



Global consortium for the classification of fungi and fungus-like taxa

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Global consortium for the classification of fungi and fungus-like taxa

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Olariaga I, Orlando FP, Pang KL, Papp V, Pawłowska J, Peintner U, Pem D, Pereira OL, Perera RH, Perez-Moreno J, Perez-Ortega S, Péter G, Phillips AJL, Phonemany M, Phukhamsakda, Phutthacharoen K, Piepenbring M, Pires-Zottarelli CLA, Poinar G, Pošta A, Prieto M, Promputtha I, Quandt CA, Radek R, Rahnema K, Raj KNA, Rajeshkumar KC, Rämä T, Rambold G, Ramírez-Cruz V, Rasconi S, Rathnayaka AR, Raza M, Ren GC, Robledo GL, Rodriguez-Flakus P, Ronikier A, Rossi W, Ryberg M, Ryvarde LR, Salvador-Montoya CA, Samant B, Samarakoon BC, Samarakoon MC, Sánchez-Castro I, Sánchez-García M, Sandoval-Denis M, Santiago ALCMA, Santamaria B, Santos ACS, Sarma VV, Savchenko A, Savchenko K, Saxena RK, Scholler M, Schouttet N, Seifollahi E, Selbmann L, Selcuk F, Senanayake IC, Shabashova TG, Shen HW, Shen YM, Silva-Filho AGS, Simmons DR, Singh R, Sir EB, Song Chang-Ge, Souza-Motta CM Sruthi OP, Stadler M, Stchigel AM, Stemler J, Stephenson SL, Strasser JFH, Su HL Su L, Suetrong S, Sulistyo B, Sun YF, Sun YR, Svantesson Sten Sysouphanthong P, Takamatsu S, Tan TH, Tanaka K, Tang AMC, Tang X, Tanney JB, Tavakol NM, Taylor JE, Taylor PWJ, Tedersoo L, Tennakoon DS, Thamodini GK, Thines M, Thiagaraja V, Thongklang N, Tiago PV, Tian Q, Tian WH, Tibell L, Tibell S, Tibpromma S, Tkalčec Z, Tomšovský M, Toome-Heller M, Torruella G, Tsurukau A, Udayanga D, Ulukapi M, Untereiner WA, Uzunov BA, Valle LG, Van Caenegem W, Van den Wyngaert S, Van Vooren N, Velez P, Verma RK, Vieira LC, Vieira WAS, Vizzini A, Walker A, Walker AK, Wanasinghe DN, Wang CG, Wang K, Wang SX, Wang XY, Wang Y, Wannasawang N, Wartchow F, Wei DP, Wei XL, White JF, Wijayawardene NN, Wijesinghe SN, Wijesundara DSA, Wisitrasameewong K, Worthy FR, Wu F, Wu G, Wu HX, Wu N, Wu WP, Wurzbacher C, Xiao YP, Xiong YR, Xu LJ, Xu R, Xu RF, Xu RJ, Xu TM, Yakovchenko L, Yan JY, Yang H, Yang J, Yang ZL, Yang YH, Yapa N, Yasanthika E, Youssef NH, Yu FM, Yu Q, fD, Yu YX, Yu ZF, Yuan HS, Yuan Y, Yurkov A, Zafari D, Zamora JC, Zare R, Zeng M, Zeng NK, Zeng XY, Zhang F, Zhang H, Zhang JF, Zhang JY, Zhang QY, Zhang SN, Zhang W, Zhang Y, Zhang YX, Zhao CL, Zhao H, Zhao Q, Zhao RL, Zhou LW, Zhou M, Zhurbenko MP, Zin HH, Zucconi L 2023 – Global consortium for the classification of fungi and fungus-like taxa. *Mycosphere* 14(1), 1960–2012, Doi 10.5943/mycosphere/14/1/23

Abstract

The Global Consortium for the Classification of Fungi and fungus-like taxa is an international initiative of more than 550 mycologists to develop an electronic structure for the classification of these organisms. The members of the Consortium originate from 55 countries/regions worldwide, from a wide range of disciplines, and include senior, mid-career and early-career mycologists and plant pathologists. The Consortium will publish a biannual update of the *Outline of Fungi and fungus-like taxa*, to act as an international scheme for other scientists. Notes on all newly published taxa at or above the level of species will be prepared and published online on the *Outline of Fungi* website (<https://www.outlineoffungi.org/>), and these will be finally published in the biannual edition of the *Outline of Fungi and fungus-like taxa*. Comments on recent important taxonomic opinions on controversial topics will be included in the biannual outline. For example, ‘to promote a more stable taxonomy in *Fusarium* given the divergences over its generic delimitation’, or ‘are there too many genera in the *Boletales*?’ and even more importantly, ‘what should be done with the tremendously diverse ‘dark fungal taxa?’ There are undeniable differences in mycologists’ perceptions and opinions regarding species classification as well as the establishment of new species. Given the pluralistic nature of fungal taxonomy and its implications for species concepts and the nature of species, this consortium aims to provide a platform to better refine and stabilise fungal classification, taking into consideration views from different parties. In the future, a confidential voting system will be set up to gauge the opinions of all mycologists in the Consortium on important topics. The results of such surveys will be presented to the International Commission on the Taxonomy of Fungi (ICTF) and the Nomenclature Committee for Fungi (NCF) with opinions and percentages of votes for and against. Criticisms based on scientific evidence with regards to nomenclature, classifications, and taxonomic concepts will be welcomed, and any recommendations on specific taxonomic issues will also be encouraged; however, we will encourage professionally and ethically responsible criticisms

of others' work. This biannual ongoing project will provide an outlet for advances in various topics of fungal classification, nomenclature, and taxonomic concepts and lead to a community-agreed classification scheme for the fungi and fungus-like taxa. Interested parties should contact the lead author if they would like to be involved in future outlines.

Keywords – classification – nomenclature – scientific criticism – taxonomy

Introduction

The series *Outline of Fungi and fungus-like taxa* (including fossil fungi) commenced with its first publication in 2020, has garnered over 450 citations to date, and is proving to be a very important publication in fungal classification. Since the inaugural outline by Wijayawardene et al. (2020a), we have strived to improve the effectiveness and accuracy of the outline, and this resulted in an updated 2022 outline (Wijayawardene et al. 2022a) featuring contributions from 57 authors. Nevertheless, worldwide participation was not sufficient to overcome arguments that the outline was not representative of most mycologists. Therefore, in 2022, we launched the Global Consortium for the Classification of Fungi and fungus-like taxa and its associated webpage, outlineoffungi.org, and invited numerous interested parties from around the world to form an internationally representative consortium. In this paper, we have more than 550 members representing 55 countries with a range of disciplines, providing a balanced participation in the Global Consortium for the Classification of Fungi and fungus-like taxa. As the project progresses, we will publish the *Outline of Fungi and fungus-like taxa* biannually, with notes on new taxa at or above the level of species. Along with the updated classification scheme for fungi and fungus-like taxa, any notes, critiques, or remarks on controversial topics, especially those pertaining to taxonomy and the establishment of novel taxa, will also be included. Where possible, we will provide appropriate parties with opposing arguments or any clarifications on these topics. Given the dynamic nature of fungal taxonomy as a field of study, it undergoes frequent updates and revisions as new data is acquired from various disciplines such as biochemistry, ecology, evolution, genomics, genetics, morphology, metabolomics, transcriptomics, phylogenetics, physiology, and proteomics. These advancements contribute to the modification of classification and taxonomic concepts at different taxonomic hierarchy. Therefore, it is essential to publish an *Outline of Fungi and fungus-like taxa* biannually to stay up-to-date on the changes and provide a universal platform to discuss controversial topics.

Values and numbers of fungi

The estimation of fungal species ranges from 1 to 11 million, depending on the criteria employed by various researchers (Hyde et al. 2020a). Among these estimates, Hawksworth & Lücking (2017) have proposed a potentially more accurate range of 2.3 to 3.8 million species. In 2022, the journal *Fungal Diversity* published a special issue on the numbers of fungi with nine papers dealing with different taxonomic groups (e.g., *Ascomycota*, *Basidiomycota* – He et al. 2022a, Wijayawardene et al. 2022b, Yeasts – Boekhout et al. 2022). High-throughput sequencing approaches yielded the highest estimates (OTUs; Baldrian et al. 2022). In the editorial of that special issue, Hyde (2022) had planned to provide a more accurate estimate following these various reviews; however, in the end, this editorial was only able to propose prospective research needed to accomplish better estimates of total fungal numbers.

While the discussion of fungal species numbers is still ongoing, the value of fungi is, however, indisputable with both beneficial and negative impacts. In terms of forest health, Niego et al. (2023a) showed how important and undervalued fungi are. They placed the value of fungi at USD 54.61 trillion annually and reported numerous benefits that fungi provide (e.g., food, industrial products, and novel drug discovery) (Niego et al. 2023b). Although any such appraisal has yet to be perfected, the data of Niego et al. (2023b) serves as an important baseline. The cumulative negative roles of fungi for humans, agriculture, and the environment have not been fully considered by Niego et al. (2023b). However, various studies show that human fungal infections are a global concern, causing ~1.7 million deaths annually. Growers worldwide experience losses of 10% to 23% of their crops

due to fungal infections each year, with an additional 10-20% lost during post-harvest (Stukenbrock & Gurr 2023). Though having great monetary value despite difficulties in quantitatively estimating fungal populations, the framework of the Fungi and fungus-like taxa will give scientists a much-needed categorization model to work from.

History of fungal classification

The history of fungal classification systems dates back to the late 18th and the first third of the 19th century and connects with the writings of Persoon (1794, 1801, 1822–1828), Nees von Esenbeck (1817), Fries (1821–1832, 1825, 1835, 1836–1838, 1849), and Link (1833). Those systems were based on the external characters and morphology of the fruit-bodies, characters of hymenophore, and the place and mode of spore formation. By the mid-19th century, the knowledge pertaining to the classification and hierarchy of taxa in the field of mycology was not uniformly established and exhibited discrepancies between different authors. However, throughout this period, significant progress had been made in identifying and categorizing major fungal groupings, including hymenomycetes, discomycetes, pyrenomycetes, and gasteromycetes. The most important books of those times that made significant contributions to fungal classification include ‘*Synopsis methodica fungorum*’ (Persoon 1801), ‘*Systema mycologicum*’ with additional ‘*Index*’ and ‘*Elenchus fungorum*’ (Fries 1821–1832), not only because they were a base for subsequent fungal classifications and systems (e.g., Bonorden 1851, Gillet 1879–1887), as well as regional checklists (e.g., Berkeley 1860, Fuckel 1860, Crouan & Crouan 1867, Cooke 1871, Bernard 1882, Karsten 1871–1879, Quélet 1886, Phillips 1887), but also because of their influence on contemporary nomenclature of fungi. For a considerable period, they served as a starting point for fungal nomenclature up to the Shenzhen Code (Turland et al. 2018) and are now treated as sanctioning works (Turland et al. 2018).

The next major step in fungal classification was a series of twenty-five volumes, the ‘*Sylloge Fungorum*’, led by P.A. Saccardo (1882-1931). Among these publications, the significance of Saccardo & Sydow’s work in 1899 lies in their use of distinct terminology regarding conidial fungi, i.e., deuteromycetes, along with other ranks for fungi and fungus-like taxa. Meanwhile, novel systematics based on minutious microscopical observations were proposed for hymenomycetes by Fayod (1889) and Patouillard (1900), and for discomycetes by Boudier (1907). Subsequent studies by Ainsworth (1966) and Moore (1971) introduced, respectively, *Deuteromycotina* and *Deuteromycota* to accommodate conidial fungi.

Ainsworth (1966) made some of the most important compilations on the classification of fungi. The subsequent series *Systema Ascomycetum* (Eriksson 1982, Eriksson & Hawksworth 1998), which was conceived by Eriksson & Hawksworth (1998), can be considered as the foundation of compilations of fungal names, particularly when it comes to genera of *Ascomycota*. In addition to this series, several issues were published exclusively on the classification of ascomycetous taxa (i.e., Eriksson & Hawksworth 1998). Since 1997, *Myconet* has been published as hard copies and online (<http://archive.fieldmuseum.org/myconet/printed.asp>) (Lumbsch & Huhndorf 2007). Nonetheless, all these efforts have focused on sexually typified genera and their classification, i.e., prior to the use of DNA sequences for fungal taxonomy and classification based on phylogenetic reconstructions.

Hyde et al. (2011) were the first to attempt to list all asexually typified genera in a natural classification. However, Kirk et al. (2008) (i.e., *The Dictionary of Fungi*) also provided higher-level classifications of asexually typified genera, but in their classification, they listed them alphabetically. Subsequent publications by Wijayawardene et al. (2012, 2017) provided the current classification of asexually typified genera, and Wijayawardene et al. (2021) compiled the classification of asexually typified genera with notes on pleomorphic genera.

Since the paper of White et al. (1990), molecular biology techniques have widely been used in mycology, and thus, taxonomists have started to use DNA sequences in taxonomy and classification (Chethana et al. 2021). With these implementations, the dual nomenclature (e.g., Saccardo 1904) was abandoned and the ‘one fungus, one name’ concept for pleomorphic taxa was implemented (McNeill et al. 2011). Thus, maintaining separate classification systems for asexually typified genera was redundant, and all genera were incorporated into a natural classification. Wijayawardene et al.

(2020a) compiled both sexually typified and asexually typified genera into one classification. At the same time, the authors recognized the importance and necessity of developing and maintaining a continuously updated webpage based on new publications and new concepts or ideas. Hence, Wijayawardene et al. (2020a) introduced ‘*outlineoffungi.org*’, which provides the classification of the kingdom *Fungi*. The website is currently being updated based on new studies and publications.

Operation of Outline of Fungi and fungus-like taxa

With the advent of molecular techniques, fungal taxonomy and classification have undergone a revolution (Ullah et al. 2022). Thus, the availability and accessibility of data to the end user are critical (Durkin et al. 2020). In the past decade, numerous databases have been established that provide easy access to fungal data (Jayasiri et al. 2015, Prakash et al. 2017, Nilsson et al. 2019, Pölme et al. 2020, Zanne et al. 2020, Ullah et al. 2022, Zhou & May 2022). Some databases are restricted to molecular, morphological, or ecological data (Nilsson et al. 2019, Ullah et al. 2022, Zhou & May 2022), while others are designed for specific fungal groups. They also mainly deal with taxonomy, such as <https://marinefungi.org/> (Jones et al. 2019), www.freshwaterfungi.org (Calabon et al. 2020), <https://gmsmicrofungi.org> (deals with microfungi from the Greater Mekong Subregion; Chaiwan et al. 2021), theyeasts.org (yeasts), <https://eumycetozoa.com> (fungus-like taxa such as *Myxomycetes*, *Dictyosteliomycetes* and *Protosteliomycetes*; Lado 2005–2023), <https://invertebratefungi.org/> (invertebrate-associated fungi and fungus-like taxa; Wei et al. 2022), <https://botryosphaerales.org> (Wu et al. 2021) and <https://www.fusarium.org/> (commonly referred to as FUSARIOID ID database that deals with *Fusarium* and fusarium-like genera, primarily for DNA-based identification and taxonomy). The classification of fungi is constantly and inevitably changing due to the discovery of new taxa, the use of novel DNA based techniques to better understand relationships, and the incorporation of more DNA sequences from multigenes and increasingly whole genome datasets to reanalyse existing classification schemes. Sometimes databases may also become obsolete over time (Prakash et al. 2017) often due to a lack of curation. Many taxonomic studies tend to overlook important features, such as ecology, which are crucial sources of information for fungal identification and biological conservation (Durkin et al. 2020). Where possible, this type of information should be made available.

The registration of new taxa, combinations, and typifications in one of the three taxonomic repositories, Index Fungorum, MycoBank (Crous et al. 2004), and Fungal Names (<https://nmdc.cn/fungalnames>) is a condition of validity of these operations (May 2017, May et al. 2019, art. 5.F) and as they are linked to the other repositories, they are constantly being updated. Subsequently, the *Outline of Fungi and fungus-like taxa* database will provide a biannual update on new information, which will be curated by members of the consortium. The cross-database communications will help to identify and fill gaps, increase the discovery of, and improve the focus on genetic, ecological, and evolutionary information (Zanne et al. 2020). Thus, we expect to derive a stable classification of the Fungi and fungus-like taxa over time (Lado & Eliasson 2022).

Notes on problems with classifications, nomenclature and taxonomic concepts

The *Outline of Fungi* online database presented here will provide updated information on taxonomic changes in the notes part. Newly introduced taxa will be assigned to curators by the head curators. A note for newly introduced genera and higher-level taxa will be provided, which includes the current classification, synonyms, morphological characters, habitat, host, lifestyle, molecular evidence, phylogenetic placement, and current issues in the classification and nomenclature, including controversial topics. The curators will write notes on their expertise, which will be corrected and edited by the head curator. The author(s) of the original paper, where the genera or higher-level taxa were introduced, will not usually write the entry to avoid partiality.

The notes will be linked to the repositories Index Fungorum, MycoBank, and Fungal Names. Furthermore, the fungal names will be linked to relevant databases such as *coelomycetes* (<https://www.coelomycetes.org>; Huanraluek et al. 2021), *Dothideomycetes* (<https://dothideomycetes.org/>, Pem et al. 2019), Faces of Fungi (<http://www.facesoffungi.org>;

Jayasiri et al. 2015), Freshwater fungi (<http://fungi.life.illinois.edu/>; Calabon et al. 2020), Genera of Fungi (<https://fungalgenera.org/>), Lichenicolous fungi (<http://www.lichenicolous.net/>), Macrofungi (<https://nmdc.cn/macrofungi/>; He et al. 2022b), Marine fungi (<https://marinefungi.org/>; Jones et al. 2019), One stop shop to genera of phytopathogens (<https://onestopshopfungi.org/>; Jayawardena et al. 2019), fungus-like taxa (<https://eumycetozoa.com/>; Lado 2005–2023), *Sordariomycetes* (<https://sordariomycetes.org/>, Bundhun et al. 2020), theyeasts.org and UNITE (<https://unite.ut.ee/>; Nilsson et al. 2019). The online preprint of notes will be sent to the corresponding curator for final approval before the notes are posted on the outline webpage periodically as new taxa are published. All the notes and the new classification will be published biannually in the ‘*Outline of Fungi and fungus-like taxa*’ towards the end of the following year.

While new genera and higher-level taxa introduced in the preceding year are easy to determine and include in the biannual outline, it is difficult to trace changes in the classifications that are published in papers that do not include new taxa. This problem has also been encountered on other webpages, such as Index Fungorum (P. Kirk, personal communication). It can be reduced by the participation of more than 500 curators who are experts on various groups of fungi and can provide an updated classification of their expert group. However, it is unlikely that even with more than 500 curators, the whole spectrum of fungi can be curated adequately. Therefore, alongside the *Outline*, a database *Fungalpedia* (Hyde et al. in press) will, over time, provide up-to-date notes on all genera of fungi so that the classification can also be updated. If there is a major disagreement in any classification, both sides of the disagreement will be encouraged to present entries in the outline justifying their opinion. The links to the entries in *Fungalpedia* will be added to the entry in the master file of the outline. Thus, this database will act as a user-friendly and informative platform that directs and allows users to browse and retrieve all the relevant updated information.

Use of molecular and evolutionary data to improve fungal classification

The classification of fungal species has historically relied heavily on the study of morphology (Taylor et al. 2000, Hyde et al. 2010). In fact, the initial investigations into fungal diversity were primarily conducted through field observations of macro- and micro-morphological characteristics (Truong et al. 2017, Cazabonne et al. 2022), establishing morphology as a fundamental aspect of early fungal diversity studies. However, morphology alone can lead to misidentifications due to overlapping structural characters shown by fungi (Hyde et al. 2009, Marin-Felix et al. 2020, Bhunjun et al. 2021b, Senanayake et al. 2022). Several studies have demonstrated that morphological cryptic masks the true diversity of taxa, whereas circumscriptions based on molecular data often reveal the presence of distinct lineages (Hyde et al. 2009, Manamgoda et al. 2014, Haelewaters et al. 2022, Leontyev et al. 2023a). On the other hand, one particular phylogenetically circumscribed species can also exhibit phenotypic plasticity which ultimately can result in categorizing taxon below species level (Van Caenegem et al. 2023). Accurate species identification is crucial to more accurately estimate the number of species, considering that the kingdom *Fungi* comprises, perhaps, 2.3–3.8 million species, but only about 156,000 of these have been properly named and classified (Hawksworth & Lücking 2017, Hyde et al. 2020a, Bhunjun et al. 2022, 2023, Phukhamsakda et al. 2022). Accurate species identification is also important to take necessary actions for effective plant disease control, quarantine measures, medical and veterinary mycology treatment (Opathy & Gabaldón 2019, Bhunjun et al. 2021a, Jayawardena et al. 2021a, b), biotech industry and patenting, agro-food industries (both in terms of spoilage and technological fungi), product authorisation (EFSA 2021), as well as for species conservation. Accurate species identification is a fundamental requirement for the comprehensive assessment of various aspects pertaining to specific fungal species, such as their geographic distribution, population dynamics, habitat preferences, and ecological interactions. These crucial criteria are employed to further evaluate the potential threats faced by these species and determine their conservation status. However, the process of identifying fungal species and individuals is often impeded by various challenges, thereby hindering the accurate evaluation of these aforementioned factors (Dahlberg & Mueller 2011, Mueller et al. 2022).

Molecular studies have enhanced the way in which fungal species are defined and identified, clarifying inter- and intra-species phylogenetic relationships and correcting taxonomical errors arising from the phenotypic classification and identification methods used in the past. For this reason, the long-held convention of fungal species having two or more valid names for their teleomorph (sexual) and anamorph (asexual) states was abandoned in 2013 (Hawksworth et al. 2011). Moreover, advances in DNA based techniques and analyses revealed extensive genetic variation within species, leading to the description of new species (Kidd et al. 2023). The ITS region is often considered to include the whole ITS1-5.8S-ITS2 fragment of the ribosomal DNA and is the universal barcode marker for fungi, and it is commonly used to identify taxa to genus level in the case of speciose genera (Schoch et al. 2012, Bhunjun et al. 2021b); however, this is not the case with, e.g., within some groups of rust fungi (*Pucciniales*) (Ebinghaus et al. 2022, 2023a,b) or fungus-like protists (Leontyev & Schnittler 2022). For some fungal groupings, high levels of intragenomic variation compromise the utility of ITS. However, the introduction of the full ribosomal operon as extended fungal barcode alleviated some of these problems (Wurzbacher et al. 2019). Thus, accurate species-level identification now mainly relies on multi-gene analyses, and it is recommended to use a polyphasic approach based on multiple species recognition criteria (Simões et al. 2013, Jeewon & Hyde 2016, Bhunjun et al. 2020, Phukhamsakda et al. 2020, Chethana et al. 2021, Gannibal 2022, Haelewaters et al. 2022). Phylogenetic analyses are also the most commonly used method to infer the evolutionary relationships of fungal species based on molecular data (Laurence et al. 2014, Naranjo-Ortiz & Gabaldón 2019, Bhunjun et al. 2021b, Chethana et al. 2021, Strasser et al. 2021., Ebinghaus et al. 2022, Su et al. 2022 García-Martín et al. 2023).

Divergence time estimates (based on molecular clocks/dating) is also increasingly being used to unravel evolutionary relationships, origin and divergence of species. These analyses have also provided evidence to support the ranking of taxa (Zhao et al. 2016a, 2017, Hyde et al. 2017, Liu et al. 2017a, Guterres et al. 2018, Zhang et al. 2018b, He et al. 2019). Several studies have used divergence time estimates as additional evidence to introduce new families (Mapook et al. 2016, Phukhamsakda et al. 2016, Bhunjun et al. 2021c) and to support the ranking of taxa at higher levels (Pérez-Ortega et al. 2016, Samarakoon et al. 2016, Hyde et al. 2017, Zhao et al. 2017, Haelewaters et al. 2019). An ultrametric tree derived from divergence time estimates is also needed for analyses such as the general mixed Yule coalescent method and ancestral character state analysis (Parnmen et al. 2012, Zhao et al. 2016b, Thiyagaraja et al. 2020, Bhunjun et al. 2021b, Samarakoon et al. 2022). Coalescence methods play an important role in demarcating species as they provide a solution for incongruence among gene trees (Fujisawa & Barraclough 2013). These methods are becoming increasingly important in resolving cryptic species (Fujita et al. 2012, Fujisawa & Barraclough 2013, Sánchez-Ramírez et al. 2015, Bhunjun et al. 2021b).

The use of whole genome data for classification

Fungi, being one of the most diverse and speciose kingdoms, is estimated to have 2.3–3.8 million species, among which less than 10% have been identified (Blackwell 2011, Hawksworth & Lücking 2017, Baldrian et al. 2022). Several studies proposed the use of genome-wide phylogenies for species delimitation, as genome data can limit the impact caused by individual genes and produce a phylogeny that gives a snapshot of the entire genome (Fitzpatrick et al. 2006, Sobel et al. 2010, Steele & Pires 2011, Bobay & Ochman 2017, Hibbett et al. 2017, Zhao et al. 2017, Matute & Sepúlveda 2019, Xu 2020, Chethana et al. 2021, Chen et al. 2023). As this technique becomes widely used and prices become more acceptable, dedicated pipelines to facilitate genome-wide phylogenetic analyses of fungi are beginning to emerge (Kim et al. 2023). Molecular data have shown whether taxonomic groups that have been classified and named based on common morphological or phenotypic characters share a single common ancestor (i.e., monophyletic) or whether they have mixed ancestry (i.e., polyphyletic). In the case of polyphyletic genera, transferring the species that do not share a common ancestry into a more appropriate genus is clearly justified (Kidd et al. 2023). Molecular techniques, specifically multi-gene phylogenetic analyses, have become common approaches in most research studies, improving fungal taxonomy (Hibbett et al. 2007). However,

research has shown that phylogenetic analyses using multi-genes may lead to erroneous phylogenetic interpretations due to insufficient information, gene-specific noises, the availability of sequences from only a few markers (mostly for ribosomal genes only), and incongruent phylogenies generated from different individual gene trees. The latter two issues cause poor resolution in the deep internal branches and poorly supported clades (Ebersberger et al. 2012, Xu 2016, 2020, Matute & Sepúlveda 2019, Chethana et al. 2021, García-Cunchillos et al. 2022, Liimatainen et al. 2022). In addition, whole genomes provide sufficient data to resolve internal nodes deeper in phylogenomic trees, and relationships evolved in short divergence times (James et al. 2020, Chen et al. 2023, Han et al. 2023). For example, there are many controversies around the class *Sordariomycetes* due to the introduction of numerous families and other higher ranks based mainly on a few markers, resulting in a grouping of phylogenetically unrelated taxa (Hyde et al. 2020b, Maharachchikumbura et al. 2022), low-resolution phylogenies and phylogenetic inconsistencies among different studies (Senanayake et al. 2018, Voglmayr et al. 2018, Hyde et al. 2020b, Samarakoon et al. 2022, Sun et al. 2022). Chen et al. (2023) conducted a phylogenomics analysis with 1,224 conserved protein sequences, covering 625 species across 50 families, 17 orders, and five subclasses. Their phylogenomic analyses demonstrated well-supported higher-level ranks, species-level phylogenies, and a strengthened backbone for *Sordariomycetes*, providing confirmative phylogenomic evidence to resolve some long-term debates in the mycological community. In addition to phylogenomics, comparative genomics establishes a robust evolutionary framework for fungal classification by decoding the genomic content responsible for functional and morphological similarities and divergences among closely related taxa (Floudas et al. 2012, Shen et al. 2018, Chethana et al. 2021, Wibberg et al. 2021, Díaz-Escandón et al. 2022).

Among different phylogenomic approaches, the two most commonly used are i) the concatenated approach, which mainly infers relationships at deeper internal nodes, and ii) the coalescence approach, which resolves relationships at shallow nodes of the fungal tree (Matute & Sepúlveda 2019, James et al. 2020, Chen et al. 2023). Some studies employ both (Shen et al. 2018, Davis et al. 2019, Li et al. 2021, Strasser & Monaghan 2022), whereas some employ only one (Shen et al. 2016). Both nucleotides and amino acids (protein sequences) have been used for phylogenomics (Li et al. 2021, Wibberg et al. 2021, Strasser & Monaghan 2022, Chen et al. 2023). A previous study suggested that protein-level phylogeny reflects evolutionary divergence better as it directly correlates with the morphology and function of fungi (Chowdhury & Garai 2017). Furthermore, protein sequences evolve more slowly, as slight “silent” changes at the nucleotide level do not necessarily alter the protein sequences. Regier et al. (2008) showed that relatively slow-evolving genes produce higher congruence in their respective gene trees compared to those of fast-evolving ones, and the exclusion of the latter resulted in improved node support (Philippe et al. 2000, Nozaki et al. 2007). Similarly, Wibberg et al. (2021) demonstrated that the use of protein sequences facilitated a more robust inference of relationships between fungal families and higher ranks.

Li et al. (2021) established a robust phylogenetic framework to assess fungal evolution and resolve conflict-prone and poorly supported major lineages in the fungal kingdom. They also established those that are sisters and the degree to which current taxonomy reflects their evolutionary relationships using 1,707 publicly available genomes of 1,679 taxa, representing every known major lineage across fungi and 28 taxa representing the outgroup. This study provided evidence that the relative evolutionary divergence (RED) of the current taxonomic ranks is consistent with their relative divergence times, resulting from the relaxed molecular clock approach, supporting the use of divergence times as a ranking criterion in fungal classification as suggested by previous studies (Avice & Johns 1999, Zhao et al. 2016a, 2017, Tedersoo et al. 2018). Using a smaller taxon-reduced but more balanced dataset, which allowed for computationally intensive analyses using best-fitting evolutionary models, Strasser & Monaghan (2022) resolved several contested deep nodes in the fungal tree of life, such as a sister relationship of *Chytridiomycota* to all other non-*Opisthosporidia* fungi (with *Chytridiomycota* being sister to *Monoblepharomycota* + *Neocallimastigomycota*), a branching of *Blastocladiomycota* + *Sanchytriomycota* after *Chytridiomycota* but before other non-*Opisthosporidia* fungi, and a branching of *Glomeromycota* as sister to the *Dikarya*. Recently, Groenewald et al. (2023) used the RED approach to reclassify the subphylum *Saccharomycotina* to

make it consistent with high level classifications of another *Ascomycota*. Since the 2010s, several phylogenomic studies have been conducted separately for diverse *Fungi* and fungus-like taxonomic groups for species delineations, such as *Aspergillaceae* (Steenwyk et al. 2019), *Cortinariaceae* (Liimatainen et al. 2022), *Glomeromycota* (Montoliu-Nerin et al. 2021), *Hypoxylaceae* (Wibberg et al. 2021), *Peronosporomycetes* (McCarthy & Fitzpatrick 2017), *Parmeliaceae* (Pizarro et al. 2018), *Peltigera* (Magain et al. 2017), *Rhizopus* (Gryganskyi et al. 2018), *Sordariomycetes* (Chen et al. 2023), *Trichoderma* (Druzhinina et al. 2018) and *Tilletia* (Nguyen et al. 2019), as well as to establish higher level classifications (Fitzpatrick et al. 2006, Spatafora et al. 2016, Shen et al. 2018, 2020, Johnston et al. 2019, Haridas et al. 2020, Li et al. 2021, Montoliu-Nerin et al. 2021). Based on the ability of the genomic data to eliminate inconsistencies in multi-gene phylogeny and to integrate diverse criteria in fungal taxonomy, Xu (2020) proposed a new genome sequence-based fungal recognition criterion, the genomic species recognition.

Comparative genomics approaches such as percentage of conserved proteins (POCP), average nucleotide identities (ANI), average amino acid identities (AAI), and shared and individual genes and gene families between taxa facilitate the establishment of relationships and taxonomic hierarchies as well as possible lifestyles (Wibberg et al. 2021). Changes to genomic content can occur because of selection pressure or other evolutionary forces like gene flow and bottleneck effects, hence reflecting evolution way better than sequence data. Whiston & Taylor (2016) suggested that gene family expansions and contractions influenced by adaptive radiation led to species or generic-level adaptations. Therefore, changes in genome content are often more suitable to distinguish species than those in nucleotide sequences of the selected markers. Wibberg et al. (2021) successfully used these genomic comparisons to differentiate *Hypoxylaceae* species. Though this approach has been applied previously to other organisms (Nobrega & Pennacchio 2004), this is the first study to apply genomic comparisons to deduce taxonomic hierarchies in fungi.

Since these are all sequence-based classification approaches, the accuracy of the completeness and whole genome sequences, their annotation and the associated metadata must be ensured for effective and efficient phylogenomic analyses. Furthermore, sequencing errors and misassemblies can strongly influence protein-level phylogenomic reconstructions. Therefore, prior to analysis, it is important to establish that the target genomes are of high quality (Zhou 2023). Collectively, these studies demonstrate the success achieved using genomic data via phylogenomic reconstructions and comparative genomic approaches to re-evaluate current taxonomic concepts.

Morphology in the molecular era of fungal classification

Morphological characterization of newly described fungal taxa is still needed in the molecular era of fungal classification (Hyde et al. 2010). The written parts of a description should focus on the shapes, colours and typical dimensions (length, width, breadth) of the fungal elements (usually hyphae or yeast cells, mature spores, and sporogenesis), focusing on those with a distinctive diagnostic value over similar taxa. The shape descriptions (if possible) should be made with examination in the living state (Baral 1992, Dominguez de Toledo 1994), following the recommendations given in the Dictionary of Fungi (Kirk et al. 2008). Image analysis is a novel, high-throughput method that allows the automated recording and evaluation of microscopic images (Posch et al. 2012). Colony colours can be determined by the 'RGB profiling' procedure (Puchkov 2016). Line drawings and microphotographs (preferably both) are essential elements of a useful description. Authors should consider which illustration technique is most relevant to show key characteristics (Fawcett 1987). Details hardly visible on photographs should be illustrated with line drawings, SEM, or different focus /illumination settings of a light microscope. High quality descriptions should show more than one spore, all of them rotated in the same orientation, which will facilitate visual recognition (Harman et al. 1999). The appearance of the colony on the host, natural, and/or artificial substrate is also required in some taxa. Scale bars should be used instead of an indication of magnification. Figure legends should contain the full *genus* and *species* names and the techniques (e.g., staining) used to produce the figure.

The use of ecology to improve fungal classification

Fungi are often considered a hidden component of the ecosystem and play crucial roles as decomposers, antagonistic or mutualistic symbionts of animals, plants, and other organisms. Fungi are essential for the recycling of nutrients in all habitats and interact in various ways with themselves, with representatives of other phylogenetic groups, and with organic and inorganic substrates (Dilly & Munch 2001, Dilly et al. 2004, Osono 2017, Jeewon et al. 2018, Zhang et al. 2018a, Gkoutselis et al. 2021, Chen et al. 2022a). Pieces of evidence also tend to suggest that aquatic fungi may be important promoters of nutrient and energy transfer in aquatic ecosystems (Danger et al. 2016). In addition, fungi exist in almost every conceivable habitat where organic carbon is available (e.g., freshwater, marine water, soil, rock surfaces, plants and animals, microplastic), which causes a vast range of variation in their morphology, reproduction, life cycles and modes of dispersal (Tsui et al. 2016, Grossart et al. 2019, Hyde et al. 2020a, Chen et al. 2022b). Ecological information, together with fungal identification, is important to achieve the predicted fungal diversity and ultimately fungal classification (Hyde et al. 2020b). However, although only some 156,000 species of fungi have been formally described and are accepted in the fungal kingdom so far, the ecological strategies they have evolved have been very successful even in adverse (Cantrell et al. 2011) or special environmental conditions, e.g., plant trichomes (Pereira-Carvalho et al. 2009). Giant diverse ecosystems such as those present in the African savannas are unexplored, while Neotropical vegetation is also underexplored (Dianese et al. 2022).

In recent years, an enormous number of unidentified molecular operational taxonomic units (OTUs) or amplified sequence variants (ASVs) were discovered because of ecological studies of fungal diversity (e.g., fungal succession) using high-throughput sequencing techniques (O'Brien et al. 2005, Porter et al. 2008, Ge et al. 2017, Li et al. 2017, Pietsch et al. 2019, Gui et al. 2020, Purahong et al. 2022). These sequences show the high diversity of fungal resources; however, the naming of taxa is required for fungal classification under the International Code of Nomenclature for Algae, Fungi and Plants. Numerous deposited sequences, however, lack taxonomic assignment, resulting in a great amount of 'uncultured fungus' unvouchered sequences (Hofstetter et al. 2019) unlikely to be integrated into any fungal classification. Numerous mycologists have suggested that an integrated naming system is needed to facilitate unambiguous communication (Hibbett et al. 2011, Hawksworth et al. 2018, Ryberg & Nilsson 2018, Nilsson et al. 2023). Mycologists have debated the inclusion of molecular operational taxonomic units in taxonomy (Zamora et al. 2018), and the subject is still being discussed. Hongsanan et al. (2018) provided case studies on some genera (*Botryosphaeria*, *Colletotrichum*, *Penicillium*, and *Xylaria*) and illustrated that it is inappropriate to use DNA as holotypes in assigning names to fungal species due to the shorter fragments of internal transcribed spacer (ITS) obtained from environmental sequencing. In the meantime, Wu et al. (2019) proposed that attempts to obtain cultures of specimens as physical types should be the priority, the complete genome sequence of fungi (single-cell genome) as a DNA type is the second choice, and fungal sequence data generated from environmental genomic DNA can be a temporary digital type. Thus, these ecology-based studies have remarkable significance for revealing unknown fungal taxa and supporting fungal classification. As shown by Nilsson et al. (2023) "species discovery through environmental sequencing vastly outpaces traditional, Sanger sequencing-based efforts, in a strongly increasing trend over the last five years".

Fungal ecology-related aspects of fungal classification provide many merits, but there are also some misconceptions. One is that most historical fungal identifications were made based on cyanobacterial, algal, plant, or animal host associations (Jeewon et al. 2004, Dayarathne et al. 2016, Liu et al. 2017). This approach is quite error-prone and has resulted in species with few character differences and egregious misidentifications. For instance, according to assessments of *Pestalotiopsis* species by Jeewon et al. (2004) and Maharachchikumbura et al. (2014), numerous species that have been described based on host association (without phylogenetic data) are probably not valid species. An assumed very narrow natural host range of a fungus may potentially be much wider, as shown in an experimental setup with a carabidicolous *Laboulbenia* species (De Kesel 1996). On the other hand, a single host can support different species belonging to the same genus. For example, Jeewon et al.

(2004) revealed two species of the endophytic genus *Pestalotiopsis* (*P. sydowiana* (Bres.) B. Sutton and *P. theae* (Sawada) Steyaert) from *Protea mellifera* Thunb., and neither species appears to be closely related. Liu et al. (2017) introduced eight *Pestalotiopsis* species and three *Pseudopestalotiopsis* species from a single host. Thus, host-based fungal species nomenclature reflects multiple misleading points and needs molecular approaches for better resolution for identification and ultimately fungal classification. New host records are also extremely important (Hyde et al. 2020c) because they can reveal the diversity of adaptations and evolutionary traits of a species.

The use of chemical profiles to improve fungal classification

Fungi are diverse in terms of their morphology, ecology, and chemical profiles (Naranjo-Ortiz & Gabaldón 2019). There are 845 publications and 26,288 citations on the Web of Science website using the keywords ‘fungi’, ‘natural product’ and ‘classification’ and 259 publications with 4,662 citations with the words ‘fungi’ and ‘chemotaxonomy’ from 2010 to 2022. Many publications highlight the advantages of involving chemical profiles in fungal classifications (Frisvad et al. 2008, Raja et al. 2017, Reich & Labes 2017, Guo et al. 2021, Maharachchikumbura et al. 2021). Morphological characters in speciose groups can be misleading due to cryptic speciation, hybridization, and convergent evolution (Raja et al. 2017, Sun et al. 2019, Boekhout et al. 2022); therefore, the application of chemotaxonomy has often been used to increase the efficiency of identifying, exploring and exploiting fungi (Frisvad 2015). However, studies have suggested that the secondary metabolite, also referred to as specialized metabolite profiles in fungi can be strain-specific, species-specific, or common to all species. This could be because fungal extracts include secondary as well as primary metabolites. In yeasts, growth patterns have been used for decades, as well as biochemical tests, i.e., chemotaxonomy (Kurtzman et al. 2011). Also, it is crucial to note that even minor changes in cultivation conditions can lead to a profound shift in the fungal metabolomic profile, underscoring the importance of maximizing the number of culture media and conditions to comprehensively assess the fungal metabolome (Rédou et al. 2016)

Chemotaxonomy is commonly used to classify and identify filamentous fungi using their chemical diversity for taxonomic purposes. This commonly consists of compounds produced on different media and includes toxins, antibiotics and other compounds defined very broadly, such as fatty acids, proteins, carbohydrates, or secondary metabolites, (Frisvad et al. 2008). However, not all compounds can be used for chemotaxonomy as the profile is based only on compounds with differentiation ability (Frisvad et al. 2008). Most fungi are fast-growing and have a high reproductive capacity; thus, metabolite profiles are generally unique in an individual group (Walker & White 2017). Different fungal species can produce one or more common secondary metabolites. For example, cytochalasin D has been reported as being produced by several fungal species in phylogenetically different groups, such as *Basidiomycota* (*Coriolus vernicipes* (Berk.) Murrill) and *Ascomycota* (*Hypoxylon terricola* J.H. Mill., *Metarhizium anisopliae* (Metschn.) Sorokīn and *Zygosporium masonii* S. Hughes) (Cole et al. 2003, Vicente et al. 2003). The hypocrealean genus *Pochonia* produces several secondary metabolites such as monordens and other resorcylic acid lactones, citreoviridin A and aurovertin B, common to *Penicillium* and *Aspergillus* species (Stadler et al. 2003).

Chemotaxonomy is very helpful in delimiting species, especially in the resolution of species complexes that could not have been distinguished based on classical morphology and can be used as chemotaxonomic markers in comparative studies (Saag et al. 2009, Læssøe et al. 2010, Surup et al. 2014, Kuhnert et al. 2017, Dickschat et al. 2018, Rinkel et al. 2018, Lambert et al. 2019, Ekman & Tønsberg 2022). Fatty acids have been used as potential chemotaxonomic markers for identification in *Albugo*, *Cunninghamella*, *Mortierella*, *Mucor*, *Plasmopara*, *Puccinia*, *Pustula*, *Rhizomucor* and *Wilsoniana* species (Blomquist et al. 1992, Weete & Gandhi 1999, Spring & Haas 2002, Spring et al. 2005, Wołczańska et al. 2021). Some hypoxylean taxa, such as *Hypoxylon griseobrunneum* (B.S. Mehrotra) J. Fourn., Kuhnert & M. Stadler, *H. invadens* J. Fourn. and *H. macrocarpum* Pouzar, yielded several new natural volatiles that can be used as chemotaxonomic markers for a comparative

volatiles study (Dickschat et al. 2018, Rinkel et al. 2018). In the myxomycete genus *Lycogala*, the presence and structure of crystalline lime in peridial vesicles were shown to be a useful criterion for delimiting species (Leontyev et al. 2022, 2023b).

Use of integrative approaches to improve fungal classification

Concurrent application of multiple characters or integrative approaches has the power to reduce confusion in identifications and help to improve contrasting classifications arising from various species concepts based on phenetics, phylogeny, ecology, evolution, chemistry, and physiology. Using polyphasic approaches based on morphological, molecular, and chemotaxonomic data is recommended and appears to provide a more useful classification tool, and is helpful in delimiting species (Stadler et al. 2014, Cao et al. 2021, Maharachchikumbura et al. 2021). In addition, biosynthesis, physiological, and genotypic information show functional characteristics that can improve the potential industrial production of fungal metabolites (Keller 2019).

The use of physiology to improve fungal classification

Although not so common, physiological tests can be a useful tool for fungal classification. Basidiomycetous yeasts produce urease amongst other enzymes (i.e., see Kurtzman et al. 2011 and theyeasts.org), with quite extensive growth profiles, whereas in ascomycetous yeasts that enzyme is mostly lacking. Splitting of esculin by *Apophysomyces elegans* P.C. Misra, K.J. Srivast. & Lata growing on bile esculin agar is sufficient to separate that species from the rest of the genus (Alvarez et al. 2010). Fermentation and utilisation of compounds have proven useful for circumscription of genera, for example, *Mrakia* (glucose-fermenting basidiomycete), *Ogataea* (methanol assimilation), and *Scheffersomyces* (xylose fermentation).

Professional criticism of mycological scientific work

Mycologists have different opinions, which could be subject to different interpretations, and unlike computers, humans make mistakes. This might involve missing references, poor alignments, ambiguous trees, and incorrectly deposited or missing data, amongst others. Phylogenomic information obtained from multi-gene sequences must be coupled and complemented with morphological characters during taxonomic studies (Hyde et al. 2010). In this context, reference to type specimens should be emphasized to adequately calibrate the morphological definition of species. Efforts should further include obtaining DNA sequences from type specimens of already described species and using these sequences in phylogenetic analyses whenever possible to ensure a direct reference to taxa within the phylogeny (e.g., Forin et al. 2018, Ronikier et al. 2022). The separation of genotype and phenotype criteria increases the frequency of mistakes by mycologists, which can be observed in mycological publications. It is essential that when other scientists encounter these mistakes, they should point them out. This might involve notifying the authors, asking for data that were not deposited, or discussing the work in publications. Most importantly, though, any criticism should be written professionally. It is rare that scientists deliberately publish incorrect research or data, although it is known to happen. However, it is not always possible to pick up every error. An eminent Chinese mycologist once stated that the job of the supervisor “is to find the silly hidden mistakes that students make in papers submitted for comment”. Unfortunately, scientists can make mistakes, and professionally worded criticism or helpful advice will be much better received. Unhelpful or spiteful criticism does not help the situation and may discourage new scientists from continuing in their careers. The number of mycologists has been declining rapidly in Western countries; meanwhile, there have been an increasing number of mycologists being trained in other countries, such as Brazil, Thailand, and China. Members of the community should engage in encouraging and helping all who are interested in continuing their careers (Hyde et al. 2010).

Therefore, in the *Outline of Fungi and fungus-like taxa* and other related publications, we will follow our ethics of professional criticism of mycological scientific work. We hope that these ethics will be adopted throughout the mycological literature.

Voting for opinions on problems of classification, nomenclature and taxonomic concepts

In cases where there are major differences in opinion regarding classification, nomenclature, and taxonomic concepts, we will encourage authors with opposing views to write arguments supporting their approaches and publish these in the outline. In some cases, we may need to follow one approach and also list a different one in the notes or outline. We may also send arguments, disseminated through electronic emails, to the consortium and ask them to vote on their preference, including a comment on their point of view, in a confidential online vote. The results of the vote can then be presented to the International Commission on the Taxonomy of Fungi and the Nomenclature Committee for Fungi with opinions and percentages of votes for and against each view. The members of the consortium are listed in Table 1 with their expertise and country.

Table 1 List of mycologist names, expertise, and countries.

Name	Expertise	Country/Region
Abdel-Wahab Mohamed A	Marine fungi	Egypt
Abdollahzadeh Jafar	<i>Dothideomycetes</i> , phytopathogens	Iran
Abeywickrama Pranami D.	<i>Dothideomycetes</i> , phytopathogens	China
Absalan Sahar	<i>Eurotiomycetes</i>	Thailand
Afshari Naghmeh	<i>Ascomycota</i>	Thailand
Ainsworth A. Martyn	Poroid and corticioid <i>Basidiomycota</i> , <i>Hygrocybe</i> s.l. and stipitate hydroids	UK
Akulov Olexander Yu	<i>Ascomycota</i> , fungicolous and plant-associated fungi	Ukraine
Aleoshin VV	Eukaryotes (in general), <i>Holomycota</i>	Russia
Al-Sadi Abdullah Mohammed	Phytopathogens	Oman
Alvarado Pablo	<i>Pezizales</i>	Spain
Alves Artur	<i>Botryosphaeriales</i> , phytopathogens, marine fungi	Portugal
Alves-Silva Genivaldo	Polypores (<i>Polyporales</i> / <i>Hymenochaetales</i>)	Brazil
Amalfi Mario	Polypores / wood decay fungi / (<i>Polyporales</i> / <i>Hymenochaetales</i> / <i>Cantharellales</i> / <i>Boletales</i> / <i>Russulales</i>)	Belgium
Amira Yacoub	<i>Leotiomycetes</i>	Brazil
Amuhenage Tharindu Bhagya	Aquatic fungi	Thailand
Anderson Jennifer	Aquatic fungi	Sweden
Antonín Vladimír	<i>Basidiomycota</i> (macrofungi)	Czechia
Aouali Souhila	Macrofungi and forest tree pathogenic fungi	Algeria
Aptroot Andre	<i>Dothideomycetes</i> , lichenized fungi	Netherlands
Apurillo Carlo Chris S	Mangrove fungi, marine fungi	Philippines
Araújo João PM	Insect-associated hypocrealean fungi	Brazil
Ariyawansa Hiran A.	<i>Dothideomycetes</i> , phytopathogens	Taiwan
Armand Alireza	<i>Sordariomycetes</i> , phytopathogens	Iran, Thailand
Arumugum Elangovan	<i>Hymenochaetaceae</i>	India
Asghari Raheleh	Marine fungi	Iran, Thailand
Assis Daniele Magna Azevedo	<i>Glomeromycota</i>	Brazil
Atienza Violeta	Lichenized fungi, lichenicolous fungi	Spain
Avasthi S	Phytopathogens	India
Azevedo Egídia	Marine fungi	Portugal
Bai Fengyan	Asco- and basidiomycetous yeasts	China
Bakhshi Mounes	<i>Hyphomycetes</i> , <i>Dothideomycetes</i> , <i>Mycosphaerellales</i> , phytopathogens	Iran
Banihashemi Zia	Fungus-like organisms, <i>Phytophthora</i> and <i>Pythium</i> spp.	Iran

Table 1 Continued.

Name	Expertise	Country/Region
Bao Danfeng	Freshwater fungi, <i>Dothideomycetes</i>	China
Baral Hans-Otto	<i>Leotiomycetes</i> , <i>Orbiliomycetes</i>	Germany
Barata Margarida	Marine fungi	Portugal
Barbosa Flavia	Freshwater and terrestrial asexual <i>Ascomycota</i>	Brazil
Barbosa Renan do Nascimento	<i>Eurotiales</i> (<i>Aspergillaceae</i> , <i>Trichocomaceae</i> , <i>Thermoascaceae</i>)	Brazil
Barreto Robert W	<i>Mycosphaerellaceae</i> , phytopathogens, fungicolous and endophytic fungi and oomycetes	Brazil
Baschien Christiane	Aquatic fungi	Germany
Belamesiatseva DB	Forest phytopathology, invasive pathogens of forest species	Belarus
Bennett Reuel M	Basal fungi, fungus-like organisms	Philippines
Bera I	<i>Basidiomycota</i> (macrofungi)	India, Thailand
Bezerra Jadson Diogo Pereira	<i>Ascomycota</i>	Brazil
Bezerra JL	<i>Ascomycota</i>	Brazil
Bhat D Jayarama	<i>Dothideomycetes</i> , asexual <i>Ascomycota</i>	India
Bhunjun Chitrabhanu S.	<i>Dothideomycetes</i> , <i>Eurotiomycetes</i> , phytopathogens	Thailand
Bianchinotti M Virginia	Fossil fungi, <i>Ascomycota</i>	Argentina
Błaszowski Janusz	<i>Glomeromycota</i>	Poland
Blondelle Aimée	<i>Laboulbeniales</i>	Belgium
Boekhout Teun	Asco- and basidiomycetous yeasts	Netherlands
Bonito Gregory	<i>Pezizales</i> , <i>Mucorales</i> , <i>Endogonales</i> , <i>Mortierellales</i> , truffles	USA
Boonmee Saranyaphat	<i>Dothideomycetes</i>	Thailand
Boonyuen Nattawut	<i>Sordariomycetes</i> , freshwater fungi	Thailand
Bregant Carlo	<i>Botryosphaeriales</i> , <i>Peronosporales</i>	Italy
Buchanan Peter	<i>Basidiomycota</i> (macrofungi)	New Zealand
Bundhun Digvijayini	<i>Sordariomycetes</i>	Thailand
Burgaud Gaëtan	General fungi	France
Burgess Treena	Phytopathogens	Australia
Buyck Bart	<i>Basidiomycota</i> (<i>Russulales</i> , <i>Cantharellales</i> , tropical ECM fungi)	France
Cabarroi-Hernández M.	Polypores / wood decaying fungi / <i>Polyporales</i>	Mexico
Caceres Marcela E. da Silva	Lichenized fungi (tropical crustose, foliicolous)	Brazil
Cadež Neža	Ascomycetous yeasts	Slovenia
Caeiro M. F.	<i>Lulworthiales</i> , <i>Halosphaeriaceae</i>	Portugal
Cai Lei	<i>Sordariomycetes</i>	China
Cai M. Feng	<i>Hypocreales</i> , halophilic fungi	China
Calabon Mark S	Freshwater fungi, marine fungi	Philippines
Calaça Francisco J. Simões	Dung-inhabiting fungi, <i>Ascomycota</i> , <i>Basidiomycota</i>	Brazil
Callalli Chanchhuaña, Mario	<i>Basidiomycota</i> , <i>Agaricomycetes</i>	Peru
Camara Marcos Paz Saraiva	Phytopathogens	Brazil
Cano-Lira JF	<i>Ascomycota</i>	Spain
Cantillo Taimy	Asexual <i>Ascomycota</i> , <i>Sordariomycetes</i>	Brazil
Cao Bin	<i>Basidiomycota</i>	China
Carlavilla Juan Ramón	General fungi, especially <i>Pezizales</i> and <i>Agaricales</i>	Spain
Carvalho A	Medically relevant fungi	Portugal
Castañeda-Ruiz Rafael F.	<i>hyphomycetes</i>	Cuba
Castlebury Lisa	<i>Diaporthales</i> , <i>Ustilaginales</i>	USA
Castro-Jauregui Oscar	Macrofungi, myxomycetes	Mexico

Table 1 Continued.

Name	Expertise	Country/Region
Catania Myriam del Valle	<i>Ascomycota</i>	Argentina
Cavalcanti Laíse H.	Myxomycetes	Brazil
Cazabonne Jonathan	General macrofungi, <i>Laboulbeniales</i>	France, Canada
Cedeño-Sanchez Marjorie Lisset	<i>Xylariales</i>	Germany
Chaharmiri-Dokhaharani S	<i>Polyporales</i>	Thailand
Chaiwan Napalai	<i>Ascomycota</i>	Thailand
Chakraborty Nilanjan	<i>Geoglossales</i>	India
Chaverri Priscila	<i>Ascomycota</i> with emphasis on <i>Hypocreales</i> and <i>Trichoderma</i>	Costa Rica, United States
Cheewangkoon R	Phytopathogens	Thailand
Chen Chao	Coelomycetes	China
Chen Chiyu	General fungi	Taiwan
Chen Jie	<i>Basidiomycota</i>	Mexico
Chen Kohsuan	<i>Eurotiomycetes</i>	Taiwan
Chen Qian	<i>Dothideomycetes</i>	China
Chen Wenhao	Insect fungi	China
Chen Yanpeng	<i>Ascomycota</i>	China
Chethana K.W. Thilini	<i>Dothideomycetes</i> , discomycetes	Thailand
Coleine Claudia	Black fungi, <i>Dothideomycetes Capnodiales</i>	Italy
Corazon-Guivin Mike Anderson	<i>Glomeromycota</i>	Peru
Cortés-Pérez Alonso	<i>Agaricales</i> , <i>Mycenaceae</i> , <i>Psilocybe</i>	Mexico
Costa-Rezende Diogo Henrique	Polypores (<i>Polyporales</i> / <i>Hymenochaetales</i>)	Brazil
Courtecuisse Régis	<i>Basidiomycota</i> (mainly gilled) – mainly Europe and the Neotropics	France
Crouch Jo Anne	Phytopathogens (<i>Calonectria</i> , <i>Clariireedia</i> , <i>Waitea</i> , <i>Colletotrichum</i>), <i>Peronosporaceae</i>	USA
Crous Pedro W	General fungi	Netherlands
Cui Baokai	Polypores, <i>Hymenochaetales</i>	China
Cui Yangyang		China
Czachura Paweł	Resiniculus fungi, sooty moulds	Poland
Da Silva Danielle Karla Alves	<i>Glomeromycota</i>	Brazil
da Silva Gladstone Alves	<i>Glomeromycota</i> , endophytes	Brazil
da Silva Iolanda Ramalho	<i>Glomeromycota</i>	Brazil, USA
da Silva Rejane M Ferreira	<i>Ascomycota</i>	Brazil
da Silva Santos Ana Carla	<i>Fusarium</i> , <i>Hypocreales</i> , insect-associated fungi	Brazil
Dai Dongqin	<i>Dothideomycetes</i>	China
Dai Yucheng	<i>Basidiomycota</i>	China
Dal Forno Manuela	Lichenized fungi	Brazil
Damm Ulrike	<i>Ascomycota</i> (<i>Cadophora</i> , <i>Colletotrichum</i> , <i>Phaeomoniellales</i> , <i>Tympanidaceae</i>)	Germany
Darmostuk Valerii	Lichenicolous fungi, <i>Hypocreales</i> , <i>Acrospermales</i>	Poland
Daroodi Zoha	<i>Xylariomycetidae</i>	Iran
Das Kallol	Soil fungi	Korea
Das Kanad	<i>Basidiomycota</i>	India
Davoodian Naveed	<i>Boletales</i> , <i>Hysterangiales</i>	Australia, USA
Davydov Evgeny A	Lichenized fungi	Russia
Dayarathne Monika	Freshwater fungi, marine fungi	Sri Lanka
de Groot Michiel	<i>Laboulbeniomycetes</i>	Netherlands, Belgium
De Kesel André	<i>Laboulbeniomycetes</i> , <i>Agaricomycetes</i>	Belgium
De Lange Ruben	<i>Russulaceae</i>	Belgium
de Oliveira Neiva Tinti	Phytopathogens	Brazil

Table 1 Continued.

Name	Expertise	Country/Region
de Silva NI	<i>Ascomycota</i>	Thailand
de Souza FA	<i>Glomeromycota</i>	Brazil
Decock Cony	Polypores, wood decay fungi (<i>Polyporales</i> , <i>Hymenochaetales</i> , <i>Russulales</i>), asexual <i>Ascomycota</i>	Belgium
dela Cruz Thomas Edison E	Fungal endophytes, endolichenic fungi, myxomycetes	Philippines
Delgado Gregorio	Asexual <i>Ascomycota</i>	USA
Denchev Cvetomir M	Smuts	Bulgaria
Denchev Teodor T	Smuts	Bulgaria
Dentinger Bryn	<i>Agaricales</i> , <i>Boletales</i>	USA
Devadatha B	Marine fungi	India
Dianese Jose C	<i>Pucciniales</i> , <i>Sordariomycetes</i>	Brazil
Dima Bálint	<i>Entolomataceae</i> , <i>Cortinariaceae</i> , EcM <i>Basidiomycota</i>	Hungary
Diniz Athaline Gonçalves	Fungal entomopathogens	Brazil
Dissanayake Asha J	<i>Dothideomycetes</i>	China
Dissanayake Lakmali S	<i>Sordariomycetes</i>	China
Doğan Hasan Hüseyin	<i>Basidiomycota</i>	Turkey
Doilom Mingkwan	<i>Ascomycota</i>	China, Thailand
Dolatabadi S	<i>Mucorales</i>	Iran
Dong Wei	Freshwater fungi	China, Thailand
Dong Zhangyong	<i>Fusarium</i> , <i>Trichoderma</i>	China
Dos Santos LA	Lichenized fungi	Brazil
Drechsler-Santos Elisandro Ricardo	<i>Hymenochaetaceae</i> (<i>Hymenochaetales</i>), <i>Ganodermataceae</i> , <i>Polyporaceae</i> (<i>Polyporales</i>)	Brazil
Du Tianye	Asexual <i>Ascomycota</i>	China
Dubey Manish Kumar	Zoosporic fungi	India
Dutta Arun Kumar	<i>Basidiomycota</i>	India
Egidi Eleonora	<i>Dothideomycetes</i>	Australia
Elliott Todd F	<i>Ascomycota</i> , <i>Basidiomycota</i> , truffles, fungal ecology	Australia, USA
Elshahed Mostafa S	<i>Neocallimastigomycota</i>	USA
Erdoğan M	General fungi	Turkey
Ertz Damien	<i>Arthoniomycetes</i> , <i>Dothideomycetes</i> , <i>Basidiomycota</i> , lichenicolous fungi	Belgium
Etayo Javier	Lichenicolous fungi	Spain
Evans Harry Charles	Endophytes, entomogenous, phytopathogens	UK
Fan Xinlei	<i>Sordariomycetes</i>	China
Fan Yuguang	<i>Inocybaceae</i> , <i>Agaricales</i>	China
Fedosova Anna G	<i>Ascomycota</i> , <i>Geoglossomycetes</i>	Russia
Fell Jack	Basidiomycetous yeasts	USA
Fernandes Isabel	Aquatic asexual <i>Ascomycota</i>	Portugal
Firmino André Luiz	Epifoliar fungi, entomogenous, phytopathogens, forest pathology	Brazil
Fiuza Patrícia Oliveira	Freshwater fungi	Brazil
Flakus Adam	Lichenicolous and lichenized fungi (tropical)	Bolivia, Poland
Fragoso de Souza CA	Zygosporic fungi (<i>Mucoromycota</i> and <i>Mortierellomycota</i>)	Brazil
Frisvad Jens Christian	<i>Ascomycota</i> , especially <i>Apiospora</i> , <i>Aspergillus</i> , <i>Fusarium</i> , <i>Monascus</i> , <i>Paecilomyces</i> , <i>Penicillium</i> and <i>Talaromyces</i>	Denmark
Fryar Sally C	Freshwater and marine fungi	Australia
Gabaldon Toni	Yeast	Spain
Gábor Péter	<i>Taphrinales</i> , ascomycetous yeasts	Hungary
Gajanyake Achala J	Fungicolous fungi	Thailand

Table 1 Continued.

Name	Expertise	Country/Region
Galindo Luis Javier	Zoosporic fungi and unicellular <i>Holomycota</i>	UK
Gannibal Philipp B	<i>Dothideomycetes</i>	Russia
Garcia Dania	<i>Ascomycota</i>	Spain
Garcia-Sandoval Ricardo	<i>Gloeophyllales</i>	Mexico
Garrido-Benavent Isaac	Lichenized fungi and <i>Basidiomycota</i> (<i>Cortinarius</i>)	Spain
Garzoli Laura	Marine and freshwater <i>Ascomycota</i> , freshwater zoosporic parasites	Italy
Gautam Ajay K	Phytopathogens	India
Ge Zaiwei	<i>Basidiomycota</i>	China
Gené Díaz Josepa	<i>Ascomycota</i>	Spain
Gentekaki Eleni	Basal fungi	Thailand
Ghobad-Nejhad Masoomeh	Corticoid and poroid fungi, wood-inhabiting <i>Basidiomycota</i> , <i>Corticiales</i>	Iran
Giachini Admir J	<i>Gomphales</i> , ECM, agriculture soil fungi	Brazil
Gibertoni Tatiana Baptista	<i>Agaricomycotina</i>	Brazil
Góes-Neto Aristóteles	<i>Basidiomycota</i> , especially <i>Hymenochaetales</i> , <i>Polyporales</i> , <i>Ganodermatales</i>	Brazil
Gomdola Deeksha	Saprobies and forest pathogens	Thailand
Gorjón Sergio P	Corticoid fungi, polypores	Spain
Goto BT	<i>Glomeromycota</i>	Brazil
Granados-Montero María del Milagro	Phytopathogens	Costa Rica
Griffith Gareth W	Anaerobic fungi, grassland <i>Basidiomycota</i> , <i>Hygrophoraceae</i> , <i>Microglossum</i> , <i>Pterulaceae</i>	UK
Groenewald Ewald JZ	<i>Dothideomycetes</i>	Netherlands
Groenewald Marizeth	<i>Ascomycete</i> yeasts	Netherlands
Grossart Hans-Peter Grube Martin	Aquatic fungi, <i>Chytridiomycota</i> lichenized fungi	Germany, Austria
Gueidan Cecile	Lichenized fungi (<i>Verrucariales</i> , <i>Pyrenulales</i>)	Australia
Gunarathne Anujani	Fungi on basal plants	Thailand
Gunaseelan Sugantha	<i>Hymenochaetaceae</i> , <i>Polyporales</i>	India
Gusmão Luis F. Pascholati	Asexual <i>Ascomycota</i>	Brazil
Gutierrez Alejandra C	Entomopathogenic fungi, <i>Laboulbeniomyces</i>	Argentina
Guzmán-Dávalos Laura	Macrofungi	Mexico
Haelewaters Danny	<i>Laboulbeniomyces</i> , <i>Leotiomyces</i> , entomopathogenic fungi	Belgium
Halling Roy	<i>Basidiomycota</i>	USA
Han Yanfeng	Soil fungi	China
Hapuarachchi Kalani K.	<i>Ganodermataceae</i>	China
Harder Christoffer Bugge	<i>Mycenaceae</i>	Denmark
Harrington Thomas C	Forest pathogens	USA
Hattori Tsutomu	Polypores	Japan
He Maoqiang	<i>Basidiomycota</i>	China
He Shuanghui	Corticoid fungi	China
He Shucheng	Phytopathogens	China
Healy Rosanne	<i>Pezizales</i>	USA
Heredia Gabriela	Asexual <i>Ascomycota</i>	Mexico
Hernández-Restrepo Margarita	Asexual <i>Ascomycota</i>	Netherlands
Hodge Kathie T	Insect pathogenic fungi, <i>Ascomycota</i>	USA
Holgado-Rojas Maria Encarnacion	<i>Agaricales</i>	Peru
Hongsanan Sinang	Epi-foliar fungi, <i>Dothideomycetes</i> , <i>Sordariomycetes</i>	China, Thailand

Table 1 Continued.

Name	Expertise	Country/Region
Horak Egon	<i>Basidiomycota, Agaricales and Boletales</i>	Switzerland
Hosoya Tsuyoshi	Discomycetes	Japan
Houbraken Jos	<i>Eurotiomycetes, food and indoor fungi</i>	Netherlands
Huang Shike	<i>Sordariomycetes</i>	China
Huanraluek Naruemon	<i>Dothideomycetes</i>	Thailand
Hur Jae Seoun	Lichenized fungi	Korea
Hurdeal Vedprakash G	Basal fungi/ <i>Chytridiomycota/Mucorales</i>	Thailand
Hustad Vincent P	Discomycetes	USA
Iotti Mirco	Macrofungi (truffles)	Italy
Iturriaga Teresa	<i>Leotiomyces</i>	USA
Janik Paulina	<i>Myxomycetes</i>	Poland
Jany Jean-Luc	<i>Mucoromycota (Mucor), Ascomycota (Cladosporium, Bisifusarium)</i>	France
Jayalal Udeni	Lichenized fungi	Sri Lanka
Jayasiri Subashini C	<i>Dothideomycetes</i>	Australia
Jayawardena Ruvishika S	Phytopathogens	Thailand
Jeewon Rajesh	Phytopathogens	Mauritius
Jerônimo Gustavo Henrique	Zoosporic eufungi	Brazil
Jesus Ana Lucia	<i>Zoosporic eufungi</i>	Brazil
Jin Jing	<i>Ascomycota</i>	China
Johnston Peter R.	Discomycetes	New Zealand
Jones E.B. Gareth	<i>Dothideomycetes</i>	UK
Joshi Y	Lichenicolous fungi	India
Justo Alfredo	<i>Basidiomycota</i>	Canada
Kaishian Patricia	<i>Laboulbeniomyces</i>	USA
Kakishima Makoto	<i>Pucciniales</i>	Japan
Kang Gongping	General macrofungi	China
Kang Jichuan	<i>Amphisphaeriales</i>	China
Karimi Omid	<i>Xylariomycetidae</i>	Thailand
Karpov Sergey A	Basal fungi, <i>Aphelida</i>	Russia
Karunarathna Samantha C.	<i>Basidiomycota</i> (macrofungi)	China, Sri Lanka
Kaufmann Moritz	Bioinformatics	Switzerland
Kemler Martin	Smuts	Germany
Kezhocuyi Kezo	<i>Hymenochaetaeae, Polyporales</i>	India
Khyaju S	<i>Basidiomycota</i> (macrofungi)	Thailand
Kirchmair Martin	<i>Agaricomycotina</i> , asexual <i>Ascomycota</i>	Austria
Kirk PM	General fungi	UK
Kitaura Marcos Junji	Cyanolichens, especially <i>Leptogium</i>	Brazil
Klawonn Isabell	Marine fungi	Germany
Kolarik Miroslav	<i>Ascomycota</i>	Czechia
Kong Alejandro	<i>Russulaceae</i> , edible & ectomycorrhizal fungi	Mexico
Kossmann Thiago	<i>Leotiomyces, Agaricomycotina</i>	Brazil, USA
Kuhar Francisco	Sequestrate fungi, corticioid, tomentelloid fungi, <i>Gasteromyces</i>	Argentina
Kukwa Martin	Lichenized and lichenicolous fungi	Poland
Kumar Shambhu	Phytopathogenic fungi	India
Kušan Ivana	<i>Onygenales, Mycoliciales, Sclerococcales, Geoglossomycetes, Ostropales, Helotiales, Leotiales, Marthamycetales, Thelebolales, Orbiliomyces, Pezizomyces</i>	Croatia
Lachance Marc-André	Ascomycetous yeasts	Canada
Lado Carlos	Myxomycetes	Spain
Larsson Karl-Henrik	Corticioid <i>Agaricomycetes</i>	Sweden
Latha K.P. Deepna	<i>Basidiomycota</i> (macrofungi)	India
Lee Hyang Burm	Basal fungi	Korea
Leonardi Marco	<i>Laboulbeniales</i> , macrofungi (tuffles)	Italy

Table 1 Continued.

Name	Expertise	Country/Region
Leontyev Dmytro L	Myxomycetes	Ukraine
Lestari Anis Sri	Discomycetes	Indonesia, Thailand
Li Cuijinyi	Discomycetes	China, Thailand
Li CY	<i>Basidiomycota</i>	China
Li Dewei	Asexual fungi, phytopathogens	USA
Li Hua	<i>Ascomycota</i>	China
Li Haiyan	Endophytes	China
Li Lu	Microfungi	China
Li Qirui	<i>Xylariomycetidae</i>	China
Li Wenli	<i>Ascomycota</i>	China
Li Yanchun	Macrofungi	China
Li Yue	<i>Basidiomycota</i>	China
Li Yanxia	<i>Xylariomycetidae</i>	China
Liao Chunfang	<i>Ascomycota</i>	China
Libkind Diego	Asco- and basidiomycetous yeasts	Argentina
Liimatainen Kare	<i>Basidiomycota (Cortinariaceae, Inocybaceae)</i>	UK
Lim YW	<i>Basidiomycota Ascomycota</i> (marine fungi)	Korea
Lin Chuangen	Hyphomycetes	China
Linaldeddu Benedetto Teodoro	<i>Botryosphaeriales</i> and <i>Peronosporales</i>	Italy
Linde Celeste	Orchid mycorrhizal fungi	Australia
Linn Maung Maung	Yeasts	Thailand
Liu Fei	<i>Basidiomycota</i>	China
Liu Jiankui	<i>Dothideomycetes</i>	China
Liu Ningguo	Hyphomycetes	China
Liu Shiliang	<i>Basidiomycota</i>	China
Liu Shun	<i>Polyporales</i>	China
Liu Xiangfu	Bat associated fungi	China
Liu Xiaoyong	Zygomycota	China
Liu Xingzhong	Nematode trapping fungi	China
Liu Zhanbo	<i>Basidiomycota</i>	China
Lu Yongzhong	<i>Dothideomycetes</i> , helicosporous fungi	China
Luangharn Thatsanee	<i>Basidiomycota</i>	Thailand
Luangsa-ard Jennifer J	Insect fungi	Thailand
LumbschThorsten	Lichenized fungi	USA
Lumyong Saisamorn	<i>Basidiomycota</i>	Thailand
Luo Le	Discomycetes	China
Luo Mei	Endophytes, <i>Trichoderma</i>	China
Luo Zonglong	<i>Dothideomycetes</i>	China
Ma Jian	<i>Dothideomycetes</i> , helicosporous fungi	China
Machado Alexandre Reis	<i>Botryosphaeriales, Mycosphaerellaceae, Fusarium</i> , phytopathogens	Brazil
Madagammana AD	<i>Dothideomycetes</i>	Thailand
Madrid Hugo	Coelomycetes, <i>Eurotiomycetes</i> , hyphomycetes	Chile
Magurno F	<i>Glomeromycota</i>	Poland
Magyar Donat	<i>Hagnosaceae</i> ; hyphomycetes on pollen grains	Hungary
Mahadevan Niranjana	Phytopathogens	Japan, Sri Lanka
Maharachchikumbura Sajeewa	Phytopathogens, <i>Sordariomycetes</i>	China
Maimaiti Y	Biotrophic fungi	China
Malarvizhi Kaliyaperumal	<i>Hymenochaetales, Polyporales</i>	India
Malosso Elaine	Asexual <i>Ascomycota</i> , Ingoldian fungi	Brazil
Manamgoda Dimuthu S.	Phytopathogens	Sri Lanka
Manawasinghe Ishara	Phytopathogens	China
Mapook Ausana	<i>Dothideomycetes</i>	Thailand
Marasinghe Diana S.	<i>Dothideomycetes</i> , epi-foliar fungi	Sri Lanka

Table 1 Continued.

Name	Expertise	Country/Region
Mardones Melissa	<i>Phyllachorales, Coronophorales</i> , mainly the genus <i>Lichenochora</i>	Costa Rica
Marin-Felix Yasmina	<i>Sordariales, Melanosporales</i> , helminthosporioid fungi	Germany
Márquez Rodrigo	<i>Cantharellales</i>	Spain
Masigol Hossein	<i>Oomycota</i>	Iran, Germany
Matošec Neven	<i>Onygenales, Mycoliciales, Sclerococcales, Geoglossomycetes, Ostropales, Helotiales, Leotiales, Marthamycetales, Thelebolales, Orbiliomycetes, Pezizomycetes</i>	Croatia
May Tom W	<i>Basidiomycota</i>	Australia
McKenzie Eric	Rusts	New Zealand
Meiras-Otoni A	<i>Ascomycota</i>	Brazil
Melo Roger Fagner Ribeiro	Coprophilous <i>Ascomycota</i> (<i>Podospora, Saccobolus, Sporormiella</i>)	Brazil
Mendes Alvarenga Renato Lúcio	<i>Auriculariales, Tremellales, Dacrymycetes</i>	Brazil
Mendieta Yañez Stephany	Entomopathogenic fungi	Peru
Meng Qingfeng	Lichenicolous fungi, lichenized fungi	China
Menkis Audrius	Forest Pathology	Sweden
Menolli Nelson Jr.	Agaricoid fungi	Brazil
Mešić Armin	<i>Agaricomycotina</i>	Croatia
Meza Calvo Jackeline	Entomopathogenic fungi	Peru
Mikhailov KV	Eukaryotes (in general), <i>Holomycota</i>	Russia
Miller Steven L	<i>Russulaceae, Sequestrate Basidiomycota, ectomycorrhizal Basidiomycota</i>	USA
Moncada Bibiana	Lichenized fungi	Colombia, Germany
Moncalvo Jean-Marc	<i>Agaricales, Ganodermataceae</i>	Canada
Monteiro Josiane Santana	Asexual <i>Ascomycota</i>	Brazil
Monteiro, Marcela	<i>Hymenochaete, Hymenochaetaceae (Hymenochaetales)</i>	Brazil
Mora-Montes Héctor M.	Clinical yeasts	Mexico
Moreau Pierre-Arthur	<i>Agaricales, Tricholomataceae</i> and other white-spored agarics, <i>Hymenogastraceae, Strophariaceae, Morchellaceae</i>	France
Mostert Lizel	<i>Togniniales, Phaeomoniellales, Diatrypaceae, Botryosphaeriaceae, Diaporthe</i>	South Africa
Mueller Greg M	<i>Basidiomycota</i>	USA
Mukhopadhyay Samhita	Marine fungi	India, Thailand
Murugadoss Ramesh	<i>Hymenochaetaceae</i>	India
Nagy László G.	Coprinoid <i>Agaricales</i>	Hungary
Najafiniya Mousa	Phytopathogens	Iran
Nanayakkara Chandrika M	Phytopathogenic and endophytic fungi	Sri Lanka
Nascimento Cristiano Coelho	Agaricoid fungi	Brazil
Nei Yong	Entomophthoroid fungi	China
Neuhauser Sigrid	<i>Phytomyxea</i> , plant-associated fungi, zoosporic fungi	Austria
Neves Maria Alice	Ectomycorrhizae, <i>Agaricales, Boletales</i>	Brazil
Niego Allen Grace	<i>Basidiomycota</i>	Philippines
Nilsson Henrik	<i>Basidiomycota</i>	Sweden
Niskanen Tuula	<i>Basidiomycota</i>	Finland
Niveiro Nicolás	<i>Agaricales</i>	Argentina
Núñez Otaño Noelia B	Fossil fungi	Argentina
O'Donnell Ryan Patric	Orchid mycorrhizal fungi (<i>Ceratobasidiaceae</i>)	Australia
Oehl Fritz	<i>Glomeromycota</i>	Switzerland

Table 1 Continued.

Name	Expertise	Country/Region
Olariaga Ibai	<i>Cantharellales</i> overall, <i>Ceratellopsis</i> , <i>Typhula</i> , <i>Macrotyphula</i> , <i>Clavariaceae</i> , <i>Tricholomopsis</i> , <i>Otidea</i> , <i>Sclerococcum</i>	Spain
Pang Kalai	Aquatic fungi	Taiwan
Papp Viktor	Polypores, <i>Basidiomycota</i> , phytopathogens	Hungary
Pawłowska Julia	Basal fungi	Poland
Peintner Ursula	<i>Mucorales</i> , <i>Mortierellaceae</i> , <i>Agaricales</i> (<i>Cortinariaceae</i>), polyporoid taxa, Endophytes	Austria, Italy
Pem Dhandevi	<i>Dothideomycetes</i>	Thailand
Pereira Olinto Liparini	<i>Ascomycota</i> (fungicolous and plant-associated fungi), orchid mycorrhizal fungi (<i>Ceratobasidiaceae</i> , <i>Sebacinaceae</i> , <i>Tulasnellaceae</i>)	Brazil
Perera Rekhani Hansika	<i>Sordariomycetes</i>	Korea
Pérez-Ortega Sergio	<i>Collemopsidiales</i> , <i>Verrucariaceae</i> (Marine genera), <i>Lecanoraceae</i> , <i>Ramalina</i>	Spain
Phillips Alan J. L.	<i>Dothideomycetes</i> , phytopathogens	Portugal
Phonemany Monthien	<i>Basidiomycota</i>	Laos, Thailand
Phukhamsakda Chayanard	<i>Dothideomycetes</i>	Thailand
Phutthacharoen K	Discomycetes	Thailand
Piątek Marcin	Black yeasts, sooty moulds, smut fungi	Poland
Piepenbring M	<i>Pucciniales</i> , <i>Meliolales</i> , <i>Ustilaginales</i> and other smut fungi	Germany
Pires-Zottarelli Carmen L A	Zoosporic eufungi	Brazil
Poinar George	Fossil fungi	USA
Popoff Orlando Fabián	Corticoid fungi, <i>Polyporales</i>	Argentina
Pošta Ana	<i>Agaricomycotina</i> , <i>Helotiales</i> , <i>Xylariales</i>	Croatia
Prieto M	<i>Coniocybomycetes</i>	Spain
Prompttha Itthayakorn	Endophytic fungi	Thailand
Quandt Alisha	<i>Leotiomyces</i> , <i>Hypocreales</i> , <i>Cryptomycota</i> , mycoparasites	USA
Radek R	<i>Nephridiophagales</i> (<i>Chytridiomycota</i>)	Germany
Rahnama Kamran	Fungal endophytes, <i>Ascomycota Venturiales</i> & phytopathogen	Iran
Raj K.N. Anil	<i>Basidiomycota</i> (macrofungi)	India
Rajeshkumar KC	Asexual <i>Ascomycota</i> , <i>Xenospadicoidales</i>	India
Rämä Teppo	Aquatic fungi	Norway
Rambold Gerhard	Lichenized fungi	Germany
Ramírez-Cruz Virginia	<i>Agaricales</i> (<i>Basidiomycota</i>)	Mexico
Rasconi Serena	<i>Chytrids</i> and zoosporic parasites	France
Rathnayaka Achala	<i>Botryosphaeriales</i>	Sri Lanka, Thailand
Raymundo Tania	<i>Sarcoscyphaceae</i> , <i>Sarcosomataceae</i> , <i>Patellariaceae</i> , <i>Pyronematceae</i> , <i>Mytilinidiales</i> , <i>Hysteriaceae</i> , <i>Hypoxylaceae</i> and <i>Xylariaceae</i>	Mexico
Raza Mubashar	Phytopathogens	China, Pakistan
Ren Guangcong	<i>Ascomycota</i>	China
Robledo Gerardo Lucio	Polypores (<i>Antrodia</i> clade, <i>Ganodermataceae</i> , <i>Polyporus s.l.</i> , <i>Hymenochaetaceae</i> , <i>Phlebioid</i> clade)	Argentina
Rodriguez-Flakus P	Lichenized fungi including <i>Lecidea s.l.</i>	Bolivia, Poland
Ronikier Anna	Myxomycetes	Poland
Rossi Valter	<i>Laboulbeniales</i>	Italy
Ryberg Martin	<i>Basidiomycota</i>	Sweden
Ryvarden Leif R	Polypores	Norway
Salvador-Montoya, Carlos A.	Polypores (<i>Hymenochaetales</i> , <i>Polyporales</i>)	Peru
Samant Bandana	Fossil fungi	India

Table 1 Continued.

Name	Expertise	Country/Region
Samarakoon Binu Chamini	Asexual <i>Ascomycota</i>	Thailand
Samarakoon Milan C.	<i>Sordariomycetes</i>	Thailand
Sánchez-Castro I	<i>Glomeromycota</i>	Spain
Sánchez-García Marisol	<i>Agaricales</i> , mainly <i>Tricholomataceae</i>	Sweden
Sandoval-Denis Marcelo	<i>Microascales</i> , <i>Hypocreales</i> , <i>Fusarium</i>	Netherlands
Santamaria Brianna	<i>Laboulbeniales</i>	Belgium
Santiago, André Luiz C.M.de A	<i>Mucoromycota</i> , <i>Zoopagomycota</i>	Brazil
Sarma VV	Marine fungi	India
Savchenko Anton	<i>Dacrymycetes</i> , heterobasidiomycetes	Ukraine, Estonia
Savchenko Kyryll	Phytopathogens	Estonia
Saxena RK	Fossil fungi	India
Scholler Markus	<i>Pucciniales</i> (rust fungi)	Germany
Schoutteten Nathan	<i>Corticaceae</i> , <i>Heterobasidiomycetes</i> , Mycoparasitic fungi	Belgium
Seifollahi Ellaheh	Phytopathogens	Thailand
Selbmann L	<i>Black fungi</i> , <i>Dothideomycetes</i> <i>Capnodiales</i>	Italy
Selçuk Faruk	Asexual <i>Ascomycota</i>	Turkey
Senanayake I Chinthani	Coelomycetes	China
Shabashova Tatiana G	<i>Basidiomycota</i> , myxomycetes	Belarus
Shen Hongwei	<i>Spathulosporales</i>	China
Shen Yuanmin	General fungi	Taiwan
Silva-Filho Alexandre G.S.	Agaricoid fungi	Brazil
Simmons D. Rabern	Zoosporic eufungi / basal fungi, <i>Chytridiomycota</i>	USA
Singh Raghvendra	Pathogenic fungi, saprobic fungi related to <i>Ascomycota</i> and <i>Basidiomycota</i> (Rust fungi)	India
Sir Esteban B.	<i>Xylariales</i>	Argentina
Song Chang-Ge	<i>Basidiomycota</i>	China
Souza-Motta Cristina M	<i>Ascomycota</i>	Brazil
Sruthi OP	Asexual <i>Ascomycota</i>	India
Stadler Marc	<i>Sordariomycetes</i>	Germany
Stchigel Alberto Miguel	<i>Ascomycota</i> , coelomycetes, <i>Mucoromycota</i>	Spain
Stemler Jannik	Phytopathogens	Germany
Stephenson Steven L	Myxomycetes	USA
Strassert JFH	<i>Chytridiomycota</i> (parasites of insects and phytoplankton)	Germany
Stryjak-Bogacka Monika	Endophytic fungi of bryophytes, sooty moulds	Poland
Su Hongli	Discomycetes	China, Thailand
Su Lei	Lichenized fungi, endophytes, phytopathogens, coprophilous fungi (<i>Anthracina</i> , <i>Rupestriomyces</i> , <i>Spissiomyces</i> , <i>Talaromyces</i> , <i>Penicillium</i> , <i>Phialemoniopsis</i> , <i>Plectosphaerella</i> , <i>Lecanicillium</i> , <i>Kernia</i> , <i>Acaulium</i>)	China
Suetrong Satinee	<i>Dothideomycetes</i>	Thailand
Sulistyo Bobby	<i>Atheliales</i>	Belgium, Indonesia
Sun Yaru	Phytopathogens	China
Sun Yifei	<i>Polyporales</i> , <i>Ganodermataceae</i>	China
Svantesson Sten	<i>Atheliales</i> and <i>Thelephorales</i>	Sweden
Sysouphanthong Phongeun	<i>Basidiomycota</i>	Laos, Thailand
Takamatsu Susumu	<i>Erysiphaceae</i>	Japan
Takashima Masako	Asco- and basidiomycetous yeasts	Japan
Tan Tinghong	Macrofungi	China
Tanaka Kazuaki	<i>Dothideomycetes</i>	Japan

Table 1 Continued.

Name	Expertise	Country/Region
Tang Alvin MC	<i>Xylariales</i>	Hong Kong
Tang Xia	Forest fungi	China
Tanney Joey B	<i>Leotiomyces</i> , endophytes, forest fungi	Canada
Tavakol Maryam	<i>Eurotiomyces</i>	China
Taylor Joanne	<i>Ascomycota</i>	UK
Taylor Paul WJ	Phytopathogens, <i>Colletotrichum</i> , <i>Pythium</i>	Australia
Tedersoo Leho	Basal fungi, <i>Sebaciniales</i>	Estonia
Tennakoon Danushka S.	<i>Dothideomyces</i>	Thailand
Thamodini GK	<i>Ascomycota</i>	Oman
Thines Marco	<i>Oomycota</i> , <i>Peronosporomycetes</i> , <i>Saprolegniomycetes</i> , <i>Basidiomycota</i> , <i>Bartheletiomycetes</i> , <i>Ustilaginomycetes</i> , <i>Exobasidiomycetes</i>	Germany
Thiyagaraja Vinodhini	<i>Dothideomyces</i> , lichenicolous fungi, lichenized fungi, <i>Eurotiomyces</i>	China
Thongklang Naritsada	<i>Basidiomycota</i> (macrofungi)	Thailand
Tiago Patricia Vieira	Fungal entomopathogens	Brazil
Tian Qing	<i>Eurotiomyces</i> , <i>Melanommataceae</i>	China
Tian WH	<i>Ascomycota</i>	China
Tibell Leif	Lichenized fungi	Sweden
Tibell Sanja	Lichenized fungi	Sweden
Tibpromma Saowaluck	<i>Dothideomyces</i> , endophytic fungi, <i>Sordariomycetes</i>	China, Thailand
Tkalčec Zdenko	<i>Agaricomycotina</i>)	Croatia
Tomšovský M	<i>Polyporales</i> , <i>Hymenochaetaceae</i> , <i>Armillaria</i> , <i>Melanoleuca</i> , phytopathogens	Czechia
Toome-Heller Merje	Phytopathogens	New Zealand
Torruella G	Sister lineages of fungi	Spain
Tsurykau Andrei	<i>Eurotiomyces</i> , lichenized fungi, lichenicolous fungi	Belarus
Turchetti Benedetta	Asco- and basidiomycetous yeasts	Italy
Udayanga Danuska	Phytopathogens	Sri Lanka
Ulukapi Merve	Asexual <i>Ascomycota</i>	Turkey
Untereiner Wendy	<i>Leotiomyces</i>	USA
Uzunov Blagoy Angelov	General fungi (incl. lichenized fungi)	Bulgaria
Valenzuela Ricardo	<i>Polyporales</i>	Mexico
Valle Laia Guardia	Freshwater fungi	Spain
Van Caenegem Warre	<i>Laboulbeniomyces</i>	Belgium
Van den Wyngaert Silke	Phytoplankton associated zoosporic fungi, <i>Chytridiomycota</i>	Finland
Van Vooren Nicolas	<i>Pezizomycetes</i>	France
Velez P	<i>Ascomycota</i>	Mexico
Verma Rajnish Kumar	Phytopathogens	India
Vieira LC	<i>Glomeromycota</i>	Brazil
Vieira Willie Anderson dos Santos	<i>Colletotrichum</i>	Brazil
Vizzini Alfredo	<i>Basidiomycota</i> and <i>Ascomycota</i> (<i>Pezizales</i>)	Italy
Walker Allison K		Canada
Walker Arttapon	<i>Basidiomycota</i>	Thailand
Wanasinghe Dhanushka N.	<i>Dothideomyces</i> , epi-foliar fungi	China
Wang Chaoge	Macrofungi	China
Wang Ke	Macrofungi	China
Wang SX	<i>Basidiomycota</i>	China
Wang Xinyu	Lichenized fungi, <i>Caliciales</i>	China
Wang Yong	Phytopathogens	China
Wannasawang Narumon	General fungi	Thailand

Table 1 Continued.

Name	Expertise	Country/Region
Wartchow Felipe	Agaricoid fungi	Brazil
Wei Deping	Insect pathogens	China
Wei Xinli	Lichenized fungi	China
Westphalen Mauro	<i>Steccherinaceae</i>	Brazil
White Jim F	Endophytes, <i>Ascomycota</i>	USA
Wijayawardene Nalin N.	Coelomycetes	China, Sri Lanka
Wijesinghe Nuwanthika	<i>Ascomycota</i>	Sri Lanka
Wijesundara DSA	Fungal ecology	Sri Lanka
Wisitrassameewong Komsit	<i>Basidiomycota</i>	Thailand
Worthy Fiona Ruth	Lichenized fungi	China
Wu Fang	<i>Auriculariales</i> , <i>Tremellales</i> , jelly fungi	China
Wu Gang	<i>Boletales</i>	China
Wu Haixia	Epi-foliar fungi, <i>Ascomycota</i>	China
Wu Na	<i>Ascomycota</i>	China
Wu Wenping	Asexual fungi, including chaetosphaeriaceous, <i>Chalara</i> -like, <i>Sporidesmium</i> -like fungi	China
Wurzbacher Christian	<i>Aquatic fungi</i>	Germany
Xiao Yuanpin	Insect fungi	China
Xiong Yinru	<i>Ascomycota</i>	China
Xu Biao	Phytopathogens	China
Xu Lijian	<i>Ascomycota</i>	China
Xu Rongju	<i>Ascomycota</i>	China
Xu Rong	<i>Ascomycota</i>	China
Xu Ruifang	Rubber associated fungi	China
Xu Taimin	Macrofungi	China
Yakovchenko Lidia	Lichenized fungi	Russia
Yan Jiye	Phytopathogens	China
Yang Hongde	Phytopathogens	China
Yang Yunhui	<i>Ascomycota</i>	China
Yang Jing	Asexual <i>Ascomycota</i>	China
Yang Zhuliang	<i>Basidiomycota</i>	China
Yapa N	<i>Ascomycota</i>	Sri Lanka
Yasanthika Erandi	Soil fungi	Thailand
Youssef Noha H	<i>Neocallimastigomycota</i>	USA
Yu Fengming	Discomycetes	China
Yu Quan	<i>Chaetothyriales</i>	China
Yu R	<i>Basidiomycota</i> (macrofungi)	China
Yu Xiandong	<i>Ascomycota</i>	China
Yu Yongxiu	<i>Ascomycota</i>	China
Yu Zefen	Nematode trapping fungi	China
Yuan Haisheng	<i>Thelephorales</i> in <i>Basidiomycota</i> , hydneous, polyporoid and corticioid <i>Basidiomycota</i>	China
Yuan Yuan	<i>Polyporales</i> , <i>Hymenochaetales</i>	China
Yurkov Andrey	Ascomycetous and basidiomycetous yeasts	Germany
Zafari D	<i>Ascomycota</i> , <i>Hypocreales</i>	Iran
Zamora Juan Carlos	<i>Geastrales</i> , <i>Dacrymycetes</i> , <i>Tremellales</i>	Spain/Switzerland
Zare Rasoul	Phialidic hyphomycetes (phytopathogens, entomogenous and nematophagous fungi)	Iran
Zeng Ming	Discomycetes	China
Zeng Niankai	<i>Basidiomycota</i>	China
Zeng Xiangyu	Phytopathogens, epi-foliar fungi (or epiphytes)	China
Zhangyong Dong	<i>Ascomycota</i>	China
Zhang Fa	<i>Ascomycota</i>	China
Zhang Huang	Freshwater fungi	China
Zhang Jinfeng	<i>Ascomycota</i>	China
Zhang Jingyi	<i>Ascomycota</i>	China

Table 1 Continued.

Name	Expertise	Country/Region
Zhang Qiuyue	<i>Mycenaceae (Favolaschia, Panellus)</i>	China
Zhang Shengnan	<i>Dothideomycetes</i>	China
Zhang Wei	Phytopathogens	China
Zhang Ying	<i>Dothideomycetes</i>	China
Zhang Yunxia	Phytopathogens	China
Zhang Zhiyuan	<i>Arthrodermataceae</i>	China
Zhao Changlin	<i>Basidiomycota</i>	China
Zhao Heng	<i>Mucoromycota</i>	China
Zhao Qi	<i>Pezizales</i>	China
Zhao Ruilin	<i>Basidiomycota</i>	China
Zhou Liwei	Macrofungi, <i>Basidiomycota</i>	China
Zhou Meng	Macrofungi	China
Zhurbenko Mikhail P.	Lichenicolous fungi	Russia
Zin Hnin Htet	<i>Ascomycota</i>	Thailand
Zucconi Laura	<i>Ascomycota</i>	Italy

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References

- Ainsworth GC. 1966 – A general purpose classification of fungi. *Bibliography of Systematic Mycology* 1, 1–4.
- Alvarez E, Stchigel AM, Cano J, Sutton DA et al. 2010 – Molecular phylogenetic diversity of the emerging mucoralean fungus *Apophysomyces*: proposal of three new species. *Revista Iberoamericana de Micología* 27(2), 80–89.
- Avise JC, Johns GC. 1999 – Proposal for a standardized temporal scheme of biological classification for extant species. *Proceedings of the National Academy of Science, USA* 96(13), 7358–7363.
- Baldrian P, Větrovský T, Lepinay C et al. 2022 – High-throughput sequencing view on the magnitude of global fungal diversity. *Fungal Diversity* 114, 539–547.
- Baral HO. 1992 – Vital versus herbarium taxonomy: Morphological differences between living and dead cells of ascomycetes, and their taxonomic implications. *Mycotaxon* 44, 333–390.
- Berkeley MJ. 1860 – *Outlines of British fungology; containing characters of above a thousand species of Fungi, and a complete list of all that have been described as natives of the British Isles.* – London: Lovell Reeve, 442 p.
- Bernard GE. 1882 – *Champignons observés à la Rochelle et dans les environs.* – Paris: Germer Baillière et cie, 300 p.
- Bhunjun CS, Dong Y, Jayawardena RS, Jeewon R et al. 2020 – A polyphasic approach to delineate species in *Bipolaris*. *Fungal Diversity* 102, 225–256.
- Bhunjun CS, Phillips AJL, Jayawardena RS, Promputtha I et al. 2021a – Importance of molecular data to identify fungal plant pathogens and guidelines for pathogenicity testing based on Koch's postulates. *Pathogens* 10(9), 1096.
- Bhunjun CS, Phukhamsakda C, Jayawardena RS, Jeewon R et al. 2021b – Investigating species boundaries in *Colletotrichum*. *Fungal Diversity* 107, 107–127.
- Bhunjun CS, Phukhamsakda C, Hyde KD, McKenzie EH et al. 2023 – Do all fungi have ancestors with endophytic lifestyles? *Fungal Diversity* 16, 1–26.
- Bhunjun CS, Phukhamsakda C, Jeewon R, Promputtha I et al. 2021c – Integrating different lines of evidence to establish a novel ascomycete genus and family (*Anastomitrabeculia*, *Anastomitrabeculiaceae*) in *Pleosporales*. *Journal of Fungi* 7(2), 94.
- Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N et al. 2022 – The numbers of fungi: are the most speciose genera truly diverse? *Fungal Diversity* 114, 387–462.
- Blackwell M. 2011 – The fungi: 1, 2, 3 ... 5.1 million species? *American Journal of Botany* 98(3), 426–438.
- Blomquist G, Anderson B, Anderson K, Brondz I. 1992 – Analysis of fatty acids. A new method for characterization of moulds. *Journal of Microbiological Methods* 16(1), 59–68.
- Bobay LM, Ochman H. 2017 – The evolution of bacterial genome architecture. *Frontiers in Genetics* 8, 72.
- Boekhout T, Amend AS, El Baidouri F, Gabaldón T et al. 2022 – Trends in yeast diversity discovery. *Fungal Diversity* 114, 491–537.
- Bonorden HF. 1851 – *Handbuch der allgemeinen Mykologie als Anleitung zum Studium derselben, nebst speciellen Beiträgen zur Vervollkommnung dieses Zweiges der Naturkunde.* – Stuttgart: E. Schweizerbart'sche Verlagshandlung und Druckerei, 336 s.
- Boudier J-L É. 1909 – *Histoire et classification des discomycètes d'Europe.* Librairie des sciences naturelles, P. Klincksieck, Paris, France.
- Bundhun D, Maharachchikumbura SSN, Jeewon R, Senanayake IC et al. 2020 – <https://sordariomycetes.org/>, a platform for the identification, ranking and classification of taxa within Sordariomycetes. *Asian Journal of Mycology* 3(1), 13–21.
- Calabon MS, Hyde KD, Jones EBG, Chandrasiri S et al. 2020 – www.freshwaterfungi.org, an online platform for the taxonomic classification of freshwater fungi. *Asian Journal of Mycology* 3(1), 419–445.
- Cao B, Haelewaters D, Schoutteten N, Begerow D et al. 2021 – Delimiting species in *Basidiomycota*: a review. *Fungal Diversity* 109, 181–237.

- Cantrell SA, Dianese JC, Fell J, Gunde-Cimerman N, Zalar P. 2011 – Unusual fungal niches. *Mycologia* 103, 1161–1174.
- Cazabonne J, Bartrop L, Dierickx G, Gafforov Y et al. 2022 – Molecular-based diversity studies and field surveys are not mutually exclusive: on the importance of integrated methodologies in mycological research. *Frontiers in Fungal Biology* 3, 860777.
- Chaiwan N, Gomdola D, Wang S, Monkai J et al. 2021 – an online database providing updated information of microfungi in the Greater Mekong Subregion. *Mycosphere* 12(1), 1409–1422.
- Chen WH, Liang JD, Ren XX, Zhao JH et al. 2022a – Phylogenetic, ecological and morphological characteristics reveal two new spider-associated genera in *Clavicipitaceae*. *MycoKeys* 91, 49–66.
- Chen WH, Liang JD, Ren XX, Zhao JH et al. 2022b – Species diversity of cordyceps-like fungi in the region of China. *Microbiology Spectrum* 10(5), 1–17.
- Chen YP, Su PW, Hyde KD, Maharachchikumbura SSN. 2023 – Phylogenomics and diversification of *Sordariomycetes*. *Mycosphere* 14(1), 414–451.
- Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS et al. 2021 – What are fungal species and how to delineate them? *Fungal Diversity* 109, 1–25.
- Chowdhury B, Garai G. 2017 – A review on multiple sequence alignment from the perspective of genetic algorithm. *Genomics* 109, 419–431.
- Cole RJ, Jarvis BB, Schweikert MA. 2003 – *Handbook of Secondary Fungal Metabolites*. Academic Press, Amsterdam, Netherlands.
- Cooke MC. 1871 – *Handbook of British fungi: with full descriptions of all the species, and illustrations of the genera*. In 2 vol. Vol. 2. – London; New York: Macmillan and Co., p. 489–981.
- Crouan PL, Crouan HM. 1867 – *Florule du Finistère. Contenant les descriptions de 360 espèces nouvelles de sporogames, de nombreuses observations et une synonymie des plantes cellulaires et vasculaires qui croissent spontanément dans ce département; accompagnées de trente-deux planches où est représentée l'organographie, faite sur l'état vif, des fruits et des tissus de 198 genres d'algues avec la plante grandeur naturelle ou réduite plus une planche supplémentaire ou sont figurés 24 champignons nouveaux*. – Paris: F. Klincksieck, 262 p.
- Crous PW, Gams W, Stalpers JA, Robert V, Stegehuis G. 2004 – MycoBank: an online initiative to launch mycology into the 21st century. *Studies in Mycology* 50(1), 19–22.
- Dahlberg A, Mueller GM. 2011 – Applying IUCN red-listing criteria for assessing and reporting on the conservation status of fungal species. *Fungal Ecology* 4(2), 147–162.
- Danger M, Gessner MO, Bärlocher F. 2016 – Ecological stoichiometry of aquatic fungi: current knowledge and perspectives. *Fungal Ecology* 19, 100–111.
- Davis WJ, Amses KR, Benny GL, Carter-House D et al. 2019 – Genome-scale phylogenetics reveals a monophyletic *Zoopagales* (*Zoopagomycota*, *Fungi*). *Molecular Phylogenetics and Evolution* 133, 152–163.
- Dayarathne MC, Boonmee S, Braun U, Crous PW et al. 2016 – Taxonomic utility of old names in current fungal classification and nomenclature: conflicts, confusion & clarifications. *Mycosphere* 7(11), 1622–1648.
- De Kesel A. 1996 – Host specificity and habitat preference of *Laboulbenia slackensis*. *Mycologia* 88, 565–573.
- Dianese JC, Inácio CA, Carvalho-Junior AA, Santos MDM et al. 2022 – Exploring the overlooked diversity of plant-associated Cerrado microfungi. *Revisão Anual de Patologia de Plantas* 28, 69–101.
- Díaz-Escandón D, Tagirdzhanova G, Vanderpool D, Allen CCG et al. 2022 – Genome-level analyses resolve an ancient lineage of symbiotic ascomycetes. *Current Biology* 32(23), 5209–5218.
- Dickschat JS, Wang T, Stadler M. 2018 – Volatiles from the xylarialean fungus *Hypoxylon invadens*. *Beilstein Journal of Organic Chemistry* 14, 734–746.

- Dilly O, Bartsch S, Rosenbrock P, Buscot F et al. 2001 – Shifts in physiological capabilities of the microbiota during the decomposition of leaf litter in a black alder (*Alnus glutinosa* (Gaertn.) L.) forest. *Soil Biology and Biochemistry* 33(7–8), 921–930.
- Dilly O, Bloem J, Vos A, Munch JC. 2004 – Bacterial diversity in agricultural soils during litter decomposition. *Applied and Environmental Microbiology* 70(1), 468–474.
- Dominguez de Toledo LS 1994 – Suggestions for describing and illustrating fungal spores. *Mycotaxon* 52(1), 259–270.
- Druzhinina IS, Chenthamara K, Zhang J, Atanasova L et al. 2018 – Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus *Trichoderma* from its plant-associated hosts. *PLOS Genetics* 14(4), e1007322.
- Durkin L, Jansson T, Sanchez M, Khomich M et al. 2020 – When mycologists describe new species, not all relevant information is provided (clearly enough). *MycKeys* 72, 109–128.
- Ebersberger I, de Matos Simoes R, Kupczok A, Gube M et al. 2012 – A consistent phylogenetic backbone for the fungi. *Molecular Biology and Evolution* 29(5), 1319–1334.
- Ebinghaus M, dos Santos MDM, Souza ESC, Barnes CW et al. 2022 – Reinstatement and phylogenetic allocation of the palm rust genus *Cerradoa* in the *Pucciniaceae*, and establishment of *Pseudocerradoa*, gen. nov. *Mycologia* 114(5), 868–886.
- Ebinghaus M, Santos MDM, Tonelli GSSS G, Macagnan D et al. 2023a – *Raveneliopsis*, a new genus of ravenelioid rust fungi on *Cenostigma* (*Caesalpinioideae*) from the Brazilian Cerrado and Caatinga. *Mycologia* 115(2), 263–276.
- Ebinghaus M, Martins JMT, Santos MDM, Tonelli GSSS et al. 2023b – *Cerradopsora*, a new genus of neotropical rust fungi. *Mycologia*, 115(6), 802–812.
- EFSA. 2021 – (EUROPEAN FOOD SAFETY AUTHORITY)
<https://efsa.onlinelibrary.wiley.com/doi/full/10.2903/j.efsa.2021.6506>
- Ekman S, Tønsberg T. 2002 – Most species of *Lepraria* and *Leproloma* form a monophyletic group closely related to *Stereocaulon*. *Mycological Research* 106(11), 1262–1276.
- Eriksson O. 1982 – Outline of the *Ascomycetes*-1982. *Mycotaxon* 15, 203–248.
- Eriksson OE, Hawksworth DL. 1998 – Outline of the ascomycetes. *Systema Ascomycetum* 16, 83–296.
- Fawcett PK. 1987 – *Botanical Illustrations: Preparation for Publication*. The New York Botanical Garden, New York, USA.
- Fayod V. 1889 – Prodrôme d'une histoire naturelle des Agaricinés. *Annales des Sciences Naturelles, Botanique, 7e Série* 9, 181–411
- Fitzpatrick DA, Logue ME, Stajich JE, Butler G. 2006 – A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. *BMC Ecology and Evolutionary* 6, 99.
- Floudas D, Binder M, Riley R, Barry K et al. 2012 – The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* 336(6089), 1715–1719.
- Forin N, Higris S, Voyron S, Girlanda M et al. 2018 – Next generation sequencing of ancient fungal specimens: The case of the Saccardo Mycological Herbarium. *Frontiers in Ecology and Evolution* 6, 129.
- Fries E. 1821–1832 – *Systema mycologicum: sistens fungorum ordines, genera et species, huc usque cognitae, quas ad normam methodi naturalis determinavit*. – Lundæ: Officina Berlingiana; Greifswald (vol. 3).
- Fries E. 1835 – *Corpus florarum provincialium Sueciæ. I. Floram Scanicam*. – Upsaliæ: Typis Palmblad, Sebell et C., 394 p.
- Fries EM. 1825 – *Systema orbis vegetabilis. Primas lineas novæ constructionis periclitatur Elias Fries. Pars I. Plantæ homonemææ*. – Lundæ: Typographia Academica, 374 p.
- Fries EM. 1836–1838 – *Epicrisis systematis mycologici, seu synopsis Hymenomycetum*. – Upsaliæ: Typographia Academica, 610 p.
- Fries EM. 1849 – *Summa vegetabilium Scandinaviae, seu enumeratio systematica et critica plantarum quum cotyledonearum, tum nemearum inter mare occidentale et album, inter*

- Eidoram et Nordkap, hactenus lectarum, indicata simul distributione geographica. Sectio posterior. – Uppsaliae: Typograph. Academici, 259–572 p.
- Frisvad JC. 2015 – Fungal Chemotaxonomy. In: Zeilinger, S., Martín, JF., García-Estrada, C. (eds) Biosynthesis and Molecular Genetics of Fungal Secondary Metabolites, Fungal Biology. Springer, New York, NY.
- Frisvad JC, Andersen B, Thrane U. 2008 – The use of secondary metabolite profiling in chemotaxonomy of filamentous fungi. *Mycological Research* 112(2), 231–240.
- Fuckel L. 1860 – Enumeratio Fungorum Nassoviae a Leopoldo Fuckel collectorum. Series 1. *Jahrbücher des Nassauischen Vereins für Naturkunde*. Jahrg. 15. Pp. 1–123.
- Fujisawa T, Barraclough TG. 2013 – Delimiting species using single-locus data and the generalized mixed yule coalescent approach: a revised method and evaluation on simulated data sets. *Systematic Biology* 62(5), 707–724.
- Fujita MK, Leaché AD, Burbrink FT, McGuire JA et al. 2012 – Coalescent-based species delimitation in an integrative taxonomy. *Trends in Ecology and Evolution* 27(9), 480–488.
- Gannibal PhB. 2022 – Polyphasic approach to fungal taxonomy. *Biology Bulletin Reviews* 12(1), 18–28.
- García-Cunchillos I, Zamora JC, Ryberg M, Lado C. 2022 – Phylogeny and evolution of morphological structures in a highly diverse lineage of fruiting-body-forming amoebae, order *Trichiales* (*Myxomycetes*, *Amoebozoa*). *Molecular Phylogenetics and Evolution* 177, 107609.
- García-Martín JM, Zamora JC, Lado C. 2023 – Multigene phylogeny of the order *Physarales* (*Myxomycetes*, *Amoebozoa*): shedding light on the dark-spored clade. *Persoonia* 51, 89–124.
- Ge ZW, Brenneman T, Bonito G, Smith ME. 2017 – Soil pH and mineral nutrients strongly influence truffles and other ectomycorrhizal fungi associated with commercial pecans (*Carya illinoensis*). *Plant and Soil* 418: 493–505.
- Gillet CC. 1879–1887 – Champignons de France. Les discomycètes. [Livraison 1]. – Alençon: E. de Broise, 230 p.
- Gkoutselis G, Rohrbach S, Harjes J, Obst M et al. 2021 – Microplastics accumulate fungal pathogens in terrestrial ecosystems. *Scientific Reports* 11, 13214.
- Grossart HP, Van den Wyngaert S, Kagami M, Wurzbacher C et al. 2019 – Fungi in aquatic ecosystems. *Nature Reviews Microbiology* 17(6), 339–354.
- Groenewald M, Hittinger CT, Bensch K, Opulente DA et al. 2023 – A genome-informed higher rank classification of the biotechnologically important fungal subphylum *Saccharomycotina*. *Studies in Mycology* 105, 1–22.
- Gryganskyi AP, Golan J, Dolatabadi S, Mondo S et al. 2018 – Phylogenetic and phylogenomic definition of *Rhizopus* species. *G3: Genes Genom Genet* 8(6), 2007–2018.
- Gui H, Purahong W, Wubet T, Peršoh D et al. 2020 – *Funneliformis mosseae* alters soil fungal community dynamics and composition during litter decomposition. *Fungal Ecology* 43, 100864.
- Guo Y, Jud W, Weikl F, Ghirardo A et al. 2021 – Volatile organic compound patterns predict fungal trophic mode and lifestyle. *Communications Biology* 4, 673.
- Guterres DC, Galvão-Elias S, de Souza BCP, Pinho DB et al. 2018 – Taxonomy, phylogeny, and divergence time estimation for *Apiosphaeria guaranitica*, a Neotropical parasite on bignoniaceous hosts. *Mycologia* 110(3), 526–545.
- Haelewaters D, Pfliegler WP, Gorczak M, Pfister DH. 2019 – Birth of an order: comprehensive molecular phylogenetic study reveals that *Herpomyces* (*Fungi*, *Laboulbeniomycetes*) is not part of *Laboulbeniales*. *Molecular Phylogenetics and Evolution* 133, 286–301.
- Haelewaters D, Van Caenegem W, De Kesel A. 2022 – *Hesperomyces harmoniae*, a new name for a common ectoparasitic fungus on the invasive alien ladybird *Harmonia axyridis*. *Sydowia* 75, 53–74.
- Han SL, Wang MM, Ma ZY, Raza M et al. 2023 – *Fusarium* diversity associated with diseased cereals in China, with an updated phylogenomic assessment of the genus. *Studies in Mycology* 104(1), 87–148.

- Haridas S, Albert R, Binder M, Bloem J et al. 2020 – 101 *Dothideomycetes* genomes: a test case for predicting lifestyles and emergence of pathogens. *Studies in Mycology* 96(1), 141–153.
- Harman KL, Humphrey GK, Goodale MA. 1999 – Active manual control of object views facilitates visual recognition. *Current Biology* 9(22), 1315–1318.
- Hawksworth DL, Crous PW, Redhead SA, Reynolds DR et al. 2011 – The Amsterdam declaration on fungal nomenclature. *IMA Fungus*, 2, 105–111.
- Hawksworth DL, Lücking R. 2017 – Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum* 5(4), FUNK-0052-2016.
- Hawksworth DL, Hibbett DS, Kirk PM, Lücking R. 2018 – (F-005-006) Proposals to permit DNA sequence data to be used as types of names of fungi. *IMA Fungus* 9, V–VI.
- He MQ, Zhao RL, Hyde KD, Begerow D et al. 2019 – Notes, outline and divergence times of *Basidiomycota*. *Fungal Diversity* 99, 105–367.
- He MQ, Zhao RL, Liu DM, Denchev TT et al. 2022a – Species diversity of *Basidiomycota*. *Fungal Diversity* 114, 281–325.
- He MQ, Zhu XY, Li TH, Cui BK et al. 2022b – Macrofungal classification system and information platform <http://www.nmdc.cn/macrofungi/> is launched. *Mycosystema* 41(6), 899–905
- Hibbett D, Abarenkov K, Kõljalg U, Öpik M et al. 2017 – Sequence-based classification and identification of *Fungi*. *Mycologia* 108(6), 1049–1068.
- Hibbett DS, Binder M, Bischoff JF, Blackwell M et al. 2007 – A higher-level phylogenetic classification of the *Fungi*. *Mycological Research* 111(5), 509–547.
- Hibbett DS, Ohman A, Glotzer D, Nuhn M et al. 2011 – Progress in molecular and morphological taxon discovery in *Fungi* and options for formal classification of environmental sequences. *Fungal Biology Reviews* 25(1), 38–47.
- Hofstetter V, Buyck B, Eyssartier G, Schnee S et al. 2019 – The unbearable lightness of sequenced-based identification. *Fungal Diversity* 96(1), 243–284.
- Hongsanan S, Jeewon R, Purahong W, Xie N et al. 2018 – Can we use environmental DNA as holotypes? *Fungal Diversity* 92, 1–30.
- Huanraluek N, Padaruth OD, Jayawardena RS, Li WJ et al. 2021 – <https://www.coelomycetes.org/>: Databank that contributes for the classification, identification and nomenclature of coelomycetes. *Asian Journal of Mycology* 4(2), 114–122.
- Hyde KD. 2022 – The numbers of fungi. *Fungal Diversity* 114, 1
- Hyde KD, Cai L, McKenzie EHC, Yang YL et al. 2009 – *Colletotrichum*: a catalogue of confusion. *Fungal Diversity* 39, 1–17.
- Hyde KD, Abd-Elsalam K, Cai L. 2010 – Morphology: still essential in a molecular world. *Mycotaxon* 114, 439–451.
- Hyde KD, McKenzie EH, KoKo TW. 2011 – Towards incorporating anamorphic fungi in a natural classification – checklist and notes for 2010. *Mycosphere* 2(1), 1–88.
- Hyde KD, Maharachchikumbura SSN, Hongsanan S, Samarakoon MC et al. 2017 – The ranking of fungi: a tribute to David L. Hawksworth on his 70th birthday. *Fungal Diversity* 84, 1–23.
- Hyde KD, Jeewon R, Chen YJ, Bhunjun CS et al. 2020a – The numbers of fungi: is the descriptive curve flattening? *Fungal Diversity* 103, 219–271.
- Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ et al. 2020b – Refined families of *Sordariomycetes*. *Mycosphere* 11(1), 305–1059.
- Hyde KD, de Silva N, Jeewon R, Bhat DJ et al. 2020c – AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology* 3(1), 22–294.
- Index Fungorum. 2023 – <https://www.indexfungorum.org/Names/Names.asp>
- James TY, Stajich JE, Hittinger CT, Rokas A. 2020 – Toward a fully resolved fungal tree of life. *Annual Review of Microbiology* 74, 291–313.
- Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity* 74(1), 3–18.

- Jayawardena RS, McKenzie EHC, Chen YJ, Phillips AJL et al. 2019 – <https://onestopshopfungi.org/>, a database to enhance identification of phytopathogenic genera. *Asian Journal of Mycology* 2(1), 281–286.
- Jayawardena RS, Bhunjun CS, Hyde KD, Gentekaki E et al. 2021a – *Colletotrichum*: lifestyles, biology, morpho-species, species complexes and accepted species. *Mycosphere* 12, 519–669.
- Jayawardena RS, Hyde KD, de Farias ARG, Bhunjun CS et al. 2021b – What is a species in fungal plant pathogens? *Fungal Diversity* 109, 239–266.
- Jeewon R, Liew ECY, Hyde KD. 2004 – Phylogenetic evaluation of species nomenclature of *Pestalotiopsis* in relation to host association. *Fungal Diversity* 17, 39–55.
- Jeewon R, Yeung QSY, Wannasinghe DN, Ramapadarath S et al. 2018 – Hidden mycota of pine needles: molecular signatures from PCR-DGGE and ribosomal DNA phylogenetic characterization of novel phylotypes. *Scientific Reports* 8, 18053.
- Johnston PR, Quijada L, Smith CA, Baral H-O et al. 2019 – A multigene phylogeny toward a new phylogenetic classification for the *Leotiomyces*. *IMA Fungus* 10, 1.
- Jones EB, Pang KL, Abdel-Wahab MA, Scholz B et al. 2019 – An online resource for marine fungi. *Fungal Diversity* 96, 347–433.
- Karsten PA. 1871–1879 – *Mycologia Fennica* Helsingfors, Finska Litteratur-sllskapets Tryckeri Series: Bidrag till kannedom av Finlands natur och folk h. 19.
- Keller NP. 2019 – Fungal secondary metabolism: regulation, function and drug discovery. *Nature Reviews Microbiology* 17, 167–180.
- Kendrick WB. 1989 – Subdivision Deuteromycotina a fungal chimera. *Sydowia* 41, 6–14.
- Kidd SE, Abdolrasouli A, Hagen F. 2023 – Fungal nomenclature: managing change is the name of the game. *Open forum infectious diseases* 10, ofac559.
- Kim D, Gilchrist CL, Chun J, Steinegger M. 2023 – UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi. *Nucleic Acids Research*, 51(D1), D777–D784.
- Kirk PM, Cannon PF, Minter DW, Stalpers JA. 2008 – *Ainsworth & Bisby's Dictionary of the Fungi*, 10th edn. CABI, Wallingford.
- Kock JLF, Botha A. 1998 – Fatty acids in fungal taxonomy. In: Frisvad JC, Bridge PD, Arora DK (eds), *Chemical Fungal Taxonomy* Marcel Dekker, New York, pp. 219–246.
- Kuhnert E, Sir EB, Lambert C, Hyde KD et al. 2017 – Phylogenetic and chemotaxonomic resolution of the genus *Annulohyphoxylon* (*Xylariaceae*) including four new species. *Fungal Diversity* 85, 1–43.
- Kurtzman CP, Fell JW, Boekhout T. 2011 – *The Yeasts, a Taxonomic Study* 5th edition.
- Læssøe T, Srikitikulchai P, Fournier J, Köpcke B, Stadler M. 2010 – Lepranic acid derivatives as chemotaxonomic markers in *Hypoxylon aeruginosum*, *Chlorostroma subcubisporum* and *C. cyaninum*, sp. nov. *Fungal Biology* 114, 481–489.
- Lado C. 2005–2023 – An online nomenclatural information system of *Eumycetozoa*. Real Jardín Botánico, CSIC. Madrid, Spain. <https://eumycetozoa.com>
- Lado C, Eliasson U. 2022 – Taxonomy and systematics: current knowledge and approaches on the taxonomic treatment of *Myxomycetes*: updated version. In: Rojas C, Stephenson SL. (eds.) *Myxomycetes: Biology, Systematics, Biogeography and Ecology*, 2021. pp. 269–324.
- Lambert C, Wendt L, Hladki A, Stadler M, Sir EB. 2019 – *Hypomontagnella* (*Hypoxylaceae*): a new genus segregated from *Hypoxylon* by a polyphasic taxonomic approach. *Mycological Progress* 18, 187–201.
- Laurence MH, Summerell BA, Burgess LW, Liew ECY. 2014 – Genealogical concordance phylogenetic species recognition in the *Fusarium oxysporum* species complex. *Fungal Biology* 118, 374–384.
- Leontyev DV, Schnittler M. 2022 – The phylogeny and phylogenetically based classification of myxomycetes. In: *Myxomycetes: Biology, Systematics, Biogeography and Ecology*, 2021, pp. 97–124.

- Leontyev DV, Schnittler M, Ishchenko Y, Quade A et al. 2022 – Another species complex in myxomycetes: diversity of peridial structures in *Lycogala epidendrum*. *Nova Hedwigia* 114(3–4), 413–434.
- Leontyev DV, Buttgerit M, Kochergina A, Shchepin ON, Schnittler M. 2023a – Two independent genetic markers support separation of the myxomycete *Lycogala epidendrum* into numerous biological species. *Mycologia* 115(1), 32–43.
- Leontyev DV, Ishchenko Y, Schnittler M. 2023b – Fifteen new species from the genus *Lycogala* (*Myxomycetes*). *Mycologia* 115 (4), 524–560.
- Li Q, Huang J, Li Y, Zhang Y et al. 2017 – Fungal community succession and major components change during manufacturing process of Fu brick tea. *Scientific Reports* 7(1), 1–9.
- Li Y, Steenwyk JL, Chang Y, Wang Y et al. 2021 – A genome-scale phylogeny of the kingdom *Fungi*. *Current Biology* 31, 1653–1665.
- Liimatainen K, Kim JT, Pokorny L, Kirk PM et al. 2022 – Taming the beast: a revised classification of *Cortinariaceae* based on genomic data. *Fungal Diversity* 112, 89–170.
- Link HF. 1833 – Handbuch zur Erkennung der nutzbarsten und am häufigsten vorkommenden Gewächse. Theil 3. – Berlin: in der Haude und Spenerschen Buchhandlung (S. J. Josepey), 536 s.
- Liu F, Hou L, Raza M, Cai L. 2017a – *Pestalotiopsis* and allied genera from *Camellia*, with description of 11 new species from China. *Scientific Reports* 7(1), 1–19.
- Liu JK, Hyde KD, Jeewon R, Phillips AJ et al. 2017 – Ranking higher taxa using divergence times: a case study in *Dothideomycetes*. *Fungal Diversity* 84, 75–99.
- Lumbsch HT, Huhndorf SM. 2007 – Notes on ascomycete systematics. Nos. 4408 – 4750. *Myconet* 13, 59 – 99.
- Magain N, Miadlikowska J, Mueller O, Gajdeczka M et al. 2017 – Conserved genomic collinearity as a source of broadly applicable, fast evolving, markers to resolve species complexes: a case study using the lichen-forming genus *Peltigera* section *Polydactylon*. *Molecular Phylogenetics and Evolution* 117, 10–29.
- Maharachchikumbura SSN, Hyde KD, Groenewald JZ, Xu J, Crous PW. 2014 – *Pestalotiopsis* revisited. *Studies in Mycology* 79, 121–186.
- Maharachchikumbura SSN, Chen Y, Ariyawansa HA, Hyde KD et al. 2021 – Integrative approaches for species delimitation in *Ascomycota*. *Fungal Diversity* 109, 155–179.
- Maharachchikumbura SSN, Wanasinghe DN, Elgorban AM, Al-Rejaie SS et al. 2022 – *Brunneosporopsis yunnanensis* gen. et sp. nov. and *Allocryptovalsa xishuangbanica* sp. nov., new terrestrial *Sordariomycetes* from Southwest China. *Life* 12, 635.
- Manamgoda DS, Rossman AY, Castlebury LA, Crous PW et al. 2014 – The genus *Bipolaris*. *Studies in Mycology* 79, 221–288.
- Mapook A, Boonmee S, Liu JK, Jones EBG et al. 2016 – Taxonomic and phylogenetic placement of *Phaeodimeriella* (*Pseudoperisporiaceae*, *Pleosporales*). *Cryptogamie, Mycologie* 37, 157–176.
- Marin-Felix Y, Miller AN, Cano-Lira JF, Guarro J et al. 2020 – Re-evaluation of the Order *Sordariales*: delimitation of *Lasiosphaeriaceae* s. str., and introduction of the New families *Diplogelasinosporaceae*, *Naviculisporaceae*, and *Schizotheciaceae*. *Microorganisms* 8, 1430.
- Matute DR, Sepúlveda VE. 2019 – Fungal species boundaries in the genomics era. *Fungal Genetics and Biology* 131, 103249.
- May TW. 2017 – Report of the Nomenclature Committee for Fungi – 20. *Taxon* 66, 483–495.
- May TW, Redhead SA, Bensch K et al. 2019 – Chapter F of the International Code of Nomenclature for algae, fungi, and plants as approved by the 11th International Mycological Congress, San Juan, Puerto Rico, July 2018. *IMA Fungus* 10, 21.
- McCarthy CG, Fitzpatrick DA. 2017 – Phylogenomic reconstruction of the oomycete phylogeny derived from 37 genomes. *Mycosphere* 2, e00095–e117.

- McNeill J, Barrie FR, Buck WR, Demoulin V et al. 2011 – International Code of Nomenclature for algae, fungi, and plants (Melbourne Code) adopted by the Eighteenth International Botanical Congress Melbourne, Australia, July 2011. Koeltz Scientific Books.
- Montoliu-Nerin M, Sánchez-García M, Bergin C, Kutschera VE et al. 2021 – In-depth phylogenomic analysis of arbuscular mycorrhizal fungi based on a comprehensive set of de novo genome assemblies. *Frontiers in Fungal Biology* 2, 716385.
- Moore RT. 1971 – Recent Advances in Microbiology, 1–623.
- Mueller GM, Cunha KM, May TW, Allen JL et al. 2022 – What do the first 597 global fungal red list assessments tell us about the threat status of fungi? *Diversity* 14(9), 736.
- MycoBank. 2023 – <https://www.mycobank.org/>
- Naranjo-Ortiz MA, Gabaldón T. 2019 – Fungal evolution: major ecological adaptations and evolutionary transitions. *Biological Reviews* 94, 1443–1476.
- Nees von Esenbeck CGD. 1817 – Das System der Pilze und Schwämme. Ein Versuch von Dr. C.G. Nees von Esenbeck. Würzburg: Stahelschen Buchhandlung, 334 s.
- Nguyen HDT, Sultana T, Kesanakurti P, Hambleton S. 2019 – Genome sequencing and comparison of five *Tilletia* species to identify candidate genes for the detection of regulated species infecting wheat. *IMA Fungus* 10, 1–7.
- Niego AGT, Rapior S, Thongklang N, Raspé O et al. 2023a – Reviewing the contributions of macrofungi to forest ecosystem processes and services. *Fungal Biology Reviews* 44:100294.
- Niego AGT, Lambert C, Mortimer P, Thongklang N et al. 2023b – The contribution of fungi to the global economy. *Fungal Diversity* 121, 95–137.
- Nilsson RH, Larsson KH, Taylor AFS, Bengtsson-Palme J et al. 2019 – The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. *Nucleic Acids Research* 47(D1), D259–D264.
- Nilsson RH, Ryberg M, Wurzbacher C, Tedersoo L et al. 2023 – How, not if, is the question mycologists should be asking about DNA-based typification. *Mycology* 96: 143–157.
- Nobrega MA, Pennacchio LA. 2004 – Comparative genomic analysis as a tool for biological discovery. *The Journal of Physiology* 554, 31–39.
- Nozaki H, Iseki M, Hasegawa M, Misawa K et al. 2007 – Phylogeny of primary photosynthetic eukaryotes as deduced from slowly evolving nuclear genes. *Molecular Biology and Evolution* 24, 1592–1595.
- O'Brien HE, Parrent JL, Jackson JA, Moncalvo JM, Vilgalys R. 2005 – Fungal community analysis by large-scale sequencing of environmental samples. *Applied and Environmental Microbiology* 71, 5544–5550.
- Opathy C, Gabaldón T. 2019 – Recent trends in molecular diagnostics of yeast infections: from PCR to NGS. *FEMS Microbiol Reviews* 43(5), 517–547.
- Osono T. 2017 – Leaf litter decomposition of 12 tree species in a subtropical forest in Japan. *Ecological Research* 32, 413–422.
- Parnmen S, Rangsiruji A, Mongkolsuk P, Boonpragob K et al. 2012 – Using phylogenetic and coalescent methods to understand the species diversity in the *Cladia aggregata* complex (*Ascomycota, Lecanorales*). *PLoS One* 7, e52245.
- Patouillard NT. 1887 – Les Hyménomycètes d'Europe. Anatomie générale et classification des champignons supérieurs. Matériaux pour l'Histoire des Champignons I. P. Klinksieck, Paris, France.
- Pem D, Hongsanan S, Doilom M, Tibpromma S et al. 2019 – <https://www.dothideomycetes.org/>: an online taxonomic resource for the classification, identification, and nomenclature of *Dothideomycetes*. *Asian Journal of Mycology* 2(1), 287–297.
- Pereira-Carvalho RC, Dianese JC, Sepulveda-Chavera G, Armando EAS. 2009 – An overlooked source of fungal diversity: novel hyphomycete genera on trichomes of Cerrado plants. *Mycological Research* 113, 261–274.

- Pérez-Ortega S, Garrido-Benavent I, Grube M, Olmo R et al. 2016 – Hidden diversity of marine borderline lichens and a new order of fungi: *Collemopsidiales* (*Dothideomyceta*). *Fungal Diversity* 80, 285–300.
- Persoon CH. 1794 – Neuer Versuch einer systematischen Eintheilung der Schwämme // Neues Magazin für die Botanik. H. 1. – S. 63–80.
- Persoon CH. 1801 – Synopsis methodica fungorum. Sistens enumerationem omnium huc usque detectarum specierum, cum brevibus descriptionibus nec non. Pars secunda. – Gottingae: Henricum Dieterich, 241–706 p.
- Persoon CH. 1822–1828 – Mycologia europea seu completa omnium fungorum in variis europaeae regionibus detectorum enumeratio, methodo naturali disposita; descriptione succincta, synonymia selecta et observationibus criticis additis. Sectio prima [-tertia]. – Erlangae: Joann Jacob Palm.
- Persoon CH. 1828 – Elenchus fungorum, sistens commentarium in Sistema mycologicum. vol. 1–2 Gryphiswaldiae: Sumptibus Ernesti Mauritii 1828.
- Philippe H, Lopez P, Brinkmann H, Budin K et al. 2000 – Early-branching or fast-evolving eukaryotes? An answer based on slowly evolving positions. *Proceedings of the Royal Society B: Biological Sciences* 267, 1213–1221.
- Phillips WA. 1887 – Manual of the British *Discomycetes* with descriptions of all the species of fungi hitherto found in Britain, included in the family and illustrations of the genera. – London: Kegan Paul, Trench et Co., 462 p.
- Phukhamsakda C, Hongsanan S, Ryberg M, Ariyawansa HA et al. 2016 – The evolution of *Massarineae* with *Longipedicellataceae* fam. nov. *Mycosphere* 7, 1713–1731.
- Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG et al. 2020 – Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. *Fungal Diversity* 102, 1–203.
- Phukhamsakda C, Nilsson RH, Bhunjun CS, Gomes de Farias AR et al. 2022 – The numbers of fungi; contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity* 114, 327–386.
- Pietsch KA, Eichenberg D, Nadrowski K, Bauhus J et al. 2019 – Wood decomposition is more strongly controlled by temperature than by tree species and decomposer diversity in highly species rich subtropical forests. *Oikos*, 128(5), 701–715.
- Pizarro D, Divakar PK, Grewe F, Leavitt SD et al. 2018 – Phylogenomic analysis of 2556 single-copy protein-coding genes resolves most evolutionary relationships for the major clades in the most diverse group of lichen-forming fungi. *Fungal Diversity* 92, 31–41.
- Pölme S, Abarenkov K, Henrik Nilsson R et al. 2020 – FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. *Fungal Diversity* 105, 1–16.
- Porter TM, Schadt CW, Rizvi L, Martin AP et al. 2008 – Widespread occurrence and phylogenetic placement of a soil clone group add a prominent new branch to the fungal tree of life. *Molecular Phylogenetics and Evolution* 46, 635–644.
- Posch AE, Spadiut O, Herwig C. 2012 – A novel method for fast and statistically verified morphological characterization of filamentous fungi. *Fungal Genetics and Biology*, 49(7), 499–510.
- Prakash PY, Irinyi L, Halliday C, Chen S et al. 2017 – Online databases for taxonomy and identification of pathogenic fungi and proposal for a cloud-based dynamic data network platform. *Journal of Clinical Microbiology* 55(4), 1011–1024.
- Puchkov E. 2016 – Image analysis in microbiology: A review. *Journal of Computer and Communications* 4(15), 8.
- Purahong W, Tanunchai B, Muszynski S, Maurer F et al. 2022 – Cross-kingdom interactions and functional patterns of active microbiota matter in governing deadwood decay. *Proceedings of the Royal Society B*, 289, 20220130.
- Quélet L. 1886 – Enchiridion fungorum in Europa media et praesertim in Gallia vigentium. – Lutetiae: Octavii Doin, 352 p.

- Raja HA, Miller AN, Pearce CJ, Oberlies NH. 2017 – Fungal identification using molecular tools: a primer for the natural products research community. *Journal of Natural Products* 80, 756–770.
- Rédou V, Vallet M, Meslet-Cladière L, Kuma A et al. 2016 – Marine fungi. The Marine Microbiome: an Untapped Source of Biodiversity and Biotechnological Potential, 99–153.
- Regier JC, Shultz JW, Ganley ARD, Hussey A et al. 2008 – Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. *Systematic Biology* 57, 920–938.
- Reich M, Labes A. 2017 – How to boost marine fungal research: a first step towards a multidisciplinary approach by combining molecular fungal ecology and natural products chemistry. *Marine Genomics* 36, 57–75.
- Rinkel J, Babczyk A, Wang T, Stadler M, Dickschat JS. 2018 – Volatiles from the hypoxylaceous fungi *Hypoxylon griseobrunneum* and *Hypoxylon macrocarpum*. *Beilstein Journal of Organic Chemistry* 14, 2974–2990.
- Robert V, Vu D, Amor ABH, de Wiele NV et al. 2013 – MycoBank gearing up for new horizons. *IMA Fungus* 4, 371–379.
- Ronikier A, Janik P, de Haan M, Kuhnt A, Zankowicz M. 2022 – Importance of type specimen study for understanding genus boundaries – taxonomical clarifications in *Lepidoderma* based on integrative taxonomy approach leading to resurrection of the old genus *Polyschismium*. *Mycologia* 114, 1008–1031.
- Ryberg M, Nilsson RH. 2018 – New light on names and naming of dark taxa. *MycKeys* 23, 31–39.
- Saag L, Saag A, Randle T. 2009 – World survey of the genus *Lepraria* (*Stereocaulaceae*, lichenized *Ascomycota*). *Lichenologist* 41, 25–60.
- Saccardo PA. 1904 – De Diagnostica et nomenclatura mycologica, Admonita quaedam. *Annales Mycologici* 2, 195–198. [English translation by Clements FE (1904) *J Mycol* 10, 109–112.
- Saccardo PA, Sydow P. 1899 – Supplementum Universale, Pars IV. *Sylloge Fungorum* 14, 1–1316.
- Samarakoon MC, Hyde KD, Promputtha I, Hongsanan S et al. 2016 – Evolution of *Xylariomycetidae* (*Ascomycota*: *Sordariomycetes*). *Mycosphere* 7, 1746–1761.
- Samarakoon MC, Hyde KD, Maharachchikumbura SSN, Stadler M et al. 2022 – Taxonomy, phylogeny, molecular dating and ancestral state reconstruction of *Xylariomycetidae* (*Sordariomycetes*). *Fungal Diversity* 112, 1–88.
- Sánchez-Ramírez S, Tulloss RE, Guzmán-Dávalos L, Cifuentes-Blanco J et al. 2015 – In and out of refugia: historical patterns of diversity and demography in the North American Caesar’s mushroom species complex. *Molecular Ecology* 24, 5938–5956.
- Schoch CL, Seifert KA, Huhndorf S, Robert V et al. 2012 – Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for fungi. *Proceedings of the National Academy of Sciences* 109, 6241–6246.
- Senanayake IC, Jeewon R, Chomnunti P, Wanasinghe DW et al. 2018 – Taxonomic circumscription of *Diaporthales* based on multigene phylogeny and morphology. *Fungal Diversity* 93, 241–443.
- Senanayake IC, Pem D, Rathnayaka AR, Wijesinghe SN et al. 2022 – Predicting global numbers of teleomorphic ascomycetes. *Fungal Diversity* 114(1), 237–278.
- Shen XX, Zhou XF, Kominek J, Kurtzman CP et al. 2016 – Reconstructing the backbone of the *Saccharomycotina* yeast phylogeny using genome-scale data. *G3* 6: 3927–3939.
- Shen XX, Opulente DA, Kominek J, Zhou X et al. 2018 – Tempo and mode of genome evolution in the budding yeast subphylum. *Cell* 175(6), 1533–1545.
- Shen XX, Steenwyk JL, LaBella AL, Opulente DA et al. 2020 – Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum *Ascomycota*. *Science Advances* 6, 45.
- Simões MF, Pereira L, Santos C, Lima N. 2013 – Polyphasic identification and preservation of fungal diversity: concepts and applications. *Management of microbial resources in the environment*, Springer, 91–117.

- Sobel JM, Chen GF, Watt LR, Schemske DW. 2010 – The biology of speciation. *Evolution* 64, 295–315.
- Spatafora JW, Chang Y, Benny GL, Lazarus K et al. 2016 – A phylum-level phylogenetic classification of Zygomycete fungi based on genome-scale data. *Mycologia* 108, 1028–1046.
- Spring O, Haas K. 2002 – The fatty acid composition of *Plasmopara halstedii* and its taxonomic significance. *European Journal of Plant Pathology* 108, 263–267.
- Spring O, Haas K, Lamla I, Thurnhofer S, Vetter W. 2005 – The composition and taxonomic significance of fatty acid patterns in three white rust species: *Albugo amaranthi*, *A. candida* and *A. tragopogonis* (*Peronosporales*, *Albuginaceae*). *Mycological Progress* 4, 179–184.
- Stadler M, Tichy HV, Katsiou E, Hellwig V. 2003 – Chemotaxonomy of *Pochonia* and other conidial fungi with verticillium-like anamorphs. *Mycological Progress* 2, 95–122.
- Stadler M, Hawksworth DL, Fournier J. 2014 – The application of the name *Xylaria hypoxylon*, based on *Clavaria hypoxylon* of Linnaeus. *IMA Fungus* 5, 57–66.
- Steele PR, Pires JC. 2011 – Biodiversity assessment: State-of-the-art techniques in phylogenomics and species identification. *American Journal of Botany* 98, 415–425.
- Steenwyk JL, Shen XX, Lind AL, Goldman GH et al. 2019 – A robust phylogenomic time tree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *MBio* 10, 1–25.
- Strassert JFH, Wurzbacher C, Hervé V, Antany T et al. 2021 – Long rDNA amplicon sequencing of insect-infecting nephridiophagids reveals their affiliation to the *Chytridiomycota* and a potential to switch between hosts. *Scientific Reports* 11, 396.
- Strassert JFH, Monaghan MT. 2022 – Phylogenomic insights into the early diversification of fungi. *Current Biology* 32, 3628–3635.e3
- Stukenbrock E, Gurr S. 2023 – Address the growing urgency of fungal disease in crops. *Nature*, 617(7959), 31–34.
- Su W, Xu R, Bhunjun CS, Tian S et al. 2022 – Diversity of *Ascomycota* in Jilin: introducing novel woody litter taxa in *Cucurbitariaceae*. *Journal of Fungi* 8, 905.
- Sun J, Yu S, Lu Y, Liu H et al. 2022 – Proposal of a new family *Pseudodiploösporeaceae* fam. nov. (*Hypocreales*) based on phylogeny of *Diploöspora longispora* and *Paecilomyces penicillatus*. *Mycology* 14, 60–73.
- Sun S, Coelho MA, Heitman J, Nowrousian M. 2019 – Convergent evolution of linked mating-type loci in basidiomycete fungi. *PLOS Genetics* 15(9), e1008365.
- Surup F, Kuhnert E, Lehmann E, Heitkämper S et al. 2014 – Sporothriolide derivatives as chemotaxonomic markers for *Hypoxylon monticulosum*. *Mycology* 5, 110–119.
- Sutton BC. 1980 – The *Coelomycetes* (CAB, IMI) Kew, Surrey, U.K. pp. 696.
- Taylor JW, Jacobson DJ, Kroken S, Kasuga T et al. 2000 – Phylogenetic species recognition and species concepts in fungi. *Fungal Genetics and Biology* 31, 21–32.
- Tedersoo L, Sánchez-Ramírez S, Kõljalg U, Bahram M et al. 2018 – High-level classification of the fungi and a tool for evolutionary ecological analyses. *Fungal Diversity* 90, 135–159.
- Thiyagaraja V, Lücking R, Ertz D, Wanasinghe DN et al. 2020 – Evolution of non-lichenized, saprotrophic species of *Arthonia* (*Ascomycota*, *Arthoniales*) and resurrection of *Naevia*, with notes on *Mycoporum*. *Fungal Diversity* 102, 205–224.
- Truong C, Mujic AB, Healy R, Kuhar F et al. 2017 – How to know the fungi: combining field inventories and DNA-barcoding to document fungal diversity. *New Phytologist* 214, 913–919.
- Tsui CKM, Baschien C, Goh TK. 2016 – Biology and ecology of freshwater fungi. *Biology of Microfungi* 285–313.
- Turland NJ, Wiersema JH, Barrie FR, Greuter W et al. 2018 – International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017. *Regnum Vegetabile* 159. Glashütten: Koeltz Botanical Books.
- Ullah S, Rahman W, Ullah F, Jehan R et al. 2022 – FDBC: a comprehensive platform of the fungi databases collection. *Journal of Biology* 11(3), 001–006.

- Van Caenegem W, Blondelle A, Dumolein I, Santamaria B et al. 2023 – Five new species of *Gloeandromyces* (*Fungi*, *Laboulbeniales*) from tropical American bat flies (*Diptera*, *Streblidae*), revealed by morphology and phylogenetic reconstruction. *Mycologia* 115(5), 714–737.
- Vicente MF, Basilio A, Cabello A, Pelaez F. 2003 – Microbial natural products as a source of antifungals. *Clinical Microbiology and Infection* 9, 15–32.
- Voglmayr H, Friebe G, Gardiennet A, Jaklitsch WM. 2018 – *Barrmaelia* and *Entosordaria* in *Barrmaeliaceae* (fam. nov., *Xylariales*) and critical notes on *Anthostomella*-like genera based on multigene phylogenies. *Mycological Progress* 17, 155–177.
- Walker GM, White NA. 2017 – Introduction to fungal physiology. *Fungi: Biology and Applications*, 1–35.
- Weete JD, Gandhi SR. 1999 – Sterols and fatty acids of the *Mortierellaceae*: taxonomic implications. *Mycologia* 91, 642–649.
- Wei DP, Gentekaki E, Hyde KD, Xiao YP et al. 2022 – <https://invertebratefungi.org>: an expert-curated web-based platform for the identification and classification of invertebrate-associated fungi and fungus-like organisms. Database, article ID baac021.
- Whiston E, Taylor JW. 2016 – Comparative phylogenomics of pathogenic and nonpathogenic species. *G3 Genes, Genomes, Genetics* 6, 235–244.
- White TJ, Bruns T, Lee SJ, Taylor J. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications* 18(1), 315–322.
- Wibberg D, Stadler M, Lambert C, Bunk B et al. 2021 – High quality genome sequences of thirteen *Hypoxylaceae* (*Ascomycota*) strengthen the phylogenetic family backbone and enable the discovery of new taxa. *Fungal Diversity* 106, 7–28.
- Wijayawardene DN, McKenzie EH, Hyde KD. 2012 – Towards incorporating anamorphic fungi in a natural classification – checklist and notes for 2011. *Mycosphere* 3(2), 157–228.
- Wijayawardene NN, Hyde KD, Tibpromma S, Wanasinghe DN et al. 2017 – Towards incorporating asexual fungi in a natural classification: checklist and notes 2012–2016. *Mycosphere* 8, 1457–1555.
- Wijayawardene NN, Hyde KD, Al-Ani LK, Tedersoo L et al. 2020a – Outline of *Fungi* and fungus-like taxa. *Mycosphere* 11, 1060–1456
- Wijayawardene NN, Hyde KD, Dai DQ, Tang LZ et al. 2020b – A dynamic portal for a community-driven, continuously updated classification of *Fungi* and fungus-like organisms: outlineoffungi.org. *Mycosphere* 11, 1514–1526.
- Wijayawardene NN, Hyde KD, Anand G, Dissanayake LS et al. 2021 – Towards incorporating asexually reproducing fungi in the natural classification and notes for pleomorphic genera. *Mycosphere* 12, 238–405.
- Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M et al. 2022a – Outline of *Fungi* and fungus-like taxa – 2021. *Mycosphere* 13, 53–453.
- Wijayawardene NN, Phillips AJL, Pereira DS, Dai DQ et al. 2022b – Forecasting the number of species of asexually reproducing fungi (*Ascomycota* and *Basidiomycota*). *Fungal Diversity* 114, 463–490.
- Wolczańska A, Christie WW, Fuchs B, Galuska CE et al. 2021– Fatty acid composition and lipid profiles as chemotaxonomic markers of phytopathogenic fungi *Puccinia malvacearum* and *P. glechomatis*. *Fungal Biology* 125, 869–878.
- Wu B, Hussain M, Zhang W, Stadler M et al. 2019 – Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. *Mycology* 10(3), 127–140.
- Wu NA, Dissanayake AJ, Manawasinghe IS, Rathnayaka AR et al. 2021 – <https://botryosphaeriales.org/>, an online platform for up-to-date classification and account of taxa of *Botryosphaeriales*. Database, article ID baab061.

- Wurzbacher C, Larsson E, Bengtsson-Palme J, Van den Wyngaert S et al. 2019 – Introducing ribosomal tandem repeat barcoding for fungi. *Molecular Ecology Resources* 19(1), 118–127.
- Xu J. 2016 – Fungal DNA barcoding. *Genome* 59, 913–932.
- Xu J. 2020 – Fungal species concepts in the genomics era. *Genome* 63, 459–468.
- Zamora JC, Svensson M, Kirschner R, Olariaga I et al. 2018 – Considerations and consequences of allowing DNA sequence data as types of fungal taxa. *IMA Fungus* 9(1), 167–175.
- Zanne AE, Abarenkov K, Afkhami ME, Aguilar-Trigueros CA et al. 2020 – Fungal functional ecology: bringing a trait-based approach to plant-associated fungi. *Biological Reviews* 95(2), 409–433.
- Zhang N, Li Y, Wubet T, Bruelheide H et al. 2018a – Tree species richness and fungi in freshly fallen leaf litter: unique patterns of fungal species composition and their implications for enzymatic decomposition. *Soil Biology and Biochemistry* 127, 120–126.
- Zhang ZF, Zhao P, Cai L. 2018b – Origin of cave fungi. *Frontiers in Microbiology* 9, 1407.
- Zhao P, Liu F, Li YM, Cai L. 2016b – Inferring phylogeny and speciation of *Gymnosporangium* species and their coevolution with host plants. *Scientific Reports* 6(1), 29339.
- Zhao RL, Zhou JL, Chen J, Margaritescu S et al. 2016a – Towards standardizing taxonomic ranks using divergence times – a case study with reconstruction of *Agaricus* taxonomic system. *Fungal Diversity* 78, 239–292.
- Zhao RL, Li GJ, Sánchez-Ramírez S, Stata M et al. 2017 – A six-genes phylogenetic overview of *Basidiomycota* and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. *Fungal Diversity* 84, 43–74.
- Zhou LW, May TW. 2022 – Fungal taxonomy: current status and research agendas for the interdisciplinary and globalisation era. *Mycology* 14, 52–59.
- Zhou LW. 2023 – Microbial taxonomy with DNA sequence data as nomenclatural type: How far should we go? *The Innovation Life* 1, 100017.