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Patterns and trends in research on endophytic fungi associated with plants: gaps and biotechnological implications (2015–2025)

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ABSTRACT

Endophytic fungi associated with plants have received increasing scientific attention due to their ecological relevance and high biotechnological potential, especially for the production of bioactive metabolites with agricultural, pharmacological, and environmental applications. This study aimed to analyze patterns, trends, and gaps in scientific production on endophytic fungi associated with plants from 2015 to 2025, using a descriptive scientometric approach. Articles indexed in the Web of Science Core Collection, selected based on predefined criteria, were analyzed. Data were evaluated using descriptive statistics and multivariate analyses, including Principal Coordinate Analysis (PCoA). The results showed continuous growth in scientific production, concentrated in countries such as China, Brazil, India, and the United States. An asymmetrical pattern was observed in the selection of host botanical families, with a predominance of Poaceae, Fabaceae, Bignoniaceae, Meliaceae, Zingiberaceae, and Asteraceae, indicating taxonomic biases associated with the economic and medicinal relevance of these plants. PCoA demonstrated that the selection of botanical families follows scientific trends and temporal dynamics throughout the analyzed period. It is concluded that, although the area is consolidated, expanding the taxonomic and geographic scope of research is fundamental to reducing knowledge gaps and enhancing the discovery of new endophytic fungi and bioactive metabolites.

RESUMO

Os fungos endofíticos associados a plantas têm recebido crescente atenção científica devido à sua relevância ecológica e ao elevado potencial biotecnológico, especialmente pela produção de metabólitos bioativos com aplicações agrícolas, farmacológicas e ambientais. Este estudo teve como objetivo analisar padrões, tendências e lacunas na produção científica sobre fungos endofíticos associados a plantas no período de 2015 a 2025, por meio de uma abordagem cienciométrica descritiva. Foram analisados artigos indexados na Web of Science Core Collection, selecionados com base em critérios previamente definidos. Os dados foram avaliados por estatística descritiva e análises multivariadas, incluindo Análise de Coordenadas Principais (PCoA). Os resultados evidenciaram crescimento contínuo da produção científica, com concentração em países como China, Brasil, Índia e Estados Unidos. Observou-se um padrão assimétrico na seleção das famílias botânicas hospedeiras, com predominância de Poaceae, Fabaceae, Bignoniaceae, Meliaceae, Zingiberaceae e Asteraceae, indicando vieses taxonômicos associados à relevância econômica e medicinal dessas plantas. A PCoA demonstrou que a seleção das famílias botânicas acompanha tendências científicas e dinâmicas temporais ao longo do período analisado. Conclui-se que, embora a área esteja consolidada, a ampliação do escopo taxonômico e geográfico das pesquisas é fundamental para reduzir lacunas de conhecimento e potencializar a descoberta de novos fungos endofíticos e metabólitos bioativos.

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Introduction

The high plant richness and diversity observed in preserved natural ecosystems establish favorable conditions for colonization by endophytic microorganisms. The environmental heterogeneity and structural complexity of plant communities favor the establishment of intimate interactions between plants and endophytic fungi, which colonize the internal tissues of the hosts without causing harm (Coertjens; Mascarenhas; Batistote, 2024). These microorganisms have aroused increasing scientific interest due to their significant biotechnological potential, acting as promising sources of enzymes, secondary metabolites, and bioactive compounds with applications in the agricultural, pharmaceutical, and industrial sectors (Bogas et al., 2022). In this context, highly diverse plant ecosystems are configured as strategic reservoirs of endophytic fungi that are still underexplored from a biotechnological perspective.

Plant colonization by endophytic fungi can occur through multiple pathways, including natural openings such as stomata and hydathodes, wounds caused by insects or pathogens, as well as vertical transmission via seeds (Papik et al., 2020). Different species of endophytic fungi can coexist within the same plant, establishing functional associations that favor the adaptation and survival of both organisms (Yan et al., 2019; Mattoo; Nonzom, 2021). Throughout coevolution, these interactions have resulted in highly integrated symbiotic systems, based on the exchange of metabolic resources, protection, and biochemical signals essential to maintaining the association (Malicka; Magurno; Piotrowska-Seget, 2022).

As a result of this interaction, endophytic fungi play a central role in plant physiology by synthesizing biologically active molecules that contribute to plant tolerance to biotic and abiotic stresses, especially through the production of metabolites with antifungal, antioxidant, and plant growth-regulating properties (Harman et al., 2021; Lee et al., 2021). Conversely, these microorganisms gain continuous access to nutrients and a protected environment within plant tissues, which favors the stability of the interaction. The ability to produce a wide variety of compounds, such as enzymes, alkaloids, antibiotics, and other secondary metabolites, highlights the ecological relevance of endophytic fungi and reinforces their significant biotechnological potential (Baron; Rigobelo, 2022; Wen et al., 2022).

In this scenario, endophytic fungi stand out for the production of bioactive molecules with applications in multiple sectors, including pharmacology, health, industry, and bioremediation. Studies indicate that endophytic communities associated with highly diverse plants exhibit significant taxonomic richness and high biotechnological value, although they are still underexplored in terms of systematic prospecting (Devi et al., 2023; Noriler et al., 2018). Among the products of greatest interest are hydrolytic enzymes, such as cellulases, lipases, proteases, and amylases, which are widely applicable in industrial and biotechnological processes (Bezerra et al., 2021; Sharma; Dhar; Kaul, 2023).

In addition to enzyme production, endophytic fungi constitute a highly promising source of structurally diverse secondary metabolites, including steroids, alkaloids, phenols, flavonoids, isocoumarins, xanthones, quinones, and terpenoids, which are widely recognized for their pharmacological properties (Satheesan; Sabu, 2020; Adeleke; Babalola, 2021; Rai et al., 2021). Many of these compounds exhibit antimicrobial, antifungal, antiparasitic, anticancer, and antiviral activities, reinforcing the role of endophytic fungi as strategic sources for the development of new drugs and therapeutic agents (Manganyi; Ateba, 2020).

However, despite the significant progress in research in this area, scientific production on endophytic fungi still presents relevant structural limitations. A heterogeneous distribution of scientific production is observed on a global scale, with concentration in certain countries and taxonomic groups of host plants, in addition to a predominance of approaches focused on bioprospecting metabolites and specific biotechnological applications. These characteristics indicate the existence of gaps and potential biases in the literature, hindering an integrated understanding of the diversity and functional potential of these microorganisms.

In this context, the adoption of descriptive scientometric approaches proves particularly relevant, as it allows for the systematic and quantitative analysis of scientific production, enabling not only the identification of patterns, trends, and gaps in knowledge, but also the structural organization of available information. Unlike traditional narrative reviews, this approach provides greater analytical rigor and reproducibility, contributing to a more integrated understanding of the dynamics of research at scale.

Materials and Methods

Nature of the study

This study is configured as a descriptive and exploratory scientometric analysis, aimed at identifying structural patterns in scientific production related to host plants and the biotechnological potential of endophytic fungi. The approach adopted prioritizes the analysis of biological, taxonomic, and thematic attributes present in the literature, focusing on identifying trends, gaps, and research biases.

Although it does not fully encompass the traditional metrics of classical bibliometrics, such as co-authorship networks, citation analysis, or keyword co-occurrence, the study incorporates bibliometric principles by employing quantitative analysis of scientific production, allowing the identification of relevant temporal and geographical patterns (Snyder, 2019; Xiao & Watson, 2019; Palmatier et al., 2018).

Data Sources and Search Strategy

Initially, the bibliographic search was conducted in widely recognized scientific databases, including Web of Science, Scopus, Google Scholar, and SciELO, with the aim of ensuring broad coverage of indexed scientific production. However, due to the high volume of records retrieved and the need for standardization and consistency of data, the Web of Science Core Collection database was chosen exclusively as the main source for constructing the analytical corpus, since it presents rigorous indexing criteria and greater standardization of bibliometric information.

The search strategy was structured systematically, based on a combination of controlled descriptors and free terms, associated by Boolean operators (AND, OR), applied in English and Portuguese. Searches were conducted in the title, abstract, and keyword fields, aiming to maximize sensitivity and comprehensiveness in retrieving relevant studies. The search was conducted in the Web of Science Core Collection database, using the following string: TS = ("endophytic fungi" OR "endophytes" OR "plant-associated fungi") AND ("metabolites" OR "secondary metabolites"). Additionally, equivalent terms in Portuguese ("fungos endofíticos" AND "metabólitos") were considered, as well as semantic variations and truncation operators, when applicable, in order to broaden the scope of the search. The searches were performed on January 5, 2026, ensuring the temporal traceability of the analyzed records.

The adopted time frame encompassed the period from 2015 to 2025, allowing for the analysis of the evolution of scientific production over a recent decade, characterized by the intensification of research in bioprospecting and biotechnological applications of endophytic fungi.

Inclusion and exclusion criteria

For the selection of studies included in this review, inclusion and exclusion criteria were established in order to delimit the scope of the research and ensure the relevance and quality of the analyzed database. Table 1 presents, in a summarized form, the criteria adopted for the screening of articles.

Table 1. Criteria adopted for the composition of the bibliometric database.

Inclusion criteria	Exclusion criteria
Research articles published in peer-reviewed scientific journals	Conference abstracts
Publications fully available online	Book chapters, dissertations, and theses
Studies addressing endophytic fungi associated with plants	Duplicate records
Studies reporting host plant botanical family and plant tissue used	Studies not directly related to endophytic fungi
Studies with a biotechnological focus	

Source: Authors.

Study selection and data extraction, organization, and analysis

The records were exported in .csv format, including information such as title, authors, year of publication, journal, abstract, and keywords.

The article selection process was conducted in three sequential stages, following an adaptation of the PRISMA Statement guidelines for bibliometric reviews. Initially, records were identified and duplicates were removed. Then, titles and abstracts were screened based on their adherence to the study's objectives. Finally, the full texts were evaluated for eligibility, considering the previously established inclusion criteria. Initially, 2440 records were identified in the consulted databases. After the screening stage, which included the removal of duplicates and the application of inclusion and exclusion criteria, 2325 articles were considered for the composition of the study's textual corpus. The relevant information from these studies was extracted, organized, and systematized in spreadsheets using Microsoft Excel® 2019 software.

The structured textual corpus was used as a basis for conducting descriptive statistical analyses and for creating tables and graphical representations using RStudio (version 2026.01.0), utilizing specific packages for data manipulation, analysis, and visualization, including dplyr, tidyr, and readr for data organization, ggplot2 for creating graphs, and vegan for multivariate analyses, such as Principal Coordinate Analysis (PCoA) based on the Bray-Curtis distance.

Data interpretation

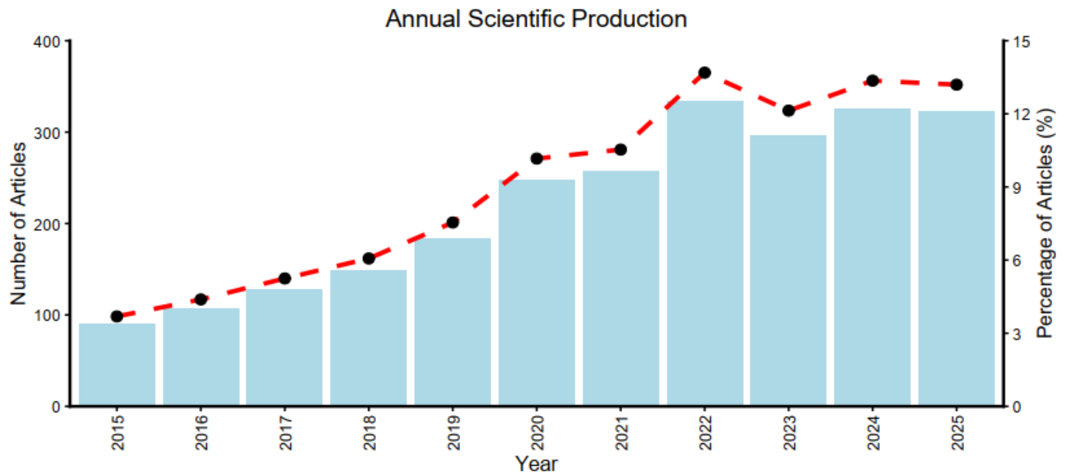
The results obtained were interpreted using an integrated descriptive and analytical approach, allowing the identification of dominant patterns, emerging trends, and knowledge gaps. This strategy made it possible to critically discuss the current state of research on endophytic fungi and to point out opportunities for future studies, especially those focused on the isolation, characterization, and biotechnological exploration of these microorganisms and their metabolites.

Results and Discussion

An analysis of the landscape of scientific publications on the isolation and bioprospecting of endophytic fungi from 2015 to 2025 shows a significant growth in scientific production throughout the time series (Figure 1). In 2015, 90 articles were recorded, a number that progressively increased to 185 publications in 2019, corresponding to an increase of 105.6% compared to the beginning of the analyzed period. From 2020 onwards, an intensification of scientific production is observed, with 245 articles published in 2020 and 260 in 2021. The highest volume of publications was recorded in 2022, with 335 articles. In 2023, there was a reduction to 300 publications, followed by a new increase in 2024, with 330 articles. In 2025, production showed relative stabilization, with 325 articles published. These results highlight the occurrence of interannual fluctuations, although maintaining a general growth trend throughout the analyzed period, indicating a consistent expansion of scientific production in the area.

Figure 1.

Annual expansion of publications on endophytic fungi isolated from plants between 2015 and 2025.



Source: Prepared by the author based on data extracted from the Web of Science Core Collection database (2026). The bars represent the total number of articles published per year, while the dotted line indicates the annual percentage variation in scientific output.

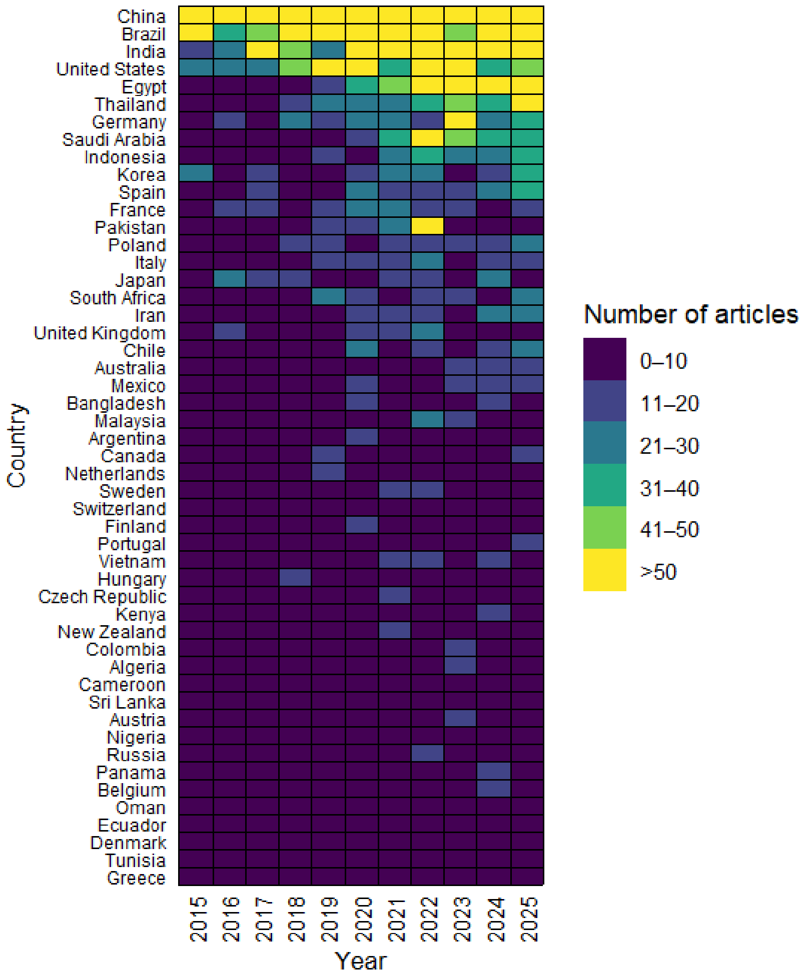
Research on endophytic fungi has shown a continuous process of expansion in the international scientific landscape over the last decade. This pattern reflects not only the quantitative increase in academic production, but also the diversification of analytical approaches and the advancement of methodological strategies employed in the area, including techniques for isolation, characterization, and analysis of secondary metabolites (Wen et al., 2022; Jha et al., 2023). The observed growth may also be associated with the increased scientific interest in the ecological and biotechnological potential of endophytic fungi, especially in the context of bioprospecting for bioactive compounds of economic and environmental interest, as reported in the literature (Kumar et al., 2017; Ancheeva et al., 2020). In this context, the evolution of scientific production suggests the progressive consolidation of the topic on the international research agenda, with increasing relevance in studies focused on the interface between biodiversity, microbiology, and biotechnology.

In parallel, advances in bioprospecting techniques and analytical tools, especially omics approaches and high-resolution molecular methods, have played a fundamental role in intensifying research aimed at identifying and characterizing bioactive metabolites produced by endophytic fungi, allowing for a more detailed analysis of the biosynthetic pathways and chemical diversity of these compounds (Dos Reis et al., 2024; Verma et al., 2024). These methodological advances have significantly expanded the capacity to detect new molecules and understand endophyte-host interactions, driving studies directed towards pharmacological, agricultural, food, and environmental applications. Integrated omics analysis approaches have been applied to unravel molecular mechanisms and metabolic profiles of endophytic fungi associated with medicinal and food plants (Sena et al., Goyal et al., 2025); Recent research has also demonstrated the ability of these microorganisms to produce metabolites with pharmacological properties and resistance to biotic stresses, reinforcing their biotechnological relevance (Prajapati et al., 2025; Ramatsitsi & Manyevere, 2025).

The spatiotemporal analysis of scientific production on the isolation of endophytic fungi associated with plants, based on the heatmap of annual publications by country from 2015 to 2025, reveals an asymmetrical distribution of scientific activity. China, Brazil, India, and the United States stand out as the main global production hubs, showing, especially from 2019 onwards, high volumes of publications, exceeding 40–50 articles per year (Figure 2). China exhibits continuous growth throughout the period. Brazil shows a consistent growth trajectory from 2018 onwards. India and the United States maintain significant production, but with greater interannual variability, indicating heterogeneity in the dynamics of scientific production.

Figure 2.

Spatiotemporal distribution of scientific production on endophytic fungi associated with plants by country, from 2015 to 2025.



Source: The colors represent annual publication frequency classes, ranging from low (0–10 articles) to high (>50 articles), according to the color scale. Countries are ordered according to total productivity in the analyzed period. Data obtained from the Web of Science Core Collection (search performed on January 5, 2026; n = 2325).

The predominance of China, Brazil, India, and the United States as the main centers of scientific production highlights the relevance of these countries in advancing research on endophytic fungi, especially in areas related to the exploration of bioactive metabolites and biotechnological applications (Dos Santos et al., 2022). According to Hu (2020), the continuous growth observed in China may be associated with institutional policies aimed at strengthening science and technology, as well as expanding research infrastructure and encouraging innovation in biotechnology.

In the Brazilian case, the upward trajectory of scientific production may be related to the country's high floristic richness and the consolidation of research groups focused on environmental microbiology and the ecology of microorganisms associated with plants (Mayrhofer et al., 2024; Coertjens et al., 2024). Additionally, the growing interest in sustainable agricultural applications and the prospecting of bioactive compounds has been identified as a relevant factor for the intensification of research on endophytic fungi (Gakuubi et al., 2021).

The significant scientific output observed suggests a progressively diversified research agenda, characterized by the integration of different thematic approaches. In this context, studies of an ecological, physiological, pharmacological, and industrial nature stand out, with an emphasis on interactions between plants and microorganisms, microbial genetics, and bioprospecting for bioactive metabolites. These approaches have broadened the scope of investigations, considering plants not only as hosts but also as structuring elements of endophytic communities and the expression of associated metabolic potential (Gao et al., 2025; Li et al., 2025).

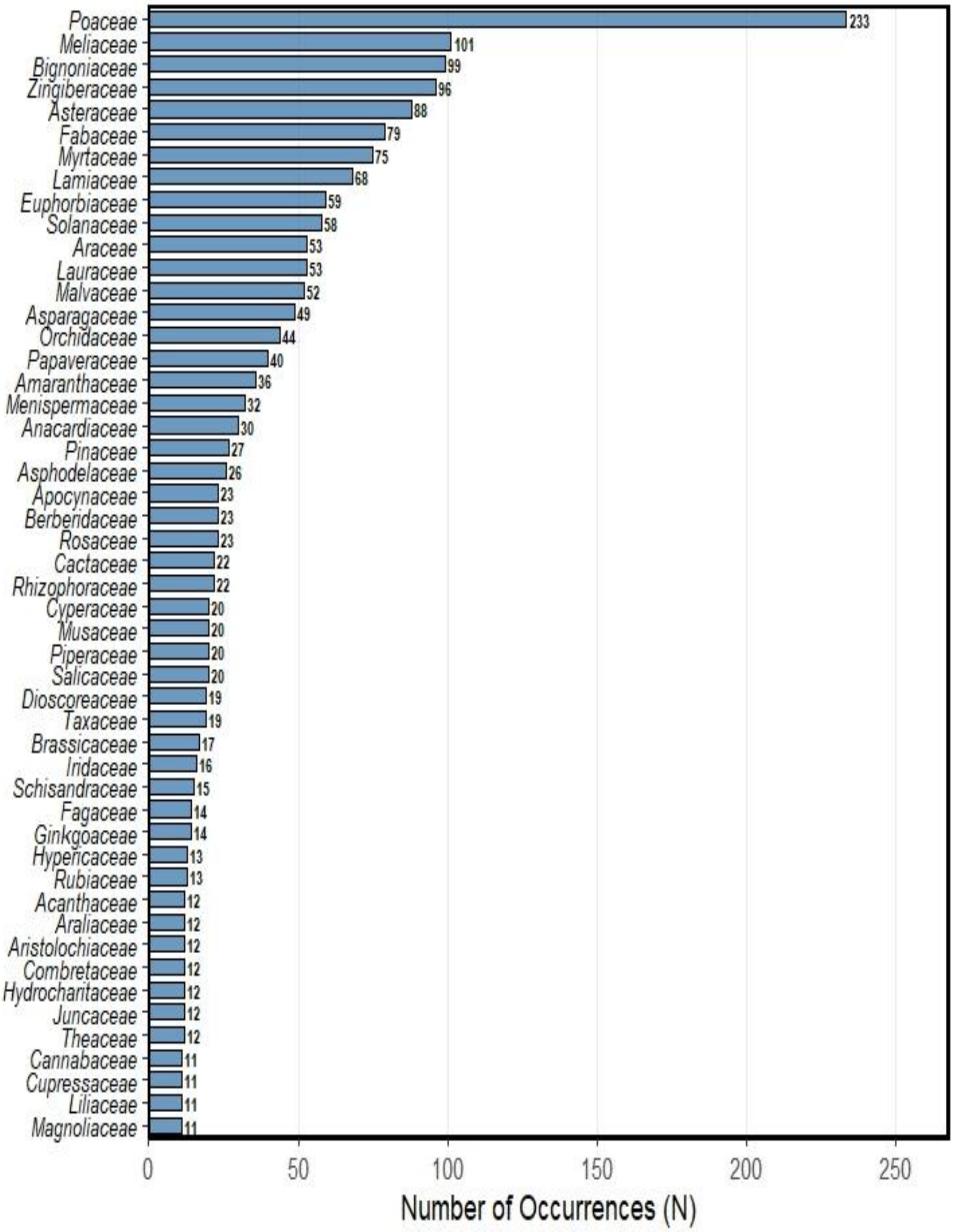
In general, the panorama of scientific production throughout the analyzed period suggests the consolidation of research focused on the bioprospecting of endophytic fungi. This process may be associated with plant diversity and the ecological characteristics of the hosts, as discussed in the literature. Furthermore, recent analyses highlight the potential of international cooperation as a strategy to broaden the geographic and thematic diversity of research, favoring comparative approaches between different plants and taxonomic groups (Yadigarova, 2025).

The analysis of the frequency of occurrence of host botanical families in studies on endophytic fungi from 2015 to 2025 reveals an asymmetrical distribution of scientific production, with a concentration in a restricted set of plant families. The Poaceae family has the highest number of records (n = 233), standing out in relation to the others. Following this, Meliaceae (n = 101), Bignoniaceae (n = 99), Zingiberaceae (n = 96), and Asteraceae (n = 88) stand out, comprising the group of the most frequently investigated families. Other families with high representation include Fabaceae (n = 79), Myrtaceae (n = 75), Lamiaceae (n = 68), and Euphorbiaceae (n = 59). An intermediate group is composed of Solanaceae (n = 58), Araceae and Lauraceae (n = 53 each), Malvaceae (n = 52), Asparagaceae (n = 49) and

Orchidaceae (n = 44). In contrast, a high number of families with low frequency of occurrence are observed, presenting values lower than 20 records. This pattern indicates an uneven distribution of the research, characterized by concentration in a few highly represented groups and by a long tail of poorly explored families (Figure 3).

Figure 3.

Frequency of occurrence of host botanical families in the literature on endophytic fungi from 2015 to 2025.



Source: The bars represent the number of articles in which each family was reported, highlighting the most recurrent groups in the analyzed scientific production. Data obtained from the Web of Science Core Collection (search performed on January 5, 2026; n = 2325).

The predominance of the Poaceae family may be related to its wide geographic distribution, high economic importance, and recurrent use as an experimental model in plant-microorganism interaction studies (Vandenkoornhuyse et al., 2015; Santoyo, 2025; Sharma et al., 2025). Globally relevant agricultural species, such as rice, wheat, corn, and sugarcane, belonging to this family, are frequently used in investigations aimed at increasing productivity, tolerance to biotic and abiotic stresses, and the development of biotechnological applications, which may contribute to its high representation in the scientific literature on endophytic fungi (Verma et al., 2022; Ansabayeva et al., 2025; Majhi et al., 2025).

The high frequency of occurrence of Meliaceae, Bignoniaceae, Zingiberaceae, and Asteraceae may be associated with the taxonomic diversity of these groups, their predominance in tropical and subtropical regions, and the scientific interest focused on medicinal and forest plants (Thangavel et al., 2025). These families are frequently explored in bioprospecting studies, especially in the identification of secondary metabolites with antimicrobial, antioxidant, antifungal, and cytotoxic activities (Hashem et al., 2023; Mulyani et al., 2023; Mendieta-Brito et al., 2025).

Families such as Fabaceae, Myrtaceae, and Lamiaceae reinforce the trend of prioritizing plants with recognized ecological, ethnobotanical, and pharmacological relevance, widely used in agricultural and medicinal systems (Guo et al., 2024; Thangavel et al., 2025). On the other hand, the high proportion of families with fewer than 20 records indicates a possible taxonomic bias in scientific production, in which a significant portion of global plant diversity remains underexplored as a host for endophytic fungi. The results suggest that research on endophytic fungi tends to focus on botanical families of direct economic interest. This pattern may reflect gaps in knowledge associated with less investigated plants and highlights opportunities for expanding studies in plant families related to natural ecosystems, endemic or underexplored species, which may constitute promising sources of new endophytic fungi and bioactive compounds with biotechnological potential.

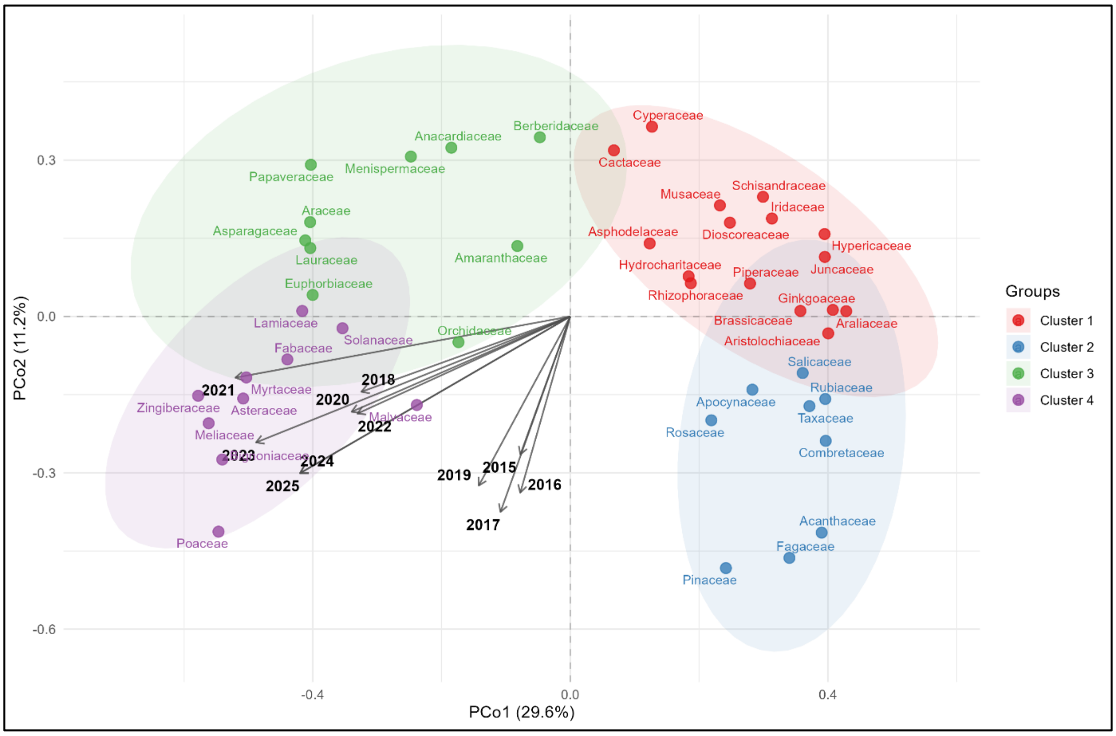
Principal coordinate analysis (PCoA), based on the Bray–Curtis distance, revealed a well-defined structure of the main host botanical families associated with endophytic fungal isolation studies throughout the period from 2015 to 2025. The first two ordination axes together explained 40.8% of the total data variation, with 29.6% attributed to the PCo1 axis and 11.2% to the PCo2 axis (Figure 4). Multivariate ordination showed the formation of four distinct clusters of botanical families, defined by k-means analysis. These clusters reflect differences in the frequency of occurrence of families in the studies and their distribution along the temporal gradient. Families such as Poaceae, Asteraceae, Myrtaceae, and Zingiberaceae were associated with the most recent temporal vectors, indicating greater recurrence in studies published in the final years of the analyzed period. On the other hand, families such as Pinaceae, Fagaceae, and Acanthaceae showed a more isolated position in the ordination, suggesting a lower relative frequency or more punctual occurrence in the studies considered.

The temporal gradient represented by the year vectors indicated a progressive shift in the center of the ordination, evidencing changes in the distribution of host botanical families throughout the time series. This pattern suggests a reorganization in the composition of the families investigated over the analyzed period.

The structuring observed in the PCoA indicates that the distribution of host botanical families in studies on endophytic fungi does not occur randomly, reflecting structural patterns in the analyzed literature. The association of families such as Poaceae, Asteraceae, and Myrtaceae with more recent years may be related to the greater recurrence of these families in contemporary studies, as evidenced by the data from the textual corpus.

Figure 4.

Principal Coordinates Analysis (PCoA) of the main botanical host families reported in studies on the isolation of endophytic fungi, based on Bray–Curtis distance.



Source: The points represent botanical families, while the colors indicate the groupings defined by k-means analysis (k = 4). The ellipses represent the confidence regions of the clusters, highlighting patterns of similarity in the composition of the families. The vectors indicate the temporal contribution of the publication years throughout the analyzed period. Data obtained from the Web of Science Core Collection (search performed on January 5, 2026; n = 2325).

The grouping of families with intermediate frequency, such as Anacardiaceae and Euphorbiaceae, suggests an exploratory approach in studies, often associated with bioprospecting for secondary metabolites, investigating endophytic diversity in natural environments, and evaluating potential pharmacological and environmental applications, as discussed by Singh et al. (2023). In contrast, the more isolated position of families such as Pinaceae and Fagaceae may be associated with ecological, geographic, or methodological factors, as well as the lower representation of these families in certain lines of research, as reported by Dos Reis et al. (2023) and Silva et al. (2023).

The displacement of temporal vectors along the ordination suggests changes in the organization of scientific production over the analyzed period, indicating a possible transition from predominantly descriptive studies to more integrated approaches, involving ecology, biotechnology, and sustainable applications. Thus, the PCoA highlights not only the heterogeneity of the botanical host families investigated, but also changes in research patterns over the last decade.

In this context, the distribution of host plants of endophytic fungi presents an asymmetrical pattern, in which a limited number of botanical families concentrate most of the records observed in the textual corpus. The predominance of families such as Poaceae, Fabaceae, Bignoniaceae, Meliaceae, and Asteraceae may be associated with recurring taxonomic biases in the literature, possibly related to the economic, agronomic, forestry, and medicinal relevance of these plants, which are widely used in experimental studies (Table 2).

Table 2. Botanical families and their respective host plants reported in studies on endophytic fungi from 2015 to 2025.

Botanical family	Host plants
Poaceae	*Agrostis stolonifera; Andropogon gerardii; Anthoxanthum odoratum; Arundo donax; Avena fatua; Bambusa vulgaris; Bambusoideae; Bambusoideae (Bamboo); Bouteloua gracilis; Bromus tectorum; Coix lacryma-jobi; Cynodon dactylon; Dactylis glomerata; Distichlis spicata; Eleusine coracana; Elymus repens; Festuca arundinacea; Festuca rubra; Festuca sp.; Hordeum vulgare; Lolium multiflorum; Lolium perenne; Oryza sativa; Panicum virgatum; Paspalum dilatatum; Paspalum vaginatum; Phleum pratense; Phragmites australis; Poa pratensis; Saccharum officinarum; Saccharum sp.; Schizachyrium scoparium; Sorghum halepense; Spartina alterniflora; Spartina sp.; Sweet grass species; Triticum aestivum; Zea mays; Zizania aquatica*
Bignoniaceae	*Adenocalymma sp.; Amphilophium mansoanum; Anemopaegma arvense; Anemopaegma glaucum; Arrabidaea chica; Bignonia binata; Bignonia sp.; Callichlamys latifolia; Campsis radicans; Catalpa bignonioides; Crescentia cujete; Cuspidaria argentea; Cybistax antisyphilitica; Cydista aequinoctialis; Dolichandra unguis-cati; Fridericia chica; Fridericia platyphylla; Handroanthus impetiginosus; Handroanthus sp.; Jacaranda mimosifolia; Kigelia africana; Lundia corymbifera; Macfadyena unguis-cati; Mansoa alliacea; Mansoa hymenaea; Martinella obovata; Pleonotoma variabilis; Pyrostegia venusta; Sparattosperma leucanthum; Spathodea campanulata; Stizophyllum perforatum; Tabebuia aurea; Tabebuia roseo-alba; Tanaecium nocturnum; Tecoma stans; Tynanthus fasciculatus; Xylophragma carvalhoi; Zeyheria montana*
Fabaceae	*Arachis hypogaea; Astragalus membranaceus; Butea monosperma; Cassia fistula; Centrosema pubescens; Cicer arietinum; Crotalaria juncea; Cytisus scoparius; Dalbergia sissoo; Desmodium uncinatum; Gleditsia triacanthos; Glycine max; Glycyrrhiza glabra; Indigofera tinctoria; Laburnum anagyroides; Lens culinaris; Lotus corniculatus; Lupinus albus; Medicago lupulina; Medicago sativa; Melilotus albus; Phaseolus vulgaris; Pisum sativum; Pongamia pinnata; Pterocarpus marsupium; Pterocarpus santalinus; Pueraria lobata; Robinia pseudoacacia; Saraca asoca; Sophora flavescens; Stylosanthes guianensis; Tephrosia purpurea; Trifolium repens; Ulex europaeus; Vigna radiata; Vigna unguiculata*
Meliaceae	*Aglaia odorata; Amoora rohituka; Aphanamixis polystachya; Azadirachta indica; Carapa guianensis; Cedrela odorata; Chukrasia tabularis; Cipadessa baccifera; Dysoxylum binectariferum; Dysoxylum densiflorum; Dysoxylum sp.; Khaya senegalensis; Melia azedarach; Melia dubia; Munronia pinnata; Naregamia alata; Sandoricum koetjape; Soymida febrifuga; Swietenia macrophylla; Toona ciliata; Turraea villosa; Walsura robusta; Xylocarpus granatum; Xylocarpus moluccensis*
Asteraceae	*Ageratina adenophora; Ageratum conyzoides; Arnica montana; Artemisia annua; Atractylodes macrocephala; Baccharis dracunculifolia; Calendula officinalis; Cirsium arvense; Cynara scolymus; Echinacea angustifolia; Echinacea purpurea; Eclipta alba; Helianthus annuus;*

	Lactuca sativa; Matricaria chamomilla; Matricaria recutita; Saussurea costus; Senecio jacobaea; Silybum marianum; Stevia rebaudiana; Tanacetum parthenium
Orchidaceae	*Anacamptis morio; Bletilla striata; Cattleya walkeriana; Cephalanthera damasonium; Cyrtochilum myanthum; Dactylorhiza fuchsii; Dendrobium sp.; Dendrobium spp.; Epipactis helleborine; Goodyera repens; Ludisia discolor; Macodes petola; Neottia nidus-avis; Ophrys apifera; Orchid species; Platanthera bifolia; Scaphyglottis punctulata; Spiranthes spiralis; Stelis superbiens; Vanilla planifolia*
Malvaceae	*Abutilon theophrasti; Adansonia digitata; Althaea officinalis; Bombax ceiba; Ceiba pentandra; Cola nitida; Gossypium barbadense; Gossypium hirsutum; Heritiera fomes; Heritiera littoralis; Hibiscus sabdariffa; Kosteletzkya virginica; Luehea divaricata; Ochroma pyramidale; Sida rhombifolia; Sterculia foetida; Theobroma cacao; Tilia cordata; Tilia sp.*
Myrtaceae	*Campomanesia sp.; Corymbia citriodora; Eucalyptus globulus; Eucalyptus grandis; Eucalyptus sideroxylon; Eucalyptus sp.; Eugenia dysenterica; Eugenia jambolana; Eugenia uniflora; Melaleuca alternifolia; Myrcia sp.; Myrtus communis; Pimenta dioica; Pimenta pseudocaryophyllus; Plinia cauliflora; Psidium guajava; Syzygium aromaticum; Syzygium cumini*
Lamiaceae	*Hyssopus officinalis; Lavandula angustifolia; Lavandula sp.; Melissa officinalis; Mentha aquatica; Mentha piperita; Mentha spicata; Ocimum basilicum; Ocimum sanctum; Origanum vulgare; Plectranthus amboinicus; Premna serratifolia; Rosmarinus officinalis; Salvia miltiorrhiza; Salvia officinalis; Scutellaria baicalensis; Thymus vulgaris*
Zingiberaceae	*Alpinia galanga; Alpinia officinarum; Amomum subulatum; Amomum villosum; Boesenbergia rotunda; Curcuma amada; Curcuma longa; Elettaria cardamomum; Hedychium coronarium; Kaempferia galanga; Zingiber cassumunar; Zingiber montanum; Zingiber officinale; Zingiber zerumbet; Zingiberaceae (6 spp.)*
Amaranthaceae	*Amaranthus caudatus; Arthrocnemum macrostachyum; Atriplex canescens; Atriplex lentiformis; Chenopodium quinoa; Halimione portulacoides; Salicornia europaea; Salsola kali; Spinacia oleracea; Suaeda australis; Suaeda glauca; Suaeda maritima*
Asparagaceae	*Agave americana; Agave tequilana; Asparagus adscendens; Asparagus officinalis; Asparagus racemosus; Chlorophytum borivilianum; Convallaria majalis; Dracaena draco; Polygonatum odoratum; Ruscus aculeatus; Sansevieria trifasciata; Yucca filamentosa*
Pinaceae	*Abies alba; Abies sp.; Larix decidua; Larix kaempferi; Larix sp.; Picea abies; Picea glauca; Picea sp.; Pinus radiata; Pinus sp.; Pinus sylvestris; Pinus tabuliformis*
Rosaceae	*Crataegus laevigata; Crataegus monogyna; Crataegus sp.; Fragaria ananassa; Malus domestica; Prunus dulcis; Prunus persica; Prunus spinosa; Pyrus communis; Rosa canina; Rosa roxburghii; Sorbus aucuparia*
Cupressaceae	*Callitris columellaris; Chamaecyparis obtusa; Cryptomeria japonica; Cunninghamia lanceolata; Cupressus sempervirens; Juniperus communis; Juniperus virginiana; Metasequoia glyptostroboides; Sequoia sempervirens; Taxodium distichum; Thuja occidentalis*
Araceae	*Amorphophallus konjac; Colocasia esculenta; Dracontium spruceanum; Lemna minor; Monstera deliciosa; Philodendron sp.; Pistia stratiotes; Typhonodorum lindleyanum; Wolffia arrhiza; Zantedeschia aethiopica*
Menispermaceae	*Abuta sandwithiana; Anamirta cocculus; Chondrodendron tomentosum; Cocculus hirsutus; Cyclea peltata; Jateorhiza palmata; Menispermum canadense; Stephania tetrandra; Tinospora cordifolia; Tinospora crispa*

Source: Data obtained from the Web of Science Core Collection (search performed on January 5, 2026; n = 2325).

The Poaceae and Fabaceae families are highly represented in the studies analyzed, possibly associated with their importance in agricultural systems and the scientific interest in understanding the role of endophytic fungi in promoting plant growth, stress tolerance, and the sustainability of production systems. In contrast, the lower representation of several botanical families highlights knowledge gaps, especially regarding native plants and groups that are still little explored. This pattern indicates that the endophytic diversity reported in the literature reflects, in part, the direction of scientific investigations, rather than the actual ecological distribution of these microorganisms among different plant groups.

In this context, it is observed that, although scientific production on endophytic fungi associated with plants has advanced consistently over the last decade, structural limitations still persist that should be considered in the interpretation of the results. The taxonomic and geographical concentration of research reveals biases that can influence the representativeness of the knowledge produced, especially when associated with the restrictions inherent in the database used. In this context, it becomes necessary to broaden the taxonomic and geographic scope of investigations, as well as to develop integrative approaches that incorporate different data sources and more robust analytical strategies. This direction is fundamental to reducing existing gaps and enhancing the prospecting of new endophytic fungi and bioactive metabolites of biotechnological interest.

Final Considerations

This study highlights a consistent growth in research on endophytic fungi associated with plants between 2015 and 2025, indicating an expansion of scientific and applied interest in the area, possibly associated with its ecological relevance and the biotechnological potential of these microorganisms. Scientific production was mainly concentrated in China, Brazil, India, and the United States, evidencing the presence of consolidated research centers, while a gradual process of internationalization of the field is observed.

The analysis of host botanical families revealed an asymmetrical pattern of investigation, with a predominance of groups of high economic and medicinal relevance, especially Poaceae, Meliaceae, Bignoniaceae, Zingiberaceae, and Asteraceae, which may be associated with taxonomic biases in the scientific literature. The limited representation of several families indicates possible knowledge gaps and points to opportunities for studies focused on native, endemic, and little-explored plant species, as well as natural ecosystems.

Multivariate analyses indicated that the distribution of host families follows structural patterns in the analyzed literature, associated with scientific trends and temporal dynamics over the period. This pattern suggests changes in research approaches, with a possible transition to more integrative strategies focused on biotechnology and sustainability.

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