

The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts

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Abstract Taxonomic names are key links between various databases that store information on different organisms. Several global fungal nomenclural and taxonomic databases (no-

tably Index Fungorum, Species Fungorum and MycoBank) can be sourced to find taxonomic details about fungi, while DNA sequence data can be sourced from NCBI, EBI and

Database URL: www.Facesoffungi.org

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UNITE databases. Although the sequence data may be linked to a name, the quality of the metadata is variable and generally there is no corresponding link to images, descriptions or herbarium material. There is generally no way to establish the accuracy of the names in these genomic databases, other than whether the submission is from a reputable source. To tackle this problem, a new database (FacesofFungi), accessible at www.facesoffungi.org (FoF) has been established. This fungal database allows deposition of taxonomic data, phenotypic details and other useful data, which will enhance our current taxonomic understanding and ultimately enable mycologists to gain better and updated insights into the current fungal classification system. In addition, the database will also allow access to comprehensive metadata including descriptions of voucher and type specimens. This database is user-friendly, providing links and easy access between taxonomic ranks, with the classification system based primarily on molecular data (from the literature and via updated web-based phylogenetic trees), and to a lesser extent on morphological data when molecular data are unavailable. In FoF species are not only linked to the closest

phylogenetic representatives, but also relevant data is provided, wherever available, on various applied aspects, such as ecological, industrial, quarantine and chemical uses. The data include the three main fungal groups (Ascomycota, Basidiomycota, Basal fungi) and fungus-like organisms. The FoF webpage is an output funded by the Mushroom Research Foundation which is an NGO with seven directors with mycological expertise. The webpage has 76 curators, and with the help of these specialists, FoF will provide an updated natural classification of the fungi, with illustrated accounts of species linked to molecular data. The present paper introduces the FoF database to the scientific community and briefly reviews some of the problems associated with classification and identification of the main fungal groups. The structure and use of the database is then explained. We would like to invite all mycologists to contribute to these web pages.

Keywords Classification · Database · FacesofFungi · Fungi · Phylogeny · Taxonomy

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Introduction

Fungi encompass a diverse group of eukaryotic organisms ranging from microscopic, single celled yeasts to macroscopic multicellular mushrooms (Kendrick 1985; Schoch et al. 2014) and are numerically among the most abundant eukaryotes in the Earth's biosphere (Smil 2003; Gherbawy and Voigt 2010; Blackwell 2011; Hawksworth 2015). They are vital to ecosystem functioning, play important roles in natural nutrient cycling, and cause disease of humans, animals and plants. They are increasingly being used as food and in biotechnological industries to produce enzymes, alcoholic drinks, medicines, biocontrol agents, natural fertilizers, natural pigments, cosmetics and foods (Marcel et al. 1998; Duránad et al. 2002; Hyde et al. 2010a; Lange 2010; Muzzarelli et al. 2012; Gupta et al. 2015; Bandara et al. 2015), fermented foods, to enhance storage stability and to improve human health and wealth (Knorr 1998; Laitila et al. 2002; Martins et al. 2009). In nature, fungi are specialized in breaking down plant materials by means of a wide range of enzyme systems (Eggin and Pugh 1962; Tian et al. 2009). In industry, such fungal products can be used to convert bio-waste and agricultural crop residues into bioenergy, biomaterials, biochemical and biofertilizers (Arvanitoyannis 2008; Lange 2014). The world is warming at an unprecedented rate and the resulting climate change will impact the distribution and biodiversity of living organisms (Bellard et al. 2012; Hutchings et al. 2012). Climate change will lead to increasing stress on agricultural productivity, and fungi could be exploited as a new generation of agricultural inoculants to provide more robust, nutrient efficient, and drought tolerant crop plants (Lange et al. 2012). It is therefore, important to scientifically document and record fungal, diversity and classification in a phylogenetic based system so that they can be preserved and used more efficiently (Lange 2010). As such a dedicated fungal database providing efficient storage and organization of information will allow improved fungal identification and possibly provide an indication of potential fungal candidates for future applied purposes.

Classification using morphological versus molecular data

Morphological characters, which are relatively easy to observe and record, have been used over the last 300 years to identify, classify, and infer the relationships of fungi (Talbot 1971); a system known as the phenotypic classification concept (Inui et al. 1965). Over the past 20 years the use of molecular data, especially DNA sequence data, has allowed reconstruction of the evolutionary relationship of all life, revolutionizing the process of classifying an organism and leading to a renaissance in taxonomy (Seifert et al. 2011). Morphological characters may not reflect phylogenetic

relationships as many of them are subject for example to plasticity, parallelism, and reversal (Judd et al. 2002). Morphology-based identification of a species can be very difficult and highly subjective in many cases, especially among asexual or non sporulating fungi (Jeewon et al. 2002; Promputtha et al. 2005, 2007).

While morphology formed the base for taxonomy, modern classification systems increasingly use phylogenetic analyses of DNA sequence data to reveal major evolutionary trends among fungi (e.g., O'Donnell 1979; Hibbett et al. 1997; Jensen et al. 1998; Sugiyama 1998; Tanabe et al. 2000, 2004, 2005; Moncalvo et al. 2000, 2002; Gottlieb and Lichtwardt 2001; White et al. 2001; White 2002, 2006; Cafaro 2005; Seif et al. 2005; Dentinger et al. 2015). It is now commonplace to combine morphological and molecular data to resolve taxonomic problems and provide a more holistic approach towards a classification system that reflects past evolutionary pathways.

Higher level classifications

Classification of a fungus into a taxonomic rank is largely based on convergent morphologies. Incorporation of molecular data has profoundly changed the systematics of fungal classes, subclasses, orders, families, genera, and species (Schoch et al. 2006; Hibbett et al. 2007; Gherbawy and Voigt 2010), e.g., recent revisions of the classes Arthoniomycetes, Dothideomycetes and Sordariomycetes (Ertz et al. 2013; Hyde et al. 2013a; Wijayawardene et al. 2014; Maharachchikumbura et al. 2015), the subclasses Lulworthiomycetidae and Xylariomycetidae (Senanayake et al. 2015) the orders *Asterinales*, *Dothideales* and *Erysiphales* (Braun and Cook 2012; Hongsanan et al. 2014; Thambugala et al. 2014; Ertz and Diederich 2015), and the genera *Pestalotiopsis* and *Diaporthe* (Maharachchikumbura et al. 2011, 2012, 2013b; Udayanga et al. 2011, 2012a). Although the classification of Hibbett et al. (2007) has been amended at all levels since its publication (e.g., Binder et al. 2010; Jones et al. 2011; Bauer et al. 2015), its fundamental structure remains the same. These are used as the baseline classification system in the FoF database.

Hibbett et al. (2007) accepted one kingdom, one subkingdom, seven phyla, and ten subphyla for classification of fungi (Table 1). The Basal lineages and Dikarya (Ascomycota and Basidiomycota) are two main groups among seven phyla of fungi. The most dramatic changes in this classification concern the 'basal fungal lineages', which include taxa that have traditionally been placed in the Zygomycota and Chytridiomycota (Hibbett et al. 2007). These groups have long been recognized to be polyphyletic, based on analyses of rRNA, TEF1, and RPB1 (James et al. 2000; Tanabe et al. 2004, 2005).

Table 1 Higher level classification of the Kingdom Fungi based on phylogenetic analyses (Hibbett et al. 2007)

| Kingdom | Subkingdom | Phylum | Subphylum |
|---------|------------|--------------------------------|--|
| Fungi | Dikarya | Ascomycota | Taphrinomycotina Saccharomycotina Pezizomycotina |
| | | Basidiomycota | Pucciniomycotina Ustilaginomycotina Agaricomycotina |
| | | Blastocladiomycota | |
| | | Chytridiomycota | |
| | | Glomeromycota | |
| | | Microsporidia | |
| | | Neocallimastigomycota | |
| | | Subphyla <i>Incertae sedis</i> | Mucoromycotina Kickxellomycotina Zoopagomycotina Entomophthoromycotina |

Ascomycota

The classification of ascomycete genera at the family and order levels based on morphological characters was previously very difficult and subjective. The most important characters used to circumscribe major groups of Ascomycota were the type of asci, septation of ascospores, the morphology and development of the ascoma, as well as the structure and organization of the centrum (Barr 1987, 1992). Morphological characters can assist in the identification of fungal genera as is evident from a plethora of identification keys and morphological descriptions (Cummins and Hiratsuka 2003; Heffer et al. 2006; Diba et al. 2007; Shenoy et al. 2007; Petrini and Petrini 2013). The most detailed morphological assessment of the class Dothideomycetes was that of Barr (1987) and her subclasses were interpreted based on characters of the centrum, including its absence or presence and types of hamathecial tissues. In line with several earlier authors (as outlined in Barr 1979, 1987), Barr's ordinal classifications were based on ascomatal type (perithecioid or apothecioid) and the manner in which nutrients were obtained by the fungus (Barr 1987). In addition to these characters she emphasized the importance of further distinction in the hamathecium, i.e. the shape and structure of the pseudoparaphyses (Barr 1979, 1987), the latter of which, has now been shown to be phylogenetically misleading (Liew et al. 2000).

In another large class, Sordariomycetes, the shape, size, pigmentation, texture and position of ascomata were used in traditional classifications (Zhang et al. 2006). For example the position of ascomata in relation to substrates was used in family delimitation of the order *Diaporthales*, but this classification was not supported by later molecular phylogenetic analyses based on DNA sequence characters (Zhang and Blackwell 2001; Castlebury et al. 2002; Maharachchikumbura et al. 2015). In *Erysiphales* (powdery mildews), dramatic changes in the classification structure have been proposed following

several comprehensive phylogenetic studies at generic and higher levels of this fungal group (Braun and Cook 2012). Sexual morph-based characters systematic of *Erysiphales* were found to be misleading, and now the molecular phylogeny of *Erysiphales* is primarily reflected by morphological characters of the asexual morphs (Mori et al. 2000; Braun and Cook 2012).

Basidiomycota

Historical classification of the basidiomycetes into genera, families and orders used characters such as basidia shape, spore shape and deposit colour, hymenial structures such as cystidia, ultrastructure of hyphal septa and spindle pole bodies, presence or absence of yeast phases, "spore repetition" (production of secondary spores directly from spores), and cell-wall carbohydrate composition characters (Oberwinkler 1987; Prillinger et al. 1990, 1991; McLaughlin et al. 1995). Sequences from ribosomal RNA genes (rDNA), recently supplemented by protein-coding genes (e.g., *rpb1*, *rpb2* and *tef1*; Matheny et al. 2007), have played a major role in increasing our understanding of the relationships within the Basidiomycota, and have demonstrated that some morphological attributes which have been given importance in higher-level classification, such as the form of basidia, are subject to homoplasy (Swann and Taylor 1993, 1995; Swann et al. 1999). There is therefore a need for a modern outline of Basidiomycota in a similar way as provided for Ascomycota by Lumbsch and Huhndorf (2010) and more recently by Wijayawardene et al. (2014) for Dothideomycetes and by Maharachchikumbura et al. (2015) for Sordariomycetes. Partial outlines of higher-level taxa of Basidiomycota were provided by Aime et al. (2014) for Pucciniomycotina, Begerow et al. (2014) for Ustilaginomycotina, Weiss et al. (2014) for Tremellomycetes

and allies, Oberwinkler (2014) for Dacrymycetes and Hibbett et al. (2014) for Agaricomycetes. Recently, due to whole genomes becoming available for an increasing number of species across all the known phyla of fungi, systematics is entering a new era: the so-called genome-enabled mycology where genome-scale data are used in phylogenomic analyses to detect more reliable natural relationships within fungi (Hibbett et al. 2013; Hibbett and Taylor 2013). The preliminary phylogenomic studies by Binder et al. (2013) and Dentinger et al. (2015) shed light on the phylogeny of *Polyporales* and *Agaricales*, respectively. In particular, Dentinger et al. (2015), after analyzing a genomic dataset composed of 39 genomes representing 26 family-level clades, recognized seven suborders within *Agaricales*.

Myxomycota

In addition to the true fungi, the database described herein also considers the organisms generally known as slime molds, plasmodial slime molds, myxogastrids or (the term likely to be familiar to most mycologists) Myxomycetes. Members of the group have been traditionally studied by mycologists, and specimens of myxomycetes are curated in much the same way as fungi and are almost invariably deposited in the same herbaria. However, molecular data have confirmed that Myxomycetes belong on a different branch of the eukaryotic tree of life and now are placed within the assemblage of amoeboid protists referred to as the supergroup Amoebozoa (Fiore-Donno et al. 2010). However, the well-established tradition of Myxomycetes being studied almost exclusively by mycologists was considered sufficient justification for including these organisms in the database. A recent review of the biology, ecology and classification of the group was provided by Stephenson (2011). Other groups on different branches of the eukaryotic tree of life, traditionally studied by mycologists, i.e. Trichomycetes may also be included if the need arises.

Resolving species

The phenotypic concept based on morphological and physiological characteristics was the classic approach for delimiting species (Inui et al. 1965). The use of morphology and host-specificity to recognize plant-associated fungi may have resulted in the description of an excessive number of species, with few character differences (Hibbett et al. 2007), or in contrast, may have overlooked cryptic species that can be detected from mating tests (e.g., in *Armillaria*, Anderson and Ullrich 1979) or multigene phylogenies (e.g., in *Amanita*, Sánchez-Ramírez et al. 2015). For example, in the ascomycetes, species of the genus *Pestalotiopsis* were mostly introduced based on host-specificity (Espinoza et al. 2008). However a series of papers

by Maharachchikumbura (Maharachchikumbura et al. 2011, 2012, 2013a, b, c), have shown that most *Pestalotiopsis* species are generalists. Similar species concepts based on host association are known from other genera (e.g., *Colletotrichum*, *Diaporthe*). Recent findings based on molecular data have shown most species to have reasonably wide host ranges, and unexpectedly high species diversity (Photita et al. 2005; Udayanga et al. 2011; Manamgoda et al. 2013). The genus *Diaporthe* comprises pathogenic, endophytic and saprobic species with both temperate and tropical geographic distributions (Rehner and Uecker 1994; Rossmann et al. 2007; Udayanga et al. 2011; Huang et al. 2013). Species recognition criteria in *Diaporthe* have evolved from a concept based on morphology and host associations (Wehmeyer 1933) to the recent concept of phylogenetic species recognition (Castlebury et al. 2003; Santos and Phillips 2009; Santos et al. 2011; Udayanga et al. 2012a, b, 2014; Tan et al. 2013). In a similar manner Phillips et al. (2013) used DNA sequence data together with morphology to provide robust concepts for genera and species in the Botryosphaeriaceae. In the basidiomycetes, the use of DNA sequence data to improve species recognition in morphologically similar taxa were also conducted (e.g., in *Inocybe* Matheny et al. 2001; *Ganoderma*, Moncalvo and Buchanan 2008).

Unlike phenotypic characters, which are often difficult to interpret given the amount of homoplasy in fungi, molecular data are generally more reliable to delimit species. The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) has been widely used for delimiting fungal species as proposed by Taylor et al. (2000) and recently a growing number of studies have used cohesion-based approaches for species delimitation (reviewed in Leavitt et al. 2015). The former was based on the genealogical concordance species concept (Avice and Ball 1990) requiring the analysis of several unlinked genes. The GCPSR is applicable to any set of independent characters, whether they are molecular, morphological or other (Dettman et al. 2003). However, only a few studies have evaluated the utility of the GPDSR to delineate closely related species in genera with broad host ranges and wide geographic distributions (Huang et al. 2013; Giraud et al. 2008; Dupis et al. 2012; Groenewald et al. 2013; Salgado-Salazar et al. 2013). Recently, multispecies coalescence methods have emerged as a powerful approach for phylogenetic inference and species demarcation (Pammern et al. 2012; Leavitt et al. 2012, 2013; Hyde et al. 2013b; Jones et al. 2014; Sánchez-Ramírez et al. 2015).

Linking sexual (teleomorphs) and asexual morphs (anamorphs) to genera and species

The sexual morph of a fungus has been traditionally classified and named separately from their asexual morph (see Index Fungorum where asexual morph and sexual morph names

are now commonly synonymized). Each morph was provided with a different binomial as if it was a different species, and the morphs were even subjected to different classification systems (Hennebert and Weresub 1977; Kendrick 1979; Weresub and Hennebert 1979; Hennebert 1987; Sugiyama 1987; Reynolds and Taylor 1993; Seifert et al. 2000; Kirk et al. 2001). Molecular techniques now allow most asexual taxa to be connected to their corresponding sexual morphs or integrated into appropriate higher taxonomic ranks which are recognized by changes in the nomenclatural code (Guarro et al. 1999; Hawksworth 2011; Braun and Cook 2012).

Epitypification and neotypification

An epitype is a specimen or illustration selected to serve as an interpretative type when the holotype, lectotype, or previously designated neotype, or all original material associated with a validly published name, is demonstrably ambiguous and cannot be critically identified for purposes of the precise application of the name to a taxon (McNeill et al. 2012). Designation of an epitype is not effected unless the holotype, lectotype, or neotype that the epitype supports is explicitly cited (McNeill and Turland 2011). Epitypification and neotypification can help to resolve taxonomic confusion and stabilize the nomenclature of fungi. Ariyawansa et al. (2014) demonstrated the importance of epitypification and also illustrated the value of proposing reference specimens when epitypification is not advisable. Designating an epitype with molecular data along with complete or adequate descriptions is the best option to stabilize the understanding of species, genera, family and orders (Ariyawansa et al. 2014). Collaboration among mycologists will be vital key for the success of epitypification and neotypification of many fungal names worldwide.

The need for comprehensive fungal databases in a phylogenetic framework

The development of the polymerase chain reaction method (PCR; Bartlett and Stirling 2003) has revolutionized many fields of biology, including fungal systematics (Schesser et al. 1991; Gargas and Taylor 1992; Valones et al. 2009). In the last two decades, phylogenetic classifications of the kingdom Fungi have been proposed with reference to molecular phylogenetic analyses of one or more genes with input from diverse members of the fungal taxonomic community (Hibbett et al. 2007; Nilsson et al. 2008).

Databases have a role to play in aggregating these scattered data. There are numerous fungal databases which provide name lists of fungi, literature, fungal DNA sequences and genomic data and photographs for morphological identification. Some have greatly simplified the understanding of fungi

compared with other organisms. Mycologists should be responsible for providing informative outreach materials, made easily accessible on the internet, in a free way or under an open access license. It is a responsibility of mycologists to ensure that data and results are available to end users (Gregory et al. 2007; Lange 2010; Mesirov 2010). Some important online mycological resources are listed in Table 2.

Fungal database

The taxonomic name of an organism is the key link between different databases that store information on that organism (Roderic 2005; Abarenkov et al. 2010). A correct name enables access to complete information and may have a major economic impact on, for example, agriculture (phytopathology, epidemiology) or pharmaceuticals (ethnobiology), and in fact on the total scientific community (Crous et al. 2004a; Hyde et al. 2010b).

An excellent source of nomenclatural information that provides classification of fungal species is *Index Fungorum*, a community resource coordinated and supported by the partnerships among CABI Bioscience and Landcare Research-NZ (Lincoln, New Zealand) (White 2006). *Index Fungorum* is a database of over 370,000 names of fungi, primarily at the species level (Roderic 2005). Its partner database, *Species Fungorum*, is a RBG Kew coordinated initiative delivering the fungal component of the Species 2000 project and a contribution, in partnership with Integrated Taxonomic Information System, to the Catalogue of Life (currently used in the Global Biodiversity Information Facility portal); this global initiative is presented at <http://www.speciesfungorum.org/>.

MycoBank (<http://www.MycoBank.org>) was launched with a remit to document mycological nomenclatural novelties and their associated descriptions and illustrations (Crous et al. 2004a, b). This allows mycologists to deposit new names. It also requires some basic information, both nomenclatural (example, the basionym or type information) and taxonomical (e.g., a description). Depositors of nomenclatural novelties are asked to deposit, in addition to a description and type information, as much other data as they feel appropriate or have available. This includes illustrations, molecular sequence data, physiological data, and links to web-based data. This name registration is also offered by *Index Fungorum* and Fungal Names (<http://fungalinfo.im.ac.cn/fungalname/fungalname.html>).

GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>) is the most comprehensive collection of publicly available nucleotide and protein sequences (Benson et al. 2015). GenBank, together with its collaborative partners in the International Nucleotide Sequence Databases Collaboration (INSDC), i.e., the DNA Data Bank of Japan (DDBJ) and the European Nucleotide Archive (ENA) has long been the most

Table 2 Examples of useful mycological websites and basic concept of contents

| Web site | Content |
|--|--|
| <i>Aspergillus</i> & Aspergillosis Website (http://www.aspergillus.org.uk/) | Taxonomic—providing detailed information on <i>Aspergillus</i> and the diseases it can cause |
| Cybertruffle (http://www.cybertruffle.org.uk/eng/index.htm) | Nomenclatural and taxonomic—information about fungi and their associated organisms |
| Freshwater Ascomycete Database (http://fungi.life.illinois.edu/) | Taxonomic—devoted to Ascomycetes that occur in freshwater habitats |
| FungiDB: an integrated functional genomics database for fungi (http://FungiDB.org) | Taxonomic—integrated genomic and functional genomic database for the kingdom Fungi |
| Fungi—Tree of Life Web Project (http://tolweb.org/fungi) | Taxonomic—morphological, biochemical information and DNA-based comprehensive multigene phylogeny |
| GenBank (http://www.ncbi.nlm.nih.gov/genbank/) | Taxonomic—annotated collection of all publicly available DNA sequences comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI |
| Index Fungorum (http://www.indexfungorum.org/) | Nomenclatural—list of names of fungal taxa at all taxonomic ranks |
| International Commission on the Taxonomy of Fungi (http://www.fungaltaxonomy.org) | Taxonomic—information on fungal taxonomy |
| ISTH (International Sub-commission on <i>Trichoderma</i> and <i>Hypocrea</i> Taxonomy), a Sub-commission of ICTF (International Commission on the Taxonomy of Fungi), TrichoKEY 2, TrichoBLAST v.1, MycoBank (http://www.MycoBank.org) | Taxonomic—information and on online method for the quick molecular identification <i>Trichoderma</i> and <i>Hypocrea</i> Taxonomy. |
| Myconet (http://www.fieldmuseum.org/myconet) | Nomenclatural and taxonomic—nomenclatural novelties and their associated descriptions and illustrations |
| Q-bank Fungi (http://www.q-bank.eu/Fungi/) | Nomenclatural and taxonomic—continuously updated “Outline of Ascomycota” and “Notes on ascomycete systematics” |
| Systematic Mycology and Microbiology Laboratory Fungal Database, U.S. Department of Agriculture, Agricultural Research Service (http://nt.ars-grin.gov/fungaldatabases/) | Taxonomic—DNA sequence data (barcodes), and for some species morphological, phenotypical and ecological data relevance to mycological phytopathology |
| UNITE ITS database (http://unite.ut.ee) | Literature sources and various metadata of fungi including those in the U.S. National Fungus Collections |
| | Taxonomic—feature-rich ITS database for molecular identification and unambiguous naming of all fungi from environmental as well as taxonomic samples |

comprehensive resource for nucleotide data (Nakamura et al. 2013). The National Center for Biotechnology Information taxonomy database is a curated database of names of all organisms for which sequences have been submitted to GenBank. Each taxon regardless of taxonomic level is assigned a unique identifier (the “taxid”), which jointly provides a classification for the taxa in NCBI. If a taxon has more than one scientific name, each name has the same taxid, but only one is indicated as the “scientific name”. The other names are represented as synonyms and common names. This database taxonomy is not intended to be an authoritative source of taxonomic information. However it does contain many taxa that are not found in other databases. In GenBank, every sequence is assigned to an organism, whose exact identity may be unknown in some cases (Roderic 2005).

Another source for sequence data is UNITE (Kõljalg et al. 2013), which is a database comprising all publicly available fungal ITS sequences. UNITE seeks to offer unambiguous, standardized reference to all fungi recovered in environmental and taxonomic sequencing efforts of fungi and fungal

communities through assigning a unique identifier (a DOI) to all fungal OTUs known from two or more ITS sequences. Metadata e.g., on country and host of collection are assembled for all such Operational Taxonomic Units, and several measures are taken to identify and exclude technically substandard entries (Nilsson et al. 2015). All sequence entries are open to web-based third-party annotation, and sequences from type material are given special attention. UNITE serves as data provider for a range of downstream efforts (Bates et al. 2013; Lindahl et al. 2013), including several sequence analysis pipelines and mycological databases (<https://unite.ut.ee/repository.php>).

The Tree of Life Web Project is another important on-line classification system. Ascomycota classification is being updated regularly through the on-line Myconet series and this has been the basis for recent revisions at GenBank, but for the other major groups of fungi no comparable on-line resource is available (James et al. 2006; Liu et al. 2006; Seif et al. 2005; Steenkamp et al. 2006). Myconet volume 14, part one, outline of Ascomycota—2009 is the latest update for the Ascomycota (Lumbsch and Huhndorf 2010).

The major clades of fungi have broad agreement regarding their composition; however, there is still considerable variation in the names that have been applied to the recognizable groups. The tenth edition of the Dictionary of fungi and the Mycota VII (McLaughlin et al. 2015) are two important works that have influenced fungal taxonomy in the 21st century, and they both contain a comprehensive kingdom-wide classification down to genus level. Publications that survey the entire fungal kingdom based on molecular phylogenies include the chapter by Taylor et al. (2000) in *Assembling the Tree of Life* (Cracraft and Donoghue 2004) and the first large collaborative analysis of the *Assembling the Fungal Tree of Life* (AFTOL) project (Cracraft and Donoghue 2004). The first DNA-based comprehensive multigene phylogenetic views of the fungal kingdom were published by Lutzoni et al. (2004) and James et al. (2006). Hyde et al. (2013a) revised the classification of fungi above the ordinal level. The Structural and Biochemical Database (SBD), developed as part of the US NSF-funded assembling the Fungal Tree of Life (AFTOL), is a multi-investigator project. It is a major resource to present and manage morphological and biochemical information on Fungi and serves as a phyloinformatics tool for the scientific community (Kumar et al. 2013). The Mycota VII (McLaughlin et al. 2015) highlights developments in both basic and applied research and presents an overview of fungal systematics and cell structure of yeasts and mycelial fungi. Foremost authorities in research on fungi have been assembled to edit and contribute to the volumes (McLaughlin et al. 2015).

Databases and the needs of environmental sequencing

Most described fungal species lack DNA sequence data in the public databases, and only morphological information is available. Conversely, environmental sequencing is becoming commonplace and large numbers of operational taxonomic units (OTUs) are frequently reported in publications (Freeman et al. 2009; Zinger et al. 2009; Hibbett et al. 2011; Fischer et al. 2012; Bengtsson-Palme et al. 2013), including the discovery of novel fungal groups at deeper taxonomic levels that remain unnamed (Schadt et al. 2003; Porter et al. 2008). It is becoming apparent that the vast majority of fungal diversity will have to be assessed, at least for the time being, solely by comparing DNA sequences (Hibbett et al. 2011; Tedersoo et al. 2014). Although OTUs provide an estimate of diversity in a habitat, they provide no information on function other than what may be gleaned from the taxonomic name of the fungus (Nguyen et al. 2015). Chomnunti et al. (2014) found the resolution power of OTUs to be limited with reference to sooty molds. However, this may still be sufficient to assess most factors shaping sooty mold community composition, such as geographical location, climatic conditions, and

taxonomic affiliation of the host plants and honeydew-producing insects. Sequence data from environmental studies therefore need to be linked with accurate source data and a taxonomic name insofar as possible (Tedersoo et al. 2015). An attempt at such a nomenclature is presented by the UNITE database, where each fungal OTU known from at least two ITS sequences is given a stable name (a DOI) for unambiguous reference across sites and studies (Kõljalg et al. 2013; Nilsson et al. 2014). This and other infrastructure initiatives will provide the framework required to further our understanding of biology across all groups of fungi.

The need for *FacesofFungi* (FoF)

Our current concepts on fungal classification as well as our taxonomic approach undergo rapid transitions and in this context establishing a proper database is essential for management and dissemination of taxonomic information. With the future availability of more fungal molecular data and discovery of many more novel taxa, FoF will inevitably be a critical resource not only for theoretical studies, but also for those researchers involved in accurate identification of pathogens for disease management and private laboratories involved in pharmaceuticals and biotechnology. The database will also allow retrieval of relevant taxonomic information at the strain or subspecies level for better comparative purposes. The concept behind this database is to provide a platform and a more structured approach for mycologists to upload taxonomic descriptions as well as phylogenetic trees for all types of fungi and one that integrates type, reference or other specimens for ease of identification. Additional data (whether chemical, ecological industrial or molecular data) can also be stored and another peculiarity of FoF is that it will directly link images and descriptions from type, epitype, reference or other specimens of species, genera and families to allow taxonomists to update their records. Being user friendly, one can easily search and browse species, and retrieve taxonomic information.

Construction

All fungi in FoF are listed according to the most recent classifications (Hibbett et al. 2007; Lumbsch and Huhndorf 2010; Woudenberg et al. 2013; Hyde et al. 2013a; Maharachchikumbura et al. 2015). The database will include all classes of fungi in the future, including Ascomycota and Basidiomycota (Fig. 1), as well as early diverging fungi, each with records to species level. Contributions will include descriptions, photographic plates, notes, phylogenetic trees and other important data. During the initial development of the website, various genera and species of Dothideomycetes and Sordariomycetes have been linked to published data.

Fig. 1 View of data search from the home page

The screenshot displays the 'FACES OF FUNGI Fungal Phyla' website. At the top, a navigation bar includes 'Home', 'Ascomycota', 'Basidiomycota', 'Basal Fungi', and 'Other fungal-like organisms'. A large image of white mushrooms is featured on the left. Below the navigation, two taxonomic trees are shown: 'Dothideomycetes' on the left and 'BASIDIOMYCOTA' on the right. The 'Dothideomycetes' tree highlights 'Pyrenophora' within the 'Pleosporales' order. The 'BASIDIOMYCOTA' tree highlights 'AGARICOMYCOTINA' and 'Agaricomycetes'. Below these trees, a detailed entry for 'Pyrenophora phaecomes' is shown, including its Facesoffungi number (FoF 000009), a list of species (Species 1-6), a citation by Atiyawansa et al. (2015), and a detailed description of its morphology and asexual state. A list of images (A-H) is provided for the species, with a scale bar indicating 200 μm.

Database interface and visualization

The proposed FoF database provides insights into an updated classification based on morphological and molecular data of the Kingdom Fungi, starting at the phyla listed in the menu bar of the homepage. Drop down menus to each class appears for each phylum and takes you to a separate page for each class. Each class is provided with a scroll down list of families and genera. Within each genus, species are listed. A click on the genus name reveals data on the genus and provides a list of species, mainly the type species of the genus in question, and any relevant herbarium or reference material. Each entry provides information about taxa, which are descriptions,

photographic plates and other available data (role, importance, industrial relevance biosecurity issues and biochemistry) deemed as relevant and available. In addition to gaining an easy access to basic information of the phylum, subphylum, class, order, family, genus and species description, other relevant data and phylogenetic trees that are considered relevant are provided. 'Basal fungi' and 'Other fungi like-organisms' sections data entry will be improved in the same way as Ascomycota and Basidiomycota. As the database develops it will include all groups of true fungi (Ascomycota, Basidiomycota and Basal fungi) and fungi like organisms and will continually be updated to reflect the state of the art of fungal phylogenetic classification. We are also linking the webpage entries directly

Table 3 Fungal group and expert curators

| Fungal group | Expert curators |
|---------------------|--|
| Ascomycota (genera) | Kevin D. Hyde E.B. Gareth Jones Clement Tsui |
| Arthoniomycetes | Damien Ertz |
| Dothideomycetes | Mohamed A. Abdel-Wahab (marine Dothideomycetes) Hiran A. Ariyawansa Saranyaphat Boonmee (<i>Tubeufiales</i>) Kamel Abd-Elsalam Iman Hidayat (<i>Mycosphaerellaceae</i>) Sinang Hongsanan- (<i>Asterinales</i> , <i>Microthyriales</i> , <i>Zeloasporiales</i> , <i>Zopfiaceae</i>) Subashini C. Jayasiri Jian-Kui Liu Yongzhong Lu (<i>Tubeufiales</i> and <i>Dictyosporaceae</i>) Jamjan Meebon (<i>Mycosphaerellaceae</i>) Chada Norphanphoun Olinto L. Pereira (<i>Asterinales</i> , <i>Mycosphaerellaceae</i>) Alan Phillips (<i>Botryosphaeriaceae</i>) Rungtiwa Phookamsak (<i>Astrosphaeriellaceae</i> , <i>Phaeosphaeriaceae</i>) Satinee Suetrong (marine Dothideomycetes) Qing Tian (<i>Melanommataceae</i>) Kasun M. Thambugala (<i>Dothideales</i> and Lophiostoma-like taxa) |
| Eurotiomycetes | Sinang Hongsanan- (<i>Trichopeltinaceae</i>) Qing Tian (<i>Chaetothyriales</i>) |
| Lecanoromycetes | H. Thorsten Lumbsch |
| Leotiomycetes | Hasini Ekanayaka |
| Pezizomycetes | Alfredo Vizzini (<i>Pezizales</i> , <i>Tuberaceae</i>) Qi Zhao (<i>Helvellaceae</i> , <i>Gyromitra</i> , <i>Morchella</i> and <i>Verpa</i>) |
| Sordariomycetes | Dinushani A. Daranagama (<i>Xylariaceae</i>) Asha Dissanayake (<i>Diaporthe</i> , <i>Botryosphaeriaceae</i>) Sally C. Fryar (freshwater Sordariomycetes) Shike Huang - (<i>Boliniales</i> , <i>Calosphaeriales</i> , <i>Chaetosphaeriales</i> , <i>Coronophorales</i> , <i>Lasiochaeriales</i> , <i>Niessliaceae</i> , <i>Pleurotremataceae</i> , <i>Sordariaceae</i>) Ruvishika Jayawardena (<i>Colletotrichum</i>) Cai Lei Sajeewa S. N. Maharachchikumbura Rekhani H. Perera Olinto L. Pereira (<i>Meliolales</i>) Andrea Irene Romero Idunil C. Senanayake (<i>Diaporthales</i>) Qiuju Shang—(<i>Australiascaceae</i> , <i>Plectosphaerellaceae</i> , <i>Reticulascaceae</i> , <i>Coniochaetaceae</i> , <i>Cephalothecaceae</i> , <i>Chaetomiaceae</i> , <i>Batistiaceae</i> , <i>Diatrypaceae</i> , <i>Melogrammataceae</i>) Joanne Taylor Mohamed A. Abdel-Wahab (marine Sordariomycetes) |

Table 3 (continued)

| Fungal group | Expert curators |
|----------------------------------|---|
| | Ting Chi Wen (<i>Clavicipitaceae</i> , <i>Cordycepitaceae</i> , <i>Ophiocodyceps</i>) |
| Basidiomycota | Bart Buyck (Cantharellales) Yucheng Dai (Polypores) Tatiana B. Gibertoni (Corticoid, clavarioid and poroid fungi) Samantha C. Karunarathna Jean-Marc Moncalvo (<i>Agaricales</i> , <i>Ganoderma</i>) Masoomah Ghobad-Nejhad (<i>Corticiales</i> , <i>Hymenochaetales</i> , <i>Polyporales</i>) Olivier Raspé (<i>Boletales</i>) Benjarong Thongbai (<i>Amanitaceae</i>) Alfredo Vizzini (<i>Agaricales</i> , <i>Boletales</i>) Ruilin Zhao (<i>Agaricales</i>) |
| Myxomycetes | Steven L. Stephenson Adam W. Rollins |
| General fungal groups | |
| Coelomycetes | Wen-Jing Li Faruk Selcuk Nalin N. Wijayawardene |
| Hyphomycetes | Jayarama Bhat Chuangen Lin Eric McKenzie Jeewon Rajesh (Sordariomycetes) |
| Rusts and smuts | Eric McKenzie |
| Ecological fungal groups | |
| Freshwater fungi | Kevin D. Hyde Yang Jing E.B. Gareth Jones Sutakorn Kamolhan Zonglong Luo |
| Fungi of specific host groupings | Dong Qin Dai (bamboo fungi) Mingkwon Doilom (teak fungi) Ishani D. Goonasekara (Sordariomycetes on grasses) Sirimapa Konta (palm fungi) Jiang Kui Liu (palm fungi) Rungtiwa Phookamsak (fungi on monocotyledons and ferns) Saowaluck Tibpromma (fungi on <i>Pandanaceae</i>) |
| Lichenicolous fungi | Javier Etayo Damien Ertz |
| Invertebrate-pathogenic fungi | J. Jennifer Luangsa-ard Thi Chi Wen Yuanpin Xiao |
| Marine fungi | Mohamed A. Abdel-Wahab M. Dayarathna Kevin D. Hyde E.B. Gareth Jones Ka-Lai Pang |

to GenBank and UNITE numbers. We have invited international curators with various fields of expertise to monitor the web page and continuously suggest improvements. Table 3 lists the various fields and the that experts that will monitor the webpage. Other interested parties can contact the webpage and offer suggestions, or their services as curators.

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