



Advancing sustainable agriculture through beneficial microbes: From microbial physiology to synthetic community-based innovations

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Abstract

This is a review of the use of effective microorganisms (EM) in sustainable agriculture to improve soil quality, increase crop yields, and control plant diseases. This review aims to contribute to understanding sustainable agriculture using microbes for our benefit by integrating microbial physiology and synthetic microbial innovations, with respect to community-level microbial interactions. Using a literature search strategy, the physiological mechanisms by which EM may enhance soil fertility through improved nutrient cycling and increased nutrient availability to plants, and/or by creating or modifying soil structure to support root growth, were described. Results showed that EM also increase the ability of plants to grow despite biotic stressors, such as soil-borne pathogens, through both the creation of antimicrobial compounds and competitive exclusion. Microbes also enhance plant tolerance to abiotic stressors, such as water loss from drought or salt accumulation, by altering how plants respond physiologically and by retaining soil moisture. This could be achieved by using effective microbes in agriculture via synthetic microbial communities (SynCom), which will enable greater resource efficiency, a lower environmental footprint, and contribute to achieving food security while addressing current global issues such as climate change and growing populations. However, there is still much to be learned about the long-term ecological implications, scalability, regulatory environments, and socio-economic feasibility of agricultural technologies based on microorganisms and SynComs, especially in developing and climate-vulnerable countries. Therefore, a comprehensive review that links microbial physiology, SynCom design, empirical data from crop studies, and future paths to innovation is both timely and needed.

Keywords: Effective microbes, Beneficial organisms, Sustainable agriculture, Microbial physiology, Synthetic communities (SynCom)

1. Introduction

Climate change, soil degradation, biodiversity loss, and population growth are putting extreme pressure on global agricultural systems. The conventional methods of farming depend on synthetic fertilizers, Pesticides, and intensive land use, and these contribute significantly to environmental degradation, greenhouse gas emissions, and poor soil health. [1]. These challenges have intensified the search for sustainable, resilient, and ecologically

sound alternatives that maintain productivity while minimizing environmental costs. Among the most promising solutions is the strategic use of beneficial microbes as biological drivers of sustainable agriculture.

Beneficial microbes associated with plants and soil, such as bacteria and fungi, play a vital role in promoting nutrient cycles, forming soil structures, supporting plant development, and helping plants resist stress [2]. Plant growth-promoting microorganisms (PGPMs) contribute to the availability of nutrients by producing compounds that help to fix nitrogen, make phosphorus available, produce siderophores, and produce phytohormones; PGPMs also improve the ability of plants to withstand both biotic and abiotic stresses. For example, mycorrhizal fungi extend the effective root zone of a plant, allowing it to obtain more water and nutrients; Endophytes and Rhizosphere Bacteria influence how a plant metabolizes its resources and responds to pathogens and other stresses. In total, all of these functions place beneficial microbes at the center of sustainable intensive agriculture [3].

Although it is now decades since many studies demonstrated that there are many beneficial single microbe inoculum candidates for use on crops, their performance when grown on actual soils under varying environmental conditions is still highly variable due to differences in soil physical and chemical properties, temperature and moisture regimes, crop genotype, and indigenous microbial populations that can limit both the persistence and effectiveness of these candidate strains. As a result, interest has increasingly focused on investigating the complex biological processes underlying microbial physiology, interactions, and community dynamics at the population level, rather than on single-strain applications, to design more reliable and predictable microbial treatments in agroecosystems. Thus, exploiting microbial physiological characteristics such as metabolic flexibility, signaling mechanisms, stress tolerance responses, and resource partitioning is considered critical for developing more effective microbial-based treatments in agroecosystems [4].

Synthetic microbial communities (SynComs), which are communities of well-characterized microorganisms specifically selected to work together within the soil-plant system for a particular function(s), have recently evolved into an innovative tool for agricultural microbiologists. Compared with a single inoculant, SynComs were developed to better model the "functions" of native microbiomes while providing greater reproducibility, control over their application, and mechanistic insights. The potential of SynComs has been tested across several major crops (cereals, vegetables, legumes, horticultural species) and has demonstrated improved nutrient use, pathogen suppression, increased yield stability, and greater tolerance to drought, salinity, and nutrient stress [5].

The increasing focus on SynCom is indicative of an overall shift toward a systems approach in agriculture, away from the traditional microbiologist's view (microbe-centric) toward a systems-level perspective. The use of multi-omics, systems biology, and computational models has greatly enhanced our ability to identify keystone species, functional guilds, and network interactions that maintain microbiome stability and function. Additionally, these tools will allow the design of microbial consortia based on physiological and ecological knowledge of microbes, rather than relying on the empirical trial-and-error method. Finally, recent developments in precision microbiome engineering, climate-smart bioinoculants, and microbiome-assisted crop breeding are changing how beneficial microbes can be incorporated into future agricultural systems [6].

This literature review will expand our knowledge of sustainable agriculture through beneficial microbes by connecting the physiological aspects of microbes with community-level interactions and SynCom (synthetic communities) microbial innovations. The three specific goals of this literature review are: (1) synthesizing existing knowledge on how beneficial microbes function physiologically to improve plant growth, nutrient acquisition, and stress resilience; (2) critically evaluate the results of experiments using synthetic microbial communities (SynComs) in agricultural crops including the functional outcomes, design strategies and limitations; (3) identify the trends and technological advances, and innovative solutions that will shape the future of sustainable agriculture based on microbes. As the literature review offers mechanistic, applied, and forward-looking perspectives, this paper aims to provide a framework for researchers, practitioners, and policymakers seeking to develop microbial innovations for the next generation of sustainable agriculture.

2. Literature Search Strategy

A Literature search was conducted using online databases such as Google Scholar, PubMed, Scopus, and Web of Science. "effective microorganisms", "sustainable agriculture", "beneficial microbes", "microbial inoculants", "soil health", and "SynCom" were used as keywords to find relevant articles. The searches were limited to studies published between 2010-2025, ensuring that recent developments were considered. Data and results from selected studies were extracted and organized based on themes relevant to this review. The themes chosen were: (1) The benefits of effective microbes for sustainable agriculture; (2) the benefits of natural plant growth promoting mechanisms for sustainable agriculture; (3) advancing sustainable agriculture through exploiting microbial physiology; (4) exploring catalytic mechanisms of microbes; (5) exploring genetic modifications for physiological upgrade; (6) exploring microbial products for sustainable agriculture; (7) the synthetic communities breakthrough; and (8) the underexplored realms of synthetic biology and nanotechnology.

3. Sustainable Agriculture Using Beneficial Microbes

3.1 The Overall Advantage of Effective Microbes for Sustainable Agriculture

Beneficial microbes help plants resist disease through mechanisms such as competition for space, antibiotic production, and increased plant resistance to both biotic and abiotic stresses by altering hormone levels and producing antioxidants. These microbes help increase nutrient availability and thus soil fertility by making nutrients that would otherwise be unavailable available; converting insoluble forms of N, P, and other micronutrients into soluble forms; and helping stabilize soil structure (through biofilms) and increase organic matter in soils. Microbial engineering at the individual organism or community level can enhance the efficiency of these activities, targeting specific growth-promoting traits in plants and significantly reducing reliance on synthetic fertilizers and chemical pesticides in environmentally sustainable agriculture. Simply put, these beneficial microorganisms act as a single entity to improve soil fertility, suppress pathogen populations, and enhance plant resistance to environmental stresses, including drought and salt stress (Figure 1) [7].

There are positive impacts of effective microbes on plant growth and resiliency, as well as on environmental sustainability: Effective microbes can support plant growth and increase resiliency while reducing the use of chemical fertilizers and pesticides. Additionally, effective microbes may be engineered to optimize plant microbiomes, further increasing plant growth and resiliency. Effective microbes include lactic acid bacteria (LAB), photosynthetic bacteria, yeast, fermenting fungi, and Actinomycetes. In line with this, there are several ways to apply effective microbes to plants, including direct soil application, foliar spraying, and seed treatments. Each of the methods mentioned above can increase biomass accumulation, photosynthesis, and stress resistance in plants [8].

In addition to improving plant health, effective microbes also help maintain healthy soils and optimize nutrient availability for plants. Lactic acid bacteria (LAB) are involved in the breakdown of organic matter. As they break down this material, they produce lactic acid, which assists in the decomposition of other complex soil materials, making them available to plants. LAB can also solubilize phosphate, a mineral that is often bound in soil in an insoluble form. By converting insoluble phosphate to a soluble form, LAB enable plants to access it for growth and development [9]. Lastly, yeasts help break down complex organic matter and make essential nutrients, such as phosphorus and iron, more readily available to plants. Yeast also helps promote increased nutrient absorption and plant growth [10].

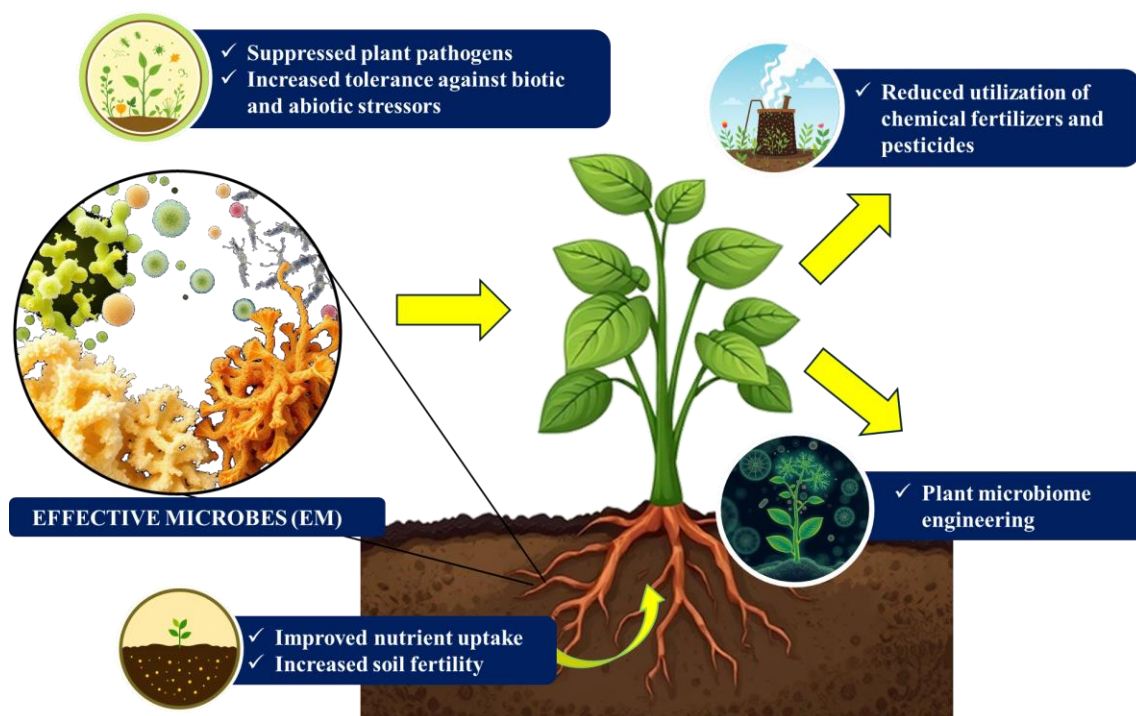


Figure 1 Beneficial effects of effective microbes in plants

Photosynthetic bacteria, and particularly purple non-sulfur bacteria (PNSB), are significant contributors to the process of nitrogen fixation; that is, they take nitrogen from the atmosphere and convert it to forms available to plant life. Nitrogen fixation eliminates the need for synthetic fertilizers and increases the bioavailability of soil

nitrogen. Additionally, actinomycetes contribute to the breakdown of complex organic compounds, thereby aiding decomposition and nutrient cycling, which are essential for maintaining soil fertility and structure [11].

Overall, the use of effective microorganisms (EM) in sustainable agriculture creates an environment where beneficial microbes can work together to support plant growth, fostering a healthy soil through biochemical processes such as fermentation, enzymatic activity, and metabolic cross-feeding. Physiologically, EM organisms, including lactic acid bacteria, photosynthetic bacteria, and yeast, affect the redox state of the rhizosphere (the area around the roots of the plant), compete with harmful microbes, produce organic acids that inhibit pathogens, and increase the availability of nutrients (N-P-micronutrients) for the plant to take up. This results in the plant producing its own hormones, developing strong roots, and being tolerant of stress. The combination of the above factors enhances the plant's ability to grow and thrive through biological interactions with the soil.

3.2 The Natural Plant Growth Promoting Mechanisms of EMs

There are different mechanisms by which EMs can increase plant growth. Phytohormone-producing photosynthetic bacteria induce IAA production, promoting root and shoot development and thereby increasing total plant biomass. The bacteria associated with LAB also help plants develop greater abiotic stress tolerance (such as drought or salinity) through increased expression of the plant's native defense systems [12] and/or indirectly by providing for improved nutrient acquisition, creating stable soil aggregates, and creating more aerobic conditions and better water retention within the soil [9].

Yeasts act as biostimulants by releasing plant hormone auxins and cytokinin, thereby enhancing root and shoot development. In addition, yeasts enhance plant stress tolerance by providing protective compounds that safeguard plants from environmental stresses [10]. Actinomycetes enhance root development by producing indole acetic acid (IAA), therefore increasing nutrient uptake. Some strains can increase root length by up to 50% in rice and other crops and promote plant health and yield. Effective microbes provide additional support to plants by controlling disease by suppressing detrimental pathogens. LAB are highly effective at producing antimicrobial compounds such as lactic acid, fatty acids, and bacteriocins, which inhibit the growth of both fungal and bacterial pathogens, including *Fusarium oxysporum*, a major cause of *Fusarium* wilt in tomatoes. LAB also compete with pathogens for nutrients/substrates in the rhizosphere and phyllosphere, reducing colonization and inducing systemic resistance in plants [11].

Yeasts control pathogenic microorganisms through various mechanisms. These microbes suppress harmful fungi and bacteria by competing with these organisms for both physical location (space) and nutrients, thus precluding the development of these pathogens. Yeast can also produce “killer” toxins and volatile organic compounds that impede the growth of harmful microorganisms. Furthermore, yeast can stimulate the plant's immune system, thereby allowing it to develop enhanced resistance against a broader range of pathogens [10]. Actinomycetes are notable for their production of antibiotics and other bioactive compounds. The production of these compounds helps suppress plant disease. In addition, certain species of actinomycetes elicit systemic resistance in plants, enabling them to be more resilient to abiotic stresses such as salinity and heavy metal toxicity [13].

Several species of microorganisms in the EM consortium support plant survival under stressful conditions; thus, they play a significant role in sustainable agriculture. The LAB (lactic acid bacteria) and photosynthetic bacteria enhance tolerance to abiotic stresses such as drought and salinity by improving soil structure and nutrient availability, while also promoting a stable root system. Yeast protects plants from environmental stresses due to high or low temperatures and a lack of moisture by producing protective compounds and promoting plant natural defenses [10]. Actinomyces (e.g., *Micromonospora aurantiaca*) reduces salt stress on plants by stimulating root growth via phytohormones, allowing plants to survive in saline soils [13].

Concisely, the primary way effective microorganisms (EMs) stimulate natural plant growth is through the increased production of indole-3-acetic acid (IAA). IAA increases root length, lateral root development, and overall nutrient absorption. While IAA production stimulates hormone-related activity in plants, EMs also enhance biological stimulation by releasing enzymes, vitamins, organic acids, and secondary metabolites, thereby activating physiological processes and improving plant vigor. EM consortia suppress phytopathogens via competitive exclusion, antimicrobial compound production, and niche occupation in the rhizosphere, thereby reducing disease pressure without chemical inputs. Working synergistically, diverse EM communities enhance plant resilience to environmental stresses such as drought, salinity, and temperature extremes by stabilizing rhizosphere function, improving osmotic balance, and reinforcing plant defense signaling networks.

4. Advancing Agriculture by Exploiting Microbial Physiology

4.1. Exploring Catalytic Mechanisms of Microbes

Microbes were recognized as the catalysts of all the cycles of the elements on our planet. Beneficial microbes play a vital role in building a sustainable, resilient agricultural system, especially as our climate changes. One of which is nitrogen fixation. Nitrogen fixation is a biological and natural process wherein the unavailable form of atmospheric nitrogen gas is converted into a usable form of ammonia; *Azotobacter*, *Azospirillum*, *Bacillus*, *Arthrobacter*, *Enterobacter*, *Pseudomonas*, *Alcaligenes*, *Klebsiella*, *Rhizobium*, *Frankia*, *blue green algae*, *Azomonas*, and *Serratia* are bacteria efficient in the fixation of nitrogen [14]. In addition, Cheng et al. [15] also include the contributions of phosphate-solubilizing bacteria (PSB) in converting immobilized P from soils, animal, and plant residues into available P for plant uptake, thereby influencing the structure of the rhizosphere microbial community and the configuration of the root system.

As stated earlier, plant growth-promoting bacteria (PGPB) have revolutionized agriculture by replacing chemical inputs and improving environmental cleanup strategies. PGPB exploits certain bacterial traits through direct physiological mechanisms, thereby promoting plant growth and development, including auxin production, ACC deaminase activity, gibberellin and cytokinin hormone production, and even nitrogen fixation [14], phosphorus solubilization [15], and the sequestration of the element iron by bacterial siderophores. On the other hand, indirect mechanisms of action by PGPB may refer to bacterial traits that suppress the activities of one or more plant pathogenic organisms (e.g., bacteria and fungi), which include ACC deaminase, antibiotics, cell wall-damaging enzymes, competition, hydrogen cyanide, induced systemic resistance, quorum quenching, and siderophores [16]. They also added that aside from these plant growth-promoting bacteria, fungi have also been demonstrated to promote plant growth. For example, the action of arbuscular mycorrhizal fungi in *Lycopersicon esculentum* Mill. conducted by Osillos and Nagpala [17] shows a faster increase in height, a higher number of leaves, and taller plants from the 2 weeks to the 10 weeks after inoculation, and AMF application resulted in earlier flower onset and fruit emergence. These microbes play a significant role in nutrient cycling, making them vital for plant growth and development [18].

Agriculture can be significantly advanced by microbial catalytic mechanisms that drive biological nitrogen fixation, converting atmospheric nitrogen into plant-available forms through enzyme systems such as nitrogenase, thereby reducing reliance on synthetic fertilizers. Beyond nitrogen supply, microbes directly promote plant growth by catalyzing phytohormone production, solubilizing phosphorus and micronutrients, and increasing root surface area for efficient nutrient acquisition. Indirectly, beneficial microbes suppress pathogens through antibiosis, competition, and induced systemic resistance, catalyzing plant defense pathways that improve crop health and yield stability. Together, these microbially mediated catalytic processes optimize nutrient cycling, strengthen plant–soil interactions, and enable more sustainable, low-input agricultural systems.

4.2. Exploring Genetic Modifications for Physiological Upgrade

Agricultural innovation is becoming apparent with the advent of genetically modified microbes (GMMs) as a means to use technology to enhance agriculture in an environmentally friendly manner. Modern molecular methods enable scientists to engineer microorganisms with specific functions to improve agricultural production and reduce environmental impacts. The use of GMM has dramatically changed agricultural processes by improving nutrient efficiency, reducing susceptibility to biotic and abiotic stresses, and decreasing the harmful impacts of environmental pollution [19].

Microbial genetic modification, using biotechnology and genomic tools, allows researchers to target and modify genes associated with desirable traits in microorganisms. The ability to edit microbial genomes, particularly through CRISPR-Cas9 gene editing, enables researchers to add, enhance, or suppress desired physiological processes in microbes, thereby optimizing their positive interactions with plants [20]. A primary example is the genetic engineering of nitrogen-fixing bacteria (*Azospirillum* and *Rhizobium*) to increase their nitrogen-fixing capacity, thereby reducing the need for artificial nitrogen-based fertilizers.

An increase in a plant's physiological activity due to enhanced expression of enzymes involved in nitrogen fixation (e.g., Nitrogenase) would provide greater amounts of available nitrogen, resulting in a long-term increase in crop yield while conserving natural resources. Genetically engineered microbes can also be designed to improve the stress tolerance of host plants by expressing stress-responsive genes. These microbes will remain viable in adverse environmental conditions (drought, salinity, extreme temperatures). In fact, *Bacillus* species engineered to express stress-tolerant genes have demonstrated promising performance in field trials and therefore have the potential to significantly enhance crop resilience under drought-stressed conditions [21]. While this innovation offers an opportunity to maintain high levels of sustainable production, it also has the potential to improve long-term food security in regions with limited access to resources and that are affected by climate variability.

Another important field of research in this area involves the genetic engineering of microbes for maximizing their potential as biocontrols. The development of genetically modified microorganisms that produce higher amounts of antimicrobial compounds, siderophores, or growth regulators provides an efficient means of reducing disease and pathogenic organisms. Thus, these microorganisms serve as a substitute for chemical pesticides, helping create a sustainable environment for agricultural practices. Examples of two such species include *Pseudomonas fluorescens* and *Trichoderma harzianum*, whose genetic engineering has effectively enhanced their ability to suppress pathogens by altering physiological responses [22].

Despite these promising outcomes, implementing genetically modified microbes in agriculture also involves addressing biosafety concerns and public acceptance. Regulatory frameworks must ensure that these genetically modified organisms (GMOs) are safe for the environment, humans, and non-target organisms. Additionally, fostering transparent communication and demonstrating clear benefits are crucial to gaining public trust and acceptance.

4.3 Exploring Microbial Inoculants in Field Trials

Microbial inoculants are beneficial bacteria or fungi applied to soil as biofertilizers, biocontrol agents (biopesticides), for bioremediation, and to improve soil characteristics. However, challenges are met along the way in improving and maximizing the effectiveness of microbial inoculants in the field. To successfully introduce microbial inoculants into the soil, adequate numbers of microbes are required to thrive in their preferred habitats. Many microbial inoculants have failed due to unrealistic expectations that a single microbe can be mass-produced, reapplied across different environments, and establish and perform specific functions. Microbial inoculants, however, will only be beneficial if they address specific soil limitations at the site of application. For example, microbial inoculants intended to manage specific plant diseases can only provide benefits if used where the target infection occurs. This is similar to how fertilizers provide benefits when specific nutrients are limited [23].

Successful research on the effects of microbes on improving growth and crop yield has been documented, including the use of mycorrhizal fungi and rhizobia as potential biofertilizers. Despite these successful research efforts, the adoption of beneficial microbes by the manufacturing industry and farming communities remained insignificant due to technical limitations that hindered the development of microbial products. The limitations are often related to advancing the efficacy of microbial products from controlled conditions, such as in the laboratory or greenhouse, to field conditions [24].

Although microbial products have been successful in field trials, results may not be consistent across crops, soils, and environmental conditions, which may limit their adoption by farmers [25]. The variability in the effectiveness of microbial products in the field may be attributed to the initial phases of microbial product testing, which are conducted in sterile, regulated environments that enable an impartial assessment of the microbes being investigated [24]. For example, native microbial communities associated with plants or in soil may outcompete introduced microbes. The microbial inoculants may disappear quickly or remain at low levels, thereby reducing their effectiveness. Aside from that, various biotic and abiotic factors, including extreme climatic conditions, poor soil quality, and environmental and soil contaminants, can hinder a strain that typically shows remarkable effectiveness under controlled conditions. Several practical challenges associated with the use of microbial inoculants include short shelf-life, potential incompatibility with agricultural chemicals, equipment, or farming practices, lack of appropriate guidance on their use, and issues related to storage and transport [26].

5. Future Trends and Emerging Solutions

5.1. The SynCom Breakthrough

Although microbial consortia such as EM have significant potential, it is difficult to predict how well they will perform across different soil types. This is largely due to variations in soil characteristics such as pH, organic matter, texture, and existing microbial populations, which all affect microbial viability and metabolic function. Typically, single-inoculum EM preparations do not yield consistent results because they provide a limited number of functions for the microbes present and may therefore be unable to outcompete other microorganisms for resources. Synthetic microbial consortia (SynComs), however, typically produce more consistent results and are also easier to predict since they combine complementary functions, allow for ecological niche partitioning, and offer stress tolerance that increases the ability of the SynCom to adapt to the various environmental conditions found in a diverse agricultural ecosystem [27].

The last few years have seen rapid advances in methods to overcome some of the challenges faced when using microbial products in agriculture. Advances made in the last decade or so in the use of culture-independent technologies (such as Next Generation Sequencing) have opened new avenues for researchers to study plant-associated microbiomes and to develop ways to modify those microorganisms in their native habitats. Using the plant-associated microbiome does not require isolating microbial strains [28]; rather, it begins by defining what

constitutes an important or "core" microbiome. The core microbiome is defined as the set of microbial species consistently identified in a specific plant type that are also highly productive. It is critical to develop effective methodologies to establish the core microbiome and enhance agricultural productivity [27].

Another conventional method for controlling microbiomes in their natural habitat involves using microbial inoculants containing plant-growth-promoting microorganisms (PGPMs) to boost the population of beneficial core microbes. The recent trend in the development of PGPM-based products is moving towards the use of combinations of microorganisms or synthetic communities (SynComs) rather than inoculants containing a single microbial strain (Table 1). Synthetic communities are often created to replicate, to some extent, the functioning and composition of the microbiome in its natural environment [28]. This approach addresses the issue of inconsistent efficacy of single inoculants by allowing a wider range of responses to different environmental conditions and enabling them to compete with native microbial communities, leading to a favorable response in the treated plants. Rapid advances in microbial ecology, genetics, and microbiology are used to develop these inoculants. Furthermore, the choice of important beneficial microorganisms for creating SynComs can be guided by their phylogeny or functional traits, which can be inferred genomically or experimentally.

Table 1. Studies that used SynComs in agricultural crops

Plant	Growth Condition	SynComs Origin	Response/Action	Reference
Tomato	Gnotobiotic system	5 bacterial strains from the root of the desert plant <i>Indigofera argentea</i>	Promotes growth under salt stress and non-sterile conditions; cross-kingdom (fungi and bacteria) SynComs were more effective in suppressing Fusarium Wilt Disease than those of fungal or bacterial SynComs alone	[29]
	Field trial and Greenhouse	205 strains of bacteria and fungi		[30]
Soybean	Pot experiment	8 bacterial strains from soybean Plant growth-promoting rhizobacteria (PGPR)	The microbial community in the endosphere and rhizosphere is enhanced in structure and function, and growth is also promoted.	[31]
Garlic	Field trial	6 <i>Pseudomonas</i> strains from garlic	Promotes garlic growth under a favorable soil type	[32]
Apple	Greenhouse experiment	8 strains, belonging to the genera <i>Bacillus</i> and <i>Streptomyces</i>	Enhance apple plant growth and combat apple pathogens	[33]
Wheat	Greenhouse experiment	14 bacterial strains derived from rhizosphere soil	Protects wheat from soil-borne fungal infection (<i>R. solani</i> AG8)	[34]
Corn	Gnotobiotic system, greenhouse, and field trial	7 bacterial strains isolated from the Jala maize landrace	Promotes growth, yield, and inhibition of fungal rust in corn	[35]
Watermelon	Field trial	16 core bacterial strains from the rhizosphere of grafted watermelon plants	Protect ungrafted watermelon plants from <i>Fusarium oxysporum</i>	[33]

Table 1 presents recent studies on the benefits of using SynComs to improve plant growth and yield, as well as to protect plants from pathogens. The studies use different growth conditions, from controlled systems to greenhouse and field trials, to assess how bacteria and fungi influence plants. Among the microbes used in SynCom formulations across different studies, *Pseudomonas* was a key contributor to plant growth promotion. Aside from that, soil type also influences the benefits of SynComs. The study by Zhuang et al. [32] examines the influence of different soil types on garlic growth. SynComs were isolated from the garlic rhizosphere and tested in field trials. Results showed that bacteria, namely *Hydrophile*, *Pseudomonas*, and *Flavobacterium*, are more abundant in sandy loam and loam soils. It was also further noticed that the rhizosphere microbiota in sandy loam and loam are different from those in sandy soil. In addition, there is a notable change in the microbiota during garlic growth, a dynamic process.

Cross-kingdom SynComs were also studied using a combination of bacteria and fungi and suggest that it is more effective at suppressing Fusarium wilt in tomatoes than fungal or bacterial SynComs alone [30]. Disease suppression caused by fungal pathogens was also observed in wheat, apple, corn, and watermelon treated with SynComs [33-35]. Plant growth was also observed in tomato plants under salt stress and non-sterile conditions in the presence of SynComs obtained from the roots of *Indigofera argentea*, a desert plant [29]. Furthermore, research suggests that effective SynComs introduced into soybean plants significantly alter the structure and function of the rhizosphere and endosphere microbial communities. This intervention led to increased microbial diversity and an elevated relative abundance of microbes [31]. It can also be inferred that most of the crops studied use SynComs obtained from the rhizosphere, where they are naturally grown.

Overall, these studies indicate that improving crop-optimized SynComs can be achieved by targeting and using the natural endophytic microbiota by introducing inoculants that are already adapted to the plant environment and

are more likely to survive and colonize the plants, as well as focusing on the core microbiota, particularly on the most influential or connected microbes in the community.

5.2 The Underexplored Realms of Synthetic Biology and Nanotechnology

In the future, traditional strategies such as microbial inoculants, PGPM, and SynComs are expected to be combined with emerging technologies, such as synthetic biology and nanotechnology, to address inconsistent efficacy and expand the use of microbes in agriculture. Advances in synthetic biology enable the transformation of crop metabolic pathways and genetic information and involve the application of microorganisms in agriculture [36]. The use of synthetic biology enables the redesign of plant and beneficial microbial genomes, as well as improving communication between them.

Plant-mediated microbiome engineering involves strategically manipulating the plant-associated microbiome to optimize plant growth, improve disease resistance, enhance nitrogen fixation, and adapt to abiotic stresses. This approach manipulates the symbiotic relationships that plants have developed with beneficial microbes, utilizing various methods to encourage beneficial interactions while suppressing the negative impacts of harmful microorganisms. This is made possible by adapting plants and microbes with enhanced capabilities using genetic engineering. For example, plants can be modified to enhance their ability to attract specific beneficial microbes or to provide more favorable niches for microbial colonization, thereby significantly altering microbiome composition [37]. Gene-editing tools in agriculture have enhanced plant-microbe interactions. The CRISPR/Cas9 system is one of the most widely used gene editing technologies in agriculture. It enables targeted alteration of specific DNA sequences in the genome, allowing the knockout or modification of genes relevant to agronomic traits. By enabling precise genome editing, researchers are using this technology to investigate and enhance the relationships between plants and their associated microbial communities.

A study conducted by Yan et al. [20] uses CRISPR-based gene editing to target apigenin breakdown in rice, thereby enhancing apigenin content and root exudation. Their results showed that modified rice plants under limiting nitrogen conditions increased grain yield. Aside from that, biofilm production also modified the root microbiome structure, favoring the enrichment of diazotrophic bacteria. It is well known that plant root exudation and microbial substrate utilization traits are the main drivers of microbial community abundance and metabolic synchronization. The same tool was used by Hao et al. [38], who demonstrated its potential to recruit beneficial microbes and control parasitic weeds by manipulating strigolactone production in sorghum.

Nanotechnology is another future trend with the potential to enhance plant-microbe interactions to achieve sustainable agriculture. Nanoparticles can be designed to stimulate specific plant-microbe interactions that enhance symbiotic relationships. For instance, nanoparticles can enhance plant recognition of beneficial microbes, leading to improved colonization and nutrient uptake, and can promote plant growth by optimizing soil physiochemical characteristics. A recent study showed that the application of carbon-based nanoparticles enhanced *Z. mays* growth by improving nutrient uptake and, by stimulating soil enzymes, significantly affecting microbial communities [39].

New technologies such as genetic engineering and nanotechnology are being integrated into agriculture to transform traditional farming practices to achieve the overall goal of sustainable agriculture for the future. The positive impact of these new technologies on beneficial plant microbes has been documented by numerous studies. However, there has been little experimental research on how these technologies might alter or enhance the structure of the rhizosphere microbiome under real conditions. For instance, the identification of growth-promoting schemes by root symbiotic fungi found in ferns [40] may be further explored through experimental research using nanotechnology.

Since every technology has its own drawbacks and advantages, new technologies are still necessary in many applications. An in-depth understanding of the impact of these technologies and their interactions with plants and microbes can help reduce the significant reliance on traditional or chemical fertilizers, improving plant nutrition, reducing plant stress, and promoting plant growth.

6. Conclusion

This review examines how beneficial microbes advance sustainable agriculture by linking microbial physiology with emerging synthetic community (SynCom) innovations. It highlights core mechanisms, including biological nitrogen fixation, phytohormone production, nutrient solubilization, pathogen suppression, and stress mitigation, that collectively enhance plant growth and soil fertility. The article contrasts traditional effective microorganism applications with engineered microbial consortia, emphasizing functional complementarity, metabolic networking, and system stability. It further discusses limitations related to soil heterogeneity and environmental variability and shows how SynCom design improves predictability and resilience. Overall, the review positions microbe-based and community-engineered solutions as viable pathways to reduce agrochemical dependence while sustaining productivity and ecosystem health.

7. Ethical Review

The study protocol (RETC code: 2025-650- Use Effective Microbes-Aban) underwent ethics review from a PHREB (Philippine Health Research Ethics Board) – accredited institution (Level 1) with accreditation number: L1-2023-056-01.

8. Declaration of Generative AI and AI-Assisted Technologies in the Writing Process

During the preparation of this work, the authors used ChatGPT in order to improve the manuscript and align its enhancement to what the peer reviewers desire. After using this tool / service, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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10. Conflict of Interest

The authors declare no conflict of interest.

11. Authors contribution

Aban, JL: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing, original draft, Writing - review & editing; de Guzman, ADL: Conceptualization, Data curation, Formal analysis, Investigation, Resources, Software, Visualization, Writing, original draft; Escobal, MJB: Conceptualization, Data curation, Formal analysis, Investigation, Resources, Software, Visualization, Writing, original draft; Estal, KNF: Conceptualization, Data curation, Formal analysis, Investigation, Resources, Software, Visualization, Writing, original draft; Milanese, NAS: Conceptualization, Data curation, Formal analysis, Investigation, Resources, Software, Visualization, Writing, original draft; Sagun, AV: Validation, Supervision

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