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A bibliometric analysis on soil microbial diversity and processes: global trends and methodologies

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Abstract

Soil is Earth's most biodiverse habitat, harboring a multitude of microbial species. Several efforts have been conducted to survey the diversity of these microbial communities in the last decades. Still, a comprehensive overview of the literature highlighting significant topics and key players was needed. We carried out a bibliometric analysis of the literature on soil microorganisms and processes between 2011 and 2022, aiming to identify research trends, methodologies, and gaps in knowledge on soil microorganisms. A database was developed in PostgreSQL and connected with the R statistical program, enabling literature review data analysis through 227 SQL customized queries. The data retrieved from the database was analyzed using R and Excel. Bacteria and fungi were the most studied among soil microorganisms, accounting for 78% and 90% of the articles and patents in the databases, respectively. China and the USA were the leading nations studying soil microbial diversity and processes. These countries were also at the forefront of applying advanced molecular methods (e.g., omics). Most other top publishers were from developed countries, especially Europe, or large developing economies such as India and Brazil. Other developing nations, such as Argentina, Egypt, Iran, Mexico, Pakistan, and the Philippines, were among the top publishers in agriculture-related topics. Altogether, the results show that groups other than bacteria and fungi are understudied, that a few countries dominate the research output on soil microbes, and that countries from Latin America, Africa, and Asia are underrepresented, highlighting the need to invest in soil microbiology science in these regions.

Keywords: biodiversity, microorganisms, publications.

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1. Introduction

Soil harbors a considerable part of the earth's species and is Earth's most biodiverse singular habitat. Among these species, soil microorganisms represent the most significant proportion (Anthony et al. 2023) and are also indispensable in sustaining life on the planet. They significantly influence biogeochemical cycles, affecting the delivery of essential ecosystem services, such as plant growth, nutrient cycling, and climate regulation (Adhikari & Hartemink 2016; Banerjee & van der Heijden 2023). These microorganisms directly and indirectly influence plant, animal, human, and environmental health, contributing to the One Health concept (Kopittke et al. 2024).

Nevertheless, soil biodiversity has been increasingly threatened by human-induced alterations such as fire, deforestation, land degradation, erosion, landslides, urbanization, surface sealing, soil compaction, agricultural intensification, depletion of soil organic matter, soil acidification, nutrient imbalance, contamination, salinization, and sodification (FAO 2020, Lindo et al. this issue).

The field of microbial diversity is strongly methods-driven and evolved significantly with the development of molecular culture-independent approaches during the 80s and 90s, which allowed the assessment of a diversity previously undetected by culture-dependent methods. Especially in the case of the soil, the estimates are that only between 0.1 - 1.0% of this diversity can be detected by culturing (Amman et al. 1995). Among those, the use of 16S rRNA gene amplification associated with several approaches, such as enzymatic restriction, electrophoresis, denaturation gradients, cloning, and sequencing, unveiled the existence of many undescribed microbes at the taxonomic level (Kirk et al. 2004). The field further evolved with the development of high-throughput sequencing technologies, which allowed the development of metagenomics to an unprecedented level. Additionally, the evolution of genomics and other omics in the last two decades allowed the in-depth genetic and phenotypic characterization of microbial isolates (Iqbal et al. 2024). Prices became more affordable for many laboratories, allowing the widespread use of such techniques.

However, the assessment of these tools may still be a challenging task in several countries. These approaches have revealed the crucial role of soil microbiomes in maintaining soil health and resilience, allowing ecosystems to better withstand perturbations (Banerjee & van der Heijden 2023). This resilience is critical in a scenario where the world seeks food security, as the soil is a repository of microbes with beneficial traits for plant growth and productivity, including pest suppression, nutrient provision, and soil structure maintenance (Gupta et al. 2022). Despite its recognized relevance as a field of study, a published overview of how soil microorganisms and microbial diversity have been studied globally was lacking. Such an overview could reveal the major players driving research in the field and in which regions to identify research gaps and determine where to invest financial resources to increase knowledge on global soil microbial diversity. This data could also contribute valuable information to implement global initiatives such as the Global Soil Biodiversity Initiative and support the establishment of a Global Soil Biodiversity Observatory by the Food and Agriculture Organization. Given this context, we performed a bibliometric analysis and a patents search related to soil microbial biodiversity to understand the practical applications and innovations emerging from this field.

2. Material and Methods

2.1 Literature review on soil microbial diversity and processes

We performed a literature review on the Web of Science (WoS) platform to identify the worldwide distribution of studies on soil microorganisms, the methods used in these studies, and the vital environmental processes or functions these microorganisms provide. The review included publications of all types (articles, books, book chapters, and reviews) published between January 2011 and December 2021 for microorganisms and between January 2012 and December 2021 for microbial processes. A comprehensive database containing all records and fields downloaded from the Web of Science (WoS) was constructed using PostgreSQL. Details regarding the database construction and subsequent analysis of the organized information are provided by Niva et al. (this issue). In our case, we had two distinct subdivisions of the database, one for the search related to microbial diversity and the other for soil microbial processes.

Search terms were carefully selected to cover major microbial taxonomic groups, related processes, and functions (Table 1). The searches within the microbial diversity database were performed for microbial groups and potential uses (biological nitrogen fixation, plant growth promotion, phosphate solubilization, potassium solubilization, bioremediation, biological control, industrial applications, antibiotics, antibiotic resistance, and biodiversity inventories). This database was also searched for many methods used to assess microbial diversity, including culture-dependent methods and culture-independent methods (genomics,

Table 1. Search terms, number of recovered papers, and percentage of papers within the major microbial groups. The searches were made within Topics in the Web of Science database between 2011 and 2021 (taxa) and 2012 to 2021 (processes).

Group	**Search terms**	**Number of papers**		**%**
		Per group	**Total**	
Bacteria	“Diversity” AND ”soil bacteria” ”Rhizobi*” ”Soil” AND ”Cyanobacteria” ”Soil” AND ”Actinobacteria” AND ”Actinomycetes” "plant growth-promoting rhizobacteria" OR ”PGPR”	31,354	12,129 8,196 1,955 6,375 2,699	43.5
Archaea	”Diversity” AND ”soil Archaea”		2,956	4.1
Fungi	”Diversity” AND ”soil fungi” ”Mycorrhiz*”	24,944	8,378 16,566	34.6
Virus	”Diversity” AND ”soil virus” ”Soil” AND ”Bacteriophage”		1,875 281	3.0
Algae	”Soil” AND ”Algae”		2,130	3.0
Lichen	”Soil” AND ”Lichen”		1,640	2.3
Microbiome	”Soil” AND ”Microbiome”		4,027	5.6
Microbiota	”Soil” AND ”Microbiota”		2,798	3.9
TOTAL			**72,005**	**100**
Soil microbial processes				
Soil enzymes	"enzymatic" OR "soil enzyme" OR "soil enzymes" OR "phosphatase" OR "urease" OR "glucosidase" OR "cellulase" OR "arylsulfatase" OR "dehydrogenase" OR "diacetate fluoresceine" OR "glucosaminidase" OR “amidase” OR “amylase” OR “phenol oxidase” OR “galactosidase” OR “invertase” OR “laccase” OR “protease” OR “xylanase” OR “FDA hydrolysis” OR “chitinase” OR "phosphomonoesterase" AND "soil"		16,389	30
Soil microbial biomass	"microbial biomass" OR "microbial-biomass" OR "fungi biomass" OR "bacteria biomass" OR "ergosterol" AND "soil"		10,971	20
Soil microbial respiration	"microbial biomass" OR "microbial-biomass" OR "fungi biomass" OR "bacteria biomass" OR "ergosterol" AND "soil"		6,737	12

Table 1 continued.

Group	Search terms	Number of papers		%
		Per group	Total papers	
Soil-mediated nitrogen processes (except BNF)	“nitrogen mineralization” OR “nitrification” OR “N-mineralization” OR “N mineralization” OR “nitrogen immobilization” OR “N immobilization” OR “denitrification” AND "soil"		12,218	23
Soil greenhouse gas emissions	“CH4 emission” OR “methane emission” OR “N2O emission” OR “nitrous oxide emission” OR “nitrous-oxide emission” OR “CO2 emission” OR “carbo dioxide emission” AND "soil"		4,869	9
Soil organic matter decomposition	”decomposition" AND "soil" AND ("organic matter" OR "SOM")		7,333	14
TOTAL			**58,517**	**100**

proteomics, metagenomics, microscopy, qPCR, RFLP, DGGE or TGGE, PLFA or FAME, fingerprinting, and metabarcoding). The searches within the microbial processes database included major processes (Table 1), methods, and enzymes. Terms formed by two words were used with quotation marks to keep the meaning of the words together. The Boolean operator “OR” was used to indicate the presence of any of the search terms.

The search results were downloaded as Excel spreadsheets with the complete records to populate the database. The number of publications per keyword query, country, and affiliation were retrieved and used to build maps and graphics in Microsoft Excel 2019, with the top ten or twenty countries in each category. Additionally, the rank of the top twenty publishing countries was correlated with their gross domestic product (GDP) and the Gross Domestic Expenditure on R&D (GERD). The GDP data was obtained from the International Monetary Fund for 2024 (IMF 2024) and the GERD data from UNESCO for 2020 (UNESCO 2024). The GERD of 2021 was used for Australia and Switzerland since the data was unavailable for 2020. The Spearman’s coefficient was calculated using the software R (R Core Team 2023) and the package agricolae (de Mendiburu 2023). Graphics were built with the package ggplot2 (Wickham 2016).

2.2 Patents search

Search terms for patents were selected based on major microbial taxonomic groups (Table 2) used for research publications in WoS. Patent applications between January 2011 and December 2021 were retrieved using the Derwent Innovations Index (DII) via the WoS interface. The search results were downloaded as Excel spreadsheets with the complete records.

2.3 Data availability

The files containing all downloaded fields from the WoS were combined into the PostgreSQL database maintained at Embrapa Cerrados. Access to this database is restricted, mainly due to the legal restrictions on reusing data obtained from WoS searches.

3. Results

3.1 Main microbial taxa assessed and distribution of studies

The bibliographic search returned 72,005 papers for all taxa (Table 1), with bacteria and fungi accounting for 78% of the total. Archaea, viruses, algae, and lichens represented only 12% of the studies (Table 1), and the remaining 10% accounted for the emergent field of “Microbiome” studies and the alternative term “Microbiota.”

Overall, China and the United States of America (USA) together published 17,037 articles, corresponding to 37% of all articles among the top 20 countries. This list includes countries of all inhabited continents except Africa. These are among the 29 countries with the most significant gross domestic product in 2024 and are large economies in their regions. The top ten countries accounted for 40% of the published articles. As an exercise, we calculated Spearman's correlation between the rank of these countries and their GDP or GERD. The correlation was 82.23% and significant with the GDP ($p < 0.001$). Conversely, the correlation was 21.50% with the GERD and not significant ($p = 0.3626$).

China and the USA contributed 43 to 56% of publications on all taxa and search terms except for lichens, primarily studied by the USA, Spain, Russia, Canada, and Germany, before China (Figures 1 and 2). Germany followed these two countries in almost all subjects. Other highlighted countries were India, the UK, France, Brazil, Spain, Australia, Canada, the Netherlands, and Japan, with diverse rankings depending on the subject.

Regarding bacteria and archaea, China and the USA accounted for almost 40% of all publications among the top 20 publishing countries, followed by India and Germany with 8% and 6%, respectively (Figure 1). When considering Rhizobia and PGPR, India and Brazil came next to the USA and China, followed by France, Spain, Germany, Mexico, Australia, and the UK. China, the USA, Germany, the UK, France, India, Australia, and Brazil accounted for 64% of publications on Fungi, and the UK was behind France and India when dealing specifically with mycorrhizal fungi. Germany and the UK were among the top five publishing on viruses and algae (Figure 2).

In the emergent field of microbiome studies, Germany, the Netherlands, and the UK stood out after the USA and China, followed by Canada, Australia, Brazil, India, and France (Figure 2). Lichens first had the US, then Spain, Russia, Canada, and Germany. The Russian Federation appeared among the top ten for algae and cyanobacteria studies. Among African countries, only South Africa and Egypt were among the top 20 countries publishing on rhizobia and PGPR. These two countries were also among the top 20 publishing on microbiome and algae, respectively.

3.2 Primary methods used in soil microbiology research

Over 12,000 papers were published between 2011 and 2022, mentioning some of the most widely used soil microbial diversity assessment methods. The ten most used methods were genomics, with 4,999 articles, representing 41% of the articles, followed by proteomics (9 %), metagenomics (7%), microscopy (7%), qPCR (6%), RFLP (5%), DGGE or TGGE, PLFA or FAME (3%), fingerprinting and metabarcoding (all around 3%) (Figure 3). These include both culture-dependent and independent methods. The countries with the highest number of publications in methods of soil microbial diversity were the USA and China, with 2,569 and 2,554 publications, respectively, followed by Germany, France, the UK, India, Spain, Australia, Brazil, and Canada.

3.3 Microbial processes and soil enzymes

The literature search yielded 42,540 publications regarding microbial processes and soil enzymes after duplicate removal. Soil enzymes were the most studied soil microbial-mediated process, with 16,389 records (Table 1) representing approximately 39% of all publications on soil microbial processes (Figure 4). Soil-mediated nitrogen processes, which include mineralization, nitrification, immobilization, and denitrification, were the second most studied topic, with 12,218 records (29% of the total), followed by studies on soil microbial biomass (26%), soil organic matter (SOM) decomposition, soil respiration activity and soil-mediated greenhouse gas (GHG) emissions (11-17% of the total; Table 1).

The top 20 countries with the most publications on soil microbial processes included countries of all continents but Africa (Figure 4). China and the USA stood out again, with China having almost 14,000 publications and the USA around 9,000. These countries were followed by Germany, India, Australia, the UK, Spain, Brazil, Canada, and France, each with over 1,600 publications.

Dehydrogenase and urease were the most studied among soil enzymes, each with around 3,000 articles published between 2012 and 2022 (Figure 4). Other frequently studied enzymes were glucosidase (1,877 articles), alkaline (1,323) and acid (1,045) phosphatases, protease (1,315), peroxidase (979), and cellulase (977). Additional enzymes with fewer publications included invertase, chitinase, laccase, amylase, phenol oxidase and glucosaminidase (each with 440-669 articles), and xylanase, fluorescein diacetate hydrolysis, arylsulfatase, galactosidase and amidase (each with 100-440 articles).

3.4 Main uses and applications of microbial diversity and their geographical distribution

As for the main uses and applications of microbial diversity, the USA and China remained among the top publishing countries, but other countries also took the lead. Brazil was the country with the most papers on biological N_2 fixation, followed by the USA, China, Argentina, Spain, Canada, South Africa, and Mexico (Figure 5). In the case of PGPR, India contributed almost twice the number of papers from China and Pakistan, followed by the USA, Brazil, Spain, Iran, Italy, South Korea, and Germany. The country also led the topic of phosphate solubilization, and it was the second after China and ahead of the USA in bioremediation. Together China, the USA, and India accounted for 54% to 60% of the articles on microbial industrial applications and antibiotics, respectively (Figure 6). For antibiotic resistance, the USA, China, the UK, and Brazil accounted for 69% of the articles.

Table 2. Number of Derwent Innovations Index (DII) patent families (inventions protected by patent) from each searched term. Terms were also grouped into significant groups: Bacteria, Archaea, Fungi, Viruses, Algae, and Microbiome. The result (in bold) is based on joining patent families but disregarding overlaps, as several patents appear in more than one term.

Group/search	Number of Patent Families	DWPI Patent Proportion (%)
Bacteria	**22,361**	**65.2**
Soil AND Bacteria	19,211	
Rhizobi*	2,942	
Soil AND Cyanobacteria	296	
Soil AND (Actinobacteria OR actinomyce*)	2,452	
PGPR OR (Plant AND Growth AND Promoting AND rizhobacteria)	193	
Archaea	**62**	**0.3**
Soil AND Archaea	62	
Fungi	**14,178**	**41.3**
Soil AND Fung*	13,173	
Mycorrhiza*	1,743	
Virus	**2,101**	**6.1**
Soil AND Virus*	2,022	
Soil AND bacteriophage	89	
Algae	**1,857**	**5.4**
Soil AND Algae	1,857	
Microbiome/microbiota	**99**	**0.3**
Soil AND Microbiome	56	
Soil AND Microbiota	46	
TOTAL	**34,314**	**100**

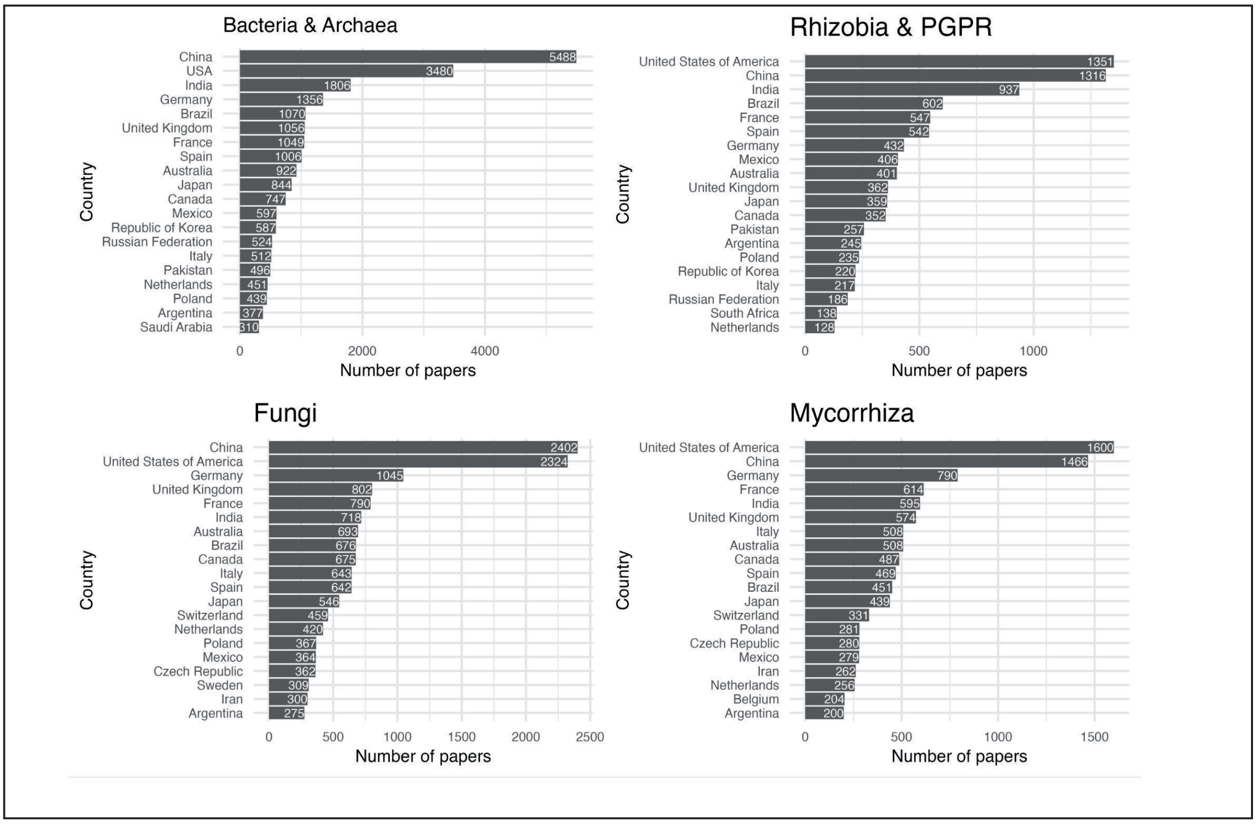

Figure 1. Top twenty countries with the most significant number of publications in Bacteria & Archaea, Rhizobia & PGPR, Fungi, and Mycorrhiza between 2011 and 2021. The frequency of publications is based on the authors' country of origin, according to Web of Science.

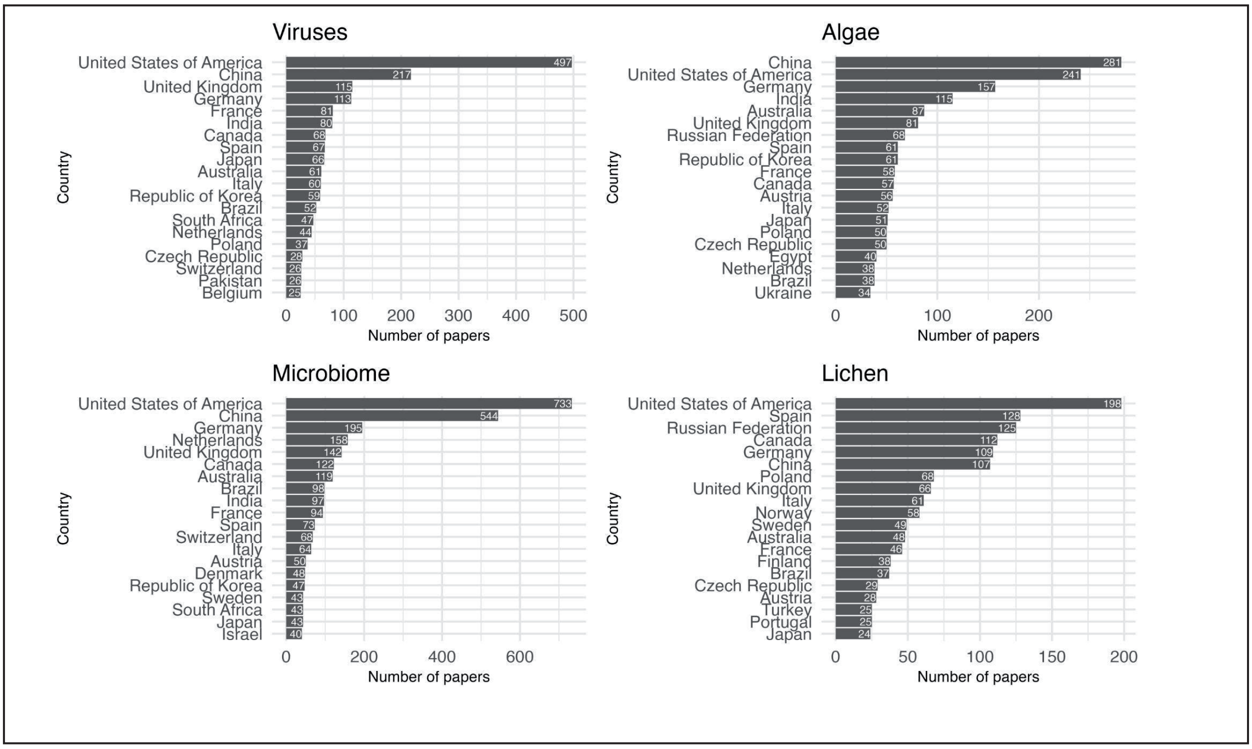

Figure 2. Top twenty countries with the most significant number of publications in viruses, algae, microbiome, and lichens between 2011 and 2021. The frequency of publications is based on the authors' country of origin, according to Web of Science.

In biological control, the top ten countries included China, the USA, India, and Brazil, followed by Egypt, Spain, Germany, Japan, Italy, and Canada (Figure 5), while China, the USA, and the Netherlands lead on suppressive soils, with 25%, 22%, and 14% of the articles published by the top ten countries, respectively. Finally, China, the USA, and Germany accounted for 51% of the publications on biodiversity inventories among the top ten countries. The remaining 49% were from the UK, Brazil, Spain, Australia, France, Italy, and Canada (Figure 6).

3.5 Main microbial taxa associated with patents and global distribution

In the patent search using the Derwent Innovations Index (WoS) between 2011 and 2021, 34,314 patent families were found. Terms related to bacteria were found in 22,361 patent families, corresponding to 65% of patents recovered, followed by the terms associated with fungi, found in 14,178 patent families (41%). The following significant terms found in patents were virus (6%), algae (5%), and microbiome and archaea (both with <0.3%; Table 2).

4. Discussion

The bibliometric analysis revealed the soil microbial groups most studied globally, the leading countries carrying out these studies, the methods used, and the processes and functions assessed. Our analysis included bacteria, archaea, fungi, viruses, algae, and lichen data. Protists were not included since they were considered microfauna in a complementary study (Correia et al., this issue). It is important to highlight that the results shown here are limited to our database, which is restricted to the queries used to search for the papers in WoS. For this reason, the number of papers may be underestimated. However, they are still a representative sample of what can be found in the whole database (72,005 papers).

Fungi and bacteria were the most studied taxa, accounting for 78% of the publications in the evaluated time frame. These organisms are directly involved in organic matter degradation and transforming different organic and inorganic elements (Madigan et al. 2008, Fierer 2017) and constitute most of the soil microbial biomass (Baldrian 2017). Despite their relevance, other groups, such as archaea, viruses, and algae, accounted for a smaller portion of the publications.

Archaea are pivotal in the N cycle and methanogenesis (Conrad et al. 2006, Stahl &de la Torre 2012, Timonen & Bomberg 2009, Brauer et al. 2020), while viruses play a crucial role in cell turnover in the soil due to their ability to infect prokaryotic and eukaryotic cells (Kimura et al. 2008, Pratama and van Elsas 2018, Sokol et al. 2022, Wang et al. 2024). The revolution of metagenomic studies, which started with prokaryotes, has arrived in virology, facilitating the assessment of viral communities (Roux 2021).

Regarding the methods used to assess soil microbial diversity, genomics was by far the most used approach, followed by proteomics, metagenomics, and microscopy. Although being surpassed by more recent techniques, fingerprinting approaches such as RFLP, DGGE, TGGE, PLFA, and FAME were still used, albeit to a lesser extent. The USA and China stood out as the countries with the most publications using the top ten methods, followed by several developed countries, including many in Europe and some developing countries such as India, Brazil, Mexico, and South Africa. These results underscore the relevance of molecular methods in the study of soil microbiology. At the same time, the increasing use of these methods raises concerns about expertise since data processing and analysis rely heavily on bioinformatics (Attwood et al. 2019).

Although sequencing costs have been reduced significantly, these analyses can still be expensive for smaller research groups. It is essential to highlight that the top twenty countries are either developed or developing countries with strong economies and considerable scientific investment (Salami & Soltanzadeh 2012; IMF 2024; UNESCO 2024).

The significant processes studied overall were soil enzymatic activity, processes linked to N and C cycles, soil microbial biomass, and respiration. Fewer studies focused on soil greenhouse gas emissions despite the importance of microbes in this process (American Society for Microbiology, 2023). The most assessed enzymes were dehydrogenases and ureases. Dehydrogenases are indicators of general microbiological activity in the soil since they occur intracellularly in all living microbial cells and do not accumulate extracellularly in the soil (Wolinska & Stepniewsk 2012). Ureases, in turn, are involved in the transformation and bioavailability of N (Cordero et al. 2019). Other frequently assessed enzymes, such as beta-glucosidase, phosphatases, and proteases, are primarily involved in C, P, and N cycles. Again, China and the USA had the most publications, with a similar pattern observed among most of the top twenty countries, including many developed nations, especially in Europe, and some developing economies with robust scientific output, such as India, Brazil, Russia, and Pakistan.

We found an extensive publication record on all evaluated functions except antibiotic resistance. It is

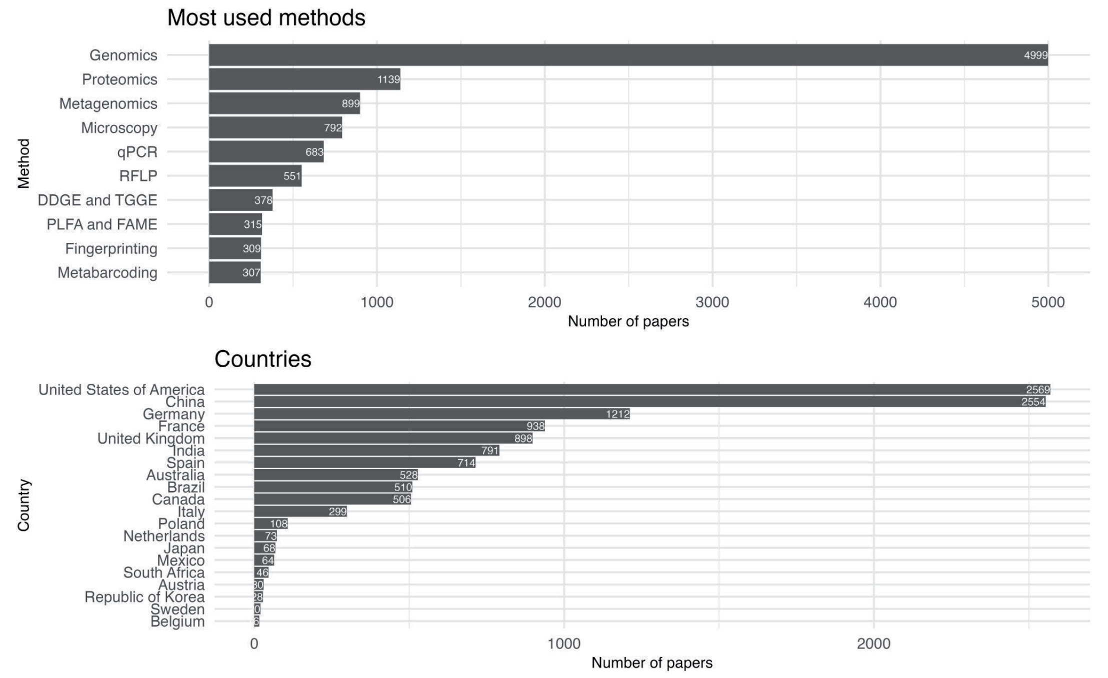

Figure 3. Top 10 main methods used to assess microbial biodiversity and countries with the highest number of publications of these in the period between 2011 and 2021. The frequency of publications is based on the country of origin of authors according to the Web of Science.

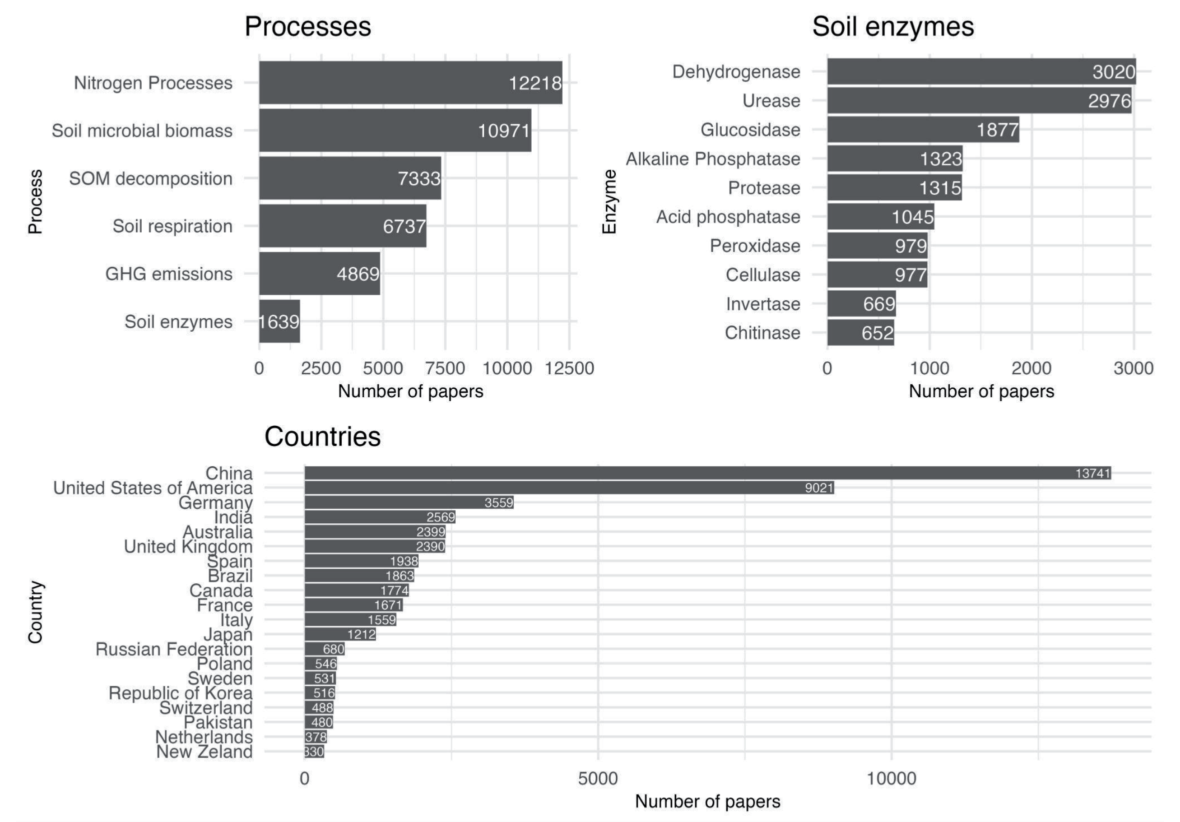

Figure 4. Number of publications per soil microbial processes, the main assessed enzymes, and the top 20 countries with the most significant number of publications between 2012 and 2022. The frequency of publications is based on the country of origin of authors according to the Web of Science.

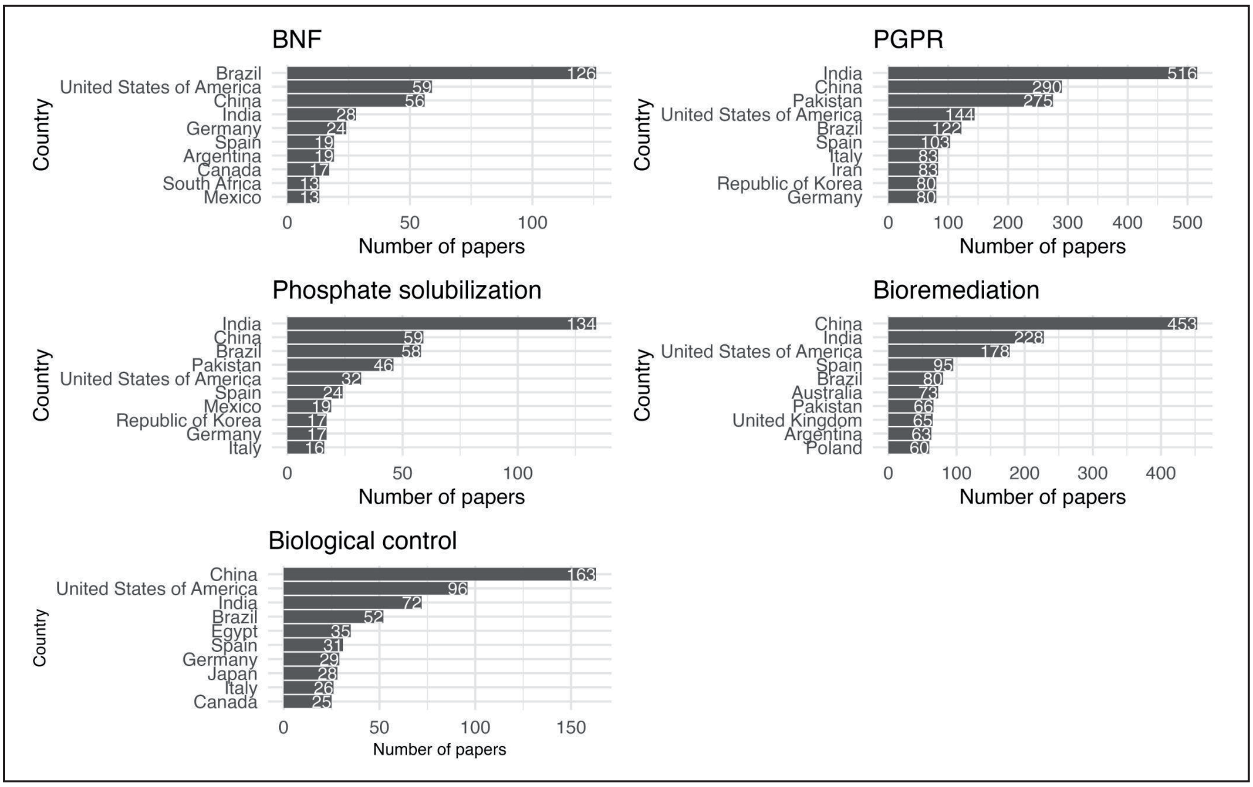

Figure 5. Top 10 countries publishing on biological nitrogen fixation (BNF), plant growth promoting-rhizobacteria (PGPR), phosphate solubilization, bioremediation, and biological control between 2011 and 2021. The frequency of publications is based on the country of origin of authors according to the Web of Science.

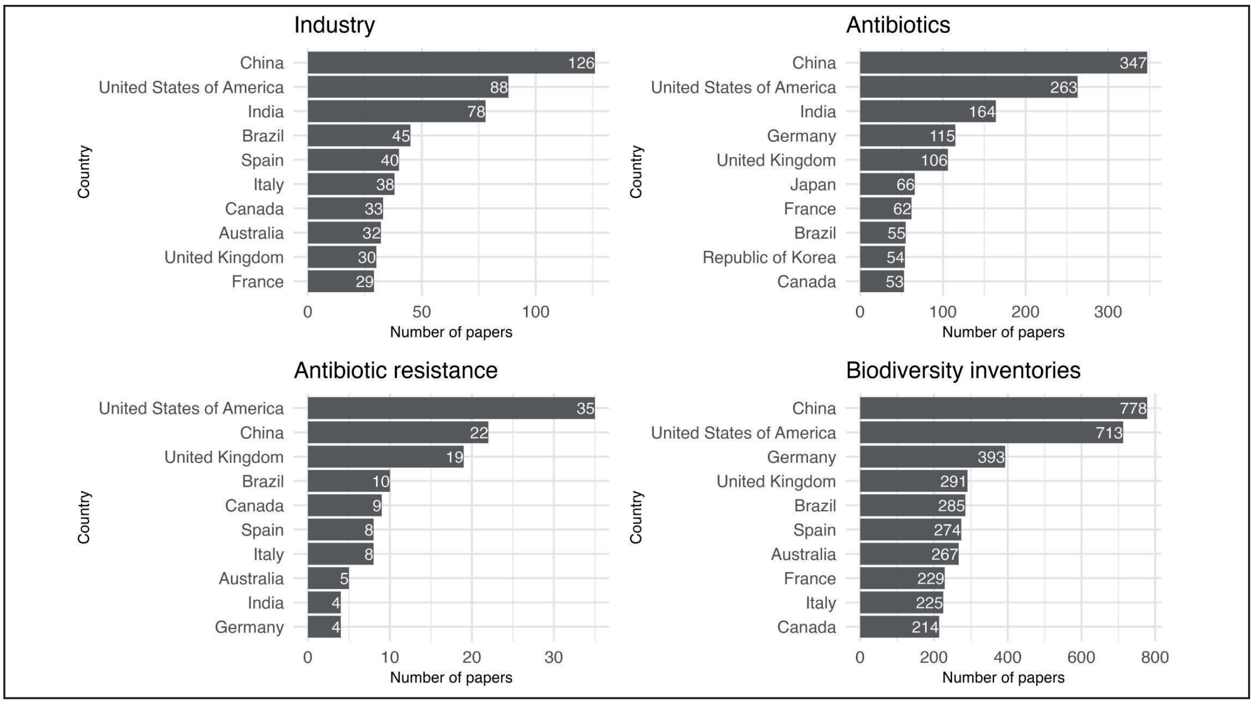

Figure 6. Top ten countries publishing on industrial applications, antibiotics, antibiotic resistance, and biodiversity inventories between 2011 and 2021. The frequency of publications is based on the country of origin of authors according to the Web of Science.

worth noting that developing countries stood out in topics related to microbial functions. For example, Brazil led the number of publications on biological nitrogen fixation, highlighting a long history of studies on this topic (Telles et al. 2023). India had the most publications on phosphate solubilization and plant growth promotion. China was the leading country in bioremediation, biological control, industrial applications, antibiotics, and biodiversity inventories. These and other developing countries such as Argentina, Mexico, Pakistan, Egypt, Chile, Iran, and the Philippines were also among the top ten countries on applied topics, together with developed countries such as the USA, Canada, France, Germany, Spain, Italy, the UK, South Korea, Japan, and Australia.

Finally, over 34,000 patents were found in our searches, primarily based on bacteria and fungi (together 90% of the total), reflecting the same pattern observed for publications in indexed journals. Fewer patents were recovered using archaea and soil microbiomes (around 0.3% each), reflecting a gap in research on archaea and the relative novelty of the microbiome field. Often referred to as an 'intellectual property right,' patents serve as a motivator for fostering innovation (Hall 2007). They cover only some possible microbe-based technologies since indigenous microorganisms cannot be patented in some countries (Balachandra Nair & Ramachandranna 2010, Cameotra 2013, Parmar 2024). However, they can still indicate technological advancements. Granting patents fosters the protection of technological inventions and the advancement of knowledge by granting inventors exclusive rights while publicly disclosing the technical details, contributing to the overall understanding of a particular technology (Florencio et al. 2020, Figueiredo et al. 2019).

China and the USA stood out as the countries with the most publications, reflecting their economic power and investment in science. These two countries spent US$526 and 656 billion dollars on research and development in 2019, accounting for roughly half of global investments in science that year (Woolston 2023). China approached the USA in Earth and Environmental Sciences and Physical Sciences in 2018 (Nature 2021) and surpassed it in Chemistry and Natural Sciences in 2018 and 2022, respectively (Nature 2021, Woolston 2023). As shown here, China and the USA published roughly the same number of papers on the most common assessment methods (2,569 and 2,554 for the USA and China, respectively). On the other hand, China published almost 5,000 more papers on soil microbial processes than the USA.

Among the ten top countries publishing on different microbial taxa, we encountered mainly developed countries such as Canada, France, Germany, Spain, Italy, the UK, South Korea, Japan, and Australia. India and Brazil, developing countries with megadiverse ecosystems, stood out among the top ten countries for most of the taxa, reflecting these countries' investments in science in the last decades (de Meis et al. 2007, Scarano 2007, Salami & Soltanzadeh 2012).

When focusing on specific functions carried out by microorganisms mainly used in agricultural settings, such as biological nitrogen fixation, plant growth promotion, and mineral solubilization, other developing countries such as Argentina, Mexico, Pakistan, Egypt, Chile, Iran, and the Philippines were also among the top ten countries together with developed countries, highlighting a particular interest of these countries in topics of agricultural importance. Besides their large diversity, these countries also have a robust agricultural sector that benefits from microbial inoculation. For example, soybeans in Brazil save billions of dollars with rhizobia inoculation that otherwise would be spent with nitrogen fertilizers (Telles et al. 2023). Inoculation with *Azospirillum* in Argentina, Brazil, and Mexico and the use of arbuscular mycorrhizal fungi in India are two other examples (Cassán et al. 2020, Kuila & Ghosh 2022).

It is important to note that many of the developing countries listed in this study are among the largest economies in their regions. Some are even among the most significant economies worldwide, such as China, India, and Brazil, which had the 2nd, 5th, and 10th largest gross domestic products in 2024 (IMF, 2024). As previously highlighted, most of the top publishing countries are among the 29 with the highest GDP in 2024 and are large economies in their regions. The number of papers was correlated with the GDP, though not with the gross domestic expenditure in research and development, perhaps because the total expenditure is not directly related to investments in soil microbiology research. These correlations are based on a small amount of data, thus only indicative, and must be explored in future research.

5. Conclusions

China and the United States are the leading nations in studying soil microbial diversity and processes, with China consolidated as a critical player in the field. These countries are at the forefront of applying advanced molecular methods, especially genomics, proteomics, and metagenomics. Other developed countries, especially some European countries, Canada, Japan, South Korea, and Australia, also significantly contribute to the study of soil microbial diversity. Nevertheless, the participation of some developing countries among the top contributors is worth noting, especially India and

Brazil. Other developing countries, such as Argentina, Egypt, Iran, Mexico, Pakistan, and the Philippines, play a significant role mainly in research on microbial groups relevant to agriculture, such as nitrogen fixers, phosphate and potassium solubilizers, and plant growth-promoting rhizobacteria (PGPR). These countries have robust economies and are relevant in a global or regional economic context. Apart from these countries, most nations in Latin America, Africa, and Asia were not included among the top publishers, highlighting the need for more significant investment in soil biodiversity science in those regions. Finally, bacteria and fungi were the most extensively studied microbial groups and withheld the most patents, indicating a well-established expertise in their potential biotechnological use. Therefore, monitoring strategies focusing on bacteria and fungi could be quicker to implement, particularly in agriculture. On the other hand, viruses and algae remain understudied, highlighting a critical gap that deserves more attention in future research efforts.

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