



REVIEW ARTICLE

# Plant probiotic microbes - trending microbes for plant growth and value addition of compost - a review

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## Abstract

New agricultural approaches, including natural and organic farming, have developed organic and microbiological goods. Beneficial microbes known as plant probiotic microorganisms (PPM) are primarily found in soil and have coevolved with plants in a symbiotic or free-living relationship. By encouraging plant growth and health, these bacteria lessen the need for artificial fertilizers, support environmentally friendly agricultural practices, and improve plant health. Agroecosystem vigour, biodiversity, biological cycles and soil biological activity are all enhanced by using plant probiotic bacteria in biologically based agriculture. By using beneficial bacteria to support the health and function of the host organism, plant probiotics aim to lessen the demand for toxic pesticides and fertilizers. Using these probiotic microorganisms will have a synergistic and advantageous effect on crop production. Plant probiotic microorganisms improve the overall quality of compost throughout the composting process by accelerating the breakdown of organic materials and introducing helpful bacteria. This rich compost adds beneficial bacteria to the soil, creating a healthy and productive environment. This review looks at the common plant probiotic bacteria, how they work, how they complement each other to improve compost quality and plant growth, how they might be used in agriculture, and how they could change how composting is done.

## Keywords

bacteria; yeast; plant probiotic microbes; growth promoting hormones; compost

## Introduction

Organic farming, natural farming, precision farming and smart farming methods demand the use of novel inorganic products to reduce or avoid the use of organic fertilizers and simultaneously promote the use of microbes for nutrient transformations in soil for plant growth and health. One such microorganisms that make trend-setting and gain importance in promoting plant growth and health is the Plant Probiotic Microorganisms (PPM). PPMs are beneficial microorganisms that coevolve with plants in a symbiotic or free-living association. This association mainly occurs in the soil, and other association types, such as microalgae-bacteria, were also reported (1). Reliance on chemical fertilizers for fundamental agronomic advancement would exacerbate soil quality degradation and increase the risk of water pollution and contamination, creating an unsupportable barrier to the economy. In contrast, biological-based agriculture, using probiotic

microorganisms and other beneficial microbes for promoting plant growth, offers comprehensive advantages such as promoting and enhancing the health of agroecosystems and sustaining bio-diversity and soil biological activity (2).

Similar to human probiotics, the idea behind plant probiotics is to promote plant health and function through helpful bacteria. The term Plant Probiotic Bacteria was used for the first time by Haas and Keel for a group of bacteria that promotes plant growth and health through effective colonization in plant roots, offer induced systemic resistance (ISR) in host plants and provide antagonistic effects on plant pathogens (3). PPMs that include bacteria, fungi, actinobacteria and algae are subsets of the bacterial group known as "Plant Growth Promoting Rhizobacteria" (PGPR). PGPRs promote plant development by producing siderophores, synthesizing phytohormones, and solubilizing plant nutrients from insoluble to soluble forms.

Apart from plant growth promotion, plant probiotic microbes aid in the faster breakdown of organic materials during composting, which is essential to managing organic waste (4). When applied to the soil, these PPM-enriched composts create a robust and fruitful environment favouring plant growth (5). Studies showed that the application of compost to the soil as organic amendment altered the topologies of the rhizosphere bacterial communities in the rice-wheat cropping system and was dominated by the phyla *Proteobacteria*, *Acidobacteria* and *Chloroflexi* (6).

This comprehensive review explores the popular plant probiotic bacteria and clarifies their action modes and complementary impacts on compost quality and plant development. We review recent research discoveries, discuss the valuable uses of these bacteria in agriculture,

and emphasize how they might completely transform composting procedures. Our goal in doing this thorough analysis is to offer a comprehensive grasp of how plant probiotic bacteria may influence composting and sustainable agriculture in the future.

### Microbial diversity of PPMs in rhizosphere, phyllosphere, endosphere and their role in plant growth promotion

PPMs include probiotic bacteria and yeast. Yeasts are well-known for their role in the fermentation industry, but their potential as plant growth probiotics is under-researched and a significant focus of current agricultural studies. Given their widespread presence in the phytobiome and significant agricultural and industrial potential, it is crucial to study these organisms further to determine their effectiveness as biofertilizers. Their diversity is immense, so the possibility of exploration is wide.

A total of 538 yeast strains were isolated from the rhizosphere of various leguminous plants, including alfalfa (*Medicago sativa*), sainfoin (*Onobrychis viciifolia*), clover (*Trifolium pratense*), sweet clover (*Melilotus officinalis*) and soybean (*Glycine max*), in dark chestnut soil from the Almaty region of Kazakhstan (7). Most isolates were obtained at a depth of 10-20 cm (47.6%) and harboured the most efficient IAA-producing strains. Endophytic yeast (*Candida* sp.) was isolated and identified from rice sprouts that showed phytase activity (8). Similarly, several studies have put forward their plant growth-promoting or antagonistic activity, which could be exploited in utilizing them as plant probiotics. An overview of some isolates is listed in Table 1.

Endophytic bacteria with plant probiotic qualities might increase agricultural output by boosting plant growth, yield and disease resistance in challenging environments. Application of *Occhrobactrum ciceri* +

**Table 1.** List of PPM isolated from different crops in various locations

| Sl. No. | PPMs isolated  | Region of isolation                                      | Location         | References |
|---------|--|--|------------------|------------|
| 1.      | <i>Aureobasidium pullulans</i> (YA05)<br><i>Rhodotorula mucilaginosa</i> (YR07)  | Rhizosphere (legumes)                                    | Kazakhstan       | 5          |
| 2.      | <i>Candida</i> sp (Y3)   | Endosphere (rice sprouts)                                | Guangzhou, China | 6          |
| 3.      | <i>Hannaella sinensis</i> (DMKU-RP45)<br><i>Kodamaea ohmeri</i> (DMKU-RP233)<br><i>Meyerozyma guilliermondii</i> (DMKU-RP168)<br><i>Pseudozyma antarctica</i> (DMKU-RP163)<br><i>Rhodotolura taiwanensis</i> (DMKU-RP105)<br><i>Torulasporea globosa</i> (DMKU-RP31)<br><i>R. paludigenum</i> (DMKU-RP301) | Phyllosphere<br>(rice leaves- epiphytic)                 | Thailand         | 7          |
| 4.      | <i>P. rugulosa</i> (DMKU-RE60)<br><i>Cryptococcus flavus</i> (DMKU-RE12)   | Phyllosphere<br>(rice leaves- endophytic)                | Thailand         | 7          |
| 5.      | <i>Rhodotorula graminis</i>  | Endosphere (stem of poplar)                              | Washington       | 8          |
| 6.      | <i>Cryptococcus albidus</i> KKUY0017<br><i>Wickerhamomyces anomalus</i> KKUY0051   | Epiphytic (surface of apricot<br>and pear, respectively) | Saudi Arabia     | 9          |
| 7.      | <i>Pichia kudriavzevii</i> POY5<br><i>Issatchenkia terricola</i> GRY4  | Endosphere<br>(seeds of pomegranate and<br>grapes)       | India            | 10         |

*Mesorhizobium cicero* bacterial consortia in chickpeas increased the nodulation by 42% and yield by 64% (9). In fenugreek application, the *Burkholderia* sp RHT8 and RHT12 cell-free extract increased the yield by 40% and controlled the plant pathogen *Fusarium oxysorum* by 37-41 % (10). Treatment of lentils with *R. leguminosarum* + *P. fluorescens* enhanced the utilization of phosphatic fertilizers, resulting in nodule number, dry weight of nodule, leghaemoglobin content in nodules and grain yield (11). In paddy, the rhizosphere bacterial population, diversity and root architecture were influenced by the application of plant probiotic bacteria. Treatment of paddy seeds with *Paraburkholderia fungorum* BRRh-4 and *Delftia* sp. BTL-M2 enhanced plant growth and seed germination. The root metagenome revealed the dominance of the phyla Bacteroidetes (42.91%) followed by Firmicutes (29.03%) and the modulation of the microbiome signature of rice by application of these probiotic bacteria (12). In maize, seed treatment with *Pseudomonas taiwanensis* influenced the diversity of microbes. The genera, namely *Pseudomonas* (36.27%), *Luteolibacter* (1.93%), *Flavisolibacter* (1.64%) and *Opitutus* (0.55%) were found in abundance compared to control (13)

### Plant growth promoting indices of PPMs

An essential mechanism of growth promotion by PPMs involves the production of hormones, particularly auxins. The effects of PPMs on plant growth promotion are given in Figure 1. IAA produced by the yeast strains stimulates seed germination, resulting in elongation of stems and roots and promoting plant growth (7). The endophytic yeasts utilized the tryptophan from plants, providing IAA for plant growth (24). The gene *aux/IAA* was responsible for auxin production. *Serratia marcescens* PLR, which possessed the gene, promoted plant growth in *Arabidopsis* by triggering auxin rapid response genes like GHs, Aux/IAAs and SAURs. (14). Aux/IAA gene expression in tomato leaves promoted leaf, root and stem growth in tomato (15). Apart from auxins, they can also synthesize other hormones like gibberellins, cytokinin and even amino acids and vitamins (16). ACC deaminases, enzymes found in endophytic yeasts, cleave ACC (1-aminocyclopropane-1-

carboxylate), the precursor of the stress hormone ethylene. Because of the ACC deaminase activity, yeasts could prevent the growth inhibitory activity associated with ethylene, thus providing stress tolerance (17). The ACC deaminase gene *acdS* identified in *Pseudomonas migulae* 8R6 negatively affected ethylene signalling. It was proved that ACC deaminase significantly increased plant growth and productivity under salt stress in *Camelina sativa* (18). The recombinant strain *Azoarchus* sp. CIB (pseva237ACDs) cloned with the *acdS* gene expressed ACC deaminase activity and imparted stress tolerance to cadmium in rice (19).

Phytase, also called phosphomonoesters, had a crucial role in hydrolyzing the phytic acid, the predominant reserved and unavailable form of organic phosphorus in soil, seeds and straws (20), and an anti-nutritional factor. It was demonstrated that the probiotic yeast *Candida tropicalis* was capable of producing the phytase and was found to be associated with enhanced phytase activity during seed germination (21). Similar results were obtained when the effect of endophytic yeasts in seedling germination and promotion of shoot length, shoot fresh weight and roots fresh weight by 35%, 80%, and 60% were studied, respectively (6). When three yeast genera (*Kluyveromyces waltii*, *Pachytrichospora transvaalensis* and *Sacharromyces cataeensis*) were used for identifying the growth promotion activity in sugarbeet, it is also identified the presence of important secondary metabolites like methyl undecane, adipate, Dioctyl sebacate and Bacchotricuneatin C, through gas chromatography-mass spectrometry (GC-MS) analysis (22). It was assumed that such compounds enhanced soil's physical and chemical properties, thereby improving water holding capacity, preventing nutrient leaching and adding more mineral nutrients to the soil, which could enhance plant growth promotion. They also observed the production of capric ether, a form of fatty acid from *S. cataeensis* that could be a potential precursor for growth hormones (23). Hence, these compounds could directly or indirectly enhance the crop plants' growth and productivity.

A study on various endophytic yeast isolates from rice and sugarcane leaves elucidated the role of phosphate solubilizing and zinc oxide solubilizing ability of the isolate DMKU-RP31 (*Torulaspota globosa*). It was attributed to the growth of those crops (7). Along with this, other two isolates, viz., *Pseudozyma rugulosa* DMKU-RE60 and *P. antarctica* DMKU-RP213, exhibited polyamine production in the culture broth, which is an organic polycation that could contribute to root cell elongation, thereby influencing the root growth.

The plant health-promoting probiotics from *Ananas comosus*, namely *Bacillus* sp., *Providencia* sp., and *Staphylococcus* sp. (Acb12&13), possessed nitrogen fixating potential, ACC deaminase activity and IAA production. These bacteria possessed drought tolerance. Ability. The *Bacillus* sp. released the antifungal compound surfactin (24) and these isolates from *Ananas comosus* proved their probiotic ability.

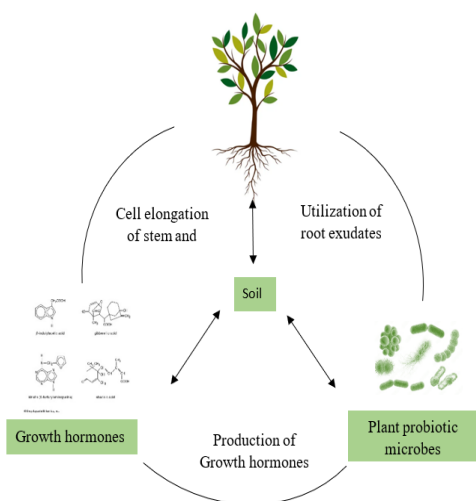


Fig. 1. The effect of PPMs on plant growth promoting

## Plant health promoting indices of PPMs

Apart from promising plant growth-promoting probiotics, these organisms also play a role as antagonists against plant pathogens. The use of bacteria and filamentous fungal biocontrol agents has always taken the upper hand and the role of yeasts is often underexploited (23).

The biocontrol ability of the yeast *Torulaspora globosa* was experimentally demonstrated against *Colletotrichum graminicola*, the cause of maize anthracnose (2). Similarly, the role of *Saccharomyces cerevisiae* as a biocontrol agent was proved against sugar beet damping-off caused by soil-borne fungus, *Fusarium oxysporum* F4 (22). Production of siderophore, the iron chelating compound, is a potential mechanism of antagonism. This was one of the mechanisms employed by the "black yeast", *Aureobasidium pullulans*, to inhibit the phytopathogen *Glomerella cingulata*, which causes several diseases in fruits (25). In a study conducted in (10), where they isolated 20 seed-borne yeasts, they came up with two effective yeast isolates. These isolates, *Pichia kudriavzevii* POY5 and *Issatchenkia terricola* GRY4 could induce the production of defence-related enzymes like catalases, peroxidases, polyphenol oxidases and chitinases in *Rhizoctonia solani* challenge inoculated black gram plants. Yeast genera like *Candida*, *Rhodotorula*, *Rhodospiridium*, *Cryptococcus*, etc., were reported to have potential antagonistic properties against pathogens like *Botrytis cinerea*, *Penicillium sp.*, *Colletotrichum sp.* etc (26).

The 13 yeast isolates studied in (7) possessed catalase activity, directly involved in protection against oxidative damage by reactive oxygen species (ROS). Some of the isolates also possessed hydrolytic enzymes that directly contributed to antagonism. The isolate *Torulaspora globosa* (DMKU-RP31) has shown antagonism against important rice pathogens like *Fusarium moniliforme*, *Helminthosporium oryzae* and *Rhizoctonia bataticola*, which was thought to be associated with the production of antifungal volatile compounds.

### Influence of PPMs on crop growth

Unscrupulous and unprecedented usage of chemical fertilizers and pesticides pushed by the need for increased productivity has not only resulted in soil and water pollution but has also led to chemical contamination of soil, air and water, thereby affecting human health and hygiene. This is where the use of plant probiotic microorganisms as an alternative means for chemical pesticides and fertilizers gains importance. The effects of PPMs on crop growth are given in Figure 2.

Studies on *Candida tropicalis* CtHY, an essential component of the multi-strain biofertilizer BioGro, promote rice growth and yield in seasonal field experiments in Vietnam. (24). The results of these studies demonstrated that CtHY was shown to exhibit several plant growth-promoting characteristics such as ability to produce IAA, growth on ACC as a sole N source, mobilized organic and inorganic phosphates and synthesized polyamines and was capable of enhancing rice seedling growth. It has been shown that rhizophagy, previously believed to be a way for

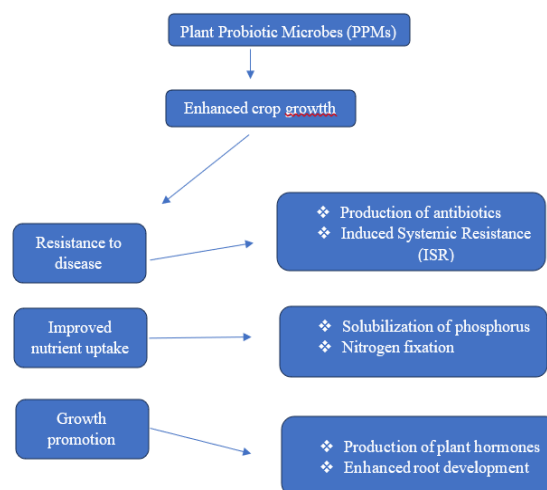


Fig. 2. Effect of PPMs on crop growth

dicotyledons to acquire nutrients, also takes place in monocotyledons by using yeast cells that constitutively produce green fluorescent protein (27). Sugarcane plants with living yeast produced 47% more root biomass and enhanced tiller numbers by at least 23%. These results were consistent with an increase in root: shoot ratio in plants supplied with organic sources of N and P, including amides, amino acids, small peptides and DNA. Researchers came up with two potent isolates, one from the seeds of pomegranate (POY5) and the other one from grapes (GRY4) and found that they had antimicrobial activity (28). Subsequently, these isolates were assessed for plant growth-promoting characteristics such as phosphorus solubilization, zinc solubilization, auxin, siderophore, ACC deaminase and hydrogen cyanide production that could be classified as plant probiotics. Seed imbibition with probiotic yeast led to a significant increase in germination rates, with POY5 and GRY4 isolates showing a rise of 9% and 8.8%, respectively, compared to the control. Considerable differences in root and shoot length of black gram seedlings treated with probiotic yeast were also noted. Hence, this multifunctional yeast could be exploited as bio-formulation for better crop nutritional security in black gram. Researchers developed a synthetic probiotic formulation for treating black Sigatoka consisting of several bacterial endophytic strains (29). This probiotic formula was known to reduce the impact of fungal disease on naturally infected plantations in Colima, Mexico. It is reported that the addition of the dry yeast to *Rhizoctonia*-inoculated potato plants showed a marked increase in all parameters related to growth when compared to the controls to the control while it dramatically reduced in terms of disease incidence and severity (30)

### Metagenomic approach to study the diversity of PPMs

Probiotic bacteria have garnered the scientific community's attention due to their beneficial effects on human, plant and animal health. One of the reasons for the wide use of probiotic concepts in plant-microorganism relationships has been due to the development of these new sequencing technologies-mainly metagenomics analysis-which has recently highlighted the complex composition of symbioses,

showing a rich microbial community living together within healthy plants (31) Study of plant probiotic microorganisms forms the core for understanding their ecological role and their interaction with plants which in turn enables the biotechnological application of these beneficial microbes in terms of crop management. When it comes to the study of these microbes, we have both culture-independent and dependent methods (1) a culture-dependent approach wherein the microorganisms, isolated from the plant material, are cultivated on a suitable media and then identified by a combination of phenotypic and molecular methods; whereas in culture-independent approach where the microorganisms are detected without cultivation, based on extraction and specific DNA analyses (32).

The assessment of the genotypic and phenotypic diversity in populations of plant-probiotic *Pseudomonas* spp. Colonizing roots using various culture-independent methods, even though initial steps involve cultivation- and isolation-based methods, currently remains the first common step in studying the diversity of soil and rhizosphere populations of plant-probiotic fluorescent *pseudomonads* (PFP) (33). The various culture-independent methods used in the study of PFP include DNA-based typing methods generally used for investigating the diversity of isolated PFP populations, which were based on the analysis of (1) the whole genome, such as repetitive extragenic palindromic polymerase chain reaction (rep-PCR) and random amplification of polymorphic DNA (RAPD), (2) the ribosomal region, like ARDRA and ribotyping and (3) antimicrobial-coding genes, like restriction fragment length polymorphism of PCR products (PCR-RFLP), denaturing gradient gel electrophoresis of PCR products (PCR-DGGE) and sequencing. Experiments conducted in (34) resulted in a well-put and thorough investigation into the plant systemic responses to the interactions with beneficial components of the soil microbiome, which are often associated with small perturbations in the gene transcription rate (34). The subtractive library approach resulted in the compilation of an inventory of 40 tomato genes related to the colonization by the rhizosphere microbes, which was found to be enriched with transcripts displaying even slight differences in gene expression levels. Transcript annotation and interrogation of available ESTs and microarray data further demonstrated that different signalling pathways interact to activate the ISR and growth-promoting response induced in tomatoes by MK1.

### Value addition of compost with PPMs

Compost treated with plant probiotic microorganisms (PPMs) had the potential to speed up the decomposition process. It increased the agronomic value of the final organic matter by enhancing its biochemical complexity (35). PPMs help to create a more robust and nutrient-dense compost composition by promoting the absorption of essential macronutrients and micronutrients through complex microbial processes. Furthermore, a dynamic range of bioactive substances was introduced by the enzymatic activity of these bacteria, strengthening the compost against pathogenic invasion and promoting a variety of soil microbiota (36). Complementary PPMs and

compost substrates provided a microbially rich environment that enhanced soil aeration, water retention, and soil structure (37). The effects of PPMs on compost are given in Figure 3.

Using plant probiotic microbes significantly accelerated the rice straw leftovers into probiotic bacterial compost. Compost reinforced with *K. pneumoniae* RSI9 and *B. cereus* RSDa2 increased shoot and root length by 19.6% and 14.2%, respectively, over control. Nutrition and the encouragement of plant development depend heavily on the microbial population in the rhizosphere. By promoting the development of additional bacterial species and modifying the microbiome in the rice rhizosphere, plant probiotic bacterial compost augmentation enhanced plant growth (38).

Value addition of liquid compost was recorded using a probiotic consortium of *Lactobacillus* sp., *Rhodopseudomonas* sp., *Actinomyces* sp., and *Streptomyces* sp., resulting in an increase of N by 1-12.3%. P by 0.6-2.2% and K by 1-3.2% (39).

A study examined the application of *Lactobacillus plantarum*, *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus natto* and *Saccharomyces cerevisiae* during composting enhanced the cellulose breakdown, along with value addition of nutrients and lowering of mycotoxin content (40).

Plant-probiotic bacteria *Stenotrophomonas maltophilia* RSD6, with the production of lignases, xylanases and cellulases, improved the rice straw to bioactive compost. The application of this compost enhanced the growth of rice (41).

*Bacillus velezensis* T-B, *Bacillus haynesii* R-1, and *Bacillus methylotrophicus* F-6. Improved the lignocellulose breakdown and compost fertility of bovine dung and wheat straw. The addition of *Bacillus* resulted in a more prolonged thermophilic phase, reduced respiration activity and higher rates of cellulose, hemicellulose and lignin breakdown (42). These results supported the value addition of compost with PPMs and the prospects to reduce or replace chemical fertilizers for a greener future

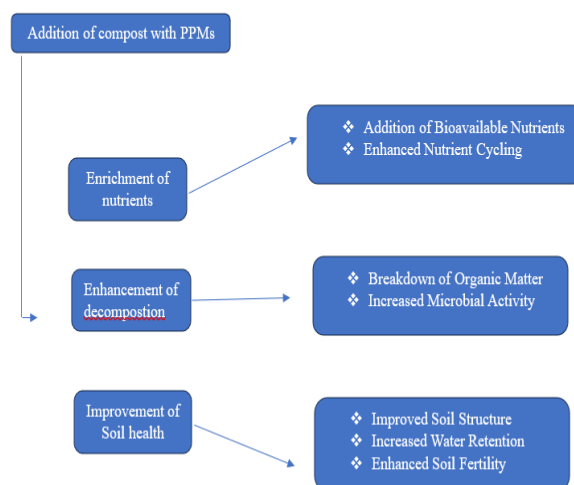


Fig. 3. Effect of PPMs on composting

## Conclusion

In a scenario where sustainable development has gained its importance, shifting to a more ecologically safer method of agriculture is acceptable over the widespread use of chemicals and pesticides. In this context, relying on a safer plant growth promotion and protection method is worth mentioning. Plant probiotic microorganisms can be a potential and emerging alternative to these chemicals, along with other biofertilizers and biopesticides prevailing. Considering their immense role in plant growth promotion through (i) effectiveness and competitiveness in niche colonization, (ii) the ability to induce systemic resistance (ISR) in their hosts and (iii) the presence of antagonistic traits on pathogens (43), use of these probiotic microorganisms would give a synergistic and advantageous effect on crops.

The researchers may concentrate on the mechanistic insight of plant probiotic microorganisms in promoting plant growth and health in the future. Some non-culturable probiotic microbes may be researched by studying the homologous proteins or recombinantly expressing specific genes or gene clusters in cultivable strains. The behaviour and interactions of these PPMs with plants, environment and other microorganisms (the microbiome) remain poorly understood, even though many of these relationships are well-documented and the majority provide favourable consequences. However, a lot of consortiums have already been commercialized.

In the future, there should be a rise in the integration of PPMs with cutting-edge agricultural technology, including smart farming methods and precision agriculture. By enabling more efficient monitoring of plant and soil health, these technologies guarantee that PPMs can be applied in agricultural production systems in the most advantageous way possible. It is anticipated that the creation of regulatory frameworks would promote the safe and efficient application of PPMs in agricultural activities, opening the door for more precise regulations on microbial product use. The increased consumer demand for organic and sustainably produced food is expected to fuel the market for sustainable farming techniques using PPMs.

The increasing inclination towards eco-friendly pursuits and the need for sustainably cultivated and organic food may further enhance the financial feasibility of PPMs. Adding plant probiotic microorganisms (PPMs) to composting processes results in a compost that is improved in several ways, including its nutritional profiles and microbial diversity. As a result, the deliberate use of PPMs signifies a paradigm change in handling organic waste and producing compost that significantly increases agricultural sustainability and production (44).

Developing specialized microbial consortia for composting applications, process optimization, and compost quality enhancement would be the main goals of future developments in microbial technology. Utilizing sensors and data analytics to maximize probiotic activity and integrate PPMs with smart composting systems would

improve the monitoring and control of composting conditions. Regulations may be implemented as PPMs become more widely used to guarantee these microbial products' quality assurance and efficient usage.

PPMs are considered next-generation bio-fertilizers, and more research could be focussed on understanding molecular mechanisms in growth promotion. Using PPMs for sustainable and regenerative agriculture is broad and gives a bright scope for naturally promoting soil and plant health.

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## Authors' contributions

AR and JPB conceived the idea and wrote the manuscript. JPB gave ideas, and AR designed the diagrams and tables. RPT revised the manuscript. JPB, GM, RPT and HM finalized the manuscript. All authors read and approved the final manuscript.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interest to declare.

**Ethical issues:** None.

## Declaration of generative AI and AI-assisted technologies in the writing process

While preparing this work, the authors used Grammarly to improve the language and readability. After using this tool/service, the authors reviewed and edited the content as needed and took full responsibility for the publication's content.

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