

A class-wide phylogenetic assessment of *Dothideomycetes*

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Abstract: We present a comprehensive phylogeny derived from 5 genes, nucSSU, nuLSU rDNA, *TEF1*, *RPB1* and *RPB2*, for 356 isolates and 41 families (six newly described in this volume) in *Dothideomycetes*. All currently accepted orders in the class are represented for the first time in addition to numerous previously unplaced lineages. Subclass *Pleosporomycetidae* is expanded to include the aquatic order *Jahnulales*. An ancestral reconstruction of basic nutritional modes supports numerous transitions from saprobic life histories to plant associated and lichenised modes and a transition from terrestrial to aquatic habitats are confirmed. Finally, a genomic comparison of 6 dothideomycete genomes with other fungi finds a high level of unique protein associated with the class, supporting its delineation as a separate taxon.

Key words: *Ascomycota*, *Pezizomycotina*, Dothideomyceta, fungal evolution, lichens, multigene phylogeny, phylogenomics, plant pathogens, saprobes, Tree of Life.

INTRODUCTION

Multi laboratory collaborative research in various biological disciplines is providing a high level of interaction amongst researchers with diverse interests and backgrounds. For the mycological community, the “Assembling the Fungal Tree of Life” project (AFTOL) provided the first DNA-based comprehensive multigene phylogenetic view of the fungal Kingdom (Lutzoni *et al.* 2004, James *et al.* 2006). This has also made it possible to revise the classification of the fungi above the ordinal level (Hibbett *et al.* 2007). Subsequent work is focused on elucidating poorly resolved nodes that were highlighted in the initial DNA-based phylogeny (McLaughlin *et al.* 2009).

At the other end of the scale from the tree of life projects, taxon sampling with relatively small numbers of sequence characters are also progressing in various barcoding projects (Seifert *et al.* 2007, Chase *et al.* 2009, Seifert 2009). It remains important to link these two ends of the spectrum by also sampling intensively at foci of interest between barcoding and the tree of life. With this in mind it is the aim of this paper and subsequent ones in this volume to provide a broadly sampled phylogeny at class level and below for *Dothideomycetes*. This result is combined efforts and data from a diverse group of researchers to focus on systematic sampling, therefore developing a more robust fungal class wide phylogeny of *Dothideomycetes*. This is especially important as a framework

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for comprehending how fungi have evolved as they shift ecological habitats and adapt to new environments and nutritional modes.

It is apparent that the assemblage of fungi, now defined as *Dothideomycetes*, exemplifies a dynamic evolutionary history. This is by far the largest and arguably most phylogenetically diverse class within the largest fungal phylum, *Ascomycota* (Kirk *et al.* 2008). It contains a heterogeneous group of fungi that subsist in the majority of the niches where fungi can be found. The best-known members of the group are plant pathogens that cause serious crop losses. Species in the genera *Cochliobolus*, *Didymella*, *Phaeosphaeria*, *Pyrenophora*, *Venturia*, *Mycosphaerella* and *Leptosphaeria*, or their anamorphs, are major pathogens of corn, melons, wheat, barley, apples, bananas and brassicas respectively, in most areas of the world where they are cultivated. Other species are important pathogens in forestry *e.g.* species in the genera *Botryosphaeria* and *Mycosphaerella* and their anamorphs that attack economically important tree species.

Despite a large body of work containing taxonomic, phytopathological, genetic and genomic research, the majority of fungi hypothesised to be members of *Dothideomycetes* remain under-sampled within a systematic framework. Several studies performed during the course of the last four years have advanced our understanding of these fungi, but phylogenetic relationships of the saprobes, aquatic, asexual and lichenised species remain particularly poorly studied. Indeed, their conspicuous absence in phylogenetic analyses frustrates a broader understanding of dothideomycete evolution.

Dothideomycetes share a number of morphological characters with other fungal classes. It was recently formally described (Eriksson & Winka 1997) replacing in part the long-recognised loculoascomycetes (Luttrell 1955). This redefinition of the loculoascomycetes was mainly prompted by DNA sequencing comparisons of ribosomal RNA genes (Berbee & Taylor 1992, Spatafora *et al.* 1995) that was subsequently expanded and confirmed (Berbee 1996, Silva-Hanlin & Hanlin 1999, Lindemuth *et al.* 2001, Lumbsch & Lindemuth 2001). These early phylogenetic studies demonstrated that loculoascomycetes, as it was defined, is not monophyletic, although contrary views exist (Liu & Hall 2004). Nevertheless the majority of analyses have shown that some loculoascomycete taxa, such as the "black yeasts" in *Chaetothyriales* as well as the lichenised *Verrucariales*, reside within *Eurotiomycetes* as subclass *Chaetothyriomycetidae* (Spatafora *et al.* 1995, Winka *et al.* 1998, Geiser *et al.* 2006, Gueidan *et al.* 2008). The majority of the remaining loculoascomycete species are now placed in *Dothideomycetes*. Although finer morphological distinctions between the distantly related members of loculoascomycetes can be made, their synapomorphies remain elusive (Lumbsch & Huhndorf 2007). These findings all point to the fact that a number of loculoascomycete morphological characters are either retained ancestral traits or that they exhibit convergence due to similar selection pressures.

Traditionally the most important morphological characters used to define major groups in *Ascomycota* were the type of ascus, septation of ascospores, the morphology and development of the ascoma, as well as the structure and organisation of the centrum. *Dothideomycetes* (and previously, loculoascomycetes) have fissitunicate (or functionally bitunicate) asci, that emerge from ascolocular development in preformed locules within vegetative tissue, that represents the ascoma. The reproductive structures in ascolocular development are derived from cells before fusion of opposing mating types occurs and can contain one or several locules. This form of ascolocular development is in contrast

to the ascohyemial development found in most other fungal classes. During ascohyemial development asci are generated in a hymenium and the reproductive structure is derived from cells after fusion of opposing mating types. The fissitunicate ascus has been described for more than a century, but the importance of ascolocular development was first emphasised in 1932 (Nannfeldt 1932). Importantly Nannfeldt's concepts were also the basis for the Santesson's integration of lichens into the fungal classification (Santesson 1952). In fissitunicate asci, generally, the ascospores are dispersed by the rupture of the thick outer layers (ectotunica) at its apex, allowing the thinner inner layer (endotunica) to elongate similar to a "jack in a box". The elongated endotunica ruptures apically and releases the ascospores forcefully through the ascoma opening. The spores are then released in the air, or in aquatic species, under water. Building on this work and that of others (Miller 1949), Luttrell proposed Loculoascomycetes, synonymous to Nannfeldt's "Ascoloculares" (Luttrell 1955). Importantly, he proposed a correlation between fissitunicate asci and ascolocular development, also emphasising the importance of ascus morphology and dehiscence as well as the development of surrounding elements within the ascoma.

Although the concept of a group of fungi (including the *Dothideomycetes*) with fissitunicate asci and ascolocular development has been accepted by several authors, much less agreement could be found on ordinal definitions in the era before molecular characters. This ranged from proposing a single order (von Arx & Müller 1975) to three (Müller & von Arx 1962), five (Luttrell 1951, 1955) six (Barr 1979), or seven (Barr 1987). Luttrell initially described a number of important development types centered on descriptions of all tissues inside the ascoma (the centrum concept) and combined this with ascoma structure to define his five orders (Luttrell 1951, 1955). Of Luttrell's initial centrum concepts three are applicable to the *Dothideomycetes* as they are presently defined. Thus, the *Pleospora* type, the *Dothidea* type and the *Elsinoë* type centra correspond to the dothideomycete orders *Pleosporales*, *Dothideales* and *Myriangiales*, respectively. An important refinement to Luttrell's ideas was introduced with the concept of the hamathecium by Eriksson (Eriksson 1981). This is defined as a neutral term for sterile hyphae or other tissues between the asci in the ascoma (Kirk *et al.* 2008). For example, hamathecial types can include the presence or absence of pseudoparaphyses, which are sterile cells that extend down from the upper portion of the ascomatal cavity. They become attached at both ends, although the upper part may become free at maturity. Other important concepts introduced by Müller and von Arx (Müller & von Arx 1962) focused on the morphology of the ascoma opening and ascus shape. The *Dothidea* type centrum in the type species of *Dothidea*, *D. sambuci* illustrates several typical dothideomycete morphologies (Fig. 1). These include the thick-walled fissitunicate asci produced within a multilocular stroma.

The most recent dothideomycete class-wide morphological assessments were carried out by Barr (Barr 1979, 1987). Her subclasses were determined based on characters in the centrum, including the absence, presence and types of hamathecial tissues. Consistent with several earlier authors, Barr's ordinal classifications were based on ascomatal shape (perithecioid or apothecioid) and manner in which nutrients are obtained by the fungus (Barr 1987). In addition to these characters she emphasised the importance of finer distinctions in the hamathecium such as the shape and structure of the pseudoparaphyses (Barr 1979, 1987).

The introduction of molecular phylogenies for *Dothideomycetes* (Berbee 1996) provided an opportunity to verify the significance

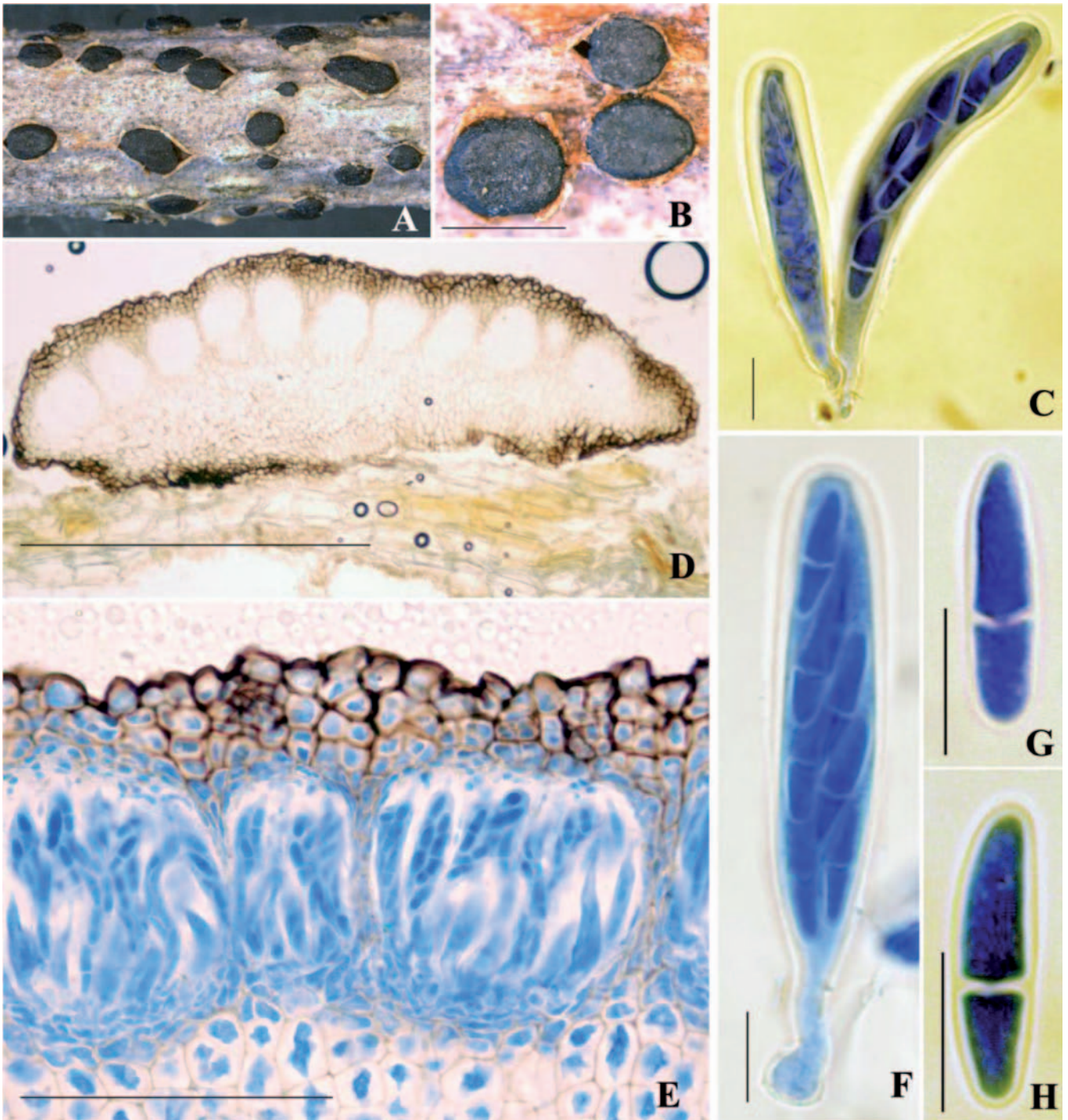


Fig. 1. *Dothidea sambuci*. A–B. Appearance of ascomata on the host surface. C, F. Asci in cotton blue reagent. D. Vertical section through ascomata illustrating the multilocule at the upper layer. E. Vertical section through ascomata in cotton blue reagent illustrating the locule. G–H. Ascospores in cotton blue reagent. Scale bars: B = 1000 μ m; C = 500 μ m; E = 100 μ m; F–H = 10 μ m.

of various morphological characters used in the aforementioned classifications. The clearest correlation with a DNA sequence-based phylogeny was for the presence or absence of pseudoparaphyses, largely agreeing with the first orders proposed by Luttrell (Liew *et al.* 2000, Lumbsch & Lindemuth 2001). Barr's concept of applying the shape of the pseudoparaphyses to define orders was rejected by molecular phylogenies (Liew *et al.* 2000). This set the stage for more comprehensive analyses incorporating protein data, and resulted in the definition of two subclasses, *Pleosporomycetidae* (pseudoparaphyses present) and the *Dothideomycetidae* (pseudoparaphyses absent; Schoch *et al.* 2006). Numerous orders and other taxa remained unresolved outside of these two subclasses.

The most recent class level phylogenetic analyses combining sequences from protein coding genes with ribosomal RNA sequences fortified the view that *Dothideomycetes* is a monophyletic group (Schoch *et al.* 2009a, b). Furthermore, strong support was found for a sister relationship between *Dothideomycetes* and the lichenised class *Arthoniomycetes* (Lumbsch *et al.* 2005, Spatafora *et al.* 2006, Schoch *et al.* 2009a). This clade was recently defined as a rankless taxon "Dothideomyceta" (Schoch *et al.* 2009a, b). The *Arthoniomycetes* consists of a single order (*Arthoniales*) of lichens and lichenicolous fungi (Ertz *et al.* 2009) that produce bitunicate asci in ascohymenial apothecia and was proposed as an intermediate group or "Zwischengruppe" (Henssen & Thor 1994). This placement raises intriguing questions regarding the origins of

ascococcal development and further illustrates the importance of including lichen-forming fungi in dothideomycete phylogenies.

While considerable progress has been made in defining these fungi the placement of *Dothideomycetes* in relation to the majority of other *Ascomycota* classes remains unresolved. Here, greater clarity would likely require a huge increase of characters from genome projects. In this regard, the first phylogenomic studies have shown low resolution for this relationship (Fitzpatrick *et al.* 2006, Kuramae *et al.* 2006, Robbertse *et al.* 2006). This could indicate a rapid radiation event, but more likely suggests taxon sampling bias. This latter view is supported by the fact that none of these studies has included lichenised species that represent about 25 % of the number of species in *Ascomycota*.

The authors of this volume have focused on two primary goals. These are to considerably expand the taxon sampling of existing orders by including saprobes, asexual species and other poorly sampled groups. Secondly we aim to sample widely within specific environmental niches and present a multigene phylogeny that exposes the highly diverse nature of *Dothideomycetes*.

MATERIAL AND METHODS

DNA extraction, amplification and sequencing

The majority of fungal cultures were obtained from the CBS culture collection and additional sources mentioned in other papers of this volume. DNA was also provided by authors of several papers presented in this volume and the reader is referred to Boehm *et al.* (2009a), Crous *et al.* (2009a), Suetrong *et al.* (2009) and Zhang *et al.* (2009). For additional details see Table 1 - see online Supplementary Information. Fungal genomic DNA was obtained by scraping mycelium from PDA plates. Samples were subsequently pulverised and the DNA was extracted using the FastDNA® kit and the FastPrep® instrument from MPI Biochemicals (Irvine, CA, U.S.A.). DNA amplifications were completed using *Taq* polymerase (GenScript, Piscataway, NJ, U.S.A.), with FailSafe™ PCR 2× PreMix E (Epicentre, San Diego, CA, U.S.A.). Primers were used as noted in the Assembling the Fungal Tree of Life project (AFTOL; Schoch *et al.* 2009a). This resulted in DNA sequence data obtained from the small and large subunits of the nuclear ribosomal RNA genes (SSU, LSU) and three protein coding genes, namely the translation elongation factor-1 alpha (*TEF1*) and the largest and second largest subunits of RNA polymerase II (*RPB1*, *RPB2*). Primer sets used for these genes were as follows: SSU: NS1/NS4; LSU: LR0R/LR5; *TEF1* 983/2218R (initially obtained from S. Rehner: ocid.nacse.org/research/deephyphae/EF1primer.pdf); *RPB2*: fRPB2-SF/fRPB2-7cR; *RPB1*: RPB1-Ac/RPB1-Cr (obtained from V. Hofstetter). Primer sequences are available at the WASABI database at the AFTOL website (aftol.org). PCRs for these genes were performed in various laboratories of the coauthors mentioned but the majority of reactions were run under conditions described previously (Lutzoni *et al.* 2004, Schoch *et al.* 2009a). Two duplicate sets of sequences were inadvertently included in the analysis (indicated in Table 1).

Sequence alignment and phylogenetic analyses

Sequences were obtained from WASABI (Kauff *et al.* 2007) as well as from previous publications (*e.g.* Lutzoni *et al.* 2004, Schoch *et al.* 2009a). Introns were removed and an initial core set of 171 taxa were aligned by using default options for a simultaneous method of estimating alignments and tree phylogenies, SATé (Liu *et al.* 2009). In order to consider codons without the insertion of unwanted gaps, protein coding fragments were translated in BioEdit v. 7.0.1 (Hall 2004) and aligned within SATé as amino acids. These were then realigned with their respective DNA sequences using the RevTrans 1.4 Server (Wernersson & Pedersen 2003). After the removal of intron sequences the alignment was examined manually in BioEdit with a shade threshold of 40 % and regions with high amounts of gap characters were excluded. This resulted in a reduction of 99 columns in the LSU data set, 118 in *RPB1* and 162 in *RPB2*, for a total of 379. Nothing was removed for *TEF1*. In order to allow for the extension of our alignment as newly generated sequences became available from other studies in this volume, these were subsequently added to this core alignment with MAFFT v. 6.713 (Katoh *et al.* 2009). The E-INS-i setting, focused on high accuracy with a high percentage of unalignable regions such as introns, was applied and the SATé alignment was used as a seed. This resulted in a supermatrix of five genes (LSU, SSU *TEF1*, *RPB1*, *RPB2*) consisting of 52 % gaps and undetermined characters out of a total of 6 582 characters. GenBank accession numbers are shown in Table 1.

Conflict tests

Conflict tests on the initial core set of 204 taxa were conducted by selecting single gene data sets and doing comparisons on a gene by gene basis. This was done using the “bootstopping” criterion in RAxML v. 7.0.4 (Stamatakis *et al.* 2008) under the CIPRES v. 2.1 webportal to produce trees of comparative gene sets where all taxa have the gene present. Comparisons between all potential sets of gene trees with no missing taxa were done using a script (Kauff & Lutzoni 2002) obtained through the Lutzoni lab website and to detect present or absent taxa within clades with a cut-off bootstrap value of 70 %. This is described in more detail elsewhere (Miadlikowska *et al.* 2006, Schoch *et al.* 2009a).

Phylogeny

A phylogenetic analysis was performed using RAxML v. 7.0.4 (Stamatakis 2006) applying unique model parameters for each gene and codon. The dataset was divided in 11 partitions as previously described in Schoch *et al.* (2009a). A general time reversible model (GTR) was applied with a discrete gamma distribution and four rate classes following procedures laid out in Schoch *et al.* (2009). Ten thorough maximum likelihood (ML) tree searches were done in RAxML v. 7.0.4 under the same model, each one starting from a randomised tree. Bootstrap pseudo replicates were performed 2000 times using the fast bootstrapping option and the best scoring tree from 10 separate runs were selected. The resulting trees were printed with TreeDyn v. 198.3 (Chevenet *et al.* 2006). All alignments are deposited in TreeBASE. Additionally, the data sets were analyzed in GARLI v. 0.96 (Zwickl 2006) using the GTR-gamma-invariant model. In this case 200 bootstraps were run under default conditions.

Fig. 2A–C. (Page 5–7). Best scoring ML tree with RAxML and GARLI bootstrap values respectively above (green) and below (red) the nodes. Values below 50 % were removed and branches with more than 90 % bootstrap for both methods are thickened without values. Environmental sources relevant to the papers in this volume are indicated in the key (R-Rock; M-Marine; F-Freshwater; D-Dung; B-Bamboo). Nutritional characters are indicated by colour as per the key.

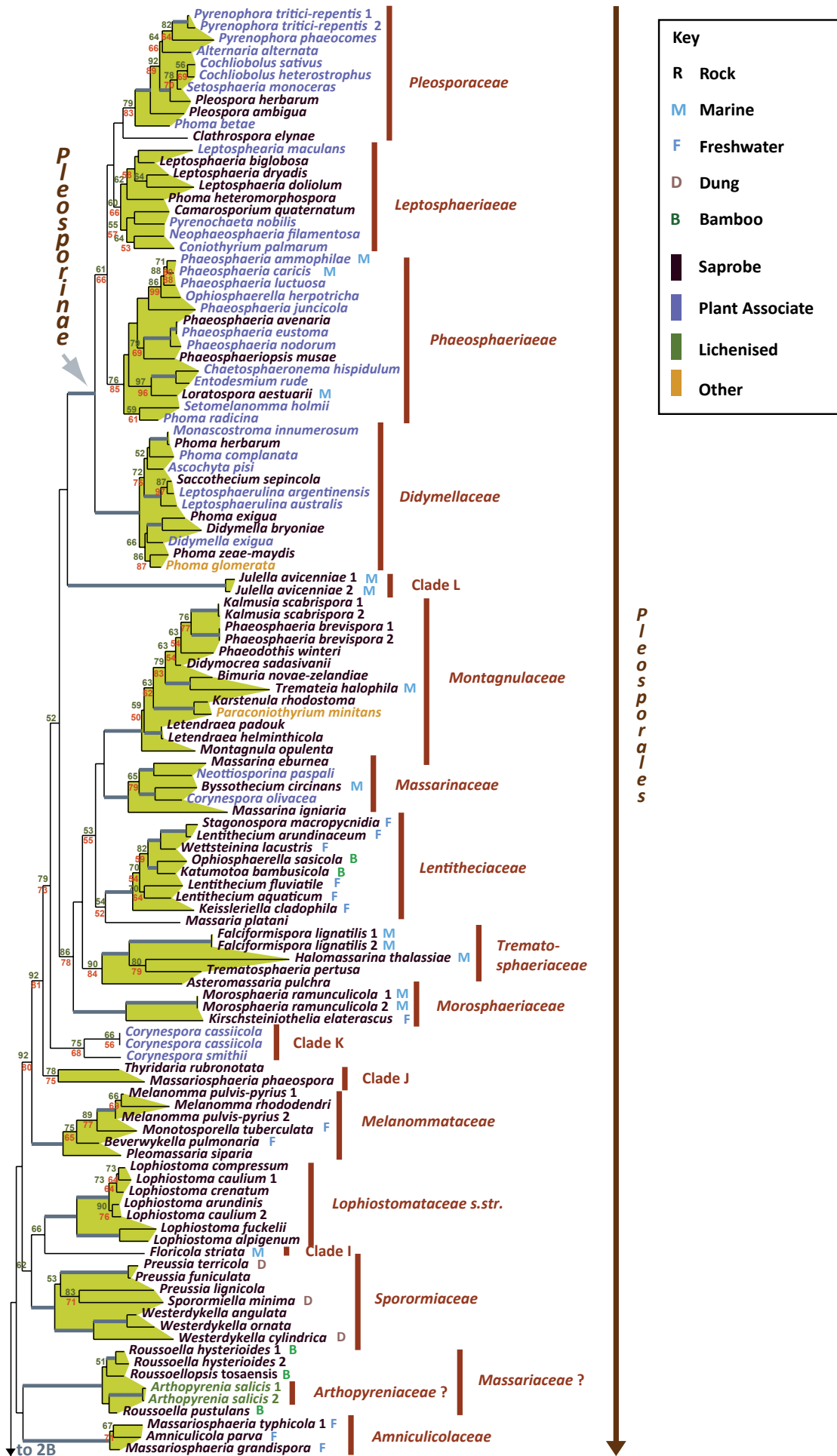


Fig. 2A.

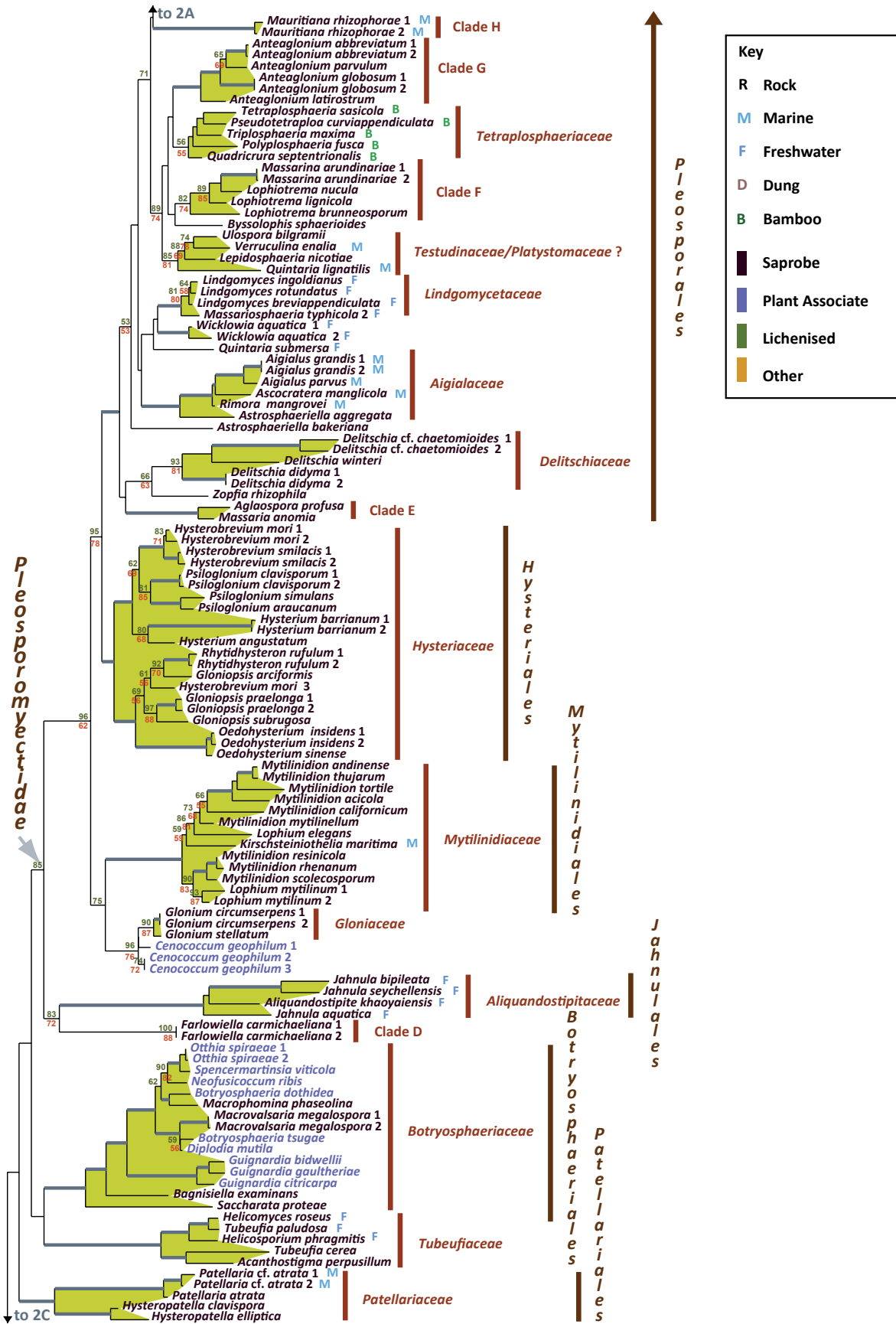


Fig. 2B.

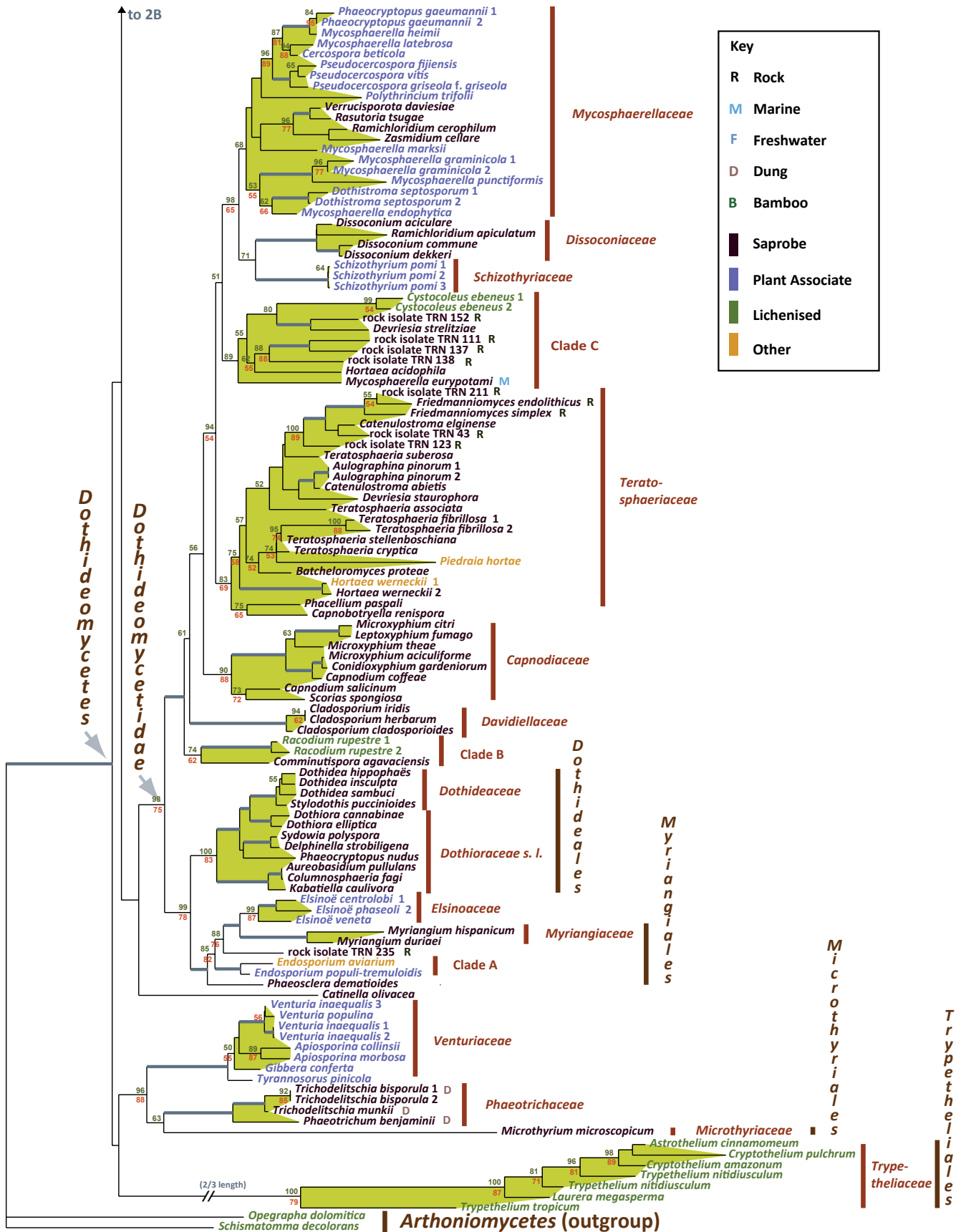


Fig. 2C.

Ancestral reconstruction

Ancestral reconstructions were performed in Mesquite v. 2.6 with character states traced over 2000 bootstrapped trees obtained with RAxML-MPI v. 7.0.4 (Stamatakis 2006). Following the phylogeny presented (Fig. 2) this reconstruction was performed with a maximum-likelihood criterion using the single parameter Mk1 model. Ancestral states were assigned to a node if the raw likelihood was higher by at least 2 log units than the likelihood value of the other ancestral state(s) according to default settings. Character states were also mapped using TreeDyn v. 198.3 (Chevenet *et al.* 2006), shown in Fig. 3. This is presented as a clockwise circular tree, starting with outgroup taxa. Only clades with more than two taxa of the same state are shown and bootstrap recovery was not considered in assigning character states. In applying the character states of saprobes (including rock heterotrophs), plant associated fungi (including pathogens, endophytes and mycorrhizae) and lichenised fungi the broad concepts presented were followed as laid out in Schoch *et al.* (2009a). Some character assessments were taken from Zhang *et al.* (2009; this volume). Ecological characters of sampling sources, terrestrial, fresh water and marine were assessed based on papers elsewhere in this volume (Suetrong *et al.* 2009, Shearer *et al.* 2009).

Genome analyses

A MCL (Markov Cluster Algorithm) protein analysis of 52 fungi and one metazoan (*Drosophila melanogaster*) (Table 2 - see online Supplementary Information) and the phylogenetic placement of these species was used to characterise the phylogenetic profile of each cluster. *Chytridiomycota* and *Mucoromycotina* each were represented by one and two species, respectively. In *Dikarya*, *Basidiomycota* and *Ascomycota* were represented by 8 and 40 species respectively. The *Pezizomycotina* (filamentous ascomycetes) was presented by 26 species in four classes [*Sordariomycetes* (12), *Leotiomyces* (2), *Dothideomycetes* (6) and *Eurotiomycetes* (6)].

RESULTS AND DISCUSSION

Taxon sampling

The phylogram presented in Fig. 2 represents the largest ever phylogenetic assessment of *Dothideomycetes* to date. Here the focus has been on expanding taxon diversity in the class while specifically avoiding a small number of taxa that other analyses suggest reside on long unstable branches. This still allowed for an extensive sweep of dothideomycete taxon diversity; in doing so we followed the premise of allowing for missing data in our supermatrix (Wiens 2006). An effort was made to intersperse taxa with poor character sampling amongst those having better sampling throughout the tree, but the inclusion of missing characters could still have unanticipated effects on phylogenetic assessments (Lemmon *et al.* 2009). While recognising this caveat, a recent expansive data set covering all of *Ascomycota* noted very little changes in major nodes even after the removal of taxa with high proportions of missing characters (Schoch *et al.* 2009a). The phylogeny presented here agrees well with broad phylogenies in this volume and elsewhere (Schoch *et al.* 2006, Crous *et al.* 2007a, Zhang *et al.* 2008, Crous *et al.* 2009b). After all introns and 379 ambiguous character positions were removed, the matrix consisted of 52 % missing and indeterminate characters. This maximum-likelihood analysis had 5 069 distinct alignment patterns and produced a best known likely tree with a log likelihood of -207247.761117.

Evolution of nutritional modes

The ancestral reconstructions in Fig. 3 indicate that phytopathogenicity can be confined to a number of terminal clades throughout the tree and that these always reside within saprobic lineages. A maximum of seven transitions likely occurred in several lineages of the orders *Pleosporales*, *Capnodiales* and singular lineages in *Myriangiiales*, *Botryosphaerales* and *Venturiaceae* (also see in this volume; Crous *et al.* 2009a, Zhang *et al.* 2009). Several transitions to lichenisation have also occurred, although phylogenetic uncertainty may limit this to a minimum of two. Due to the use of lichenised *Arthoniomycetes* as outgroup a broader assessment is required to determine whether the *Dothideomycetes* evolved from a lichenised ancestor. Previous studies suggested that the saprobic habit is an ancestral trait but only with marginal support (Schoch *et al.* 2009a). Similar conclusions can be reached for the aquatic ecological characters – the majority of fresh water and marine clades reside within terrestrial clades as has been shown previously *e.g.* (Spatafora *et al.* 1998, Vijaykrishna *et al.* 2006). Transitions from a terrestrial life style to fresh water likely occurred at least three times and transitions to marine environments up to six times. Phylogenetic uncertainty for the placement of some marine clades can limit this to a minimum of four times (Fig. 2). Reversions from aquatic to terrestrial environments are rare, with one possible exception in the *Lentitheciaceae* where bambusicolous saprobes reside, nested within several fungi occurring in freshwater habitats (for additional details see Zhang *et al.* 2009; this volume). Phylogenetic resolution will have to improve to test this further.

An analysis of recently released genomes was compared to consider whether genome composition reinforces phylogenetic support for *Dothideomycetes* (Fig. 4). Relative to a clustering analysis of proteins from 52 sequenced fungi and *Drosophila melanogaster*, about 5 515 protein coding genes from *Dothideomycetes* shared protein clusters with proteins from other dothideomycete fungi only. This comprises roughly 8–11 % of the protein coding genes in each of six sequenced *Dothideomycetes*. The species profile of each protein cluster was used to assign a phylogenetically informed designation. The profiles most frequently seen were those of the most conserved proteins, namely clusters designated as having a shared Ophistokont phylogenetic profile. Among the more derived nodes of the *Dothideomycetes*, protein clusters were observed that had a species composition that could reflect the result of selection pressure on more distantly related fungi that share the same niche.

A phylogenomic profile (Fig. 4) of the proteins from six *Dothideomycetes* from the two largest orders seen in Fig. 1 is presented (*Mycosphaerella graminicola*, *Mycosphaerella fijiensis*, *Phaeosphaeria nodorum*, *Alternaria brassicicola*, *Pyrenophora tritici-repentis*, *Cochliobolus heterostrophus*). The highest percentage of proteins (excluding species specific proteins) were conserved outside kingdom *Fungi* (Ophistokont node, 23 %), followed by proteins specific for the *Dikarya* (14 %) and the *Pezizomycotina* (13 %). This breakdown was also prevalent within other *Pezizomycotina* classes. Approximately 8 % of the proteins from the six *Dothideomycetes* were conserved across and within derived nodes in this class. Relative to this analysis 28 % of the proteins were specific to the *Dothideomycetes* (including species specific proteins). The other class containing loculoascomycetes, *Eurotiomycetes*, had 19.5 % proteins characterised as class specific. This means the percentage dothideomycete specific proteins were about 8.5 % more. *Eurotiomycetes* in the analysis were mostly human pathogens, with most having no known sexual state whereas the *Dothideomycetes* in the analysis were all plant

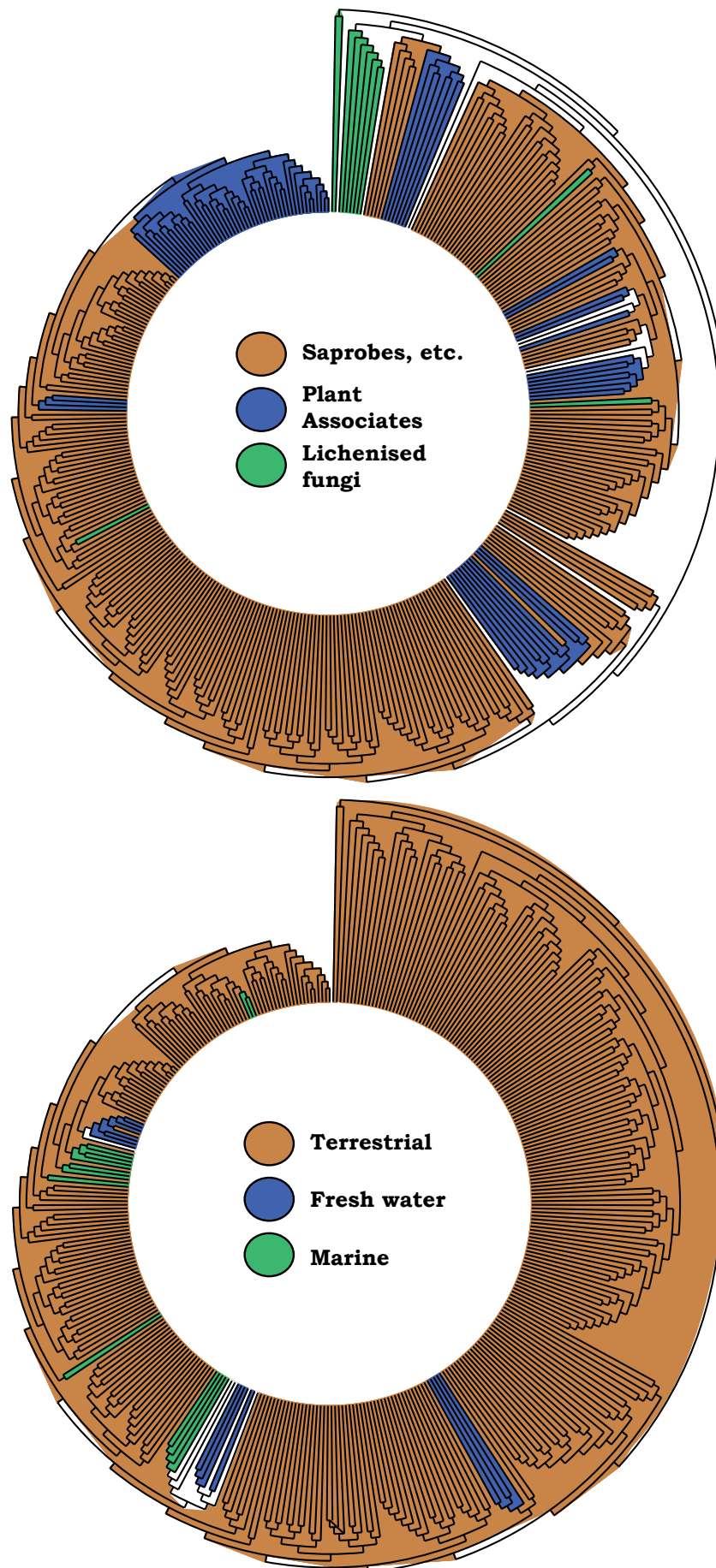


Fig. 3. Simplified ancestral state reconstructions, showing potential transitions between character states. The same phylogeny as in Fig. 2A–C is shown, with the outgroups positioned at twelve o’ clock and subsequent clades arranged in a clockwise manner. Characters were traced over 2 000 bootstrap trees and those that were recovered in the majority are coloured on the nodes. In the case of equivocal construction no colour was used (white). To simplify the figure, only clades with two or more neighbouring character states are shown.

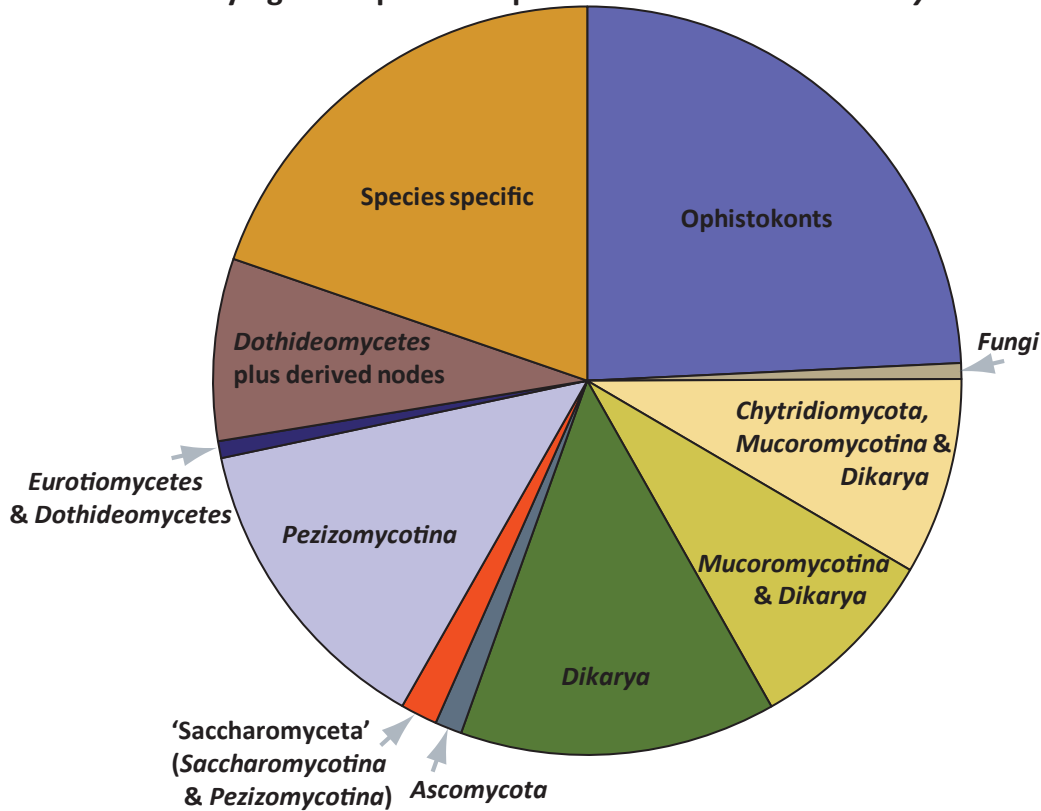
Phylogenetic profile of proteins from six *Dothideomycetes*

Fig. 4. Pie chart showing relative numbers of unique proteins per genome according to taxonomic classification.

pathogens and mostly with known sexual states. This breakdown of nutritional modes, although not comprehensive for these two classes, is somewhat representative. In *Eurotiomycetes* human pathogens are more diverse and plant pathogens uncommon, with the converse being true for *Dothideomycetes*. Both classes contain melanised species with similar morphologies and more comprehensive comparative studies need to expand sampling to incorporate species from the different nutritional modes for both classes.

Phylogenetic relationships

In the phylogram presented (Fig. 2) the two dothideomycete subclasses previously described based on presence or absence of pseudoparaphyses (Schoch *et al.* 2006) could be recovered with varying levels of bootstrap representation. Subclass *Pleosporomycetidae* previously included *Pleosporales* plus a single species, representing *Mytiliniaceae*, namely *Lophium mytilinum* (Schoch *et al.* 2006). Taxon sampling for the *Mytiliniaceae* was considerably expanded by Boehm *et al.* (2009b), with the addition of a number of new taxa, leading to the establishment of the *Mytiliniales*. Likewise, extensive taxon sampling for the family *Hysteriaceae* led to a newly redefined *Hysteriales* also included in this subclass (Boehm *et al.* 2009a; this volume). It appears that persistent, hysterothecious carbonaceous ascomata that dehiscence via a longitudinal slit (e.g., hysterothecia) have evolved multiple times within *Pleosporomycetidae* (Mugambi & Huhndorf 2009). *Pleosporomycetidae* can be expanded to tentatively include *Jahnulales* (Fig. 2B) based on strong bootstrap support from RAxML analyses and morphology. Perithecioid ascomata and a hamathecium of wide cellular pseudoparaphyses are characteristic of *Jahnulales* (Inderbitzin *et al.* 2001, Pang *et al.* 2002; Shearer

et al. 2009; this volume) and agree with diagnostic features for *Pleosporomycetidae*. We also recommend that the definition of the subclass be reassessed with more inclusive character sets. Also, *Leptosphaerulina* species characterised by the absence of pseudoparaphyses reside within the pseudoparaphysate *Pleosporales* (Fig. 2C; Silva-Hanlin & Hanlin 1999, Kodsueb *et al.* 2006), indicating that pseudoparaphyses could have been lost multiple times. It should be noted that the maturity of ascomata may play an important role in these assessments. Immature specimens may contain pseudoparaphyses that dehiscence when mature and these characteristics need to be evaluated with more complete sampling of the numerous aparaphysate taxa still listed as *incertae sedis*. The second subclass, *Dothideomycetidae*, previously circumscribed based on the absence of pseudoparaphyses remains well supported (Fig. 2C).

The results of this study provided continued support for ten orders within class *Dothideomycetes*, namely *Pleosporales*, *Hysteriales*, *Mytiliniales*, *Patellariales*, *Botryosphaerales*, *Jahnulales*, *Dothideales*, *Capnodiales*, *Myriangiales* and *Trypetheliales*. The latter order was recently proposed (Aptroot *et al.* 2008) and represents the largest lichen forming clade in *Dothideomycetes*. Another recently proposed order, *Botryosphaerales* includes only the single family, *Botryosphaeriaceae*. The analysis (Fig. 2B), however, shows strong support for a narrower interpretation of the *Botryosphaeriaceae*, typified by *Botryosphaeria dothidea* and related genera, excluding a separate clade of species residing in *Guignardia* (with *Phyllosticta* anamorphs). *Bagnisiella examinens* and *Saccharata protea* did not reside in either of the above clades, placed on early diverging branches. A more extensive taxon sampling is required to address the diversity in this order, which most likely will validate the separation of additional families. Another currently accepted order, *Microthyriales*, consisting of

species occurring as saprobes or epiphytes on stems and leaves is represented in this study by only a single sample, *Microthyrium microscopicum* (Fig. 2C). Members of this order are poorly represented in culture and have unusual thyrothecial ascomata that have a scutate covering comprising a thin layer of radiating cells. This structure is generally lacking a basal layer and is quite unlike any morphologies in other orders. This positioning adjacent to the plant parasitic *Venturiaceae* and coprophilic *Phaeotrichaceae*, is unexpected but since the single representative of the *Microthyriales* is on a long branch this is a relationship that will require more intensive taxon sampling.

Additional families that could not be placed in an order are *Tubeufiaceae* and *Gloniaceae* (Fig. 2B). Species in *Tubeufiaceae* have superficial clustered ascomata and characteristic bitunicate asci with relatively long ascospores, often with helicosporous anamorphs (Kodsueb *et al.* 2008). Members of *Tubeufiaceae*, which frequently occur in freshwater habitats include anamorph genera, such as *Helicoon* and *Helicodendron*, and are ecologically classified as aeroaquatic species. A few teleomorph taxa such as *Tubeufia asiatica* occur on submerged wood (Tsui *et al.* 2007), and *Tubeufia paludosa* occur on herbaceous substrates in wet habitats (Webster 1951). The *Gloniaceae* are saprobic, have dichotomously branched, laterally anastomosed pseudothecia that form radiating pseudo-stellate composites and dehisce by an inconspicuous, longitudinal, but evaginated slit. They reside sister to the saprobic *Mytiliniidiales* but due to conspicuous morphological differences and moderate statistical support they are placed in *Pleosporomycetidae incertae sedis* (Boehm *et al.* 2009a, this volume).

Several other well supported clades representing families were evident in this study (Fig. 2). These include several families in *Pleosporales*, treated elsewhere (Zhang *et al.* 2009; this volume). Other clades have lower levels of support. For example *Leptosphaeriaceae* (Fig. 2A) have moderate bootstrap support and it is treated in the very broad sense here. There was also support for several newly described families treated in different papers within this volume. In *Pleosporales* these include *Amniculicolaceae* and *Lentitheciaceae* (Zhang *et al.* 2009; this volume). The *Lindgomycetaceae* (Shearer *et al.* 2009; this volume, Hirayama *et al.* 2010) encompassing a majority of species isolated from fresh water habitats. Two other novel families, *Aigialaceae* and *Morosphaeriaceae* include mainly marine species (Suetrong *et al.* 2009; this volume). In addition to these, the sampling of a wide diversity of fungi on bamboo yielded the description of *Tetraplophaeriaceae* (Tanaka *et al.* 2009; this volume). Another novel family, *Dissoconiaceae*, is proposed by Crous *et al.* 2009 (this volume) for foliicolous commensalists on *Eucalyptus* leaves, some of which are putative hyper parasites and reside in *Capnodiales*.

Results of this study suggest that sampling within existing families also requires continued expansion as familial definitions in *Dothideomycetes* remains problematic. A paper focused on two families, with poor representation in molecular data sets, *Melanommataceae* and *Lophiostomataceae* addresses this in more detail (Mugambi & Huhndorf 2009; this volume). Numerous other clades in our tree remain without familial placement. This includes a diverse group in *Capnodiales* (Fig. 2C, clade C) a newly described group of hysteriaceous fungi in *Pleosporales* (Fig. 2A, clade G) and additional marine lineages (clades H, L, Fig. 2A). An interesting clade tentatively circumscribed by Zhang *et al.* (2009; this volume) as *Massariaceae* contains bambusicolous fungi and appears related to the lichenised *Arthopyreniaceae* (Fig. 2A).

Finally, a clade including *Corynespora* anamorphs (clade K, Fig. 2A) is placed for the first time, but without clear relationship

to any other currently defined families. The genus *Corynespora* includes anamorphic fungi with tretic, percurrent, and acropetal conidiogenesis. The melanised, pseudoseptate conidia have a pronounced hilum from which the conidial germ tube emerges and are borne apically from solitary, melanised conidiophores. Though nearly 100 species are described based on differences in morphology, considerable phenotypic plasticity within individual isolates complicates species recognition, and molecular analyses that may result in taxonomic clarification have not been done. *Corynespora* species fill a diversity of roles as saprobes, pathogens, and endophytes on and in woody and herbaceous plants, other fungi, nematodes, and human skin (Dixon *et al.* 2009). One of the species represented here, *C. cassicola* is an important pathogen of rubber. The teleomorph fungi *Pleomassaria swidaea* (*Pleomassariaceae*; Tanaka *et al.* 2005) and *Corynesporasca caryotae* (*Corynesporascaceae*; Sivanesan 1996) have unnamed *Corynespora* species as anamorphs. In this study, species currently placed in *Corynespora* are not monophyletic and are positioned in at least two families: *Massariaceae* and Clade K (Fig. 2A).

Anamorph taxa

The previously mentioned *Dissoconiaceae* relies on taxonomic descriptions based on anamorph characters. This is a theme that is expected to continue for mitosporic taxa in *Dothideomycetes* as molecular data accelerates their integration. The artificial nature of the "higher" taxa of anamorphs *e.g.*, deuteromycetes (Kirk *et al.* 2001) is now well recognised, but the integration of anamorphs into the phylogenetic classification of teleomorphs remains a significant challenge in fungal systematics (Shenoy *et al.* 2007). The correlation of teleomorphs and anamorphs (Seifert *et al.* 2000) is not always predictive but it has been applied in some genera within *Dothideomycetes*, *e.g.* *Botryosphaeria* and *Mycosphaerella* (Crous *et al.* 2006, 2009b). However, numerous examples underscoring anamorph convergence can be found throughout the class *e.g.* *Dictyosporium* (Tsui *et al.* 2006, Kodsueb *et al.* 2008), *Sporidesmium* (Shenoy *et al.* 2006), *Cladosporium* (Crous *et al.* 2007b) and *Phoma* (Fig. 2A; Aveskamp *et al.* 2009, de Gruyter *et al.* 2009, Woudenberg *et al.* 2009) as well as *Fusicoccum* and *Diplodia* (Crous *et al.* 2006, Phillips *et al.* 2008). The use of large multigene phylogenies will be essential to bring taxonomic order to cryptic anamorph lineages.

Ecological diversity

Besides the unclassified diversity found in anamorphic genera, numerous ecological niches contain diverse lineages of fungi lacking systematically sampled molecular characters. Several examples of this knowledge gap can be found in papers in this volume. In this regard, the rock inhabiting fungi are amongst the least understood. These fungi exist ubiquitously as melanised, slow growing colonies and that usually do not produce generative structures. They subsist on bare rock surfaces and are consequently highly tolerant of the environmental stresses induced by lack of nutrients, water and extremes in radiation and temperature (Palmer *et al.* 1990, Sterflinger 1998, Ruibal 2004, Gorbushina *et al.* 2008). Members of this ecological guild are diverse and occur in two classes – *Eurotiomycetes* and *Dothideomycetes*. Ruibal *et al.* 2009 (this volume) present the results of an expanded sampling of rock-inhabiting fungi that include lineages residing within *Dothideomycetes* and sister class *Arthoniomycetes*. These rock inhabiting fungi can be placed in

Capnodiales, *Pleosporales*, *Dothideales* and *Myriangiales*, as well as some unclassified lineages of *Dothideomycetes*. Interestingly, some associated lineages were without clear placement within either *Arthoniomycetes* or *Dothideomycetes*. The rock isolates included in Fig. 2C illustrate a subsection of genetic diversity seen in these extremophiles, in particular for the *Capnodiales*, with two rock isolates-rich lineages *Teratosphaeriaceae* and Clade C (Fig. 2C). A more detailed analysis (Ruibal *et al.* 2009; this volume) allows for the presentation of hypotheses related to evolution of pathogenicity and lichenisation because these modes of nutrition are often found in close proximity of rock inhabiting fungal lineages.

The lichenised fungi allied with the *Dothideomycetes* represent another poorly sampled group of fungi. Several lichenised species remain enigmatically placed after they were confirmed as members of *Dothideomycetes* based on DNA sequence data (Lumbsch *et al.* 2005, Del Prado *et al.* 2006). Although the number of species is comparatively small, their placement can play an important link in determining how transitions to and from lichenisation influenced dothideomycete evolution. *Trypetheliaceae* known for its anastomosing, branched pseudoparaphyses was until very recently still placed within *Pyrenulales*, an ascohymental order in *Eurotiomycetes*, based on bitunicate asci and lense-shaped lumina in the ascospores (Del Prado *et al.* 2006). Attempts to resolve members of this family remain challenging as they tend to occur on long, rapidly evolving branches in our phylogenetic analyses, which often lead to artifacts. Nelsen *et al.* 2009 (this volume) demonstrate the occurrence of two additional lichen-forming lineages within *Dothideomycetes* representing the families *Strigulaceae* and *Monoblastiaceae*. The delineation of lichenised family *Arthopyreniaceae* should continue to be assessed given their placement with a clade containing bambusicolous fungi (Tanaka *et al.* 2009; this volume) and their non monophyly is also confirmed elsewhere (Nelsen *et al.* 2009; this volume). The relationship between the lichenised groups and bambusicolous genera *Roussoella* and *Roussoellopsis* (*Didymosphaeriaceae*; Ju *et al.* 1996, Lumbsch & Huhndorf 2007) is strongly supported, but their affinity is not fully understood due to their considerable morphological differences.

The fungi collected from marine and freshwater habitats contain yet more varied species that have not been assessed well within a molecular based framework. Their diversity is supported by the fact that whole orders (*Jahnulales*) and several families, already mentioned, almost exclusively consist of species collected from these environments. A recent assessment of marine fungi tallied a number of more than 500 species with more than a fifth of these suggested to reside in *Dothideomycetes* (Jones *et al.* 2009). The number for fungi from fresh water habitats is somewhat lower (about 170 taxa).

Despite similarities in their preferred medium for spore dispersal (water) an examination of phylogenetic diversity within *Dothideomycetes* indicates that these groups of fungi tend to reside in divergent parts of the tree (Figs 2, 3). However, some exceptions may occur: For example, members of *Aigialaceae* are weakly supported to share ancestry with members of freshwater clade *Lindgomycetaceae* (Raja *et al.* 2010). The *Jahnulales* represents another recently delineated aquatic lineage with an interesting mixture of fresh water and marine taxa. It was delineated based on molecular and morphological data (Inderbitzin *et al.* 2001, Pang *et al.* 2002) and now contains four genera and several species (Campbell *et al.* 2007). Previously, two anamorphic species in the *Jahnulales*, *Xylomyces rhizophorae* (described from mangrove wood of *Rhizophora*) and *X. chlamydosporus* have been reported

from mangroves and thus saline habitats (Kohlmeyer & Volkman-Kohlmeyer 1998). It has further been documented that *X. chlamydosporus* is the anamorph of *Jahnula aquatica*, a freshwater species (Sivichai, pers. comm.).

Marine *Dothideomycetes* generally exist in association with algae and plants in marine and brackish environments, usually with intertidal or secondary marine plants (e.g., mangroves). The majority of these fungi have been classified in families and genera that comprise mostly terrestrial species (e.g., *Pleospora*) and no definitive clades of marine *Dothideomycetes* have been identified. Here we find support for diverse aquatic lineages similar to the situation in *Sordariomycetes*. Papers by Suetrong *et al.* 2009 (this volume) and Shearer *et al.* 2009 (this volume) continue to address this disparity by using multigene phylogenies to describe several lineages within a class wide context. In contrast, many marine members of the *Dothideomycetes* await interrogation at the DNA sequence level, especially the genera *Belizeana*, *Thallassoascus*, *Lautospora* and *Loratospora*, all exclusively marine taxa.

The final environmentally defined group sampled in this volume is the bambusicolous fungi. More than 1 100 fungal species have been described or recorded worldwide from bamboo (Hyde *et al.* 2002). Furthermore, their ecological specialisation as pathogens, saprophytes, and endophytes has been relatively well documented (e.g. Hino 1961). However, relatively few studies based on DNA sequence comparisons have been undertaken for many bambusicolous fungi. Several unique lineages, e.g. the *Katumotoa bambusicola*-*Ophiosphaerella sasicola* clade in a freshwater lineage (*Lentitheciaceae*) and the *Roussoella*-*Roussoellopsis* clade close to lichen-forming families could be found (Fig. 2). Particularly, a new family *Tetraplophaeriaceae* including five new genera characterised by a *Tetraploa* anamorph s. l. is introduced as a lineage of fungi with bamboo habitat (Tanaka *et al.* 2009; this volume). It is clear that much additional diversity within this group of fungi remains to be sampled using DNA sequence data

A number of other niches remain poorly discussed in this volume. Coprophilous fungi occur in three families *Delitschiaceae*, *Phaeotrichaceae*, and *Sporormiaceae* (Figs 2A, C). These families are not closely related and it is clear that the fimicolous life style has arisen more than once in the *Dothideomycetes*. Also, many species from these groups are not strictly dung-inhabiting, but can be found on other substrates like soil, wood, and plant-debris. Interestingly, some are human pathogens, plant endophytes and lichenicolous fungi. As is true throughout the *Ascomycota*, a change in substrate is apparently not a substantial evolutionary step in these taxa (Kruys & Wedin 2009).

Additional observations

Several orders e.g. *Dothideales*, *Myriangiales* and *Microthyriales* have not been treated using the extensive systematic sampling that is true for studies treated in this volume. However, individual smaller studies continue to provide interesting and surprising results. One such example is the first described meristematic and endoconidial species residing in *Myriangiales* (Fig. 2C) reported by Tsuneda *et al.* (2008). These *Endosporium* species were isolated from very different substrates such as: poplar twigs and a dead bird. They also have a close relationship to a single lineage of rock inhabiting fungi. The nutritional shifts represented by these closely related species correlate well with scenarios described by Ruibal *et al.* (2009; this volume) for rock inhabiting fungi. Another melanised meristematic fungus, *Sarcinomyces crustaceus*, isolated from pine trees appears in a similar position in a phylogeny presented in the aforementioned paper (Ruibal *et al.* 2009; this volume).

Another unusual species, *Catinella olivacea* is included in Fig. 2C, but without any clearly resolved position, diverging early to *Dothideomycetidae*. This species was initially placed in *Leotiomyces*, due to their flattened apothecia, found on the underside of moist, well-decayed logs of hardwood. Asci are unitunicate but they appear to form after ascolocular development. As in the previous analysis, it was not possible to identify relationships between this species and any known order, although there are indications of a close relationship with the *Dothideomycetidae* (Greif *et al.* 2007).

The placement of the single asexual mycorrhizal lineage representing *Cenococcum geophilum* in the *Dothideomycetes* (LoBuglio *et al.* 1996), allied to members of the saprobic *Gloniaceae* is intriguing (Fig. 2B; Boehm *et al.* 2009a; this volume). No resolved placement for this species in *Dothideomycetes* has been possible in the past. The results of this study were also unexpected because no biological data suggest a connection to the family. *Cenococcum* is a fungus that is intensively used in environmental studies and this could suggest a very interesting biology for members of the ostensibly saprobic *Gloniaceae*. Results of this study advocate a more expansive sampling of *Cenococcum* in order to confirm this intriguing result.

CONCLUSIONS

One of the major obstacles in dothideomycete systematics remains the lack of a clear understanding of what species are members of the class based on morphology alone. Throughout most of the 20th Century, comparative morphological studies have been the only character on which to base phylogenetic relationships. The advent of large DNA-sequence data sets should allow for a substantially improved interpretation of morphological characters for this class of fungi. Studies in this volume and elsewhere have provided a clear understanding that many of the characters classically used in taxonomy and systematics of the group are homoplastic and not helpful for reconstructing phylogenetic relationships. Dothideomycete taxonomy also needs to keep pace with the rapid advances being made in phylogenetics, genomics and related fields. The important principle here is that our classification should communicate diversity accurately and allow dothideomycete biologists from disparate fields to have access to an agreed upon set of taxonomic names to aid communication. In addition, it should allow for a focus on under-sampled groups and clades (i.e. poorly sampled saprobes and others). A major task ahead will be to add asexual genera to present phylogenetic schemes, and integrate these into the existing familial and ordinal classification. As most of these asexual genera are in fact poly- and paraphyletic, their type species will need to be recollected to clarify their phylogenetic position. In addition to this, it appears that even some concepts of teleomorphic taxa will require extensive reconsideration. Finally, we should attempt to incorporate valuable biological information from past workers, such as the three mycologists to which this volume is dedicated, by reliably assessing culture and sequence identity. It is hoped that the papers in this volume will make a meaningful contribution towards these goals.

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SUPPLEMENTARY INFORMATION

Table 1. Isolates of *Dothideomycetes* included in this study. Newly deposited sequences are shown in bold.

Taxon	voucher/culture ¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Acanthostigma perpusillum</i>	UAMH	AY856937	AY856892			
<i>Aglaospora profusa</i>	CBS 123109	GU296130	GU301792			GU349062
<i>Aigialus grandis</i> 1	2Q	GU296132	GU301794			GU349063
<i>Aigialus grandis</i> 2	JK 5244A	GU296131	GU301793		GU371762	
<i>Aigialus parvus</i>	A6	GU296133	GU301795		GU371771	GU349064
<i>Aliquandostipite khaoyaiensis</i>	CBS 118232	AF201453	GU301796		FJ238360	GU349048
<i>Alternaria alternata</i>	CBS 916.96	DQ678031	DQ678082		DQ677980	DQ677927
<i>Amniculicola parva</i>	CBS 123092	GU296134	FJ795497			GU349065
<i>Anteaglonium abbreviatum</i> 1	ANM 925.1		GQ221877			GQ221924
<i>Anteaglonium abbreviatum</i> 2	GKM 1029		GQ221878			GQ221915
<i>Anteaglonium globosum</i> 1	SMH 5283		GQ221911			GQ221919
<i>Anteaglonium globosum</i> 2	ANM 925.2		GQ221879			GQ221925
<i>Anteaglonium latirostrum</i>	L100N 2		GQ221876			GQ221938
<i>Anteaglonium parvulum</i>	SMH 5210		GQ221907			GQ221917
<i>Apiosporina collinsii</i>	CBS 118973	GU296135	GU301798	GU357778		GU349057
<i>Apiosporina morbosa</i>	dimosp		EF114694			
<i>Arthopyrenia salicis</i> 1	1994 Coppins		AY607730	AY607742		
<i>Arthopyrenia salicis</i> 2	CBS 368.94	AY538333	AY538339	GU371814		
<i>Ascochyta pisi</i>	CBS 126.54	DQ678018	DQ678070		DQ677967	DQ677913
<i>Ascocratera manglicola</i>	JK 5262C	GU296136	GU301799		GU371763	
<i>Asteromassaria pulchra</i>	CBS 124082	GU296137	GU301800		GU371772	GU349066
<i>Astrosphaeriella aggregata</i>	MAFF 239486	AB524450	AB524591		AB539105	AB539092
<i>Astrosphaeriella bakeriana</i>	CBS 115556		GU301801	GU357752		GU349015
<i>Astrothelium cinnamomeum</i>	DUKE 0000007		AY584652			DQ782896
<i>Aulographina pinorum</i> 1	CBS 302.71				GU371766	
<i>Aulographina pinorum</i> 2	CBS 174.90	GU296138	GU301802	GU357763	GU371737	GU349046
<i>Aureobasidium pullulans</i>	CBS 584.75	DQ471004	DQ470956	DQ471148	DQ470906	DQ471075
<i>Bagnisiella examinans</i>	CBS 551.66	GU296139	GU301803	GU357776	GU371746	GU349056
<i>Batcheloromyces proteae</i>	CBS 110696	AY251102	EU019247			
<i>Beverlykella pulmonaria</i>	CBS 283.53		GU301804		GU371768	
<i>Bimuria novae-zelandiae</i>	CBS 107.79	AY016338	AY016356	DQ471159	DQ470917	DQ471087
<i>Botryosphaeria dothidea</i>	CBS 115476	DQ677998	DQ678051	GU357802	DQ677944	DQ676637
<i>Botryosphaeria tsugae</i>	CBS 418.64	AF271127	DQ767655		DQ767644	DQ677914
<i>Byssolophis sphaerioides</i>	IFRDCC2053	GU296140	GU301805		GU456348	GU456263
<i>Byssothecium circinans</i>	CBS 675.92	AY016339	AY016357		DQ767646	GU349061
<i>Camarosporium quaternatum</i>	CBS 483.95	GU296141	GU301806	GU357761		GU349044
<i>Capnobotryella renispora</i>	CBS 215.90	AY220613	GQ852582			
<i>Capnodium coffeae</i>	CBS 147.52	DQ247808	DQ247800	DQ471162	DQ247788	DQ471089
<i>Capnodium salicinum</i>	CBS 131.34	DQ677997	DQ678050			DQ677889
<i>Catenulostroma abietis</i> (as <i>Trimmatostroma abietis</i>)	CBS 459.93	DQ678040	DQ678092	GU357797		DQ677933
<i>Catenulostroma elginense</i>	CBS 111030	GU214517	EU019252			
<i>Catinella olivacea</i>	UAMH 10679	DQ915484	EF622212			
<i>Cenococcum geophilum</i> 1	HUNT A1	L76616				
<i>Cenococcum geophilum</i> 2	CGMONT	L76617				
<i>Cenococcum geophilum</i> 3	10	L76618				

Table 1. (Continued).

Taxon	voucher/culture¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Cercospora beticola</i>	CBS 116456	DQ678039	DQ678091			DQ677932
<i>Chaetosphaeronema hispidulum</i>	CBS 216.75	EU754045	EU754144	GU357808	GU371777	
<i>Cladosporium cladosporioides</i>	CBS 170.54	DQ678004	DQ678057	GU357790	DQ677952	DQ677898
<i>Cladosporium iridis</i> (teleomorph <i>Davidiella macrospora</i>)	CBS 138.40		DQ008148			
<i>Clathrospora elynae</i>	CBS 196.54	GU296142	GU323214			
<i>Cochliobolus heterostrophus</i>	CBS 134.39	AY544727	AY544645		DQ247790	DQ497603
<i>Cochliobolus sativus</i>	DAOM 226212	DQ677995	DQ678045		DQ677939	
<i>Columnosphaeria fagi</i>	CBS 171.93	AY016342	AY016359		DQ677966	
<i>Comminutispora agavaciensis</i>	CBS 619.95	Y18699	EU981286			
<i>Conidioxypium gardeniorum</i>	CPC 14327	GU296143	GU301807	GU357774	GU371743	GU349054
<i>Coniothyrium palmarum</i>	CBS 400.71	DQ678008	DQ767653		DQ677956	DQ677903
<i>Corynespora cassicola</i> 1	CBS 100822	GU296144	GU301808	GU357772	GU371742	GU349052
<i>Corynespora cassicola</i> 2	CCP	GU296145				
<i>Corynespora olivacea</i>	CBS 114450		GU301809			GU349014
<i>Corynespora smithii</i>	CABI 5649b		GU323201	GU371804	GU371783	GU349018
<i>Cryptothelium amazonum</i>	47		GU327713			GU327731
<i>Cryptothelium pulchrum</i>	63C		GU327714			
<i>Cystocoleus ebeneus</i> 1	L348	EU048573	EU048580			
<i>Cystocoleus ebeneus</i> 2	L315	EU048572				
<i>Davidiella tassiana</i>	CBS 399.80	DQ678022	DQ678074	GU357793	DQ677971	DQ677918
<i>Delitschia</i> cf. <i>chaetomioides</i> 1	GKM 3253.2		GU390656			
<i>Delitschia</i> cf. <i>chaetomioides</i> 2	GKM 1283		GU385172			
<i>Delitschia didyma</i> 1 (duplicate)	UME 31411		DQ384090			
<i>Delitschia didyma</i> 2	UME 31411	AF242264	DQ384090			
<i>Delitschia winteri</i>	CBS 225.62	DQ678026	DQ678077		DQ677975	DQ677922
<i>Delphinella strobiligena</i>	CBS 735.71		DQ470977	DQ471175	DQ677951	DQ471100
<i>Devriesia staurophora</i>	CBS 375.81	EF137359	DQ008151			
<i>Devriesia strelitziae</i>	CBS 122379	GU296146	GU301810		GU371738	GU349049
<i>Didymella bryoniae</i> (as <i>Phoma cucurbitacearum</i>)	CBS 133.96		GU301863		GU371767	
<i>Didymella exigua</i>	CBS 183.55	GU296147		GU357800	GU371764	
<i>Didymocrea sadasivanii</i>	CBS 438.65	DQ384066	DQ384103			
<i>Diplodia mutila</i> (teleomorph <i>Botryosphaeria stevensii</i>)	CBS 431.82	DQ678012	DQ678064		DQ677960	DQ677907
<i>Dissoconium aciculare</i>	CBS 204.89	GU214523	GQ852587			
<i>Dissoconium commune</i> (teleomorph <i>Mycosphaerella communis</i>)	CBS 110747	GU214525	GQ852589			
<i>Dissoconium dekkeri</i> (teleomorph <i>Mycosphaerella lateralis</i>)	CBS 111282	GU214531	GU214425			
<i>Dothidea hippophaës</i>	CBS 188.58	U42475	DQ678048	GU357801	DQ677942	DQ677887
<i>Dothidea insculpta</i>	CBS 189.58	DQ247810	DQ247802	DQ471154	AF107800	DQ471081
<i>Dothidea sambuci</i>	DAOM 231303	AY544722	AY544681		DQ522854	DQ497606
<i>Dothiora cannabinae</i>	CBS 737.71	DQ479933	DQ470984	DQ471182	DQ470936	DQ471107
<i>Dothiora elliptica</i>	CBS 736.71		GU301811			GU349013
<i>Dothistroma septosporum</i> 1 (teleomorph <i>Mycosphaerella pini</i>)	CBS 543.74		GU301853		GU371730	
<i>Dothistroma septosporum</i> 2	CBS 112498	GU214533	GQ852597			
<i>Elsinoë centrolobi</i>	CBS 222.50	DQ678041	DQ678094	GU357798		DQ677934
<i>Elsinoë phaseoli</i>	CBS 165.31	DQ678042	DQ678095	GU357799		DQ677935
<i>Elsinoë veneta</i>	CBS 150.27	DQ767651	DQ767658			DQ767641
<i>Endosporium aviarium</i>	UAMH 10530	EU304349	EU304351			

Table 1. (Continued).

Taxon	voucher/culture ¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Endosporium populi-tremuloidis</i>	UAMH 10529	EU304346	EU304348			
<i>Entodesmium rude</i>	CBS 650.86		GU301812			GU349012
<i>Falciformispora lignatilis</i> 1	BCC 21118	GU371835	GU371827			GU371820
<i>Falciformispora lignatilis</i> 2	BCC 21117	GU371834	GU371826			GU371819
<i>Farlowiella carmichaeliana</i> 2	CBS 179.73	GU296148				
<i>Farlowiella carmichaeliana</i> 1 (as anamorph <i>Acrogenospora sphaerocephala</i>)	CBS 164.76	GU296129	GU301791	GU357780	GU371748	GU349059
<i>Floricola striata</i>	JK 56781	GU296149	GU301813		GU371758	
<i>Friedmanniomyces endolithicus</i>	CCFEE 522	DQ066715				
<i>Friedmanniomyces simplex</i>	CBS 116775	DQ066716				
<i>Gibbera conferta</i>	CBS 191.53	GU296150	GU301814	GU357758		GU349041
<i>Gloniopsis arciformis</i>	GKM L166A	GU323180	GU323211			
<i>Gloniopsis praelonga</i> 1	CBS 112415	FJ161134	FJ161173		FJ161113	FJ161090
<i>Gloniopsis praelonga</i> 2	CBS 123337	FJ161154	FJ161195	FJ161103		FJ161103
<i>Gloniopsis subrugosa</i>	CBS 123346	FJ161170	FJ161210	GU371808	FJ161131	
<i>Glonium circumserpens</i> 1	CBS 123342	FJ161168	FJ161208			
<i>Glonium circumserpens</i> 2	CBS 123343	FJ161160	FJ161200	GU371806	FJ161126	FJ161108
<i>Glonium stellatum</i>	CBS 207.34	FJ161140	FJ161179			FJ161095
<i>Guignardia bidwellii</i>	CBS 237.48	DQ678034	DQ678085	GU357794	DQ677983	
<i>Guignardia citricarpa</i>	CBS 102374	GU296151	GU301815	GU357773		GU349053
<i>Guignardia gaultheriae</i>	CBS 447.70		DQ678089	GU357796	DQ677987	
<i>Halomassarina ramunculicola</i> 1 (as <i>Massarina ramunculicola</i>)	BCC 18404	GQ925838	GQ925853			
<i>Halomassarina ramunculicola</i> 2 (as <i>Massarina ramunculicola</i>)	BCC 18405	GQ925839	GQ925854			
<i>Halomassarina thalassiae</i> (as <i>Massarina thalassiae</i>)	JK 5262D		GU301816			GU349011
<i>Helicomycetes roseus</i>	CBS 283.51	DQ678032	DQ678083		DQ677981	DQ677928
<i>Hortaea acidophila</i>	CBS 113389		GU323202	GU357768		
<i>Hortaea werneckii</i>	CBS 708.76	GU296153	GU301818	GU357779	GU371747	GU349058
<i>Hortaea werneckii</i>	CBS 100496	GU296152	GU301817		GU371739	GU349050
<i>Hysterium angustatum</i>	CBS 123334	FJ161167	FJ161207		FJ161129	FJ161111
<i>Hysterium barrianum</i> 1	ANM 1495	GU323182	GQ221885			
<i>Hysterium barrianum</i> 2	ANM 1442	GU323181	GQ221884			
<i>Hysterobrevium mori</i> 1	CBS 123336	FJ161164	FJ161204			
<i>Hysterobrevium mori</i> 2	SMH 5273		GU301820			GQ221936
<i>Hysterobrevium mori</i> 3	GKM 1013		GU301819			GU397338
<i>Hysterobrevium smilacis</i> 1	CBS 114601	FJ161135	FJ161174	GU357806	FJ161114	FJ161091
<i>Hysterobrevium smilacis</i> 2	SMH 5280	GU323183	GQ221912	GU371810	GU371784	
<i>Hysteropatella clavisporea</i>	CBS 247.34	DQ678006	AY541493		DQ677955	DQ677901
<i>Hysteropatella elliptica</i>	CBS 935.97	EF495114	DQ767657		DQ767647	DQ767640
<i>Jahnula aquatica</i>	R68-1	EF175633	EF175655			
<i>Jahnula bipileata</i>	F49-1	EF175635	EF175657			
<i>Jahnula seychellensis</i>	SS2113.1	EF175644	EF175665			
<i>Julella avicenniae</i> 1	BCC 18422	GU371831	GU371823		GU371787	GU371816
<i>Julella avicenniae</i> 2	BCC 20173	GU371830	GU371822		GU371786	GU371815
<i>Kabatiella caulivora</i>	CBS 242.64	EU167576	EU167576	GU357765		
<i>Kalmusia scabriscpora</i> 1	MAFF 239517	AB524452	AB524593		AB539093	AB539106
<i>Kalmusia scabriscpora</i> 2	NBRC 106237	AB524453	AB524594		AB539094	AB539107

Table 1. (Continued).

Taxon	voucher/culture¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Karstenula rhodostoma</i>	CBS 690.94	GU296154	GU301821		GU371788	GU349067
<i>Katumotoa bambusicola</i>	MAFF 239641	AB524454	AB524595		AB539095	AB539108
<i>Keissleriella cladophila</i>	CBS 104.55	GU296155	GU301822		GU371735	GU349043
<i>Kirschsteinothelia elaterascus</i>	A22-5A / HKUCC7769	AF053727	AY787934			
<i>Kirschsteinothelia maritima</i>	CBS 221.60		GU323203			GU349001
<i>Laurera megasperma</i>	AFTOL 2094		FJ267702			
<i>Lentithecium aquaticum</i>	CBS 123099	GU296156	GU301823		GU371789	GU349068
<i>Lentithecium arundinaceum</i>	CBS 619.86	GU296157	GU301824		FJ795473	
<i>Lentithecium fluviatile</i>	CBS 122367	GU296158	GU301825			GU349074
<i>Lepidosphaeria nicotiae</i>	CBS 101341		DQ678067		DQ677963	DQ677910
<i>Leptosphaeria biglobosa</i>	CBS 303.51		GU301826			GU349010
<i>Leptosphaeria doliolum</i>	CBS 505.75	GU296159	GU301827			GU349069
<i>Leptosphaeria dryadis</i>	CBS 643.86		GU301828		GU371733	GU349009
<i>Leptosphaerulina argentinensis</i>	CBS 569.94		GU301829	GU357759		GU349008
<i>Leptosphaerulina australis</i>	CBS 317.83	GU296160	GU301830		GU371790	GU349070
<i>Leptosphaeria maculans</i>	DAOM 229267	DQ470993	DQ470946	DQ471136	DQ470894	DQ471062
<i>Leptoxylum fumago</i>	CBS 123.26	GU296161	GU301831	GU357771	GU371741	GU349051
<i>Letendreaa helminthicola</i>	CBS 884.85	AY016345	AY016362			
<i>Letendreaa padouk</i>	CBS 485.70	GU296162	AY849951			
<i>Lindgomyces breviappendiculata</i>	HHUF 28193	AB521733	AB521748			
<i>Lindgomyces ingoldianus</i>	ATCC_200398	AB521719	AB521736			
<i>Lindgomyces rotundatus</i>	HHUF_27999	AB521723	AB521740			
<i>Lophiostoma alpigenum</i>	GKM 1091b		GU385193			
<i>Lophiostoma arundinis</i>	CBS 621.86	DQ782383	DQ782384		DQ782386	DQ782387
<i>Lophiostoma caulium</i> 1	CBS 623.86	GU296163	GU301833		GU371791	
<i>Lophiostoma caulium</i> 2	CBS 624.86		GU301832			GU349007
<i>Lophiostoma compressum</i>	IFRD 2014	GU296164	GU301834		FJ795457	
<i>Lophiostoma crenatum</i>	CBS 629.86	DQ678017	DQ678069		DQ677965	DQ677912
<i>Lophiostoma fuckelii</i>	GKM 1063		GU385192			
<i>Lophiotrema brunneosporum</i>	CBS 123095	GU296165	GU301835			GU349071
<i>Lophiotrema lignicola</i>	CBS 122364	GU296166	GU301836			GU349072
<i>Lophiotrema nucula</i>	CBS 627.86	GU296167	GU301837		GU371792	GU349073
<i>Lophium elegans</i>	EB 0366	GU323184	GU323210			
<i>Lophium mytilinum</i> 1	CBS 114111	EF596819	EF596819			
<i>Lophium mytilinum</i> 2	CBS 269.34	DQ678030	DQ678081		DQ677979	DQ677926
<i>Loratospora aestuarii</i>	JK 5535B	GU296168	GU301838		GU371760	
<i>Macrophomina phaseolina</i>	CBS 227.33	DQ678037	DQ678088		DQ677986	DQ677929
<i>Macrovalsa megalospora</i> 1	178150	FJ215707	FJ215701			
<i>Macrovalsa megalospora</i> 2	178149	FJ215706	FJ215700			
<i>Massaria anomia</i>	CBS 591.78	GU296169	GU301839		GU371769	
<i>Massaria platani</i>	CBS 221.37	DQ678013	DQ678065		DQ677961	DQ677908
<i>Massarina arundinariae</i> 1	MAFF 239641	AB524455	AB524596		AB539096	AB524817
<i>Massarina arundinariae</i> 2	NBRC 106238	AB524456	AB524597		AB539097	AB524818
<i>Massarina eburnea</i>	CBS 473.64	GU296170	GU301840	GU357755	GU371732	GU349040
<i>Massarina igniaria</i>	CBS 845.96	GU296171	GU301841		GU371793	
<i>Massariosphaeria grandispora</i>	CBS 613.86	GU296172	GU301842	GU357747	GU371725	GU349036

Table 1. (Continued).

Taxon	voucher/culture ¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Massariosphaeria phaeospora</i>	CBS 611.86	GU296173	GU301843		GU371794	
<i>Massariosphaeria typhicola</i> 1	CBS 123126	GU296174	GU301844		GU371795	
<i>Massariosphaeria typhicola</i> 2	KT 797	AB521730	AB521747			
<i>Mauritiana rhizophorae</i> 1	BCC 28866	GU371832	GU371824		GU371796	GU371817
<i>Mauritiana rhizophorae</i> 2	BCC 28867	GU371833	GU371825		GU371797	GU371818
<i>Melanomma pulvis-pyrius</i> 1	SMH 3291		GU385197			
<i>Melanomma pulvis-pyrius</i> 2	CBS 371.75		GU301845		GU371798	GU349019
<i>Melanomma rhododendri</i>	ANM 73		GU385198			
<i>Microthyrium microscopicum</i>	CBS 115976	GU296175	GU301846		GU371734	GU349042
<i>Microxyphium aciculiforme</i>	CBS 892.73	GU296176	GU301847	GU357762	GU371736	GU349045
<i>Microxyphium citri</i>	CBS 451.66	GU296177	GU301848	GU357750	GU371727	GU349039
<i>Microxyphium theae</i>	CBS 202.30	GU296178	GU301849	GU357781		GU349060
<i>Monascostroma innumerosum</i>	CBS 345.50	GU296179	GU301850			GU349033
<i>Monotosporella tuberculata</i>	CBS 256.84		GU301851			GU349006
<i>Montagnula opulenta</i>	CBS 168.34	AF164370	DQ678086		DQ677984	
<i>Mycosphaerella endophytica</i>	CBS 114662	GU214538	DQ246255			
<i>Mycosphaerella euryptami</i>	JK 5586J		GU301852		GU371722	
<i>Mycosphaerella graminicola</i> 1	CBS 292.38	DQ678033	DQ678084		DQ677982	
<i>Mycosphaerella graminicola</i> 2	CBS 115943	GU214540	GU214436			
<i>Mycosphaerella heimii</i>	CBS 110682	GU214541	GQ852604			
<i>Mycosphaerella latebrosa</i>	CBS 687.94	DQ848331	GU214444			
<i>Mycosphaerella marksii</i>	CBS 110942	GU214549	GQ852612			
<i>Mycosphaerella punctiformis</i> (anamorph <i>Ramularia endophylla</i>)	CBS 113265	DQ471017	DQ470968	DQ471165	DQ470920	DQ471092
<i>Myriangium duriaei</i>	CBS 260.36	AY016347	DQ678059		DQ677954	DQ677900
<i>Myriangium hispanicum</i>	CBS 247.33	GU296180	GU301854	GU357775	GU371744	GU349055
<i>Mytilinidion acicola</i>	EB 0349	GU323185	GU323209		GU371757	
<i>Mytilinidion andinense</i>	CBS 123562	FJ161159	FJ161199		FJ161125	FJ161107
<i>Mytilinidion californicum</i>	EB 0385	GU323186	GU323208			
<i>Mytilinidion mytilinellum</i>	CBS 303.34	FJ161144	FJ161184	GU357810	FJ161119	FJ161100
<i>Mytilinidion resinicola</i>	CBS 304.34	FJ161145	FJ161185	FJ161101	FJ161101	FJ161120
<i>Mytilinidion rhenanum</i>	EB 0341	GU323187	GU323207			
<i>Mytilinidion scolecosporum</i>	CBS 305.34	FJ161146	FJ161186	GU357811	FJ161121	FJ161102
<i>Mytilinidion thujarum</i>	EB 0268	GU323188	GU323206			
<i>Mytilinidion tortile</i>	EB 0377	GU323189	GU323205			
<i>Neofusicoccum ribis</i> (teleomorph <i>Botryosphaeria ribis</i>)	CBS 115475	DQ678000	DQ678053	GU357789	DQ677947	DQ677893
<i>Neophaeosphaeria filamentosa</i>	CBS 102202	GQ387516	GQ387577	GU357803	GU371773	GU349084
<i>Neottiosporina paspali</i>	CBS 331.37	EU754073	EU754172	GU357812	GU371779	GU349079
<i>Oedohysterium insidens</i> 1	CBS 238.34	FJ161142	FJ161182		FJ161118	FJ161097
<i>Oedohysterium insidens</i> 2	ANM 1443	GU323190	GQ221882	GU371811	GU371785	
<i>Oedohysterium sinense</i>	CBS 123345	FJ161169	FJ161209	GU371807	FJ161130	
<i>Opegapha dolomitica</i>	DUKE 0047528	DQ883706		DQ883717	DQ883714	DQ883732
<i>Ophiosphaerella herpotricha</i>	CBS 620.86	DQ678010	DQ678062		DQ677958	DQ677905
<i>Ophiosphaerella sasicola</i>	MAFF 239644	AB524458	AB524599		AB539098	AB539111
<i>Otthia spiraeae</i> 1	CBS 114124	EF204515	EF204498			
<i>Otthia spiraeae</i> 2	CBS 113091	EF204516	EF204499	GU357777		
<i>Paraconiothyrium minitans</i>	CBS 122788	EU754074	EU754173	GU357807	GU371776	GU349083

Table 1. (Continued).

Taxon	voucher/culture¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Patellaria atrata</i>	CBS 958.97	GU296181	GU301855	GU357749	GU371726	GU349038
<i>Patellaria</i> cf. <i>atrata</i> 1	BCC 28876	GU371836	GU371828			
<i>Patellaria</i> cf. <i>atrata</i> 2	BCC 28877	GU371837	GU371829			
<i>Phacellium paspali</i>	CBS 113093	GU214669	GQ852627			
<i>Phaeocryptopus gaeumannii</i> 1	CBS 244.38			GU357766	GU371740	
<i>Phaeocryptopus gaeumannii</i> 2	CBS 267.37	EF114722	EF114698	GU357770		
<i>Phaeocryptopus nudus</i>	CBS 268.37	GU296182	GU301856	GU357745		GU349034
<i>Phaeodothis winteri</i>	CBS 182.58	GU296183	GU301857			DQ677917
<i>Phaeosclera dematioides</i>	CBS 157.81	GU296184	GU301858	GU357764		GU349047
<i>Phaeosphaeria ammophilae</i>	CBS 114595	GU296185	GU301859	GU357746	GU371724	GU349035
<i>Phaeosphaeria avenaria</i>	DAOM 226215	AY544725	AY544684		DQ677941	DQ677885
<i>Phaeosphaeria brevispora</i> 1	NBRC 106240	AB524460	AB524601		AB539100	AB539113
<i>Phaeosphaeria brevispora</i> 2	MAFF 239276	AB524459	AB524600		AB539099	AB539112
<i>Phaeosphaeria caricis</i>	CBS 120249		GU301860			GU349005
<i>Phaeosphaeria eustoma</i>	CBS 573.86	DQ678011	DQ678063		DQ677959	DQ677906
<i>Phaeosphaeria juncicola</i>	CBS 595.86					GU349016
<i>Phaeosphaeria luctuosa</i>	CBS 308.79		GU301861			GU349004
<i>Phaeosphaeria nodorum</i>	Broad	Genome	Genome	Genome	Genome	Genome
<i>Phaeosphaeriopsis musae</i>	CBS 120026	GU296186	GU301862	GU357748		GU349037
<i>Phaeotrichum benjaminii</i>	CBS 541.72	AY016348	AY004340	GU357788	DQ677946	DQ677892
<i>Phoma betae</i>	CBS 109410	EU754079	EU754178	GU357804	GU371774	GU349075
<i>Phoma complanata</i>	CBS 268.92	EU754081	EU754180	GU357809	GU371778	GU349078
<i>Phoma exigua</i>	CBS 431.74	EU754084	EU754183	GU357813	GU371780	GU349080
<i>Phoma glomerata</i>	CBS 528.66	EU754085	EU754184		GU371781	GU349081
<i>Phoma herbarum</i>	CBS 276.37	DQ678014	DQ678066	GU357792	DQ677962	DQ677909
<i>Phoma heteromorphospora</i>	CBS 115.96	EU754089	EU754188		GU371775	GU349077
<i>Phoma radicina</i>	CBS 111.79	EU754092	EU754191	GU357805		GU349076
<i>Phoma zae-maydis</i>	CBS 588.69	EU754093	EU754192	GU357814	GU371782	GU349082
<i>Piedraia hortae</i>	CBS 480.64	AY016349	AY016366		DQ677990	
<i>Pleomassaria siparia</i>	CBS 279.74	DQ678027	DQ678078		DQ677976	DQ677923
<i>Pleospora ambigua</i>	CBS 113979		AY787937	GU357760		
<i>Pleospora herbarum</i>	CBS 191.86	DQ247812	DQ247804	DQ471163	DQ247794	DQ471090
<i>Polyposphaeria fusca</i>	MAFF 239685	AB524463	AB524604			
<i>Polythrincium trifolii</i> (as <i>Cymadothea trifolii</i>)	133	EU167612	EU167612			
<i>Preussia funiculata</i>	CBS 659.74	GU296187	GU301864		GU371799	GU349032
<i>Preussia lignicola</i> (as <i>Sporormia lignicola</i>)	CBS 264.69	GU296197	GU301872		GU371765	GU349027
<i>Preussia terricola</i>	DAOM 230091	AY544726	AY544686	DQ471137	DQ470895	DQ471063
<i>Pseudocercospora fijiensis</i> (teleomorph <i>Mycosphaerella fijiensis</i>)	OSC 100622	DQ767652	DQ678098		DQ677993	
<i>Pseudocercospora griseola</i> f. <i>griseola</i>	CPC 10461	GU323191	GU348997			
<i>Pseudocercospora vitis</i>	CPC 11595	DQ289864	GU214483			
<i>Pseudotetraploa curviappendiculata</i>	MAFF 239495	AB524467	AB524608			
<i>Psiloglonium araucanum</i>	CBS 112412	FJ161133	FJ161172	GU357743	FJ161112	FJ161089
<i>Psiloglonium clavisporum</i> 1	CBS 123338	FJ161156	FJ161197		FJ161123	
<i>Psiloglonium clavisporum</i> 2	GKM L172A	GU323192	GU323204			
<i>Psiloglonium simulans</i>	CBS 206.34	FJ161139	FJ161178		FJ161116	FJ161094
<i>Pyrenochaeta nobilis</i>	CBS 407.76		DQ678096		DQ677991	DQ677936

Table 1. (Continued).

Taxon	voucher/culture ¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Pyrenophora phaeocomes</i>	DAOM 222769	DQ499595	DQ499596		DQ497614	DQ497607
<i>Pyrenophora tritici-repentis</i> 1	OSC 100066		AY544672			DQ677882
<i>Pyrenophora tritici-repentis</i> 2	CBS 328.53					GU349017
<i>Quadricrura septentrionalis</i>	CBS 125429	AB524474	AB524615			
<i>Quintaria lignatilis</i>	CBS 117700	GU296188	GU301865		GU371761	
<i>Quintaria submersa</i>	CBS 115553		GU301866	GU357751		GU349003
<i>Racodium rupestre</i> 1	L423	EU048576	EU048581			
<i>Racodium rupestre</i> 2	L424	EU048577	EU048582			
<i>Ramichloridium apiculatum</i>	CBS 156.59	GU296189			GU371770	
<i>Ramichloridium cerophilum</i>	CBS 103.59	GU296190	EU041855			
<i>Rasutoria tsugae</i>	ratstk	EF114730	EF114705	GU371809		
<i>Rhynchostyrium rufulum</i> 2	CBS 306.38	GU296191	FJ469672	FJ238444		GU349031
<i>Rhynchostyrium rufulum</i> 1	GKM 361A	GU296192	GU301867			
<i>Rimora mangrovei</i>	JK 5246A	GU296193	GU301868		GU371759	
rock isolate TRN 111	CBS 118294	GU323193	GU323220	GU357783	GU371751	GU349088
rock isolate TRN 123	CBS 117932	GU323194	GU323219	GU357784	GU371753	
rock isolate TRN 137	CBS 118300	GU323195	GU323218	GU357782	GU371749	
rock isolate TRN 138	CBS 118301	GU323196	GU323217		GU371750	
rock isolate TRN 152	CBS 118346	GU323197	GU323223		GU371752	
rock isolate TRN 211	CBS 117937	GU323198	GU323222	GU357785	GU371754	
rock isolate TRN 235	CBS 118605	GU323199		GU357787	GU371756	GU349087
rock isolate TRN 43	CBS 117950	GU323200	GU323221	GU357786	GU371755	GU349086
<i>Roussoella hysteroioides</i> 1	MAFF 239636	AB524480	AB524621		AB539101	AB539114
<i>Roussoella hysteroioides</i> 2	CBS 125434	AB524481	AB524622		AB539102	AB539115
<i>Roussoella pustulans</i>	MAFF 239637	AB524482	AB524623		AB539103	AB539116
<i>Roussoellopsis tosaensis</i>	MAFF 239638		AB524625		AB539104	AB539117
<i>Saccharata proteae</i>	CBS 115206	GU296194	GU301869	GU357753	GU371729	GU349030
<i>Sacothecium sepincola</i>	CBS 278.32	GU296195	GU301870		GU371745	GU349029
<i>Schismatomma decolorans</i>	DUKE 0047570	AY548809	AY548815		DQ883715	DQ883725
<i>Schizothyrium pomi</i> 1	CBS 406.61	EF134949	EF134949			
<i>Schizothyrium pomi</i> 2	CBS 486.50	EF134948	EF134948			
<i>Schizothyrium pomi</i> 3	CBS 228.57	EF134947	EF134947			
<i>Scorias spongiosa</i>	CBS 325.33	DQ678024	DQ678075		DQ677973	DQ677920
<i>Setomelanomma holmii</i>	CBS 110217	GU296196	GU301871		GU371800	GU349028
<i>Setosphaeria monoceras</i>	AY016368		AY016368			
<i>Spenceriartinsia viticola</i> (teleomorph <i>Botryosphaeria viticola</i>)	CBS 117009	DQ678036	DQ678087	GU357795	DQ677985	
<i>Sporormiella minima</i>	CBS 524.50	DQ678003	DQ678056		DQ677950	DQ677897
<i>Stagonospora macropycnidia</i>	CBS 114202	GU296198	GU301873			GU349026
<i>Stylothis puccinioides</i>	CBS 193.58		AY004342	FJ238427		DQ677886
<i>Sydowia polyspora</i>	CBS 116.29	DQ678005	DQ678058	GU357791	DQ677953	DQ677899
<i>Teratosphaeria associata</i> (as <i>Teratosphaeria jonkershoekensis</i>)	CBS 112224	GU296200	GU301874	GU357744	GU371723	GU349025
<i>Teratosphaeria cryptica</i> (as <i>Mycosphaerella cryptica</i>)	CBS 110975	GU214602	GQ852682			
<i>Teratosphaeria fibrillosa</i> 1	CBS 121707	GU296199	GU323213	GU357767		
<i>Teratosphaeria fibrillosa</i> 2	CPC 1876		GU214506			
<i>Teratosphaeria stellenboschiana</i> (as <i>Colletogloeopsis stellenboschiana</i>)	CBS 116428	GU214583	EU019295			

Table 1. (Continued).

Taxon	voucher/culture¹	SSU	LSU	RPB1	RPB2	TEF1
<i>Teratosphaeria suberosa</i> (as <i>Mycosphaerella suberosa</i>)	CPC 11032	GU214614	GQ852718			
<i>Tetraplosphaeria sasicola</i>	MAFF 239677	AB524490	AB524631			
<i>Thyridaria rubronotata</i>	CBS 419.85		GU301875		GU371728	GU349002
<i>Tremateia halophila</i>	JK 5517J	GU296201			GU371721	
<i>Trematosphaeria pertusa</i>	CBS 122371	GU348999	GU301876		GU371801	GU349085
<i>Trichodelitschia bisporula</i> 1	CBS 262.69	GU349000	GU348996	GU371812	GU371802	GU349020
<i>Trichodelitschia bisporula</i> 2 (duplicate)	CBS 262.69	GU296202				
<i>Trichodelitschia munkii</i>	Kruys201	DQ384070	DQ384096			
<i>Triplosphaeria maxima</i>	MAFF 239682	AB524496	AB524637			
<i>Trypethelium nitidiusculum</i> 1	139		GU327728			GU327732
<i>Trypethelium nitidiusculum</i> 2	AFTOL 2099		FJ267701			
<i>Trypethelium tropicum</i>	25		GU327730			
<i>Tubeufia cerea</i>	CBS 254.75	DQ471034	DQ470982	DQ471180	DQ470934	DQ471105
<i>Tubeufia paludosa</i>	CBS 120503	GU296203	GU301877	GU357754	GU371731	GU349024
<i>Tubeufia paludosa</i> (as anamorph <i>Helicosporium phragmitis</i>)	CBS 245.49	DQ767649	DQ767654		DQ767643	DQ767638
<i>Tyrannosorus pinicola</i>	CBS 124.88	DQ471025	DQ470974	DQ471171	DQ470928	DQ471098
<i>Ulospora bilgramii</i>	CBS 110020	DQ678025	DQ678076		DQ677974	DQ677921
<i>Venturia inaequalis</i> 1	CBS 594.70	GU296205	GU301879	GU357757		GU349022
<i>Venturia inaequalis</i> 2	CBS 815.69	GU296204	GU301878	GU357756		GU349023
<i>Venturia inaequalis</i> 3 (as <i>Spilocaea pomi</i>)	CBS 176.42		GU348998			GU349089
<i>Venturia populina</i>	CBS 256.38	GU296206	GU323212	GU357769		
<i>Verrucisporota daviesiae</i>	CBS 116002	GU296207	GQ852730			
<i>Verruculina enalia</i>	JK 5253A	DQ678028	DQ678079		DQ677977	DQ677924
<i>Westerdykella angulata</i> (as <i>Eremodthis angulata</i>)	CBS 610.74	DQ384067	DQ384105	GU371805		GU371821
<i>Westerdykella cylindrica</i>	CBS 454.72	AY016355	AY004343	DQ471168	DQ470925	DQ497610
<i>Westerdykella ornata</i>	CBS 379.55	GU296208	GU301880		GU371803	GU349021
<i>Wettsteinina lacustris</i>	CBS 618.86	DQ678023			DQ677972	DQ677919
<i>Wicklowia aquatica</i>	AF289-1		GU045446			
<i>Wicklowia aquatica</i>	CBS 125634	GU266232	GU045445	GU371813		
<i>Zasmidium cellare</i>	CBS 146.36	EF137362	EU041878			
<i>Zopfia rhizophila</i>	CBS 207.26	DQ384086	DQ384104			

¹BCC: Belgian Coordinated Collections of Microorganisms; CABI: International Mycological Institute, CABI-Bioscience, Egham, Basingstoke, U.K.; CBS: Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DUKE: Duke University Herbarium, Durham, North Carolina, U.S.A.; HHUF: Herbarium of Hirosaki University, Japan; IFRDCC: Culture Collection, International Fungal Research & Development Centre, Chinese Academy of Forestry, Kunming, China; MAFF: Ministry of Agriculture, Forestry and Fisheries, Japan; NBRC: NITE Biological Resource Centre, Japan; OSC: Oregon State University Herbarium, U.S.A.; UAMH: University of Alberta Microfungus Collection and Herbarium, Edmonton, Alberta, Canada; UME: Herbarium of the University of Umeå, Umeå, Sweden; Culture and specimen abbreviations: ANM: A.N. Miller; CPC; P.W. Crous; EB: E.W.A. Boehm; EG: E.B.G. Jones; GKM: G.K. Mugambi; JK: J. Kohlmeyer; KT: K. Tanaka; SMH: S.M. Huhndorf.

SUPPLEMENTARY INFORMATION

Table 2. Genomes used for phylogenetic profile. All are opisthokonts; remaining classifications used in Fig. 4 are indicated in columns: Do – *Dothideomycetes*, ED – *Eurotiomycetes* & *Dothideomycetes*, S – *Saccharomyceta*, A – *Ascomycota*, Di – *Dikarya*, MD – *Mucoromycotina* & *Dikarya*, CMD – *Chytridiomycota*, F – *Fungi*.

Genomes	Classifications							
	Do	ED	S	A	Di	MD	CMD	F
<i>Alternaria brassicicola</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Cochliobolus heterostrophus</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Mycosphaerella fijiensis</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Mycosphaerella graminicola</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Pyrenophora tritici-repentis</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Stagonospora nodorum</i>	Do	ED	S	A	Di	MD	CMD	F
<i>Aspergillus fumigatus</i>		ED	S	A	Di	MD	CMD	F
<i>Aspergillus nidulans</i>		ED	S	A	Di	MD	CMD	F
<i>Aspergillus terreus</i>		ED	S	A	Di	MD	CMD	F
<i>Coccidioides immitis</i>		ED	S	A	Di	MD	CMD	F
<i>Histoplasma capsulatum</i>		ED	S	A	Di	MD	CMD	F
<i>Uncinocarpus reesii</i>		ED	S	A	Di	MD	CMD	F
<i>Ashbya gossypii</i>			S	A	Di	MD	CMD	F
<i>Botrytis cinerea</i>			S	A	Di	MD	CMD	F
<i>Candida albicans</i>			S	A	Di	MD	CMD	F
<i>Candida glabrata</i>			S	A	Di	MD	CMD	F
<i>Candida guilliermondii</i>			S	A	Di	MD	CMD	F
<i>Candida lusitanae</i>			S	A	Di	MD	CMD	F
<i>Chaetomium globosum</i>			S	A	Di	MD	CMD	F
<i>Debaryomyces hansenii</i>			S	A	Di	MD	CMD	F
<i>Fusarium graminearum</i>			S	A	Di	MD	CMD	F
<i>Fusarium oxysporum</i>			S	A	Di	MD	CMD	F
<i>Fusarium verticillioides</i>			S	A	Di	MD	CMD	F
<i>Kluyveromyces lactis</i>			S	A	Di	MD	CMD	F
<i>Laccaria bicolor</i>			S	A	Di	MD	CMD	F
<i>Lodderomyces elongisporus</i>			S	A	Di	MD	CMD	F
<i>Magnaporthe grisea</i>			S	A	Di	MD	CMD	F
<i>Nectria haematococca</i>			S	A	Di	MD	CMD	F
<i>Neurospora crassa</i>			S	A	Di	MD	CMD	F
<i>Pichia stipitis</i>			S	A	Di	MD	CMD	F
<i>Podospira anserina</i>			S	A	Di	MD	CMD	F
<i>Saccharomyces cerevisiae</i>			S	A	Di	MD	CMD	F
<i>Sclerotinia sclerotiorum</i>			S	A	Di	MD	CMD	F
<i>Sporobolomyces roseus</i>			S	A	Di	MD	CMD	F
<i>Trichoderma atroviride</i>			S	A	Di	MD	CMD	F
<i>Trichoderma reesei</i>			S	A	Di	MD	CMD	F
<i>Trichoderma virens</i>			S	A	Di	MD	CMD	F
<i>Verticillium dahliae</i>			S	A	Di	MD	CMD	F
<i>Yarrowia lipolytica</i>			S	A	Di	MD	CMD	F
<i>Schizosaccharomyces japonicus</i>				A	Di	MD	CMD	F
<i>Schizosaccharomyces octosporus</i>				A	Di	MD	CMD	F
<i>Schizosaccharomyces pombe</i>				A	Di	MD	CMD	F
<i>Coprinus cinereus</i>					Di	MD	CMD	F
<i>Cryptococcus neoformans</i>					Di	MD	CMD	F
<i>Phanerochaete chrysosporium</i>					Di	MD	CMD	F

Table 1. (Continued).

Genomes	Classifications			
<i>Postia placenta</i>	Di	MD	CMD	F
<i>Puccinia graminis</i> f. sp. <i>tritici</i>	Di	MD	CMD	F
<i>Ustilago maydis</i>	Di	MD	CMD	F
<i>Phycomyces blakesleeanus</i>		MD	CMD	F
<i>Rhizopus oryzae</i>		MD	CMD	F
<i>Batrachochytrium dendrobatidis</i>			CMD	F
<i>Encephalitozoon cuniculi</i>				F
<i>Drosophila melanogaster</i>				