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A dynamic portal for a community-driven, continuously updated classification of *Fungi* and fungus-like organisms: outlineoffungi.org

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Abstract

The website http://outlineoffungi.org, is launched to provide a continuous up-to-date classification of the kingdom *Fungi* (including fossil fungi) and fungus-like taxa. This is based on

recent publications and on the outline of fungi and fungus-like taxa published recently (Mycosphere 11, 1060–1456, doi 10.5943/mycosphere/11/1/8). The website is continuously updated according to latest classification schemes, and will present an important platform for researchers, industries, government officials and other users. Users can provide input about missing genera, new genera, and new data. They will also have the opportunity to express their opinions on classifications with notes published in the 'Notes' section of the webpage following review and editing by the curators and independent experts. The website will provide a system to stay abreast of the continuous changes in fungal classification and provide a general consensus on the systematics of fungi.

Keywords – classification – community-driven – higher ranks – outline – portal – taxa

Introduction

Classification of fungi is a topic of key concern among mycologists and other researchers, such as plant pathologists and those in the applied sciences. Accurate species identification and classification are prerequisites for precise scientific communication and for future comparative studies. Morphology-based classification was widely used before DNA sequence data became available and opened up a more objective tool to infer natural relationships (White et al. 1990). In traditional taxonomy, asexual fungi have been placed in the Subdivision *Deuteromycotina* (Ainsworth 1966), which comprised three classes, *Coelomycetes*, *Hyphomycetes* and *Agonomycetes* (*mycelia sterilia*) (Sutton 1980). None of these taxa are used anymore, but the designations, coelomycetes and hyphomycetes, are still frequently used in an informal, descriptive manner. Kendrick (1989) stressed the importance of incorporating asexual fungi and sexual fungi into one classification system and Taylor (1995) discussed the possibility of using one classification system with the application of DNA sequences and phylogeny. In recent years, multi-locus phylogenetic analyses have come at the forefront of modern fungal taxonomy (e.g. Jiang et al. 2020, Samarakoon et al. 2020, Wibberg et al. 2020). Furthermore, DNA sequence analyses are used to link asexual morphs with sexual morphs. As a result of these developments, dual nomenclature that existed for asexual and sexual morphs was discontinued (Hawksworth et al. 2011), and a base for a global classification scheme for fungi developed.

Previous outlines of fungi and their limitations

Classification of sexual fungi has been presented as an outline by Eriksson (1982, 1999, 2001, 2005), Eriksson & Hawksworth (1986, 1998a, b), and Lumbsch & Huhndorf (2007, 2010). Hyde et al. (2011) published the first outline of asexual genera with links to their sexual genera, and this was updated by Wijayawardene et al. (2017b). Wijayawardene et al. (2018) incorporated both asexual and sexual genera in the most recent Outline of the *Ascomycota*. Wijayawardene et al. (2017a, b, 2018, 2020) and He et al. (2019) provided notes for all fungal (including fossil fungi) and fungus-like genera. Most recently, Wijayawardene et al. (2020) provided a classification of all fungi and fungus-like taxa as an outline that was authored by over 150 mycologists. These authors recognized two crucial limitations while compiling the outline.

1. As classification is not an exact science, there can be disagreement and dispute among different research groups on taxonomic boundaries of genera and higher taxa.
2. As phylogenetic data are still being collected at a very high pace and increasingly being used in taxonomy, there is the necessity of constantly updating classification schemes and incorporate new findings.

Overcoming limitations of static publication

Disagreements on the classification and identification of fungi can occur as a result of different types of DNA analyses performed, different gene regions analysed, the impact of taxonomic sampling, the significance of specific morphs used in species delineation, and the inclusion of type species and type specimens in analyses. Therefore, Wijayawardene et al. (2020)

included some alternative views on higher-level classification. It is important for readers to evaluate different classification proposals and make decisions as to which ones they will follow based on the available data and expert opinion. Collection of updated data was also a huge challenge while compiling the outline of Wijayawardene et al. (2020) as fungi and fungus-like organisms are extremely diverse and their classification and taxonomy is in a constant state of flux. As a consequence, a 'cut-off' date for gathering published data was set by Wijayawardene et al. (2020), as the authors were well-aware that continuous updating of the classification scheme would be necessary. As a result, the importance of a flexible, online platform has been discussed as a means to overcome static classification proposals.

Other online databases

Online databases are used as tools in current studies in mycology, including taxonomy, nomenclature and classification (Prakash et al. 2017, Větrovský et al. 2020). For example, Index Fungorum (http://www.indexfungorum.org), MycoBank (https://www.mycobank.org) and FungalNames (http://www.fungalinfo.net/) are important web tools that mainly deal with nomenclature. Several other important web based databases such as onestopshopfungi.org (https://onestopshopfungi.org/), dothideomycetes.org (https://dothideomycetes.org/), fungalgenera.org (https://fungalgenera.org/), facesoffungi.org (http://www.facesoffungi.org/), theyeasts.org (https://theyeasts.org/) provide information on pathogenic genera, Dothideomycetes genera, typification data, descriptions of species and other taxonomic ranks, and yeast genera, respectively (Jayasiri et al. 2015, Jayawardena et al. 2019, Monkai et al. 2019, Pem et al. 2019). Doctor Fungus (http://www.mycosesstudygroup.org/), Mycology Online (http://www.mycology.adelaide.edu.au/), and the *Aspergillus* and Aspergillosis Website (http://www.aspergillus.org.uk/) are dedicated websites for clinically important fungi. The website http://www.marinefungi.org deals with the latest taxonomy of marine fungi (Jones et al. 2019). None of these databases provides general changes in consensus classification and the reasons for changes. Hence, it is essential to have a database, which, based on new studies, is being continuously updated with balanced changes of a community-supported consensus classification.

Outline of *Fungi* web page

The Outline of *Fungi* web site is established to address the limitations recognized during the compilation of the published Outline of *Fungi* (Wijayawardene et al. 2020). The main objectives of the online resource, 'outlineoffungi.org' are to:

1. Present a continually updated consensus classification of fungi and fungus-like organisms based on recent literature and expert opinion.
2. Provide notes for important changes and additions to the outline.
3. Provide an opportunity for researchers to add missing data, suggestions to modify data, and provide critical comments on the consensus outline, based on their expert opinion.

Fossil fungi

Fossil fungi are the ancestors of current fungi and represent extinct lineages, some of which evolved relatively early, probably more than 1500 million years ago. They were buried in sediments, silicified or trapped in amber, and have been preserved until now in sedimentary rocks (Samarakoon et al. 2020). They generally tend to be microscopic. However, a few large fungal bodies, such as mushrooms, have also been found as fossils. Fossil fungal remnants are found in the form of spores, mycelia, sporophores, symbiotic associations, and are commonly observed in macerated residues prepared for palynological studies. Although fungal remains are encountered in sediments of all ages, their frequency increases remarkably in the Tertiary Period (Dilcher 1965, Pirozynski & Weresub 1979, Kalgutkar & Jansonius 2000, Saxena & Tripathi 2011). Because of the fragmentary remains that make up the vast majority of fungal remains, fossil fungi usually lack characteristic features that are diagnostic, hampering their classification with extant fungi. Since DNA survival is limited, they are described on the basis of morphological characters only. For

example, spore taxa are characterised on their shape, size, symmetry, number and nature of apertures, septa and spore wall characters, which often allow up to genus-level classifications. In addition, fossil sporocarps without spores or hyphal details can mostly be assigned to order level or above. All fossil fungal taxa are registered with a recognized nomenclatural repository, e.g. Index Fungorum/MycoBank, to make their references accessible world-wide. This also helps ensuring that they are validly published, avoiding unnecessary introductions of later homonyms.

Fungus-like taxa

Fungal-like characteristics have evolved multiple times, both in prokaryotes (e.g. *Myxobacteria*) and eukaryotes (e.g. slime molds, *Labyrinthulomycota*, *Oomycota*). *Myxobacteria* are, however, almost exclusively studied by bacteriologists, and many members of *Labyrinthulomycota* have been described under the zoological code in the corresponding phylum *Labyrinthulida*. In more recent classifications of myxomycetes, which have long been described under the *International Code of Nomenclature for algae, fungi and plants* (ICNafp), a classification entirely based on the *International Code of Zoological Nomenclature* (ICZN) is adopted (Adl et al. 2005). However, but this approach was criticized by Ronikier & Halamski (2018), who emphasized that the transfer of myxomycetes to zoological nomenclature would destabilize the nomenclature of the group, due to the existence of numerous homonyms. For this reason, the most recent published classification of *Eumycetozoa* was based on the botanical nomenclature (Leontyev et al. 2019). However, most of the non-Eumycetozoan slime molds, such as protosteloids, acrasids, copromyxids, fonticulids, or guttulinopsids, were described by protozoologists using zoological nomenclature. These groups, therefore, should be covered by ICZN. However, the Preamble 8 of the ICNafp states that the 'slime molds' are considered among the organisms for which the Code is applied, while ICZN does not mention these organisms at all, so coordination between ICZN and ICNafp is needed to resolve this issue.

The group most closely resembling opisthokont fungi are *Oomycota*, because of their hyphal growth, osmotrophic nutrition and formation of large numbers of asexual spores (Dick 2001, Beakes & Thines 2017). Because of these similarities, they have always been described under the ICNafp and its predecessors. Their early-diverging lineages mostly form only small, holocarpic thalli, i.e. the entire thallus converts into a sporangium. This is similar to the trophocytes found in some other members of the *Straminipila-Alveolata-Rhizaria* supergroup (Burki et al. 2007) groups, such as *Perkinsozoa*. However, the monophyletic branch starting from *Miraculaceae* (Buaya et al. 2017) until the highly diversified downy mildews (Thines & Choi 2016) is commonly recognised as the phylum *Oomycota* (Beakes & Thines 2017), and thus, treated under the ICNafp. Within *Oomycota*, the higher-level classification is still not fully resolved, owing to the difficulties in obtaining multiple genes for in-depth phylogenetic analyses from the often obligate biotrophic and holocarpic lineages that diverge before the main split into *Saprolegniomycetes* and *Peronosporomycetes* (Beakes & Thines 2017). Another poorly-known group related to *Oomycota*, *Hyphochytriomycota*, is usually treated under the ICNafp as well, but only few species of this group have been discovered and their higher-level relationships, as well as their relationships to some bacteriovorous protists and oomycetes are still poorly resolved. Thus, it is expected that for both oomycetes and hyphochytrids, there will be considerable efforts necessary to stabilise their nomenclature, which will also be reflected in the Outline of Fungi website.

Construction

As a starting point, all fungal genera in the database are listed according to Wijayawardene et al. (2020). The database will be updated based on new studies and observations by the users.

Database interface and visualization

The homepage comprises nine tabs. Viewers can follow them and use the underlying functions with a simple and user-friendly interface (Fig. 1).

Tools included in homepage

1. Home: The homepage provides an overview of the kingdom *Fungi*. Objectives of launching the website are also provided. (Fig. 1)
2. Outline: The 'Outline' provides a recent consensus taxonomic classification of the kingdom *Fungi* and fungus-like taxa of other kingdoms (e.g., slime moulds, oomycetes). (Fig. 2)
3. Archives: The 'Archives' provides recently published outlines.
4. Sexual-asexual links: This will be updated with all pleomorphic genera.
5. Curators: This section provides a list and contact details of the curators of the website (see Table 1).
6. History: This section provides a brief history of the classification of kingdom *Fungi* and fungus-like taxa.
7. References: This section provides reference list of citations used in the entries, history and related information.
8. Notes: The 'Notes' section publishes recent changes in outline since Wijayawardene et al. 2020 (see below for further details).
9. Contact: The 'Contact' section provides contact details for the website and allows users to address any comments and suggestions.

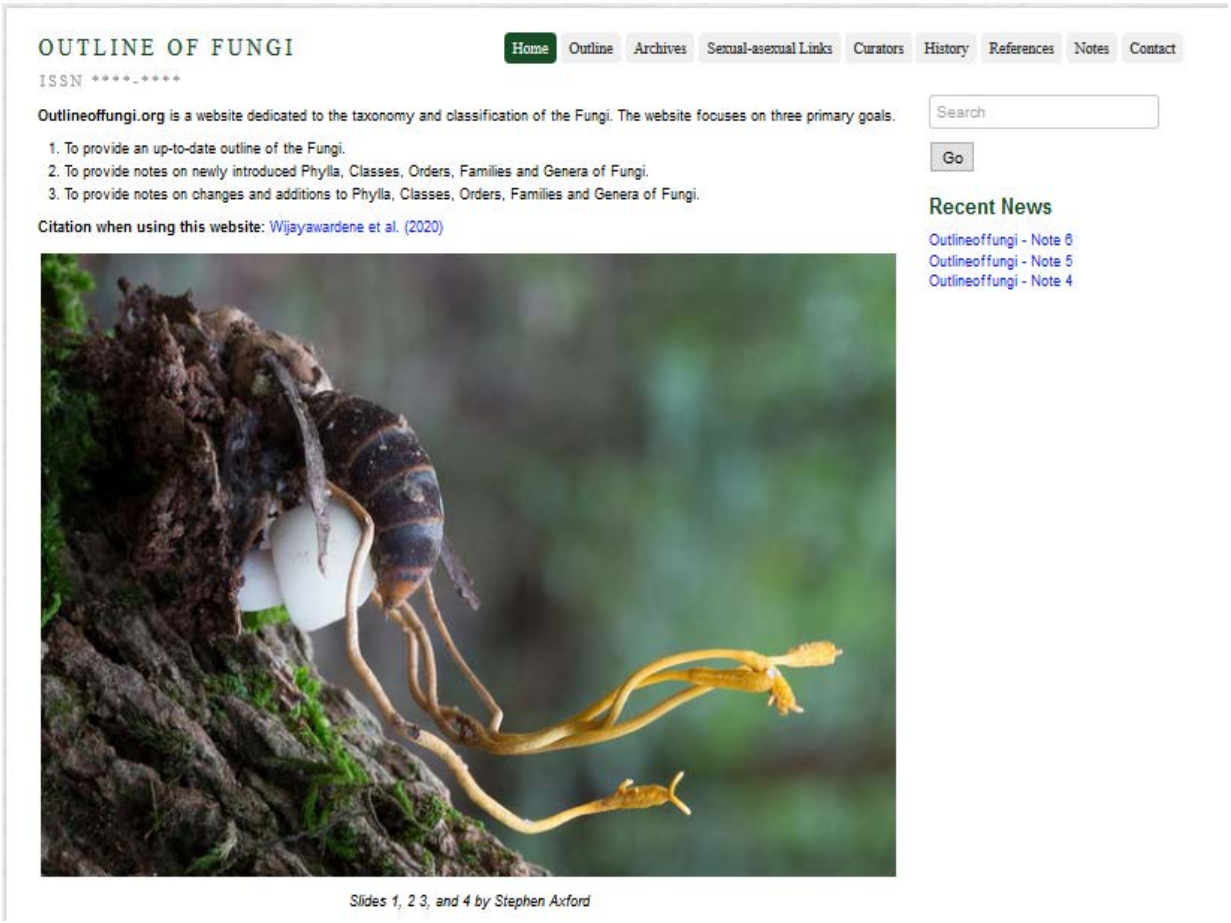

Figure 1 – The homepage view of outlineoffungi.org

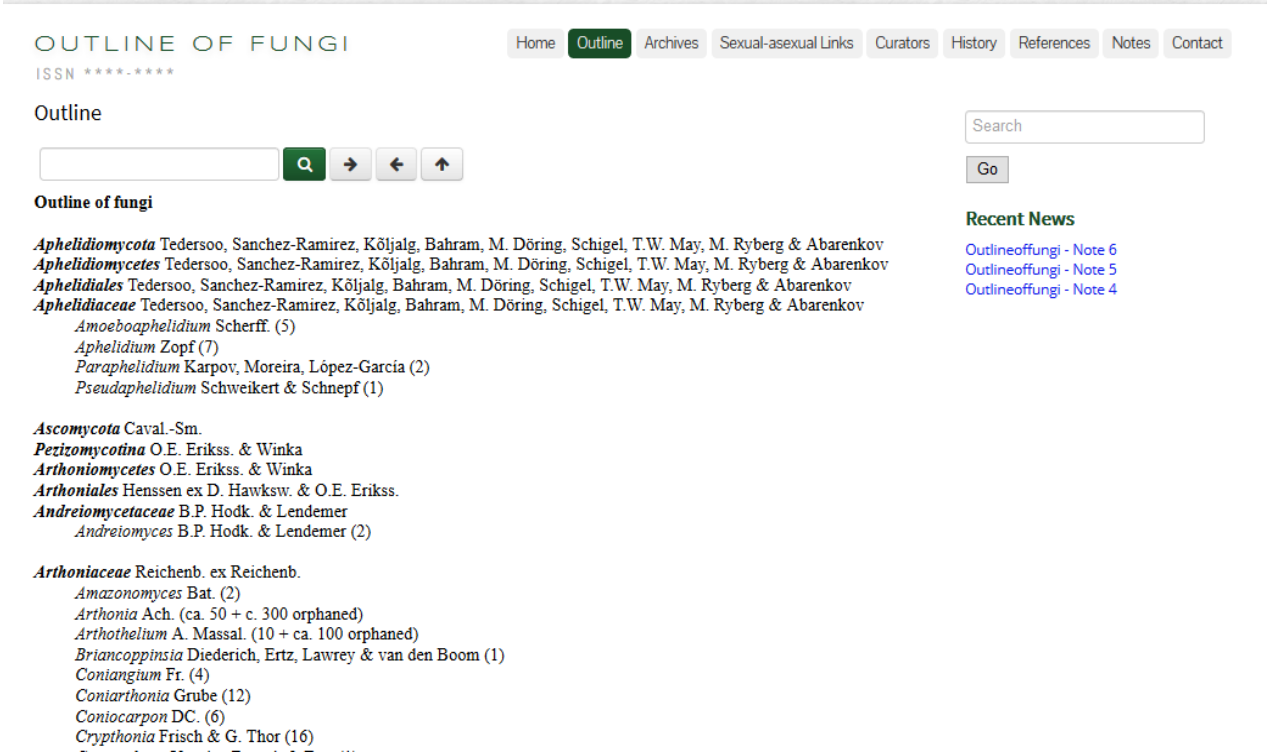

Figure 2 – Outline of fungi

Table 1 List of expert curators for Outline of *Fungi* webpage

Position	Name	Field of specialty	Contact details
Head curator	Nalin N. Wijayawardene	Asexual fungi, nomenclature	nalinwijayawardene@yahoo.com
Senior Curator	Kevin D. Hyde	*Dothideomycetes*, *Sordariomycetes*	kdhyde3@gmail.com
Managing curators	Makbule Erdoğdu	Fungal plant pathogens	merdogdu@ahievran.edu.tr
	Andrei Tsurykau	Lichens, lichenicolous fungi	tsurykau@gmail.com
	Shiva Prakash Nedle	*Basidiomycota*, hyphomycetes	shivanedle@gmail.com
	Josiane S. Monteiro	Asexual fungi	kiotobelbio2003@yahoo.com.br
Curators	Alan J.L. Phillips	*Botryosphaeriales*, pathogens	alan.jl.phillips@gmail.com
	André Aptroot	Lichens	andreaptroot@gmail.com
	Bruno T. Goto	*Glomeromycota*	brunogoto@hotmail.com
	Danny Haelewaters	*Leotiomycetes*, *Laboulbeniomycetes*	danny.haelewaters@gmail.com
	Eleni Gentekaki	Basal fungi	gentekaki.ele@mfu.ac.th
	Damien Ertz	Lichens, lichenicolous fungi	damien.ertz@jardinbotaniquemeise.be
	Hugo Madrid	hyphomycetes, *Eurotiomycetes*	hugo.madrid@gmail.com
	Marc Stadler	*Xylariales*, secondary metabolites of fungi	marc.stadler@helmholtz-hzi.de
	Alfredo Vizzini	*Basidiomycota*, *Agaricales*, *Boletales*	alfredo.vizzini@unito.it
	Marco Thines	*Oomycota*, *Ustilaginomycotina*, nomenclature	marco.thines@senckenberg.de
	Chuan-Gen Lin	Hyphomycetes	chuangenlin@gmail.com

Table 1 Continued.

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	Paul M. Kirk	Nomenclature	P.Kirk@kew.org
	Don-Qin Dai	*Dothideomycetes*	cicidaidongqin@gmail.com
	Ramesh K. Saxena	Fossil fungi	rksaxena2207@yahoo.com
	Rafael F. Castañeda-Ruiz	hyphomycetes	rfcastanedaruiz@gmail.com
	Irina S. Druzhinina	Asexual fungi	irina.s.druzhinina@mail.ru
	Feng Cai	Asexual fungi	czfscf@hotmail.com
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	Sinang Hongsanan	Sooty moulds	sinang333@gmail.com
	E.B. Gareth Jones	Aquatic fungi	torperadgj@gmail.com
	Walter P. Pfliegler	Yeast (Ascomycota)	pfliegler.valter@science.unideb.hu
	Samantha C. Karunarathna	*Basidiomycota*	samanthakarunarathna@gmail.com
	Hyang Burm Lee	Basal fungi	hblee@jnu.ac.kr
	Javier Etayo	Lichens, lichenicolous fungi	jetayosa@educacion.navarra.es
	H. Thorsten Lumbsch	Lichens	tlumbsch@fieldmuseum.org
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	R.G. Udeni Jayalal	Lichens	jayalal@appsc.sab.ac.lk
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	Dhanushka N. Wanasinghe	*Pleosporales*	dnadeeshan@gmail.com
	Xinlei Fan	*Diaporthales*, *Botryosphaeriales*, forest pathogenic fungi	xinleifan@bjfu.edu.cn
	Eric H.C. McKenzie	*Pucciniomycotina*, *Ustilaginomycotina*, hyphomycetes	mckenziee@landcareresearch.co.nz
	Teun Boekhout	Yeasts	t.boekhout@wi.knaw.nl
	Vince Hustad	*Geoglossales*	vhustad@gmail.com
	Dmitry Leontyev	Slime moulds	alwisiamorula@gmail.com
	Sybren de Hoog	Clinical fungi	Sybren.deHoog@radboudumc.nl.
	Tuula Niskanen	*Agaricomycetes*	t.niskanen@kew.org
	Roger G. Shivas	Plant pathogens	roger.shivas@usq.edu.au
	Gaya Ester	Lichens	e.gaya@kew.org
	Wen-Jing Li	Asexual fungi	winnie20070653026@163.com

Notes section

The publication of notes is recognized as an important part of outlineoffungi.org, which provides details of new additions, changes or opinions. This provides an opportunity for interested parties to better understand recent changes. It will also provide a platform to express opinions and judgements on fungal taxonomy with respect to the identification and placement of fungi in different classification schemes.

Changes to the outline/ classification could be due to three main reasons:

1. Changes to classification following recent publications.
2. Additions of taxa missing in Wijayawardene et al. (2020).
3. Correction or errors in Wijayawardene et al. (2020) (e.g. duplication of names, wrong placement of taxa).

Preparing notes

1. Addition of new taxa from new publications

The addition of new taxa will be coordinated with repositories such as Index Fungorum. The published materials/research articles that introduce new taxa will cross checked against repository lists by the four managing curators. Their main task will be to prepare entries for new additions. As the second step, the entries will be sent to curator/s for checking. Once the managing curator has edited the entry according to curators' comments, the senior curator and the head curator will check the entries. The head curator will cross check the validity of the taxa against repositories (e.g. Index Fungorum) and upload the entry.

A list of new taxa (genus level and above) will be gathered from Index Fungorum twice a year and cross checked against the entries provided in outlineoffungi.org. This will help to maintain a current outline.

Authors who publish new taxa are also encouraged to provide entries. This includes resurrection of synonymized genera in recent publications (e.g. Thiyagaraja et al. 2020).

2. Addition of missing taxa

Notes for missing taxa will be mainly expected from expert mycologists. They can prepare the entries and send these to the head curator. The curator/s will check and correct the entries which will be uploaded to the webpage.

3. Correcting mistakes in the existing outline

Notes which correct mistakes (such as duplication of names, incorrect author citations) will also be acceptable. However, the senior curator and the head curator will decide whether it is necessary to upload the note, or correct the web version of the outline.

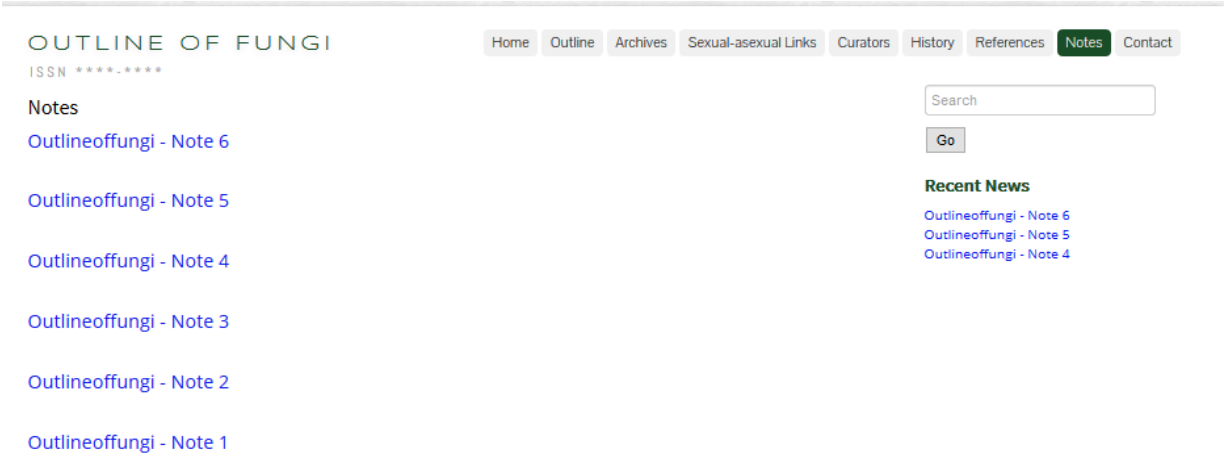

Figure 3 – Notes section

A platform to exchange different opinions

Different opinions on higher classification and synonymy of pleomorphic genera (Art. 59.1) are two important topics that can lead to confusion. For example, the higher-level classification of *Leotiomycetes* in Ekanayaka et al. (2019) is different from the classification in Johnston et al. (2019). Two main differences account for the alternative classification schemes: (i) the amount of sequence data [5-locus by Ekanayaka et al. (2019) vs 15-locus and genomic-scale by Johnston et al. (2019)] and (ii) the inclusion of type species and ex-type sequences in Johnston et al's (2019) analyses. However, the presentation of the alternative classifications provide perspective for

general users and mycologists interested in *Leotiomycetes* taxonomy. Further, if other authors have different opinions on existing classifications, we encourage them to provide them in the notes section.

Adopted or proposed names for pleomorphic genera are also controversial in some cases. For example, Wijayawardene et al. (2014) proposed to adopt *Anthracostroma* Petr. 1954 over *Camarosporula* Petr. 1954, but Rossman et al. (2015) did not agree and proposed to adopt the latter name over the former. This type of disagreement and controversial opinions might cause confusion among users if future authors referred to only one publication. Thus, it is essential to have a platform such as http://outlineoffungi.org to provide different opinions, which can eventually culminate in a consensus towards species concepts.

Links between sexual and asexual morphs

The new webpage also provides links between sexual and asexual morphs with the names that have been adopted for pleomorphic genera since 2011 (Art. 59.1). Wijayawardene et al. (2017b) provided the adopted names of pleomorphic genera based on previous studies (e.g. Wijayawardene et al. 2014, Rossman et al. 2015), but it is intended to include all pleomorphic genera according to recent developments and recommendations from the *International Commission on the Taxonomy of Fungi*.

A place to obtain data (from genus to higher rank) for phylogenetic analyses

Selecting taxa for phylogenetic studies is a challenge as it is important to include closely related genera in the analyses. Extracting data from static publications might cause problems due to outdated views on phylogenetic relationships. Thus, it is important to obtain data from a database that is kept updated. Since outlineoffungi.org will be continuously updated, with the supervision of senior taxonomists, users can obtain a list of related genera from it for their phylogenetic analyses and morphological comparisons.

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