



Global Perspectives on Environmental Microbiome Research: Current Status and Future Directions

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Abstract

The environmental microbiome plays an important role in various ecosystems around the world, influencing nutrient cycling, disease dynamics and ecosystem stability. This bibliometric analysis provides a comprehensive overview of the current state and future directions of environmental microbiome research from a global perspective from 2009–2024. Through systematic examination of Scopus publications, 2154 documents were found. The results show a significant increase in the number of publications since 2017 and a peak in 2024. The most cited document was "The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes" with 1887 citations and "Structure and function of the global ocean microbiome" with 1843 citations. The most productive countries in environmental microbiome research are the United States (n = 748), China (n = 533), India (n = 308), Germany (n = 172) and the United Kingdom (n = 157). Microbiome, microbial community, microflora, microbiota, microbiology, bacteria, and bacterium are the most popular topics that will continue to develop in the future. Although the United States has published the highest total number of papers, more recent studies have predominantly been published from China, indicating shift in the centre of study from the United States to China. Insights gained from this analysis contribute to a deeper understanding of the environmental microbiome research landscape, guiding future research priorities and collaborations in the field.

Keywords: environmental microbiomes; global perspective; interdisciplinary approaches; research trends; sustainable management

1. INTRODUCTION

The microbiome consists of diverse microorganisms, including bacteria, archaea, fungi, and viruses, that inhabit specific environments with unique physical and chemical characteristics [1]. These microorganisms interact with biotic and abiotic factors, influencing various ecosystem processes such as decomposition, bioremediation, biofuel production, biogeochemical cycling, and wastewater treatment [2]-[7]. Decomposition is the breakdown of organic matter with the help of microflora such as fungi, bacteria, actinomycetes, protozoa, and other microorganisms. In soil, decomposition produces humus, which can increase soil fertility and become a source of nutrients for soil organisms [8]. The decomposition of soil

organic matter is influenced by both fungi and bacterial activity. Decomposition by fungi involved ectomycorrhizal (ECM) and saprotrophic fungi, which play distinct roles in nutrient cycling [9]. Bacteria such as *Priestia aryabhattai*, *Trichoderma reesei*, and *Bacillus megaterium* are also known to be involved in the decomposition of soil organic matter through their phosphate solubilization and cellulolytic activities [10]-[13]. In the aquatic environment, decomposition process plays a crucial role in nutrient cycling and maintenance of ecosystem balance by releasing essential nutrients into the water column and sediments. Microorganism such as heterotrophic bacteria and aquatic fungi, especially hyphomycete, play a key role in the decomposition process in this environment [14]. Both in terrestrial and aquatic environments, decomposition of organic matter occurs due to the enzymatic activity of microorganisms in breaking down proteins, lipids, cellulose, hemicellulose, chitin, and lignin [15][16].

Bioremediation refers to the process of reducing or removing environmental contaminants through biological means, which can involve plants, fungi, bacteria, or other organisms. Some microorganisms that play a role in soil bioremediation include *Achromobacter denitrificans*, *Klebsiella oxytoca*, and *Rhizobium radiobacter* [17]. While

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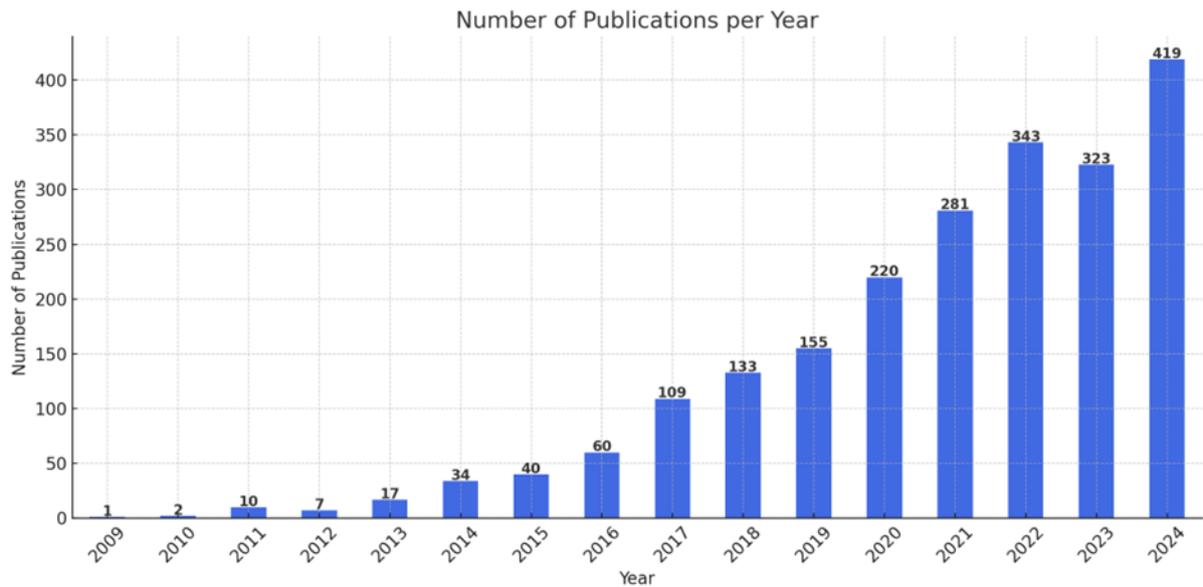


Figure 1. The global trend of environmental microbiome publications. A steady increase since 2017 was observed, reaching a peak in 2024.

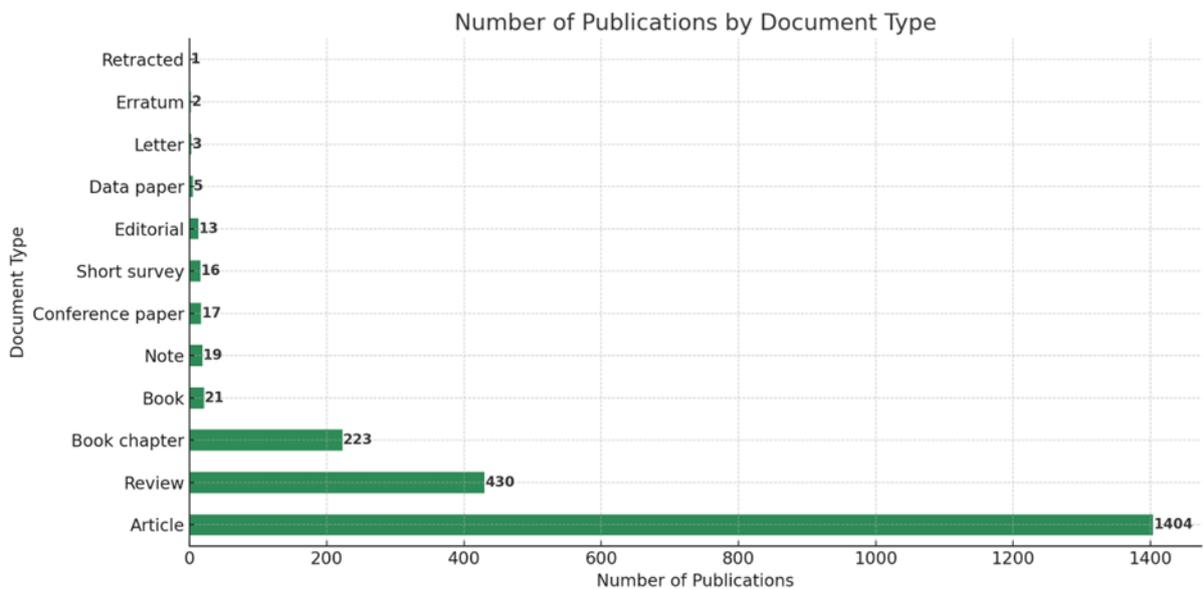


Figure 2. Type of publications in environmental microbiome research.

microorganisms such as *Oceanobacillus profundus*, *Bacillus coagulans*, *Aspergillus flavus* are capable of reducing heavy metals in the aquatic environment [18]. Microorganisms also contribute to biofuel production by fermenting lignocellulosic biomass [19]. They also play a crucial role in biogeochemical cycles, regulating the carbon, nitrogen, phosphorus, and sulfur cycles [20]. For example, *Rhizobium leguminosarum*, *Bradyrhizobium japonicum*, and *Azirrhizobium caulinodans* are well-known nitrogen-fixing organisms that are symbiotic with plant roots [8].

Meanwhile, various members of SAR11 bacteria (Pelagibacterales), Chloroflexi, and Planctomycetes have been reported to play a major role in the nitrogen cycle in both ocean and freshwater ecosystems [21].

The utilization of microorganisms in overcoming various environmental problems is an interesting topic that will always be researched and developed. One promising approach is environmental microbiome engineering, which involves introducing microbial inoculants into natural microbial communities to enhance ecosystem

Table 1. The top cited articles of environmental microbiome research.

No.	Title	Authors	Journal	Year	Citation	Article Type
1	The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes [29]	Hardoim et al.	Microbiology and Molecular Biology Reviews	2015	1887	Review
2	Structure and function of the global ocean microbiome [30]	Sunagawa et al.	Science	2016	1843	Article
3	The ecology of the microbiome: Networks, competition, and stability [31]	Coyte et al.	Science	2015	1711	Article
4	Improved bacterial 16S rRNA gene (V4 and V4-5) and fungal internal transcribed spacer marker gene primers for microbial community surveys [32]	Walters et al.	mSystems	2016	1474	Article
5	Habitat degradation impacts black howler monkey (<i>Alouatta pigra</i>) gastrointestinal microbiomes [33]	Amato et al.	ISME Journal	2013	1042	Article
6	EMPeror: A tool for visualizing high-throughput microbial community data [34]	Vázquez-Baeza et al.	GigaScience	2013	959	Article
7	Where less may be more: How the rare biosphere pulls ecosystems strings [35]	Jousset et al.	ISME Journal	2017	827	Review
8	Biofertilizers function as key player in sustainable agriculture by improving soil fertility, plant tolerance and crop productivity [36]	Bhardwaj et al.	Microbial Cell Factories	2014	809	Review
9	Next-generation beneficial microbes: The case of <i>Akkermansia muciniphila</i> [37]	Cani and deVos	Frontiers in Microbiology	2017	757	Short Survey
10	Disentangling interactions in the microbiome: A network perspective [38]	Layeghifard et al.	Trends in Microbiology	2017	582	Review

Table 2. The institutions with the most publications.

No.	Institution	Country	Documents
1	University of Chinese Academy of Sciences	China	29
2	Research Center for Eco-Environmental Sciences	China	14
3	University of Colorado	United States	8
4	Australian Institute of Marine Science	Australia	7
5	Harbin Institute of Technology	China	5

functions, such as carbon stabilization and nitrogen fixation [22]. Therefore, a method is needed to analyze research trends related to the environmental microbiome over time. One method that can be used is bibliometric analysis, enabling quantitative analysis of publications and productivity of researchers and institutions for topics that are widely researched [23][24]. Bibliometric analysis has been widely used to analyze research trends globally, such as in organoids in regenerative medicine, the prevalence of chikungunya cases in ASEAN and South Asian countries, the prevalence of non-alcoholic fatty liver disease, Indonesian biodiversity identification through DNA barcoding, and the prevalence of monkeypox cases to snake venom research [23]-[28]. In this study, bibliometric analysis was used to determine the trend of environmental microbiome research globally from 2009 to 2024.

2. MATERIALS AND METHODS

2.1. Materials

Environmental microbiome publication trends were collected from the Scopus database between 2009 and 2024. Data collection was conducted on March 10, 2025. The keywords used to filter the documents displayed were "environmental" and "microbes". Here, we define environmental microbiome research as studies focusing on all microorganisms (including bacteria, archaea, fungi, viruses, and other microbes) and their genomes, along with the surrounding environmental conditions that influence their activity and interactions. The definition extends to various environments, including soil, water, air, and even the built environment. To ensure alignment with the scope, we manually screened the initial 3588 publications based on their titles and abstracts,

excluding studies related to clinical research in human and animal systems, resulting in 2154 relevant publications.

2.2. Methods

The bibliometric indicators used were publication year, citations, journal titles, institutions, countries, and keywords. The results were then analyzed to determine the pattern of environmental microbiome research. Bibliometric analysis was conducted with VOSviewer [27]. We included publications of all document types and languages to provide a comprehensive perspective.

3. RESULTS AND DISCUSSIONS

3.1. The Global Trend of Environmental Microbiome Publications

The environmental microbiome has been a topic of growing interest from 2009 to 2024. Our analysis identified a total of 2154 documents, of which 2131 (98.93%) were published in English and 23 (1.07%) in other languages. Starting in 2017, environmental microbiome publications have increased significantly, and the highest number of publications occurred in 2024 with 419 publications (Figure 1).

The most frequent types of publications on environmental microbiome are research articles, reviews, and book chapters with 1404, 430, and 223 documents, respectively (Figure 2).

The top ten cited articles show publications that are widely referenced in environmental microbiome research. The article with the highest number of citations is "The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes" with 1887 citations published by Microbiology and Molecular Biology Reviews. The article titled

"Habitat degradation impacts black howler monkey (*Alouatta pigra*) gastrointestinal microbiomes" and "EMPeror: A tool for visualizing high-throughput microbial community data" published in 2013, are the oldest of the top ten cited articles (Table 1).

The top five institutions with the highest publications are listed in Table 2. The Chinese Academy of Sciences is the institution with the highest number of publications at 29 documents, while the institution with the lowest number of documents within the top five is the State Key Laboratory of Urban Water Resource and Environment, Harbin Institute of Technology, with 5 documents.

The top ten journals with the highest number of publications are listed in Table 3. The *Frontiers in Microbiology* journal has the highest number of documents at 152, and the *Applied and Environmental Microbiology Journal* has the lowest number of documents within the top five at 27 documents.

The top ten countries contributing to environmental microbiome research are listed in Table 4. The country with the highest number of publications is the United States, with 748 documents while collaborating with 43 countries. Within the top ten list, the Netherlands has the lowest number of publications, with 68 documents, and collaborated with 33 countries.

Figure 3 illustrates six distinct collaboration clusters, each represented by a different color (red, green, blue, yellow, purple, and light blue). These colors indicate grouping within the network, where

countries within the same-colored cluster tend to collaborate more frequently with each other. For instance, countries like China, Australia, New Zealand, Hong Kong, Singapore, Pakistan, and Malaysia form a cluster based on their collaboration records and are represented by yellow nodes. Figure 3(b) maps research contributions based on publication year, where colors transition from purple (older publications) to yellow (newer publications), highlighting the shift in research focus over time (Figure 3).

In 2020, countries such as Canada, France, Finland, Norway, and the United States were the primary contributors to environmental microbiome research. However, more recent studies have predominantly been conducted in China, New Zealand, Pakistan, Malaysia, and Egypt. Notably, China has emerged as the second-largest node after the United States, with a brighter yellow color in the visualization, indicating a shift in research dominance toward this country. This trend suggests that China will likely play an increasingly significant role in future research contributions and collaborations. Additionally, Table 4 shows that China has surpassed the United States in the number of published documents from 2020 to 2024, reinforcing the notion of China's growing influence in the field in recent years.

Table 5 shows the top ten authors of environmental microbiome research. Knight, R. is the author with the highest number of publications with 23 documents, while the authors with the lowest number of publications within the top ten are

Table 3. The top ten journals of environmental microbiome research.

No.	Journal	Documents	H-index
1	Frontiers in Microbiology	152	233
2	Science of The Total Environment	103	353
3	Microbiome	57	143
4	mSystems	41	76
5	Environmental Pollution	33	301
6	Microbial Ecology	32	150
7	Journal of Hazardous Materials	31	352
8	Scientific Reports	31	315
9	FEMS Microbiology Ecology	31	183
10	Applied and Environmental Microbiology	27	367

Table 4. The top ten countries in the publication of environmental microbiome research.

No.	Country	Documents		Number of collaborating countries
		(2009–2024)	(2020–2024)	
1	United States	748	463	43
2	China	533	475	41
3	India	308	262	34
4	Germany	172	121	39
5	United Kingdom	157	105	40
6	Canada	136	88	36
7	Australia	126	90	38
8	France	78	47	40
9	Italy	69	55	33
10	Netherlands	68	47	33

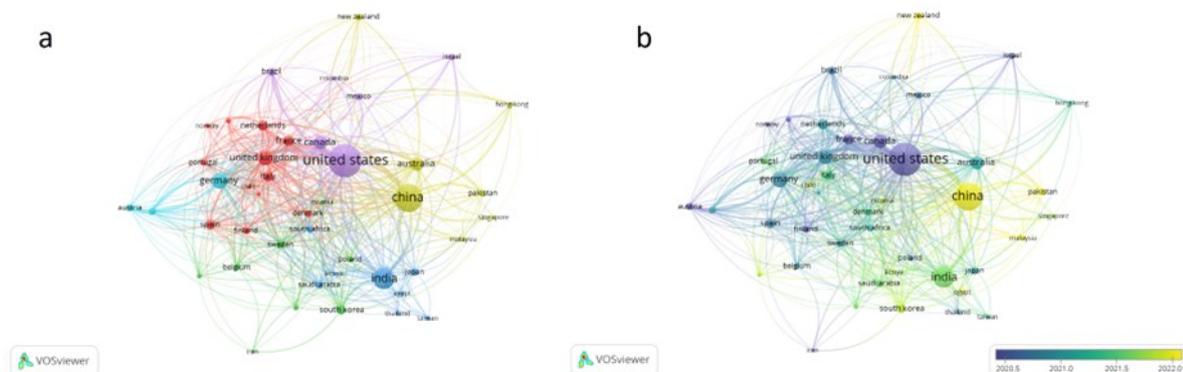


Figure 3. Mapping of countries' collaboration in environmental microbiome research. (a) Network visualization of international research collaborations, where node colors indicate different collaboration clusters based on co-authorship patterns. (b) The overlay visualization represents the temporal distribution of research contributions, where a color gradient from purple to yellow indicates older to more recent average publication years. The length of the connections between countries reflects the strength of their collaboration, with a minimum threshold of 10 documents per country.

Jansson, J. K., Dinsdale, E. A., and Kohl, K. D. with 7 documents. Figure 4 shows the cluster of authors with a threshold of 5 documents per author. Five clusters of authors are observed, different colors of red, green, blue, yellow, and purple indicate the different clusters (Figure 4(a)). Figure 4 (b) shows the mapping of the year where the article published by the top ten authors. There is a color gradation from purple (year 2016) to yellow (year 2022), indicating old to new publications from the top ten authors

3.2. Popular Topics in Environmental Microbiome Research

The popular topics in environmental microbiome

research are presented in Figure 5. The keywords representing popular topics in environmental microbiome research.

Figure 5(a) shows keyword clusters with a threshold of 200 occurrences. The clusters formed are marked with different colors of red, green, blue, and yellow. (b) The maps of year when the article containing the keywords are published. There is a purple-to-yellow color gradation that indicates old to new publications. (c) The most used keywords, where the lighter the color, the more frequent the topic is researched. Some of the prominent topics related to environmental microbiome are microbiome, microbial community, microflora microbiota, microbiology, bacteria, and bacterium.

3.3. Current Status

The study of the environmental microbiome has experienced significant growth over the past decade, particularly from 2017 onward. This surge can be attributed to several key factors, including advancements in sequencing technologies, the increasing application of multi-omics approaches, and a heightened interest and awareness of the role of microbiomes in ecosystem functions. Next-generation sequencing (NGS) and metagenomic techniques have revolutionized microbiome research, enabling high-throughput analysis of microbial communities with greater precision and depth at lower cost [39]. The integration of metatranscriptomics, metabolomics, and metaproteomics has further expanded our understanding of microbial interactions, functional capabilities, and responses to environmental changes [40]. The growing concern over climate change, pollution, and ecosystem degradation has also driven interest in studying environmental microbiomes [41]. Furthermore, international collaborations and large-scale microbiome initiatives, such as the Earth Microbiome Project and the Human Microbiome Project, have provided standardized methodologies and global datasets, fostering a more systematic exploration of environmental microbiomes [42].

The United States led environmental microbiome research with 748 publications and 43 international collaborations, followed by China (533, 41) and

India (308, 34). Germany, the UK, Canada, and Australia also made significant contributions, highlighting strong global collaboration in this field (Table 4). The majority of publications were research articles (1404), followed by review papers (430) and book chapters (223), indicating a strong emphasis on original research and synthesis of existing knowledge in environmental microbiome studies (Figure 2).

The most cited works in environmental microbiome research, such as *"The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes"* (Hardoim et al. (2015) with 1887 citations) [29] and *"Structure and function of the global ocean microbiome"* (Sunagawa et al. (2016) with 1843 citations) [30], underscore the pivotal role of microbial communities in shaping ecosystem functions and stability. These studies highlight how diverse microbial assemblages drive nutrient cycling, host-microbe interactions, and biogeochemical processes across terrestrial and aquatic environments.

Recent research has expanded on these foundations, leveraging network-based approaches to unravel the complexity of microbial interactions, moving beyond reductionist methods to holistic frameworks that capture polymicrobial dynamics. As highlighted by Layeghifard et al. (2017) with 582 citations, microbial communities are not merely collections of independent species,

Table 5. The top ten authors of environmental microbiome research.

No.	Author	Documents	Scopus ID ^b	H-index ^c
1	Knight, R.	23	57202526255	221
2	Gilbert, J. A.	14	7401452139	103
3	Zhu, Y. G.	13	7406073704	143
4	Wu, Wei-Min	10	57202196184	29
5	Berg, G.	9	7201431307	89
6	Voolstra, C. R.	8	25224158700	72
7	Babalola, O. O.	8	36166570300	61
8	Jansson, J. K.	7	7102590766	83
9	Dinsdale, E. A.	7	6602355182	40
10	Kohl, K. D.	7	26635408000	38

^bScopus ID or Scopus author identifier is a unique number that matches authorship to groups of documents. ^cH-index is an author-level metric that measures both the productivity and citation impact of the publications.

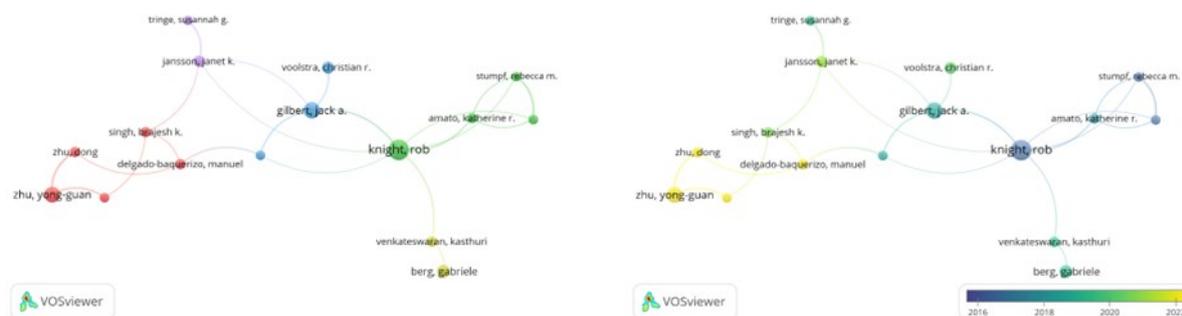


Figure 4. Mapping of authors' collaboration in environmental microbiome research. (a) Network visualization of research collaboration between authors, where node colors indicate different collaboration clusters based on co-authorship patterns. (b) The overlay visualization represents the temporal distribution of the collaboration, where a color gradient from blue to yellow indicates older to more recent collaboration. The length of the connections between authors reflects the strength of their collaboration, with a minimum of 5 documents per author.

but interconnected networks shaped by ecological and evolutionary processes. For instance, co-occurrence networks constructed from soil, aquatic, and rhizosphere microbiomes have revealed keystone species and functional modules critical for ecosystem processes like carbon cycling and nitrogen fixation [38]. Additionally, innovations in DNA extraction and high-throughput sequencing (e.g., Walters et al. (2016) with 1474 citations) have enabled deeper exploration of microbial responses to pollution, habitat degradation, and climate change [32].

The prominent research keywords include microbiome, microbial community, microflora, microbiota, microbiology, bacteria, and bacterium (Figure 5(c)). The frequent occurrence of terms such as microbiome, microbial community, microflora, and microbiota aligns with the widespread use of metagenomic methods to analyze microbial composition in specific environments. Advances in NGS technology have made such analyses more accessible and cost-effective, further driving their use in environmental microbiome research. Additionally, the higher prevalence of bacterial-related keywords compared to other microorganisms suggests a strong research focus on bacteria, this can be attributed to several factors, including methodological and ecological factors. Many laboratory and molecular protocols are optimized for bacterial works, compared to other microorganisms (e.g., fungi, archaea, viruses). For

example, bacterial 16S rRNA gene sequencing is well-established, cost-effective, and supported by robust reference databases, while fungal (ITS) or viral sequencing is less standardized [32][43]. Ecologically, bacteria dominate microbial biomass in most environments (soil, water, rhizosphere) and drive key processes like nutrient cycling (e.g., nitrogen fixation, decomposition) [30][44]. Their metabolic versatility allows them to thrive in diverse conditions, making them focal points for bioremediation and climate studies [45]. Additionally, bacterial communities are more frequently linked to host health (e.g., plant growth promotion, human and animal gut symbiosis) than other microbes in both environmental and clinical contexts [29][45][46].

3.4. Future Direction

The global center of environmental microbiome research is poised to shift from the US to China in the coming decade, driven by China's rapidly expanding scientific output and substantial investments in research funding. By 2017, China ranked second globally in research output, contributing 19% of all Scopus-indexed papers, a significant rise from 10% in 2005. This growth is driven by substantial government funding, with R&D investment reaching 2.12% of GDP, (2.06% of GDP) but still trailing behind the USA (2.74%) [47][48]. Additionally, China's increasing international co-publications, particularly with the

US and EU, have enhanced the global impact of its research. China's share of international co-publications rose from 14% to 22%, with collaborations with leading scientific nations. The country has also benefited from talent return programs, attracting scientists trained abroad to strengthen domestic research networks. With a strong focus on key scientific fields including microbiome applications for: soil remediation, circular agriculture, and carbon neutrality [47]-[49]. Chinese researchers are also highly prolific in paper writing, with many of them affiliated with institutions in the United States and European countries (Tables 2 and 4). Collaboration among researchers from different Chinese research institutions is extensive (Table 2), with scholars like Zhu and Wei-Min being the most prolific authors (Table 5). Additionally, researchers from other countries, such as Singh and Delgado, also tend to collaborate predominantly with Chinese researchers (Figure 4).

Future research will increasingly focus on microbial contributions to environmental and climate feedback mechanisms, driving advancements in analytical technologies. Emerging innovations include (1) third-generation sequencing platforms, such as Oxford Nanopore's adaptive sampling, which enable the enrichment of low-abundance species in metagenomic samples [50]; (2) high-throughput single-cell sequencing and phenotyping integration, allowing precise analysis of individual microbial cells within complex communities [51]; and (3) integrated multi-omics analysis, providing a comprehensive understanding

of microbial functions, interactions, and ecosystem roles [52]. Additionally, molecular methods will continue to evolve with techniques such as microfluidic digital PCR for absolute quantification of keystone taxa [53] and CRISPR-based nucleic acid enrichment, enhancing the detection of low-biomass samples [54]. These advancements will be further accelerated by AI-driven bioinformatics pipelines, integrating multi-omics data with remote sensing and environmental models for deeper ecological insights [55].

The field of microbiome research is expected to grow significantly following discoveries in various systems, including soil and plant microbiomes. Future studies will likely extend beyond characterization to explore microbial communication, molecular physiology, and its environmental impacts. Currently, microbial studies are largely focused on bacteria (Figure 5(c)), but future research is expected to expand to fungi, protists, and viruses, providing a more comprehensive understanding of microbial communities. This is essential, as interkingdom interactions can enhance our understanding of microbial community structure and assembly, emphasizing the complexity of microbial interactions across species and kingdoms [56]. Moreover, the increasing demand for new antibacterial and antifungal agents, driven by antibiotic resistance, will further accelerate the search for bioactive compounds within microbial ecosystems [57]. This growing interest is likely to stimulate greater collaboration among researchers and institutions, fostering advancements in

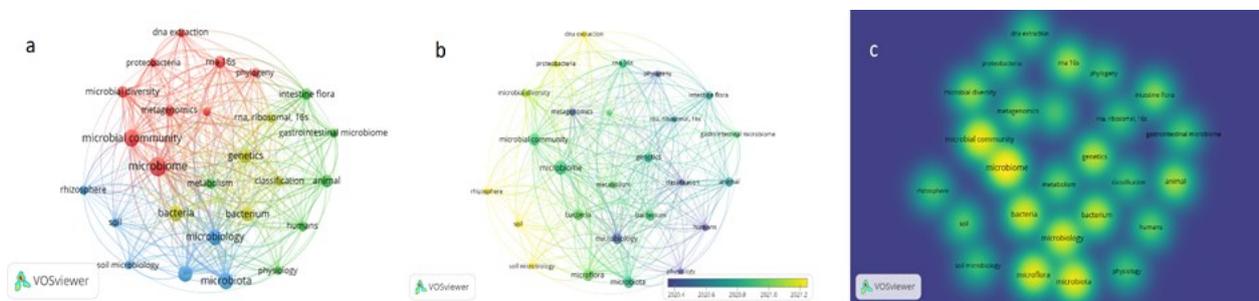


Figure 5. Mapping of keywords in environmental microbiome research. (a) Network visualization of co-occurrence between keywords, where node colors indicate different keyword clusters based on co-occurrence patterns. (b) The overlay visualization represents the temporal distribution of the keywords co-occurrence, where a color gradient from blue to yellow indicates older to more recent co-occurrence in publications. (c) Density cluster visualization.

environmental microbiome research. Collaborations across countries and disciplines will be essential in advancing our understanding of environmental microbiomes and addressing global ecological challenges. To make progress in the understanding of environmental microbiomes and solve global ecological problems, it is crucial to establish multicounty collaborations. This emergent landscape calls for more integrative research endeavors, integrating microbiome insights in other environmental studies towards achieving ecosystem resilience and sustainability.

4. CONCLUSIONS

Bibliometric analysis shows an increasing trend of environmental microbiome publications from 2009 to 2024. This shows that the environmental microbiome is an interesting topic that continues to be researched by various renowned institutions. In addition, this study also provides an overview of the potential development of the utilization of environmental microbiomes in the future.

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Conflicts of Interest

The authors declare no conflict of interest.

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REFERENCES

- [1] G. Berg, D. Rybakova, D. Fischer, T. Cernava, M.-C. C. Vergès, T. Charles, X. Chen, L. Cocolin, K. Eversole, G. H. Corral, M. Kazou, L. Kinkel, L. Lange, N. Lima, A. Loy, J. A. Macklin, E. Maguin, T. Mauchline, R. McClure, B. Mitter, M. Ryan, I. Sarand, H. Smidt, B. Schelkle, H. Roume, G. S. Kiran, J. Selvin, R. S. C. d. Souza, L. v. Overbeek, B. K. Singh, M. Wagner, A. Walsh, A. Sessitsch, and M. Schlöter. (2020). "Microbiome definition re-visited: old concepts and new challenges". *Microbiome*. **8** (1): 103. [10.1186/s40168-020-00875-0](https://doi.org/10.1186/s40168-020-00875-0).
- [2] R. Simarmata, T. Widowati, L. Nurjanah, Nuriyanah, and S. J. R. Lekatompessy. (2021). "The role of microbes in organic material decomposition and formation of compost bacterial communities". *IOP Conference Series: Earth and Environmental Science*. **762** (1). [10.1088/1755-1315/762/1/012044](https://doi.org/10.1088/1755-1315/762/1/012044).
- [3] Y. A. Purwestri, T. R. Nuringtyas, A. T. Wibowo, H. Nugrahapraja, Y. C. F. Salsinha, A. Sebastian, S. Nurbaiti, N. Kumalasari, R. R. Annisa, S. P. Manik Putri, S. Az-Zahra, and L. Al Umami. (2024). "Application of osmoprotectant enhance tolerance to drought stress in rice and trigger changes in root microbial composition". *Journal of Plant Biochemistry and Biotechnology*. [10.1007/s13562-024-00933-w](https://doi.org/10.1007/s13562-024-00933-w).
- [4] N. H. Alami. (2014). "The Influence of Microbial Consortium in Bioremediation Process using Bioreactor". *IPTEK Journal of Science*. **1** (1). [10.12962/j23378530.v1i1.a436](https://doi.org/10.12962/j23378530.v1i1.a436).
- [5] S. Meng, T. Peng, X. Liu, H. Wang, T. Huang, J. D. Gu, and Z. Hu. (2022). "Ecological Role of Bacteria Involved in the Biogeochemical Cycles of Mangroves Based on Functional Genes Detected through GeoChip 5.0". *mSphere*. **7** (1): e0093621. [10.1128/msphere.00936-21](https://doi.org/10.1128/msphere.00936-21).
- [6] X. Zhu, C. Lei, J. Qi, G. Zhen, X. Lu, S. Xu, J. Zhang, H. Liu, X. Zhang, and Z. Wu. (2022). "The role of microbiome in carbon sequestration and environment security during wastewater treatment". *Science of the Total Environment*. **837** : 155793. [10.1016/j.scitotenv.2022.155793](https://doi.org/10.1016/j.scitotenv.2022.155793).
- [7] M. F. Adegboye, O. B. Ojuederie, P. M. Talia, and O. O. Babalola. (2021). "Bioprospecting of microbial strains for biofuel production: metabolic engineering, applications, and challenges". *Biotechnology for Biofuels and Bioproducts*. **14** (1): 5. [10.1186/s13068-020-01853-2](https://doi.org/10.1186/s13068-020-01853-2).
- [8] S. Usman, Y. Muhammad, and A. Chiroman. (2016). "Roles of soil biota and biodiversity in soil environment – A concise communication". *Eurasian Journal of Soil Science (Ejss)*. **5** (4). [10.18393/ejss.2016.4.255-265](https://doi.org/10.18393/ejss.2016.4.255-265).
- [9] J. M. Talbot, T. D. Bruns, D. P. Smith, S. Branco, S. I. Glassman, S. Erlandson, R. Vilgalys, and K. G. Peay. (2013). "Independent roles of ectomycorrhizal and saprotrophic communities in soil organic matter decomposition". *Soil Biology and Biochemistry*. **57** : 282-291. [10.1016/j.soilbio.2012.10.004](https://doi.org/10.1016/j.soilbio.2012.10.004).
- [10] R. Y. Khusna, A. Geraldi, A. T. Wibowo, U. Fatimah, C. Clement, Y. S. W. Manuhara, H. Santoso, F. N. Fauzia, Y. K. Putro, R. N. Arsad, R. Setiawan, A. Luqman, and S. Hariyanto. (2024). "Isolation and identification of plant growth-promoting rhizobacteria from *Spinifex littoreus* in Parangkusumo Coastal Sand Dunes, Indonesia". *Brazilian Journal of Biology*. **84** : e284907. [10.1590/1519-6984.284907](https://doi.org/10.1590/1519-6984.284907).
- [11] M. T. Vu, A. Geraldi, H. D. K. Do, A. Luqman, H. D. Nguyen, F. N. Fauzia, F. I.

- Amalludin, A. Y. Sadila, N. H. Wijaya, H. Santoso, Y. S. W. Manuhara, L. M. Bui, S. Hariyanto, and A. T. Wibowo. (2022). "Soil Mineral Composition and Salinity Are the Main Factors Regulating the Bacterial Community Associated with the Roots of Coastal Sand Dune Halophytes". *Biology (Basel)*. **11** (5). [10.3390/biology11050695](https://doi.org/10.3390/biology11050695).
- [12] A. Geraldi, C. Clement, M. D. Pertiwi, Y. Lestari, D. H. Parinnata, R. N. Arsad, R. A. Sadikin, A. Luqman, H. Santoso, A. N. Kristanti, Y. S. W. Manuhara, and A. T. Wibowo. (2024). "Isolation and characterization of plant growth-promoting bacteria from medicinal plants Java cardamom (*Amomum compactum*) and bitter ginger (*Zingiber zerumbet*)". *Biodiversitas Journal of Biological Diversity*. **25** (6). [10.13057/biodiv/d250626](https://doi.org/10.13057/biodiv/d250626).
- [13] A. Jurys and D. Feiziene. (2021). "The Effect of Specific Soil Microorganisms on Soil Quality Parameters and Organic Matter Content for Cereal Production". *Plants (Basel)*. **10** (10). [10.3390/plants10102000](https://doi.org/10.3390/plants10102000).
- [14] S. R. Shah Walter, U. Jaekel, H. Osterholz, A. T. Fisher, J. A. Huber, A. Pearson, T. Dittmar, and P. R. Girguis. (2018). "Microbial decomposition of marine dissolved organic matter in cool oceanic crust". *Nature Geoscience*. **11** (5): 334-339. [10.1038/s41561-018-0109-5](https://doi.org/10.1038/s41561-018-0109-5).
- [15] P. Solanki, S. S. Meena, M. Narayan, H. Khatoun, and L. Tewari. (2017). "Denitrification Process as an Indicator of Soil Health". *International Journal of Current Microbiology and Applied Sciences*. **6** (5): 2645-2657. [10.20546/ijemas.2017.605.296](https://doi.org/10.20546/ijemas.2017.605.296).
- [16] H. P. Grossart, S. Van den Wyngaert, M. Kagami, C. Wurzbacher, M. Cunliffe, and K. Rojas-Jimenez. (2019). "Fungi in aquatic ecosystems". *Nature Reviews Microbiology*. **17** (6): 339-354. [10.1038/s41579-019-0175-8](https://doi.org/10.1038/s41579-019-0175-8).
- [17] A. N. Alabssawy and A. H. Hashem. (2024). "Bioremediation of hazardous heavy metals by marine microorganisms: a recent review". *Archives of Microbiology*. **206** (3): 103. [10.1007/s00203-023-03793-5](https://doi.org/10.1007/s00203-023-03793-5).
- [18] M. S. Ayilara and O. O. Babalola. (2023). "Bioremediation of environmental wastes: the role of microorganisms". *Frontiers in Agronomy*. **5**. [10.3389/fagro.2023.1183691](https://doi.org/10.3389/fagro.2023.1183691).
- [19] V. V. Atuchin, L. K. Asyakina, Y. R. Serazetdinova, A. S. Frolova, N. S. Velichkovich, and A. Y. Prosekov. (2023). "Microorganisms for Bioremediation of Soils Contaminated with Heavy Metals". *Microorganisms*. **11** (4). [10.3390/microorganisms11040864](https://doi.org/10.3390/microorganisms11040864).
- [20] A. D. Chintagunta, G. Zuccaro, M. Kumar, S. P. J. Kumar, V. K. Garlapati, P. D. Postemsky, N. S. S. Kumar, A. K. Chandel, and J. Simal-Gandara. (2021). "Biodiesel Production From Lignocellulosic Biomass Using Oleaginous Microbes: Prospects for Integrated Biofuel Production". *Frontiers in Microbiology*. **12** : 658284. [10.3389/fmicb.2021.658284](https://doi.org/10.3389/fmicb.2021.658284).
- [21] S. C. Wagner.(2011)." Biological Nitrogen Fixation". Nature Education Knowledge.
- [22] M. R. Silverstein, D. Segre, and J. M. Bhatnagar. (2023). "Environmental microbiome engineering for the mitigation of climate change". *Global Change Biology*. **29** (8): 2050-2066. [10.1111/gcb.16609](https://doi.org/10.1111/gcb.16609).
- [23] J. Setiawan, D. M. Rizal, F. Sofyantoro, D. S. Priyono, N. I. Septriani, W. U. Mafiroh, T. Kotani, T. Matozaki, and W. A. Putri. (2024). "Bibliometric analysis of organoids in regenerative medicine-related research worldwide over two decades (2002-2022)". *Regenerative Medicine*. **19** (3): 119-133. [10.2217/rme-2023-0176](https://doi.org/10.2217/rme-2023-0176).
- [24] F. Sofyantoro, A. Frediansyah, D. S. Priyono, W. A. Putri, N. I. Septriani, N. Wijayanti, W. A. Ramadaningrum, S. A. Turkistani, M. Garout, M. Aljeldah, B. R. Al Shammari, A. S. S. Alwashmi, A. H. Alfaraj, A. Alawfi, A. Alshengeti, M. H. Aljohani, S. Aldossary, and A. A. Rabaan. (2023). "Growth in chikungunya virus-related research in ASEAN and South Asian countries from 1967 to 2022 following disease emergence: a bibliometric and graphical analysis". *Global Health*. **19** (1): 9. [10.1186/s12992-023-00906-z](https://doi.org/10.1186/s12992-023-00906-z).

- [25] W. A. Putri, J. Setiawan, F. Sofyantoro, D. S. Priyono, N. I. Septriani, W. U. Mafiroh, Y. Yano, and W. Wasityastuti. (2023). "Global research trends in non-alcoholic fatty liver disease". *Bratislavske Lekarske Listy*. **124** (8): 590-598. [10.4149/BLL_2023_092](https://doi.org/10.4149/BLL_2023_092).
- [26] D. S. Priyono, F. Sofyantoro, W. A. Putri, N. I. Septriani, A. Rabbani, and T. Arisuryanti. (2023). "A Bibliometric Analysis of Indonesia Biodiversity Identification through DNA Barcoding Research from 2004-2021". *Natural and Life Sciences Communications*. **22** (1). [10.12982/nlsc.2023.006](https://doi.org/10.12982/nlsc.2023.006).
- [27] F. Sofyantoro, H. I. Kusuma, S. Vento, M. Rademaker, and A. Frediansyah. (2022). "Global research profile on monkeypox-related literature (1962-2022): A bibliometric analysis". *Narra J*. **2** (3): e96. [10.52225/narra.v2i3.96](https://doi.org/10.52225/narra.v2i3.96).
- [28] F. Sofyantoro, D. S. Yudha, K. Lischer, T. R. Nuringtyas, W. A. Putri, W. A. Kusuma, Y. A. Purwestri, and R. T. Swasono. (2022). "Bibliometric Analysis of Literature in Snake Venom-Related Research Worldwide (1933-2022)". *Animals (Basel)*. **12** (16). [10.3390/ani12162058](https://doi.org/10.3390/ani12162058).
- [29] P. R. Hardoim, L. S. van Overbeek, G. Berg, A. M. Pirttila, S. Compant, A. Campisano, M. Doring, and A. Sessitsch. (2015). "The Hidden World within Plants: Ecological and Evolutionary Considerations for Defining Functioning of Microbial Endophytes". *Microbiology and Molecular Biology Reviews*. **79** (3): 293-320. [10.1128/MMBR.00050-14](https://doi.org/10.1128/MMBR.00050-14).
- [30] S. Sunagawa, L. P. Coelho, S. Chaffron, J. R. Kultima, K. Labadie, G. Salazar, B. Djahanschiri, G. Zeller, D. R. Mende, A. Alberti, F. M. Cornejo-Castillo, P. I. Costea, C. Cruaud, F. d'Ovidio, S. Engelen, I. Ferrera, J. M. Gasol, L. Guidi, F. Hildebrand, F. Kokoszka, C. Lepoivre, G. Lima-Mendez, J. Poulain, B. T. Poulos, M. Royo-Llonch, H. Sarmiento, S. Vieira-Silva, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, c. Tara Oceans, C. Bowler, C. de Vargas, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, O. Jaillon, F. Not, H. Ogata, S. Pesant, S. Speich, L. Stemann, M. B. Sullivan, J. Weissenbach, P. Wincker, E. Karsenti, J. Raes, S. G. Acinas, and P. Bork. (2015). "Ocean plankton. Structure and function of the global ocean microbiome". *Science*. **348** (6237): 1261359. [10.1126/science.1261359](https://doi.org/10.1126/science.1261359).
- [31] K. Z. Coyte, J. Schluter, and K. R. Foster. (2015). "The ecology of the microbiome: Networks, competition, and stability". *Science*. **350** (6261): 663-6. [10.1126/science.aad2602](https://doi.org/10.1126/science.aad2602).
- [32] W. Walters, E. R. Hyde, D. Berg-Lyons, G. Ackermann, G. Humphrey, A. Parada, J. A. Gilbert, J. K. Jansson, J. G. Caporaso, J. A. Fuhrman, A. Apprill, and R. Knight. (2016). "Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys". *mSystems*. **1** (1). [10.1128/mSystems.00009-15](https://doi.org/10.1128/mSystems.00009-15).
- [33] K. R. Amato, C. J. Yeoman, A. Kent, N. Righini, F. Carbonero, A. Estrada, H. R. Gaskins, R. M. Stumpf, S. Yildirim, M. Torralba, M. Gillis, B. A. Wilson, K. E. Nelson, B. A. White, and S. R. Leigh. (2013). "Habitat degradation impacts black howler monkey (*Alouatta pigra*) gastrointestinal microbiomes". *ISME Journal*. **7** (7): 1344-53. [10.1038/ismej.2013.16](https://doi.org/10.1038/ismej.2013.16).
- [34] Y. Vazquez-Baeza, M. Pirrung, A. Gonzalez, and R. Knight. (2013). "EMPeror: a tool for visualizing high-throughput microbial community data". *Gigascience*. **2** (1): 16. [10.1186/2047-217X-2-16](https://doi.org/10.1186/2047-217X-2-16).
- [35] A. Jousset, C. Bienhold, A. Chatzinotas, L. Gallien, A. Gobet, V. Kurm, K. Kusel, M. C. Rillig, D. W. Rivett, J. F. Salles, M. G. van der Heijden, N. H. Youssef, X. Zhang, Z. Wei, and W. H. Hol. (2017). "Where less may be more: how the rare biosphere pulls ecosystems strings". *ISME Journal*. **11** (4): 853-862. [10.1038/ismej.2016.174](https://doi.org/10.1038/ismej.2016.174).
- [36] D. Bhardwaj, M. W. Ansari, R. K. Sahoo, and N. Tuteja. (2014). "Biofertilizers function as key player in sustainable agriculture by improving soil fertility, plant tolerance and crop productivity". *Microbial Cell Factories*. **13** : 66. [10.1186/1475-2859-13-66](https://doi.org/10.1186/1475-2859-13-66).

- [37] P. D. Cani and W. M. de Vos. (2017). "Next-Generation Beneficial Microbes: The Case of *Akkermansia muciniphila*". *Frontiers in Microbiology*. **8** : 1765. [10.3389/fmicb.2017.01765](https://doi.org/10.3389/fmicb.2017.01765).
- [38] M. Layeghifard, D. M. Hwang, and D. S. Guttman. (2017). "Disentangling Interactions in the Microbiome: A Network Perspective". *Trends in Microbiology*. **25** (3): 217-228. [10.1016/j.tim.2016.11.008](https://doi.org/10.1016/j.tim.2016.11.008).
- [39] H. Satam, K. Joshi, U. Mangrolia, S. Waghoo, G. Zaidi, S. Rawool, R. P. Thakare, S. Banday, A. K. Mishra, G. Das, and S. K. Malonia. (2023). "Next-Generation Sequencing Technology: Current Trends and Advancements". *Biology (Basel)*. **12** (7). [10.3390/biology12070997](https://doi.org/10.3390/biology12070997).
- [40] J. K. Jansson and K. S. Hofmockel. (2018). "The soil microbiome-from metagenomics to metaphenomics". *Current Opinion in Microbiology*. **43** : 162-168. [10.1016/j.mib.2018.01.013](https://doi.org/10.1016/j.mib.2018.01.013).
- [41] R. Cavicchioli, W. J. Ripple, K. N. Timmis, F. Azam, L. R. Bakken, M. Baylis, M. J. Behrenfeld, A. Boetius, P. W. Boyd, A. T. Classen, T. W. Crowther, R. Danovaro, C. M. Foreman, J. Huisman, D. A. Hutchins, J. K. Jansson, D. M. Karl, B. Koskella, D. B. Mark Welch, J. B. H. Martiny, M. A. Moran, V. J. Orphan, D. S. Reay, J. V. Remais, V. I. Rich, B. K. Singh, L. Y. Stein, F. J. Stewart, M. B. Sullivan, M. J. H. van Oppen, S. C. Weaver, E. A. Webb, and N. S. Webster. (2019). "Scientists' warning to humanity: microorganisms and climate change". *Nature Reviews Microbiology*. **17** (9): 569-586. [10.1038/s41579-019-0222-5](https://doi.org/10.1038/s41579-019-0222-5).
- [42] L. R. Thompson, J. G. Sanders, D. McDonald, A. Amir, J. Ladau, K. J. Locey, R. J. Prill, A. Tripathi, S. M. Gibbons, G. Ackermann, J. A. Navas-Molina, S. Janssen, E. Kopylova, Y. Vazquez-Baeza, A. Gonzalez, J. T. Morton, S. Mirarab, Z. Zech Xu, L. Jiang, M. F. Haroon, J. Kanbar, Q. Zhu, S. Jin Song, T. Kosciolk, N. A. Bokulich, J. Lefler, C. J. Brislawn, G. Humphrey, S. M. Owens, J. Hampton-Marcell, D. Berg-Lyons, V. McKenzie, N. Fierer, J. A. Fuhrman, A. Clauset, R. L. Stevens, A. Shade, K. S. Pollard, K. D. Goodwin, J. K. Jansson, J. A. Gilbert, R. Knight, and C. Earth Microbiome Project. (2017). "A communal catalogue reveals Earth's multiscale microbial diversity". *Nature*. **551** (7681): 457-463. [10.1038/nature24621](https://doi.org/10.1038/nature24621).
- [43] L. Tedersoo, A. Tooming-Klunderud, and S. Anslan. (2018). "PacBio metabarcoding of Fungi and other eukaryotes: errors, biases and perspectives". *New Phytologist*. **217** (3): 1370-1385. [10.1111/nph.14776](https://doi.org/10.1111/nph.14776).
- [44] P. G. Falkowski, T. Fenchel, and E. F. Delong. (2008). "The microbial engines that drive Earth's biogeochemical cycles". *Science*. **320** (5879): 1034-9. [10.1126/science.1153213](https://doi.org/10.1126/science.1153213).
- [45] S. V. Lynch and O. Pedersen. (2016). "The Human Intestinal Microbiome in Health and Disease". *New England Journal of Medicine*. **375** (24): 2369-2379. [10.1056/NEJMra1600266](https://doi.org/10.1056/NEJMra1600266).
- [46] T. L. Karasov, M. Neumann, L. Leventhal, E. Symeonidi, G. Shirsekar, A. Hawks, G. Monroe, T. Pathodopsis, M. Exposito-Alonso, J. Bergelson, D. Weigel, and R. Schwab. (2024). "Continental-scale associations of *Arabidopsis thaliana* phyllosphere members with host genotype and drought". *Nature Microbiology*. **9** (10): 2748-2758. [10.1038/s41564-024-01773-z](https://doi.org/10.1038/s41564-024-01773-z).
- [47] K. Jonkers, C. S. Wagner, J. Baas, and C. Cao. (2020). "Returning scientists and the emergence of China's science system". *Science and Public Policy*. **47** (2): 172-183. [10.1093/scipol/scz056](https://doi.org/10.1093/scipol/scz056).
- [48] R. P. Appelbaum, C. Cao, X. Han, R. Parker, and D. Simon. (2018). "Challenging the global science and technology system". Polity Press, Cambridge.
- [49] K. Chen, K. Flaherty, and Y. Zhang. (2012). "China: recent developments in public agricultural research".
- [50] S. Martin, D. Heavens, Y. Lan, S. Horsfield, M. D. Clark, and R. M. Leggett. (2022). "Nanopore adaptive sampling: a tool for enrichment of low abundance species in metagenomic samples". *Genome Biology*. **23** (1): 11. [10.1186/s13059-021-02582-x](https://doi.org/10.1186/s13059-021-02582-x).

- [51] Y. Zhang, B. Xue, Y. Mao, X. Chen, W. Yan, Y. Wang, Y. Wang, L. Liu, J. Yu, X. Zhang, S. Chao, E. Topp, W. Zheng, and T. Zhang. (2025). "High-throughput single-cell sequencing of activated sludge microbiome". *Environmental Science and Ecotechnology*. **23** : 100493. [10.1016/j.ese.2024.100493](https://doi.org/10.1016/j.ese.2024.100493).
- [52] M. Arikan and T. Muth. (2023). "Integrated multi-omics analyses of microbial communities: a review of the current state and future directions". *Molecular Omics*. **19** (8): 607-623. [10.1039/d3mo00089c](https://doi.org/10.1039/d3mo00089c).
- [53] X. Wang, S. Howe, F. Deng, and J. Zhao. (2021). "Current Applications of Absolute Bacterial Quantification in Microbiome Studies and Decision-Making Regarding Different Biological Questions". *Microorganisms*. **9** (9). [10.3390/microorganisms9091797](https://doi.org/10.3390/microorganisms9091797).
- [54] J. Zhou, Z. Li, J. Seun Olajide, and G. Wang. (2024). "CRISPR/Cas-based nucleic acid detection strategies: Trends and challenges". *Heliyon*. **10** (4): e26179. [10.1016/j.heliyon.2024.e26179](https://doi.org/10.1016/j.heliyon.2024.e26179).
- [55] B. Ambaru, R. Manvitha, and R. Madas. (2025). "Synergistic integration of remote sensing and soil metagenomics data: advancing precision agriculture through interdisciplinary approaches". *Frontiers in Sustainable Food Systems*. **8**. [10.3389/fsufs.2024.1499973](https://doi.org/10.3389/fsufs.2024.1499973).
- [56] W. Ren, R. Penttila, R. Kasanen, and F. O. Asiegbu. (2023). "Interkingdom and intrakingdom interactions in the microbiome of *Heterobasidion* fruiting body and associated decayed woody tissues". *Applied and Environmental Microbiology*. **89** (12): e0140623. [10.1128/aem.01406-23](https://doi.org/10.1128/aem.01406-23).
- [57] R. Urban-Chmiel, A. Marek, D. Stepień-Pysniak, K. Wiczorek, M. Dec, A. Nowaczek, and J. Osek. (2022). "Antibiotic Resistance in Bacteria-A Review". *Antibiotics (Basel)*. **11** (8). [10.3390/antibiotics11081079](https://doi.org/10.3390/antibiotics11081079).