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ARTICLE

Global fungal diversity and distribution patterns within the order Hymenochaetales (Agaricomycetes, Basidiomycota)

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Abstract

The taxonomy and phylogeny within the order Hymenochaetales have advanced considerably worldwide, however, knowledge of their global fungal diversity and distribution patterns remains limited. In this study, we compiled a checklist of Hymenochaetales using the Fungal Names Database, and validated the records with MycoBank, Index Fungorum, and authoritative literatures. The result revealed that Hymenochaetales comprises 1,651 species belonging to 101 genera across 18 families, with 25 genera classified as incertae sedis. Among these taxa, the family Hymenochaetaceae has the greatest species richness, encompassing 44 genera and 973 species, which account for 59.12% of all species in the order. The most species-rich genera were *Hymenochaete*, *Xylodon*, *Fuscoporia*, *Inonotus*, *Phylloporia*, *Fulvifomes*, *Fomitiporia*, *Coltricia*, *Lyomyces*, and *Tropicoporus*. At the continental scale, Asia exhibited the highest species richness, while Africa had the lowest. The number of families, genera, and species shared across the six continents showed a decreasing trend, with Europe and North America displaying the highest similarity, whereas Asia and South America exhibited the lowest. Across climate zones, species richness was highest in temperate zones, followed by tropical, subtropical, and boreal zones. Distribution patterns of Hymenochaetales species across four climatic zones on the six continents demonstrated three main trends: 1) dominance of temperate species, 2) dominance of tropical species, and 3) continuous distributed from temperate to tropical regions. Morphologically, the species were primarily poroid, followed by corticioid, hydnoid, and others. Overall, this study provides a comprehensive overview of the global diversity and distribution patterns of the order Hymenochaetales, offering a valuable foundation for resource utilization and ecological conservation.

Keywords – Corticioid and hydnoid fungi – Hymenochaetaceae – Macrofungi – Polypores – White-rot – Wood-inhabiting fungi

INTRODUCTION

Fungi, the second largest group of organisms on Earth, inhabit an extraordinary range of environments, from the stratosphere to the depths of the Dead Sea, and from Antarctic glaciers to

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scorching deserts. They play indispensable roles in ecosystems as saprotrophs, symbionts (including ectomycorrhizal, ericoid, endophytic, and lichenized fungi), and as pathogens of plants and animals (Lutzoni et al. 2018, Wu et al. 2022a, 2022b, Zhao et al. 2023a, 2023b, Abrego et al. 2024, Bao et al. 2025, Deng et al. 2025a, Hibbett et al. 2025, Hongsanan et al. 2025, Lin et al. 2025, Samaradiwakara et al. 2025). And they are also vital to human life, contributing significantly to food production, medicine, healthcare, and industry (Dai & Yang 2008; Dai et al. 2010, Si et al. 2011, Wang et al. 2013, Wu et al. 2016, Cui et al. 2018, Niego et al. 2023, Barua et al. 2024, Pawłowicz et al. 2024). Despite their ecological and economic importance, fungal diversity remains strikingly underexplored. Current estimates of global fungal species richness vary widely, ranging from 0.5 million to 12 million species (Hawksworth & Lücking 2017, Bhunjun et al. 2022, Niskanen et al. 2023). To date, more than 160,000 fungal species have been formally described and classified (https://nmdc.cn/fungalnames/), representing only about 5% of the conservative estimate, implying that the vast majority of fungal diversity is still unknown (Hibbett et al. 2025). Furthermore, with the increasing use of molecular tools in taxonomy, the annual number of newly described species has risen from approximately 1,000 to over 3,000 in recent years (Bhunjun et al. 2022, Hibbett et al. 2025). These findings underscore both the vast number of fungal species yet to be discovered and continued importance of discovering and descripting new fungal taxa as a central, long-term goal for mycologists.

The order Hymenochaetales, belonging to the class Agaricomycetes within the phylum Basidiomycota, was established by Oberwinkler in 1977, with *Hymenochaete* designated as the type of genus (https://indexfungorum.org/). This order is species-rich and represents one of the major groups of wood-inhabiting fungi, characterized by diverse morphologies and a wide range of host plants (Figure 1, Wu et al. 2022b, Liu et al. 2025a). The biggest fungus in the word, *Phellinus ellipsoideus* (B.K. Cui & Y.C. Dai) B.K. Cui, Y.C. Dai & Decock, belongs to this order (Dai & Cui 2011). The majority of Hymenochaetales species are wood-decaying fungi that cause white rot (Wu et al. 2022b, Liu et al. 2025a). Some species are pathogenic to a broad range of tree hosts, and a small number are capable of forming ectomycorrhizal associations with trees (Tedersoo et al. 2007, Wu et al. 2022b, Yuan et al. 2023, Zhao et al. 2023a). In addition, some Hymenochaetales species are renowned for their medicinal value, such as *Sanghuangporus sanghuang* (桑黄) and *Inonotus obliquus* (桦树茸) (Zheng et al. 2011, Wu and Dai 2020, Szychowski et al. 2021, Wang et al. 2023a, Yang et al. 2023, Ghobad-Nejhad et al. 2024).

In recent years, significant advances have been made in the studies of Hymenochaetales, particularly in the areas of taxonomy, phylogeny, evolutionary origins, multi-omics, and resource utilization (Cui et al. 2011, Zhou et al. 2016a, 2016b, Miettinen et al. 2019, Wu et al. 2022b, Zhao et al. 2023a, 2025a, Zhou et al. 2023, Cho et al. 2024, 2025, Ghobad-Nejhad et al. 2024, Liu et al. 2025a). For example, systematic revision of both poroid (Wu et al. 2022b) and non-poroid (Liu et al. 2025a) species in the family Hymenochaetaceae resulted in the recognition of seven genera and 81 species. Moreover, new species from other families, especially in Schizoporaceae, within Hymenochaetales have been proposed based on combined morphological, phylogenetical, and molecular dating evidence (Guan et al. 2023, Zhou et al. 2023, Cho et al. 2024, Viner et al. 2024, Zhang et al. 2025a).

In the past decades, the documented diversity of Hymenochaetales has increased rapidly, driven by expanded specimen collections from diverse geographic regions and continued advances in phylogenetic studies. The Dictionary of the Fungi 10th recorded approximately 600 species (Kirk et al. 2008). Subsequently, Hibbett et al. (2014) recorded around 900 species in 75 genera across three families. He et al. (2019) summarized 1,205 species within 80 genera and seven families. And then Wijayawardene et al. (2020) recognized 1,174 species in 79 genera across six families, updated classification to 1,229 species in 83 genera and 6 families (Wijayawardene et al. 2022). He et al. (2022) updated 1,305 species, and the most recent assessment listed 1,462 species currently recognized in Hymenochaetales (Hyde et al. 2024). All in all, the number of recognized species in this order has grown by more than 800 since 2008—an increase of 2.4-fold—yet their global distribution patterns remain poorly understood.

Currently, a series studies of species diversity within Hymenochaetales have focused primarily on taxonomy, such as construction of phylogenetic trees and the description of new taxa (Parmasto et al. 2014, Ji et al. 2017a, 2017b, 2018, Wu et al. 2017, Miettinen et al. 2019, Wu et al. 2022b, Zhou et al. 2023, Liu et al. 2025a). Some investigations have examined the morphology of basidiomata, often as part of broader studies on polypores or fungal (macrofungal) communities (Dai et al. 2021, Ryvarden et al. 2022, Wu et al. 2022a, Cui et al. 2024, Zhao et al. 2024, Gafforov et al. 2025). A smaller number of studies have addressed the species richness of Hymenochaetales in specific regions or countries (Fiasson & Niemelä 1984, Vinjusha & Kumar 2024). Overall, however, comprehensive research on the global species richness and biogeographic patterns of Hymenochaetales remains scarce.

This study aims to provide a comprehensive assessment of the global species richness of Hymenochaetales, elucidating their taxonomic composition as well as their climatic and geographic distribution patterns.

MATERIALS AND METHODS

Checklist collection of Hymenochaetales

In this study, the comprehensive checklist of Hymenochaetales was compiled based on the Fungal Names database (https://nmdc.cn/fungalnames/) and cross-validated against MycoBank (https://mycobank.org) and Index Fungorum (https://indexfungorum.org) databases. The taxonomic framework of Hymenochaetales followed the most recent studies (Zhou et al. 2023, Hyde et al. 2024, Zhao et al. 2025a), with newly described taxa incorporated up to June 17, 2025 (Bolaños-Nuñez et al. 2025, Chen et al. 2025a, Choudhary & Uniyal 2025, Dai et al. 2025, Deng et al. 2025b, Jerusalem et al. 2025, Liu et al. 2025a, Ma et al. 2025, Oliveira et al. 2025, Shao et al. 2025, Yang et al. 2025, Zeng et al. 2025, Zhang et al. 2025a).

The checklist contains information on taxonomy, current accepted names, basidiomata morphology, climatic and continental distribution, type locality, year of publication, and references (deposited in National Microbiology Data Center (NMDC) with accession numbers NMDCX0002160 (https://nmdc.cn/resource/attachment/detail/NMDCX0002160)).

Classification and distribution patterns of Hymenochaetales

A classification hierarchy tree was constructed based on previously studies (Zhou et al. 2023, Hyde et al. 2024, Zhao et al. 2025a) using the complied species checklist. The tree, together with abundance data, was visualized with iTOL version 6.9.1 (https://itol.embl.de/). Climatic zones were classified into four categories: boreal, temperate, subtropical, and tropical. The six continents considered were Africa, Asia, Europe, North America, Oceania, and South America.

Data analyses

To assess the similarity of species composition among six continents, the Sørensen Similarity Index (SS) was applied, calculated as $SS = 2C / (A + B)$, where A and B denote the number of species in two different continents, and C represents the number of species shared by both (Sørensen 1948, Wu et al. 2022a, Zhao et al. 2024), according to the checklist of Hymenochaetales. Column and line charts were generated using the ggplot2 package (Wilkinson, 2011) in R version 4.1.2 (R Core Team 2013). Flower plots were created and tested using the ImageGP 2 web platform (Chen et al. 2024).

RESULTS

Species composition of the order Hymenochaetales

The nomenclature of Hymenochaetales species dates back to 1753, beginning with Linnaeus's binomial naming of *Boletus igniarius* L. (currently *Phellinus igniarius* (L.) Quél.) and *Boletus perennis* L. (currently Coltricia perennis (L.) Murrill). In recent years, the number of newly

established families, genera, and species within Hymenochaetales has steadily increased through the morphological, phylogenetic, and molecular dating analyses. As of June 17, 2025, a total of 1,651 species have been recorded, belonging to 101 genera (including 25 incertae sedis), and 18 families (Figure 2 and Figure 3). Of these, 22 species were described between 1753 and 1799, 198 species from 1800 to 1899, 531 species from 1900 to 1999, and 900 species since 2000. In the 21st century, number species in Hymenochaetales has increased rapidly, surpassing 1,000 by 2014, reaching 1,028 species (Figure 3a). Notably, the highest number of newly described species occurred in 2024, with a total of 114.

Figure 1 Basidiomata of represented taxa of the order Hymenochaetales. (a) *Coltricia weii*. (b) *Fibrodontia alba*. (c) *Fomitiporella chinensis*. (d) *Fomitiporia punicata*. (e) *Fulvoderma australe*. (f) *Fuscoporia senex*. (g) *Hydnoporia yasudae*. (h) *Hymenochaete yunnanensis*. (i) *Hyphodontia juniperi*. (j) *Kneiffiella pseudoabdita*. (k) *Lyomyces mascarensis*. (l) *Peniophorella pinicola*. (m) *Phellinopsis junipericola*. (n) *Phellinus tremulae*. (o) *Porodaedalea alpicola*. (p) *Resinicium bicolor*. (q) *Rickenella fibula*. (r) *Rigidoporus philadelphi*. (s) *Sanghuangporus baumii*. (t) *Sidera malaysiana*. (u) *Skvortzovia furfuracea*. (v) *Trichaptum fuscoviolaceum*. (w) *Tubulicrinis yunnanensis*. (x) *Xylodon flaviporus*. Photos credit Prof. Dr. Yu-Cheng Dai, Prof. Dr. Fang Wu, and Dr. Heng Zhao.

Among the 18 families, Hymenochaetaceae is the most species-rich, containing 44 genera and 973 species, which accounts for 59.12% of all Hymenochaetales species. This is followed by Schizoporaceae, with nine genera and 274 species (16.60%), Coltriciaceae, with one genus and 73 species (4.42%), Rigidoporaceae, with four genera and 57 species (3.45%), and Tubulicrinaceae, with one genus and 40 species (2.42%). Other families include Peniophorellaceae (one genus, 38 species, 2.30%), Hirschioporaceae (four genera, 37 species, 2.24%), Sideraceae (one genus, 19 species, 1.15%), Resiniciaceae (one genus, 17 species, 1.03%), Repetobasidiaceae (one genus, 13 species, 0.79%), Odonticiaceae (two genera, ten species, 0.61%), Rickenellaceae (one genus, nine species, 0.55%), Skvortzoviaceae (one genus, nine species, 0.55%), Trichaptaceae (one genus, eight species, 0.48%), Schizocorticiaceae (one genus, four species, 0.24%), Umbellaceae (one genus, four species, 0.24%), Nigrofomitaceae (one genus, three species, 0.18%), and Neoantrodiellaceae (one genus, two species, 0.12%). In addition, 25 genera comprising 58 species remain unassigned to any family (incertae sedis), representing 3.50% of the total species (Figure 3b).

Among the 101 genera within Hymenochaetales, 11 genera each contain more than 50 species, totaling 1,061 species and accounting for 64.26% of all species. In contrast, the remaining 90 genera comprise 590 species, representing 35.74%. *Hymenochaete*, the type of genus of both Hymenochaetaceae and Hymenochaetales, has the highest number of known species, with 218 species (Figure 2 and Table 1). This is followed by *Xylodon* (137 species), *Fuscoporia* (105 species), *Inonotus* (101 species), *Phylloporia* (96 species), *Fulvifomes* (79 species), *Fomitiporia* (76 species), *Coltricia* (73 species), *Lyomyces* (64 species), *Tropicoporus* (60 species), and *Rigidoporus* (52 species). Notably, 30 genera in this order are currently monotypic, each containing by a single known species.

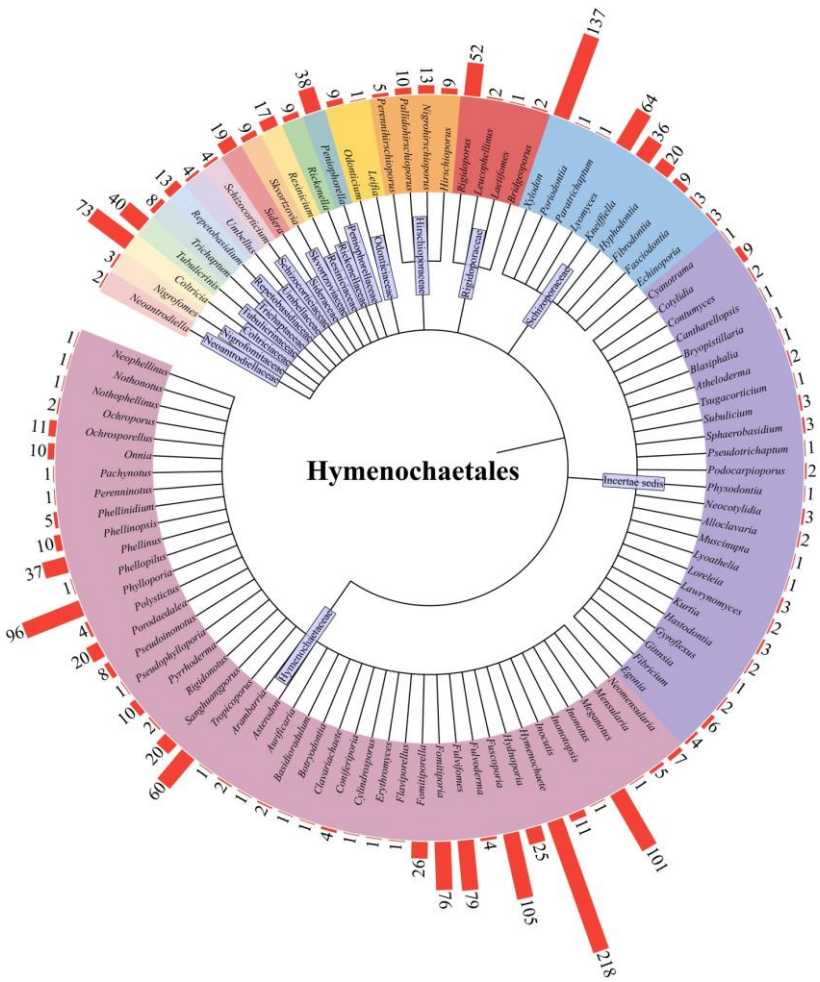

Figure 2 – Diagram illustrating the global species richness of Hymenochaetales. The red bars on the outer circle indicate the number of species in each corresponding genus.

Table 1 Global species composition of the order Hymenochaetales.

Families (number of genera)	Genera	Number of species	Africa	Asia	Europe	North America	Oceania	South America
Coltriciaceae (1)	*Coltricia*	73	6	49	5	11	10	13
Hirschioporaceae (4)	*Hirschioporus*	9	0	8	2	3	0	0
	Nigrohirschioporus	13	1	5	0	2	7	5
	Pallidohirschioporus	10	0	8	2	3	6	0
	Perennihirschioporus	5	0	2	0	2	0	2
Hymenochaetaceae (44)	*Arambarria*	1	0	0	0	0	0	1
	Asterodon	2	0	0	1	0	0	1
	Aurificaria	1	0	0	0	1	0	0
	Basidioradulum	2	0	0	0	1	7	0
	Botryodontia	1	0	0	0	0	0	1
	Clavariachaete	1	0	0	0	0	0	1
	Coniferiporia	4	0	3	0	1	0	0
	Cylindrosporus	1	0	1	0	0	0	0
	Erythromyces	1	1	1	0	0	6	0
	Flaviporellus	1	0	0	0	0	0	1
	Fomitiporella	26	2	12	1	7	8	9
	Fomitiporia	76	9	22	7	18	11	24
	Fulvifomes	79	9	47	1	19	13	11
	Fulvoderma	4	0	4	0	0	0	0
	Fuscoporia	105	9	50	7	36	14	20
	Hydnoporia	25	1	22	4	6	0	3
	Hymenochaete	218	24	127	16	49	50	50
	Inocutis	11	2	8	3	5	0	1
	Inonotopsis	1	0	1	1	1	0	0
	Inonotus	101	13	52	7	28	17	16
	Meganotus	1	0	0	0	1	0	0
	Mensularia	5	0	5	2	1	0	0
	Neomensularia	7	0	4	0	2	0	1
	Neophellinus	1	0	0	0	0	0	1
	Nothonotus	1	0	0	0	0	6	0

Table 1 Continued

Families (number of genera)	Genera	Number of species	Africa	Asia	Europe	North America	Oceania	South America
	Nothophellinus	1	0	0	0	0	0	1
	Ochroporus	2	0	0	2	0	0	0
	Ochrosporellus	11	0	7	0	2	6	1
	Onnia	10	0	8	3	3	0	0
	Pachynotus	1	0	1	0	0	0	0
	Perenninotus	1	0	1	0	0	0	0
	Phellinidium	5	0	3	2	2	0	0
	Phellinopsis	10	0	8	1	2	0	1
	Phellinus	37	3	22	9	15	6	1
	Phellopilus	1	0	1	1	1	0	0
	Phylloporia	96	20	51	1	13	9	19
	Polystictus	4	0	1	0	1	0	2
	Porodaedalea	20	1	14	4	4	0	0
	Pseudoinonotus	8	0	3	3	2	8	1
	Pseudophylloporia	1	0	0	0	0	6	0
	Pyrrhoderma	10	0	9	0	0	6	0
	Rigidonotus	2	0	1	0	1	0	0
	Sanghuangporus	20	1	15	1	2	6	0
	Tropicoporus	60	7	35	0	11	9	16
Incertae sedis (25)	*Alloclavaria*	2	0	2	1	1	0	0
	Atheloderma	2	0	1	1	0	0	0
	Blasiphalia	1	0	0	0	1	0	0
	Bryopistillaria	1	0	0	1	0	0	0
	Cantharellopsis	1	0	0	1	1	0	0
	Contumyces	2	0	0	2	0	0	0
	Cotylidia	9	1	6	7	4	6	1
	Cyanotrama	1	1	1	0	1	0	0
	Egonia	4	0	2	3	2	0	0
	Fibricium	6	1	3	3	1	0	1
	Ginnsia	2	0	2	0	1	6	0

Table 1 Continued

Families (number of genera)	Genera	Number of species	Africa	Asia	Europe	North America	Oceania	South America
	Gyroflexus	1	0	1	0	0	0	0
	Hastodontia	2	0	1	2	1	6	0
	Kurtia	3	1	1	2	1	7	1
	Lawrynomyces	2	0	0	2	0	0	0
	Loreleia	3	0	1	3	2	6	0
	Lyoathelia	1	0	1	1	1	0	0
	Muscinupta	1	0	0	1	1	0	0
	Neocotylidia	3	1	3	1	1	6	1
	Physodontia	1	0	1	1	0	0	0
	Podocarpioporus	2	0	2	0	0	0	0
	Pseudotrichaptum	1	0	1	1	1	0	0
	Sphaerobasidium	3	0	1	1	2	6	0
	Subulicium	3	0	1	3	2	0	0
	Tsugacorticium	1	0	0	0	1	0	0
Neoantrodiellaceae (1)	*Neoantrodiella*	2	0	2	0	0	0	0
Nigrofomitaceae (1)	*Nigrofomes*	3	1	3	1	1	6	1
Odonticiaceae (2)	*Leifia*	1	0	1	0	0	0	0
	Odonticium	9	0	3	4	1	0	2
Peniophorellaceae (1)	*Peniophorella*	38	9	26	10	14	12	8
Repetobasidiaceae (1)	*Repetobasidium*	13	1	2	9	7	6	0
Resiniciaceae (1)	*Resinicium*	17	3	6	2	11	8	7
Rickenellaceae (1)	*Rickenella*	9	1	6	5	3	7	2
Rigidoporaceae (4)	*Bridgeoporus*	2	0	1	0	1	0	0
	Laetifomes	1	0	0	0	0	6	0
	Leucophellinus	2	1	2	0	0	6	0
	Rigidoporus	52	14	32	8	15	15	18
Schizocorticiaceae (1)	*Schizocorticium*	4	0	4	0	0	0	0
Schizoporaceae (9)	*Echinoporia*	3	1	1	0	1	0	2
	Fasciodontia	3	0	1	1	0	0	1
	Fibrodontia	9	1	6	1	3	0	3

Table 1 Continued

Families (number of genera)	Genera	Number of species	Africa	Asia	Europe	North America	Oceania	South America
	Hyphodontia	20	5	14	4	6	10	7
	Kneiffiella	36	2	18	15	12	6	4
	Lyomyces	64	8	44	7	14	11	13
	Paratrichaptum	1	0	1	0	0	0	0
	Poriodontia	1	0	1	0	0	0	0
	Xylodon	137	16	74	20	19	31	32
Sideraceae (1)	*Sidera*	19	0	14	3	3	10	2
Skvortzoviaceae (1)	*Skvortzovia*	9	0	8	4	4	0	2
Trichaptaceae (1)	*Trichaptum*	8	1	4	0	4	6	2
Tubulicrinaceae (1)	*Tubulicrinis*	40	6	20	23	18	13	5
Umbellaceae (1)	*Umbellus*	4	0	3	1	1	6	0

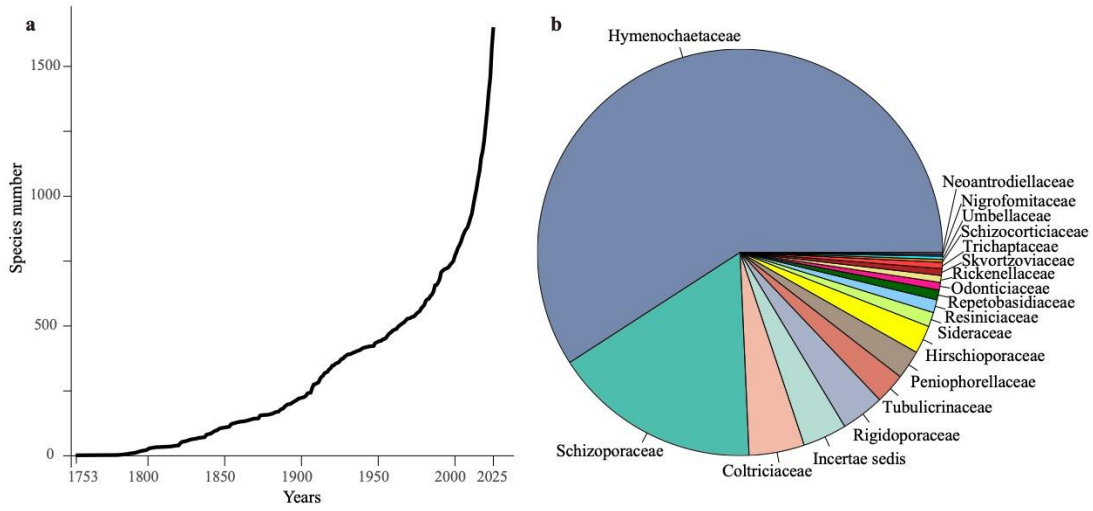

Figure 3 – Diagram illustrating the global species richness of Hymenochaetales. The red bars on the outer circle indicate the number of species in each corresponding genus.

Species richness of six continents

This study, the species richness and distribution patterns of Hymenochaetales species were analyzed across six continents, namely Africa, Asia, Europe, North America, Oceania, and South America. The results showed that Asia exhibited the highest species richness, encompassing 18 families, 80 genera, and 939 species (Figure 4). This is followed by North America (16 families, 70 genera, 419 species), South America (14 families, 47 genera, 318 species), Europe (15 families, 60 genera, 241 species), Oceania (14 families, 43 genera, 198 species), and Africa (12 families, 36 genera, 184 species).

The proportion of shared families, genera, and species across all continents declines progressively (Figure 4). Of the 18 families in Hymenochaetales, 10 families (accounting for 55.56%) are present on all six continents. Among the 101 genera, only 22 genera (21.78%) are globally distribution. At the species level, just 28 species of the 1,651 species, (1.70%) occur on six continents.

The SS revealed patterns of species-level similarity among continents (Figure 5). The highest similarity was observed between Europe and North America (SS = 0.40), followed by North and South America (SS = 0.35). In contrast, the lowest similarities were found between Asia and South America (SS = 0.13), and between Asia and Oceania (SS = 0.14).

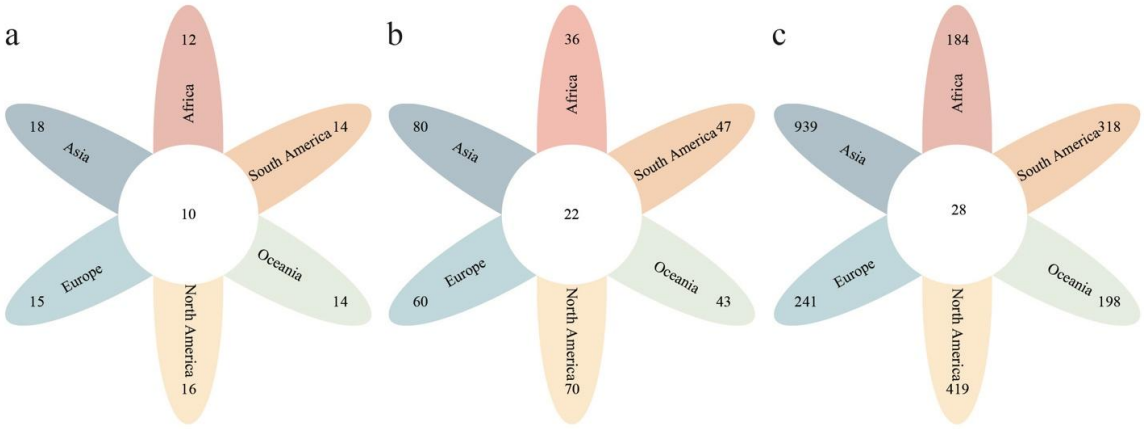

Figure 4 – The number of families (a), genera (b), and species (c) of Hymenochaetales found in Africa ( ), Asia ( ), Europe ( ), North America ( ), Oceania ( ), and South America ( ) with the shared families, genera, and species in central.

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The highly species richness in temperate and tropical zones

In this study, the global distribution of Hymenochaetales species was classified into four climatic zones, including boreal, temperate, subtropical, and tropical. Species richness was highest in the temperate and tropical zones, while the subtropical and boreal zones exhibited comparatively lower richness (Figure 6). Among the 18 families, 17 families were recorded in the temperate and subtropical zones, followed by 16 families in the tropical zones and 11 families in the boreal zones (Figure 6). At the genus level, the temperate zones had the highest number, with 84 genera, followed by 59 in the tropical zones, 56 in the subtropical zones, and 30 genera in the boreal zones. At the species level, of the 1,651 total Hymenochaetales species, the temperate and tropical zones had the most species, with 700 and 693, respectively. The subtropical zoned contained 490 species, whereas the boreal zones had the fewest, with only 74 species.

An analysis of species distribution across different climatic zones on each of the six continents revealed three major biogeographic patterns (Table 2). In the Northern Hemisphere, including Asia, Europe, and North America, Hymenochaetales species are predominantly distributed in temperate zones. In contract, in Africa and South America, species are mainly found in tropical zones. In Oceania, species are more similarly distributed from temperate to tropical zones.

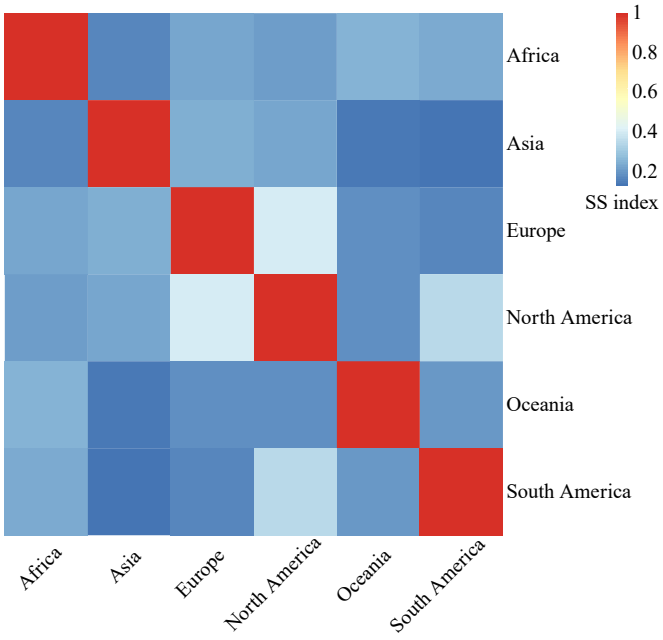

Figure 5 – The heatmap of Sørensen Similarity Index (SS) among the six continents.

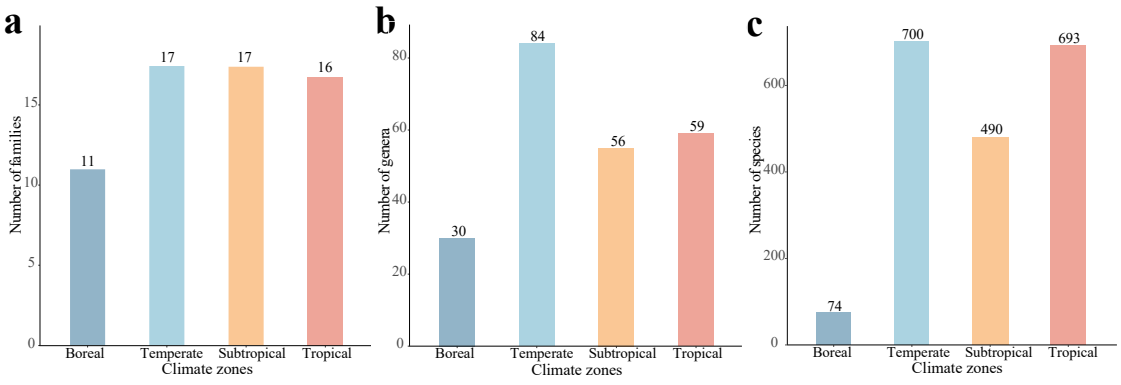

Figure 6 – The number of families (a), genera (b), and species (c) of Hymenochaetales found in boreal (), temperate (), subtropical (), and tropical ().

Table 2 Hymenochaetales species found in four climate zones within six continents. Four climate zones were represented boreal, temperate, subtropical, and tropical. Six continents were represented Africa, Asia, Europe, North America, Oceania, and South America.

Continents	Climate zones			
	Boreal	**Temperate**	**Subtropical**	**Tropical**
Africa	24	57	45	132
Asia	57	428	307	331
Europe	65	232	40	0
North America	53	230	115	187
Oceania	22	96	111	87
South America	22	116	89	210

Basidiomata types of Hymenochaetales species

Hymenochaetales species exhibit highly diverse basidiomata (fruiting body) morphologies. In this study, statistical analyses revealed that poroid species are the most abundant, comprising 944 species and accounting for 57.18% of all species (Figure 7a). This is followed by corticioid species, with 429 species (25.98%), and hydnoid species, with 220 species (13.33%). In addition to these three morphological types, Hymenochaetales also includes species with other basidiomata types, such as agaricoid, clavarioid, poroid to hydnoid, corticioid to hydnoid, poroid to corticioid, hydnoid to irpicoid, poroid to irpicoid, and lamellae to poroid. These were collectively categorized as "others", comprising 58 species (3.51%).

The relative abundance of basidiomata types varies across continents (Figure 7b). Poroid species are the dominant form on all continents except Europe, where they account for 33.61% (81/241) of species. The highest proportion of poroid species is observed in Africa, at 58.15% (107/184). Corticioid species are least abundant in South America (24.84%, 79/318) and the most abundant in Oceania (37.37%, 74/198). Hydnoid species are least represented in North America (11.69%, 49/419) and the most common in Europe (19.09%, 46/241). Others basidiomata types are least represented in Africa (1.09%, 2/184) and the abundant in Europe (11.62%, 28/241).

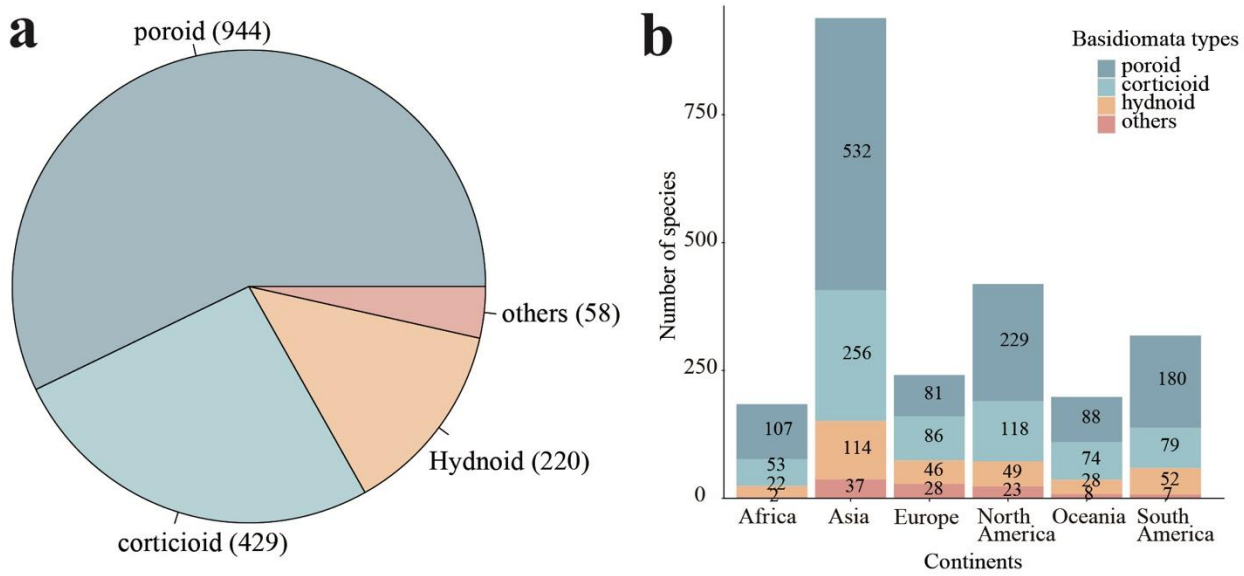

Figure 7 – The number of families (a), genera (b), and species (c) of Hymenochaetales found in boreal (■), temperate (■), subtropical (■), and tropical (■).

Origins of type specimens and the corresponding publication sources for Hymenochaetales species.

The origins of type specimen for Hymenochaetales species showed that among the 1,651 species, 1,621 species (98.18%) have derived from 112 countries or regions, while the type localities for 30 species (1.82%) remains unknown (Table 3). Among these 112 countries or regions, six contributed more than 50 type specimens, including China (438 species, 26.53%), United States (123 species, 7.45%), Brazil (97 species, 5.88%), India (67 species, 4.06%), Australia (58 species, 3.51%), and Malaysia (53 species, 3.21%). Collectively, these six countries account for 50.64% of all type specimen, while the remaining 106 countries or regions are contributed 47.54%.

In this study, the type specimens of 1,651 Hymenochaetales species were published across 160 journals or books, with the majority appearing in mycological journals (Figure 8). Notable examples include Fungal Diversity with 266 species (16.11% of the total), Mycological Progress with 141 species (8.54%), Mycologia with 113 species (6.84%), Mycotaxon with 107 species (6.48%), Synopsis Fungorum with 101 species (6.12%), and MycoKeys with 95 species (5.75%). In addition, 132 journals or books each published fewer than ten species, collectively accounting for 292 species.

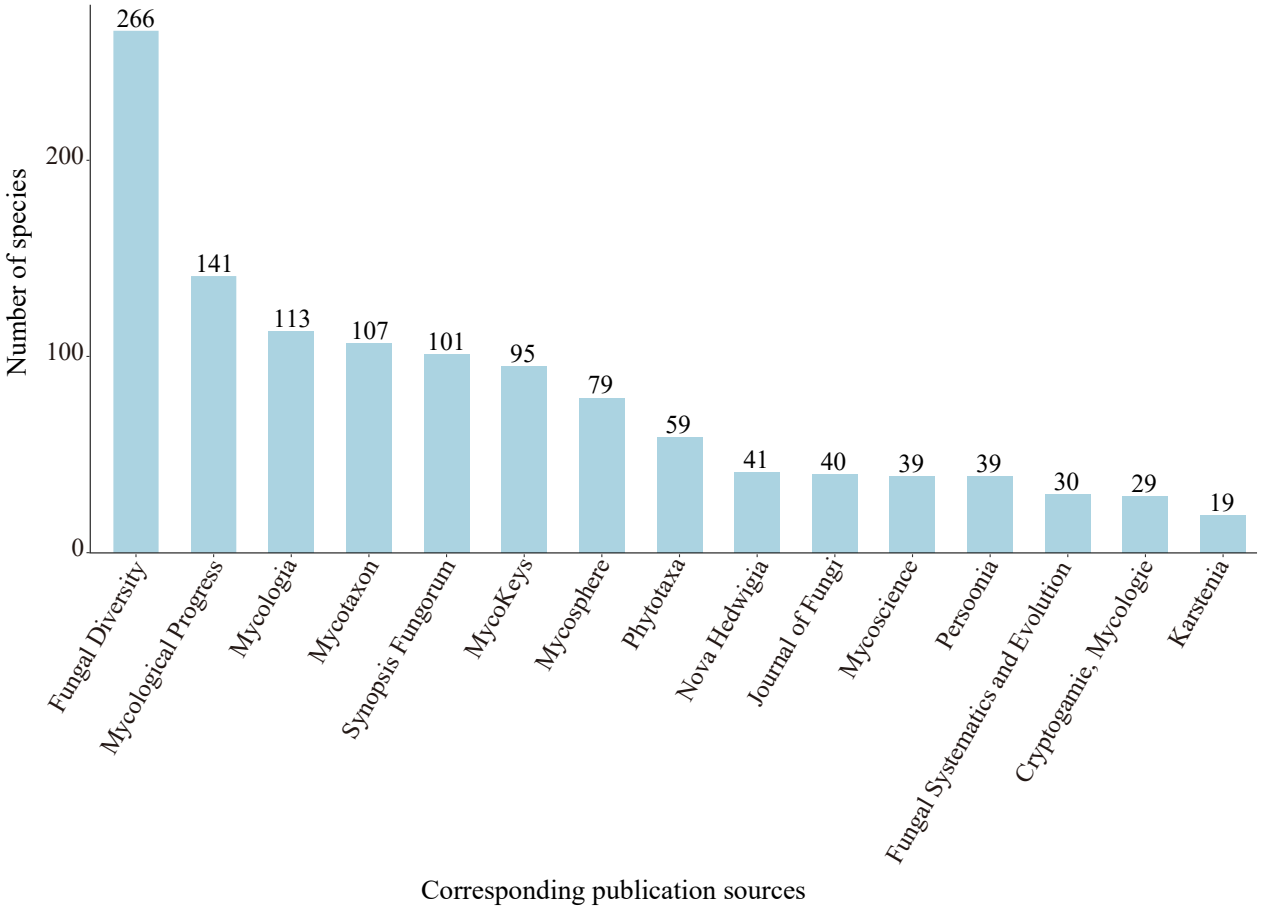

Figure 8 – The top 15 corresponding publication sources of type specimens of Hymenochaetales species.

Table 3 Types species of Hymenochaetales originated from countries or zones.

Rank	Countries or zones	Number of types	Rank	Countries or zones	Number of types
1	China	438	57	Guyana	3
2	USA	123	58	Iran	3

Table 3 Continued

Rank	Countries or zones	Number of types	Rank	Countries or zones	Number of types
3	Brazil	97	59	Kazakhstan	3
4	India	67	60	Pakistan	3
5	Australia	58	61	Papua New Guinea	3
6	Malaysia	53	62	Paraguay	3
7	Argentina	46	63	Poland	3
8	New Zealand	44	64	Samoa	3
9	Japan	39	65	Algeria	2
10	Sweden	38	66	Czechoslovakia	2
11	Russia	31	67	Dominican Republic	2
12	Costa Rica	30	68	Estonia	2
13	Unknown	30	69	Ethiopia	2
14	Cuba	28	70	Georgia	2
15	France	28	71	Ghana	2
16	Finland	23	72	Madagascar	2
17	Mexico	22	73	Malawi	2
18	Sri Lanka	21	74	Martinique	2
19	Indonesia	19	75	Micronesia Federated States	2
20	Ecuador	18	76	Morocco	2
21	Reunion	18	77	Nicaragua	2
22	Gabon	17	78	Solomon Islands	2
23	Germany	17	79	Suriname	2
24	Venezuela	17	80	Switzerland	2
25	Philippines	15	81	Tasmania	2
26	Thailand	14	82	Zambia	2
27	Vietnam	14	83	Angola	1
28	Canada	13	84	Buka Island	1
29	French Guiana	13	85	Cambodia	1
30	Singapore	12	86	Croatia	1
31	Jamaica	11	87	Equatorial Guinea	1
32	South Africa	11	88	Fiji	1
33	Italy	10	89	former Soviet Union	1
34	Cameroon	9	90	Grenada	1
35	Tanzania	9	91	Guadeloupe	1
36	Korea	8	92	Guatemala	1
37	Panama	8	93	Guinea	1
38	Chile	7	94	Hungary	1
39	Colombia	7	95	Kyrgyzstan	1
40	Nepal	7	96	Mauritius	1
41	Zimbabwe	7	97	Mayotte	1
42	Kenya	6	98	Montserrat	1
43	Uzbekistan	6	99	Mozambique	1
44	Czech Republic	5	100	Netherlands	1
45	Norway	5	101	New Caledonia	1
46	Puerto Rico	5	102	Oman	1
47	Spain	5	103	Peru	1
48	Austria	4	104	Rwanda	1

Table 3 Continued

Rank	Countries or zones	Number of types	Rank	Countries or zones	Number of types
49	Benin	4	105	Sao Tome and Principe	1
50	Portugal	4	106	Seychelles	1
51	Uganda	4	107	Slovenia	1
52	UK	4	108	Sudan	1
53	Belize	3	109	Tunisia	1
54	Central African	3	110	Turkmenistan	1
55	Congo	3	111	Ukraine	1
56	Denmark	3	112	Yugoslavia	1

DISCUSSION

The order Hymenochaetales, as the primarily wood-inhabiting fungi, play a vital role in forest ecosystem by contributing to nutrient cycling and forest regeneration through the decomposition of key structural components of plant cell walls, including lignin, hemicellulose, and pectin, causing white rot (Larsson et al. 2006, Dai 2010, Wu et al. 2022b, Gafforov et al. 2025). The scientific naming of Hymenochaetales began in 1753 with Linnaeus's introduction of binomial nomenclature, and subsequent species descriptions have become increasingly systematic, with morphological traits long serving as the foundation of fungal taxonomy. Since the advent of molecular biology in the 21st century, the number of recognized Hymenochaetales species has increased substantially.

In China, mycologists have made significant contributions to the taxonomy of this group by describing new families, genera, species, and combinations, documenting distribution patterns, reconstructing phylogenies, estimating divergence times, and exploring historical biogeography (Dai 2010, Dai et al. 2021, Ma et al. 2022, Wu et al. 2022b, Zhao et al. 2023a, 2025a, 2025b, Zhou et al. 2023, Liu et al. 2025a). Internationally, Ryvarden and collaborators have played a pioneering role in advancing the taxonomy and ecology of Hymenochaetales, particularly in Africa, Europe, and tropical America. Their work has included the description of numerous new taxa and the publication of a series of influential studies (Ryvarden 1991, 2000, 2004, 2018, 2023, Ryvarden & Melo 2014, 2017, Decock et al. 2021, Ryvarden et al. 2022, Spirin & Ryvarden 2024). Additionally, new taxa of Hymenochaetales continuously are described (Chen et al. 2025b, 2025c, Patil et al. 2025, Wei et al. 2025, Zhao et al. 2025b). All in all, remarkable progress has been made in the taxonomy and phylogeny of Hymenochaetales.

Despite growing interest and expanded collection efforts worldwide, many Hymenochaetales species may undescribed due to factors such as geographic isolation, limited funding, and difficultly of accessing remote or extreme environments (Wu et al. 2022a, Zhao et al. 2024). In our study, Asia was identified as the continent with the highest species richness. Species richness in Africa remains poorly documented, and the number of described species is the lowest, highlighting the need for intensified systematic surveys. Encouragingly, several countries that have historically been underrepresented in fungal research, such as India (Jayawardena et al. 2022, Gunaseelan et al. 2024, Arumugam et al. 2024, Vinjusha & Kumar 2024), Pakistan (Bashir et al. 2024, Ghobad-Nejhad et al. 2024, Cao et al. 2025), and Mexico (Chamorro-Martínez et al. 2022, Suh et al. 2024), have reported increasing numbers of newly described species in the past several years.

Many previous studies have proposed new taxa within Hymenochaetales, but several issues remain unresolved, including inconsistent nomenclature, underexplored species richness, and incomplete fungal diversity analyses (Dai 2010, Wu et al. 2022b, Vinjusha & Kumar 2024, Cho et al. 2024, Mendes-Freire & Soares 2025). To address these gaps, this study aimed to systematically investigate the global species richness of Hymenochaetales. Since the establishment of scientific naming in 1753, the documented species richness of the order has shown a continuous upward trend over the past 272 years, with a marked acceleration in last two decades. Notably, in

the Dictionary of the Fungi 10th (Kirk et al. 2008) recorded about 600 species of Hymenochaetales were recorded, whereas 1,462 species were listed in 2024 (Hyde et al. 2024). In the presently study, we compiled and validated a comprehensive dataset of 1,651 species across 101 genera and 18 families, representing a 2.75-fold compared with the 2008 record. Our study provides the most updated and authoritative baseline for future taxonomic, phylogenetic, and ecological studies.

There are some synonyms and misapplied names within the order Hymenochaetales. A widely recognized example is that Oxyporaceae (*Oxyporus*) has been replaced by Rigidoporaceae (*Rigidoporus*), with most researchers accepting the latter rather than the former (Wijayawardene et al. 2022, Wang et al. 2023b, Zhou et al. 2023, Hyde et al. 2024, Zhao et al. 2025a). Although Wu et al. (2022b) treated *Coltriciella* as a synonym of *Coltricia* based on molecular phylogenetic and morphological evidence, new species have still been published under the name *Coltriciella*, adding to the difficulty of subsequent taxonomic correction (Zhou et al. 2024, Zeng et al. 2025). In addition, Hymenochaetales includes many important medicinal fungi, especially *Sanghuangporus* spp., but some studies have still used outdated names, such as *Inonotus sanghuang* and *Phellinus baumii* instead of *Sanghuangporus sanghuang* and *Sanghuangporus baumii* (Liu et al. 2022, Luo et al. 2024, Zhang et al. 2025b). Therefore, it is recommended that researchers verify species names according to the updated studies (Wu et al, 2022b, Ghobad-Nejhad et al. 2024), and this study will greatly reduce misapplied names in Hymenochaetales.

It is important to note, however, that species distribution patterns across climate zones and geographic regions remain incomplete, largely due to insufficient sampling and the lack of comprehensive records in some areas. Previous studies have suggested that members of Agaricomycetes exhibit the highest species richness in temperate zones (Varga et al. 2019), whereas the latitudinal diversity gradient (LDG) hypothesis predicts increasing species richness from the poles toward the equator (Mittelbach et al. 2007). Zhao et al. (2024) found that tropical zones (tropical Africa, Asia, and America) harbor greater polypore diversity than temperate zones (temperate China, Europe, and North America), consistent with the LDG hypothesis. However, this result showed that temperate zones host slightly more Hymenochaetales species than tropical zones, while subtropical and boreal zones show markedly lower diversity. The unexplored taxa and under-sampled regions may have an important impact on this result. In comparison to Asia (especially in China, Japan, and Korea, etc.) and Europe, less Hymenochaete species recorded in Africa is attributed to fewer investigations, for instance being fewer reports from the tropical forests of West Africa. These results suggest that many species in tropical and subtropical regions may remain undiscovered, highlighting the need for intensified surveys in these areas. Moreover, future studies should incorporate environmental factors, such as climate, precipitation, and forest type to better understand the ecological and biogeographical patterns of Hymenochaetales, particularly in the context of global climate change and ecosystem stability.

Within the order Hymenochaetales, poroid species represent the dominant basidiomata type, followed by corticioid and hydnoid species. In recent years, the number of hydnoid species has notably increased, particularly within *Xylodon* of the family Schizoporaceae (Viner et al. 2021, Dong et al. 2024, Yuan & Zhao 2024, Yurchenko et al. 2024, Yang et al. 2025, Zhang et al. 2025a). By contrast, agaricoid and clavarioid forms have remained relatively stable, with only a few described species (Wijayawardene et al. 2022, Hyde et al. 2024). With the continued description of new taxa (e.g., new families, genera, and species), the relative proportions of basidiomata types are likely to evolve over time.

In addition to their ecological importance, Hymenochaetales species also possess considerable medicinal potential. Some species have long been used in traditional medicine in China, such as *Sanghuangporus* spp., and a few, have historical applications in European herbal medicine, such as *Inonotus obliquus* (Dai 2010, Szychowski et al. 2021, Wu et al. 2022b). However, studies to date have mainly focused on a limited number of genera, such as *Sanghuangporus* and *Inonotus*, while many other taxa with potential medicinal values remained underexplored. Recent studies have shown that at least 124 species across 27 genera within the family Hymenochaetaceae produce bioactive metabolites (Wu et al. 2019, Ghobad-Nejhad et al.

2024). Over 500 compounds have been identified, including terpenoids, styrylpyrones, steroids, phenolics, polysaccharides, and others, exhibiting diverse biological activities such as antioxidant, antitumor, antidiabetic, immunomodulatory, anti-inflammatory, antibacterial, and antifungal effects (Dai et al. 2010, Wu et al. 2019, Wang et al. 2023a, Ghobad-Nejhad et al. 2024). Additionally, some species within *Trichaptum* s.l. also demonstrate promising medicinal potential (Adhikari et al. 2019, Payamnoor et al. 2020, Zhou et al. 2023, Xie et al. 2025). These findings highlight Hymenochaetales as a rich reservoir of pharmaceutical valuable metabolites. Nevertheless, many species remain unstudied, underscoring the need for future research to establish comprehensive germplasm collections to support the discovery, development, and sustainable utilization of their bioactive compounds.

Currently, the development of multi-omics technologies has provided new insights into the phylogenomics, ecological diversification, wood degradation, metabolites biosynthesis, mitochondrial genomes, and virulence factor repertoires of Hymenochaetales species (Korotkin et al. 2018, Min et al. 2015, Chung et al. 2017, Zhao et al. 2023a, 2025a, Feng et al. 2024, Garcia et al. 2024, Cho et al. 2025, Liu et al. 2025, Xie et al. 2025). For example, numerous studies have applied multi-omics approaches to *Sanghuangporus* spp. and closely related genera to investigate metabolite biosynthetic mechanisms, such as *S. sanghuang*, *S. weigelae*, *S. vannini*, and *Inonotus hispidus* (Jin et al. 2024, Zhang et al. 2022, Cho et al. 2025). Garcia et al. (2024) revealed the characteristics of virulence factor repertoires through comparative genomics. Nevertheless, compared with other fungal groups such as Botryosphaeriales, *Penicillium*, *Aspergillus*, and yeasts, multi-omics research on Hymenochaetales remains relatively underdeveloped, highlighting the need to strengthen studies in this field in the future.

All in all, this study provides a comprehensive overview of the species richness and distribution pattens of Hymenochaetales. Species richness has steadily increased since 1753, with rapid growth in the past two decades based on 1,651 species. Asia emerged as the diversity hotspot, while Africa remains underexplored. Across climatic zones, temperate and tropical regions contained the highest numbers of species, whereas subtropical and boreal zones were relatively species poor. Poroid species dominate the order, followed by corticioid and hydnoid forms. Future efforts should emphasize systematic surveys in underrepresented regions, integrative taxonomy, and omics-based approaches to better resolve ecological and evolutionary processes. Such advances will enhance biodiversity conservation while fostering the sustainable utilization of Hymenochaetales.

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DECLARATION OF COMPETING INTEREST

All authors declare that they have no competing interests.

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