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**Ecological dynamics and microbial  
consortia: Enhancing soil health and  
sustainable agriculture**

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# Ecological dynamics and microbial consortia: Enhancing soil health and sustainable agriculture

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## REVIEW ARTICLE

Sustainable agriculture faces challenges in maintaining soil health and productivity while reducing reliance on chemical inputs. There is a need for eco-friendly practices that can support soil ecosystems and enhance crop yields. This review explores microbial consortia in sustainable agriculture, focusing on their development, application, and interactions within soil ecosystems. It examines the creation and formulation of microbial inoculants, including carrier materials and application methods. This study also discusses advanced techniques like metagenomics, metatranscriptomics, metaproteomics, Stable Isotope Probing (SIP), Fluorescence In Situ Hybridization (FISH), and CRISPR-Cas9 based tracking with barcoding for understanding soil microbes, their functions and fate. This review details the effects of microbial consortia on soil health, community structure, functional roles, and fertility. It highlights the importance of microbial inoculants working in harmony with native soil microbes and the concept of functional redundancy in soil communities. The study reveals how do advanced techniques provide detailed insights into microbial community composition, active genes, and their functions. It also examines beneficial relationships within soil ecosystems and how do changes in ecological dynamics impact soil health and crop yields. Microbial consortia show significant potential for supporting sustainable agriculture and improving soil health. However, challenges still exist that hinder widespread adoption. This review emphasizes the need for long-term studies, cost-effective production methods, and a deeper understanding of microbial interactions in various agricultural systems. This overview provides valuable insights for advancing sustainable farming practices and improving ecosystem management, while acknowledging the complexities and challenges involved in implementing these approaches on a broader scale.

**Keywords:** Ecological factors, Ecosystem management, Inoculant(s) development, Molecular techniques, Soil health

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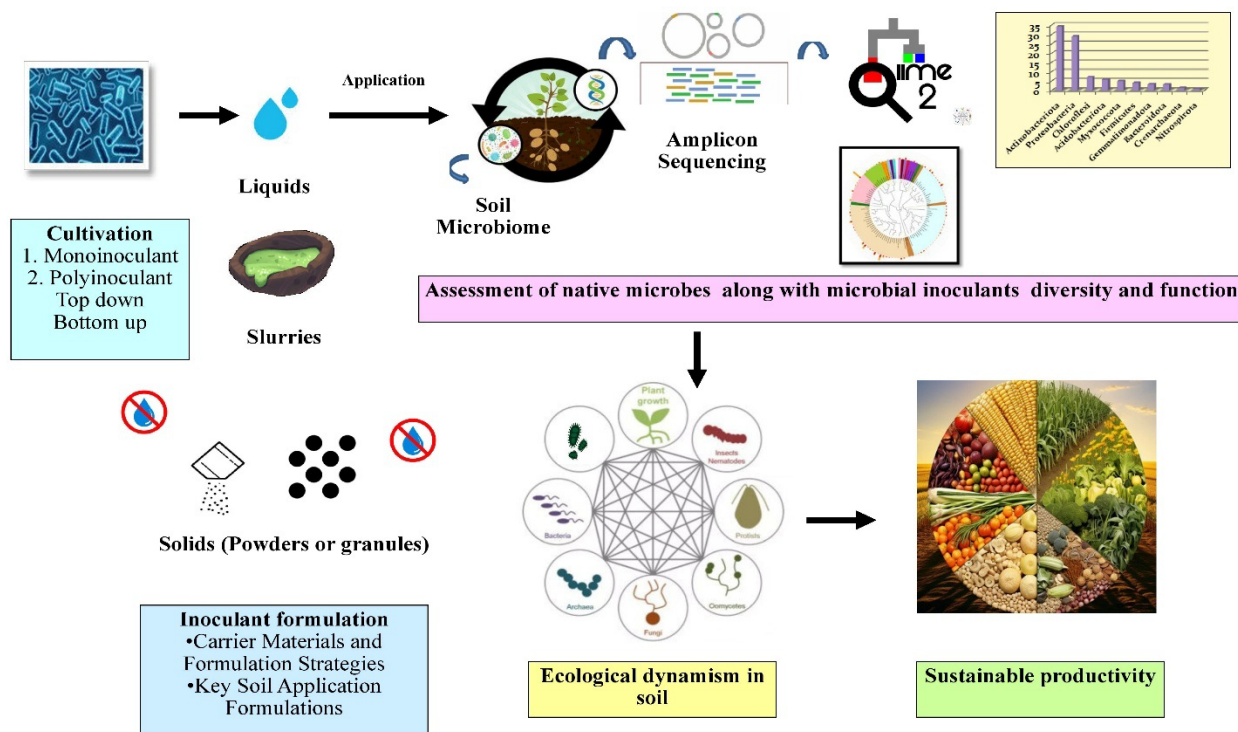
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## INTRODUCTION

Agriculture is shifting towards reducing the use of synthetic fertilizers, which provide essential macro and micronutrients like nitrogen (N), phosphorus (P), and potassium (K). This transition emphasizes the use of organic fertilizers and microbial inoculants to sustain crop yields while minimizing environmental

impact, thereby ensuring food security for a growing population. Unlike synthetic fertilizers that supply nutrients quickly and dissolve easily in water, microbial inoculants and organic fertilizers improve soil health without causing environmental pollution. The overuse of synthetic fertilizers, particularly N and

P, accelerates soil acidification and reduces fertility. In contrast, organic fertilizers rely on microbial activity to convert nutrients, improve soil structure, and boost microbial activity, promoting long-term soil health and crop growth (Adeleke et al., 2021).

Microbial inoculants contain live or dormant cells of specific bacteria and fungi that multiply in the soil rhizosphere, enhancing nutrient uptake. Countries like Brazil, India, China, the United States, and Iran increasingly use these inoculants (Koovalamkadu et al., 2021). The global market for microbial fertilizers is expected to grow by 14% annually, reaching USD 3124.5 million by 2024 (Joshi & Gauraha, 2022). Despite their benefits, challenges persist, including a lack of awareness and unfavorable comparisons to synthetic fertilizers. However, farmers' attitudes are changing, with some adopting partial substitution strategies. Different inoculants produce unique microbial consortia, which can be applied via seeds, seedlings, soil, and foliar methods. Establishing microbial inoculants in the soil requires considering soil type, biomass, moisture, biotic interactions, species specificity, and plant stages (Zhang et al., 2021).

Microbial consortia serve various sustainable agriculture purposes, including nitrogen fixation, mineral and phosphate solubilization, promoting plant growth, managing stress, protecting against pathogens, and bioremediating pesticides. The trend of developing "task-specific microbial consortia" with multiple microbial populations and established rhizospheric interactions is gaining popularity over single-strain populations (Mahmud et al., 2020). Beneficial microorganisms support farming techniques globally. However, ensuring the persistence and functionality of these microbial consortia is crucial for environmental benefits (Tsoi et al., 2019). Monitoring the fate of soil microbial inoculants is essential for optimizing their application and impact on agriculture (Canfora et al., 2021). These consortia, comprising arbuscular mycorrhizal fungi (AMF), plant growth-promoting rhizobacteria (PGPR), and Actinobacteria, contribute significantly to nutrient cycling, soil structure improvement, and disease suppression. They facilitate the decomposition of organic matter, thereby recycling essential nutrients and enhancing nutrient uptake efficiency in plants (Aguilar-Paredes et al., 2023). Moreover, microbial consortia soil regulates carbon dynamics, contributing to efforts to mitigate climate change. By harnessing the potential of these microorganisms, sustainable agricultural practices

can be promoted, ensuring both agricultural productivity and environmental sustainability.

Promoting sustainable practices and addressing environmental concerns in today's agricultural landscape is crucial. Microbial inoculants offer a promising alternative to synthetic fertilizers, providing a cost-effective, eco-friendly, and productive long-term solution, especially for small-scale farmers. To maximize their effectiveness, it is essential to understand their persistence and interaction with native microbiota in the rhizosphere and endosphere. However, there is still a lack of clear understanding of how microbial inoculants integrate into current agricultural practices. Comprehensive studies on their longevity and stability in various conditions are needed. The synergistic effects of different microbial strains and their impact on soil and plant health over multiple growing seasons remain undocumented. Research should focus on the long-term use of these inoculants on soil health and crop productivity, developing cost-effective, scalable production methods, and identifying the most effective microbial strains and consortia for different agricultural systems. Future studies must also examine the interactions between microbial inoculants and native soil microbiota to optimize their use in sustainable agriculture (Malusa and Vassilev, 2014).

## **Development and application of microbial inoculants**

### **Brief description of microbial inoculants**

Microbial inoculants, comprising specific microorganisms like bacteria and fungi from plant roots and root zones, are known as PGPR or, more broadly, plant growth-promoting microorganisms (PGPM). These inoculants boost plant growth and yield by 10%–40% and protect against biotic and abiotic stressors (Khan et al., 2020; Kumar et al., 2018). By colonizing the rhizosphere or plant interior, they enhance soil fertility and promote plant growth through nitrogen fixation, phosphate solubilization, and growth-promoting substances. PGPR and plant growth-promoting bacteria (PGPB) are common terms, but PGPM includes PGPR, PGPB, and Plant Growth-Promoting Fungi (PGPF), covering a wider range of growth-promoting microorganisms.

Microbial consortia found in the rhizosphere or endosphere and composed of cooperating microorganisms enhance plant health and provide disease defense when a biocontrol agent is included. These consortia improve plant growth, soil quality, texture, and fertility (Macik et al., 2020). Microbial

inoculant-based agriculture is crucial for sustainable farming and food safety, offering a solution to address population growth, enhance plant yield, and reduce the negative impacts of excessive agrochemical use on food safety.

Various microorganisms, including bacteria, fungi, and genetically modified organisms, are vital for sustainable agriculture's future. The efficiency and activity of these microorganisms are key to the next green revolution. Plant-microorganism interactions involve both symbiotic and nonsymbiotic pathways. Using effective microorganisms through mono-inoculant and co-inoculant approaches forms diverse microbial consortia, promoting agricultural sustainability. Tables 1 and 2 provide examples of mono-inoculants and co-inoculants.

Nitrogen, a primary nutrient limiting plant growth in agro-ecosystems, is crucial. Biological nitrogen fixation (BNF) is essential for sustainable agriculture and a healthy ecosystem. Mahmud et al., (2020) highlight that BNF reduces synthetic nitrogen fertilizer use, increases plant nutrient content and restores soil health. This can occur through symbiotic BNF in legumes and associative, endosymbiotic, and endophytic nitrogen fixation in non-legumes like rice, wheat, and maize. This process can replace synthetic fertilizers, reducing greenhouse gas emissions (NO) and underground water leaching.

#### Process of creating microbial inoculants

Liu et al. (2023) found that microbial consortia outperform single strains in living soil. These consortia, essential for crop health and productivity (Table 2), support plants from germination to yield enhancement. Their success depends on the production process.

Two approaches, top-down and bottom-up, construct or select microbial consortia with desired functions. The top-down strategy selects natural microbial communities in specialized media or conditions, like temperature, promoting the survival of adapted organisms through successive transfers (Díaz-García et al., 2021).

The bottom-up strategy designs consortia by combining microbial isolates based on their interactions. For instance, a synthetic consortium of lactic acid bacteria and a cellulolytic fungus showcases this method. *Trichoderma reesei* breaks down plant polysaccharides into saccharides, which *Lactobacillus pentosus* ferments. Recently, a combination strategy developed fungal-bacterial

consortia with numerous strains, reducing experimental needs (Lin, 2022).

Rhizospheric lignocellulosic biodegradation in microbial inoculants, along with other fertilizing and growth-enhancing properties, indicates functional stability and enrichment. Table 3 lists various processes for producing microbial inoculants.

#### Carrier Materials and Formulation Strategies for Ecosystem Application

##### Carrier characteristics and functionality

Carrier materials are substances or media used to support, protect, and deliver beneficial microorganisms in biofertilizer formulations. They serve as a vehicle for the microorganisms, maintaining their viability and efficacy from production through storage, transport, and application in agricultural settings. Ideal carriers possess a large surface area, high organic matter content, high water-holding capacity, and near-neutral pH. They create a favorable micro-environment for the microorganisms, protect their viability, support their competition with native soil microflora, and reduce losses from micro-fauna and chemical or physical agents. Carrier materials are crucial for extending the shelf life of biofertilizers, minimizing contamination, and ensuring the effective delivery of beneficial microbes to plants and soil (Sahu & Brahma Prakash, 2016; Macik et al., 2020).

##### Types and methods of inoculation

##### Natural carriers

Natural carriers like sludge ash enhance nodulation and germination and offer a longer shelf life than lignite. Combining *Pseudomonas moraviensis* and *Bacillus cereus* with ground maize straw and sugarcane husk carriers enhances microbial survival rates and aids in saline soil reclamation by reducing electrical conductivity and soil sodium levels. This approach significantly boosts soil and plant nutrient levels (N, P, K, Ca, and Mg) by 30%–40%, demonstrating its effectiveness in improving soil fertility and plant nutrition. Biochar, derived from biomass pyrolysis, stabilizes metals through ionic exchange and electrostatic interactions. Combining biochar with *Bacillus cereus* enhances crop growth, soil microbial biomass, enzyme activity, and nitrogen fixation (Azeem et al., 2021). Cocopeat extends *Pseudomonas* sp. shelf life, outperforming talc powder and farmyard manure (FYM). Sawdust promotes microbial activity, wheat bran supports acid-preferring microbes, and bagasse benefits

**Table 1.** List of Different Microbes Used as Mono-Inoculants and Their Respective Host Plant.

| Microbial inoculant                                                                                                                                                     | Role                    | Crop plant                                                                                                                                                                                    | Reference              |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------|
| <i>Rhizobium leguminosarum</i>                                                                                                                                          | N <sub>2</sub> fixation | Pea group ( <i>Pisum</i> , <i>Vicia</i> , <i>Lens</i> )                                                                                                                                       | Argaw and Mnalku, 2017 |
| Engineered <i>Azotobacter chroococcum</i> HKD15                                                                                                                         | N <sub>2</sub> fixation | Wheat ( <i>T. aestivum</i> L.)                                                                                                                                                                | Bageshwar et al., 2017 |
| <i>Paraburkholderia phytofirmans</i>                                                                                                                                    | P solubilizing          | Wheat ( <i>Triticum aestivum</i> L.)                                                                                                                                                          | Adeleke et al., 2021   |
| <i>Enterobacter hormaechei</i> J146, <i>Pseudomonas frederiksbergensis</i> J158, <i>Pseudomonas moraviensis</i> J16                                                     | Zinc-solubilizing       | Wheat ( <i>Triticum aestivum</i> L.)                                                                                                                                                          | Fahsi et al., 2021     |
| <i>Bacillus mucilaginosus</i> , <i>B. circulans</i> , <i>B. edaphicus</i> , <i>Arthrobacter</i> spp., <i>Acidithiobacillus ferrooxidans</i> , <i>Paenibacillus</i> spp. | Potassium-solubilizing  | Wheat ( <i>Triticum aestivum</i> L.), Maize ( <i>Zea mays</i> L.), Tomato ( <i>Lycopersicon esculentum</i> L.), Cotton ( <i>Gossypium herbaceum</i> L.), Sorghum ( <i>Sorghum bicolor</i> L.) | Etesami et al., 2017   |
| <i>Paecilomyces formosus</i> LWL1 (Fungal endophytes)                                                                                                                   | Temperature stress      | Rice ( <i>Oryza sativa</i> subsp. <i>japonica</i> )                                                                                                                                           | Waqas et al., 2015     |
| <i>Acrocalymma vagum</i>                                                                                                                                                | Heavy metal stress      | Tobacco ( <i>Nicotiana tabacum</i> L.)                                                                                                                                                        | Jin et al., 2018       |

**Table 2.** List of Some Microbes Used as Consortium (Co-Inoculant) and Their Role in Respective Plants.

| Microbial Consortium                                                                                                                                        | Role                                                                                                          | Crop Plant                                                                         | Reference               |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|-------------------------|
| <i>Bacillus sonorensis</i> , <i>Funneliformis mosseae</i>                                                                                                   | Raising healthy, vigorously growing seedlings under polyhouse condition                                       | Tomato ( <i>Lycopersicon esculentum</i> L.), Capsicum ( <i>Capsicum annuum</i> L.) | Desai et al., 2020      |
| <i>Bradyrhizobium japonicum</i> , <i>B. diazoefficiens</i> , <i>Bacillus subtilis</i> , <i>Azospirillum brasilense</i>                                      | Alleviate oxidative damage and increase grain yield during short dry spells.                                  | Soybean [ <i>G. max</i> (L.) Merrill]                                              | Moretti et al., 2021    |
| <i>Rhizoglossus irregularis</i> (AMF); <i>P. putida</i> (Phosphate-solubilizing bacterium, PSB)                                                             | Increased productivity and Phosphorus (P) use efficiency; altered P allocation reduces grain P concentration. | Maize ( <i>Z. mays</i> L.)                                                         | Pacheco et al., 2021    |
| <i>Pseudomonas moraviensis</i> , <i>P. frederiksbergensis</i> , <i>Bacillus halotolerans</i> , <i>Enterobacter hormaechei</i>                               | Metal tolerance: cadmium (Cd), copper (Cu), and nickel (Ni)                                                   | Wheat ( <i>T. aestivum</i> L.)                                                     | Fahsi et al., 2021      |
| <i>Trichoderma harzianum</i> , <i>Bacillus licheniformis</i> , <i>B. megaterium</i> , <i>B. polymyxa</i> , <i>B. pumilis</i> , <i>B. subtilis</i>           | Alleviate oxidative damage and stimulate hormonal cold stress adaptations                                     | Maize ( <i>Z. mays</i> L.)                                                         | Moradtabat et al., 2020 |
| <i>Candida tropicalis</i> , <i>Phanerochaete chrysosporium</i> , <i>Streptomyces globisporus</i> , <i>Lactobacillus</i> sp., <i>Photosynthetic bacteria</i> | Increased carotenoid pigment content; increased enzymatic activities at flowering                             | Marigold ( <i>Tagetes</i> sp.L.), Calendula ( <i>Calendula</i> sp.L.)              | Sharma et al., 2017     |
| <i>Azospirillum brasilense</i> , <i>Phyllobacterium brassicacearum</i>                                                                                      | Growth of plants under drought situations and nutrient limitation                                             | Rice ( <i>O. sativa</i> L.)                                                        | Mishra et al., 2015     |
| <i>Pseudomonas putida</i> , <i>Chlorella vulgaris</i>                                                                                                       | Growth promotion and Arsenic amelioration                                                                     | Rice ( <i>O. sativa</i> L.)                                                        | Awasthi et al., 2021    |

specific microbial functions. The highwater retention capacity of rice husks promotes microbial activity, while the rich N and P content of FYM enhances microbial metabolism (Aloo et al., 2022). Cyanobacteria, used as microbial inoculants in rice fields (Bashan et al., 2014), can be immobilized on natural and synthetic polymers.

### Synthetic Carriers

Synthetic carriers play a pivotal role in developing biofertilizer formulations, providing a controlled and consistent medium for beneficial microorganisms. Key synthetic carriers include polymeric substances such as alginate, methoxypectin, gellan gum, xanthan-locust bean gum, and polyvinyl pyrrolidone

(PVP). These carriers offer advantages like non-toxicity, biodegradability, and gradual release of high colony-forming units (CFU) in the field. For example, alginate beads are widely used for their ability to trap and slowly release microbes, although their high cost and potential for cell death during bio-encapsulation present challenges. PVP serves as a suspending agent and stabilizer in liquid formulations, extending the shelf life of microbial inoculants like *Azospirillum*. Additionally, polymeric clay composites containing nano zinc oxide and zinc fertilizer, combined with zinc-solubilizing microbes, have shown superior performance in zinc release during crop growth, enhancing microbial populations and plant nutrition. Other low-cost synthetic materials such as kaolin,



**Table 3.** Process of Making Microbial Inoculant(s) (Top-Down, Bottom-Up, and Combined Method).

| Method                                                                                                                                                                                                                                                                                                                                       | Source                                                                                                                         | Purpose                                                                     | Reference                       |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|---------------------------------|
| Top-down                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                |                                                                             |                                 |
| <i>Mesorhizobium</i> , <i>Cellulosimicrobium</i> , <i>Pandoraea</i> , <i>Achromobacter</i> , <i>Stenotrophomonas</i>                                                                                                                                                                                                                         | Tree trimmings                                                                                                                 | For lignin (28.7%) and cellulose (10.2%) degradation                        | Fang et al.,2018                |
| Bacteria: <i>Joostella marina</i> , <i>Flavobacterium beibuense</i> , <i>Algoriphagus ratkowskyi</i> , <i>Pseudomonas putida</i> , <i>Halomonas meridiana</i> ,<br>Fungus: <i>Sarocladium strictum</i>                                                                                                                                       | Cultured a salt marsh soil microbiome in six sequential cycles on fresh wheat straw and four cycles on predigested wheat straw | Degradation of lignocellulose under saline conditions                       | Cortes-Tolalpa et al.,2018      |
| Enterobacteriales (fast growers and highly abundant), Actinomycetales, Bacillales, and Lactobacillales                                                                                                                                                                                                                                       | <i>Megathyrsus maximus</i> (Guinea grass) phyllosphere                                                                         | Development/design of a synthetic bio-inoculant to improve silage processes | Díaz-García et al.,2021         |
| Bottom-up                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                |                                                                             |                                 |
| Fungal ( <i>Trichoderma</i> and <i>Aspergillus</i> ) and bacterial strains ( <i>Bacillus</i> , <i>Enterococcus</i> , <i>Lactococcus</i> , <i>Acinetobacter</i> , and <i>Pseudomonas</i> )                                                                                                                                                    | —                                                                                                                              | lignocellulolytic enzyme production                                         | Hu et al.,2017                  |
| <i>Stenotrophomonas maltophilia</i> , <i>Paenibacillus</i> sp., <i>Microbacterium</i> sp., <i>Chryseobacterium taiwanense</i> , and <i>Brevundimonas</i> sp.                                                                                                                                                                                 | Environmental sample                                                                                                           | Lignocellulose Degradation                                                  | Puentes-Téllez and Salles, 2018 |
| Combined                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                |                                                                             |                                 |
| Top-down method:<br>Anaerobic fungi: <i>Piromyces</i> ,<br>Bacteria: <i>Sphaerochaeta</i> and two methanogenic archaea ( <i>Methanosphaera</i> and <i>Methanocoprpusculum</i> )<br>Bottom-up method:<br>Fungi: <i>Neocallimastix californiae</i> and <i>Anaeromyces robustus</i> paired with the methanogen <i>Methanobacterium bryantii</i> | Synthetic Microbial Consortia (rumen and/or hindguts of large mammalian)                                                       | For efficient lignocellulose-to-methane bioconversion                       | Gilmore et al.,2019             |
| Sphingobacteriaceae, Enterobacteriaceae, Pseudomonadaceae, Paenibacillaceae                                                                                                                                                                                                                                                                  | Forest soil                                                                                                                    | Lignocellulolytic Bacterial Consortium                                      | Díaz-García et al.,2021         |

bentonite, perlite, starch, montmorillonite, chitin, humic acid, trehalose, and protein hydrolysate provide mechanical resistance, high cell viability, and effective soil colonization, making them valuable alternatives in biofertilizer formulations (Balla et al., 2022; Vassilev et al., 2020).

### Solid formulations

Solid formulations often use a mixture of peat and clay in forms like powder, granules, and suspensions. Clay, with its large surface area and uniform pore distribution, acts as an effective desiccant and container, while peat provides high water-holding capacity. This combination is used for various microbial inoculants, including ectomycorrhizal and AMF, and microorganisms forming microcolonies. The fluid bed drying (FBD) method enhances plant responsiveness, reduces contamination, and improves survival rates, making it suitable for seed inoculation and other delivery methods (Sahu & Brahma Prakash, 2016).

### Liquid Formulations

Liquid formulations are known for ease of use and as starter cultures, using PVP as a suspending agent and

stabilizer, with glycerol as a carbon source. PVP-enhanced formulations have a longer shelf life, as seen with *Azospirillum*. Polymeric formulations with alginate beads, which are non-toxic and biodegradable, are gradually released in the field, trapping high CFU counts. Liquid metabolite formulations with microbial metabolites like Myc Factors (Mycorrhizal factors role in plant-fungi communication) and extracellular polymeric substances (EPS) promote symbiosis, root colonization, and plant growth. However, high production costs hinder their widespread adoption (Chaudhary et al., 2020).

Both solid and liquid carriers extend shelf life and minimize contamination. The viable cell count, measured in CFU, is vital before application. Liquid carriers maintain higher bacterial loads ( $10^8$  CFU/ml) for 15–24 months and cost less than solid ones. Common methods include seed and soil inoculation, soil drench, and plant inoculation at the seedling stage. Soil inoculation introduces a large bacterial population using granular or liquid inoculants in the furrow under or alongside the seed (Macik et al., 2020). Seed inoculation involves creating a slurry with water and adhesives. Large-scale production in

fermenters includes edible Vanaspati oil (1%–2%) for lubrication and turbidity, *Acacia* powder (1%–2%) for adhesion, glycerol (2.5%–5%) for preservation, and labolene (0.5%–0.8%) to reduce surface tension. Despite the development of many microbial inoculants, few are commercialized due to poor formulations and carrier compatibility, leading to a reliance on synthetic fertilizers (Macik et al., 2020). Different types of carrier materials used for inoculum formulation are mentioned in Table 4.

Key soil application formulations include pre-biotic formulations with liquid or solid carriers, gel formulations with controlled cell release, and post-biotic formulations with cell-free extracts. Enhancing viscosity, stability, and dispersion in liquid preparations improves cell suspension. Carrier materials make handling easier, prolong storage, and enhance efficacy. This method transfers nitrogen-fixing, plant growth hormone-producing, and phosphorus-solubilizing microbes using natural and synthetic carriers (Vassilev et al., 2020).

Current research shows conflicting evidence, ongoing debates, limitations, and knowledge gaps. Shen et al. (2021) found microbial inoculants could positively influence bacterial communities and decrease alpha diversity indices in some treatments. Ladau et al. (2023) discuss the risks of using non-genetically modified microbial inoculants, emphasizing the need for major regulations and understanding these risks. Limitations include the long-term effects on soil microbial communities and interactions between beneficial microbes and phytopathogens in diverse environmental conditions (Wang et al., 2021), and the real-world efficacy of microbial interactions (Mocali et al., 2022). Hashmi (2019) highlights the need for further research on microbial interactions in various nutritional contexts. Canfora et al. (2021) note the lack of research on the persistence and fate of soil microbial inoculants. Liu et al. (2022) discuss the overlooked indirect and cascading effects of microbial inoculants on soil microbiomes and agroecosystem functions. These studies collectively highlight significant gaps in current research and emphasize the need for a more comprehensive understanding of microbial inoculants' behavior and effectiveness in agricultural ecosystems.

### Microbial Contributions to Soil Ecosystems

#### Microbial Community Structure in Soil Ecosystems

Microbes in soil interact with plants in neutral, harmful, or beneficial ways. Neutral interactions involve bacteria, fungi, and viruses in plant

microbiomes without affecting the plants. Pathogenic associations include harmful microorganisms, while beneficial microbes promote plant growth and protect against pathogens. Understanding these interactions is crucial, and recent metagenomics advancements have significantly enhanced our ability to study soil microbial communities. Metagenomics uses DNA to provide a comprehensive view of microbial diversity through 16S rRNA sequencing and function, facilitating numerous studies with next-generation sequencing (NGS) to analyze soil microbial composition and roles (Noman et al., 2021).

A study on Sorghum crops in China used NGS to identify specific bacterial genera, including *Lysobacter*, *Acidibacter*, *Steroidobacter*, and *Blastococcus* along with fungal genera such as *Fusarium* and *Guehomyces*, highlighting their roles in influencing crop yield and protein content through their interactions with the plant and soil environment (Sun et al., 2021). Another NGS-based study in Vietnam revealed a dominance of bacterial communities like Chloroflexi, Proteobacteria, Actinobacteria, Acidobacteria, and Firmicutes in agricultural soil. It found positive correlations between total nitrogen and specific phyla, such as Proteobacteria, Acidobacteria, Firmicutes, and Planctomycetes, and between certain Proteobacteria genera and the phosphorus-solubilizing gene *phoD*, highlighting the influence of soil properties on microbial abundance and phosphorus solubilization (Hegyí et al., 2021).

Disease-suppressive soils (DSS) have been studied since the 1960s for their reduced soil-borne disease incidence despite the presence of a host plant and pathogen. These soils offer an environmentally friendly alternative to pesticides and help combat agricultural productivity decline. The first occurrence of suppressive soil was documented in 1892 by Atkinson, who studied the effects of *Fusarium* wilt on cotton. DSS harbor diverse microbial communities that contribute to disease suppression through various mechanisms (Nisrina et al., 2021; Hjort et al., 2009). Nisrina et al. focused on PGPR in suppressive soils against *Fusarium oxysporum* f. sp. *cubense* in banana plantations using metagenomics. They found higher abundances of Actinobacteria and Betaproteobacteria, with active zinc/manganese transport systems enhancing nutrient availability and inhibiting pathogens. Co-occurrence patterns showed that *Pseudomonas*, *Burkholderia*, and *Streptomyces* were prevalent in suppressive soils. Hjort et al. (2009) used metagenomics and direct DNA extraction from

**Table 4.** List of Different Types of Carrier Materials Used for Inoculum Formulation.

| Carrier material                                                                                                                                              | Microbial inoculant                                                                                                                                                                                                     | Characteristics                                                                                                                                                                                     | Reference                                |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------|
| <b>Natural</b>                                                                                                                                                |                                                                                                                                                                                                                         |                                                                                                                                                                                                     |                                          |
| Composted sawdust                                                                                                                                             | <i>Bradyrhizobium</i> , <i>Rhizobium</i> and <i>Azospirillum</i> ;<br><i>Klebsiella grimontii</i> (MPUS7), <i>Serratia marcescens</i> (NGAS9), <i>Citrobacter freundii</i> (LUTT5)                                      | - Seed inoculation<br>- Good growth and survival of the inoculant strains.                                                                                                                          | Macik et al., 2020; Aloo et al., 2022    |
| Soybean oil or peanut oil loaded with lyophilized cells                                                                                                       | <i>Rhizobium</i> sp.                                                                                                                                                                                                    | - Seed inoculant<br>- Provides more protection than peat-based inoculants. When rhizobia are inoculated on seeds and exposed to conditions of drought and high temperature.                         | Macik et al., 2020                       |
| Wastewater sludge                                                                                                                                             | <i>Sinorhizobium meliloti</i>                                                                                                                                                                                           | - Seed inoculant<br>- The study showed the suitability of using sludge as a carrier because it had the same or a higher potential than peat to support the survival of <i>S. meliloti</i> .         | Macik et al., 2020                       |
| Wheat bran, sugarcane bagasse                                                                                                                                 | <i>Rhizobium</i> , <i>Bradyrhizobium</i> and rock-phosphate-solubilizing fungus <i>Aspergillus niger</i> ; <i>Klebsiella grimontii</i> (MPUS7), <i>Serratia marcescens</i> (NGAS9), <i>Citrobacter freundii</i> (LUTT5) | - Soil inoculant<br>- The number of co-cultured microorganisms was the highest with peat, followed by bran and sugarcane bagasse.                                                                   | Macik et al., 2020<br>Aloo et al., 2022  |
| Vermicast + lignite in different combinations (0:1, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, and 1:0) Charcoal and vermicompost ( <i>Perionyx excavatus</i> )            | <i>Azotobacter chroococcum</i> , <i>Bacillus megaterium</i> , <i>Rhizobium leguminosarum</i>                                                                                                                            | - Biofertilizer formulation                                                                                                                                                                         | Sahu et al., 2016                        |
| Compost and charcoal (50:50)                                                                                                                                  | <i>Azospirillum</i> sp.                                                                                                                                                                                                 | - Seed, Soil, and root-dip treatment<br>- Growth and yield of crop                                                                                                                                  | Sahu & Brahmaprakash, 2016               |
| Nanocarriers including nanoclay, natural char microparticles (NCMPs), nanoclay + alginate, NCMPs + alginate, and natural char nano-particles (NCNPs)+alginate | <i>Pseudomonas putida</i> (PP20), <i>Pseudomonas kilonensis</i>                                                                                                                                                         | - P solubilizing                                                                                                                                                                                    | Safari et al., 2020                      |
| Alginate-perlite dry granule                                                                                                                                  | <i>Rhizobium</i> sp.                                                                                                                                                                                                    | - Soil inoculation<br>- <i>Rhizobium</i> strains survived in dry granules beyond 180 days.<br>- The inoculant can be stored in a dry state without losing much viability.                           | Dey, 2021                                |
| <b>Synthetic</b>                                                                                                                                              |                                                                                                                                                                                                                         |                                                                                                                                                                                                     |                                          |
| Carrageenan (1.5%), sodium alginate (1%), trehalose (10 mM), polyvinyl pyrrolidone (2%), glycerol (10 mM)                                                     | Liquid inoculant of <i>Azospirillum brasilense</i>                                                                                                                                                                      | - Maintains the viability of the cells during the time of storage.                                                                                                                                  | Cortés-Patiño & Bonilla, 2015            |
| Carboxymethyl cellulose (CMC) and starch                                                                                                                      | <i>Rhizobium</i>                                                                                                                                                                                                        | - Soil inoculation promote cowpea ( <i>Vigna unguiculata</i> ) nodulation                                                                                                                           | Dubey et al., 2021                       |
| Sterilized oxalic acid industrial waste                                                                                                                       | <i>Rhizobium</i>                                                                                                                                                                                                        | - Seed inoculation<br>- Multiplication in carrier in ambient temperature up to 90 days.<br>- Carrier sterilization contributed a significant increase in grain yield, nodule number, and N content. | Dey, 2021                                |
| <b>Natural + Synthetic</b>                                                                                                                                    |                                                                                                                                                                                                                         |                                                                                                                                                                                                     |                                          |
| Talc and 1%, carboxymethyl cellulose                                                                                                                          | <i>P. fluorescens</i>                                                                                                                                                                                                   | - Against leaf disease                                                                                                                                                                              | Naik et al., 2020                        |
| Peat moss, a mixture of peat moss plus vermiculite 1:2 (w/w), wheat bran, rice husk, clay, and sodium alginate                                                | <i>Azotobacter chroococcum</i> ; <i>Klebsiella grimontii</i> (MPUS7), <i>Serratia marcescens</i> (NGAS9), <i>Citrobacter freundii</i> (LUTT5)                                                                           | - Effective carrier material preparation                                                                                                                                                            | Raimi et al., 2021;<br>Aloo et al., 2022 |



agar isolates to identify bacterial strains with antifungal and chitinase activities. They studied chitinase genes, revealing their abundance in suppressive soils and identifying key chitinase-producing bacteria like *Streptomyces mutomycini* and *Streptomyces clavifer*. Both studies underscore the importance of microbial diversity and functional interactions in disease suppression.

### Microbial niches and their roles in soil functioning

Soil hosts various microbial niches grouped into five main zones, each with unique communities and functions. The detritosphere, above the soil surface, includes litter, fermentation, and humification layers with significant root, mycorrhizal, and saprophytic fungal activity. The drilosphere consists of soil influenced by earthworms. The porosphere contains water films for bacteria, protozoa, nematodes, and fungal hyphae. The aggregatusphere concentrates microorganisms, and the rhizosphere is influenced by roots and mycorrhizal hyphae (Miller and Lodge, 1997).

The aggregatusphere, crucial for microbial research, divides into macroaggregates and microaggregates. Macroaggregates, larger than 250 µm, decompose quickly, providing organic resources. Microaggregates, smaller than 20 µm, are stable soil units made of mineral, organic, and biotic elements. They influence soil structure, nutrient content, and water movement, affecting microbial diversity. Different aggregate fractions house various bacterial species, such as *Ralstonia* in microaggregates linked to diseases (Totsche et al., 2018).

Soil particle size impacts microbial interactions. Surface roughness within 10–100 nm promotes selective bacterial adhesion, affecting gene transfer and morphology. Bacterial cell sizes (1–2 µm) fit soil microaggregate pores, influencing nitrogen fixation. Fungal hyphae (1–15 µm) and bacterial biofilm in sand enhance aggregate strength and binding. Close bacterial interactions (10–30 µm) within microaggregate pores affect denitrification and quorum sensing, showing how soil particle sizes outline microbial interactions and soil functions. Prokaryotic communities, including PGPM, inhabit both microaggregates and macroaggregates (Wilpiszeski et al., 2019).

Preferences for specific soil particle size fractions are important, but other factors like soil moisture, conservation strategies, and soil quality (physical, chemical, and biochemical) are also crucial. These

factors help plants withstand abiotic stresses, with microbial diversity playing a key role. Specific microbes dominate nutrient cycling and regulate plant productivity (Hossain et al., 2022). Changes in soil microbial community composition and diversity influenced by plant-microbe interactions, soil conditions, and environmental stressors, lead to niche selection. This favors microorganisms providing protection and essential nutrients to plants, impacting nutrient cycling and plant growth.

### Enhancing soil fertility and health through microbial activities

Microbes, especially bacteria and fungi, play pivotal roles in enhancing soil fertility through diverse processes. Decomposer microbes break down plant and microbial residues, forming soil organic matter (SOM) through the detritus food chain. SOM acts as a reservoir of essential nutrients, influencing soil structure, water retention, and nutrient cycling. Microbes in SOM aid organic matter decomposition, contributing to soil organic carbon (SOC) and microbial biomass carbon (MBC). The MBC-to-SOC ratio indicates how efficiently soil microbes utilize absorbed carbon, known as microbial carbon use efficiency (CUE). Higher CUE values suggest better carbon utilization by microbes, leading to increased SOM and improved soil fertility. Nitrogen use efficiency (NUE) assesses nitrogen availability and transformation crucial for plant uptake (Kaur et al., 2017).

Microorganisms, including nitrogen-fixing bacteria, nitrifying bacteria, denitrifying bacteria, ammonifying bacteria, and proteolytic bacteria, regulate nitrogen cycling in soil, influencing key soil fertility indicators:

**Microbial biomass carbon:** Reflects the size and activity of the soil microbial community, impacting soil functions like structure, water filtration, and carbon storage. The MBC-to-SOC ratio provides insights into SOM turnover and carbon sequestration efficiency (Zhu et al., 2021).

**Soil respiration:** Indicates soil metabolic activity and carbon cycling through the release of carbon dioxide during microbial SOM decomposition. Influenced by factors like SOM quantity, temperature, moisture, and pH, soil respiration correlates with the soil's ability to sustain plant growth. The ratio of soil aerobic respiration to MBC reveals microbial CUE, showing how microbes allocate carbon between growth and respiration (Dijkstra et al., 2015).

**Soil enzymes:** Indicators of soil quality, sourced from microbes, plant residues, and other soil organisms. Enzymes like  $\beta$ -glucosidase, amidase, urease, and phosphatase break down organic compounds, contributing to carbon, nitrogen, phosphorus, and sulfur cycling. They offer practical tools for assessing soil health (Karaca et al., 2011).

**Molecular markers:** Identify and quantify distinct groups or functions of microorganisms within soil ecosystems (Wellington et al., 1994). Techniques like polymerase chain reaction (PCR), quantitative PCR (qPCR), DNA microarrays, and high-throughput sequencing enable molecular marker detection and analysis.

High-throughput sequencing methods, including amplicon and metagenomic sequencing, are used to study soil microbial communities. Amplicon sequencing targets specific DNA regions (e.g., 16S rRNA for bacteria or ITS for fungi) used to classify microbial taxa but has limited scope compared to metagenomic sequencing. Metagenomic sequencing examines all DNA fragments in a sample, providing comprehensive insights into taxonomic diversity and microbial community functions, including nutrient cycling through metabolic pathways and enzymes.

Amplicon sequencing offers simplicity and speed but may overlook complete microbial diversity due to primer biases. Metagenomic sequencing, though thorough, requires substantial computational resources, particularly for large or contaminated datasets. Molecular markers can target specific taxa or functional groups of microorganisms, such as  $N_2$ -fixing bacteria (e.g., *nifH* gene), AMF (e.g., SSU rRNA gene), phytopathogens (e.g., *Fusarium oxysporum* f.sp. *lycopersici* gene), or their antagonists (e.g., *Bacillus subtilis* gene). They can also target specific metabolic pathways or enzymes involved in nutrient cycling or degradation processes, such as nitrification (e.g., *amoA* gene), denitrification (e.g., *nirK* gene),  $PO_4^{3-}$  solubilization (e.g., *phoD* gene), or lignin degradation (e.g., *lcc* gene).

Assessing soil ecological functions relies heavily on molecular indicators, yet evaluating soil fertility demands diverse indicators. No single indicator fully captures the soil microbiome's complexity, necessitating a combination of approaches to encompass various aspects effectively. Factors such as spatial and temporal variability, soil type, land use, and management practices must be considered for accurate interpretation. Developing standardized methods and protocols, coupled with ongoing

research, is essential to overcome challenges and enhance molecular indicators' utility in assessing soil quality.

Despite the benefits of microbial inoculants, several challenges need addressing. These include soil microbial community variability, potential competition with native soil microbes, and microbial formulation stability during storage and application. Ecological factors like soil pH, moisture, and temperature can influence microbial inoculants' efficacy, necessitating site-specific adjustments. The presence of microbial inoculants in soil necessitates the analysis of both pre- and post-harvest, as illustrated in Figure 1.

### Ecological factors in achieving successful establishment of microbial inoculants

#### Compatibility With Native Soil Microbiomes

Microbial inoculants must coexist with native soil microbes to thrive. Cardoso and Ferreira, 2021 studied a mix of beneficial microbes (*Rhizobium tropici*, *Azospirillum brasilense*, and *Trichoderma asperellum*) on common beans. Inoculating with *Rhizobium* alone or in combination with *Azospirillum* boosted grain yields (2946.27 kg and 2892.42 kg per hectare, respectively), suggesting these inoculants integrate well into the soil's microbial community, enhancing plant growth and productivity. Factors influencing compatibility include niche overlap, functional redundancy, microbial interactions, environmental conditions, and mutualistic relationships (Bashan et al., 2014).

Practical implications include selecting microbial inoculants well-adapted to local soils, often involving testing and choosing strains that perform well in similar environments for inoculants formulation. Using soil amendments like organic matter can create favorable conditions for inoculants, promoting functional redundancy. Post-inoculation monitoring is crucial to assess inoculants establishment and performance. For these applied inoculants prove ineffective, alternative strains or additional soil management practices might be needed to ensure niche availability for these microbes (Malusá et al., 2012).

#### Functional redundancy and mutualistic interactions

Successful microbial inoculant integration relies on how well newcomers mesh with native microbes. Functional redundancy, where multiple species perform similar roles, is key. Fetzer et al. (2015)

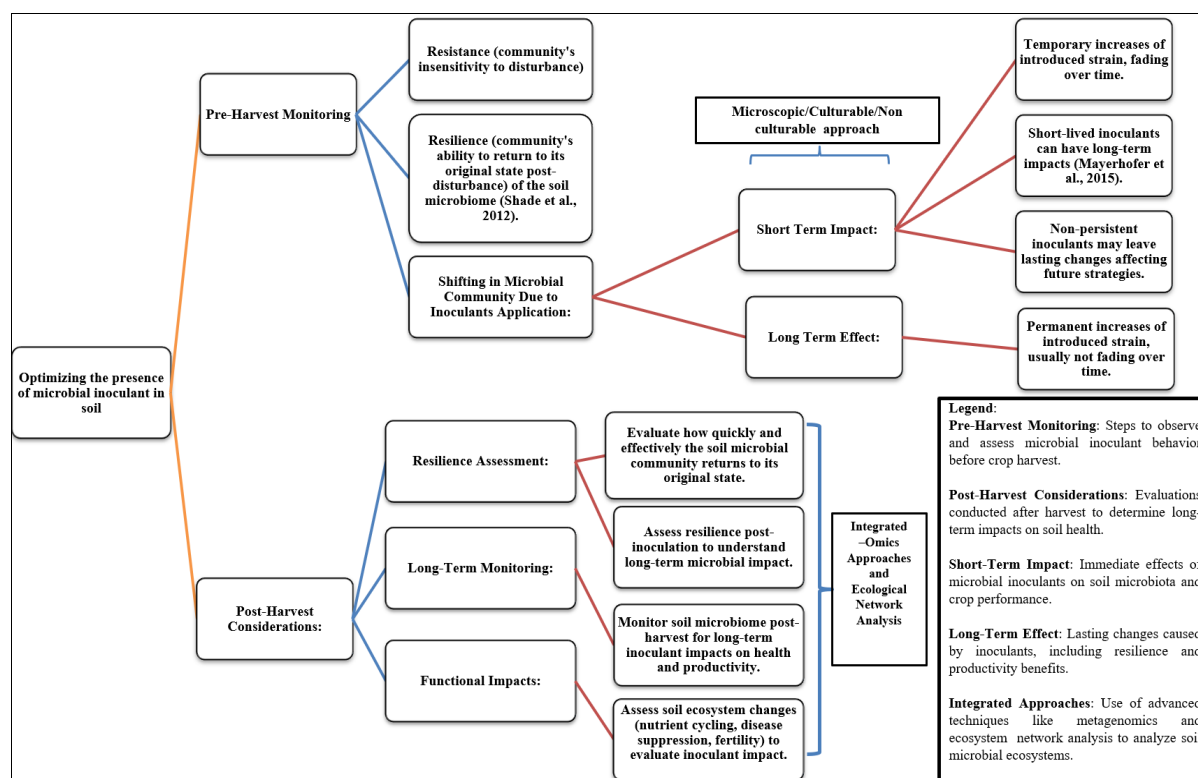


Figure 1. Optimizing the presence of microbial inoculants(s) in soil (Philippot et al., 2013).

showed that microbial roles shift with changing environments, making functional redundancy context-dependent. Yu and Whalen (2020) challenged the idea of distinct metabolic niches, suggesting most microbes perform basic functions while few handle rare tasks. The Phylogenetic Niche Conservatism Theory explains this, showing overlapping metabolic capabilities among species. These findings highlight the importance of maintaining species diversity for ecosystem resilience.

Mutualistic interactions between plants and microorganisms play a crucial role in enhancing nutrient acquisition and plant growth. For instance, the symbiosis between *Rhizobium* spp. and legumes involves the formation of root nodules where nitrogen fixation occurs, and promoting the plant (Oldroyd and Downie, 2008). Techniques to study this interaction include PCR, qPCR, genomic analysis of nod genes, and stable isotope labeling ( $^{15}\text{N}$ ), which help in understanding the presence and function of key genes involved in this process. AMF such as *Glomus* spp. and *Rhizophagus* spp., improve phosphorus uptake in plants (Smith and Read, 2008). Techniques used to investigate these interactions

include root staining, PCR with AMF-specific primers, high-throughput sequencing, and confocal microscopy, which allow for detailed visualization and quantification of fungal colonization and activity. PGPR, such as *Bacillus* spp. and *Pseudomonas* spp., enhance plant growth by interacting with the rhizosphere (Kloepper et al., 1980). Methods like DGGE, T-RFLP, metagenomics, whole-genome sequencing, and GFP tagging are employed to study these bacteria, offering insights into their community dynamics, functional roles, and interactions with plant roots. Endophytic bacteria, such as *Azospirillum* spp. and *Enterobacter* spp., live within plant tissues and contribute to growth and resilience (Compant et al., 2005). Techniques for examining these endophytes include isolation, 16S rRNA gene sequencing, metabolomics, confocal microscopy, and proteomics, which help in identifying and quantifying these bacteria and their effects on plant health. These techniques, including GFP tagging for visualizing microbial networks and stable isotope labeling for tracking nutrient absorption, provide a comprehensive understanding of the complex interactions and contributions of mutualistic microbes to plant health and growth.

### Shifting ecological dynamics along with soil health and plant yields

The ability of microbial inoculants to colonize and thrive in soil is essential. Investigating the application of microbial co-inoculants—specifically *Ensifer* sp. NYM3 (Alphaproteobacteria), *Acinetobacter* sp. P16 (Gammaproteobacteria), and *Flavobacterium* sp. KYM3 (Bacteroidetes)—on cucumbers, revealed that a 2:1:2 ratio improved soil fertility, while a 1:10:1 ratio increased available phosphate. Both ratios significantly increased cucumber yields by enhancing microbial activity. This study shows that well-designed microbial inoculants can mediate beneficial bacterial community structures and functions, promoting plant growth and yield. Traits-based integration of multi-species inoculants facilitates shifts in indigenous soil bacterial communities, highlighting the ecological dynamics involved (Wang et al., 2018).

### Advanced approaches for studying soil microbial dynamics, both applied and native, and inoculant adaptation to shifting environments

Recent advancements in molecular techniques have revolutionized our understanding of soil microbial communities and their functions. These advancements provide crucial insights into community composition, potential functions, and ecological interactions, which are essential for developing strategies for sustainable agriculture and ecosystem management.

Metagenomics, for instance, enables comprehensive sequencing of soil microbial DNA, offering detailed insights into community composition and potential functions (Tiedje et al., 1999). Network analysis of metagenomic data can further explore co-occurrence patterns in soil microbial communities, revealing potential ecological interactions (Barberán et al., 2012). However, metagenomics does not distinguish between active and inactive microbial states, as it sequences DNA from microbes in various physiological conditions.

To address this limitation, researchers have turned to metatranscriptomics, which reveals active gene expression in complex soil microbial communities. This RNA-centered approach provides simultaneous insights into both taxonomic structure and functional characteristics (Urich et al., 2008). Metatranscriptomics offers several advantages, including comprehensive community profiling, detection of rare taxa, functional insights through

mRNA-tag analysis, unbiased methodology, quantitative abundance data, and the ability to link community structure with active functions. Integrating metagenomics with metatranscriptomics and other techniques like metaproteomics enhances our understanding of how soil microorganisms support plant growth, cycle nutrients, and respond to environmental changes.

SIP is another technique that tracks labeled nutrient utilization, revealing active microbial populations and their functional roles (Neufeld et al., 2007). For example, in a methanol-fed sequencing batch reactor (SBR), SIP with ( $^{13}\text{C}$ ) methanol identified Methylophilales bacteria as the dominant denitrifiers, crucial for efficient denitrification. Similarly, FISH visualizes microbial interactions. In the same SBR study, FISH probes confirmed the correlation between SBR denitrification levels and the abundance of DEN67-targeted bacteria (Ginige et al., 2004).

Recent developments in CRISPR-Cas9 technology have allowed real-time observation of microbial dynamics. This method, known as CREATE (CRISPR EnAbleD Trackable genome Engineering), involves designing and introducing a sgRNA library targeting specific genomic loci, creating genomic edits (insertions, deletions, substitutions), integrating unique DNA barcodes with edits, culturing engineered bacteria under desired conditions, sampling at various time points, performing high-throughput sequencing of edited regions and barcodes, and analyzing data to determine barcode frequency over time (Garst et al., 2017). Single-cell genomics also plays a crucial role in analyzing unculturable microorganisms in the soil, revealing new phylogenetic lineages and metabolic features (Rinke et al., 2013).

High-resolution imaging techniques like Nanoscale Secondary Ion Mass Spectrometry (NanoSIMS) enable visualization of nutrient uptake and exchange at the single-cell level. Keiluweit et al., 2015 used NanoSIMS to map carbon flow in soil microaggregates, demonstrating that microbial necromass contributes significantly to stable soil organic matter formation. Additionally, microfluidic devices provide a controlled environment for studying microbial behavior and interactions in soil-like conditions. Stanley et al. (2016) developed a “soil-on-a-chip” device to investigate bacterial motility in simulated soil pore spaces, revealing that *Pseudomonas putida* exhibits different swimming

behaviors depending on pore size and connectivity, influencing bacterial dispersal in soil.

Bioreporter technology enables real-time monitoring of microbial activity and environmental conditions. Herron et al. (2010) employed a lux-based bioreporter to monitor arsenic bioavailability in soil, observing significant variations across different soil types influenced by factors such as pH and organic matter content.

To see the impact of soil physiochemical conditions on microbial inoculants, it is essential to consider variations in soil conditions such as pH, moisture, temperature, and nutrient availability, which significantly impact the survival and functionality of microbial inoculants. Various techniques can be employed to study these effects. High-throughput sequencing analyzes microbial community composition, while qPCR tracks specific microbial groups or genes. SIP identifies active microbes by tracing labeled substrates, and metaproteomics analyzes the microbial community protein complements. Additionally, microfluidics and micromodels study microbial behavior and interactions under controlled conditions. These methodologies provide a comprehensive understanding of microbial community structure and function, highlighting the active roles of specific microbial taxa in processes like denitrification and nutrient cycling, thereby contributing to advancements in sustainable agriculture and ecosystem management.

## CONCLUSION

This comprehensive review highlights the pivotal role of microbial consortia in enhancing soil health and promoting sustainable agriculture. Developing and applying microbial inoculants represents a promising approach to ecosystem management, offering potential solutions to modern agricultural challenges. The analysis underscores the complexity of microbial community structures in soil ecosystems and their multifaceted contributions to soil functioning and fertility. The successful establishment of introduced microbial consortia hinges on various ecological factors, including compatibility with native microbiomes and the presence of functional redundancy. Advanced techniques for observing microbial interactions and studying microbial dynamics have opened new avenues for research in this field. Key areas warranting further investigation include long-term ecological impact studies, optimization of microbial formulations, integration of

-omics technologies, and the development of climate-resilient consortia. Additionally, exploring the potential of microbiome engineering, expanding bioremediation applications, and integrating microbial inoculants into precision agriculture systems present exciting opportunities for future research. Understanding the complexities of microbial ecology and effectively utilizing microbial consortia paves the way for sustainable agricultural practices that not only address global food demands but also protect and maintain ecosystem health. The path forward requires interdisciplinary collaborations and a holistic approach to ecosystem management, promising significant advancements in our understanding and application of microbial ecology in sustainable agriculture.

## LIST OF ABBREVIATIONS

SIP: Stable Isotope Probing  
 FISH: Fluorescence In Situ Hybridization  
 CRISPR-Cas9: Clustered Regularly Interspaced Short Palindromic Repeats  
 PGPR: Plant Growth-Promoting Rhizobacteria  
 PGPM: Plant Growth-Promoting Microorganisms  
 PGPB: Plant Growth-Promoting Bacteria  
 PGPF: Plant Growth-Promoting Fungi  
 BNF: Biological Nitrogen Fixation  
 FYM: Farmyard Manure  
 PVP: Polyvinyl pyrrolidone  
 CFU: Colony-Forming Units  
 AMF: Arbuscular Mycorrhizal Fungi  
 FBD: Fluid Bed Drying  
 Myc factors: Mycorrhizal factors  
 EPS: Extracellular Polymeric Substances  
 NGS: Next-Generation Sequencing  
 DSS: Disease-Suppressive Soils  
 SOM: Soil Organic Matter  
 MBC: Microbial Biomass Carbon  
 CUE: Carbon Use Efficiency  
 NUE: Nitrogen Use Efficiency  
 SIP: Stable Isotope Probing  
 DGGE: Denaturing Gradient Gel Electrophoresis  
 T-RFLP: Terminal Restriction Fragment Length Polymorphism  
 GFP: Green Fluorescent Protein  
 SBR: Methanol-Fed Sequencing Batch Reactor  
 CREATE: CRISPR EnAbleD Trackable Genome Engineering  
 NanoSIMS: Nanoscale Secondary Ion Mass Spectrometry

## ETHICS APPROVAL AND CONSENT TO PARTICIPATE

This article does not contain any studies with human participants or animals performed by any of the authors.

## CONSENT FOR PUBLICATION

Both authors declare their consent for publication.



## CONFLICTS OF INTEREST

The author declares no conflict of interest.

## CONTRIBUTION OF AUTHORS

Both authors shared writing, editing, and revising the MS and agree to its publication.

## AVAILABILITY OF DATA AND MATERIAL

Not applicable.

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