

Review

A Bibliometric Review of Global Research Trends in Corticioid Fungi (2016–2025)

Ewelina Bagińska ^{1,*}, Tomasz Oszako ² and Sławomir Bakier ¹¹ Institute of Forest Sciences, Białystok University of Technology, Wiejska 45E St., 15-351 Białystok, Poland² Forest Protection Department, Forest Research Institute, Braci Leśnej 3 St., 05-090 Sękocin Stary, Poland

* Correspondence: e.baginska@pb.edu.pl

Abstract

Corticioid fungi play important ecological roles in forest ecosystems by contributing to wood decomposition, nutrient cycling, and habitat formation. Their simplified morphology has long-complicated taxonomic classification, while molecular phylogenetics has revealed this group to be highly polyphyletic. This bibliometric review assessed global publication trends, research dynamics, and geographical patterns in corticioid fungi research between 2016 and 2025. After duplicate removal and manual screening, 231 publications were retained for analysis. The results showed that original research articles strongly dominate the literature, whereas review papers remain scarce. Publication output peaked in 2021, when integrative taxonomic studies combining traditional morphology and molecular phylogenetic approaches predominated. Geographically, European research centers laid the historical foundations of corticioid fungi research. In recent years, however, Chinese research groups have contributed substantially to the increase in species discoveries and taxonomic revisions, whereas megadiverse regions of Africa and Central and South America remain underexplored due to limited research infrastructure. These findings underscore the importance of international collaboration for advancing research in underexplored regions and enhancing global assessments of fungal biodiversity.

Keywords: corticioid fungi; bibliometrics; molecular phylogenetics; wood decomposition; global research trends; taxonomical review; forest ecosystems

1. Introduction

Fungi play a crucial ecological role in forest ecosystems. Some of them create mycorrhizal associations with plant roots, enhancing their ability to take up vital compounds from the soil [1,2]. In addition to their role in nutrient cycling, fungi create ecological niches for other organisms. By decomposing wood, they soften its structure, allowing birds to create tree cavities [3]. Even old fruiting bodies can provide feeding grounds for invertebrates [4,5]. Tree-parasitic species (e.g., *Phellinus igniarius*, *Inonotus obliquus*) impact the health of forest stands. Although they may seem harmful, they actually accelerate the process of tree generation, creating space for young individuals and increasing species diversity [6]. However, when focusing on corticioid fungi, although the vast majority are saprotrophic, a minor group also exhibits specialized parasitic or mycoparasitic behaviors, as observed within Atheliales (e.g., *Athelia arachnoidea*), Corticiales (e.g., *Laetisaria* sp.), and Tremellales (e.g., *Christiansenia* sp.) [7]. Several species, particularly among the polypores, serve as valuable bioindicators [8–10]—their presence indicates forest continuity



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(e.g., species associated with dead wood in old stands and primeval forests) and the degree of naturalness of the habitat.

Despite their ecological importance, the taxonomic classification of corticioid fungi has long been the subject of intense debate, primarily due to their simplified morphology. Corticioid fungi belong to the class *Agaricomycetes* in the *Basidiomycota* phylum. Mycologists recognize this group as an artificial assemblage of taxa that share similar morphological features of basidia and fruiting bodies, as well as a common methodological approach in taxonomic studies. Most of these fungi develop flattened, inconspicuous fruitbodies on woody substrates, remaining active year-round, with the exception of frosty periods. Corticioid fungi are characterized by effused or effused-reflexed basidiomata with a diverse hymenophore, ranging from smooth to raduloid, while poroid and lamellate forms are specifically excluded [11,12].

The history of research on this group of fungi, dating back to the late 18th century [13], clearly demonstrates how researchers' approaches to classification have evolved over the years. The taxonomic history of corticioid fungi shifted from Chevallier's (1826) [14] broad concept of *Thelephoraceae* to Patouillard's (1900) [15] restriction of this family to mycorrhizal species ("Série des Phylactéries"). To accommodate the remaining resupinate taxa, Herter (1910) [16] established *Corticiaceae*, which was later expanded by Donk (1964) [17] sensu lato to encompass most wood-decaying basidiomycetes with a typically smooth hymenophore [18,19].

Advances in phylogenetic studies based on molecular data have significantly deepened our understanding of fungal evolution. As a result, the traditional use of the name *Corticiaceae* is no longer justified. Genetic studies now allow for a rigorous and precise definition of the family of *Corticiaceae*, rather than treating it as a broad morphological group. Phylogenetic analyses have shown that this group of fungi does not constitute a single evolutionary lineage and is highly polyphyletic. Corticioid fungi have been found to occur in all major evolutionary lineages of the class *Agaricomycetes* and show relationships with almost all classical morphological groups. Due to their wide evolutionary distribution, corticioid fungi play a key role in understanding the evolution of homobasidiomycetes. Some evolutionary analyses even suggest that the ancestor of all homobasidiomycetes may have been a corticioid fungus, although this hypothesis remains debated [18].

The primary objective of this review is to evaluate the current status and visibility of corticioid fungi within modern mycology. Despite their fundamental role in forest carbon cycling and wood decomposition, this group has often been perceived as taxonomically challenging and less charismatic than gilled or poroid mushrooms. This study aims to determine whether scientific interest in corticioid fungi continues to grow or whether they remain comparatively underrepresented in contemporary biological research.

Specifically, the review seeks to:

1. **Assess Publication Dynamics:** by analyzing the volume of scientific output between 2016 and 2025, we aim to identify whether there is an upward trend in publications. An increase in the number of papers would indicate a growing research potential and a renewed interest in the ecological and taxonomic significance of this group.
2. **Identify Global Leadership:** the study will map the geographical distribution of research productivity to identify which countries (by affiliations) are currently leading the field. This allows for a clear visualization of where the expertise is concentrated and which regions are shaping the global knowledge on corticioid fungi.

This comparison is not intended to critique regional pace, but rather to identify untapped opportunities for further mycological exploration and international collaboration.

3. Identify Current Trends and Future Directions: based on monitoring leading journals and analyzing the themes that dominate most articles, the study will highlight the future perspective of the field.

Ultimately, this review serves as a diagnostic tool to demonstrate that corticioid fungi are a dynamic and evolving field of study, deserving continued investment and scientific attention.

The period 2016–2025 was intentionally selected to capture the most recent decade of corticioid fungi research, characterized by the widespread adoption of molecular phylogenetic methods, rapid growth of sequence databases, and increasing use of integrative taxonomic approaches. The study was designed to assess contemporary developments rather than provide a historical review of the field.

2. Methodology

2.1. Search Strategy and Data Sources

Bibliographic data were collected from the Web of Science Core Collection (WoSCC) and Scopus databases. Searches were conducted using title, abstract, and keyword fields in Scopus and the Topic (TS) field in WoSCC, which encompasses these fields.

2.2. Keywords

The search strategy combined both contemporary taxonomic terminology and traditional descriptors commonly used in the literature on corticioid fungi. The following search terms were applied: “corticioid fungi”, “resupinate fungi”, “crust fungi” and “Aphyllophorales”. Although additional searches using selected genus names could retrieve further publications, broad group-level terms were deliberately used to identify studies explicitly referring to corticioid fungi as a collective research subject.

The query was implemented using Boolean operators in both databases.

2.3. Eligibility Criteria

Publications were selected according to the following criteria:

- (1) Publication period: studies published between 2016 and 2025, including early-access articles. The selected period was intended to capture the most recent decade of corticioid fungi research and to assess contemporary developments associated with modern molecular approaches.
- (2) Document type: original research articles, review papers, books, and book chapters. Editorials, conference abstracts, meeting reports, and book reviews were excluded.
- (3) Subject scope: studies focusing on corticioid fungi, including taxonomy, morphology, phylogeny, ecology, environmental significance, and bioactive compounds.
- (4) Language: no language restrictions were applied, as relevant non-English publications could be assessed using translation tools. However, the final dataset was dominated by English-language articles.

2.4. Data Screening and Selection

Although this study is designed as a bibliometric review rather than a formal systematic review, the literature selection process (Figure 1) was structured following the general reporting logic of the PRISMA 2020 (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines to ensure transparency, objectivity, and reproducibility.

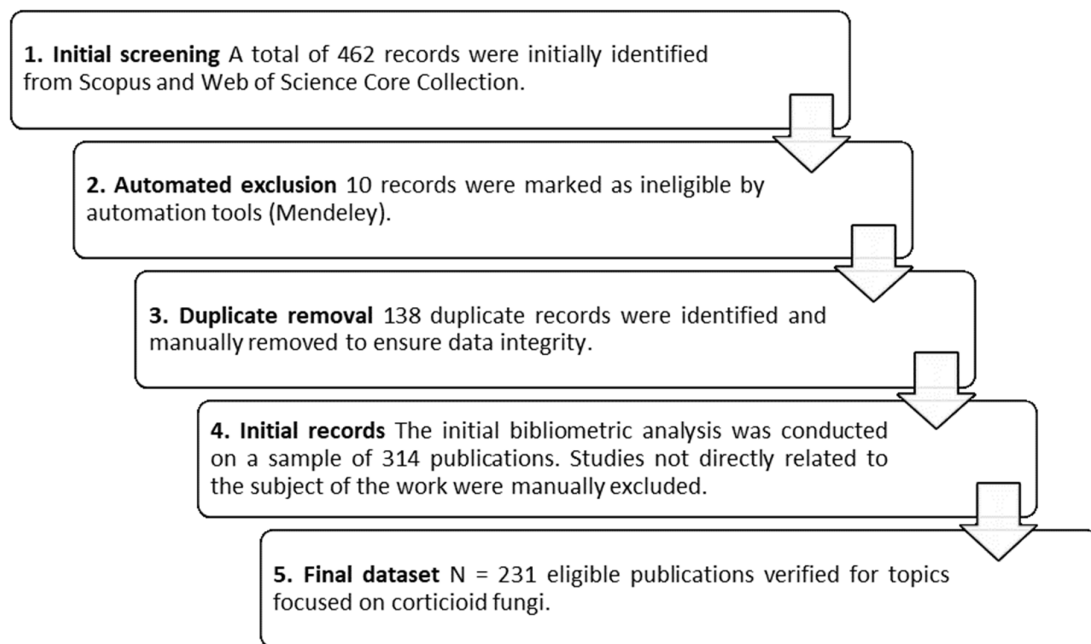


Figure 1. Flowchart of the data selection process.

File *PRISMA_2020_checklist* is provided in the Supplementary Materials.

Records retrieved from WoSCC and Scopus were exported to Mendeley Reference Manager. Automated screening identified 10 ineligible records, which were removed prior to duplicate checking. Subsequently, 138 duplicate records were eliminated, resulting in a dataset of 314 publications.

The search strategy included the term *Aphylllophorales*, which encompasses a broad range of non-gilled macrofungi with diverse morphologies, including corticioid and poroid fungi. Consequently, the initial dataset contained several records that fell outside the primary scope of this study.

All remaining records were manually screened by the first author based on titles, abstracts, and, when necessary, full-text content. Ambiguous records were discussed with the co-authors before final inclusion or exclusion. Articles not directly related to corticioid fungi (e.g., focusing exclusively on strictly poroid species such as *Ganoderma* or *Trametes*) were removed from the final dataset. Uncertainties regarding the taxonomic placement of species within corticioid fungi were resolved using key taxonomic references [7,11,20,21]. The final dataset of 231 publications used for the bibliometric analysis, obtained after manual selection, is attached as Supplementary Material (file named *Data after manual selection*). Selection procedure is summarized in Figure 1.

2.5. Bibliometric Analysis

The final dataset was analyzed to assess publication dynamics, document types, journal distribution, and geographical patterns of scientific productivity. Descriptive bibliometric indicators were calculated based on publication counts and author affiliations.

2.5.1. Co-Authorship Network Analysis

The co-authorship network was constructed and visualized using VOSviewer (version 1.6.20). To ensure maximum clarity, legibility, and substantive interpretability, the network generation process underwent deliberate parametric optimization. First, a minimum threshold of 4 publications per author was applied. Restricting the analysis to researchers with at least 4 documents during the studied period filtered out incidental contributors and reduced informational noise, thereby focusing the network on key, consistently active

representatives of the field. Second, a minimum link strength threshold of 2 was established, ensuring that connections represent at least two co-authored publications.

To optimize the spatial layout of the graph, we tested several visualization configurations and refined the default parameters: the attraction was set to 2 and the repulsion force was increased to -8 . This stronger repulsion physically expanded the network structure and improved cluster separation, effectively resolving label overlap and ensuring full readability even within smaller nodes. Node sizes correspond to overall publication output, while line thickness indicates the strength of collaborative links.

2.5.2. Publication Output by Affiliation Analysis

Item density visualization of regions based on affiliations (Figure 2) was visualized using VOSviewer (version 1.6.20). A minimum threshold of two publications per region was applied, resulting in a total of 38 included in the final analysis. For layout optimization, the attraction parameter was set to 4 and repulsion to -1 . In the density visualization, node sizes were weighted by publication volume (number of documents), using the item density display mode.

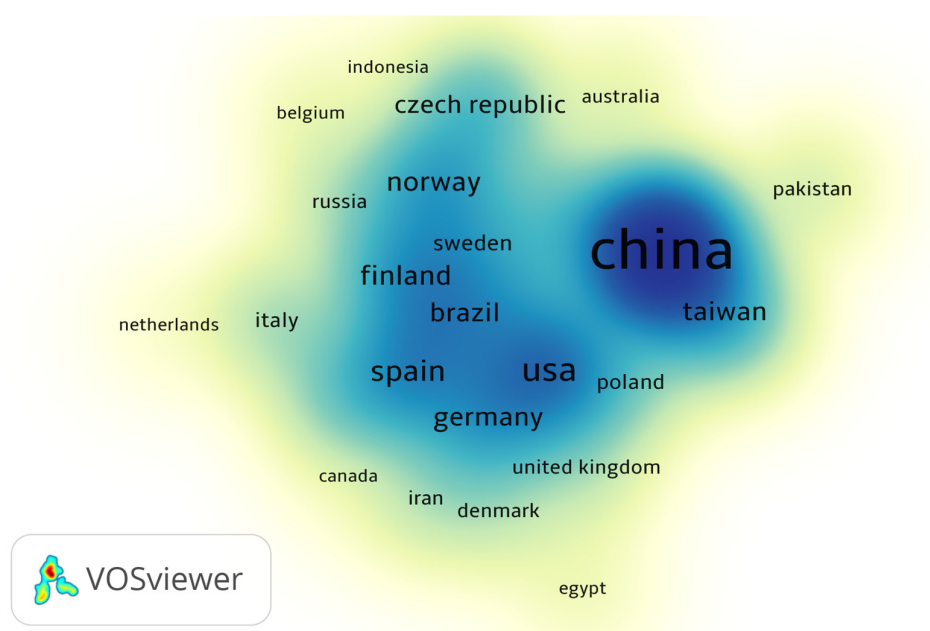


Figure 2. Density map of publication output by affiliation. Font size and color intensity reflect the total number of publications produced by authors from each region.

3. Results

3.1. Raw Data

A quantitative summary of the bibliographic records identified in the Web of Science and Scopus databases, broken down by document type, is provided in Table 1.

The search identified 216 records in WoSCC and 246 records in Scopus. In both databases, original research articles accounted for the vast majority of records. Research articles represented 97.2% of all Scopus records (239 publications) and 99.1% of all WoSCC records (214 publications). The share of review articles and book chapters is marginal in both. The WoSCC database recorded only 1 for each of these document types. In Scopus, these figures are slightly higher (3 reviews and 4 book chapters), which confirms the database's higher sensitivity to monographic and non-journal literature.

Table 1. Distribution of retrieved publications by document type in the WoSCC and Scopus databases (2016–2025).

Document Type	WoSCC	Scopus	Total Raw Records	Deleted Duplicates (Mendeley/Manually)	Unique Records
Article	214	239	453	10/136	307
Review	1	3	4	0/2	2
Book Chapter	1	4	5	0/0	5
Total Records	216	246	462	10/138	314

3.2. Results After Manual Selection

After automated screening, duplicate removal, and manual assessment, 231 publications were included in the final dataset. Of these, 98.3% (227 papers) were original research articles, whereas only two books and two review articles were identified. This distribution highlights the scarcity of synthetic publications within the field.

All 138 duplicate records were identified across the two databases (inter-database overlap), highlighting the specific level of coverage shared between WoSCC and Scopus.

3.2.1. Publication Dynamics

Research interest in corticioid fungi changed markedly over the last decade. The total number of publications indexed annually in the Web of Science and Scopus databases was subject to significant fluctuations, demonstrating considerable year-to-year variability rather than a consistent temporal trend (Figure 3).

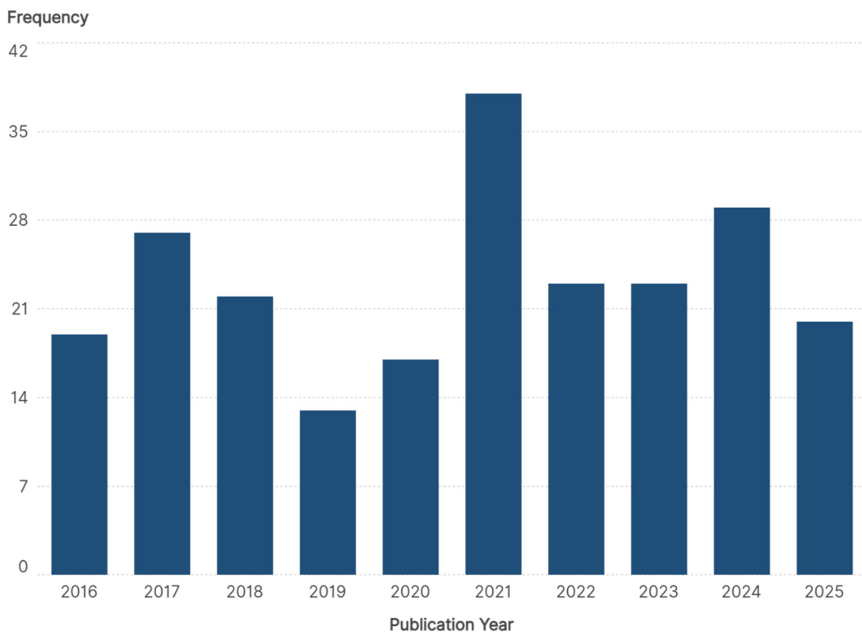


Figure 3. Annual publication output on corticioid fungi indexed in the WoSCC and Scopus databases between 2016 and 2025. Source: created using Scimago Graphica Beta 1.0.55.

In the initial period, a sharp increase in the number of articles was recorded, rising from 19 in 2016 to 27 in 2017. Over the following two years, scientific productivity gradually declined, reaching the lowest point of the decade in 2019. However, immediately after this decline, research activity distinctly resurged, culminating in 2021 with a record 38 papers published. After this peak, between 2022 and 2023, publication volume stabilised at 23 articles per year. A renewed surge in interest occurred in 2024, when the number

of publications reached 29, matching the previous high from 2017. The analysed period concludes in 2025 with a noticeable drop to 20 published papers.

3.2.2. Co-Authorship Network Analysis

The presented co-authorship network (Figure 4), generated using VOSviewer software, illustrates the structure of scientific relationships and the dynamic temporal evolution of publications within the studied field.

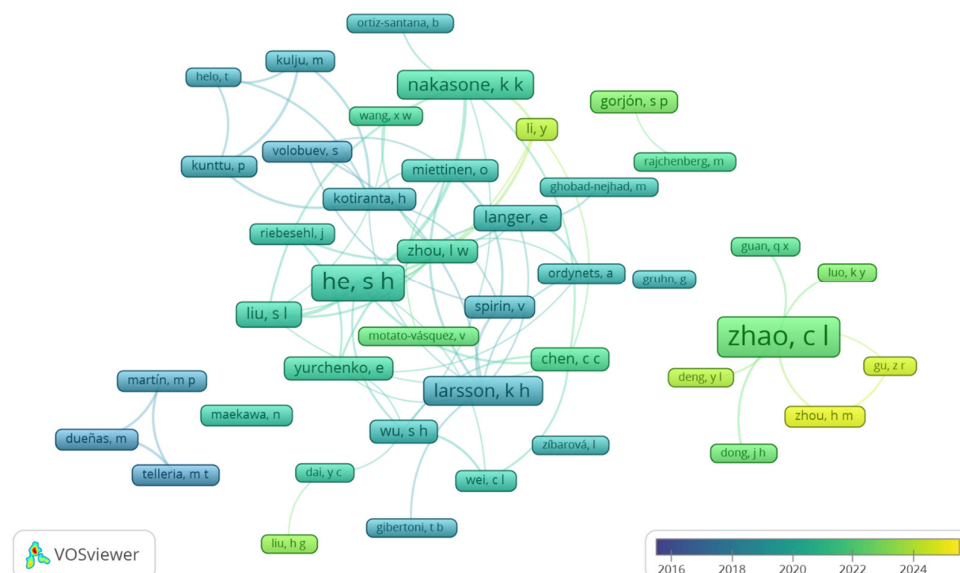


Figure 4. Overlay visualization of the co-authorship network. Node size corresponds to publication output, whereas colors indicate the period of highest research activity, from earlier (dark blue) to more recent (yellow) publications.

The size of the nodes (representing individual authors) corresponds to the volume of their publication output. The distance between researchers reflects the strength of their collaborative relationship: a shorter distance indicates a higher frequency of co-authorship, while a greater distance signifies a weaker or non-existent direct link between researchers. The colours visualize the average publication year (according to the chronological scale from 2016 to 2025).

3.2.3. Most Productive Journals

A key element of bibliometric analysis is identifying the leading journals (so-called core journals) that shape the dissemination of knowledge within a given discipline. Mapping source titles not only reveals the publishing preferences of researchers but also highlights the periodicals that exert the greatest influence on the advancement of knowledge regarding corticioid fungi. The result of this analysis is presented in Figure 5.

More than half of all examined records (58.87%) are concentrated within a narrow group of ten key specialized journals. Taxonomic and systematic periodicals, such as *Phytotaxa*, *MycoKeys*, and *Mycological Progress*, play a dominant role here. The strong position of these journals confirms a modern developmental trend in the field, emphasizing rapid information dissemination and open access to descriptions of new taxa as well as revisions of those already known to science. The remaining 41.13% of papers were published across a broad spectrum of other journals (categorized as “Other”), where the number of publications covering corticioid fungi was five or fewer.

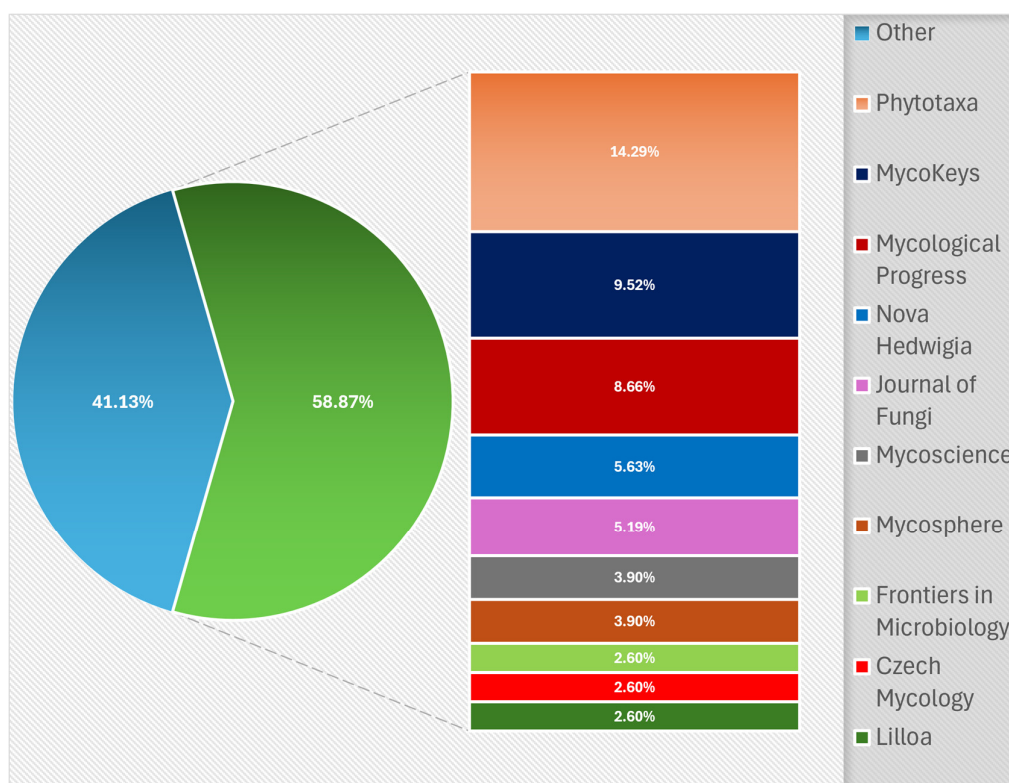


Figure 5. Most productive journals in the analyzed literature dataset. The pie chart presents the proportion of publications concentrated within the ten most productive journals (58.87%) relative to all remaining 10 sources (41.13%). The adjacent chart expands the core-journal category and presents the contribution of individual journals. Source: own study based on data from Scopus and WoSCC databases.

3.2.4. Most Cited Publications

To identify the publications that have exerted the greatest influence on the development of research on the studied group of fungi, a subset of the 20 most cited articles was selected from the primary database of 231 publications (Table 2).

By far the most influential article in the analyzed dataset was the publication by [1], which dominated the bibliometric ranking with 333 citations—more than double the second most cited record (141 citations). Such a high citation count strongly underscores its status as a benchmark paper in modern mycology. The inclusion of this publication in the review is justified by its groundbreaking significance for the taxonomy of both major morphological groups within the *Polyporales*. Although the study largely focuses on polyporoid fungi, further analysis reveals that it also formally defines and characterizes families (e.g., *Phanerochaetaceae*, *Irpicaceae*), where corticioid species either constitute the vast majority or intermix with polyporoid forms. By combining multigene phylogenetic analyses with the reconstruction of anatomical traits, the authors established a coherent classification for the order and delineated family boundaries that encompass corticioid fungi.

A substantial share of the most cited publications is represented by systematic revisions of higher taxa (e.g., *Polyporales*, *Atheliales*) and multigene phylogenetic analyses. A significant proportion of studies addressing regional biodiversity highlights the growing importance of describing new wood-decay species for modern mycology. This citation profile proves that stabilizing systematics and ensuring precise species identification provide a critical foundation for further ecological and applied research.

Table 2. Most frequently cited publications among the papers included in the bibliometric analysis.

No.	Citation Count	Journal Name	Reference
1.	333	Fungal Biology	[22]
2.	141	Mycolog	[23]
3.	121	Mycosphere	[24]
4.	94	Fungal Diversity	[25]
5.	67	Mycologia	[26]
6.	65	Journal of Fungi	[27]
7.	57	Mycobiology	[28]
8.	55	Mycological Progress	[29]
9.	45	MycoKeys	[30]
10.	42	Frontiers in Microbiology	[31]
11.	40	Bioresource Technology	[32]
12.	38	Frontiers in Microbiology	[33]
13.	35	Fungal Biology	[34]
14.	34	Mycosphere	[35]
15.	34	Fungal Biology	[36]
16.	34	Mycological Progress	[37]
17.	33	MycoKeys	[38]
18.	33	IMA Fungus	[39]
19.	32	Botany	[40]
20.	30	MycoKeys	[41]

4. Discussion

This review provides a comprehensive overview of global publication trends in corticioid fungi research during 2016–2025. To the best of our knowledge, our study addresses this gap and provides a novel contribution as the first bibliometric analysis tailored specifically to corticioid fungi. Existing bibliometric reviews in the literature generally concentrate on broad functional groups or specific applications, such as the biotechnological use of white-rot fungi [42] or the role of specific taxa in ecosystem processes (e.g., arbuscular mycorrhizal fungi) [43].

Furthermore, bibliometric data on wood-decay fungi research highlight its strong interdisciplinary nature, with Forestry emerging as one of the leading research disciplines alongside applied biotechnology, environmental sciences, and wood material science. This reflects the dual interest in these organisms-both as critical drivers of forest ecosystem functioning and as subjects for applied forestry management and wood protection.

Our bibliometric analysis reveals the evolution of research interest in corticioid fungi group, characterized by an initial steady increase in publication output, a pronounced peak in 2021, and subsequent stabilization. Among the 38 analyzed publications from 2021, an integrative approach clearly dominates, combining traditional taxonomy with modern molecular biology tools. Only five studies relied exclusively on classical morphological criteria without incorporating genetic analyses. Most publications were based on molecular phylogenetic methods and focused on the description of new species, documentation of new regional records, or taxonomic revision of problematic groups.

The increase in publications related to fungal phylogenetics and ecology identified in the bibliometric analysis likely reflects methodological advances and the widespread standardization of next-generation sequencing (NGS) and third-generation sequencing technologies, including nanopore platforms. The transition from conventional Sanger sequencing to high-throughput metabarcoding has transformed fungal research, including studies of corticioid fungi that are difficult to identify using morphological methods alone [44–46]. Large-scale sequencing of environmental DNA (eDNA) from substrates such

as soil and deadwood has enabled a comprehensive exploration of microbial communities, contributing to the rapid growth of published research.

The analysis further demonstrated that phylogenetic approaches based on the rRNA ITS, 28S, EF1 α , RPB1, and RPB2 loci played a central role throughout the study period, becoming the standard for species delimitation and reconstruction of evolutionary relationships in corticioid fungi. In studies of fungal diversity and community structure, the choice of molecular markers is critical. The internal transcribed spacer (ITS) region of ribosomal DNA is widely accepted as the universal DNA barcode for fungi [47,48]. Its broad application stems from high amplification success, rapid evolutionary rate, substantial interspecific variation, and extensive representation in reference databases such as UNITE and GenBank [44,49–51].

In addition to ITS, several complementary markers improve phylogenetic resolution and analytical robustness. These include ribosomal regions such as the 28S large subunit (LSU) rRNA gene, as well as informative protein-coding loci. The latter comprise RPB1 and RPB2, encoding the largest and second-largest subunits of RNA polymerase II, respectively, and EF1 α , encoding translation elongation factor 1-alpha [47,51,52].

The analyzed literature is dominated by specialized journals with a strong taxonomic and evolutionary focus, particularly those dedicated to the description of new taxa and phylogenetic revision of fungal groups (e.g., *Phytotaxa* and *MycKeys*). A smaller, yet still substantial, proportion of studies was published in interdisciplinary journals or journals covering broader aspects of mycology. These publications less frequently address taxonomy alone and more often investigate ecology, biodiversity, physiology, and the applied importance of fungi, including their roles in forestry (e.g., wood decomposition) and agriculture.

This pattern suggests that species inventories and systematic revisions have remained the dominant research direction over the last decade, consistent with the high frequency of new species discoveries reported from East Asia. At the same time, the literature demonstrates a clear shift toward integrative taxonomy, in which molecular markers and morphological characters function as complementary and indispensable tools. Their combined application is essential for accurate species delimitation and taxonomic description [53,54].

A marked increase in research activity by Chinese authors during 2022–2025 is evident from the bright-yellow-green and yellow nodes shown in Figure 4. The clear leader, represented by the largest node in the network and serving as the core of a distinct research cluster, is Changlin Zhao. According to [55], Chinese mycologists described 20,826 new fungal taxa, of which approximately 65% were published during the last decade. Publication output increased rapidly from 2020 onward and has continued to rise steadily. Authors [55] further emphasized that the majority of fungal research conducted by Chinese scientists focuses on *Basidiomycota*, including wood-inhabiting taxa.

The increasing contribution of Chinese researchers appears to be closely associated with the rapid expansion of the national mushroom industry. The growing economic importance of fungi has been accompanied by sustained investments in taxonomic research, scientific infrastructure, and biodiversity inventory programs. The emergence of mushroom cultivation as the fifth-largest agricultural sector in China [56] has created a strong economic incentive for research on edible and medicinal macrofungi, thereby stimulating scientific interest in fungal diversity and systematics.

This development has been further supported by large-scale national initiatives, including the incorporation of fungi into the Catalogue of Life China project and the establishment of the Checklist of Fungi in China database. Owing to China's exceptionally rich flora, comprising more than 40,000 plant species, and based on the currently accepted estimate of approximately 10 fungal species per plant species [54,57], the country's fungal diversity

may reach as many as 400,000 species [55]. Such a vast and still incompletely explored mycobiota provides substantial opportunities for taxonomic discovery and likely contributes to the growing volume of fungal research, including studies on corticioid fungi.

Crucially, our findings align with the broader trends observed across mycological research. For instance, a bibliometric overview [58] of wood-decay fungi research spanning 1913–2020 demonstrated that scientific productivity is heavily concentrated in Northern Europe, the USA, and China, highlighting significant geographic disparities and the relative underrepresentation of tropical regions.

The co-authorship network demonstrates that the development of this research field is driven not only by the high productivity of individual authors but also by extensive collaborative relationships. A particularly prominent role is played by Shuang-Hui He, whose central position and numerous connections to other researchers suggest that this author serves as a bridge between collaboration clusters within the field. The network surrounding Shuang-Hui He encompasses both well-established researchers and authors whose publication activity has intensified in recent years. Furthermore, the links connecting researchers from China, Europe (Karl-Henrik Larsson, Norway), and North America (Karen K. Nakasone, USA) highlight the highly international character of corticioid fungi research and underscore the growing importance of intercontinental scientific collaboration.

The literature survey also identified several key researchers and research centers in Northern and Central Europe. Temporal visualization of the co-authorship network (dark-blue and turquoise nodes in Figure 4 suggests that their most influential publication period occurred predominantly before 2020. Notable contributors include K.-H. Larsson, E. Langer (Germany), E. Yurchenko (Belarus, Poland), and the Finnish mycologists O. Miettinen and H. Kotiranta, with additional contributions from V. Spirin (Norway, Finland) and S. Volobuev (Russia). European research institutions played a pivotal role in establishing the foundations of corticioid fungi research and continue to provide the taxonomic framework upon which the discipline is built, as documented both by the present bibliometric analysis and previous studies [55,59]. Among the most influential references is the multi-volume monograph series *The Corticiaceae of North Europe* [60–67], which remains a cornerstone of corticioid fungi taxonomy. This historical foundation and sustained scientific impact, continuing right up to the present day, are clearly mirrored in the region-density publication map (Figure 2), which reveals dense research clusters across Northern and Central European nations, particularly Norway, Finland, Sweden, Spain, Germany, and Poland. Together with China and the USA, these nodes represent the primary centers of global publication activity in corticioid mycology.

According to [68], the majority of corticioid fungi are associated with deadwood, including trunks and branches. At least 80% of species cause white rot through lignin degradation, whereas approximately 5% cause brown rot by decomposing cellulose. The remaining species are either mycorrhizal or involved in the decomposition of plant litter. The spatial distribution of deadwood in European forests [69] suggests that these ecosystems may represent an underappreciated hotspot of corticioid fungi diversity. As deadwood constitutes the primary substrate for many species, regions characterized by high deadwood volumes warrant particular research attention.

Southern and eastern Poland, the Czech Republic, and Slovakia are distinguished by exceptionally high deadwood stocks, frequently reaching up to 100 m³/ha [69]. This pattern largely coincides with the Carpathian arc and the Sudeten mountain ranges. Similarly, substantial deadwood resources occur in the southern Alpine regions of Germany and across the Baltic states, including Estonia, Latvia, and Lithuania [69]. Importantly, the abundance of woody substrates reflects not only conservation-oriented forest management and biodiversity protection measures, but also the increasing effects of climate change.

Prolonged droughts and large-scale forest dieback events, including extensive outbreaks of the spruce bark beetle (*Ips typographus*), have substantially increased the availability of deadwood. These disturbances expand habitat resources for wood-decaying fungi, including facultative pathogens, and have stimulated European research groups to undertake new biodiversity surveys and long-term monitoring programs.

Despite a long history of investigation (e.g., [6,70–77]), European forest ecosystems continue to offer considerable potential for the discovery of previously undocumented taxa and for further taxonomic refinement of known corticioid fungi.

Among the publications analyzed, only seven addressed the African continent. Nevertheless, vast tropical regions, including the Neotropical zone of Central and South America and sub-Saharan Africa, remain severely underexplored with respect to fungal diversity and are believed to harbor a large reservoir of undescribed taxa [78–80]. Available estimates suggest that South Africa alone may support up to 200,000 fungal species [81], while the African continent accounts for more than 25% of global macrofungal diversity [82]. Central Africa is considered a particularly important biodiversity hotspot due to its high heterogeneity of landscapes, vegetation types, and soils [83]. However, mycological research in the region is constrained by a lack of specialized institutions, limited scientific infrastructure, and shortages of trained personnel, local experts, and educational programs [83,84].

As noted by [85], the poor understanding of fungal diversity in tropical regions is largely attributable to the scarcity of long-term research programs. This limitation stems primarily from disparities in financial resources between researchers working in temperate regions and those in tropical countries. Consequently, areas characterized by low publication output may still contain substantial undocumented fungal diversity.

Overall, the bibliometric patterns identified in this study indicate that future advances in corticioid fungi research will rely on the integration of advanced molecular approaches with strengthened international collaboration. Local partners could support international researchers by providing travel logistics, obtaining permits for sample collection and export, and maintaining a continuous field presence. Dedicated local parataxonomists, while stationed in research areas, would play a pivotal role in year-round biological sampling across all forest types. This would allow for the generation of unique phenological and ecological data that would otherwise be unattainable through short-term visits by foreign teams.

In return, international partners could offer specialized expertise by conducting field and university training for parataxonomists and students, as well as providing scientific infrastructure. Access to international reference collections, key publications, and identification keys would be essential for precise taxonomic identification of samples. Furthermore, foreign partners could provide valuable support in the publication process and the dissemination of results. Additionally, international institutions could ensure long-term maintenance, digitization, and curation of collections in the event of local financial depletion.

An example of such collaboration-highlighted alongside other successful initiatives in [86]-is the project *The Costa Rican National Fungal Inventory* (1999–2005). International research involving Costa Rican institutions resulted in the collection of materials that were subsequently divided and deposited at the Field Museum in Chicago (USA) and the New York Botanical Garden (USA), where they were cataloged and digitized.

Another fruitful example of international collaboration, focused on botany and biodiversity conservation, involves the partnership between Guinea (West Africa) and international institutions including the Royal Botanic Gardens, Kew (UK) and Ghent University (Belgium) [83]. This joint initiative aimed to establish a national herbarium, organize long-term field exploration programs, and provide academic training-including Master's and PhD programs, and the identification of Tropical Important Plant Areas (TIPAs) [87].

Expanding research efforts into biodiversity-rich yet under-sampled regions has the potential to substantially improve current estimates of fungal diversity and foster a more balanced global understanding of fungal evolution, taxonomy, and ecology.

5. Study Limitations

Several limitations of the present study should be acknowledged. First, the analysis was restricted to the period 2016–2025, which was intentionally selected to capture recent developments in corticioid fungi research and the growing influence of molecular approaches. Consequently, the results do not fully reflect the historical development of the field, particularly the profound taxonomic changes initiated during the early DNA era in the mid-1990s. Second, the bibliometric dataset was generated using a limited set of broad search terms. Although these keywords were chosen to identify publications explicitly addressing corticioid fungi as a research group, some relevant studies may have been omitted because they focused primarily on individual genera or species and did not include the selected umbrella terms in their titles, abstracts, or keywords. Third, the study focused on publication output and collaboration patterns rather than on comprehensive citation-based metrics, which may provide additional insights into scientific influence and knowledge dissemination. Finally, the relatively small number of retrieved publications reflects not only methodological constraints but also the cryptic and frequently overlooked nature of corticioid fungi themselves. Many species produce inconspicuous mycelia and fruiting bodies, and their diversity remains insufficiently documented in many regions of the world. Therefore, the presented results should be interpreted as a contemporary overview of visible research activity rather than a complete representation of the global knowledge on corticioid fungi. Future studies should incorporate a broader range of search terms, additional bibliometric indicators, and a longer temporal framework, ideally covering approximately three decades, to provide a more comprehensive assessment of research development in this field.

6. Conclusions

The bibliometric trends identified here provide a framework for understanding the current state of corticioid fungi research and for identifying geographic and thematic priorities for future investigations.

Although traditional European research centers established the foundations of corticioid fungi studies, recent years have been characterized by a quantitatively dominant contribution from Chinese research groups, particularly in the discovery and description of new taxa. Nevertheless, European forests remain an important reservoir of deadwood, providing extensive and diverse substrates that support corticioid fungi and sustain opportunities for further taxonomic and ecological research. In contrast, megadiverse regions such as Africa remain insufficiently explored because of limited scientific infrastructure and a shortage of local specialists. In this context, international collaborations represent a promising strategy for advancing fungal research. Such partnerships could combine European taxonomic expertise with biodiversity-rich but under-sampled regions, thereby accelerating the documentation and estimation of global fungal diversity.

Molecular approaches have become an integral component of contemporary mycological research. However, the present review demonstrates that modern fungal taxonomy cannot rely on molecular data alone. Phylogenetic analyses and traditional morphological investigations should be regarded as complementary rather than alternative approaches. Their integration enables robust species delimitation and taxonomic classification, with each method providing essential validation of the other.

The continuing expansion of global reference databases, such as UNITE, together with the growing number of deposited sequence records, is expected to further advance mycological research. Increased accessibility of molecular data will facilitate new species discoveries and taxonomic revisions within corticioid fungi and may stimulate a renewed surge in research activity comparable to that observed during the publication peak in 2021.

Finally, the scarcity of review papers identified in the dataset indicates a need for more synthetic studies integrating taxonomic, ecological, phylogenetic, and biogeographical knowledge. Such reviews may facilitate knowledge transfer between research groups and provide a stronger framework for future biodiversity assessments.

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