

Trends and Hotspots in Plant Microflora Research: A Comprehensive Scientific Evaluation**Diksha Negi¹; & Neeraj Padariya²**DOI: <https://doi.org/10.5281/zenodo.18648509>**Review: 04/02/2026****Acceptance: 04/02/2026****Publication: 15/02/2026**

Plant microflora serves as a crucial biological link through which plants engage with their external surroundings. Microbial communities found in the rhizosphere, phyllosphere, and endosphere regulate vital processes like nutrient uptake, pathogen control, stress resilience, and overall plant health. This study performs a focused bibliometric analysis to assess the worldwide research environment on plant microflora utilizing data obtained from the Web of Science and PubMed databases. Following a systematic review, 56 publications were examined using VOS viewer to map co-occurring keywords, determine prominent conceptual clusters, and illustrate research hotspots. The findings indicate that keywords pertaining to the rhizosphere, endophytes, phyllosphere, and biological control constitute the foundation of current research efforts, with the rhizosphere showing the greatest total link strength. Key focus areas are plant-associated microbiomes, root colonization methods, and utilizing beneficial microorganisms like *Bacillus subtilis* and *Pseudomonas* species for crop improvement and biocontrol. The overlay and density maps additionally suggest a transition from descriptive taxonomic research to functional, molecular, and application-focused studies propelled by progress in metagenomics and microbial ecology. This bibliometric evaluation underscores the evolution of plant microflora research into a cohesive area that links microbial diversity with sustainable agricultural practices and ecological stability.

Keywords: Plant microflora, Rhizosphere dynamics, Endophytic microbial communities, Phyllo sphere bacteria, Microbial biocontrol agents, Plant-associated microbiome, Root colonization

Introduction:

In the last ten years, studies have demonstrated that plants contain intricate microbial communities, with each organ harboring a distinct group of microorganisms. These microorganisms, collectively referred to as the plant microbiota or microbiome, reside in the rhizosphere, phyllosphere, and endosphere, where they are vital for plant growth, health, and resistance to stress (Compant et al., 2019). Research on plant microflora dates back to traditional farming methods that, without awareness, depended on helpful microbes to improve soil quality and plant vitality. As research advanced, it became possible to identify and characterize microorganisms associated with roots, leaves, and endophytes, uncovering their essential functions in plant growth, disease resistance, and stress resilience. Contemporary molecular methods have revealed the variety and functional capabilities of these microbial communities, emphasizing their significance for sustainable farming and biotechnological uses (Ayilara et al., 2023). Initial studies on plant microflora focused on the rhizosphere, regarded as a critical area where soil microorganisms engage intimately with plant roots. Eventually, researchers broadened their attention from the rhizosphere to additional plant environments, including the phyllosphere, endosphere, and reproductive organs. Foundational studies demonstrated the significance of soil nutrients and plant exudates in influencing microbial communities, whereas contemporary developments emphasized the impact of particular plant compounds and

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wider environmental elements. These achievements established the basis for contemporary research on plant microbiomes (Berg et al., 2014).

Various sections of a plant, including its roots, stems, branches, and leaves, offer natural environments for numerous microorganisms that coexist closely with the host. Endophytes are often present in various crops such as wheat, maize, soybean, and sorghum. These cultivable microbes exist inside the plant's internal tissues, referred to as the endospheric (Babalola & Adedayo, 2023).

Harmful blooms of cyanobacteria are rising globally as a result of climate change and nutrient pollution. These blooms emit microcystins (MCs), particularly MC-LR, which are persistent toxins that pose risks to water quality, human health, vegetation, and soil microorganisms. MCs can access drinking water, food, and crops watered with tainted water, hindering plant development and impacting soil microbial equilibrium. As conventional water treatments fail to eliminate dissolved MCs, microbial degradation is being investigated. This study examines the impacts of irrigation water contaminated with MC on plants, soil, and the buildup of toxins in consumable crops (Redouane et al., 2019). Microbes associated with plants typically belong to three categories: helpful bacteria, plant diseases, and human opportunistic pathogens. Helpful microorganisms like Burkholder, Pseudomonas, Bacillus, and Rhizobium enhance plant development by increasing nutrient accessibility, offering disease protection, and generating phytohormones. Fresh fruits and vegetables play a crucial role in the human diet, yet the incidence of foodborne illnesses associated with raw produce has risen in recent years. Pollution may happen due to unprocessed fertilizers, contaminated irrigation water, animal interaction, and inadequate post-harvest management. Numerous studies indicate that uncooked vegetables can harbor various true and opportunistic human pathogens that thrive effectively on plant exteriors and within soil. Examples consist of E. coli, Salmonella, Pseudomonas aeruginosa, Bacillus cereus, and Serratia marcescens (Ali, 2019). To tackle these issues, it is crucial to isolate endophytic bacteria from commercially significant plants in vitro, pinpointing those exhibiting antimicrobial properties that can act as targeted biocontrol agents against particular pathogens in the host (Cui et al., 2019). Various sections of a plant, including roots, stems, branches, and leaves, contain different microbes that establish intimate relationships with the plant. Numerous endophytes reside within crops such as wheat, maize, soybean, and sorghum, with culturable microbes inhabiting the plant's internal tissues (Tzschoppe et al., 2012).

Plants extract microorganisms from various nearby environments. These consist of the soil and rhizosphere, the phyllosphere (the surfaces of leaves above ground), the anthosphere (the area around flowers), the spermosphere (the region around germinating seeds), and the carposphere (the external environment of fruits) (Hardoim et al., 2015). The majority of root-associated microorganisms are obtained horizontally from the nearby soil, which contains a highly varied microbial community mainly comprised of Acidobacteria, Verrucomicrobia, Bacteroidetes, Proteobacteria, Planctomycetes, and Actinobacteria (Fierer, 2017). Aerial plant parts such as leaves, shoots, and flowers provide unique environments for both endophytic and epiphytic microorganisms. Nevertheless, the ecological environments of the endosphere and phyllosphere vary significantly. Numerous endophytes travel via the plant's xylem and disseminate to different areas like the stem, leaves, and fruits (Compant et al., 2010). Affect the microbiota of both aerial and subterranean plant components. The plant species

and genotype attract microorganisms from the soil environment, with root morphology, exudates, and types of rhizodeposits significantly influencing the recruitment of plant microbiota (Reinhold-Hurek et al., 2015).

Microorganisms are essential for life on Earth, but the majority are still not well understood in places such as soil, oceans, the atmosphere, and even within the human body. Although culture-based techniques provide insights into individual microbes, contemporary methods like metagenomics enable researchers to recognize them directly in their natural environments. These strategies assist in revealing the ecological functions of microbiomes in various ecosystems (Turner et al., 2013). The methods employed by soybean endophytic microbes to promote plant growth need to be investigated to understand their functions within the plant endosphere (Feng et al., 2017). FISH has been utilized to examine endophytic microbes in their native environment, yet isolating them in the lab proves difficult. Integrating PCR with sequencing methods can enhance our comprehension of gene networks within the plant microbiome (Adeleke et al., 2021).

A microbiome refers to the variety of microorganisms that cohabit with higher organisms like humans, animals, and plants. All examined complex life forms possess their unique microbiomes. Although progress on the human microbiome has accelerated, research is now more centered on comprehending the structure and roles of microbiomes in plants and soil. Plants harbor unique microbial communities on their leaves and roots, primarily derived from several dominant bacterial phyla. Root microbes are influenced by root exudates and plant genetics, whereas leaf microbes develop on the leaf surface. These communities aid in safeguarding plants against disease and fostering growth, particularly by aiding nutrient uptake via root bacteria (Bulgarelli et al., 2013). Harmful microbial interactions in plants can impede growth or induce disease, whereas beneficial ones can enhance growth. Bacteria associated with plants are categorized as rhizospheric, epiphytic, or endophytic depending on where they are found. Epiphytic bacteria reside on the surfaces of roots or leaves, while endophytes exist within internal plant tissues without inducing disease (Taulé et al., 2021). The mutualistic association between mycorrhizal fungi and rhizobacteria in the roots of legume plants enables them to collaborate with their host, enhancing the absorption of vital nutrients such as nitrogen, phosphorus, and potassium, while simultaneously decreasing the reliance on nitrogen fertilizers in farming soils (Oldroyd & Leyser, 2020). The composition and function of intestinal microbiota are affected by several factors, such as diet, the use of antibiotics, and even the delivery method at birth, which is essential in determining bacterial diversity (Tonon et al., 2021). Many bacteria recognized as root endophytes are said to come from the rhizosphere (Aloo et al., 2019).

Bibliometric methodology involves employing quantitative techniques, like citation analysis, to analyze bibliometric data, encompassing publications and their citations. While conversations about bibliometrics started in the 1950s, the approach itself is not novel. Bibliometric analysis serves as an effective method for recognizing research patterns and forecasting the future trajectory of a field. It is commonly utilized to assess the present condition, rising trends, and growth patterns in a particular area. As scientific papers act as crucial markers of technological and academic advancements, bibliometrics concentrates on quantitatively analyzing the external attributes of scientific literature. Depending on the format of the results, bibliometric techniques can encompass statistical evaluation, mathematical modeling, system examination, matrix analysis, and network assessment. Materials and Methods related to research (Q. Wang & Su, 2020) Cite Space and VOS viewer are popular

instruments for bibliometric analysis, providing clear scientific insights and valuable guidance for research activities (J.-H. Wang et al., 2024)

Bibliometric analysis encompasses both qualitative and quantitative assessments of research conducted in a particular area over a specified timeframe. It employs statistical and mathematical methods to assess the impact and importance of papers, journals, authors, and various academic contributions. In this research, data including authors, keywords, journals, nations, periodicals, and references were gathered for examination. Contemporary computing tools enable the incorporation of graphical and visual components when analyzing academic literature. Moreover, bibliometric research frequently employs co-citation analysis, a technique where two documents are referenced together by one or more additional documents. This method has been demonstrated to improve data analysis and assists in delivering the results in a more thorough and nuanced way (Yang et al., 2022). Alan Pritchard introduced the concept of bibliometrics in 1969. This approach offers an organized means to assess the effect and importance of research findings. Bibliometrics, through the incorporation of statistical and mathematical methods, functions as a powerful instrument for demonstrating the evolution and transformation of research fields over time (Chen et al., 2022). The bibliometric information was gathered from research articles in English listed in the Web of Science Core Collection and PubMed. The obtained records were subsequently processed and examined with VOS viewer, in conjunction with additional tools like R (version 3.5.6) and Cite Space (Ding et al., 2023)

Collection of Data:

The present research conducted a BA (Bibliometric Analysis) utilizing data and information gathered from the WoS (Web of Science) database as of November 18, 2025. The Web of Science (WoS) was selected due to its established reputation as a reliable database for research publications and citations.

Identification of Relevant Data:

To find and recognize dataset number 64, the researchers utilized the search function of the WoS (Web of Science) platform, defined keywords, and set criteria. This method guaranteed the exact and reliable collection of research-related information.

Data Screening and Cleaning:

Out of the 64 records collected, 4 were rejected due to document type, which encompassed proceeding papers, news items, and corrections. Additionally, 4 items were excluded because only the English language was selected.

Record Evaluation for Inclusion:

The subsequent step consisted of examining 56 datasets, each of which fulfilled the inclusion criteria, demonstrating their importance to the research.

Data Analysis:

To identify significant topics within the field, this research focused on analyzing the occurrence of specific keywords linked to plant microflora. It also aimed to demonstrate how expertise in this area has evolved and expanded over time. Bibliometric analysis, or BA, was performed to chart relationships among publications, authors, and keywords and examine trends in the literature. The objective of the present research was achieved

through the utilization of VOS viewer 1.6.19, enabling the management of large datasets and the generation of visual representations such as network, overlay, and density maps. These visual tools provided a comprehensive and important summary of the field's status, offering valuable insights to guide future research and highlight important developments.

Results:

Table -1: Co-occurrence of the keywords associated with plant microflora research

S. NO.	Keywords	Occurance	Total Link Strength
1.	Rhizosphere	12	33
2.	Rhizosphere microbiome	9	27
3.	Soil	6	23
4.	Diversity	6	20
5.	Colonization	4	18
6.	Endophytes	5	17
7.	Phyllosphere	6	17
8.	Biological - control	6	16
9.	Bacteria	5	15
10.	Biocontrol	4	14
11.	Growth	5	14
12.	Microbiome	3	14
13.	Microbiota	4	12
14.	Fungi	3	11
15.	Plant microbiome	4	11
16.	Arabidopsis-thaliana	3	10
17.	Pseudomonas-syringae	3	10
18.	Rhizobacteria	3	10
19.	Root microbiota	4	10
20.	Bacterial communities	3	8
21.	Endophytic bacteria	3	8
22.	Crop production	3	6
23.	Bacillus-subtilis	3	4
Total			

Table 1 encapsulates the most commonly co-existing keywords in scientific literature concerning plant microflora. The “Occurrence” figure shows the frequency of a specific term in the dataset, whereas the “Total

Link Strength” measures the strength of that term's connection to other keywords in the research network. Collectively, these parameters emphasize the key conceptual areas and developing trends in contemporary research on plant microflora.

- Rhizosphere (12 occurrences, 33 TLS) Rhizosphere” emerges as the most dominant keyword, indicating that the soil region surrounding plant roots is central to current microflora research. The high link strength shows its strong association with themes such as soil health, nutrient cycling, and microbial interactions.
- Rhizosphere microbiome (9 occurrences, 27 TLS) This term emphasizes microbial communities residing specifically in the rhizosphere. Its frequent appearance suggests a major interest in understanding the structural and functional dynamics of root-associated microbes.
- Soil (6 occurrences, 23 TLS) Soil acts as a critical ecological component influencing microbial diversity. Its strong connectivity highlights that soil properties such as texture, nutrients, and moisture are foundational in shaping plant microflora composition.
- Diversity (6 occurrences, 20 TLS) Frequent references to “diversity” indicate that biodiversity assessment of microbial communities remains a focal research area, reflecting efforts to characterize functional and taxonomic variations among microbes.
- Colonization (4 occurrences, 18 TLS) The prominence of “colonization” denotes the importance of understanding how microorganisms establish themselves on plant surfaces and within tissues, a key step in plant–microbe interactions.
- Endophytes (5 occurrences, 17 TLS) Endophytes refer to microorganisms living inside plant tissues without causing harm. Their high linkage signifies increasing interest in their roles in plant stress tolerance and growth enhancement.
- Phyllo sphere (6 occurrences, 17 TLS) This term represents the aerial parts of plants, especially leaves. Its relevance reflects growing recognition of above-ground microbial communities in plant health and environmental adaptation.
- Biological Control (6 occurrences, 16 TLS) The emphasis on biological control shows that researchers are actively exploring microflora as eco-friendly alternatives to chemical pesticides.
- Bacteria (5 occurrences, 15 TLS) Bacteria stands out as a major microbial group studied within plant microflora, underlining their central roles in nutrient transformation, disease suppression, and plant growth.
- Biocontrol (4 occurrences, 14 TLS) Closely linked with biological control, “biocontrol” reinforces the significance of plant-associated microbes as natural agents for suppressing pathogens.
- Growth (5 occurrences, 14 TLS) The keyword “growth” reflects the consistent research focus on how microflora influence plant development, productivity, and physiological functions.
- Microbiome (3 occurrences, 14 TLS) This broad term suggests an integrated approach to studying entire microbial ecosystems associated with plants, rather than isolated species.
- Microbiota (4 occurrences, 12 TLS) Similar to microbiome, “microbiota” highlights interest in community-level analysis, often in relation to plant health and environmental factors.

- Fungi (3 occurrences, 11 TLS) The presence of “fungi” signals their recognized importance as mutualists, pathogens, and decomposers within plant-associated microbial networks.
- Plant Microbiome (4 occurrences, 11 TLS) This keyword underscores holistic investigations into all microorganisms associated with plants roots, leaves, and internal tissues.
- Arabidopsis thaliana (3 occurrences, 10 TLS) The appearance of this model plant indicates its continued use in controlled studies to understand plant–microbe interactions at physiological and molecular levels.
- Pseudomonas syringe (3 occurrences, 10 TLS) This plant-pathogenic bacterium appears frequently due to its relevance in disease studies and as a model for host–pathogen interaction research.
- Rhizobacteria (3 occurrences, 10 TLS) Rhizobacteria, especially beneficial strains, are central to research exploring plant growth promotion and disease suppression in the rhizosphere.
- Root Microbiota (4 occurrences, 10 TLS) This term highlights specific focus on microbial communities inhabiting the root interior and surface, essential for understanding nutrient acquisition and stress responses.
- Bacterial Communities (3 occurrences, 8 TLS) The term signifies broader ecological studies on bacterial assemblages associated with plants and their collective functional contributions.
- Endophytic Bacteria (3 occurrences, 8 TLS) This reflects interest in bacteria that reside within plant tissues, contributing to enhanced resilience and improved metabolic functions.
- Crop Production (3 occurrences, 6 TLS) The appearance of “crop production” illustrates the applied dimension of this research particularly how beneficial microflora can improve yield and farming sustainability.
- Bacillus subtilis (3 occurrences, 4 TLS) Bacillus subtilis is widely studied as a plant-growth-promoting and biocontrol bacterium. Its presence indicates ongoing research into its mechanisms and applications in agriculture.

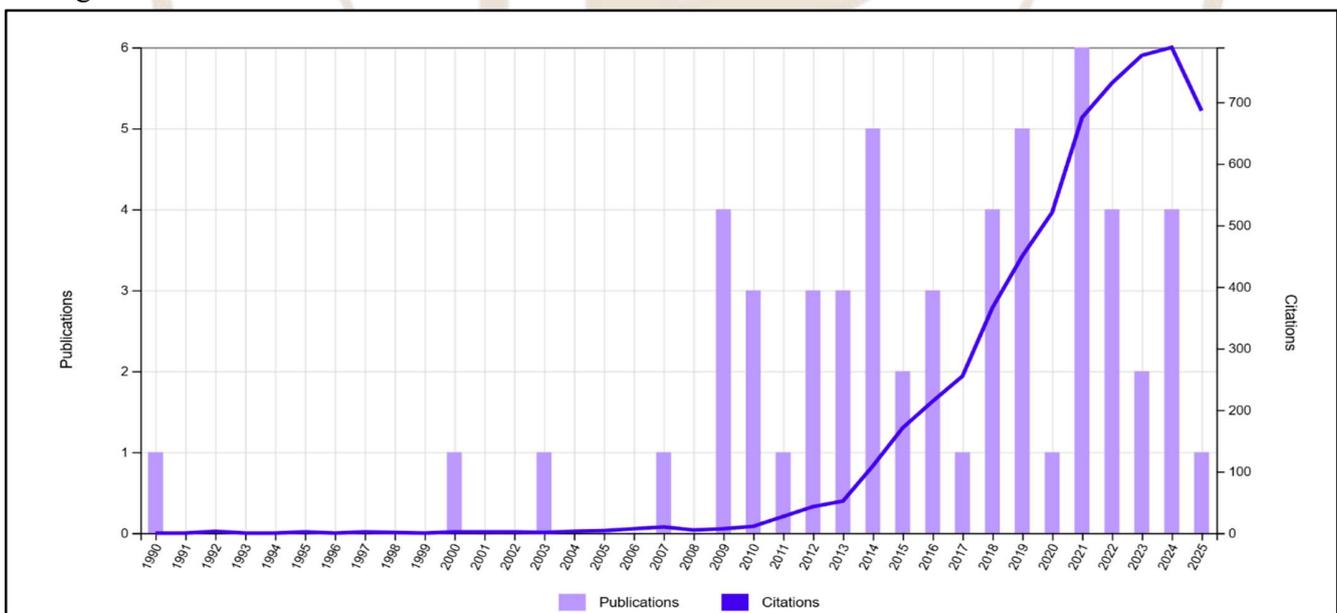
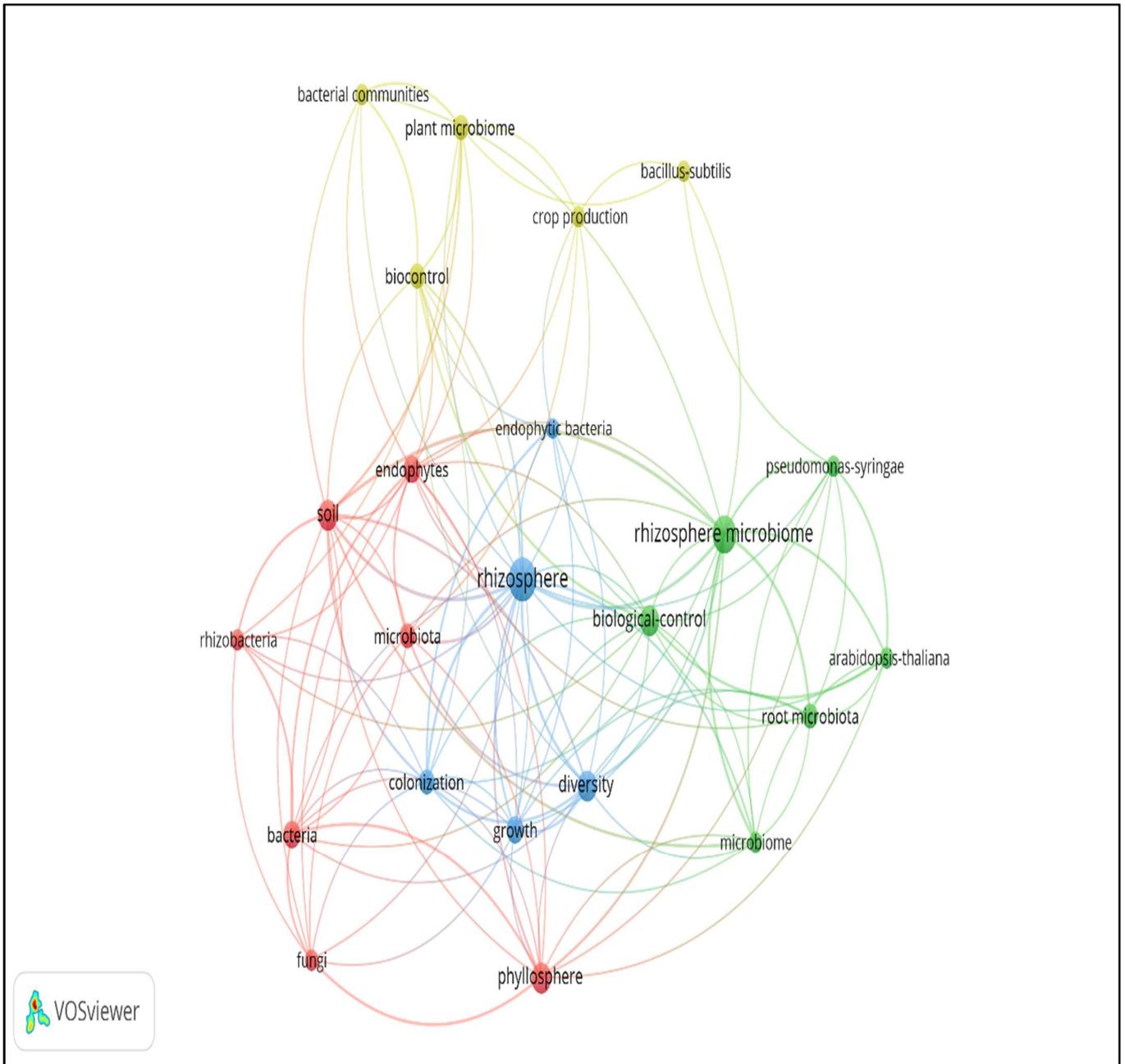


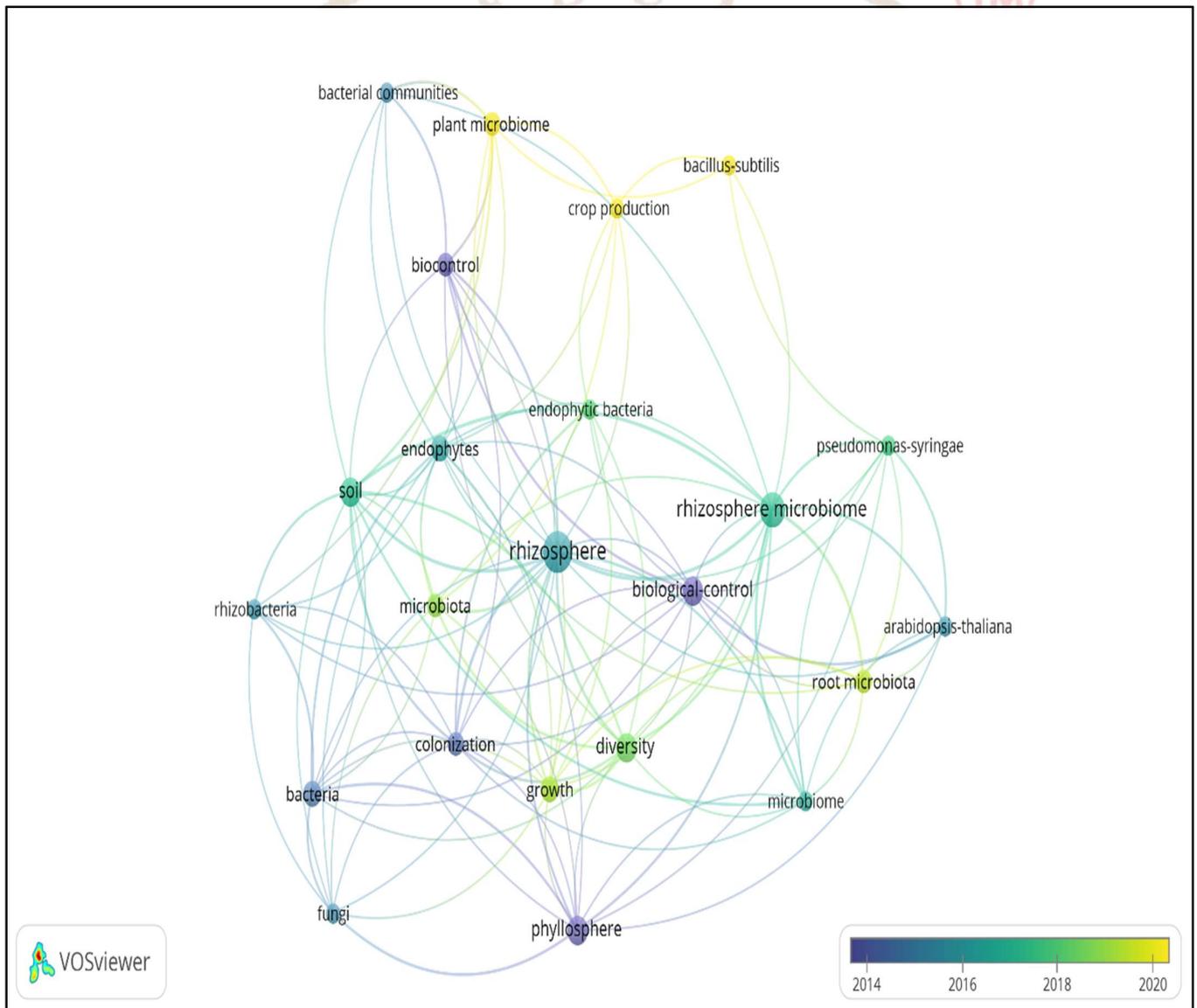
Figure: 1 Publication frequency and citation metrics for Plant Microflora research from 1994 to 2024.

The diagram shows a steady rise in academic publications related to Plant Microflora research from 1994 to 2024, indicating ongoing growth and heightened scientific interest in this area. Citation metrics show a similar upward trend, reflecting both greater research productivity and enhanced academic influence and acknowledgment. Together, the trend indicates the development of the field and its increasing importance within the wider scientific community.



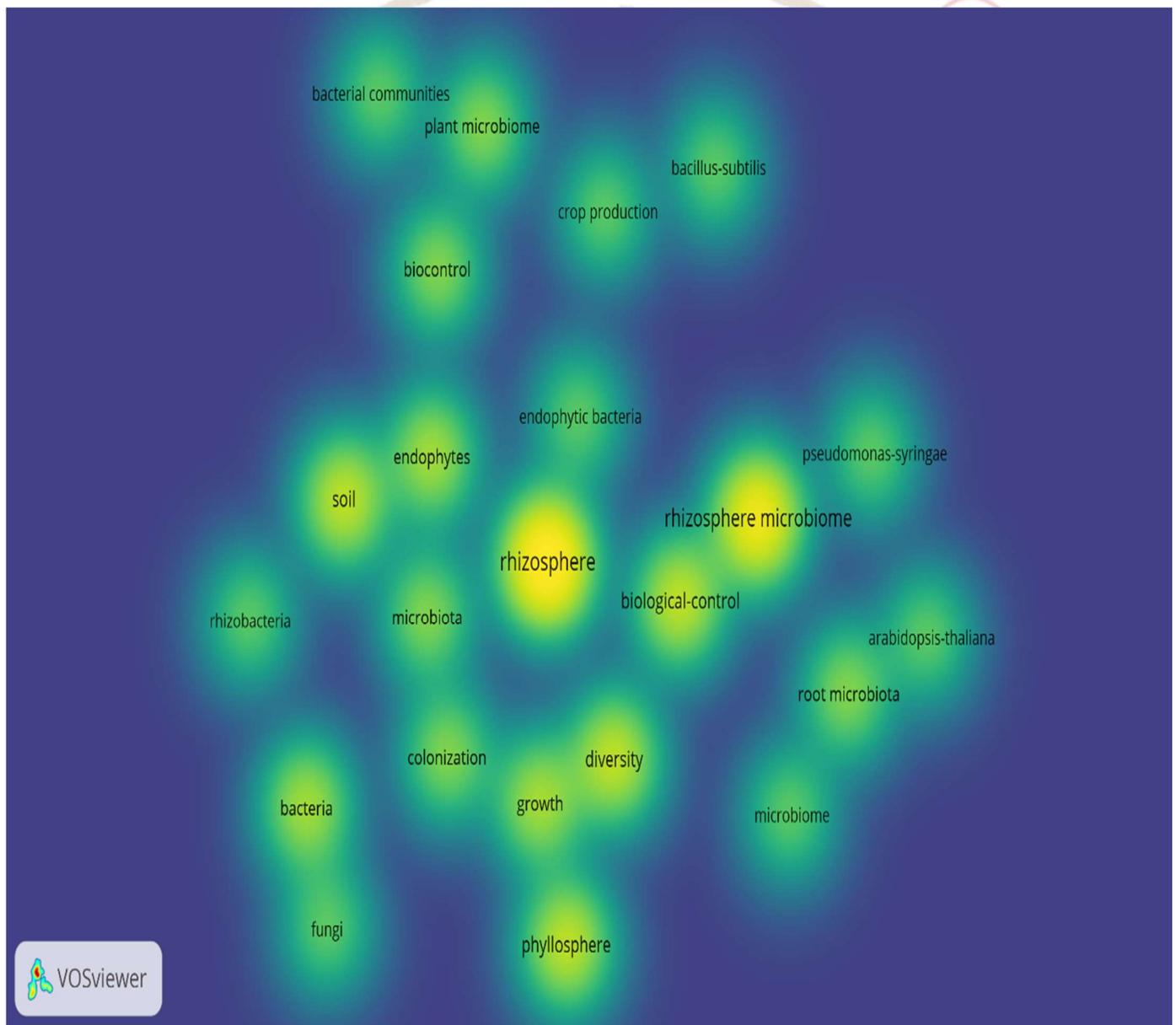
The figure: 2 Network visualization of Plant Microflora Research: A Network Analysis of Co-Occurring Keywords (Source: Prepared by Author using VOS viewer 1.6.19 software)

Figure 2 illustrates the network configuration of keyword co-occurrence produced with VOS viewer. Every node signifies a keyword, and the lines connecting them reflect the frequency of these terms appearing together in the reviewed publications. Bigger nodes represent greater frequency, while thicker links denote stronger co-occurrence. In the realm of plant microflora, commonly used terms like rhizosphere, endophytes, soil, phyllosphere, and biocontrol create tight clusters. These clusters represent well-established research topics, such as investigations into root-microbe interactions, mechanisms of biological control, and microbial diversity. The visualization illustrates the conceptual essence of the field and emphasizes the interconnections among the key research areas.



The figure: - 3 Overlay visualization of Plant Microflora Research: A Network Analysis of Co-Occurring Keywords (Source: Prepared by Author using VOS viewer 1.6.19 software)

Figure 3 provides an overlay map that displays the temporal progression of important research themes. In this form of visualization, the color gradient indicates the average publication year linked to each keyword. Themes from earlier times are depicted in blue or green hues, while yellow signifies the latest research efforts. For plant microflora, traditional terms like soil, bacteria, and rhizosphere serve as foundational aspects of early studies, whereas new themes such as microbiome, endophytic bacteria, and crop production are represented in more recent developments. This indicates a slow transition from descriptive microbial ecology to more practical and functional research utilizing molecular tools, plant physiology, and sustainable agriculture.



The figure: -4 Density visualization of Plant Microflora Research: A Network Analysis of Co-Occurring Keywords (Source: Prepared by Author using VOS viewer 1.6.19 software)

Figure 4 presents a density map in which regions of high keyword density are shown in warm hues (yellow, red), whereas terms that are less common are depicted in cooler tones (blue, green). The thick yellow area around terms such as rhizosphere, endophytes, and microbiota highlight their significant importance in the literature. These hotspots signify research areas that have attracted the most academic focus. The density visualization aids in recognizing not only the central themes but also supplementary or emerging keywords, providing useful insights for researchers looking to uncover gaps or potential research paths.

Discussion of Findings

The bibliometric analysis reveals key trends that characterize the present state of research on plant microflora. In agreement with previous research (Compant et al., 2019; Bulgarelli et al., 2013), the primary focus is the rhizosphere, which is central to all visual representations. Its strong overall link strength indicates that root-associated environments continue to be a central focus, probably because of their crucial role in nutrient absorption, soil vitality, and plant–microbe interaction. The significance of terms like rhizosphere microbiome, endophytes, phyllo sphere, and microbiota suggests that scientists are progressively viewing plant microflora as a multi-compartment ecosystem instead of a singular ecological niche. This corresponds with contemporary viewpoints that highlight the halobiont idea, where plants and their microbial associates operate as a cohesive biological entity. Keywords like biocontrol, *Bacillus subtilis*, and *Pseudomonas syringae* reflect the growing interest in utilizing microbes related to plants for effective agricultural uses. Research on biocontrol methods has increased in popularity because of the demand for eco-friendly substitutes for chemical pesticides (Cui et al., 2019; Aloo et al., 2019). The visualizations of the network and overlay indicate that biological control has emerged as one of the rapidly expanding subjects in the domain. A significant trend is the growing focus on microbiome and microbiota, propelled by the swift progress of next-generation sequencing technologies (Turner et al., 2013). These terms have emerged in recent years, indicating a methodological transition from culture-dependent methods to metagenomics, transcriptomics, and sophisticated bioinformatics techniques. This change has created new opportunities for comprehending microbial roles, host–microbe communication, and the impact of environmental change on microbial composition. The inclusion of phrases like crop production underscores the increasing emphasis on practical applications in the discipline. With agriculture confronting issues stemming from climate change, diminishing soil quality, and heightened pathogen threats, research is focusing on microbial strategies to improve plant resilience and yield (Reinhold-Hurek et al., 2015; Oldroyd & Leyser, 2020).

Conclusion

The bibliometric assessment of plant microflora research offers an extensive insight into the evolution of this field over the last thirty years. The analysis shows that the rhizosphere remains central to scientific focus, highlighting its crucial role in influencing microbial diversity and plant well-being. Simultaneously, growing interest in endophytes, microbial community composition, and biological control indicates a transition toward functional and applied studies. The generated visualization maps from VOSviewer effectively demonstrate the relationships among keywords and the evolving trends in research topics. Traditional ideas like soil-root interactions are still crucial, while contemporary molecular methods have broadened the focus to encompass entire plant microbiomes and their significance for sustainable agriculture. Research on plant microflora has evolved into a highly

interdisciplinary area that merges ecology, molecular biology, plant physiology, and biotechnology. The growing focus on microbial solutions for enhancing crops indicates that microbes associated with plants will remain pivotal in tackling global agricultural issues.

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