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Reflections on microbial genetic resources in agricultural systems

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ABSTRACT

This paper reflects on the use of microbial genetic resources in the context of agricultural systems. The benefits of harnessing the diversity of these resources in any agricultural system are highlighted, as well as the importance of knowing and preserving native agrobiodiversity, which is deemed an essential resource for Latin America. In this region, harmful effects of irrational use of agrochemicals and monocultures on the environment, economy, and health have been brought to light. In view of the growing awareness and global interest in the development of bioinputs, rational biodiversity use, environmental crisis, cost of conventional synthetic inputs, and the right to safe and quality food, agriculture requires new tools and effective strategies in its practice. Microbial genetic resources are a potential source of relevant and suitable inputs for this purpose. Using the bibliometric technique of co-occurrence of terms with the VOSviewer tool, an analysis of 60 articles published between 2020 and 2024, collected from databases such as Scopus and Web of Science, was performed. An interest in microbial resources and their potential application in plant nutrition, production of growth regulators, defenses against pests and diseases, and tolerance to limiting environmental conditions can be appreciated. However, elucidating their complex ecological dynamics is necessary to understand them in real production contexts, thus allowing the allocation of relevant technological packages and the fair management of their use and potential benefits.

1. Introduction

Soil is one of the most important components in agroecosystems. It is a system in itself, in which water, gases, minerals, organic matter in different stages of mineralization, as well as plants, macro and microorganisms interact (Nannipieri, 2020). One gram of soil can harbor millions of microbial cells of thousands of different species interacting with all system components (Nannipieri, 2020). In the Green Revolution (GR) production model, soil provides support for cultivated plants (improved, high-yielding varieties), which are produced with the addition of industrially synthesized fertilizers, herbicides, and other inputs (Cerutti, 2019). The dynamics of conventional agricultural intensification can reduce the diversity and activity of beneficial organisms that control pests and pathogens, which negatively affects the plant, animal, and human health (Wall et al., 2015). GR allowed increasing global yields of crops such as maize, rice, and wheat by more than 100% between 1960 and 2000 (Lobell et al., 2005). However, production under this scheme cannot be generalized due to the wide typology of existing agricultural systems in Mexico (LaFevor, 2022). The GR model demands the manufacture and application of inputs that require large amounts of

energy for their production, which generate harmful effects on the environment, animal, and human health, as well as on communities and local and regional economy (Martínez-Dalmau et al., 2021; Tosi et al., 2022). The effects of these synthetic inputs and the GR model on soils and microbial communities are of particular importance as they threaten food production and quality due to the disruption of Soil Organic Matter (SOM) mineralization processes, mainly carried out by fungi and bacteria, the absence of soil-microorganism-plant interactions, their bioaccumulation, and the residues they generate (Bumb et al., 2021). The increase in population –reaching more than 8 billion by 2022-, the expansion of world-wide land used for agriculture (about 1.5 billion hectares), the demand for raw materials of plant origin, the need to deal with the environmental crisis (FAO, 2009), and, in general, the need for agricultural production systems that do not compromise natural resources for future generations, reinforce the importance of paradigm shift in terms of conventional agriculture associated with GR (Suman et al., 2022).

One of the global approaches to generate new tools and strategies for sustainable or regenerative production is based on bioinput development (Aramedis et al., 2023; Bullor et al., 2023). These are products -or

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derivatives- of plant, animal, or microbial origin capable of improving productivity, quality, or health of plant crops (Aramendis et al., 2023). In the case of bioinputs of microbial origin, these have been used for soil health restoration, pest control, and plant growth and development promotion, and are often referred to as biofertilizers (Aramendis et al., 2023; Bullor et al., 2023).

Biofertilizers are substances containing microorganisms that exhibit beneficial properties for plant growth and development (Maçik et al., 2020). These are formulated with one or more types of active or latent microorganisms and improve conditions for cultivated plants to grow and develop by increasing the availability of nutrients, thus decreasing the need to apply highly soluble industrial fertilizers, as well as having a regulatory function on potentially pest organisms (Bumb et al., 2021). The identification and characterization of microorganisms useful as biofertilizers has emerged as a strategy for the substitution of inputs -now biological-, especially regarding the deep study of their dynamics in the soil, their interactions with native or specific microbiota of the rhizosphere, and in local agricultural systems (Solanki et al., 2023). This paper describes some perspectives on the use of microbial genetic resources in the context of sustainable agricultural systems. For this purpose, a bibliometric analysis was performed based on 60 research

Table 1
Key microorganisms in agricultural sustainability.

Microorganisms studied	Purpose and Agricultural Applications	Authors and year of publication
<i>Agrobacterium</i> sp., <i>Azotobacter chroococcum</i> , <i>Bacillus safensis</i> , <i>Bacillus haynesii</i> , halotolerant PGPR, <i>Pseudomonas putida</i> , <i>Bacillus subtilis</i> , <i>Micrococcus yunnanensis</i> PGPR, AMF, <i>Pseudomonas</i> spp., <i>Bacillus</i> spp., <i>Paenibacillus polymyxa</i> , <i>Streptomyces</i> spp., <i>Enterobacter</i> sp., <i>Burkholderia cepacia</i>	Promoting growth under saline and drought stress, improving water retention and nutrient absorption; increasing productivity and crop resilience in saline soils and drought conditions. Encouraging the use of biofertilizers to enhance nutrient absorption, enzymatic activity, and plant growth; improving productivity and reducing chemical input in various agricultural systems.	(Amjad et al., 2023; Borzoo et al., 2021; Castiglione et al., 2021; Gao et al., 2022; Kumar et al., 2024; Patel et al., 2023; Sharma et al., 2024; Teles et al., 2023). (Aloo et al., 2020; Avio et al., 2020; Dai et al., 2023; Dodino-Gutiérrez et al., 2023; Fan and Smith, 2021; Jyotirmayee et al., 2023; Kavková et al., 2023; Maçik et al., 2020; Pande et al., 2020; Rajkumar et al., 2024; Sharmila et al., 2021; Ünüvar et al., 2022). (Ali et al., 2022; Rajkumar et al., 2024; Raturi et al., 2021; Shabanamol et al., 2021; Sharmila et al., 2021; Surendirakumar et al., 2023; Taheri et al., 2022; Vo et al., 2023; Zahra et al., 2022). (Jurburg et al., 2020; Marois et al., 2023; Ontivero et al., 2020; Qarni et al., 2021; Rojas-Badía et al., 2022; Scotti et al., 2020; Shrivastava et al., 2024).
<i>Bacillus velezensis</i> , <i>Lysinibacillus sphaericus</i> , <i>Stenotrophomonas maltophilia</i> , <i>Fusarium oxysporum</i> , <i>Streptomyces</i> sp., endophytic bacteria	Controlling pests and diseases through volatile compounds and antifungal mechanisms; reducing pesticide dependence and serving as biocontrol agents and biopesticides in rice, banana, and other crops.	(Jurburg et al., 2020; Marois et al., 2023; Ontivero et al., 2020; Qarni et al., 2021; Rojas-Badía et al., 2022; Scotti et al., 2020; Shrivastava et al., 2024).
Soil microbial communities, AMF, <i>Bacillus</i> spp., organic amendments, <i>Penicillium</i> sp., <i>Streptomyces</i> sp.	Increasing microbial diversity and soil stability; improving fertility and promote growth in adverse conditions; use of compost and amendments for enhanced soil fertility and health.	(Dutta et al., 2024; Kajić et al., 2023; Messai et al., 2023; Zelaya-Molina et al., 2024).
<i>Acinetobacter</i> sp., <i>Lysinibacillus fusiformis</i> , MGR, PGPB bacteria	Detoxifying heavy metal-contaminated soils and improving agricultural sustainability through bioremediation; used in contaminated soils to enhance quality and promote sustainability.	(Dutta et al., 2024; Kajić et al., 2023; Messai et al., 2023; Zelaya-Molina et al., 2024).

articles published in Scopus and Web of Science (WoS) for the last five years. Table 1 features some of these microorganisms along with their purpose and applications.

1.1. Agriculture and microbial genetic resources

Microorganisms play essential roles in nature and plant physiological processes. Soil microbiota can influence ecosystem stability through their effects on plant diversity (Wang et al., 2024). Plants and associated mycobiomes, including those in soil, interact in complex and dynamic ways. These provide ecological niches, act as useful carbon sources for microbial growth, which in turn influences plant growth, development, and fitness (Vincent et al., 2020; Wang et al., 2024). Microorganisms are highly sensitive to changes in soil physicochemical features derived from agricultural activities (Moreno-Espíndola et al., 2018). Intrinsic soil variability is fundamental to understand and manage microbial genetic resources in agricultural systems such as denitrification and SOM decomposition processes (Loecke, 2012). Conventional farming techniques including crop residue removal, monocropping, tillage, and inorganic fertilizer application reduce soil fertility and alter the structure of its microbiome (Table 2) (Azarbad, 2022; Mäder et al., 2002).

Sustainable or regenerative agricultural systems, which tend to accumulate organic matter in the soil, reduce the use of external inputs and use crop rotation and relay strategies, tend to favor greater diversity and functionality of the microbial groups in the soil (Azarbad, 2022; Dessureault-Rompré, 2022; Wang et al., 2024).

The contrast in the effects of agricultural systems on microbial community has led to the acknowledgement of their ecological, economic, and cultural importance. Documents such as the Nagoya Protocol, dealing with "access to genetic resources and the fair and equitable sharing of benefits arising from their use", as well as the interest in the development of bioinputs, investment analysis, and bioinput consumption (Aramendis, 2023; Bullor et al., 2023), support the current relevance of their study.

2. Literature overview

This study employed a bibliometric analysis to explore global trends and approaches related to microbial genetic resources and their application in agricultural systems. This method, widely recognized for its ability to evaluate large volumes of scientific data, allows visualization and understanding of research patterns and relationships between publications (Donthu et al., 2021; Klarin, 2024). Scopus and Web of Science (WoS), selected for their rigorous inclusion criteria and broad coverage of peer-reviewed scientific literature, were used for data collection (Klarin, 2024).

Table 2
Conventional agricultural practices and their effects on microbial community.

Agricultural practices	Effects on microbiota and soil functions	Authors and year of publication
Tillage	Breaks up aggregates, compacts soil, and SOM mineralization processes.	(Azarbad, 2022; Dessureault-Rompré, 2022; Mäder et al., 2002; Ussiri and Lal, 2009).
Residue disposal	Reduces soil organic matter content.	(Azarbad, 2022; Bumb et al., 2021; Fuentes et al., 2009; Mäder et al., 2002).
Unmeasured applications of agrochemicals (fertilizers and herbicides)	Increases salt content and electrolytic conductivity. Decreases microbiome diversity. Promotes the presence of fungi.	(Azarbad, 2022; Lupwayi et al., 2024; Meena et al., 2020; Rezapour, 2014).
Monoculture application	Decreases microbiome diversity.	(Adeleke and Babalola, 2021; Liu et al., 2024; Moreno-Espíndola et al., 2018).

Conducted in July 2024, the search used keywords and Boolean operators: "microbial genetic resources," "bacteria," "fungi," "agricultural microbiology," "microbial resources," and "PGPB," combined with the OR operator. For articles on characterization, "characterization" and "characterizing" were used with the AND operator. "Use," "application," and "utilization" were included using the AND operator. Relevance to sustainable agriculture was ensured with the terms "sustainable agricultural systems" and "sustainable agriculture" combined with the AND operator. Articles in English were considered due to their predominance in global scientific literature, following the methodology proposed by Klarin (2024) to ensure a representative dataset (Fig 1).

Once the selection of studies was completed (Fig. 1), the bibliometric map was constructed with VOSviewer, an efficient software for data visualization and creation of term co-occurrence maps (van Eck & Waltman, 2010). This tool facilitated the identification of associations and links between key terms, organizing the findings into clusters (Klarin, 2024) that represent relevant focus areas within the microbial genetic resource literature. The "full counting" method was employed to assign equal weight to each occurrence of a term, ensuring a complete representation of its relevance in the analysis (Donthu et al., 2021). This approach captures all thematic relationships equally, ideal for studies seeking a comprehensive view of interactions in the literature (van Eck & Waltman, 2010).

A threshold of 10 co-occurrences was established after preliminary tests to ensure result validity and relevance (Klarin, 2024), which allowed 60% (26 terms) of the 44 key terms identified to be included in the final analysis, highlighting the most recurrent concepts in the field and outlining the main thematic clusters (van Eck & Waltman, 2010).

The methodology used in the selected research shows that 63% corresponds to "Isolation and characterization of microorganisms", 25% to "Evaluation of microorganisms under controlled and field conditions", 7% to "Literature reviews", and 5% to "Development and evaluation of technologies and products".

3. Cluster analysis of microbial genetic resources, characterization, and application in the context of sustainable agricultural systems

In the analysis of the abstracts of the 60 papers, 243 links were identified and four thematic groups were defined using the VOSviewer program (Fig. 2). Cluster 1 concentrated 39% of the concepts and was called "Soil microbiology and biofertilizers"; cluster 2 consisted of 27% of the concepts and was entitled "Endophytic bacteria, activities and properties"; cluster 3 comprised 19% of the concepts and was called "Role of microbial agents in enhancing crop yield and resilience to abiotic stress"; and, finally, cluster 4 included 15% of the concepts and was called "Crop tolerance to microorganism-mediated abiotic stress".

3.1. Cluster 1: soil microbiology and biofertilizers

Soil microbiology and the use of biofertilizers are pillars of agriculture as Plant Growth-Promoting Rhizobacteria (PGPR), nitrogen-fixing bacteria, and Phosphate-Solubilizing Bacteria (PSB) (Bakki et al., 2024; Khedher et al., 2021; Pande et al., 2020; Üniivar et al., 2022), can reduce the use of synthetic fertilizers (Dai et al., 2023; Maçik et al., 2020), increase the availability of plant-assimilable nutrients (Marois et al., 2023) and increase agricultural productivity (Aloo et al., 2020; Pande et al., 2020).

Species such as *Bacillus*, *Pseudomonas*, *Enterobacter*, and *Streptomyces* stand out for their ability to solubilize nutrients and produce phytohormones that promote plant growth (Dodino-Gutiérrez et al., 2023; Malayil et al., 2020; Sharmila et al., 2021; Zahra et al., 2022). The potential of isolated PGPR strains, including *Pseudomonas* (*n*), *Rhizobium* (*Y*), and *Bacillus* (*L*) has been demonstrated, showing various activities. In general, all strains exhibited nitrogen-fixing capacity, with *Pseudomonas* displaying a superior ability to solubilize phosphorus. Both *Pseudomonas* and *Bacillus* showed antagonistic effects against the growth of *Pseudomonas syringae* DC3000 and *Botrytis cinerea*, as well as tolerance to high concentrations of NaCl without compromising their antimicrobial activity. Moreover, all *Rhizobium* isolates tested positive for

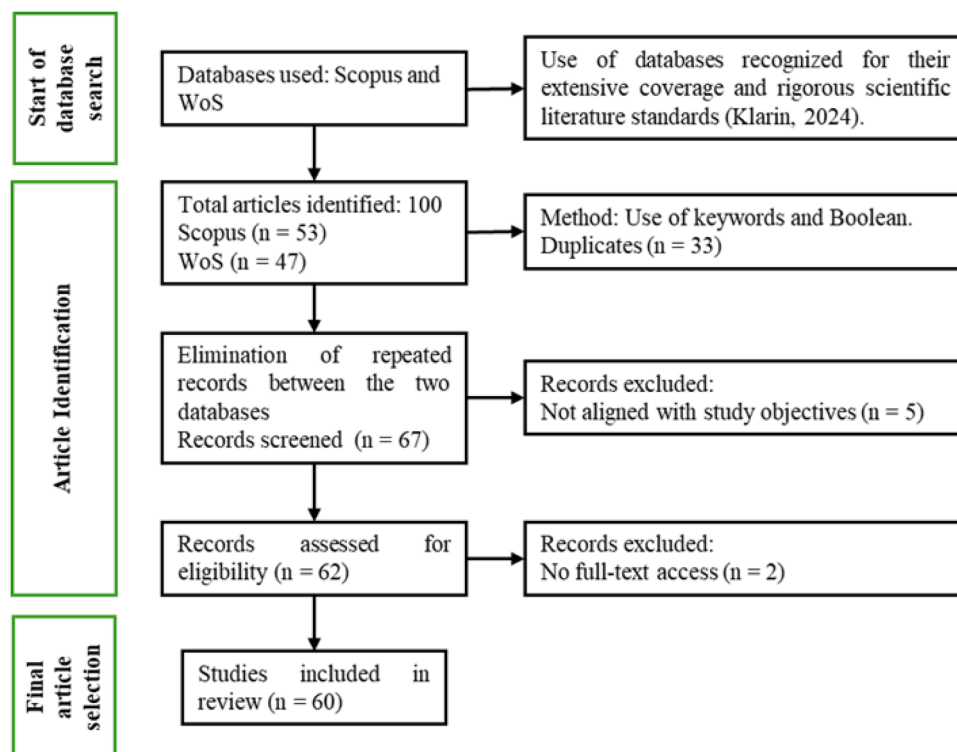


Fig 1. Article selection process and Bibliometric Analysis.

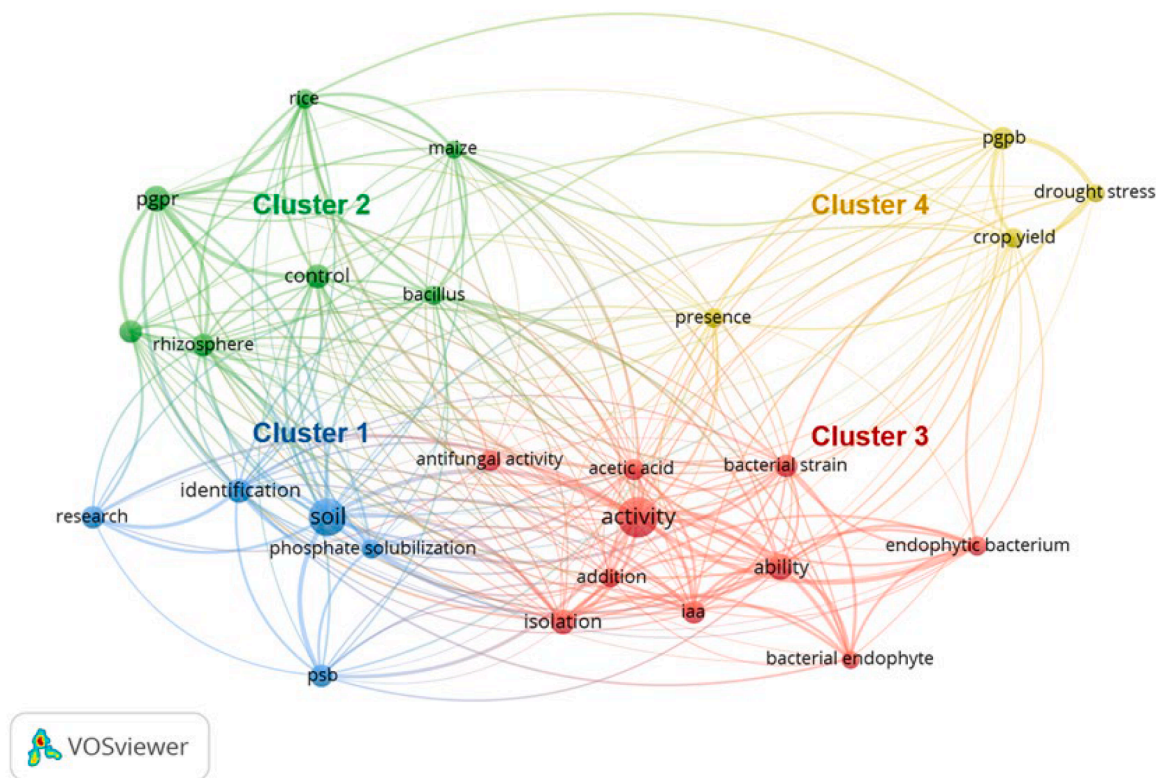


Fig 2. Bibliometric map about the study of microbial genetic resources, characterization, and application in agricultural systems.

1-aminocyclopropane-1-carboxylate deaminase activity, indole acetic acid production, and phosphorus solubilization (Fan and Smith, 2021).

Studies on microbial genetic resources have focused on improving plant growth and health, soil quality, and degradation of contaminating microorganisms (Zelaya-Molina et al., 2024). Rhizospheric bacteria from organic soils have been shown to increase nutrient content, antimicrobial activity, and crop yield of turmeric plants, highlighting the importance of using native strains adapted to local conditions to promote plant growth (Jyotirmayee et al., 2023). Certain bacterial strains have also been found to reduce heavy metal contamination through bioleaching, supporting the relevance of these approaches (Messai et al., 2023).

In light of their high tolerance to heavy metals and their ability to produce a wide range of antimicrobial peptides, the relevance of bacteria such as *Bacillus* in bioinput design has been supported by studies on Sporobiota in olive orchards (Manetsberger et al., 2023). Halotolerant bacteria isolated from the rhizosphere of *Salicornia fruticosa* and identified to the genera *Bacillus*, *Enterobacter*, *Halomonas*, *Kushneria*, *Oceanobacillus*, *Pantoea*, *Pseudomonas*, and *Staphylococcus* have been shown to be phosphate solubilizers, indicating their effectiveness in saline soils and underlining the importance of adapting microbial applications to specific contexts (Teles et al., 2023). Furthermore, the potential of *Bacillus* spp. to promote plant growth and control pathogens has also been highlighted (Rojas-Badía et al., 2022).

The addition of compost and organic amendments increases microbial diversity and stability, improving soil fertility and plant health (Scotti et al., 2020; Shrivastava et al., 2024; Marois et al., 2023). Moreover, PSB, such as *Burkholderia cepacia* and different *Bacillus* species have shown their efficacy in improving phosphorus availability in the soil (Pande et al., 2020; Qarni et al., 2021), with *Bacillus firmus*, *Bacillus licheniformis*, and *Penicillium* sp. standing out in compost-treated soils (Qarni et al., 2021).

The use of strategies based on nanoclays or encapsulation to enhance incorporation of PGPR such as *Streptomyces* sp. and *Enterobacter* sp. has been highlighted, reinforcing the need for bioformulations to optimize

the benefits these microorganisms bring to soil and crops (Syaziana et al., 2024; Zahra et al., 2022). Additionally, agroecosystem management also plays a fundamental role in the composition and functionality of microbial communities-management practices in coffee systems have been shown to significantly alter microbial diversity, affecting both bacteria and fungi, emphasizing the importance of agricultural practices that promote biodiversity and soil health (Jurburg et al., 2020).

On the other hand, arbuscular mycorrhizal fungi play an essential role in improving nutrient uptake and stress tolerance, especially in arid soils (Avio et al., 2020; Fasusi et al., 2021; Ontivero et al., 2020).

3.2. Cluster 2: endophytic bacteria, activities, and properties

Endophytic bacteria and rhizobacteria are essential for agricultural productivity and sustainability. Endophytes live inside plant tissues without causing damage, while rhizobacteria colonize the rhizosphere, interacting with roots. Both contribute to crop growth by producing growth regulators such as Indole-3-Acetic Acid (IAA) or by solubilizing nutrients (Chen et al., 2024; Khan et al., 2020; Salehin et al., 2023). In addition, they have been found to produce metabolites that act as biocontrol agents for pathogens and stressful environmental conditions (Shabanamol et al., 2021; Sharma et al., 2024; Rajkumar et al., 2024).

Salinity-tolerant *Bacillus* sp. producing growth regulators, which are lactic acid bacteria with growth suppressive activity of pathogenic fungi such as *Fusarium*, could help reduce the use of conventional inputs (Chen et al., 2024; Kavková et al., 2023; Khan et al., 2020; Mir et al., 2020; Rajkumar et al., 2024; Salehin et al., 2023; Shabanamol et al., 2021; Sharma et al., 2024; Zhang et al., 2024). *Bacillus halotolerans* LBG-1-13 has exhibited multiple growth-promoting and antifungal properties, facilitating plant growth under salt stress and drought conditions (Gao et al., 2022). Growth-promoting bacteria with bioremediation potential capable of producing substances that protect plants against pathogens have also been identified, with such capabilities being potentially influenced by the environment where the bacteria are found (Kajić et al., 2023). *Pseudomonas khazarica* produces IAA and solubilizes phosphates

(Deepika et al., 2023), *Bacillus* spp. and *Klebsiella pneumoniae* serve as growth promoters and produce metabolites that favor tolerance to salt stress conditions (Biswas et al., 2023). From these works, it is noteworthy that these microorganisms are isolated and characterized from environments with limiting conditions for plant growth.

Bacillus velezensis MS20 produces surfactin with antibiofilm and antifungal properties, inducing resistance in maize against *Rhizoctonia solani* (Ali et al., 2022). Rice-isolated *Lysinibacillus sphaericus* showed antifungal activity against *Rhizoctonia solani* by producing volatile compounds (Shabanamol et al., 2021). Characterization of endophytes of *Vicia villosa* showed that they contribute to plant growth through the production of IAA and siderophores, facilitating nutrient solubilization and control of pathogens such as *Calonectria ilicicola* (Taberi et al., 2022). Endophytic bacteria from Cavendish banana pseudostem have demonstrated the ability to produce hydrolytic enzymes, improving nutrient availability and controlling diseases caused by *Phyllosticta* sp. and *Fusarium* sp. (Vo et al., 2023).

3.3. Cluster 3: role of microbial agents in enhancing crop yield and resilience to abiotic stress

This cluster analyzes how these organisms contribute to agricultural sustainability by strengthening plant resistance to abiotic stresses and optimizing crop productivity, based on several studies that have explored their influence under different environmental stress conditions. Particularly, twenty-two specific entomopathogenic fungi adapted to local environmental conditions have been isolated, showing significant potential for formulating biocontrols and mycoinsecticides with enhanced persistence and efficacy (Anwar et al., 2021). Moreover, eight strains of root endophytic fungi exhibited potential phosphate solubilization activity and a high solubilization rate with *Phoma* sp. on PVK medium, while also producing beneficial compounds such as organic acids and phytohormones, which increase plant yield and biomass (Surendirakumar et al., 2023).

Cold-active Plant Growth-Promoting Bacteria (PGPB), including genera such as *Pseudomonas*, *Acinetobacter*, *Bacillus*, and *Stenotrophomonas*, are able to produce antifreeze proteins and express genes induced by low temperature stress, which favor their survival and enhance the ability of plants to take advantage of nutrients in the soil, reducing dependence on chemical fertilizers applied in intensive agrosystems (Rizvi et al., 2021). The relevance of *Acinetobacter* sp. TMKU7 has been highlighted for its ability to oxidize arsenic and detoxify contaminated soils. Plant growth-promoting properties have also been observed (Dutta et al., 2024). Additionally, silicate-solubilizing bacteria have been shown to regulate the solubility of silicates (mostly insoluble) and increase their bioavailability to plants, where silicon can protect plants from both abiotic and biotic stresses and increase overall plant fitness (Raturi et al., 2021).

Innovative technologies have also been developed, such as bilaminate microcapsules of *Pseudomonas putida* Rs-198 as a slow-release bacterial inoculant showing improved growth promotion of *Capsicum annum* L. under salt stress (Zhu et al., 2023). The introduction of hexaconazole nanofibers with cyclodextrin (HP γ CD) for the preparation of HEZ/HP γ CD-IC-NF has been shown to significantly improve the efficacy of insoluble fungicides and reduce fungicide dose (Liu et al., 2024). Furthermore, the combination of indigenous PGPB strains with organic and inorganic fertilizers has been found to reduce toxic effects and improve nutrient retention in soil, indirectly rehabilitating adverse soil conditions and contaminated environments (Asgar et al., 2023).

3.4. Cluster 4: crop tolerance to microorganism-mediated abiotic stress

Agricultural productivity faces significant challenges due to abiotic factors such as soil salinity and drought. Microorganisms have positioned themselves as valuable tools to improve plant tolerance under these conditions. Soil salinity, which impedes efficient water and

nutrient uptake, can be mitigated by using diazotrophs, as several PGPRs have been isolated with different abilities to benefit plants. For example, *Agrobacterium* sp. and *Azotobacter chroococcum* significantly promote seedling growth under salt stress (Kumar et al., 2024). Consortia of halotolerant bacteria, including *Bacillus* strains, have been found to be more effective than individual strains in increasing salinity tolerance in crops such as *Amaranthus viridis* (Patel et al., 2023). Furthermore, the addition of compost and the incorporation of halotolerant PGPR, including strains with diazotrophic capacity, can increase growth, biomass, and resilience to salinity and desertification stress in crops such as maize, tomato, quinoa, and sunflower (Castiglione et al., 2021).

Drought, particularly in arid regions, poses another significant challenge. However, microorganisms offer promising solutions to enhance plant resilience. Inoculant bacteria acting as growth promoters have been studied for their ability to reduce chemical inputs in conventional agricultural practices and increase nutrient uptake of P and N and stress resistance in maize sprouts (ALKahtani et al., 2020). Drought conditions during reproductive phase of *Camelina sativa* can affect its growth and seed production, and PGPB inoculation has been evidenced to improve growth and yield by decreasing reactive oxygen species and increasing proline, carbohydrates, and photosynthetic pigments (Borzo et al., 2021). The combination of endophytic bacteria such as *Pseudomonas putida* and *Bacillus subtilis* with vitamin B has been highlighted for its ability to improve plant vigor in barley crops under drought stress, decreasing the effects on early growth stages (Amjad et al., 2023). Additionally, rhizobacteria such as *Bacillus licheniformis* and *Aeromonas caviae* have shown potential to promote maize growth under water stress, significantly increasing aerial and belowground biomass even in soils with low water holding capacity (Agunbiade et al., 2024).

In addition, innovations in bioinoculant formulation and metabolite production also play a crucial role in improving crop tolerance to abiotic stress. Identified PGPRs have been shown to significantly stimulate rice morphological features as they change the chemical and physical properties of the soil surrounding the host plant roots in order to assist its nutrition (Jasrotia et al., 2021). Combined with synthetic fertilizers, this may improve rice yield and reduce fertilizer application. On the other hand, the combination of heavy metals and salinity poses another challenge in agricultural development. An innovative compound of biosynthesized selenium nanoparticles using *Rosa roxburghii* extract and chitosan has been developed, which showed outstanding antibacterial and antioxidant activities, inhibiting the spread of pathogens such as *Phylospora piricola* and *Staphylococcus aureus* in vivo tests on apples and preserving vitamin C, total acid, and water contents in red berries, highlighting their potential for sustainable applications in post-harvest fruit preservation and the development of new nano bioantibacterial compounds with agronomic interest (Ge et al., 2024).

4. Prospects

Co-occurrence analysis showed an increase in specialized publications from 2020, highlighting 27 relevant studies from India and China, leading the scientific production in this field thanks to their investment in R&D in biotechnology and agriculture. In India, characterization of beneficial bacterial strains for plant growth and disease control, production of exopolysaccharides by halotolerant bacteria, and the use of silicate solubilizing bacteria to improve soil fertility and resistance to abiotic stress are prioritized (Ali et al., 2022; Raturi et al., 2021; Shrivastava et al., 2024). China excels in characterization of bacterial strains, development of thermostable enzymes to protect crops (Gao et al., 2022), and biosynthesis of selenium nanoparticles with antibacterial and antioxidant properties (Ge et al., 2024).

A particular interest has been vested in microbial genetic resources due to their usefulness as bioinputs, their role as biofertilizers, plant growth promoters, disease control agents, and in the tolerance of cultivated plants to abiotic stress conditions, among other applications. The potential effect of their application on food quality and health of

those who consume them is also recognized (Khan et al., 2020). However, published works show an approach aimed at input substitution, without considering -at least explicitly-, aspects of microbial ecology and the complexity of agroecosystems (Azarbad, 2022; Li et al., 2022). Some relevant approaches to microorganisms and their application in sustainable agricultural systems are pointed out.

4.1. Biofertilizer ecology

This concept has not been studied in depth. There is a need to extend these studies under field conditions to analyze nutrient availability, SOM and its influence on the diversity and structure of native microbial communities over several crop cycles. The effect of climate on the permanence and efficacy of inoculants and on SOM dynamics is another approach that requires further research. In particular, the study of the native mycobiome and SOM mineralization processes, including strategies to identify local SOM strains and consortia in agroecosystems is pertinent when considering local strategies and relevant technological packages for inoculant procurement and application.

4.2. Replacing current inputs with bioinputs

Bioinput production should not be limited to the mere substitution of industrial inputs without a comprehensive analysis of the agricultural systems being worked with. Their adoption should incorporate agricultural practices that are aligned with suitable soil management, pest, and disease control, considering local strategies and the use of accessible sources of organic matter. In line with biofertilizer ecology, they should be designed as technological tools in relation to locally available sources of organic matter. In this sense, it is important to come up with local inoculant multiplication strategies.

4.3. Education, privatization, and exclusion from the use of microbial diversity

The curricular focus on the role of microorganisms in agricultural production is crucial for paradigm shift. According to GR, microorganisms and soil played a negative and merely supportive role, respectively. If this approach to agricultural education is not modified, the adoption of bioinputs in food production will be difficult to achieve. Finally, the application of regulatory instruments to the use of microbial genetic resources of local legal relevance and world-wide correspondence, such as the Nagoya Protocol, should be maintained as long as it guarantees public and collective benefit, not the conclusion of contracts that tend to limit access and corporate use of these resources for economic profit.

CRedit authorship contribution statement

Iván Pável Moreno-Espíndola: Conceptualization, Investigation, Project administration, Writing – review & editing. **Alonso Gutiérrez-Navarro:** Investigation, Conceptualization, Writing – review & editing. **Diana Carolina Franco-Vásquez:** Investigation, Visualization, Writing – review & editing. **Daniel Vega-Martínez:** Methodology, Formal analysis, Visualization, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

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