeostasis, water-use efficiency and recovery after stress. Candidate assays include drought-recovery growth, sodium/potassium balance, membrane stability, root hydraulic conductance and fruit quality after stress. A major breeding target is not maximum performance in a single stress treatment, but stable performance across variable soil moisture and temperature [21], [22].

5.5 Fruit Quality and Post-Harvest Ecology

Microbial communities associated with fruits can influence decay, aroma and metabolite accumulation. Research on tomato fruit indicates that tissue-associated bacterial communities can relate to flavour and aroma chemistry. Future MAB may therefore combine pre-harvest selection for beneficial rhizosphere recruitment with post-harvest selection for fruit-surface microbial stability. The approach must distinguish beneficial biocontrol organisms from spoilage organisms and opportunistic pathogens [23], [24].

VI. MICROBIOME-ASSISTED BREEDING FRAMEWORK

6.1 Levels of Evidence for MAB Claims

TABLE 3
LEVELS OF EVIDENCE FOR MICROBIOME-ASSISTED BREEDING CLAIMS

Level	Evidence	Permissible Interpretation
1. Association	Taxon or function correlates with a plant trait	Candidate association
2. Recruitment	Genotype or treatment repeatedly enriches the candidate	Host recruitment potential
3. Causality	Isolation, inoculation or SynCom reproduces the phenotype	Functional contribution under tested conditions
4. Stability	Benefit persists across soils, seasons and host genotypes	Breeding or deployment candidate
5. Translation	Economic, safety, regulatory and farmer validation	Deployment-ready technology

6.2 Phenotyping and Microbiome-Enabled Selection

Microbiome-assisted breeding requires phenotyping of both the host and its microbial partners. Host traits may include root length, root hair density, root biomass, exudate composition, nutrient uptake, water-use efficiency, disease severity, recovery after drought, flowering, fruit quality and post-harvest decay. Microbiome traits may include recruitment, colonization, persistence, functional gene abundance, community stability and response to management. A microbiome-enabled selection index can combine host genomic data, microbial features and field performance, but the index should be validated independently across environments [78]-[81].

6.3 Genomic Selection, QTL Mapping and Genome Editing

Host loci associated with microbial recruitment or responsiveness can be identified through genome-wide association studies, QTL mapping, transcriptomics and exudate profiling. Genomic selection models may improve prediction when microbiome data are included, but model performance depends on soil and population similarity between training and validation

environments. Genome editing could modify exudate pathways, immune thresholds, root architecture or signalling components, but editing a host trait may create unintended changes in microbial community composition. Microbiome-informed breeding should therefore measure ecological consequences alongside agronomic traits [82]-[85].

6.4 Synthetic Communities, Consortia and Ecological Restoration

SynComs provide a reproducible tool for testing causality. A rational SynCom should include complementary functions, strain-level safety information, ecological compatibility and functional redundancy. Community assembly can be improved by staged inoculation, seed coating, nursery application, rootstock inoculation, carrier optimization or soil amendments that support establishment. An alternative is ecological restoration: transplanting suppressive soil, compost-derived communities or microbiota from resilient heritage trees. Both approaches require pathogen exclusion, monitoring of persistence and comparison with untreated native communities [86]-[89].

6.5 Microbe-Enabled Breeding Approaches

TABLE 4
MICROBIOME-ASSISTED BREEDING APPROACHES FOR HORTICULTURAL CROPS

Approach	How Microbes Are Used	Best-Suited Horticultural Application	Critical Evidence	Key Citations
Microbiome-informed selection	Microbial community used as a selection environment	Vegetable and nursery crops	Repeatable host ranking with and without the community	[78]-[85]
Host × microbiome factorial breeding	Cultivars or rootstocks tested with defined soils or consortia	Fruit trees and rootstock programmes	Interaction model across independent soils	[86]-[89]
Microbial-assisted recurrent selection	Repeated selection under a functional microbial treatment	Short-cycle vegetables and legumes used in horticulture	Response persists after removal of inoculum	[5], [6], [78]
SynCom-assisted breeding	Defined bacterial/fungal community used to reveal responsive genotypes	Tomato, pepper, banana and grape	Causal function, stability and strain safety	[5], [90]-[92]
Seed and nursery holobiont breeding	Seed endophytes, coating, substrate or graft transmission	Fruit-tree nurseries and transplant crops	Persistence from nursery to field	[29]-[32], [93]-[96]
Exudate-based recruitment breeding	Selection for exudates that recruit target guilds	Drought-, salinity- and low-P-tolerant crops	Exudate chemistry linked to function and performance	[97]-[101]
Microbiome-enabled genomic selection	Host markers plus microbiome and environment data	Perennial and high-value crops	Independent cross-environment prediction	[16], [17], [49], [102]
Genome editing for holobiont design	Editing host recruitment, immunity or root traits	Targeted traits with strong mechanistic evidence	Off-target, non-target and community-level assessment	[82]-[85], [103]-[105]
Rhizosphere hybridization	Functional communities from resilient soils reconstructed for target crops	Orchards and regenerative production	Pathogen exclusion and field persistence	[106]-[109]
Microbe-supported speed breeding	High-throughput screening in controlled environments	Vegetables, ornamentals and protected crops	Field confirmation under realistic soil food webs	[28], [110]-[112]

VII. HORTICULTURAL CROP PRIORITIES

TABLE 5
HORTICULTURAL CROP PRIORITIES FOR MICROBIOME-ASSISTED BREEDING

Crop Group	Priority Trait	Microbial Targets	Breeding Experiment	Key Citations
Citrus and other fruit trees	Rootstock vigour, nutrient-use efficiency, salinity and soil-borne disease	AMF, <i>Azotobacter</i> , <i>Azospirillum</i> , <i>Bacillus</i> , <i>Pseudomonas</i>	Rootstock × inoculum × soil fertility trial over nursery and orchard stages	[90]-[94]
Banana	<i>Fusarium</i> wilt suppression and establishment	<i>Bacillus</i> , <i>Trichoderma</i> , AMF and endophytes	Plantlet microbiome tracking from tissue culture to field	[18], [35], [95]
Tomato, chilli and pepper	Heat, salinity, wilt and fruit quality	<i>Bacillus</i> , <i>Pseudomonas</i> , AMF and fruit-associated yeasts	Cultivar × SynCom × stress factorial design	[25], [95]-[98]
Grape and berry crops	Water stress, aroma and decay suppression	Yeasts, <i>Trichoderma</i> , AMF and rhizobacteria	Preharvest-postharvest microbiome and metabolome continuum	[23], [28], [66]
Apple, peach and pear	Replant disease, rootstock response and soil legacy	AMF, <i>Bacillus velezensis</i> , <i>Pseudomonas</i> , actinobacteria	Long-term orchard soil and rootstock experiment	[90], [92], [94]
Papaya and avocado	Root rot and nutrient acquisition	<i>Bacillus</i> , <i>Pseudomonas</i> , endophytes and AMF	Healthy versus symptomatic plants with causal validation	[95], [96]
Medicinal and underutilized fruits	Survival, phytochemical quality and conservation	Native AMF, drought-adapted rhizobacteria and endophytes	Voucher-linked host genotyping, soil profiling and metabolomics	[99]-[102]

7.1 Fruit Crops

Citrus, mango, guava, apple, peach, pear, grape, banana, papaya, avocado, litchi, pomegranate, strawberry and other fruit crops possess long-lived root systems and strong soil legacies. Priority topics include rootstock-AMF compatibility, replant disease, nutrient-use efficiency, soil-borne pathogens, drought recovery, salinity, fruit flavour and storage decay. Multi-year trials are essential because microbial recruitment changes with tree age, cropping load and orchard management [90]-[94].

7.2 Vegetable, Tuber and Bulb Crops

Tomato, chilli, pepper, eggplant, cucumber, melon, onion, garlic, potato, sweet potato and carrot provide faster-generation systems for testing MAB. These crops allow replicated genotype × soil × microbial treatment experiments and can link rhizosphere function with yield, nutrient density and disease resistance. Potato microbiome-interactive traits and tomato disease-suppressive rhizospheres illustrate how breeding and management should be evaluated together rather than separately [95]-[98].

7.3 Ornamental, Medicinal and Underutilized Crops

Ornamental crops require attention to flowering, rootstock performance and nursery establishment, while medicinal plants require stable phytochemical profiles and authentication. Underutilized fruit trees such as *Ximenia americana* offer opportunities to combine DNA barcoding, soil microbiome profiling, metabolomics and conservation-compatible selection. Local microbial communities should be studied in situ before recommending inoculation or community transfer [99]-[102].

VIII. RECENT DIRECTIONS AND RESEARCH GAPS

8.1 Microbiome-Interactive Traits

Recent work has formalized microbiome-interactive traits as a breeding concept that includes root length, root biomass, exudates and associated rhizosphere communities. In a potato study, cultivar identity had a stronger effect on plant growth, while agricultural treatment had a stronger effect on microbial community composition; chemical management disrupted microbial network relationships and decoupled microbial structure from plant growth. This finding has an important implication for horticulture: breeders may select a host capable of benefiting from microbes, but management determines whether that benefit remains connected to plant performance [25].

8.2 Rhizosphere Microbiome Regulation

Recent reviews emphasize that plant genotype, root traits, exudation, plant development and soil conditions regulate rhizosphere assembly. Breeding for recruitment should therefore use repeated measurements rather than a single sampling date. Root exudate chemistry and microbial function may be more transferable targets than a taxon identified in one location [26], [27].

8.3 Rhizosphere Hybridization

Rhizosphere hybridization proposes combining microbial diversity from different crop or heritage-tree rhizospheres to improve the function of a target crop's soil. Reported fruit-crop examples emphasize nutrient supply, soil enzymes, root-shoot development and defence responses. The concept is promising for regenerative horticulture but remains a hypothesis-generating framework until community transfer, safety and multi-location persistence are demonstrated [28].

8.4 Synthetic Communities and Precision Engineering

Defined SynComs make it possible to test complementarity, keystone functions, metabolite exchange and host specificity. The major challenge is ecological establishment: one or two microbes may fail because they depend on interacting partners, metabolites or native soil conditions. SynCom design should therefore include functional redundancy, compatibility testing and an explicit comparison with native communities [29], [30].

8.5 AI, Multi-Omics and Predictive Breeding

Multi-omics, machine learning and automated phenotyping can help predict host-microbe combinations, but they do not replace causal experiments. Models should include soil variables, management, plant genotype, developmental stage and climate. A prediction that works only within one soil type is not a breeding solution. The most useful future output may be a decision-support model that predicts when a genotype is likely to benefit from a given microbial community and management package [31], [32].

IX. CONSTRAINTS, BIOSAFETY AND IMPLEMENTATION

9.1 Standardization, Reproducibility and Open Data

Comparisons among studies are limited by inconsistent sampling depth, DNA extraction, primer choice, sequencing platform, taxonomic database, metadata and statistical treatment. Future studies should report soil physicochemical data, plant developmental stage, tissue sterilization, negative controls, sequencing depth, quality filtering, taxonomic assignment, functional annotation and repository accession numbers. Raw reads, sample metadata and analysis scripts should be deposited in public repositories. Standardized reporting will allow meta-analysis and reduce overinterpretation of isolated microbial signatures [103]-[106].

9.2 Risk Assessment and Regulatory Translation

Microbial products and community transfers require risk assessment for pathogenicity, antimicrobial resistance, toxin production, allergenicity, non-target effects, horizontal gene transfer and environmental persistence. Regulatory systems may differ for a single strain, a mixed consortium, a soil transplant, a genetically modified host and a genome-edited host. Claims should distinguish a research inoculum from a registered biofertilizer or biocontrol product. A traceable chain of identity, formulation, quality control and field performance is required for responsible translation [107]-[110].

9.3 Farmer-Centered Deployment and Economics

Adoption depends on cost, shelf life, ease of application, compatibility with existing practices, labour requirements and reliability under variable farms. Farmers may value reduced input risk more than maximum yield in a controlled trial. Participatory trials can reveal whether microbial technologies perform under local soil constraints, irrigation schedules and cultivar choices. Economic analysis should include inoculant production, transport, application, yield stability, quality premiums and avoided chemical inputs [111]-[114].

9.4 Data Limitations and Technical Constraints

Microbiome data are compositional: a relative increase in one taxon may reflect a decrease in another rather than true population growth. DNA detection does not prove viability, activity or tissue colonization. Amplicon sequencing can miss rare or poorly amplified organisms, while culture-based methods recover only a fraction of diversity. Multi-environment trials are expensive, and horticultural perennials require several years to evaluate. These limitations should be acknowledged explicitly in MAB manuscripts [33], [34].

9.5 Biosafety and Environmental Considerations

Safety evaluation should include strain-level identification, screening for virulence determinants, antimicrobial resistance, toxin production, allergenicity, non-target effects and environmental persistence. Community transfer from forest or protected-area soils requires collection permits, biodiversity safeguards and benefit-sharing. Commercial formulation must be compatible with nursery substrates, irrigation, fertilizers and crop-protection products. Farmer participation is needed to assess cost, labour, reliability and local acceptability [35], [36].

X. CONCLUSIONS

Microbiome-assisted breeding provides a practical bridge between plant genetics, soil health and microbial ecology. Its strongest promise lies in selecting horticultural genotypes that recruit and respond to beneficial communities for nutrient-use efficiency, disease suppression, climate resilience, fruit quality and post-harvest stability. The central unit of selection is not necessarily a fixed list of microbes, but a repeatable host-microbiome function that performs under a defined soil and management context [37], [38].

For the next decade, research should prioritize standardized soil metadata, voucher-linked host genotypes, strain-resolved functional assays, causal synthetic communities, rootstock-scion-microbiome interactions and multi-location validation. By 2050, successful horticultural systems may combine genomic selection, microbiome-interactive traits, AI-assisted community design and regenerative soil management. The central test will remain whether a host-microbiome combination provides a safe, stable and economically useful benefit in real fields. MAB should therefore be advanced as a complementary layer of precision breeding and soil stewardship [39], [40].

Limitations of this Review: This review is based on a narrative synthesis of published literature rather than a formal systematic review. The examples are selected to illustrate the diversity of approaches and should not be considered exhaustive. The focus is primarily on bacterial and fungal partners, with less attention to archaea, protists, viruses and oomycetes, reflecting the current state of the literature. The review prioritizes recent (2024-2026) and foundational literature, but may not capture all relevant studies.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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