Review

Unveiling the roles, mechanisms and prospects of soil microbial communities in sustainable agriculture

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Abstract

Soil hosts diverse microbial communities including bacteria, fungi, archaea, protozoans and nematodes among others, which are fundamental to sustainable agriculture and drive essential processes that underpin soil fertility, plant health, and ecosystem resilience. They promote plant growth through mechanisms like nitrogen fixation, phosphorus solubilization, production of growth-promoting substances, enhancement of nutrient uptake, improvement of soil structure and detoxification of harmful substances. Recently, there has been increasing interest in utilizing microorganisms to improve soil health and boost plant growth and efficiency, despite limited understanding of microbial diversity, microbe-plant interactions, and translating laboratory findings to field conditions. This interest is driven by the urgent need to feed the growing global population, placing pressure on arable land to produce high-quality yields. Conventionally, synthetic fertilizers have been extensively used to provide nutrients, promote plant growth, and increase crop productivity. Although synthetic fertilizers have revolutionized agriculture since the green revolution, their overuse has significantly harmed soil health, and reduced crop productivity. This review synthesizes the current knowledge on the mechanisms by which soil microbes influence sustainable agricultural practices, with a focus on soil nutrient cycling and plant–microbe interactions. We discuss the functions and mechanisms of important microbial groups, such as nitrogen-fixing bacteria, phosphorus-solubilizing bacteria (PSB), and fungi. Furthermore, we discuss the factors that influence soil microbial communities and highlight gaps in future research to maximize their potential use in agriculture. Understanding the significance and key mechanisms of microbial communities increases the potential of harnessing soil microbes as vital contributors to soil health and sustainable agriculture.

Keywords Nitrogen fixation · Phosphorus solubilizing bacteria · Soil microorganism · Soil health

1 Introduction

Soil serves as a habitat for a wide variety of microorganisms that play crucial roles in soil health, ecosystem stability, plant growth promotion, and productivity. These microbes encompass a diverse array of bacteria, fungi, actinomycetes, nematodes, protozoans, algae, protozoans and other soil micro faunal invertebrates that form symbiotic or associative relationships with plants, providing various benefits. Soil bacteria are the most abundant microorganisms

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in soil and their numbers range from 10^8 to 10^9 billion cells per gram of soil followed by fungi and actinomycetes respectively [1–4] (Table 1). Each group of these soil microorganisms interacts with plants in unique ways, offering specific benefits for plant growth and development. For example, free-living nitrogen-fixing organisms such as *Azotobacter*, *Clostridium*, and *Cyanobacteria* naturally inhabit the soil, where they convert atmospheric nitrogen (N_2) into ammonia (NH_3). This NH_3 is then converted into ammonium (NH_4^+) and nitrate (NO_3^-), forms that plants can absorb. In contrast, symbiotic diazotrophs, such as *Rhizobium* and *Bradyrhizobium* form symbiotic relationship with host plants, like legumes, and provide fixed nitrogen in exchange for carbon compounds to fulfil their energy needs [5, 6]. Others inhabit plant rhizosphere which include PSB microbes that intermediate in transforming insoluble phosphorus complexes into forms accessible to plants [7, 8].

Additionally, mycorrhizal fungi form symbiotic associations with plant roots, enhancing nutrient uptake, particularly phosphorus, in return for carbohydrates [9] and controlling plant diseases [10]. Ferris [11] also described soil nematodes as playing a vital role in maintaining the structure and function of the soil food web. These nematodes precisely control the population of other soil organisms, contribute to soil aggregation and aeration, supply food for other soil organisms, and consume organisms that spread plant diseases. Generally, by living in the rhizosphere of plant roots, forming symbiotic relationships or living freely in the soil, microorganisms contribute to soil fertility and promote the growth of nutrient-demanding crops.

Some soil microorganisms also act as biocontrol agents against plant pathogens. Certain bacteria and fungi produce antimicrobial compounds or compete with pathogens for resources, thus suppressing harmful organisms and reducing plant disease incidence. Moreover, some have been genetically engineered to produce enzymes and hormones, using various plant extracts and microorganisms such as bacteria, fungi, viruses, and microalgae to develop strong antimicrobial activities against plant pathogens [15]. For example, some bacteria have been discovered to produce peptides, cyclic lipopeptides, and polyketides, which primarily target fungal pathogens [16, 17]. Furthermore, soil microbes assist plants in tolerating various environmental stresses, such as drought, salinity, and extreme temperatures. They achieve this by producing stress-related hormones, enzymes and exudates, which trigger plant root mechanisms to efficiently enhance water and nutrient uptake, thereby improving plant tolerance against salinity conditions. Besides salinity, plant microbe association suggest that there are unknown molecular mechanisms reshaping the rhizosphere biota and the plant physiology to cope and adapt to drought stress and extreme temperatures [18].

Consequently, utilizing soil microorganism that promote plant growth and improve soil health aligns with principles of the United Nations Sustainable Development Goal of Zero Hunger and specifically targets sub-goal for sustainable food production using resilient agricultural practices, particularly by reducing the reliance on anthropogenic activities that degrade soil [19]. By enhancing soil fertility, nutrient cycling, and improving plant health and growth, soil microorganisms contribute to agro-ecological practices that promote long-term productivity and environmental conservation [20]. They provide a comprehensive view of soil ecosystems beyond just physical and chemical properties, helping to ensure the long-term productivity and environmental sustainability of soils.

In essence, plant-promoting microbes represent a promising avenue for revolutionizing agriculture, offering major benefits to conservation, regenerative and sustainable agriculture. An indulgent approach to interactions between plants and soil microbes opens up exciting opportunities to enhance agricultural systems and address global challenges in food security, climate sustainability, and biodiversity and ecosystem sustainability [21]. The aim of this review was to explore the roles of soil microorganisms in sustainable agriculture, with a keen interest in key microbial groups, including

Table 1 Typical summary range of numbers and biomass for different microbial groups found in the top 0–6 inches (0–15 cm) of soil

Microbial Group	Relative Number (cells/g of soil)	Biomass (µg/g of soil)	References
Bacteria	10^8–10^9	40–500	[1–4]
Fungi	10^4–10^6	100–1500	[1, 12]
Actinomycetes	10^6–10^8	10–100	[1]
Protozoa	10^3–10^5	1–10	[1]
Algae and Cyanobacteria	10^3–10^5	1–10	[1]
Archaea	10^6–10^7	10–50	[1–3]
Nematodes	10^2–10^3	1–100	[1, 13, 14]

Varies widely depending on several factors such as soil type, climate, vegetation, and land use

nitrogen-fixing bacteria, PSB, and fungi. It also examined the factors affecting soil microbial communities and pointed out areas for future research to enhance their application in agriculture.

2 Roles of soil microbial communities in sustainable agriculture

In recent years, there has been growing interest in harnessing the power of soil microorganisms in sustainable agriculture due to their essential roles in biogeochemical processes and other functions and services, such as soil structure formation, bioremediation, and the maintenance of plant health (Fig. 1) [22, 23]. These processes ensure the efficient recycling of essential nutrients, such as nitrogen, phosphorus, and carbon, maintaining soil fertility and supporting plant growth and development. Soil microbial communities act as ecosystem engineers by influencing soil aggregation, water retention, aeration, and root growth, creating a more robust and productive agricultural environment. Recent studies emphasize the synergistic interactions within diverse microbial communities, which support soil health and stimulate plant growth through intricate relationships, such as mutualistic symbiosis [20, 22, 24]. Furthermore, their diversity in soil enhances resilience to stress, facilitates adaptation to changing conditions, and ensures the continuity of vital ecosystem functions like nutrient cycling and carbon sequestration. For example, fungi are linked with the glomalin protein which is responsible for soil carbon storage and aggregate stability [25] Therefore, preserving microbial diversity through practices like crop rotation, organic farming, and minimizing pesticide use can improve soil structure, boost nutrient availability, and support long-term soil fertility [26–28].

Soil microbes also play as biological control of soil-borne diseases through competitive exclusion and antibiosis mechanisms [29]. Advances in microbiome research have identified specific microbes that can suppress plant diseases like *Fusarium, Rhizoctonia,* and *Phytophthora*, which could revolutionize integrated pest management strategies in agriculture [16, 30]. Soil microbes have been isolated and applied in synthetic biology and new insights offer the potential to engineer microorganisms through advanced molecular techniques for specific agricultural or environmental functions,
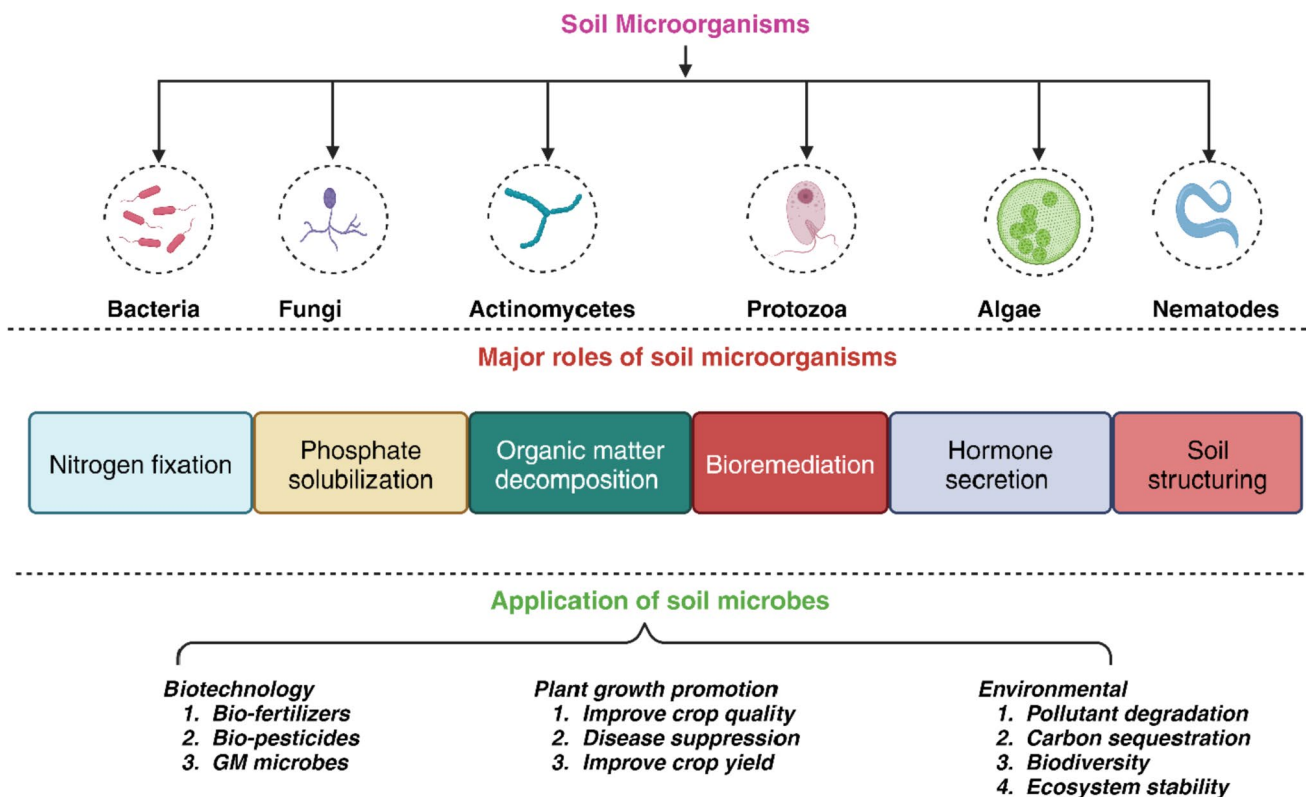

Fig. 1 Schematic illustration of soil microbes, their roles and applications in biotechnology, agriculture and environment. Source, this review. BioRender.com/v08n637

such as enhanced nutrient fixation, pollution degradation, resistance to pathogens, biofertilizers, biopesticides and carbon sequestration (Fig. 1).

These roles have significantly redesigned our insights into how life in soils function and how they can be managed for long-term agricultural productivity and soil health. Soil health management is changing because of the identification of soil microbial populations as crucial components and utilizing them in farming systems that are more robust, productive, and ecologically friendly by promoting microbial diversity, improving microbial functions, and incorporating microbial-based solutions into agricultural methods [31]. These innovative viewpoints offer fresh approaches to attain environmental sustainability, food security, and climate change mitigation in addition to challenging conventional agricultural methods. Agricultural practices that prioritize soil microbial health, including reduced tillage, crop rotation, organic farming, and agroforestry, are gaining recognition as essential components of sustainable agriculture [27, 28, 31]. These approaches foster the proliferation of beneficial microbes, support microbial biodiversity, and contribute to improved soil fertility, enhanced disease resistance, and healthy ecosystem services.

3 Soil bacteria

Soil bacteria are involved in various processes that are essential for plant growth and ecosystem stability. They inhabit the soil and then colonize plant rhizosphere (rhizosphere bacteria or rhizobacteria), reside in plant root tissues (endophytic bacteria), or on the plant root surface (epiphytic bacteria) [32]. Quantitative assessments of soil bacterial populations serve as critical indicators for evaluating soil health, enabling the determination of microbial diversity and abundance, which subsequently reflects the significance of bacterial activities in soil ecosystems. Such understanding helps in grasping ecosystem dynamics, monitoring environmental impacts, and guidance on sustainable land management practices. Listed in the subsequent subsections are some key plant growth-promoting bacteria (PGPB) that enhance plant growth and health through various mechanisms.

3.1 Nitrogen fixing bacteria

Nitrogen is one of the essential macronutrients required for plant growth and development, while it is also the most limiting. It is a crucial component of amino acids which are the building blocks of proteins. Proteins are essential for various biological processes in plants, including cell structure, enzyme functions, and metabolic pathways. Therefore, nitrogen is indispensable for the synthesis of proteins necessary for plant growth, development, and overall health. It is also vital in chlorophyll formation, making it essential for photosynthetic activity. Other functions of nitrogen include the promotion of vegetative growth, enhancing yield and quality, and finally, the regulation of metabolic processes [33].

In soil, nitrogen is present predominantly in two main forms: inorganic form making up to about 2%, while organic forms account for approximately 98% [24]. The inorganic forms comprise of NH_3, NH_4^+, NO_2^-, and nitrites (NO_3^-). Organic nitrogen is found in living or non-living organic matter such as soil biota, live animals and plant remains. Biological nitrogen is not directly available to plants and must be converted through the mineralization process to NH_3 or NO_3^-. This process is, however, very slow and its availability to plants is always competed by denitrification, soil erosion or leaching. To avail more N to plants, artificial inorganic nitrogen fertilizers using fossil fuels have been introduced to compensate for N deficiency in the soil [34]. Synthetic N is, however, detrimental to soil because it leads to pollution which adversely affects soil health and environment at large. To reduce this problem, the use of nitrogen-fixing bacteria as an alternative is considered an environmentally friendly solution.

Nitrogen-fixing bacteria collectively referred to as diazotrophic communities are microorganisms that are responsible for converting atmospheric nitrogen into forms that plants can use through a process called biological nitrogen fixation (BNF) [35]. They either form symbiotic relationships with host leguminous plants such as common beans (*Phaseolus* spp.), soybeans (*Glycine max*), peas (*Pisum* spp.), lentils (*Lens culinaris*), chickpeas (*Cicer arietinum*), peanuts (*Arachis hypogaea*), clover (*Trifolium* spp.), lupins (*Lupinus* spp.) and alfalfa (*Medicago sativa)* among others, or live freely in soils. Nodulating bacteria collectively known as rhizobia infect the host plant roots or stems, forming specialized structures known as nodules, where they multiply, and at maturity convert atmospheric nitrogen into ammonia, providing a crucial nitrogen source for the plant. These bacteria in return receive energy from the host plant in the form of photosynthates. Similarly, the non-nodulating free-living soil bacteria also contribute to soil fertility by converting atmospheric nitrogen into inorganic forms usable by plants [36]. Examples of bacteria well known for biological nitrogen fixation through nodulation include members of *Rhizobium* [37]*, Bradyrhizobium* [38]*, Frankia* [39]*, Mesorhizobium* [40]*, Sinorhizobium/Ensifer*

[41], *Paraburkholderia* [42], *Microvirga* [43] and *Methylobacterium* [44] among others. Members of free living nitrogen-fixing bacteria include *Cyanobacteria* (blue-green bacteria), *Clostridium, Azotobacter, Burkholderia, Klebsiella, Derxia* and *Azorhizobium* among others [45–48] (Table 2).

3.1.1 Mechanism of biological nitrogen fixation

The principal mechanism of biological nitrogen fixation involves the enzyme nitrogenase, which catalyzes the reduction of atmospheric N_2 to NH_3. The process begins when nitrogen fixing bacteria cells in the soil recognize specific chemical signals, collectively known as flavonoids released by plant roots in response to nitrogen deficiency in soil. In response to these signals, the bacteria *nodD* gene triggers transcription of nod genes (*nodA, nodB, nodC, nodE, NodL* and *nodM*) and encode enzymes (e.g. *Acyltransferase, chitin deacetylase and chitin synthase*) and proteins (e.g. *Symbiotic Receptor-like Kinase, Symbiosis-Specific Remorin, Nuclear Factor Y, Subunit A1 and Calcium-Dependent Protein Kinases,*) that facilitate the production of nodulating factors which are recognized by plant receptors. Most bacteria infect the root hairs and then initiate root curling and nodule formation [99, 100]. Once inside the root nodules, the bacteria differentiate into bacteroids, specialized forms capable of nitrogen fixation, and provide fixed nitrogen to the host plant (Fig. 2). They do so by undergoing morphological and physiological changes, including cell elongation and increased cell membrane permeability and utilization of plant carboxylates [101]. In the absence of oxygen during this symbiotic association, the nitrogenase enzyme complex system consists of two main components: iron (Fe) and molybdenum-iron (MoFe) proteins. The Fe protein acts as a shuttle, transferring electrons from a donor to the MoFe protein, where nitrogen fixation occurs.

The MoFe protein contains the active site where nitrogen reduction takes place, requiring a constant supply of energy in the form of ATP [35]. The electrons necessary for nitrogen reduction are provided by electron donors such as reduced ferredoxin or flavodoxin. Nitrogenase is highly sensitive to oxygen and is irreversibly inhibited by its presence. Therefore, nitrogen-fixing bacteria creates anaerobic conditions within specialized cellular structures to protect nitrogenase activity. In the case of symbiotic nitrogen-fixing bacteria such as *Rhizobium*, specialized root nodules are formed on the host plant's roots, providing an environment conducive to nitrogen fixation. Free-living nitrogen-fixing bacteria may form cysts or spores or reside in oxygen-depleted soil microsites to avoid oxygen inhibition. Nitrogenase complex catalyzes the reduction of atmospheric N_2 and convert it to NH_3 in presence of energy in form of ATP. This ammonia is then utilized by both the plant and the bacteria for their nitrogen requirements [102] (Fig. 2).

3.1.2 Role of nitrogen fixing bacteria in sustainable agriculture

The ability of nitrogen-fixing bacteria to biologically fix atmospheric nitrogen allows leguminous plants to thrive in nitrogen-deficient soils and reduces the need for synthetic nitrogen fertilizers in agriculture. These bacteria establish a highly specific symbiotic relationship with leguminous plants. A diverse species of these microbes exhibit host specificity, meaning that different strains form symbiotic relationships with specific legume species while others are fix nitrogen without forming the relationship [24]. This specificity is determined by the compatibility between the bacterial nodulation genes and nodulation receptor proteins of the plant. *Rhizobium*-legume symbioses, for example, are highly co-evolved, with each partner exerting selective pressure on the other to maintain compatibility and optimize nitrogen fixation efficiency [103].

In agriculture, nitrogen fixing inoculants are commonly used to improve soil fertility and enhance crop yields in legume cultivation [40]. These inoculants consist of selected strains of rhizobia that are applied to seeds or soil prior to planting. By introducing compatible nitrogen fixing strains to the rhizosphere of leguminous crops, farmers can promote efficient nodulation and nitrogen fixation, leading to increased plant growth, productivity, and nitrogen inputs into the soil [23]. The use of rhizobia-based inoculants offers several environmental benefits. For example, by reducing the need for synthetic nitrogen fertilizers, inoculation with nitrogen fixing bacteria helps mitigate nitrogen pollution of water bodies or underground water, greenhouse gas emissions, and soil degradation associated with conventional agricultural practices [20]. Additionally, the nitrogen fixed by soil bacteria becomes available to subsequent crops or is retained in the soil, contributing to long-term soil fertility and sustainability. On-going research on elite inoculants of biological nitrogen-fixing bacteria focuses on understanding the molecular mechanisms underlying symbiotic interactions, enhancing the efficiency of nitrogen fixation, and expanding the range of legume hosts and other plants that can form symbioses with wide range of bacteria and fungi [104].

Similarly, those living without direct interaction with other organisms, for example, members of the genus *Azotobacter* are also being investigated. Genetic engineering techniques have also been explored to improve the performance of

Table 2 Various nitrogen-fixing bacteria, their mode of association, and origin

Species	Mode of association	Isolation source/host plant	Reference
Anaeromyxobacter oryzisoli	Free living	Paddy soil	[49, 50]
Anaeromyxobacter soli sp	Free living	Paddy Soil	[50]
Anaeromyxobacter terrae sp	Free living	Paddy Soil	[50, 51]
Azospirillum lipoferum	Free living	Soil	[52]
Azotobacter beijerinckii	Free living	Laboratory	[53]
Azotobacter beijerinckii	Free living	Wheat/Rice	[54, 55]
Azotobacter chroococcum	Free living	Cow dung compost	[56]
Azotobacter vinelandii	Free living	Soil	[57]
Bacillus subtilis	Free living	Cow dung compost	[56, 58]
Bradyrhizobium diazoefficiens	Symbiosis	Pigeon Pea	[59, 60]
Bradyrhizobium japonicum	Symbiosis	Soybean nodules	[61]
Bradyrhizobium ottawaense	Symbiosis	Soybean nodules	[62, 63]
Bradyrhizobium shewense	Symbiosis	*Erythrina brucei*	[64]
Bradyrhizobium sp.	Symbiosis	Serradella	[65]
Bradyrhizobium symbiodeficiens	Symbiosis	Hog Peanut	[66]
Bradyrhizobium yuanmingense	Symbiosis	Peanut	[38, 67]
Bradyrhizobium sp	Symbiosis	Coffee	[68]
Burkholderia cepacia	Symbiosis	Chickpea	[69, 70]
Candidatus Phyllobacterium	Symbiosis	Astragalus	[71]
Ensifer medicae	Symbiosis	Medic	[72, 73]
Ensifer meliloti	Symbiosis	Medic	[74]
Klebsiella variicola	Symbiosis	Sugarcane	[75]
Kosakonia radicincitans	Free living	Maize roots	[76]
Mesorhizobium ciceri	Symbiosis	Chickpea	[77, 78]
Paenibacillus brassicae sp	Free living	Cabbage	[79]
Paenibacillus sinensis sp	Free living	Wheat	[80]
Paenibacillus vini sp.	Free living	Fermentation pit	[81]
Pseudomonas stutzeri	Free living	Maize rhizosphere	[82]
Raoultella electrica	Free living	Midgut of insect	[83]
Rhizobium anhuiense	Symbiosis	Faba bean/Pea	[84]
Rhizobium etli and R.Nodulate	Symbiosis	Common bean	[85, 86]
Rhizobium gallicum	Symbiosis	Common bean	[87]
Rhizobium mesosinicum	Symbiosis	Coffee	[68]
Rhizobium multhospitiium	Symbiosis	Coffee	[68]
Rhizobium multihospitium	Symbiosis	Chickpea	[88]
Rhizobium pusense	Symbiosis	Mung bean	[89, 90]
Rhizobium leguminosarum	Symbiosis	Clover	[91]
Rhizobium sullae	Symbiosis	Sulla	[92]
Rhizobium tropici	Symbiosis	Common bean	[93, 94]
Rhizobium phaseoli	Symbiosis	Common bean	[6]
Sinorhizobium fredii	Symbiosis	Wild Soybeans	[95]
Sinorhizobium meliloti	Symbiosis	Medic	[96, 97]
Symbiovar Sojae	Symbiosis	Soybean Nodules	[98]

beneficial strains under diverse environmental conditions and agricultural settings [105, 106]. Recent examples include modifications of *Agrobacterium rhizogenes* [107] and *Sinorhizobium meliloti* [108] using Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated protein 9 (CRISPR/Cas9) editing technology.
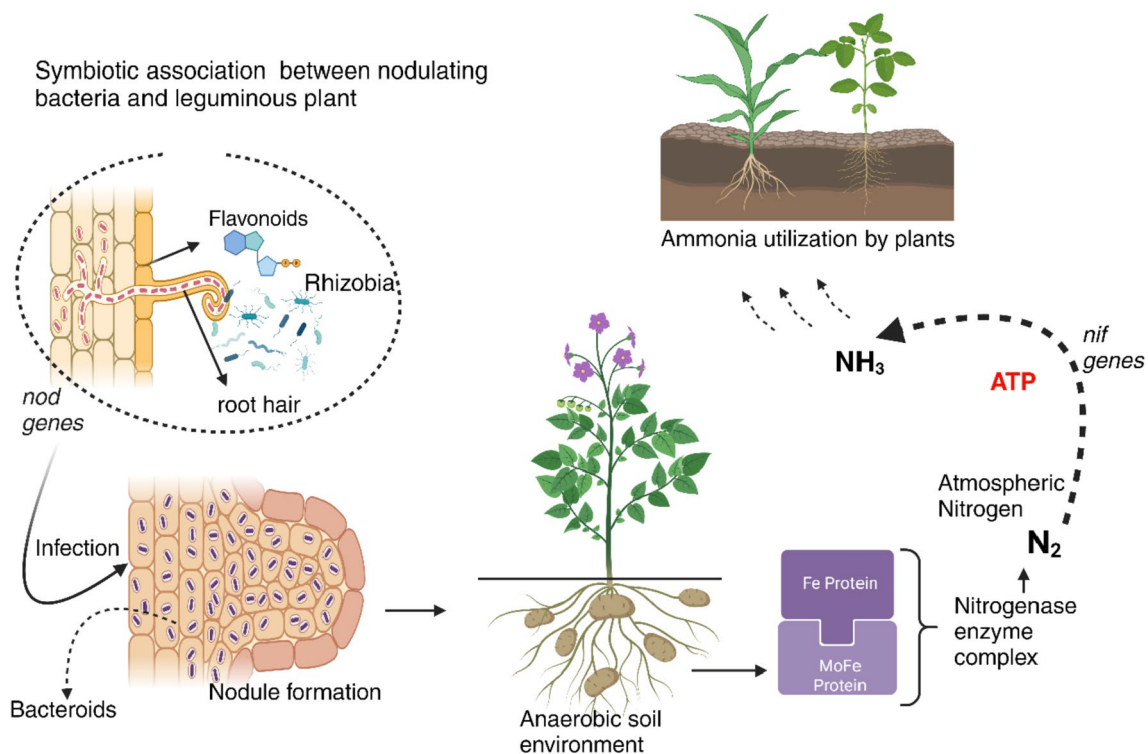
Fig. 2 The schematic illustration of the main steps involved in the nitrogen fixation process, including the recognition and infection of plant roots by nitrogen-fixing bacteria, the formation of nodules, the establishment of an anaerobic environment within nodules, the activation of nitrogenase enzyme complexes, and the conversion of atmospheric nitrogen into ammonia for plant utilization. Source, this review. BioRender.com/h22o238

3.2 Phosphorus solubilizing bacteria

P is a crucial macronutrient essential for plant growth and development, second only after N in importance. It plays a critical role during the early stages of plant growth. The main functions of phosphorus include energy storage and transfer, nucleic acid synthesis, formation and structuring of cell organelles, photosynthesis, cell division, shoot elongation, and root development [21]. When plants are deficient in phosphorus, they exhibit symptoms such as stunted growth, purplish leaves, weak stems, necrotic spots, leaf curling, poor flower and fruit development, delayed maturity, and ultimately reduced yields. In the soil, P exists in two forms: (i) organic P from decomposed plant and animal residues, which is not readily available to plants and requires mineralization, and (ii) inorganic phosphorus from mineral sources, often bound with other elements like aluminum ($AlPO_4$), iron ($FePO_4$), zinc ($Zn_3(PO_4)_2$), and calcium ($Ca_3(PO_4)_2$). These inorganic forms are available in very low quantities and are released slowly owing to their complex structure. Soil microorganisms help mitigate this issue by solubilizing phosphorus, thereby enhancing its availability for plant uptake and promoting growth and development.

PSB are highly effective microorganisms that make both organic and inorganic phosphorus compounds readily available for plant uptake [8]. These bacteria are found in diverse environments such as agricultural soils, the rhizosphere of plants, root nodules of leguminous plants, compost materials, water, sewage, and decaying organic matter. Examples of PSB that have been found to effectively solubilize and mineralize phosphorus include species from the genera *Agrobacterium* spp. [109], *Pseudomonas* spp. [110], *Bacillus* spp. [111], *Rhizobium* spp. [112], *Bradyrhizobium* spp. [113], *Enterobacter* spp. [7] and *Burkholderia* spp. [22]. Recent studies have also identified additional PSB such as *Azotobacter* spp. [55], *Kushneria (90)* spp. [114] *Paenibacillus* [115], *Rhodococcus* spp. [116], *Salmonella* spp. [117], *Sinomonas* spp. [118], *Thiobacillus* spp. [119], *Azospirillum* spp., *Klebsiella* spp., and *Serratia* spp. [8] (Table 3).

Table 3 Various bacterial species involved in phosphorous solubilization, and their origin

PSB	Source	Cultivated plant	References
Pseudomonas spp.	Cultivated bulk soil	Wheat	[120]
	Semiarid bulk soil	Wheat	[121, 122]
	Rhizosphere soil	Poplar	[123]
	Rhizosphere soil	Tomato	[124, 125]
	Rhizosphere soil	Common bean	[7]
	Cultivated bulk soil	Onion	[126]
	Cultivated bulk soil	Groundnut	[127]
	Rhizosphere soil	Wheat	[128]
	Rhizosphere soil	Soybean	[129, 130]
	Rhizosphere soil	Chilli	[131]
Enterobacter spp.	Rhizosphere soil	Cabbage	[132]
	Rhizosphere soil	Maize	[133]
	Rhizosphere soil	Common bean	[7]
	Rhizosphere soil	Wheat	[134, 135]
	Cultivated bulk soil	Pepper	[136]
	Rhizosphere soil	Rice and peanut	[137]
	Rhizosphere soil	Sugarcane	[138]
	Rhizosphere soil	Potatoes	[139]
	Rhizosphere soil	Alfa alfa	[140]
	Rhizosphere soil	Forage grasses	[141]
	Rhizosphere soil	Grapevines	[142]
Bacillus spp.	Cultivated bulk soil	Rice	[143]
	Cultivated bulk soil	Wheat	[144]
	Rhizosphere soil	Wheat, maize	[145]
	Rhizosphere soil	Wheat	[146]
	Rhizosphere soil	Tomato	[125, 147, 148]
	Cultivated bulk soil	Wheat	[120]
	Cultivated bulk soil	Groundnut	[149]
	Cultivated bulk soil	NT	[150]
	Rhizosphere soil	Guinoa	[151]
	Rhizosphere soil	Chickpea	[152]
Burkholderia spp.	Rhizosphere soil	Pigeon pea	[153]
	Cultivated bulk soil	NT	[154]
	Cultivated bulk soil	Rice	[155]
	Cultivated bulk soil	Corn, soybean, rice	[156]
	Cultivated bulk soil	Tea	[157, 158]
	Rhizosphere soil	NT	[159]
	Soybean rhizosphere	Tomato	[160]
	Rhizosphere soil	Barley	[161]
	Rhizosphere soil	Rice	[162]
Rhizobia spp.	Root nodules	Soybean	[163]
	Cultivated bulk soil	NT	[164]
	Root nodules	Soybean	[165]
	Root nodules	Several legumes	[166]
	Root nodules	Common bean	[6]
Azospirillum spp.	Rhizosphere soil	Wheat	[167, 168]
	Cultivated bulk soil	Maize	[169]
Serratia spp.	Cultivated bulk soil	Onion	[126]
	Cultivated bulk soil	Faba	[170]
	Rhizosphere soil	Peanuts and Maize	[171]
	Rhizosphere soil	Wheat	[172, 173]
Mesorhizobia spp.	Rhizosphere soil and root nodules	Chickpea	[174, 175]

NT- The strains were not tested with any plants but were evaluated in laboratory assays
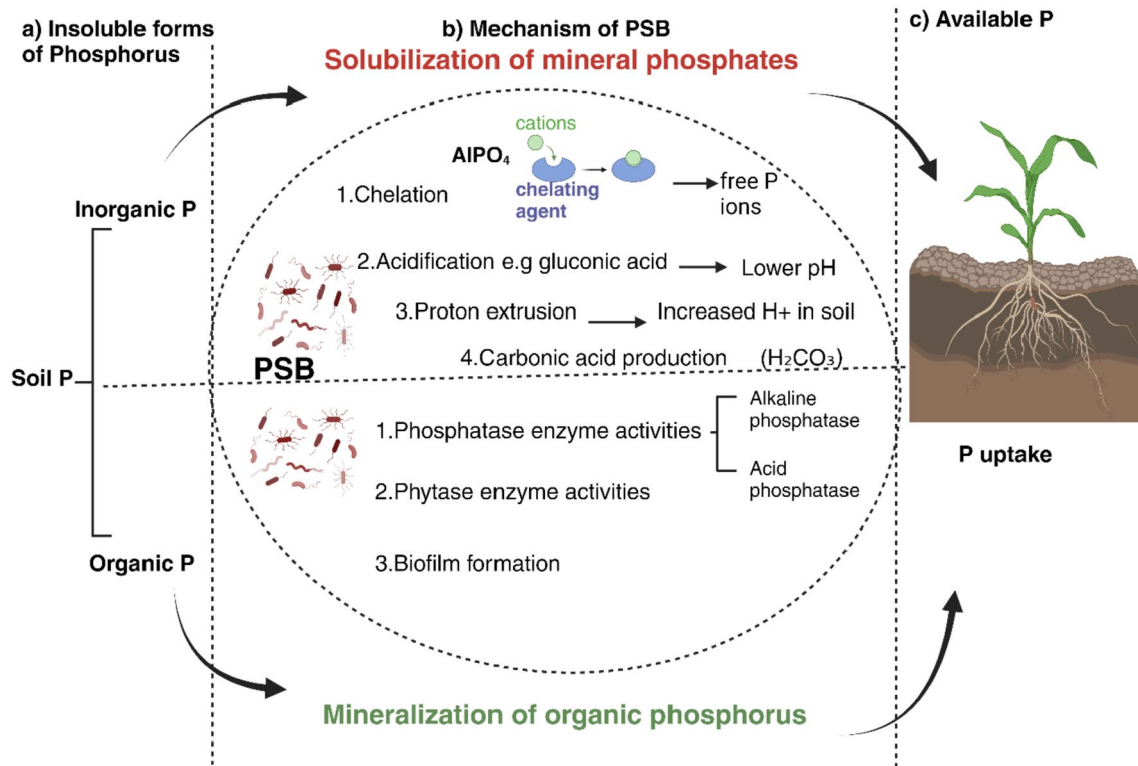
Fig. 3 A schematic illustration of the mechanisms of PSB through mineralization and solubilization of soil P into soluble forms for plant uptake. Source, this review. BioRender.com/p19q137

3.2.1 Mechanisms of phosphorus solubilizing bacteria

PSB utilizes two primary mechanisms: solubilization of mineral phosphates and mineralization of organic phosphorus. These mechanisms highlight the processes of inorganic phosphate solubilization and organic phosphorus mineralization together with other cascades of events in soil as described previously [109]. To solubilize mineral phosphates, bacteria produce organic acids, chelating agents, proton extrusion, and weak carbonic acid formation. For mineralization of organic and inorganic phosphorus, bacteria secrete phosphatase and phytase enzymes, modifying the soil environment and increasing phosphorus availability (Fig. 3).

In the acidification theory, hydrogen ions play a key role in the solubilization of mineral phosphate. PSB secretes various organic acids, such as citric acid, oxalic acid, lactic acid, gluconic acid, and acetic acid. These bacteria release acids through their oxidation and metabolic pathways into the periplasmic space, allowing organic acids to enter the soil environment and cause a pH decline [119]. The resulting decrease in pH leads to the release of free hydrogen ions (H^+) in exchange for cations present in the complexes, which then facilitates the dissolution of insoluble mineral phosphates, such as tricalcium phosphate and dicalcium phosphate, converting them into soluble phosphate ions ($H_2PO_4^-$, HPO_4^{2-}) available for plant uptake. Additionally, it has also been shown that the solubilization of mineral phosphate can occur in microbial cells and soil environment without production of organic acids through proton extrusion process. PSB participate actively in transportation of protons in form of H^+ ions from their cells into the surrounding soil environment, resulting in the solubilization of phosphorus without the production of organic acids [176]. Furthermore, the solubilization of mineral phosphates is achieved by PSB-producing chelating agents such as siderophores. Complexes, such as aluminum phosphate, zinc phosphate, and calcium phosphate, have strong metallic bonds, making phosphorus less available to plants. Chelating agents bind to metal ions (e.g., Ca^{2+}, Fe^{3+}, and Al^{3+}) that are commonly associated with these insoluble phosphate complexes, thus freeing the phosphorus for plant use [177].

To mineralize organic phosphorus, bacteria secrete enzymes such as phosphatases and phytases (Fig. 3). Alkaline phosphatase catalyzes the hydrolysis of phosphate substrates in alkaline soil environments, while acid phosphatase performs this function in acidic environments. Phytase specifically targets hydrolyzes phytate (myo-inositol hexakisphosphate), a prevalent form of organic phosphorus in soil that is not directly available to plants. The secretion of phosphatase enzymes

is related to the combined but distinct functions of phosphomonoesterase (PME) and phosphodiesterase (PDE) [119]. PME catalyzes the hydrolysis of phosphate monoesters (acid and alkaline phosphatases) releasing inorganic phosphate and alcohol. PDE hydrolyzes diesters such as nucleic acids and phospholipids into phosphomonoesters (inositol phosphates and mononucleotides), which are then transformed into bioavailable inorganic phosphorus. PSB such as *Pseudomonas, Enterobacter,* and *Pantoea* enzymatically mineralize soil phosphorus into soluble forms using these processes [21, 119].

3.2.2 Utilizing PSB for agriculture

PSB typically improves soil fertility and supports sustainable agriculture by making natural phosphorus more accessible to plants, which reduces the necessity for chemical phosphorus fertilizers [71]. This not only decreases production costs for farmers but also reduces environmental pollution caused by the overuse of chemical fertilizers. To utilize PSB, it is necessary to isolate the bacteria from various environments and assess their efficiency both in the laboratory and in the field. The rhizosphere, which is known for its high microorganism density, is a preferred source for researchers seeking effective solubilizing bacteria. Nevertheless, other sources of PSB include soil, water, decomposing organic matter/plant residues, and root nodules (Fig. 4).

To identify effective PSB, bacteria are isolated and cultured using suitable culture media such as Pikovskaya, developed by Russian scientist Raisa Yakovlevna Pikovskaya in 1948 [178] and NBRIP (National Botanical Research Institute Phosphorus Growth Medium), considered as most efficient medium which was modified by Nautiyal in 1999 [179]. Pikovskaya medium comprises 10 g of glucose, 5 g of calcium phosphate ($Ca_3(PO_4)_2$), 0.5 g of ammonium sulfate (($NH_4)_2SO_4$), 0.2 g of sodium chloride (NaCl), 0.1 g of magnesium sulfate ($MgSO_4$), 0.2 g of potassium chloride (KCl), traces of manganese sulfate ($MnSO_4$) and ferrous sulfate ($FeSO_4$) each at 0.002 g, 0.5 g of yeast extract and 15 g of agar.
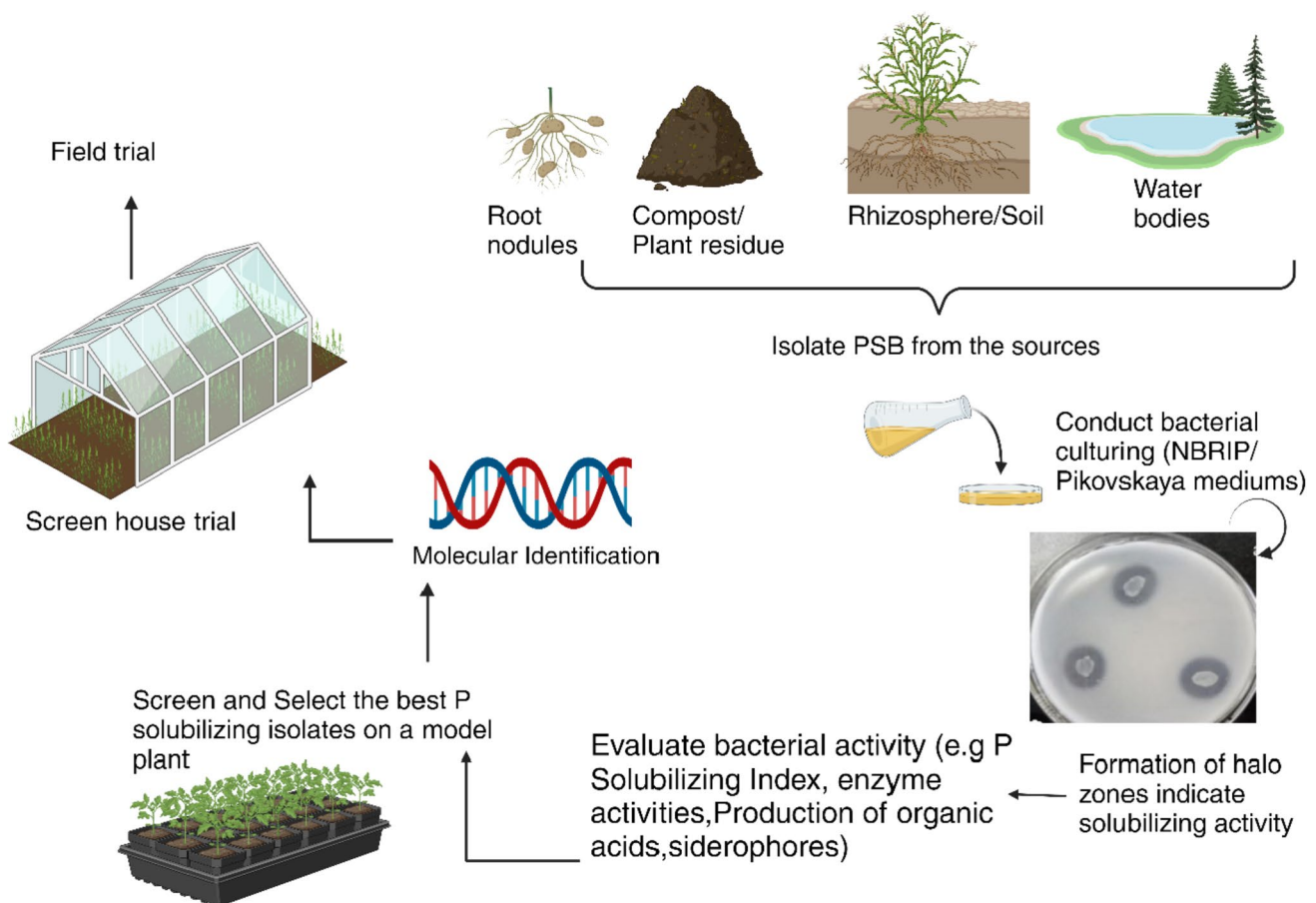

Fig. 4 Schematic representation of PSB isolation, culture, screening, molecular identification, and trials. Source, this review. BioRender.com/ z52n260

NBRIP medium without yeast extract contains 10 g of glucose, 5 g of $Ca_3(PO_4)_2$, 0.5 g of $((NH_4)_2SO_4)$, 0.2 g of NaCl, 0.1 g of $MgSO_4 \cdot 7H_2O$, 0.2 g of KCl, 0.002 g of $MnSO_4 \cdot H2O$, 0.002 g of $FeSO_4 \cdot 7H_2O$ and 15 g of agar. After culturing, in-vitro visual assays are conducted to determine the solubilizing indices, as PSB grows and forms halo zones in the agar medium, differentiating efficient solubilizers from non-solubilizers. This is followed by a colorimetric analysis of released amount of phosphorus, phosphatase enzyme activities, phytase activity, among other measurements using broth medium. Once the efficient solubilizers are identified in the laboratory, the inoculants are prepared and screened under controlled conditions for plant growth promotion using a model plant in the screen house to further determine and select efficient isolates for use as biofertilizer (Fig. 4).To identify the isolated PSB at the species level, genomic distinctiveness, and phylogenetic relationships, several advanced molecular approaches have been used, including extracting the genomic DNA of the bacteria, amplification, sequencing using a reference database, and bioinformatics analysis to comprehensively study the genetic material for a deep understanding of molecular mechanisms [7, 119].

Extensive utilization of PSB in agriculture has been documented, and numerous strains have been identified as effective inoculants (Table 3). However, although experiments in controlled environments have been well-documented, field studies are comparatively limited, leading to an urgent need for further investigations. Implementing PSB inoculants has shown to enhance plant growth and development by increasing root and shoot biomass, improving root and shoot length, improving vegetative vigor and plant biomass and yield in various crops [120, 180–183]. These findings underscore the promising future of PSB in sustainable agriculture. It is then beneficial practice in soil amelioration which contributes significantly to microbial rhizosphere management and nutrient cycling for sustainable agriculture. More research in this area is necessary to unveil more beneficial PSB and test them under field conditions for agricultural sustainability and food production.
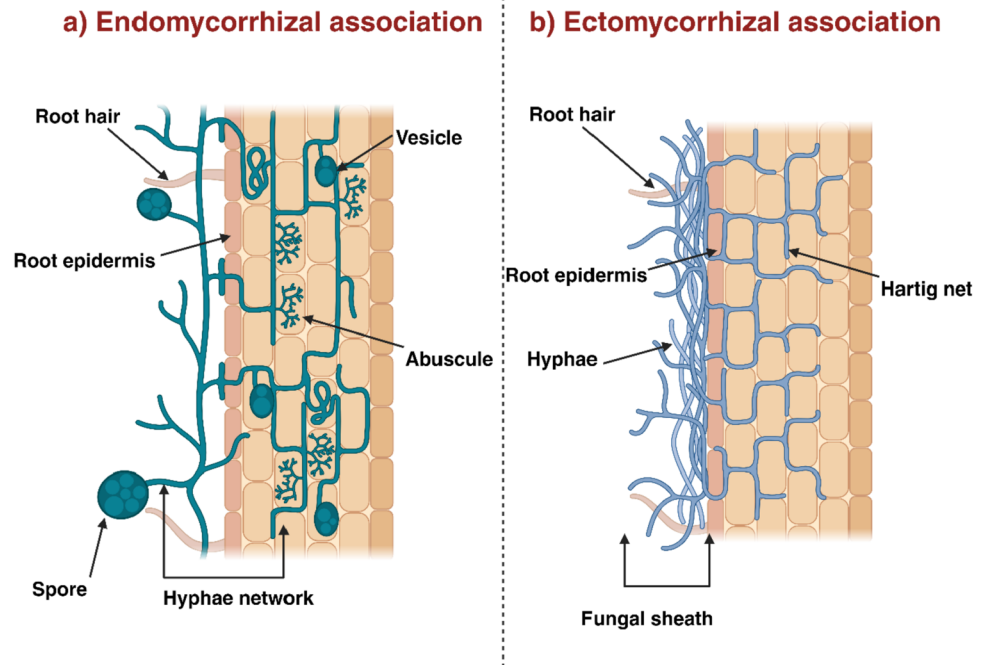
4 Soil fungi

Soil fungi are the second most critical microbes in the soil after bacteria, thriving even under adverse and unfavorable conditions due to their adaptability and high plasticity in response to physiological changes in the soil [184]. Fungi vary in size, ranging from microscopic spores that cannot be seen, to large fruiting bodies and other structures visible to the naked eye. Their primary function is to decompose organic matter and break down soil components, thereby balancing the ecosystem[185]. By secreting extracellular enzymes, fungi connect soil matter and plants, break down and decompose organic material, and play a vital role in nutrient cycling, particularly nitrogen and phosphorus. Although most fungi are beneficial, some fungi interact with other soil microorganisms, invade the plant materials and cause pathogenic effects leading to diseases.

Most beneficial fungi form symbiotic relationships with almost 90% of plants by forming hyphae networks. Fungi have filamentous bodies called hyphae that attach to the network of plant root hairs and acquire nitrogen, phosphorus, other micronutrients, and water in exchange for the carbohydrates produced by the plant. This mutually beneficial symbiotic relationship is termed as mycorrhizae network. Examples of fungi that participate in this symbiotic relationship include arbuscular mycorrhizal fungi (AMF) and ectomycorrhizal fungi[17, 186]. AMF are considered the most beneficial group of endophytic fungi, providing comprehensive benefits to plants, including tolerance to various stressful situations such as heat, salinity, drought, metals, and extreme temperatures [185]. AMF has been categorized taxonomically, primarily under the phylum *Glomeromycota*. They are classified into the orders *Glomerales, Archaeosporales, Paraglomerales,* and *Diversisporales*. The prominent families within these orders are *Glomeraceae, Gigasporaceae*, and *Acaulosporaceae*. The genera included in these families are *Glomus, Sclerocystis, Acaulospora, Entrophospora, Gigaspora*, and *Scutellospora* [187].

Members of the ectophytic fungi belonging to the phylum Ascomycota have long been known to be efficient antagonists of plant pathogenic microorganisms. Some recently investigated and confirmed to be beneficial include genera *Trichoderma* spp. *Aspergillus* spp. *Amanita* spp. *Boletus* spp. and *Laccaria* spp. and *Penicillium* spp. [188, 189]. Conversely, fungi from the Phylum Basidiomycota are primarily recognized for their role as decomposers. They secrete extracellular enzymes that enable the breakdown of lignin and the decomposition of organic materials like dead plants and wood, thus recycling nutrients back into the soil. This capability makes them important in bioremediation because they can degrade various pollutants, including pesticides and heavy metals in soil and water environments. Research has utilized these fungi to clean up contaminated soils and enhance the health of agricultural land [186, 190]. Some important species of this phylum that have proven agricultural benefits include; *Agaricus bisporus* [191], *Lentinula edodes* [192], *Pleurotus ostreatus* [193], *Tricholoma matsutake* [194], *Ganoderma lucidum* [195], *Phanerochaete chrysosporium* [196], *Coprinus comatus, Armillaria mellea* and *Scleroderma citrinum* [197].

Fig. 5 Schematic illustration of mycorrhizal association of soil fungi. **a** Endomycorrhizae association (arbuscular mycorrhizal fungi) and **b** ectomycorrhizal association. Source, this review. BioRender.com/o59n550

4.1 Mechanisms via which soil fungi support plants

Soil fungi primarily function by forming mycorrhizal associations with plants, which can be categorized into two types: Ectomycorrhizal and Endomycorrhizae (Arbuscular Mycorrhizal) associations [185]. Ectomycorrhizal association is where fungi envelop the surface of the plant's epidermal roots, forming fungal sheath without forming arbuscules. Instead, they form a Hartig network and extend hyphae into the soil to boost nutrient absorption, particularly phosphorus and nitrogen, and other nutrients required by the plants. Endomycorrhizae on the other hand, is where fungi penetrate plant root cells, forming complex structures known as arbuscules and vesicles inside the dermal cells of plant tissues (Fig. 5).

Endomycorrhizal association is commonly found in herbaceous plants and food crops. Both associations are mutualistic, benefiting plants with nutrients, water, and signaling antibiotic molecules that aid in defense against soil borne harmful pathogens and diseases, while fungi receive metabolites such as carbohydrates in return. The extensive hyphal network between fungi and plants not only enhances nutrient acquisition but also improves soil structure, increasing soil porosity and water-holding capacity, thereby enhancing water absorption by plants, particularly under drought conditions. AMF is associated with the exudation of glomalin protein which is responsible for carbon storage, stress tolerance and soil aggregate stabilization [25]. This aids plants in tolerating diverse environmental stressors and adapting to drought [190]. Fungi act as osmotic regulators in saline environments, assisting plants in adapting and surviving under such conditions. Additionally, they produce compounds that aid in detoxifying heavy metals and pollutants arising from human activities such as pesticide and herbicide use. Lastly, soil fungi are key decomposers of organic matter, breaking down complex organic compounds into simpler forms that plants can absorb as nutrients. This decomposition process releases nutrients, such as nitrogen, phosphorus, and potassium back into the soil, thereby enriching its fertility [30, 190].

5 Factors influencing soil microbial communities

Soil microbial communities play a major role in nutrient cycling and growth and development of plants. Nonetheless, certain factors constantly control their composition, organization, and roles in the soil. Agricultural management systems, soil types, climate change, plant species, and other land management practices can all have an impact on

the microbial populations in the rhizosphere and soil in agroecosystems [198, 199]. Crop rotation practices have been found to affect microbial abundance and diversity in agricultural management systems. For instance, Buyer et al. [198] found that different species of cover crops under rotation with other plants had unique root and shoot effects on soil microbial community composition. Further investigations showed that cropping sequence-induced changes in the soil microbial population had an impact on soil characteristics, suppression of plant pathogens, increased soil microbe enzymes and metabolic activities, and improved crop productivity [26, 27, 200]. Soil microbial populations can be affected by other agricultural practices, such as tillage, synthetic pesticides, and chemical fertilizers. Numerous studies have demonstrated that the use of chemical fertilizers reduces soil bacterial diversity (measured by the Shannon index) compared to the use of compost or manure [201]. In a different study, the continuous use of chemical fertilizer and long-term conventional tillage both considerably changed the composition of the microbial community, but the tillage effect was more extreme [202].

In terms of soil physical properties, the proportions of sand, silt, and clay affect pore space and water retention, which in turn influences microbial habitats [203]. Additionally, the aggregation of soil particles affects aeration and water movement, impacting microbial activity and diversity [204]. Furthermore, availability of water (soil water content) is crucial for microbial metabolic activities and influences the distribution and activity of microorganisms in soil [205]. Soil temperature has an impact on the metabolic rates and composition of microbial communities. Extreme temperatures affect the enzymatic activities of soil-dwelling microorganisms, altering their roles [206].

The availability of nutrients and the general composition of the microbial population are influenced by soil chemical properties, such as pH. While certain microbial species prefer differing pH level, for example, PSB may live in acidic or alkaline environments, the majority of microorganisms require an ideal pH between 6.0 and 7.0 [207]. The presence of essential nutrients in the soil, such as nitrogen, phosphorus, and potassium, are critical for microbial growth and activity. Organic matter provides carbon sources for microbial metabolism and influences soil community composition [208]. Saline and hypersaline environments host a vast array of prokaryotes, including bacteria and archaea. These microorganisms have adapted to thrive under high salt concentrations and elevated osmotic pressure [209].

An example of how these factors influence the activity and efficacy of PSB is dependent on many factors. The ability of PSB to convert insoluble phosphorus into soluble forms is due to the soil's nutrient richness, the bacteria's physiological capabilities, and their growth status. PSB tend to solubilize phosphate in soils under varying environmental conditions influenced by biotic and abiotic factors, such as soil acidity and alkalinity, salinity, nutrient levels, temperature, soil water content, soil type and texture, organic matter content, and human agricultural practices [210]. Studies on the impact of temperature on bacteria in phosphorus solubilization have been unreliable because most reported temperature information differs [22, 211]. For example, many studies have observed that majority of PSB at temperatures between 20 and 30 °C [22, 212–215] while others have documented between 30 °C and 40 °C [216, 217]. PSB also solubilizes phosphorus in areas with extreme temperatures [157, 218, 219].

Microbial interactions in soil coupled by vegetation cover and ecological conditions, land use, plant types and organic matter, and soil pH are all factors influencing the solubilization of P [22, 220, 221]. Hot humid climates solubilize phosphorus more quickly, whereas cool dry climates solubilize phosphorus more slowly. Compared to saturated wet soil, a well-aerated soil would allow for faster phosphorus solubilization [222]. In terms of pH, PSB tolerate both acidic soil using acid phosphatase and alkaline soils using alkaline phosphates, as well as optimal soil pH [223].

Factors influencing the roles, population, community structure, and distribution of fungi in soil include land management practices such as tillage, crop rotation, agroforestry and the use of organic or inorganic fertilizers, herbicides, and pesticides [10, 27, 202]. Additionally, general climate change affects fungi through variations in temperature, soil pH, and nutrient availability, leading to physiological changes in soil habitats [190]. Soil fungi have a significant influence on soil health, environmental sustainability, agricultural productivity, horticulture, and forestry. Furthermore, they indirectly contribute to plant physiology by influencing plant hormone levels and gene expression, leading to changes in plant growth and development, and increased yields, benefiting both humans and animals. More research is needed to determine optimal methods for preserving fungal biodiversity in soil, considering their roles and ecosystem services, such as disease control, pollution detection, and bioremediation [224].

Finally, the functions of soil microorganisms can be influenced by genetic factors. The genetic composition of microbial populations determines their metabolic capability and adaptability to environmental conditions. Genetic phenomena such as horizontal gene transfer, which involves the exchange of genetic material between microorganisms, can introduce new traits and impact community dynamics [225]. This process is common in bacteria that possess mobile genetic elements such as plasmids, transposons, and bacteriophages that facilitate genetic conjugation, transformation, and transduction. Evidence of horizontal gene transfer has been observed in symbiosis genes within and between *Rhizobia*

genera [226]. Environmental stressors, including the presence of toxic heavy metals, pesticides, and other pollutants in the soil, can lead to antibiotic resistance, metabolic changes, or increased virulence in microorganisms, thereby affecting the structure and function of the microbial community [221].

6 Knowledge gaps and prospects for research

Most research on applied microbiology, coupled with advanced molecular techniques, has laid a good foundation for exploiting the potential of the soil microbiome for sustainable agriculture. To build on this foundation, much research is needed to fully understand microbial diversity, interactions, and translation of laboratory findings to field applications. The key research gaps are as follows:

6.1 Microbial diversity and functions

Soil is a critical habitat for complex species (culturable and unculturable) of microbial communities, most of which are yet to be studied. Therefore, there is a need for a comprehensive understanding of the functional diversity of communities within diverse soil types and ecosystems. Advances in DNA sequencing platforms and methodologies such as metagenomics, metabolomics and transcriptomics will reveal functional diversity up to gene level within communities [31, 227–229]. Whole genome shotgun metagenomics sequences all the genetic material in a sample to analyze the collective genomes of the microbial community, whereas amplicon sequencing or metabarcoding approaches target specific marker genes, such as 16S rRNA for bacteria and archaea, or ITS and 18S regions for fungi, to study particular groups of microorganisms [229, 230].

6.2 Molecular mechanisms of microbial interactions

Although several molecular mechanisms of microbial communities are known, we are still far from fully understanding how microbes interact with each other and with plants in different agroecological systems. Agricultural production systems differ in terms of climate from tropical, dry, temperate, continental, polar, and high mountain (alpine) regions and different agricultural management practices, such as organic farming, crop rotations, agro-forestry, and cover cropping. A comprehensive indulgence of how microbes communicate, compete, adapt, or cooperate in diverse ecosystems using molecular mechanisms can help fine-tune agricultural practices that foster beneficial interactions in certain soils and climatic environments [25, 231]. Furthermore, particularly in developing countries, scientific evidence of the contribution of microbial communities to diverse food production systems is still limited. Therefore, more evidence is needed regarding the benefits of biological inputs over synthetic inputs or their synergetic effects.

6.3 Long-term effects of agricultural practices on microbial communities

Sustainable agriculture is shifting towards regenerative and conservation agriculture using resilient agricultural practices that favor soil health and crop productivity. These practices involve the use of reduced tillage systems, crop rotations, animal integration, cover crops, and crop diversity. There are limited studies on the roles of soil microbes in these systems and their impact, especially in developing countries. Additionally, there is limited long-term data on how these practices, such as reduced chemical inputs, crop rotation, and the use of bio-based fertilizers compared with conventional agricultural practices, affect soil microbial communities over decades. Similarly, there is limited understanding of how synthetic inputs, such as pesticides, herbicides, and chemical fertilizers, affect soil microbial diversity and functionality in the long term. Long-term data will help in understanding cumulative microbial dynamics over time [232].

6.4 Genetic manipulation and modification of microbial communities

Although some research has been conducted on the genetic manipulation and engineering of soil microbes, we are still far from fully harnessing these tools for practical applications in soil microbial management. Recent genetic engineering advancements hold potential for in situ control of microbial community composition, transforming the functionality

of existing microbiomes. A notable example is strain-specific CRISPR, which was developed to modify the composition of microbiome communities by selectively purifying or eliminating specific members of a synthetic host collection [233]. The CRISPR-Cas9 system enables rapid targeted genomic alterations in individual cells or organisms. It allows for genome-wide screening, epigenome modifications, transcription regulation, and chromosome imaging. In soil microbes, CRISPR-Cas9 systems can edit specific genes, facilitating the study of gene function and the development of beneficial traits such as availing of nutrients or disease resistance [234–236].

6.5 Microbial contributions to carbon sequestration

The global organic carbon contained in prokaryotes alone is comparable to that in plants [237]. Therefore, soil microbes are critical for soil carbon storage. This is achieved by breaking down organic matter and contributing to the formation of stable organic compounds. Although soil microbes are also involved in soil respiration, which leads to the release of greenhouse gases, these forms are immediately balanced by other microbial metabolic activities such as methanotrophs consuming methane produced through methanogenesis process in soils [238]. The long-term stabilization, carbon cycling, and metabolic pathways of these forms of carbon remain uncertain and poorly understood. The impact of climate change on microbial communities, particularly their ability to adapt to shifts in temperature and moisture, is also not fully understood. Research into the processes, mechanisms, and driving factors of soil microbial carbon dynamics and how microbes are involved, is crucial for understanding carbon sequestration and effectively addressing the growing challenges of climate change [239].

6.6 Scaling microbial solutions

The effectiveness of soil microbes isolated and used as inoculants depends on various factors, including the laboratory, greenhouse, and field conditions. While numerous studies have focused on controlled laboratory and greenhouse experiments, less attention has been paid to field trials. A key challenge is the disconnect between these controlled environments and actual field conditions, where factors such as biotic and abiotic stressors, competition with native organisms, and crop diversity affect the adaptability and stability of inoculants, as well as the development of optimal formulations. Therefore, more studies are needed to explore how to maintain the efficacy of microbial inoculants in diverse field conditions and to assess their performance under varying environmental conditions for inoculants already on the market [240]. Scaling microbial products offers a pathway to sustainable agriculture, benefiting economies, ecosystems, and societies. However, to realize these benefits equitably, supportive policies, investments in infrastructure, and educational efforts are essential. Addressing these socio-economic dimensions is critical for the inclusive and sustainable implementation of these technologies.

7 Conclusion

Integrating soil microbes into the sustainable agricultural management systems brings numerous benefits. Soil microorganisms are responsible for the decomposition and mineralization of soil organic matter, cycling of important nutrients such as nitrogen and phosphorus, maintaining and improving soil structure, enhancing water infiltration, retention, and aeration. They also serve as biological control agents for plant pests and diseases. These benefits align with the various Sustainable Development Goals of the United Nations, such as zero hunger, by promoting sustainable food production through resilient agricultural methods. Promoting microbial activity in food production systems reduces reliance on chemical fertilizers and pesticides, which are expensive and harmful to the environment. Additionally, microorganisms contribute to global biodiversity, support other soil organisms by generating byproducts that enhance their lives, and play a key role in climate change mitigation through carbon stabilization in soils. However, various gaps remain in fully understanding and harnessing the potential of soil microbiomes to transform agriculture toward sustainability. Therefore, future research should prioritize the use of advanced technologies to unravel microbial diversity, and gain deeper insights into their functionality, as these are essential for understanding their interactions with plants. Priority should also be given to translating insights from controlled environments to field conditions, where the services of microbial communities are most needed. This approach will provide a comprehensive understanding of the impacts of management

practices while addressing challenges related to biotic and abiotic stressors, competition with native organisms, the adaptability and stability of inoculants, and the development of optimal formulations for efficacy in agricultural sustainability. Such knowledge is important for exploring methods to maintain the efficacy of microbial inoculants under diverse field conditions.

Declarations

Competing interests The authors declare no competing interests.

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