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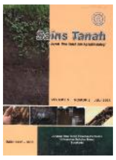

Applications of synthetic microbial communities platform through plant growth-promoting traits to enhance ecological functions in sustainable agriculture

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ABSTRACT

Synthetic microbial communities (SynCom) present a promising strategy for sustainably enhancing agricultural productivity and ecological resilience. This review critically discusses recent advancements in applying SynCom within agricultural ecosystems and highlights the practical benefits for economic sustainability. Plant growth-promoting (PGP) traits are essential for developing SynCom, as they enhance plant growth, increase nutrient uptake, improve stress tolerance, and support resistance to pathogens. SynCom demonstrates significant effectiveness as a biofertilizer, substantially improving soil health and crop yields through enhanced nutrient cycling and bioavailability. Its role as a biopesticide is also significant, as it offers an eco-friendly approach to insect pest management. The integration of SynCom into agricultural practices has proven to enhance plant disease resistance, significantly contributing to crop resilience. Moreover, SynCom plays a vital role in maintaining soil fertility, promoting carbon sequestration, and mitigating the impacts of climate change. Its applications extend to environmental remediation, where it effectively degrades hazardous pollutants in agricultural soils and efficiently processes lignocellulosic biomass, supporting sustainable biomass utilization. SynCom offers considerable advantages but also faces challenges, including community stability, environmental adaptability, and regulatory concerns. Future research efforts aim to address these limitations and enhance SynCom's efficacy regarding long-term agricultural sustainability. Our review provides valuable insights for policymakers, practitioners, and researchers to construct SynCom-based strategies that promote plant growth, enhance sustainable agriculture, and support environmental conservation.

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1. INTRODUCTION

Soil fertility is vital in agricultural development, particularly for crops, and significantly contributes to national development (Suntoro et al., 2024). Soil nutrients are essential for plant growth and productivity. Nutrients are divided into two categories: macronutrients and micronutrients. Plants require a minimum of 14 mineral elements for their nutrition, including the macronutrients nitrogen (NO_3^-, NH_4^+), phosphorus ($H_3PO_4^-$, HPO_4^{2-}), potassium (K^+), calcium (Ca^{2+}), magnesium (Mg^{2+}), and sulfur (SO_4^{2-}), as well as the micronutrients chlorine (Cl^-), boron ($B(OH)_4^-$), iron (Fe^{2+}), manganese (Mn^{2+}), copper (Cu^{2+}), zinc (Zn^{2+}), nickel (Ni^{2+}), and molybdenum (MoO_4^{2-}). These essential nutrients

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are typically sourced from the soil (White & Brown, 2010). The primary macronutrients essential for plant growth are nitrogen (N), phosphorus (P), and potassium (K), commonly referred to as NPK (Dhaliwal et al., 2024). Among these, N and P play significant roles, as they are crucial for regulating plant development and enhancing crop production (Dhaliwal et al., 2024; Wahba & Zaghloul, 2024). K also plays a key role in water regulation, nutrient transport, and disease resistance. Soil microbes are diverse microorganisms, including bacteria, fungi, archaea, and protists, essential for maintaining soil health and supporting ecosystem functions. These microorganisms play critical roles in nutrient cycling, decomposition of organic matter, and soil fertility (Chen et al., 2024; Wang et al., 2024). Plant growth-promoting bacteria (PGPB) are increasingly utilized in agriculture to enhance crop yields, reduce dependence on chemical fertilizers and pesticides, and improve soil health (Chowhan et al., 2023; Fan & Smith, 2021). SynCom involves selecting strains for specific purposes (Devi & Balachandar, 2022). The role of SynCom can effectively enhance soil ecological functions and promote environmental sustainability (Shayanthan et al., 2022; Xu et al., 2025). Synthetic consortia have the potential to enhance crop productivity via nutrient cycle and form soil aggregation, leading to improved soil porosity, and effectively address agricultural challenges (Karkaria et al., 2021). The design and assembly of SynCom require a comprehensive understanding of microbial ecology, genetics, metabolic pathways, and strain-specific characteristics (Johns et al., 2016). SynCom construction involves identifying and integrating individual microbial strains based on their desirable traits and functions, as described by Chem and Ito (2025). Depending on specific agricultural purposes, SynCom can be developed from various sources, including natural environments, microbial culture collections, and gene banks (Luo et al., 2024; Zhang et al., 2019; Zhuang et al., 2021). For instance, plant growth-promoting SynComs are often sourced from environments exhibiting exceptional plant health, growth, or stress resilience (Liu et al., 2022). Similarly, SynCom derived from the rhizosphere of healthy plants can effectively enhance crop health, growth, and stress tolerance, leading to high-yielding and disease-resistant varieties. Additionally, SynCom isolated from extreme environments, such as high salinity, drought, or contaminated soils, can significantly improve plant tolerance and resilience (Chaudhary et al., 2023). SynCom development is crucial for regulating nutrient cycles, fostering plant health, and maintaining ecosystem resilience. Therefore, this review aims to demonstrate recent advancements in research on the application of the synthetic microbial community platform in agricultural ecosystems and its practical benefits for economic sustainability. Practical insights into improving soil ecological functions through PGP traits are also included without the need for extensive investigation into the underlying scientific mechanisms.

2. Plant growth-promoting traits and their mechanisms influence crop productivity

PGP traits refer to various beneficial characteristics that microorganisms can provide to plants, leading to enhanced growth, improved nutrient uptake, and increased stress tolerance. These traits also contribute to disease suppression and promote overall soil health. PGP traits can be categorized into direct and indirect mechanisms. Direct mechanisms include nutrient solubilization (P, K, Zn-solubilization, and N-fixation), phytohormones (indole-3-acetic acid (IAA), cytokinins, and gibberellins (GAs), and the synthesis of siderophore, enhancing plant iron uptake. Indirect mechanisms include biocontrol activities in which microorganisms suppress plant pathogens by producing antibiotics, releasing hydrolytic enzymes, and generating volatile compounds such as hydrogen cyanide (HCN) (Chowhan et al., 2023; Cueva-Yesquén et al., 2021; Ünlü et al., 2024) (Table 1). *Pseudomonas* is recognized for a diverse array of PGP traits, which include antibiotic production, P-solubilization, N-fixation, 1-aminocyclopropane-1-carboxylate (ACC) deaminase activity, and phytohormone synthesis (Fan & Smith, 2021). Furthermore, *Bacillus* species are well-known for their abilities in N-fixation, P-solubilization, siderophore production, and biocontrol activities (Chowhan et al., 2023), while *Rhizobium* is mainly associated with N-fixation in legume-rhizobia symbiosis (Lindström & Mousavi, 2020). A study by Ikhwan et al. (2021) revealed that developing a bacterial consortium with PGPB can enhance maize (*Zea mays* L.) production. Furthermore, Pattani et al. (2023) indicated that utilizing the PGPB consortia can improve the overall growth of tomatoes (*Solanum lycopersicum* L.). Similarly, Devi et al. (2018) demonstrated that applying these consortia can enhance potato (*Solanum tuberosum* L.) yield. Shilev et al. (2020) studied these consortia and found that they can improve spinach (*Spinacia oleracea* L.) production. Turino Mattos et al. (2023) also reported the positive effects of using these consortia in rice (*Oryza sativa* L.) cultivation. However, the role of soil microbial communities in ecosystem functioning does not always contribute positively to soil health (Chen et al., 2024). Various challenges inhibit their capacity to enhance soil quality, including limited nutrient availability, adverse environmental conditions (Sembiring et al., 2024), soil disturbances, and pathogens (Rasheela et al., 2024).

PGP traits are crucial for microbial consortia to enhance plant growth, increase nutrient uptake, improve stress tolerance, and support resistance to pathogens. These traits have been extensively investigated in beneficial microbes, particularly in plant growth-promoting rhizobacteria (PGPR) and endophytes. Potential PGP traits for microbial applications that enhance plant growth include nutrient solubilization (P, K, and Zn), siderophore production, and N-fixation. Additionally, phytohormone production involving IAA, cytokinins, and GAs, through ACC deaminase, plays a crucial role in enhancing plant growth response to the effect of PGPR (Jaroszuk-Ściseł et al., 2019). Biocontrol and plant protection traits involve the production of antibiotics such as iturins and bacillomycins (Dunlap et al., 2019), hydrolytic enzymes including chitinases, *β*-1,3-glucanases, proteases, and cellulases (Chlebek et al., 2022), HCN (Sehrawat et al., 2022), and biosurfactant production (Jumpathong et al., 2022). A recent study by Denaya et al. (2021) emphasized the potential of a SynCom composed of *Citrobacter braakii*, *C. freundii*, and *Pseudomonas stutzeri* for promoting plant growth.

Table 1. PGP traits and nutrient acquisition mechanisms. PGP traits are beneficial characteristics of microorganisms, especially rhizobacteria and endophytes, that enhance plant growth by improving nutrient acquisition, hormone regulation, stress tolerance, and pathogen suppression. Plants obtain nutrients from soil through mass flow (nutrients move with water), diffusion (nutrients move from high to low concentration), and root interception (direct contact with roots).

PGP traits	Nutrient acquisition mechanisms
Phosphorus solubilization	Microorganisms solubilize phosphorus (P) through various biochemical and biological mechanisms, converting insoluble phosphorus into bioavailable forms that plants can absorb. These mechanisms primarily involve the secretion of organic acids and the production of phosphatase enzymes. Certain microorganisms produce and release organic acids into the soil, including gluconic, oxalic, citric, malic, lactic, and acetic acids. These acids lower the soil pH by releasing protons (H^+), which create acidic conditions that promote the dissolution of insoluble phosphate minerals, such as tricalcium phosphate, $Ca_3(PO_4)_2$. This acidification process enhances the solubility of inorganic phosphate. Additionally, these organic acids contain hydroxyl (-OH) and carboxyl (-COOH) groups that can chelate metal cations (Ca^{2+}, Fe^{2+}, Al^{3+}) commonly associated with insoluble phosphate complexes. Chelating these cations helps release phosphate ions into the soil, making them more accessible to plants. Similarly, microorganisms can produce phosphatases and phytases, breaking down organic phosphorus compounds into inorganic phosphate. These organic phosphorus compounds bond with molecules such as carbon chains, proteins, nucleic acids, and phospholipids. Phosphatases hydrolyze various organic phosphorus compounds, while phytases target phytate (inositol hexakisphosphate), a common form of organic phosphorus in soil. When these organic compounds break down, they release inorganic phosphate, which is present in the free ionic forms of orthophosphate ions ($H_2PO_4^-$, HPO_4^{2-}, and PO_4^{3-}). Through enzymatic action, phosphorus is converted from organic forms into inorganic phosphate (orthophosphate), making it readily available for plant uptake. Bacteria such as *Bacillus*, *Pseudomonas*, *Enterobacter*, and *Rhizobium*, along with fungi like *Aspergillus* and *Penicillium*, as well as arbuscular mycorrhizal fungi (AMF), have been shown to solubilize phosphorus (P) effectively.
Potassium solubilization	Although potassium (K) in soil is abundant, over 90-98% of it exists in insoluble or fixed forms that plants cannot absorb directly. Microorganisms can solubilize potassium from these insoluble mineral sources, including mica ($XY_{2\text{-}3}Z_4O_{10}(OH, F)_2$), where (X) can be K, Na, Ba, Ca, Cs, (H_3O), or (NH_4); (Y) can be Al, Mg, Fe^{2+}, Li, Cr, Mn, V, or Zn; and (Z) can be Si, Al, Fe^{2+}, Be, or Ti. Other sources include feldspar [$(Ca, Na, K)AlSi_3O_8$], and illite $(KH_3O).(Al, Mg, Fe)_2.(Si\ Al)_4.O_{10}.[(OH)_2(H_2O)]$. Certain microorganisms produce organic acids such as citric, oxalic, tartaric, gluconic, and malic acids. These acids lower soil pH by releasing H^+ ions, further promoting the dissolution of potassium-containing minerals. The lower soil pH disrupts the structure of feldspar, especially K-feldspar, a K-bearing aluminosilicate mineral ($KAlSi_3O_8$). Organic acids bind to Al^{3+}, Fe^{3+}, Si^{4+}, and other structural ions in K-bearing minerals, leading to the dissolution of the mineral matrix. Protons (H^+) secreted by certain microorganisms exchange with K^+ ions bound in these mineral matrices, causing the release of K^+ ions into the soil. These processes transform structurally bound or mineral-occluded potassium into plant-available K^+ ions.
Zinc solubilization	In soil, a significant portion of zinc (Zn) is found in insoluble forms, including zinc carbonate ($ZnCO_3$), zinc oxide (ZnO), zinc hydroxide ($Zn(OH)_2$), and zinc phosphate ($Zn_3(PO_4)_2$). These forms do not easily dissolve in water, particularly in alkaline conditions, making zinc unavailable to plants. In alkaline conditions, Zn^{2+} reacts with hydroxide (OH^-), carbonate (CO_3^{2-}), or phosphate (PO_4^{3-}) ions to form poorly soluble precipitates. Hence, alkaline soils promote zinc deficiency because Zn^{2+} precipitates or binds tightly to soil components. Similarly, certain microorganisms can solubilize zinc in the soil by producing organic acids such as gluconic acid, citric acid, oxalic acid, lactic acid, malic acid, and chelating agents. These organic acids lower the soil pH by releasing protons (H^+), increasing zinc compounds' solubility. These acids chelate Zn^{2+} ions from insoluble forms such as ZnO, $ZnCO_3$, $Zn(OH)_2$, and $Zn_3(PO_4)_2$. As Zn^{2+} is continuously chelated from insoluble forms, more Zn^{2+} is released. Chelation by organic acids helps Zn^{2+} reprecipitate with other anions, such as OH^- or PO_4^{3-}, keeping it in a soluble form available for plants. This process is critical in alkaline and calcareous soils, where zinc is commonly present but often poorly available.

PGP traits	Nutrient acquisition mechanisms
Nitrogen fixation	Atmospheric nitrogen (N_2) has a strong triple bond, which makes it chemically inert and unavailable to most organisms. However, certain microorganisms can convert atmospheric nitrogen gas (N_2) into ammonia (NH_3) through biological nitrogen fixation (BNF). This conversion occurs through an enzymatic reaction catalyzed by nitrogenase. The nitrogenase enzyme complex, which consists of dinitrogenase reductase and dinitrogenase, promotes the reduction of inert atmospheric N_2 into bioavailable ammonia (NH_3). This process requires significant energy (16 ATP molecules to fix one N_2 molecule into two NH_3 molecules) and involves transferring electrons from ferredoxin or flavodoxin to dinitrogenase reductase, which then passes the electrons on to dinitrogenase. As a result, two molecules of ammonia (NH_3) are produced from one molecule of N_2. Once produced, ammonia (NH_3) is often protonated to form ammonium (NH_4^+) under soil conditions. Plants can then directly assimilate NH_4^+ into amino acids such as glutamate and glutamine, as well as into nucleic acids and chlorophyll.
Siderophore production	Siderophores are high-affinity, low molecular-weight chelating compounds that microorganisms secrete under conditions of iron (Fe^{3+}) limitation. Iron (Fe^{3+}) is crucial for various plant processes, including chlorophyll synthesis, respiration, and enzyme function. However, Fe^{3+} can form insoluble hydroxides and oxides in aerated or alkaline soils, making it less available to plants. Microorganisms synthesize and secrete siderophores, which are iron-chelating molecules that bind tightly to Fe^{2+} and form soluble Fe^{2+}-siderophore complexes. Plants can then absorb iron from these complexes through membrane-bound transport systems.
Phytohormones	
Indole-3-acetic acid (IAA)	Indole-3-acetic acid (IAA) is an auxin, a plant hormone crucial in promoting plant growth. It influences important processes such as cell division, elongation, and differentiation. Microorganisms produce IAA as a secondary metabolite, which helps promote cell elongation by activating H^+-ATPases. Although IAA is crucial for plant development, its effects can vary depending on the dosage, with high concentrations sometimes inhibiting growth.
Cytokinins	Cytokinins support plant growth through cell division, promote shoot organogenesis, delay senescence, enhance nutrient allocation, and increase resilience to stress. This hormone activates cyclin-dependent kinases (CDKs) and cyclins that control the transition from the G1 to the S phase of the cell cycle. Additionally, cytokinins upregulate the WUSCHEL (WUS) and CLAVATA (CLV) genes, crucial for maintaining stem cell populations in the shoot apical meristem. It also inhibits the expression of senescence-associated genes (SAGs) and supports chlorophyll synthesis by maintaining the activity of enzymes. Furthermore, cytokinins regulate nitrate transporter (NRT1) genes, promoting the translocation of essential nutrients (N, P, and K) from older to younger tissues. In addition, they induce the expression of antioxidant enzyme genes, such as superoxide dismutase and catalase, which enhance tolerance to drought, salinity, and extreme temperature conditions.
Gibberellins (GAs)	Gibberellins (GAs) promote stem elongation, seed germination, flowering, and fruit development. GAs enhance RNA and protein synthesis, promoting longitudinal growth in response to light and supporting the germination process. GAs promote cell wall loosening by upregulating genes associated with expansin and xyloglucan endotransglucosylase/hydrolase (XTH). Furthermore, they activate the expression of hydrolytic enzymes, such as α-amylase and proteases, in the aleurone layer of cereal seeds. This action helps decompose stored starch and proteins in the endosperm into soluble sugars and amino acids, providing essential energy and building blocks for the developing embryo. In certain plants, particularly long-day species, GAs promote flowering by inducing the expression of floral meristem identity genes, including LEAFY (LFY) and SOC1.
ACC deaminase	Microorganisms produce 1-Aminocyclopropane-1-carboxylate (ACC) deaminase to regulate the levels of ethylene (C_2H_4), a stress-related plant hormone that can inhibit growth, especially under stress conditions. While small amounts of ethylene regulate normal growth, excessive ethylene can inhibit root elongation, lead to leaf yellowing and senescence, and delay seed germination. In response to abiotic or biotic stress, plants increase ethylene synthesis via the precursor 1-aminocyclopropane-1-carboxylic acid (ACC). The ethylene synthesis in plants follows the pathway by which methionine is converted to S-adenosyl methionine through SAM synthetase, S-adenosyl methionine is converted to ACC through ACC synthase, and ACC is converted to ethylene via ACC oxidase. In the biosynthetic pathway, ACC is the final step before ethylene synthesis. Therefore, ACC is referred to as the immediate precursor. Microorganisms produce ACC deaminase to break down ACC, the immediate precursor of ethylene, into ammonia (NH_3) and α-ketobutyrate. This process reduces ethylene production and helps mitigate its negative effects on plant growth.

PGP traits	Nutrient acquisition mechanisms
Lipopeptide antibiotics	
Iturins and bacillomycins	Iturins and bacillomycins are lipopeptide antibiotics that serve as antifungal agents, primarily produced by *Bacillus* species such as *B. subtilis*, *B. amyloliquefaciens*, and *B. velezensis*. These lipopeptides act as biocontrol agents, inhibiting plant pathogens and disrupting fungal cell membranes. Iturins and bacillomycins are inserted into fungal cell membranes through an amphiphilic structure. This insertion leads to the formation of pores or membrane disruption, resulting in ion leakage (including K^+ and Ca^{2+}), a loss of membrane potential, and, ultimately, cell lysis and death.
Enzymes	
Chitinases, *β*-1,3-glucanases, proteases, and cellulases	Certain microorganisms, particularly *Bacillus*, *Pseudomonas*, and *Trichoderma*, secrete lytic enzymes such as chitinases, *β*-1,3-glucanases, proteases, and cellulases. These enzymes primarily degrade components of pathogenic microbial cell walls, acting as biocontrol agents. Chitinases hydrolyze chitin, a major component of fungal cell walls, while *β*-1,3-glucanases break down *β*-glucans, essential for maintaining the integrity of the fungal cell wall. Proteases break down pathogens by hydrolytically cleaving the peptide bonds within protein molecules on the pathogen's surface or within its internal structures. This process reduces these proteins into smaller peptides or amino acids. As a result, proteases can effectively disrupt bacterial biofilms, dismantle structural components such as the cell wall or extracellular matrix, and degrade host defenses, including immune signaling proteins and antimicrobial peptides. Cellulases, conversely, target the exopolysaccharides (EPS) found in bacterial biofilms, which serve as a protective matrix surrounding bacterial cells. By hydrolyzing the structural *β* (1-4) glycosidic linkages within the EPS, cellulases degrade the biofilm, weakening the pathogen's structural integrity and disrupting its protective layer. These enzymatic activities can induce the lysis of phytopathogen cells.
Volatile compounds	
Hydrogen cyanide (HCN)	Certain microorganisms produce hydrogen cyanide (HCN) as a biocontrol agent. Although HCN is toxic to plants at high concentrations, the amounts produced by beneficial microbes selectively target pathogens without harming the plants. Low concentrations of HCN do not harm plants but effectively suppress pathogens. The production of HCN is tightly regulated by microbial expression and soil conditions. HCN disrupts the respiratory electron transport chain in pathogenic fungi and bacteria by inhibiting cytochrome c oxidase, an essential enzyme for cellular respiration. This inhibition blocks ATP synthesis in these pathogens, eventually leading to energy depletion and death.
Biofilm - Extracellular polymeric substances	
Exopolysaccharides (EPS)	Exopolysaccharides (EPS) are high-molecular-weight polysaccharides secreted by microorganisms such as *Bacillus*, *Pseudomonas*, *Rhizobium*, and *Azospirillum*. These substances support plant growth by enhancing root-soil interactions, promoting microbial survival, and improving plant stress tolerance. EPS are viscous compounds rich in sugar. When microorganisms colonize plant roots, they produce EPS that forms a protective biofilm for the roots. The EPS molecules contain hydrophilic (water-attracting) chemical groups, allowing them to absorb and retain water molecules. This EPS matrix effectively holds water around the root surface, even as the soil begins to dry, maintaining root hydration, particularly during drought or heat stress.

This SynCom was developed based on the strains' abilities to solubilize macronutrients and produce IAA. The findings suggest that applying a SynCom with these characteristics can significantly improve nutrient uptake, enhance systemic resistance against pathogens, and increase plant stress tolerance. Additionally, research by Kaur et al. (2022) identified another SynCom consisting of *Erwinia* sp. EU-B2SNL1, *Chryseobacterium arthrosphaerae* EU-LWNA-37, and *Pseudomonas gerardia* EU-MRK-19 promote plant growth by improving nutrient uptake, disease resistance, and stress tolerance. These strains were selected based on their unique traits, *Erwinia* sp. EU-B2SNL1 as an N-fixer, *C. arthrosphaerae* EU-LWNA-37 as a P-solubilizer, and *P. gerardia* EU-MRK-19 as a K-solubilizer. The study concluded that a SynCom based on selected strains is more effective than applying individual strains. The development of SynCom utilizing PGP traits is a practical approach to enhancing nutrient availability in the soil. These beneficial effects occur through diverse mechanisms, such as resource competition, antimicrobial compound production, and induction of plant defense responses.

3. Applications of SynCom in agricultural systems

3.1. SynCom as biofertilizers

Biofertilizers are natural fertilizers that utilize beneficial microorganisms to enhance soil fertility and support plant growth. They play an essential role in modern agriculture by improving soil health, facilitating nutrient uptake, and promoting sustainable farming practices (Ammar et al., 2023). SynCom has been developed using beneficial microorganisms as biofertilizers to enhance soil quality (Kabir et al., 2024).

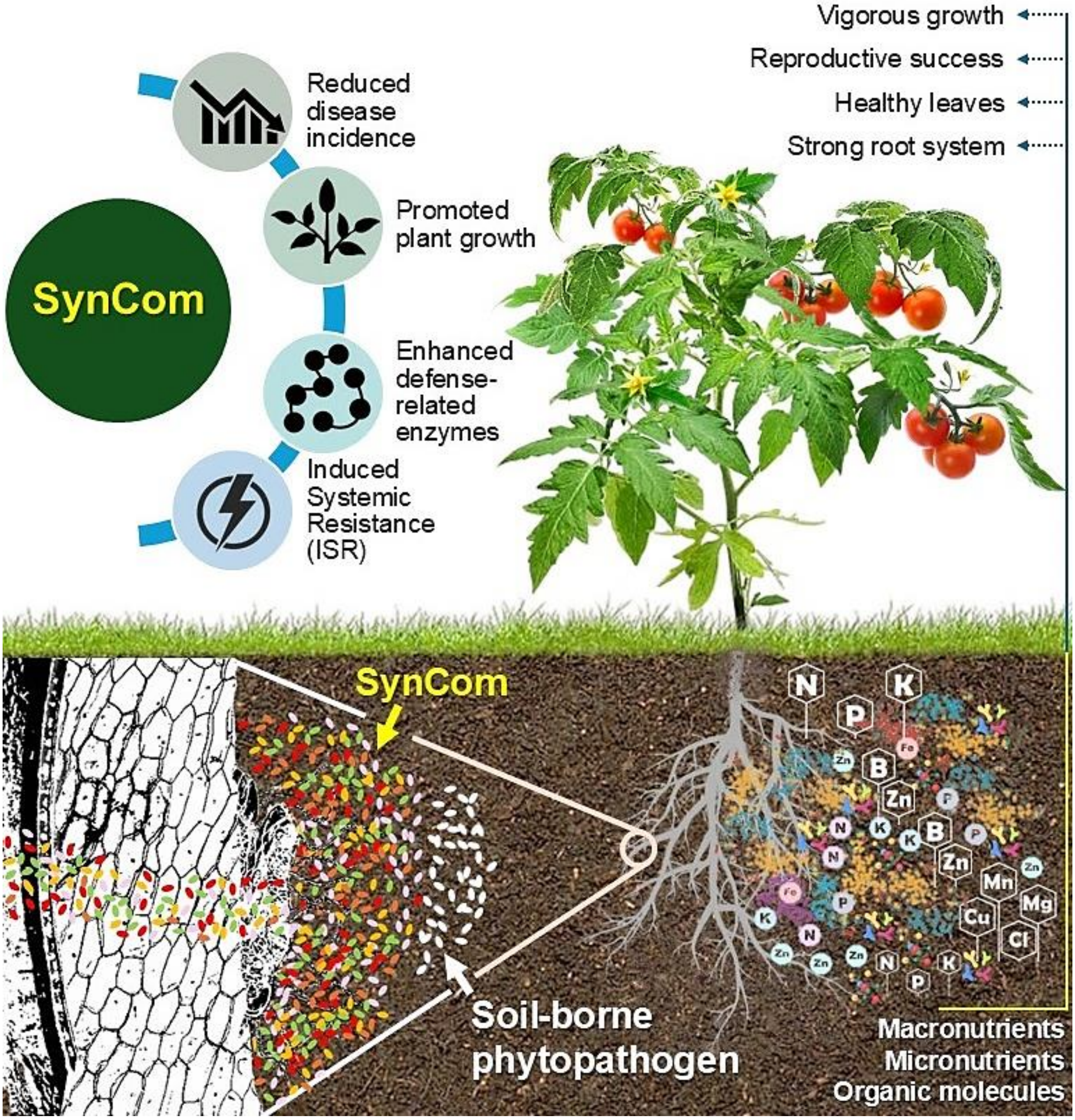

Figure 1. Synthetic microbial communities (SynCom) function as plant growth-promoting bacteria (PGPB) by enhancing nutrient uptake, protecting against pathogens, and increasing resistance to environmental stress.

Ikhwan et al. (2021) had reported that forming a SynCom with PGPB can enhance maize (*Z. mays* L.) production. The findings indicated that a specific PGPB formula could improve the yield for specific *Z. mays* L. varieties. For instance, consortia with endophytic bacteria isolates, *Azospirillum* sp., cellulolytic, and ligninolytic were the most effective formulation for Pertiwi-3 cultivation. In contrast, PGPB consortia with endophytic bacteria isolates, cellulolytic, ligninolytic, *Acetobacter* sp., and *Azospirillum* sp. produced higher yields for Talenta and Bisma. SynCom solubilizes essential nutrients and mobilizes other macro- and micronutrients to enhance nutrient uptake, protect against pathogens, and increase resistance to environmental stress (Fig. 1). Interactions between host plants and SynCom involve dynamic signaling and metabolic exchanges. Host plants release organic compounds (sugars, amino acids, and organic acids) through their roots, which attract SynCom. In response, SynCom secretes signaling molecules recognized by the plant roots, initiating colonization on the root surface or within root tissues. This interaction enhances nutrient transfer efficiency and protects roots from pathogenic microorganisms through biofilm formation, significantly influencing plant growth and overall health. This enhanced nutrient bioavailability directly promotes plant growth and productivity (Kaur et al., 2022)

Furthermore, Santoyo et al. (2021) concluded that SynCom can produce phytohormones, including auxins, cytokinins, gibberellins, ethylene, and abscisic acid, which are crucial regulators of plant growth, root development, and overall yield enhancement. Additionally, these microbial consortia can produce siderophores, antibiotics, and volatile organic compounds that protect plants from pathogens, reducing disease incidence and enhancing biocontrol efficacy (Hansen et al., 2024; Jing et al., 2024; Misra et al., 2024). Previous studies showed that SynCom secretes phosphatases, cellulases, and proteases, which decompose organic matter and release essential nutrients for plant uptake. This enzymatic activity plays a key role in sustainable agriculture and soil health (Chiaranunt & White, 2023). These substances enhance nutrient availability and root uptake, substantially enhancing plant growth. For instance, P-solubilizing bacteria can convert insoluble phosphorus compounds into soluble forms readily available for plant uptake (Zhou et al., 2024). Phosphate-solubilizing bacteria (PSBs) are crucial in enhancing phosphorus availability for plant uptake. They produce organic acids that chelate, release inorganic phosphorus, and secrete enzymes such as phosphatases to break down organic phosphorus. This process increases the accessibility of phosphorus in the soil, promoting overall plant growth and yield by ensuring that this essential nutrient is readily available for plants to absorb (Fig. 2). Plants can enhance their growth, cell division, and energy production with increased phosphorus availability, as this essential macronutrient plays a crucial role in these processes. PSBs function as biofertilizers, providing an environmentally friendly alternative to chemical fertilizers. This approach not only reduces soil pollution but also promotes ecological balance.

3.2. SynCom as biopesticides and biological control of plant disease

Integrating beneficial insecticidal bacteria can improve insect pest management strategies. Selected microbial strains exhibit potential insecticidal properties within SynCom, offering potential novel biopesticides. Utilizing multiple modes of action through various microbial agents can develop biopesticides that operate more efficiently and provide broad-spectrum activity. Integrating different bacterial strains with diverse action mechanisms can lead to stronger and more effective biocontrol than single strains.

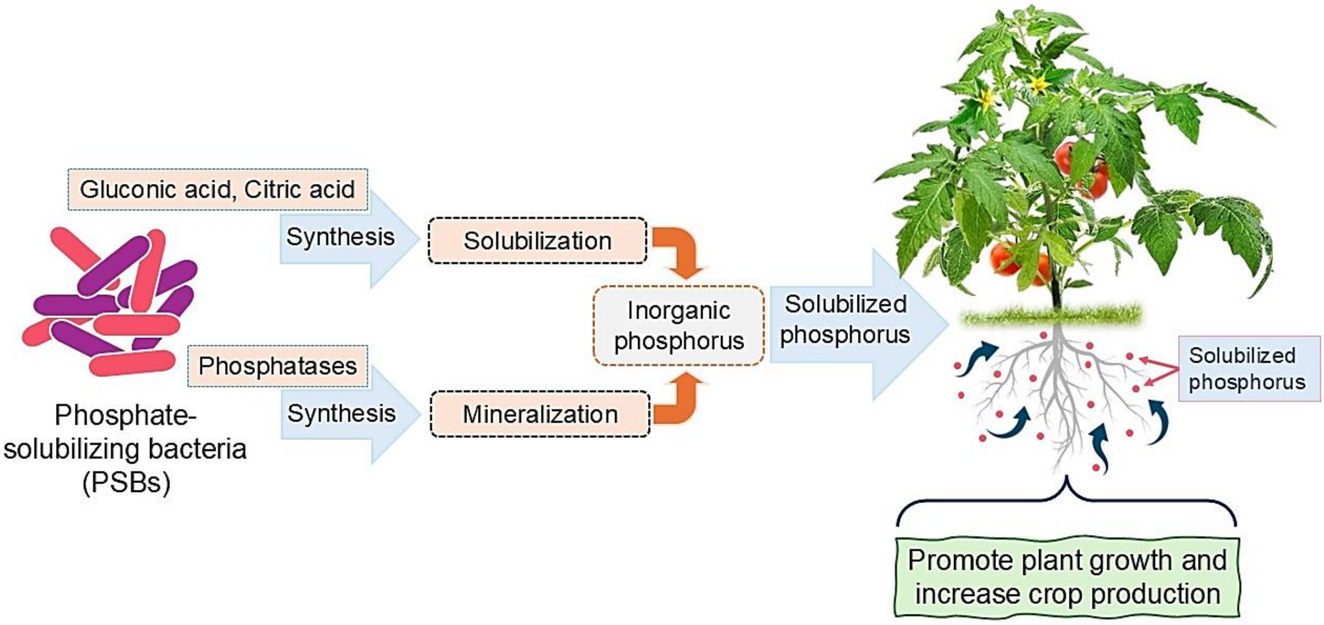

Figure 2. Phosphate-solubilizing bacteria (PSBs) enhance phosphorus availability for plants by producing organic acids that release inorganic phosphorus and secrete enzymes like phosphatases to break down organic phosphorus. This increases phosphorus accessibility in the soil, promoting plant growth and yield

A recent study by Chem et al. (2025) demonstrated that a combination of four promising non-*Bt* (beyond *Bacillus thuringiensis*) bacterial strains, *Mesobacillus thioparans* CC8, *Bacillus mobilis* CC13, *Bacillus subtilis* CC18, and *Chromobacterium rhizoryzae* 4C2, was more effective against the diamondback moth, *Plutella xylostella* L., compared to individual applications. These insecticidal bacteria produce endotoxins that can kill insect larvae (Pathma et al., 2021; Seenivasagan & Babalola, 2021). Tan et al. (2021) demonstrate that mixing two fungi, *Paranosema locustae* and *Beauveria bassiana*, effectively manages grasshopper (*Locusta migratoria*) populations. *P. locustae* is commonly used in China as a biological control agent for grasshoppers. Furthermore, the combined application of *P. locustae* and *B. bassiana* is more effective against *L. migratoria* than using either fungus alone. Similarly, a recent case study by Spescha et al. (2023) studied SynCom to control the cabbage maggot (*Delia radicum*) (Diptera: Anthomyiidae), a well-known pest that causes significant damage to Brassicaceae crops. SynCom was developed by combining *Pseudomonas chlororaphis* (bacteria), *Steinernema feltiae* (nematodes), and *Metarhizium brunneum* (fungus). *P. chlororaphis* was selected for its proven effectiveness against insect pests and fungal plant diseases, while *S. feltiae* and *M. brunneum* have a long history of commercial use against various pest insects. The study's results indicated that SynCom significantly reduced pest survival rates in greenhouse experiments. These microbial consortia perform through various mechanisms, including insecticidal proteins such as Cry, Cyt, and Vip proteins, which disrupt insect digestive systems and ultimately lead to their death.

Olanrewaju and Babalola (2019) studied the application of a SynCom composed of *B. subtilis* A1, *Pseudomonas* sp. A18, *Pseudomonas* sp. A29, *S. globisporus* NWU4, *S. griseoflavus* NWU14, and *S. heliomycini* NWU198 to control *Fusarium graminearum*. Their research demonstrated that SynCom produced antimicrobial compounds that effectively inhibited the growth of *F. graminearum*. *B. subtilis* is well-known for producing lipopeptides, including iturin, surfactin, and fengycin, which exhibit antifungal properties (Kaspar et al., 2019). Likewise, *Streptomyces* species are recognized for producing natural antibiotics, including antifungal compounds (Donald et al., 2022). *Pseudomonas* strains also generate antimicrobial compounds such as phenazines, pyoluteorin, pyrrolnitrin, and 2,4-diacetyl phloroglucinol, which are antifungal effects (Fischer et al., 2013). Antifungal lipopeptides such as iturin, surfactin, and fengycin, produced by these microbes, can effectively inhibit fungal growth by damaging cell membranes and causing cell lysis. These findings highlight the potential of the SynCom approach for controlling fungal plant pathogens.

Utilizing SynCom offers a sustainable solution for biopesticides and the biological control of plant diseases. SynCom provides a more stable and effective alternative to single-strain biocontrol agents. Approaches based on SynCom support integrated pest management (IPM) principles by reducing reliance on chemical pesticides, minimizing environmental pollution, decreasing pesticide resistance, and limiting adverse effects on non-target organisms. This method provides eco-friendly, effective, and resilient biopesticide solutions.

3.3. SynCom applications in disease resistance and stress tolerance

SynCom can protect plants from various stressors, including biotic and abiotic. The biotic stressors include pathogens (fungi, bacteria, and viruses), insects, and weeds, which can infect plants, feed on plant tissues, and compete for essential resources, adversely affecting plant health and productivity. On the other hand, abiotic stressors refer to the negative impacts of non-living environmental factors, including extreme temperatures, drought, salinity, nutrient deficiencies, and metal toxicity. SynCom represents a promising microbial consortium that not only enhances plant disease resistance but also improves stress tolerance (de Souza et al., 2020). SynCom can secrete hydrolytic enzymes, including chitinases, glucanases, and proteases, which target and break down the cell walls of fungal pathogens, enhancing plants' disease resistance (Wang et al., 2021). Additionally, SynCom can solubilize nutrients and produce phytohormones that promote plant health and resilience to stress, ultimately reducing their susceptibility to diseases (Mukherjee et al., 2021).

Bacillus and *Pseudomonas* have been widely utilized in sustainable agriculture to enhance soil health, improve crop yields, increase plant tolerance to drought, cold, and salinity stresses, and provide effective biocontrol against plant pathogens (Devi et al., 2025; Kaur et al., 2024; Raza et al., 2024; Singh et al., 2025; Swiontek Brzezinska et al., 2022; Vega-Celedón et al., 2021). They assist plants in tolerating stress and safeguarding them from pathogens. These organisms produce compounds that combat harmful microbes, including antibiotics, lytic enzymes, and biosurfactants, while also activating the plant's defense mechanisms, such as induced systemic resistance (ISR). Furthermore, they enable plants to better withstand drought, cold, and salinity by generating osmoprotectants and exopolysaccharides (EPS) (Singh et al., 2015). Ultimately, these beneficial interactions are essential for their capacity to form biofilms and colonize plant roots. These diverse microbial communities perform essential ecological functions, including nutrient cycling and N-fixation, producing plant growth hormones, and bolstering plant defense mechanisms. This approach offers an environmentally friendly alternative to chemical pesticides.

Ma et al. (2023) investigated a SynCom composed of *Bacillus* sp. HB1, *Bacillus* sp. HB9, *Burkholderia* sp. HB9, *Burkholderia* sp. MB7, *Pseudomonas* sp. MB2, *Streptomyces* sp. MB6, and *Bradyrhizobium* sp. MB15 has shown effectiveness in enhancing disease resistance against the plant pathogen *F. oxysporum*. This SynCom was developed based on its ability to fix nitrogen and P-solubilization and produce chitinase, cellulase, and xylanase. The study indicated that SynCom can significantly improve plant health, promote disease resistance, and enhance growth efficiency. A recent study by Khan et al. (2022) explored the potential of SynCom to promote wheat growth under salinity stress, using NaCl concentrations to determine strains exhibiting tolerance to salinity.

Table 2. The application of SynCom in sustainable agriculture contributes to improved soil health, increased crop yields, and enhanced plant resilience to stresses such as drought, cold, and salinity. Designing microbial consortia with specific PGP traits and enzymatic activities can adopt a strategic and promising approach to enhancing ecological functions in sustainable agriculture

SynCom	Desired function	Plant model species	Microbial construction strategies and results-based experiments	Reference
Enterobacter ludwigii EU-BEN-22, *Micrococcus indicus* EU-BRP-6, *Pseudomonas gessardii* EU-BRK-55	Improving soil health and crop yields	*Solanum melongena* L.	The isolated bacteria were assessed for N-fixation, P-solubilization, and K-solubilization. Microbial interactions can improve plant growth metrics (root and shoot length, biomass) and physiological parameters (chlorophyll, carotenoids, total soluble sugars, and phenolic content).	Kaur et al. (2024)
Claroideoglomus claroideum, *Naganishia albida*, *Burkholderia caledonica*	Helping plants tolerate drought stress	*Fragaria x ananassa*	Three types of arbuscular mycorrhizal fungi (AMF), three types of plant growth-promoting rhizobacteria (PGPR), and three types of plant growth-promoting yeasts (PGPY) were chosen for their potential to enhance plant growth under environmental stress. This combination led to improvements in biomass, relative water content, fruit quantity, photosynthetic rate, transpiration, stomatal conductance, and the quantum yield of photosystem II. Additionally, it increased the concentrations of N, P, and K and enhanced antioxidant activities and chlorophyll content.	Pérez-Moncada et al. (2024)
Serratia surfactantfaciens EU-C3SY2, *Serratia marcescens* EU-D1RNL1, *Serratia nematodiphila* EU-D2SRY4, *Erwinia persicina* EU-B1RT3.1, *Serratia* sp. EU-C1RK1	Enhancing the growth of the oats crop	*Avena sativa* L.	Isolated strains were evaluated for various PGP traits, including P, K, Zn, and Se solubilization, and the production of siderophores, NH_3, IAA, HCN, and N-fixation. The consortium can enhance oat plants' growth and physiological parameters more effectively than other developed microbial consortia, controls, and agrochemical fertilizers.	Devi et al. (2024)
Pseudomonas sp. EU-C3ST.R1, *Micrococcus indicus* IARI-JR-44, *Bacillus horikoshii* IARI-S-45	Enhancing the growth of the cereal crop	*Zea mays* L.	Bacterial strains were assessed for N-fixation, P, and K solubilization. The combination of strains can enhance plant height, biomass, and their physiological characteristics, including chlorophyll, carotenoids, flavonoids, phenolics, and total soluble sugar content.	Devi et al. (2025)
Trichoderma atrobruneum 15F, *Pseudomonas* sp. 2B, *Bacillus amyloliquefaciens* 9B, *Bacillus velezensis* 32B	Antagonistic activity against *Fusarium oxysporum f.* sp. *cumini* (*Foc*)	*Cuminum cyminum*	Bacterial, actinomycete, and fungal isolates were evaluated for their antagonistic activity against *Foc* and their tolerance to various stress conditions such as temperature, pH, salinity, and moisture. The study also assessed the production of several metabolites, including siderophores, HCN, NH_3, IAA, the solubilization of P and Zn, and the activity of hydrolytic enzymes, such as chitinase, β-1,3-glucanase, cellulase, amylase, lipase, protease, and chitosanase. This microbial consortium can enhance biomass and yield, improve disease resistance, and increase the production of secondary metabolites and antioxidant defense enzymes. Furthermore, it can help reduce electrolyte leakage, increase chlorophyll and carotenoid content, and contribute positively to plant height, dry weight, and seed yield.	Singh et al. (2025)

SynCom	Desired function	Plant model species	Microbial construction strategies and results-based experiments	Reference
Burkholderia sp. UWIGT-83, *Burkholderia* sp. UWIGT-120	Helping plants tolerate drought stress	*Capsicum chinense*	Rhizobacteria were evaluated for their ability to produce ACC-deaminase under drought stress conditions, along with PGP traits such as P solubilization, NH_3 production, siderophore synthesis, starch hydrolysis, and IAA production. The rhizobacteria consortium can improve germination and growth under drought stress.	Thomas-Barry et al. (2024)
Bacillus subtilis IS1, *Bacillus amyloliquifaciens* IS6, *Bacillus fortis* IS7	Antagonistic activity against *Fusarium oxysporum f.* sp. *pisi* (*Fop*)	*Pisum sativum*	Rhizospheric bacterial strains were assessed for their antagonistic activity against *Fop*. Combining these rhizospheric bacterial strains can help recover plants from pathogenic infections, reduce plant damage from diseases, and promote growth.	Raza et al. (2024)
Pseudomonas sp. TmR5a, *Curtobacterium* sp. BmP22c	Helping plants tolerate cold stress	*Solanum lycopersicum* L.	Bacterial strains were assessed for their ability to produce auxins, P-solubilization, nifH and acdS genes, and antimicrobial activity against phytopathogenic bacteria. A bacterial consortium can enhance tomato plant growth under normal and cold stress conditions.	Vega-Celedón et al. (2021)
Bacillus sp., *Delftia* sp., *Enterobacter* sp., *Achromobacter* sp.	Mitigation of salinity stress	*Solanum lycopersicum* L.	Halo-tolerant rhizobacterial strains were selected for their ability to solubilize P and produce siderophores, NH_3, and IAA. This consortium can enhance growth parameters, including leaf count, shoot and root length, dry weight, the number of secondary roots, and chlorophyll content, even in saline soil conditions.	Kapadia et al. (2021)
Pseudomonas sp. B14, *Sphingobacterium* sp. B16, *Microbacterium* sp. B19	Helping plants tolerate salinity stress	*Brassica napus* L.	Rhizobacteria were assessed for IAA production, ACC deaminase activity, P-solubilization, siderophore production, SA production, NH_3 production, HCN production, chitinase production, 1,3-*β*-glucanase activity, antifungal activity, and compatibility assays. The rhizobacterial consortium demonstrated the ability to increase the number of live leaves, shoot length, and chlorophyll content.	Swiontek Brzezinska et al. (2022)

The findings revealed that a SynCom combination of *Ensifer adhaerens* strain BK-30, *P. fluorescens* strain SN5, and *B. megaterium* strain SN15 significantly enhanced wheat growth and yield in saline conditions. A study by Sembiring et al. (2024) identified bacterial strains isolated from saline vegetation types-mangrove forests, grasslands, and oil palm plantations. The soil samples were analyzed, and ten bacterial species were identified, including biofilm-forming species: *P. aeruginosa*, *B. gladioli*, *E. cloacae*, *B. ciceri*, *A. xylosoxidans*, *P. flexa*, and *E. quasiroggenkampii*. These biofilm formations enhanced and stabilized the availability of N^+, P^{2+}, and K^+, potentially be utilized for promoting plant growth under salinity environments.

Designing SynCom based on PGP traits and enzymatic activities presents a strategic and promising approach to enhancing plant disease resistance and stress tolerance (Table 2). These characteristics facilitate the development of SynCom, which can protect plants by reducing pathogen viability and infection rates. It is also used in treating plant stress conditions. Biofilm formation and endophytic colonization ability are essential for root colonization and plant-microbe interaction traits. *In vitro* assays, greenhouse or pot trials, and molecular studies are recommended for evaluating the effectiveness of the constructed microbial consortium. Hence, developing a SynCom incorporating these PGP traits and their associated enzymatic activities has great potential for sustainable agriculture (Chem & Ito, 2025).

3.4. SynCom in soil fertility and carbon sequestration

The significance of SynCom in nutrient cycling and organic matter decomposition is necessary for promoting plant growth and development (El Hamss et al., 2023; Kumar & Verma, 2019). A study by Lyu et al. (2024) reveals that SynCom can effectively break down organic matter and provide essential nutrients to plants. Recent reports also indicate that SynCom has successfully produced cellulases, hemicellulases, and lignin-degrading enzymes to decompose plant matter, ultimately improving soil fertility and enhancing carbon sequestration (Bombardi et al., 2024; Vincze et al., 2024). In the decomposition of organic matter, microbes break down complex compounds, releasing simpler substances such as glucose. This process contributes to the formation of soil organic matter (SOM). The activity of these microbes, along with the resulting SOM, plays a crucial role in providing energy and carbon necessary for microbial growth and survival. Additionally, SOM serves as a reservoir of essential nutrients for plant growth and significantly influences soil health and fertility. SynCom produces EPS, stabilizes soil aggregates, protects organic carbon, and facilitates long-term storage (Vandana et al., 2023). Through the breakdown of organic matter, SynCom promotes the stabilization of a significant portion of this material in the soil, enhancing soil health. This stabilization process occurs over extended periods and is vital for maintaining soil quality and fertility.

Kaur et al. (2022) conducted a SynCom study to improve soil health and crop productivity. The SynCom was designed based on the PGP traits. These traits included IAA production, P-solubilization, N-fixation, biocontrol properties, and plant growth-promoting effects. The findings of the study revealed that SynCom, which included *Arthrobacter* sp., *Enterobacter* sp., *Brevibacterium* sp., and *Plantibacter* sp., led to a significant enhancement in soil nitrate availability by 55%, germination rates by 14.3%, plant height by 7.4%, and shoot biomass by 5.4%. These results highlight the potential of SynCom to improve soil fertility for sustainable agriculture. Furthermore, a recent study conducted by Raklami et al. (2019) exhibited the effectiveness of utilizing plant PGPR and arbuscular mycorrhizal fungi (AMF) as a SynCom to enhance crop nutrition, productivity, and soil fertility. The study evaluated various rhizobacterial strains to determine their capabilities in solubilizing P, K, and N-fixation as well as their ability to generate siderophores, EPS, IAA, and HCN. The AMF were assessed for the frequency of mycorrhizal infection in roots before their introduction into the SynCom. The research combined two PGPR strains, *Acinetobacter* sp. BS17 and *Rahnella aquatilis* PGP27, along with two rhizobia, *Ensifer meliloti* RhOF4 and *E. meliloti* RhOF155. The selected AMF included *Glomus* sp., *Sclerocystis* sp., and *Acaulospora* sp. Results indicated that SynCom inoculation showed significant increases in the shoot and root dry weight of *Vicia faba* L., along with an enhancement in leaf number by 130%, 200%, and 78%, respectively. Furthermore, mineral analyses demonstrated that the application of SynCom improved soil nutrient content, resulting in higher levels of N^+, P^{2+}, Ca^{2+}, K^+, and Na^+ and increased sugar and protein content. The construction of SynCom, which utilizes PGP traits, has been designed to support sustainable agriculture. These PGP traits include solubilization of P/K/Zn, siderophore production, auxins, and EPS. Screening SynCom based on these traits can provide a bacterial consortium that can effectively enhance nutrient availability, improving plant growth. Hence, designing SynCom using PGP traits is a crucial strategy in modern agriculture to enhance productivity in an environmentally sustainable manner.

3.5. SynCom in bioremediation of hazardous pollutants

SynCom has recently gained significant attention as a promising approach to addressing pesticide residue degradation (Lü et al., 2024; Zhang & Zhang, 2022). These bacterial consortia utilize diverse mechanisms to transform hazardous pollutants into less harmful substances (Di Giulio et al., 2020; Pang et al., 2023). SynCom possesses unique metabolic pathways capable of breaking down contaminants through enzymatic action. Enzymes produced by these consortia detoxify pollutants, converting them into non-toxic byproducts, improving environmental quality and soil health (Chem & Ito, 2025). Among these enzymes, hydrolases and oxidoreductases play crucial roles. Hydrolases degrade organophosphate pesticides through hydrolysis, converting them into less hazardous byproducts (Bhatt et al., 2021). On the other hand, oxidoreductases convert organic pesticides through oxidation-reduction reactions into friendly molecules for plants (Alneyadi et al., 2018). Additionally, certain SynCom strains produce dehalogenase enzymes capable of effectively removing halogen atoms, such as chlorine, from organochlorine pesticides (Buryska et al., 2018). This enzymatic activity significantly reduces toxicity and enhances the susceptibility of pesticide molecules to further degradation processes.

Liu et al. (2022) developed a SynCom consisting of *Rhodococcus* sp. T3-1, *Delftia* sp. T3-6, and *Sphingobium* sp. MEA3-1, which could degrade acetochlor by 97.81%. A recent study by Malla et al. (2023) explored a SynCom of *L. plantarum* JDARSH, *L. rhamnosus* ARJD, and *B. shackletonii* APMAM for pesticide (chlorpyrifos, cypermethrin, and glyphosate) degradation. SynCom achieved degradation rates of 94.93% for chlorpyrifos, 89.4% for cypermethrin, and 87.01% for glyphosate. Recent research by Shetty et al. (2023) indicates that hazardous pollutants have unique structures and varying toxicity levels. Effective degradation requires specific strains with significant metabolic pathways (Zhang & Zhang, 2022). Developing a potential SynCom relies on various factors, such as enzymatic degradation efficiency, pH, temperature, and pollutant concentration. Focusing on these factors allows us to identify potential SynCom that can effectively degrade hazardous pollutants, promoting the discovery of novel SynCom that improve degradation performance. Furthermore, these strategies can easily develop and assemble SynCom efficiently, even in irregular conditions or with various pollutants.

3.6. SynCom in the degradation of lignocellulose for sustainable biomass

Cellulose, hemicellulose, and lignin are the primary components of plant cell walls, presenting significant challenges for microbial degradation due to their complex structures. The aromatic nature of lignin makes it particularly resistant to degradation, while the presence of hemicellulose and lignin restricts microbial access to cellulose, reducing breakdown efficiency (Shikata et al., 2018; Wu et al., 2022). Nevertheless, recent studies by Zhang et al. (2023) have demonstrated that various microorganisms can degrade these polymers effectively. SynCom has emerged as a promising agent for efficiently converting lignocellulosic residues into valuable products (Lin, 2022). Through fermentation processes, SynCom employs specific enzymatic activities to degrade lignocellulosic materials, including cellulose, hemicellulose, and lignin, into simpler sugars. This enzymatic conversion is essential for the production of valuable bioproducts, such as biofuels (e.g., bioethanol and biobutanol), chemicals like hydrogen, biosurfactants, bio-based polymers, nutrients, and other commercially important compounds, supporting the sustainable utilization of biomass (Chem & Ito, 2025).

According to Lin et al. (2024), SynCom transforms agricultural residues into valuable bioproducts by mixing enzymatic breakdown with microbial fermentation. Initially, polymers are converted into simpler molecules that serve as substrates for microorganisms. During fermentation, cellulases break down cellulose into glucose units, hemicellulases degrade hemicellulose into sugar monomers, and ligninases facilitate lignin decomposition (Nargotra et al., 2023). For instance, Zheng et al. (2020) conducted a study on rice straw degradation utilizing a SynCom designed based on the degradation characteristics of specific microorganisms and lignocellulose-degrading enzymes. A SynCom of *Parabacteroides*, *Alcaligenes*, *Lysinibacillus*, *Sphingobacterium*, and *Clostridium* achieved efficient degradation rates of rice straw, breaking down cellulose (71.7%), hemicelluloses (65.6%), and lignin (12.5%). The fermentation process resulted in the production of acetic acid and butyric acid. Recently, Gad et al. (2024) investigated 86 bacterial isolates to evaluate their ability to produce endoglucanase, exoglucanases, and β-glucosidase for the degradation of cellulose. The MC29 (*C. uda* and *P. jinjuensis*) and MC31 (*C. uda* and *P. citronellolis*) SynComs exhibited the highest cellulose degradation potential, with MC31 achieving 46.15% and MC29 reaching 43.76% (Gad et al., 2024). Utilizing SynCom to break down cellulose, hemicellulose, and lignin into valuable products for sustainable development results in the innovation of sustainable biofuels and biochemicals. Nevertheless, several challenges exist, including the complex structure of lignocellulose and the necessity to identify and optimize high-activity microbial strains alongside their enzymes. Advanced technologies such as genomics, synthetic biology, and machine learning play a vital role in enhancing the efficiency of microbial degradation and advancing the industrial applications of lignocellulose utilization.

4. Challenges and limitations of the application of SynCom

SynCom has been developed to address agricultural challenges and enhance sustainable agricultural practices. Despite their potential benefits, their applications may also lead to unintended adverse effects. While SynCom can effectively enhance plant growth, reduce dependency on chemical inputs, and improve disease resistance, translating laboratory results into practical field applications remains challenging (Chem & Ito, 2025). Several factors influence their effectiveness, including interactions with indigenous soil microbes, variations in soil types, and diverse climate conditions. The development and application of SynCom can be more cost-effective than conventional agricultural inputs (Tariq et al., 2025), making their efficient utilization critical for competing with chemical fertilizers and pesticides. Moreover, creating effective SynCom requires an in-depth understanding of microbial ecology, plant-microbe interactions, systems biology, crop physiology, and environmental conditions (Chem & Ito, 2025). Furthermore, some SynCom strains may produce inhibitory substances that could negatively affect other community members (Wang et al., 2022). Additionally, the introduced SynCom can become dominant within microbial communities, potentially disrupting ecosystem balance (Afanador-Barajas et al., 2021; Dobrzyński et al., 2025). Such disruptions can alter nutrient cycling, impacting plant nutrient uptake and soil health (Korneykova et al., 2024). While SynCom might effectively suppress pathogens, it could also negatively affect plant health and crop yields if improperly designed or applied. Hence, careful design and thorough testing of SynCom are essential to maximize beneficial microbial interactions, enhance plant health, and mitigate potential risks.

5. Conclusions and future perspectives

Synthetic microbial communities (SynCom) represent an innovative and effective strategy for enhancing ecological functions and advancing sustainable agricultural practices. SynCom offers a promising alternative to conventional agricultural inputs by optimizing plant health, resilience, and productivity, significantly reducing reliance on chemical fertilizers and pesticides, mitigating environmental impacts, and helping crops adapt to climate change. Despite their substantial potential, successfully integrating SynCom into agricultural systems requires addressing critical challenges, including community stability, environmental adaptability, and regulatory frameworks. Future research efforts should prioritize evaluating SynCom's performance across diverse field conditions, exploring complex interactions within the rhizosphere, and continuously monitoring their ecological impacts. Understanding these microbial consortia will enable the refinement of strategies, ensuring long-term sustainability, productivity, and resilience of agricultural ecosystems.

CRediT authorship contribution statement

Chanchao Chem: Conceptualization, Methodology, Validation, Investigation, Data Curation, Formal analysis, Visualization, Project administration, Writing – Original Draft, Writing – Review & Editing. **Sreyneang Nhim**: Conceptualization, Methodology, Validation, Data Curation, Writing – Review & Editing. **Thev Pol**: Conceptualization, Methodology, Validation, Data Curation, Visualization, Writing – Review & Editing. **Sreylen Meas**: Conceptualization, Writing – Review & Editing. **Eneang Ourn**: Conceptualization, Writing – Review & Editing. **Techchheng San**: Writing – Review & Editing. **Channa Nget**: Writing – Review & Editing. **Tsukasa Ito** – Conceptualization, Funding Acquisition, Resources, Supervision, Writing – Review & Editing. All authors read and approved the final manuscript.

Declaration of Competing Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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