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A reappraisal of families within the order *Magnaporthales* and description of new endophytic taxa associated with *Poaceae* plants in China

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Abstract

The order *Magnaporthales* belongs to the class *Sordariomycetes* within the phylum *Ascomycota*. Through phylogenetic analyses based on the concatenated multi-locus sequence alignment, five families have been successively introduced within *Magnaporthales*. This order comprises a diverse array of plant-pathogenic and endophytic fungi, most of which are associated with monocotyledons. However, there has been a lack of systematic exploration of the phylogeny and taxonomy of endophytic *Magnaporthales* fungi. This study conducted comprehensive phylogenetic and phylogenomic analyses of *Magnaporthales*, incorporating a substantial number of newly isolated endophytic *Magnaporthales* taxa from *Poaceae* plants, one of the most diverse plant families globally. The multi-locus phylogenies revealed six well-supported main clades. One of these main clades, comprising *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*, was distinct from clusters comprising genera of *Pyriculariaceae* and *Magnaporthaceae* (excluding *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*). Phylogenomic analyses confirmed that the genus *Aquafiliformis* is sister to the cluster comprising genera of *Pyriculariaceae* and *Magnaporthaceae* (excluding *Aquafiliformis*). Consequently, we propose the introduction of a new family, *Plagiosphaeraceae*, to accommodate the genera *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*, in addition to the five previously defined families: *Ceratosphaeriaceae*, *Pseudohalonectriaceae*, *Ophioceraceae*, *Pyriculariaceae*, and *Magnaporthaceae*. Furthermore, the phylogenetic analysis of *Magnaporthales* unveiled significant endophytic taxonomic novelties associated with *Poaceae* plants in China, leading to the proposal of 11 new genera, and 24 new species within *Ophioceraceae*, *Pyriculariaceae*, and *Magnaporthaceae*. Additionally, two named species within *Pyriculariaceae* and *Magnaporthaceae* are transferred to two new genera and combinations. The previously invalid genus *Falciphora* and its type species, *Falciphora oryzae*, are also validated.

Keywords – 42 new taxa – endophytic fungi – phylogenomics – phylogeny – *Plagiosphaeraceae*

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INTRODUCTION

The order *Magnaporthales*, belonging to the class *Sordariomycetes* within the phylum *Ascomycota*, includes a diverse array of plant pathogenic fungi that primarily affect plants of the *Poaceae* family (Hyde et al. 2020). For example, the rice blast fungus *Pyricularia oryzae* causes significant losses in agriculture (Valent 1990), the take-all fungus *Gaeumannomyces graminis* affects a variety of cereal crops (Hernández-Restrepo et al. 2016), and the summer patch fungus *Magnaporthiopsis poae* damages turf grass (Luo & Zhang 2013). Recent studies have shown that certain members of this order exhibit endophytic life style by colonizing within various parts of host plants without causing any apparent harm (Klaubauf et al. 2014, Silva et al. 2019, Yuan et al. 2010). As the exploration and discovery of new *Magnaporthales* fungi continue, the importance of their precise identification becomes increasingly evident, fostering a more comprehensive understanding of taxonomy in this diverse group of fungi.

The initial studies of *Magnaporthales* began with investigations into the fungus causing rice stem rot disease (Cattaneo 1877, 1879, Cavara 1889) and rice blast disease (Cavara 1892, Saccardo 1880). Cannon (1994) proposed the first family, *Magnaporthaceae*, and later, Thongkantha et al. (2009) introduced the order *Magnaporthales* based on a phylogenetic analysis of the small and large subunits of rRNA (SSU and LSU, respectively). Klaubauf et al. (2014) defined three families within the order *Magnaporthales*: *Magnaporthaceae*, *Pyriculariaceae*, and *Ophioceraceae*. These families accommodate the *Gaeumannomyces/Magnaporthiopsis/Nakataea* generic complex, *Pyricularia* and its related genera, and *Ophioceras*, respectively. This classification was established through a morphological and multi-locus phylogenetic analysis of LSU, the internal transcribed spacer of rRNA (ITS), the largest subunit of RNA polymerase II (*RPB1*), actin (*ACT*) and calmodulin (*CAL*). In subsequent studies, Luo et al. (2015a) identified the nutritional and infection patterns of these families based on a phylogenetic analysis of representative species and genera of *Magnaporthales*. Zhang et al. (2016b) provided an update on recent advances in phylogenetic analyses of *Magnaporthales* and enumerated the 28 currently accepted genera across the three families. In a significant development, Hongsanan et al. (2017) introduced a new family, *Pseudohalonectriaceae* to accommodate *Pseudohalonectria*. Zhang et al. (2018) conducted a comprehensive phylogenomic analysis of representative species and genera of *Magnaporthales*, establishing a revised timeline for their evolution. Luo et al. (2019) introduced a new family *Ceratosphaeriaceae* within *Magnaporthales* to accommodate *Ceratosphaeria*, supported by a multi-locus phylogenetic analysis of LSU, the second largest subunit of RNA polymerase II (*RPB2*), and translation elongation factor 1-alpha (*TEF1*). More recently, Luo & Zhang (2022) delimited *Magnaporthales* into three families based on ITS, LSU, and *TEF1* loci: *Magnaporthaceae*, *Pyriculariaceae*, and *Ophioceraceae*. Wijayawardene et al. (2022) accept 5 families and 39 genera in *Magnaporthales* in the latest outline of Fungi and fungus-like organisms. However, there have been no systematic studies of endophytic *Magnaporthales* fungi on the order level.

Phylogenetic species recognition, which identifies species based on their evolutionary histories, is crucial for demarcating species with limited distinguishable morphological characters (Chethana et al. 2021c). The concatenation-based approach, which combines all gene alignments into a matrix, is frequently used for phylogenetic species recognition. However, it is subject to some degree of subjectivity when determining species limits (Taylor et al. 2000). The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) concept overcomes this drawback by demanding the concordance of genealogies from a minimum of three unlinked loci (Taylor et al. 2000). Species limits within fungal species can be determined by comparing the lineages resolved in each individual tree, with the point of transition from concordance to incongruity among branches clearly illustrated in each tree (Taylor et al. 2000). Split networks offer a comprehensive and interactive framework for estimating phylogenetic trees and networks (Chethana et al. 2021c).

The objective of this study is to analyze phylogenetic relationships of *Magnaporthales* with a large number of new endophytic *Magnaporthales* fungi in *Poaceae* plants using the GCPSR concept and concatenation-based approaches for multi-locus data and phylogenomic data.

Additionally, we aim to describe novel endophytic taxa associated with *Poaceae* plants in China to enhance our understanding of the biodiversity and ecological roles of these fungi.

MATERIALS AND METHODS

Isolation of strains and morphological observation

Fungal endophytes were isolated as described in a previous study (Feng et al. 2021). Briefly, healthy plant samples from *Poaceae* plants were collected from Yunnan, Zhejiang, and Inner Mongolia in China, representing tropical, subtropical, and mid-temperate zones, respectively, between 2015 to 2019. The roots and shoots were cut into approximately 5-cm long fragments and sequentially disinfected with 75% alcohol for three minutes and 1% (available chlorine) sodium hypochlorite for ten minutes. The disinfected fragments were then cut into approximately 0.5-cm pieces and placed on malt extract agar (MEA) media supplemented with 50 µg/mL ampicillin and streptomycin sulphate. Hyphal tips growing from the tissue pieces were transferred to new potato dextrose agar (PDA) plates to obtain fungal cultures. A total of 1821 endophytic fungal strains were isolated, including 220 strains belonging to *Magnaporthales*. The strains were stored in a 4 °C refrigerator and a –80 °C ultra-low-temperature refrigerator at the Ministry of Agriculture Key Laboratory of Molecular Biology of Crop Pathogens and Insects, Institute of Biotechnology, Zhejiang University, Hangzhou, China. Additionally, the holotype and ex-type living cultures were deposited in the China General Microbiological Culture Collection Center (CGMCC).

Morphological characteristics were observed on strains grown on MEA or synthetic low nutrient agar (SNA) medium in an incubator at 25 °C with alternating 12 h/12h light/dark cycle. Culture characteristics were observed on 9 cm Petri dishes with PDA and MEA at 25 °C. Microscopic observations were made by mounting specimens in lactic acid, and examined under a Nikon Eclipse 80i microscope (Nikon Corp.).

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from colonies grown on PDA for seven days, following the protocol described by Cubero et al. (1999). The following genomic loci were amplified using PCR and then sequenced: ITS, LSU, a partial fragment of *ACT*, minichromosome maintenance complex component 7 (*MCM7*), *RPB1*, and *TEF1*. The primers used for amplification and sequencing were: ITS1 and ITS4 (White et al. 1990), LR0R and LR5 (Rehner & Samuels 1995), ACT-512F (Carbone & Kohn 1999) and ACT-2Rd (Groenewald et al. 2013), *MCM7*-709 and *MCM7*-1348 (Schmitt et al. 2009), EF1-983F and EF1-2218R (Rehner & Buckley 2005), and *RPB1*-Ac and *RPB1*-Cr (Castlebury et al. 2004, Matheny et al. 2002). The amplification reactions were performed in a total volume of 20 µL containing 2 × Easy Flash PCR MasterMix (EASY-DO, China), 0.4 µM of each primer, and 0.4–0.8 µL (~0.2 µg) genomic DNA. PCR was conducted using a LifePro Thermal Cycler (Technology Co., Ltd. Hangzhou, China) and the resulting products were sequenced using an ABI 3730xl sequencer (Applied Biosystems, USA).

The generated DNA sequences for ITS, LSU, *ACT*, *MCM7*, *RPB1*, and *TEF1* were analyzed using sequence similarity search (BLAST) against NCBI GenBank database to identify their closest known relatives. Highly similar or identical sequences were retrieved from GenBank. The accession numbers for the sequences retrieved and generated in this study are listed in Supplementary Table 1.

Single locus and concatenated loci phylogenetic analysis

The objective of this phylogenetic analysis was to compare the tree topologies inferred from individual gene sequences as well as those obtained from combined gene sequences. The analysis was conducted in several steps. Sequence alignments were initially generated using MAFFT (Katoh & Standley 2013) and adjusted using MEGA version 7 (Kumar et al. 2016). Gap sites were removed using trimAl (Capella-Gutiérrez et al. 2009). The trimmed gene alignments were then concatenated using SequenceMatrix 1.7.8 (Vaidya et al. 2011). The best-fit partition model was

selected using ModelFinder (Kalyaanamoorthy et al. 2017) based on the Bayesian Information Criterion (BIC). Maximum likelihood (ML) phylogenies were inferred using IQ-TREE (Nguyen et al. 2015) with the edge-linked partition model, incorporating 5000 ultrafast bootstraps (Minh et al. 2013) and the Shimodaira-Hasegawa-like approximate likelihood-ratio test (Guindon et al. 2010). Bayesian inference (BI) phylogenies were inferred using MrBayes 3.2.6 (Ronquist et al. 2012) with the partition model, involving 2 parallel runs over 2,000,000 generations, with the initial 25% of data discarded as burn-in. Except alignments concatenated, other steps of the phylogenetic analysis were performed using the desktop platform PhyloSuite (Zhang et al. 2020).

Phylogenomic tree based on concatenation-based approaches

The aim of constructing the phylogenomic tree was to evaluate the relationships within *Magnaporthales* using concatenation-based IQ-TREE. The genomes were sequenced by Genedenovo Biotechnology Co., Ltd (Guangzhou, China) using the PacBio sequencing platform. Phylogenomic data matrices were constructed to infer species phylogenies using known genomic data (Luo et al. 2015a, Xu et al. 2015, Zhang et al. 2018) as well as new genomic data generated from this study. The accession numbers for the genomes retrieved and generated in this study are listed in Supplementary Table 1.

A total of 1672 single copy orthologous genes were obtained. The single copy orthologous genes were used to construct the phylogenomic tree in the several steps. Protein sequences were aligned using MUSCLE, and then the alignments were converted into nucleic acid sequences. Gap sites were removed with trimAl (Capella-Gutiérrez et al. 2009). The nucleic acid alignments were concatenated using the PhyloSuite platform (Zhang et al. 2020). ModelFinder was used to select the best-fit model for the ML phylogenies, conducted on the PhyloSuite platform (Zhang et al. 2020).

Genealogical concordance phylogenetic species recognition (GCPSR) analysis

The level of recombination among closely related species in *Magnaporthiopsis* and *Omnidemtus* was determined using single locus and concatenated sequence alignments following the GCPSR model (Taylor et al. 2000). A pairwise homoplasy index (Φ_w) test (PHI) was performed in SplitsTree6 (Huson & Bryant 2006). Additionally, a split graph was constructed using both the P Distance and Neighbor Net algorithms. A PHI index below 0.05 ($\Phi_w < 0.05$) was considered a criterion for determining recombination.

RESULTS

Phylogenetic and phylogenomic analysis of *Magnaporthales* unveils a novel family within the order

The study employs the GCPSR concept introduced by Taylor et al. (2000), which requires at least three non-contradicting, unlinked loci for reliable inference. Initially, individual locus trees were constructed based on four loci (LSU, *MCM7*, *RPB1*, and *TEF1*) at the order level of *Magnaporthales*, with the two *Diaporthales* fungi as an outgroup (*Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155) (Supplementary Figs 1–4). The phylogenetic trees inferred from LSU, *MCM7*, *RPB1*, and *TEF1* confirmed that *Magnaporthales* is a monophyletic group with statistical strong support, except for the *TEF1* phylogenetic tree, which exhibited weak ML bootstrap values (MLBS). Furthermore, *Magnaporthales* was subdivided into five or six main clades (labeled A–F), although some clades had low support, and main clades D and F could not be distinguished in the LSU phylogenetic tree. Concatenated phylogenetic trees using the four loci (LSU, *MCM7*, *RPB1*, and *TEF1*) and three loci (LSU, *MCM7* and *RPB1*) were constructed, using *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155 as outgroups. The topologies of these multi-locus phylogenetic trees (Figs 1–2) were well-resolved, showing that *Magnaporthales* is a strongly supported monophyletic group subdivided into six statistically supported main clades (A–F) in both trees. The support for main clade F in the three-locus tree (MLBS/BIPP = 78/0.999) was slightly lower than that in the four-locus tree albeit still

significant (MLBS/BIPP = 94/0.998). Notably, the separation of main clade D, which includes *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*, from main clade F, which comprises genera of *Magnaporthaceae* excluding *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*, was observed. Consequently, the genera *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera* were recognized as distinct from *Magnaporthaceae* and proposed as members of a new family named *Plagiosphaeraceae* within *Magnaporthales*.

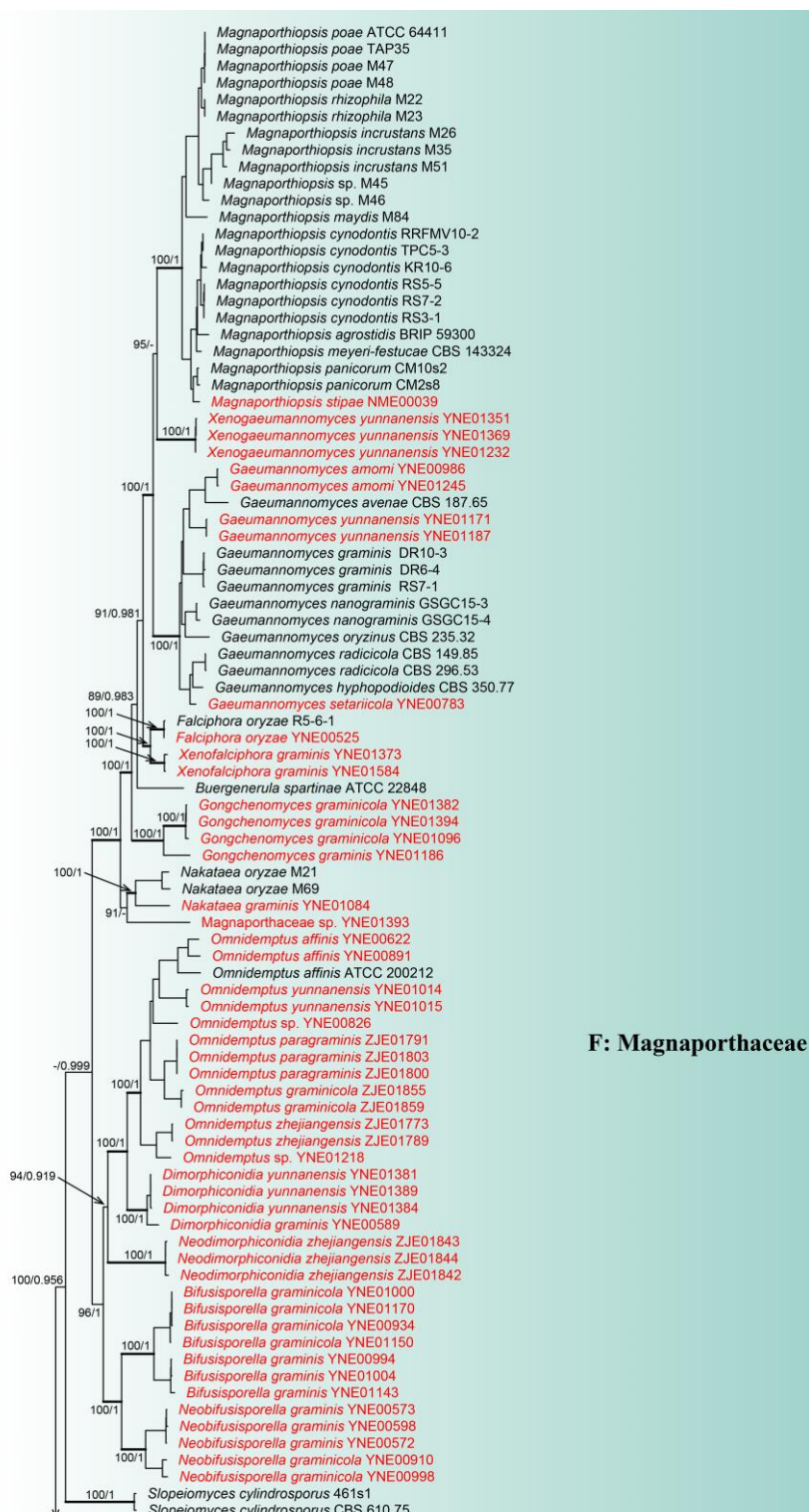


Figure 1 – Phylogenetic tree inferred from a maximum likelihood analysis using concatenated sequences of four unlinked loci (*LSU*, *MCM7*, *RPB1*, and *TEF1*) representing the order *Magnaporthales*. Nodes display corresponding ML bootstrap (MLBS) and Bayesian inference

posterior probabilities (BIPP) values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . Values for MLBS and BIPP are omitted at nodes of clades below the genus level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.

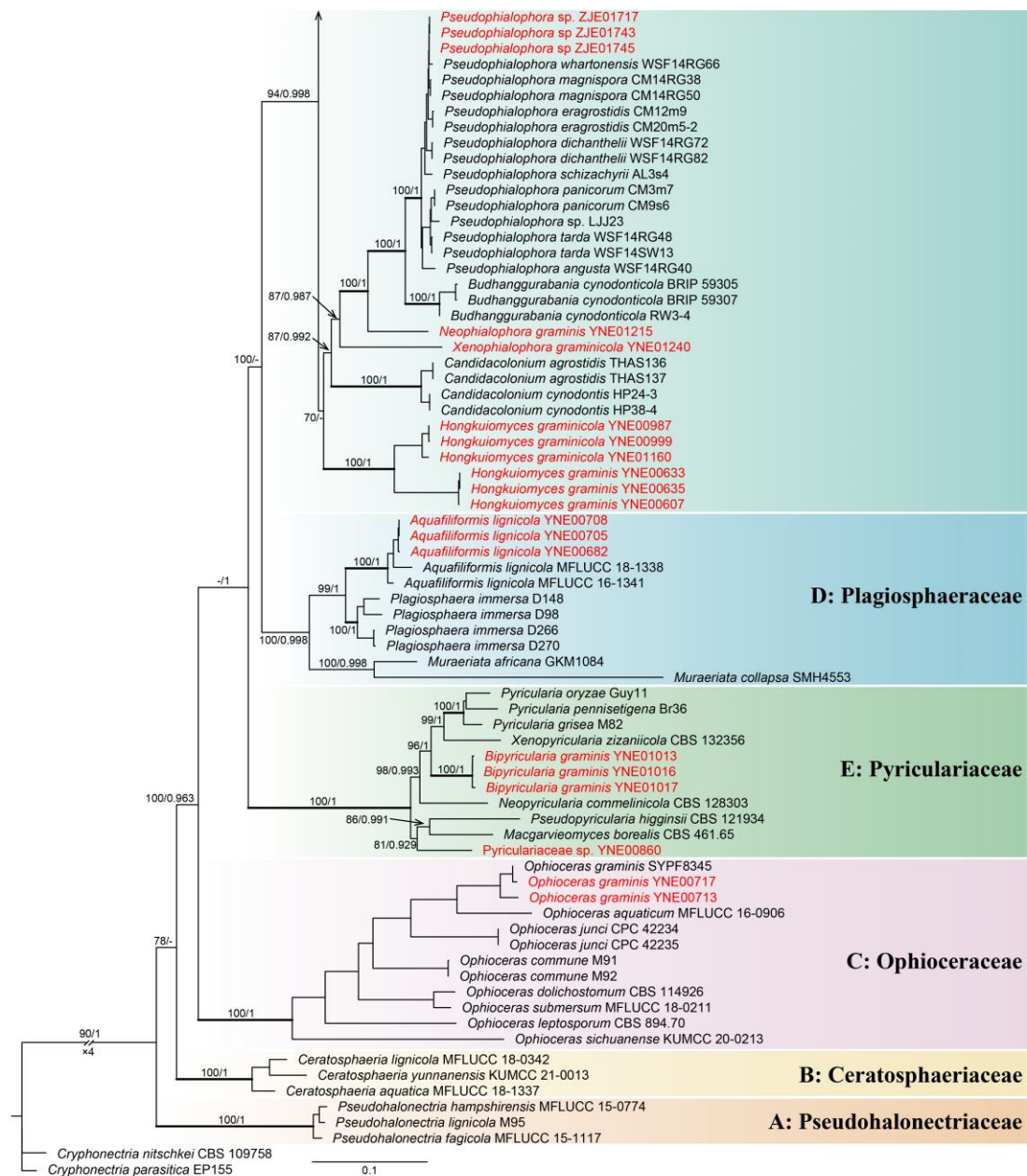


Figure 1 – Continued.

A phylogenomic analysis was conducted to determine the evolutionary history of the proposed new family *Plagiosphaeraceae* within *Magnaporthales*. A concatenation-based phylogenomic tree was constructed (Fig. 3). The analysis revealed that species within *Pyriculariaceae* (*Pyricularia grisea*, *Pyricularia oryzae*, and *Pyricularia pennisetigena*) and species within *Magnaporthaceae* (*Gaeumannomyces tritici*, *Magnaporthiopsis poae*, *Magnaporthiopsis rhizophila*, *Magnaporthiopsis incrustans*, *Falciphora oryzae*, and *Nakataea oryzae*) each form a monophyletic clade with high bootstrap values (MLBS = 100). The *Pyriculariaceae* clade was sister to the *Magnaporthaceae* clade, also with high bootstrap values (MLBS = 100). The genus *Aquafiliformis* was found to be sister to a group consisting of the genera of *Pyriculariaceae* and *Magnaporthaceae*, again with high bootstrap values (MLBS = 100). Thus, the phylogenomic analysis supports the proposed new families *Plagiosphaeraceae* within

Magnaporthales and indicates that, compared to *Pyriculariaceae*, *Plagiosphaeraceae* is not more closely related to *Magnaporthaceae*.

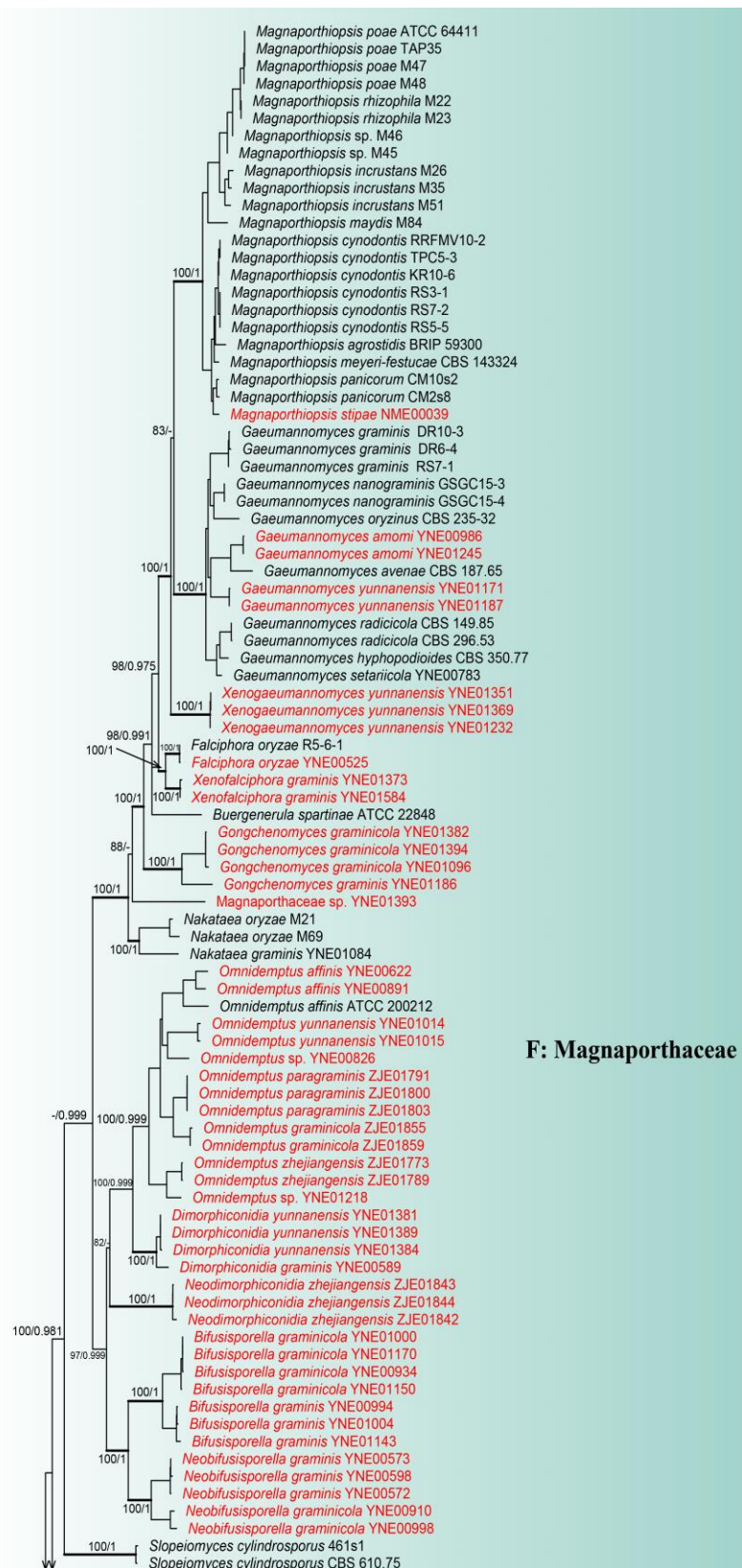


Figure 2 – Phylogenetic tree inferred from a maximum likelihood analysis using concatenated sequences of three unlinked loci (LSU, *MCM7*, and *RPB1*) representing the order *Magnaporthales*. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 .

Values for MLBS and BIPP are omitted at nodes of clades below the genus level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.

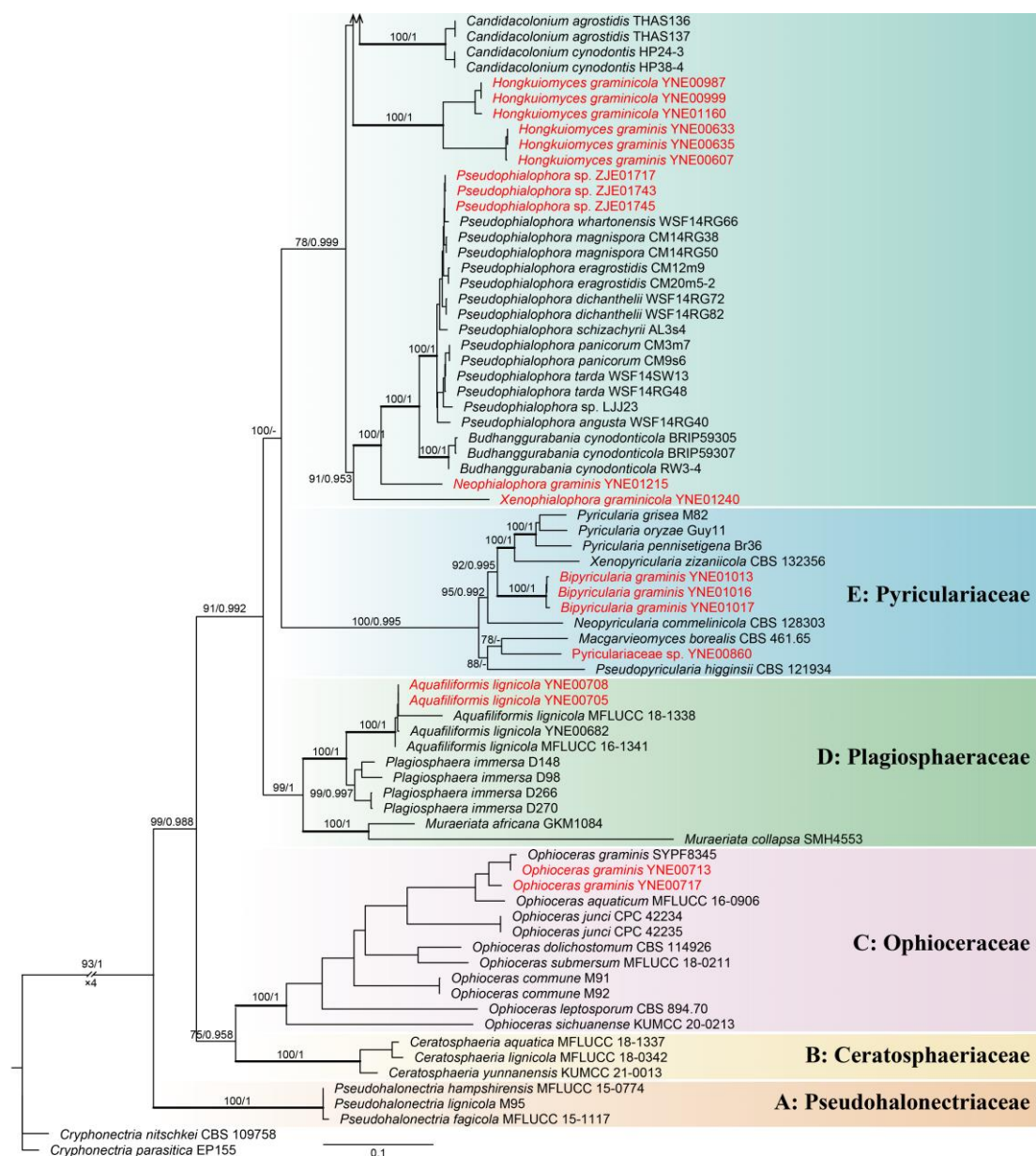


Figure 2 – Continued.

Phylogenetic analysis of *Ophiocercaceae*, *Pyriculariaceae*, and *Magnaporthaceae* reveals considerable taxonomic novelty

To improve the resolution of the clades within the families *Ophiocercaceae*, *Pyriculariaceae*, and *Magnaporthaceae*, additional individual locus trees (Supplementary Figs 5–10) were constructed at the family level using two additional loci: ITS and ACT. Subsequently, concatenations of six loci (ITS, LSU, ACT, MCM7, RPB1, and TEF1) were constructed. For the phylogenetic analyses, *Aquafiliformis lignicola* YNE00708 and *Plagiosphaera immersa* D98 were chosen as outgroups for *Ophiocercaceae*; *Magnaporthiopsis incrustans* M35 and *Magnaporthiopsis poae* ATCC64411 for *Pyriculariaceae*; and *Pyricularia oryzae* Guy11 and *Pyricularia pennisetigena* Br36 for *Magnaporthaceae*.

The phylogenetic trees inferred from ITS and ACT (Supplementary Figs 5–6) exhibited similar topologies for *Ophiocercaceae*. The six-locus phylogenetic tree for *Ophiocercaceae* (Fig. 4) consists of 13 previously described *Ophioceras* species, in addition to two isolates

(YNE00717, YNE00713) from this study and three closely related affinities (SYPF8345, clone 3183, clone FA14). Among these, YNE00713, YNE00717, SYPF8345, and clone 3183 formed a distinct lineage within *Ophioceras*, suggesting a new species named *Ophioceras graminis*. Based on both molecular phylogeny and morphological characteristics, this new species of *Ophioceras* is proposed, as detailed in the taxonomy section.

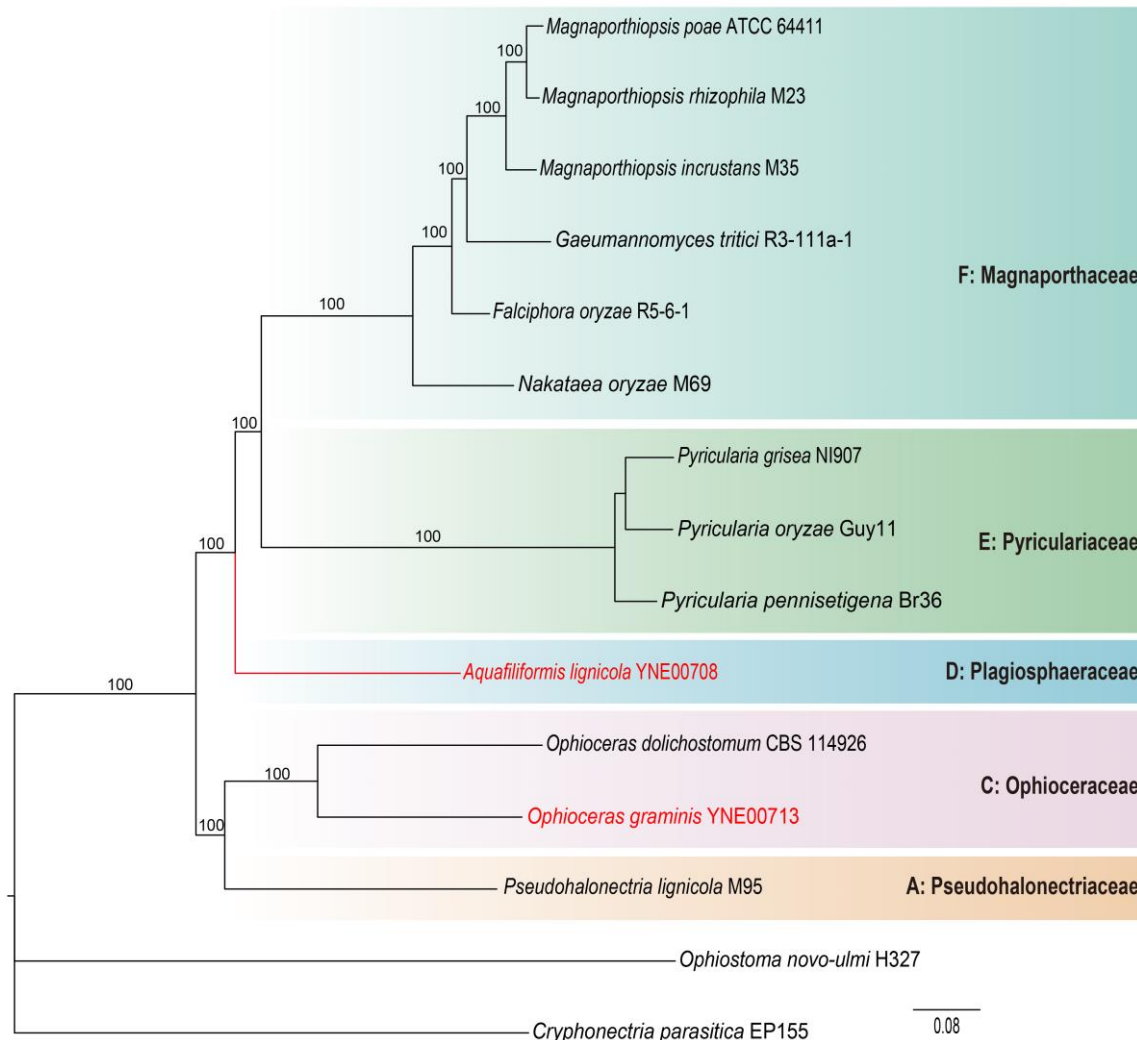


Figure 3 – Phylogenomic tree inferred from a maximum likelihood analysis using concatenated sequences of 1672 single copy orthologous genes representing the order *Magnaporthales*. Nodes display corresponding MLBS values. The tree is rooted with *Cryphonectria parasitica* EP155 and *Ophiostoma novo-ulmi* H327.

The phylogenetic trees inferred from ITS and ACT (Supplementary Figs 7–8) exhibited similar topologies for *Pyriculariaceae*. The six-locus phylogenetic tree for *Pyriculariaceae* (Fig. 5) consists of 37 species belonging to 11 genera: *Pyricularia*, *Xenopyricularia*, *Pyriculariomyces*, *Proxiopyricularia*, *Neopyricularia*, *Pseudopyricularia*, *Macgarvieomyces*, *Utrechtiana*, *Bambusicularia*, *Neocordana*, and *Barretomyces*. Four isolates (YNE00860, YNE01013, YNE01016, and YNE01017) from this study, and a closely related affinity (Otu0177) were included. Sixteen well-supported clades (E1-E16) were identified within *Pyriculariaceae*. YNE01013, YNE01016, YNE01017, and Otu0177 form a distinct clade E5 with high bootstrap support, representing a new genus and species. Additionally, YNE00860 represents a distinct clade E13 within *Pyriculariaceae*. Furthermore, *Xenopyricularia zizaniicola*, the type species of *Xenopyricularia*, represents a separate clade E3. ‘*Xenopyricularia junci*’, distinguished from

Xenopyricularia zizaniicola, forms an independent clade E6. To maintain the monophyletic concept of the genus *Xenopyricularia*, we propose transferring ‘*Xenopyricularia junci*’ to a new genus. Additionally, ‘*Pyricularia penniseti*’ and ‘*Pyricularia occidentalis*’ constitute clade E2, distinct from other taxa within *Pyricularia*. To meet the monophyletic generic concept of *Pyricularia*, ‘*Pyricularia penniseti*’ and ‘*Pyricularia occidentalis*’ are proposed to be moved out of *Pyricularia*. Based on molecular phylogeny and morphological characters, we propose two new genera, one new species, and one new combination within *Pyriculariaceae*, detailed in the taxonomy section.

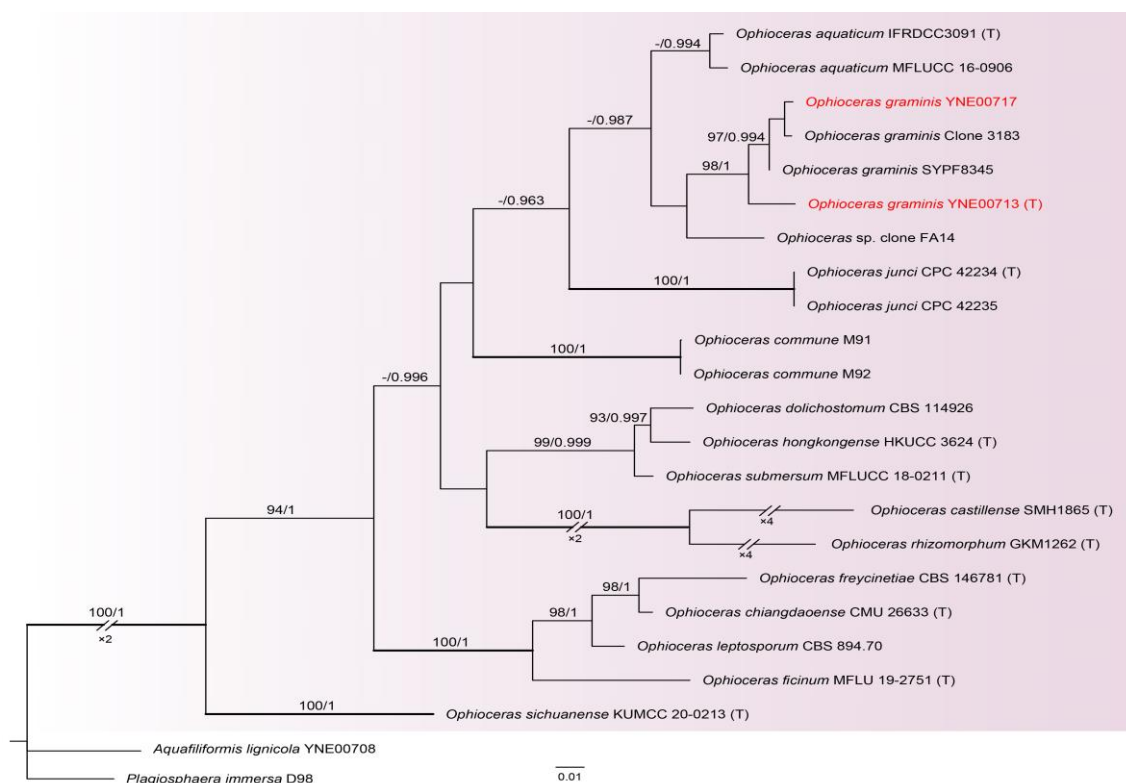


Figure 4 – Phylogenetic tree inferred from a maximum likelihood analysis using concatenated sequences of six loci (ITS, LSU, *ACT*, *MCM7*, *RPB1*, and *TEF1*) representing the family *Ophiocercaceae*. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Aquafiliformis lignicola* YNE00708 and *Plagiosphaera immersa* D98.

The phylogenetic trees inferred from ITS and *ACT* (Supplementary Figs 9–10) exhibited similar topologies for *Magnaporthaceae*. *Magnaporthaceae* was recognized as a strong supported monophyletic group, except for weak MLBS support in the *ACT* phylogenetic tree. While most clades corresponding to genera received robust support, the distinction between clades F13-F16 was not evident in the ITS tree. The six-locus phylogenetic tree for *Magnaporthaceae* (Fig. 6) consists of 55 previously described species from 18 known genera: *Atripes*, *Bifusisporiella*, *Budhanggurabania*, *Buergenerula*, *Bussabanomyces*, *Candidacolonium*, *Falciphoriella*, *Falciphora*, *Gaeumannomyces*, *Gaeumannomycella*, *Kohlmeyeriopsis*, *Magnaporthiopsis*, *Nakataea*, *Neogaeumannomyces*, *Omnidemtus*, *Pseudophialophora*, *Pyriculariopsis*, and *Slopeiomyces*. Most isolates from this study and several closely related affinities were included. Thirty-one well-supported clades (F1-F31) were identified within *Magnaporthaceae*. Based on molecular phylogeny and morphological characters, we propose 12 new genera, 23 new species, and one new combination within *Magnaporthaceae*, detailed in the taxonomy section. Furthermore, three isolates, YNE01393 from this study and CPC 26284 and CPC 26245 from Hernández-Restrepo et al. (2016), were found to represent distinct lineages within *Magnaporthaceae*. These isolates were assigned to specific, yet unnamed, generic lineages within *Magnaporthaceae*.

combinations. The previously invalid genus *Falciphora* and its type species, *Falciphora oryzae*, are also validated.

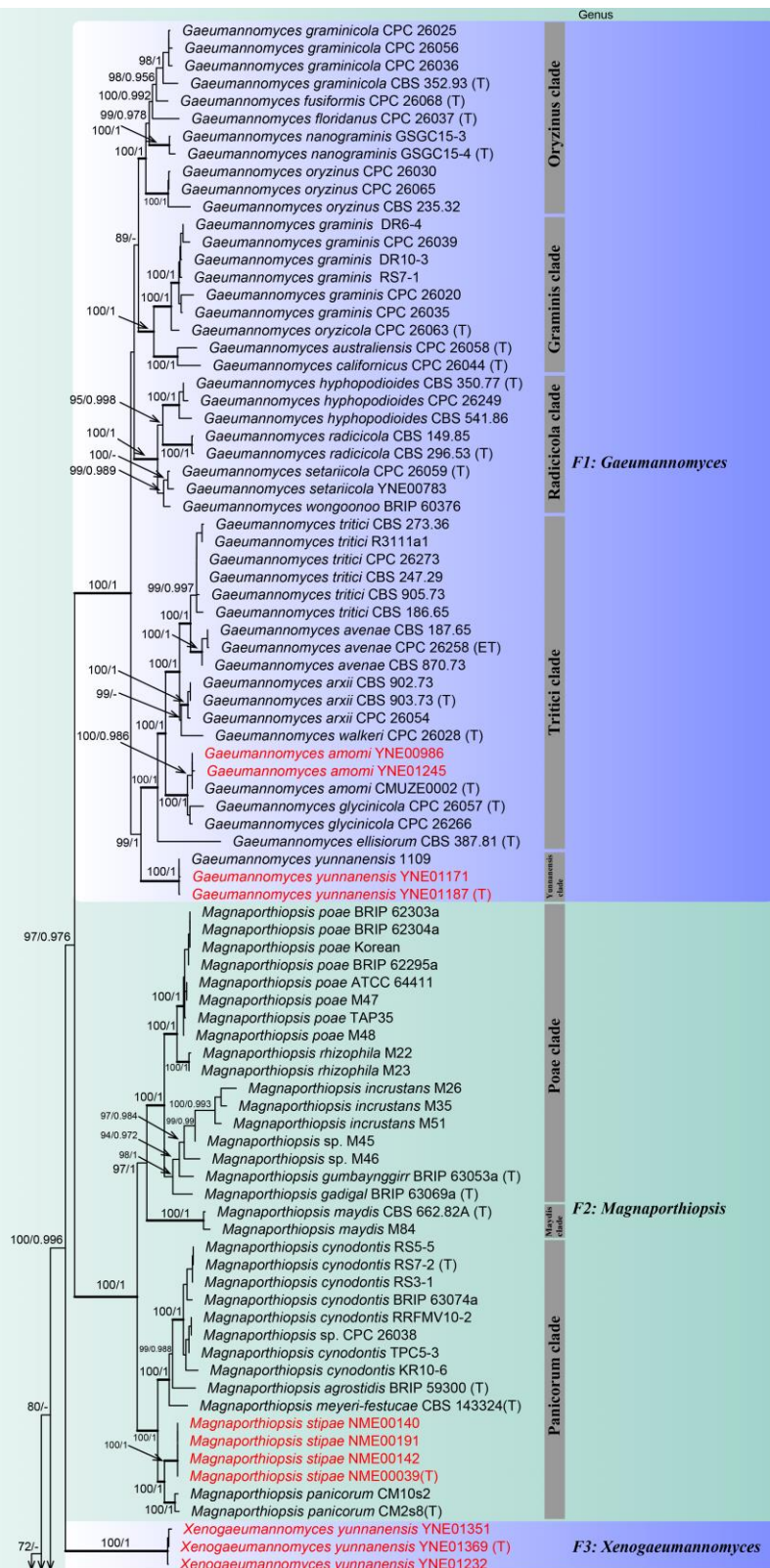


Figure 6 – Phylogenetic tree inferred from a maximum likelihood analysis using concatenated sequences of six loci (ITS, LSU, *ACT*, *MCM7*, *RBP1*, and *TEF1*) representing the family *Magnaporthaceae*. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Pyricularia oryzae* Guy11 and *Pyricularia pennisetigena* Br36.

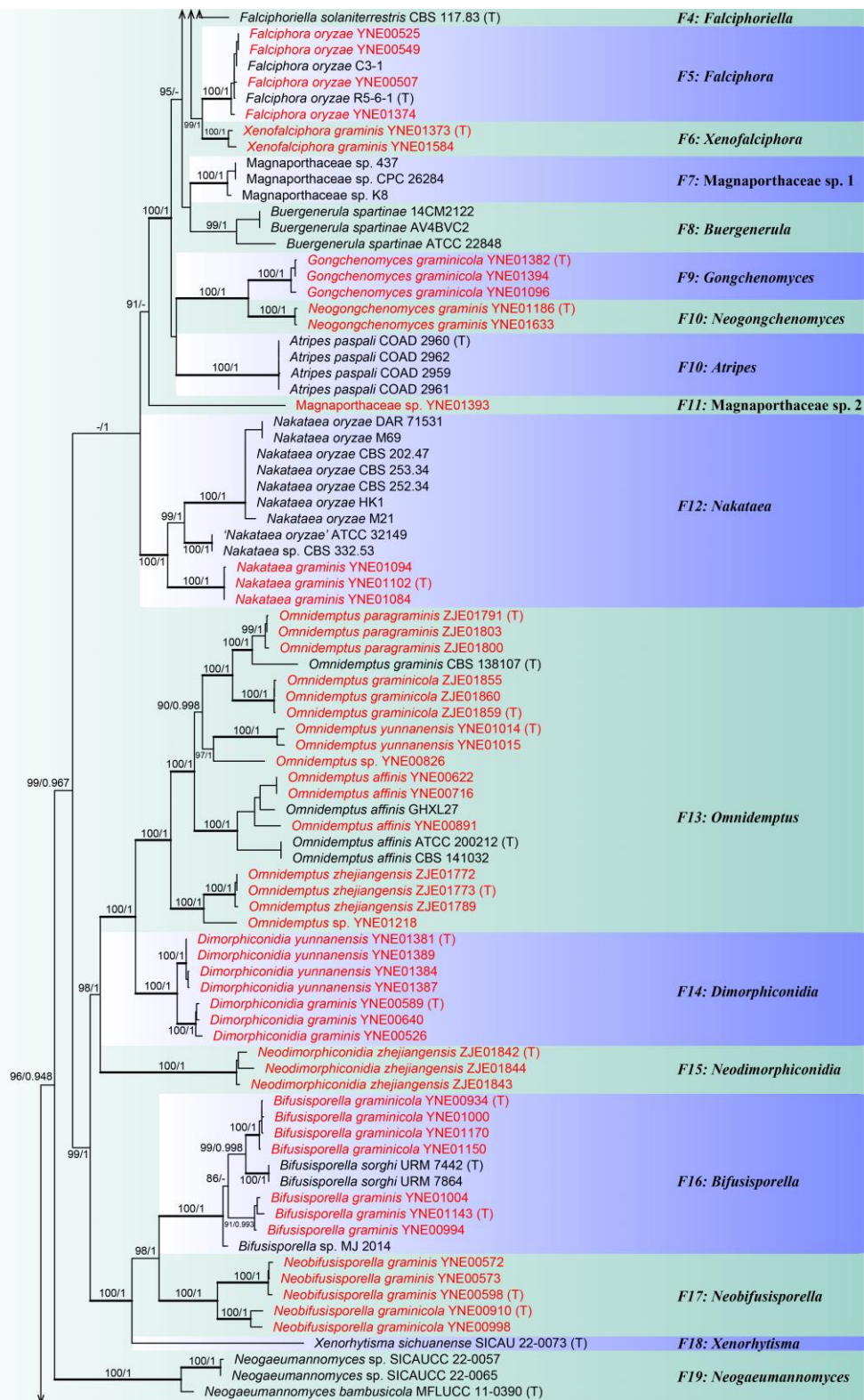


Figure 6 – Continued.

***Plagiosphaeraceae* C.L. Zhang, fam. nov.**

MycoBank number: MB849530; Facesoffungi number: FoF16911

Etymology – The name refers to the type genus *Plagiosphaera*.

Type genus – *Plagiosphaera* Petr., Annales Mycologici 39 (4–6): 289 (1941).

Saprobic on decaying wood or endophytes in plants. Sexual morph: Ascomata perithecial, immersed with neck, lageniform, subglobose to globose, dark brown to black. Peridium continuous, with pale brown to dark brown cells of textura angularis. Paraphyses hyaline, septate, unbranched.

Asci 8-spored, unitunicate, fusoid, cylindrical to clavate, hyaline. Ascospores aseptate to septate, guttulate, hyaline, smooth-walled, ranging in shape from substraight, slightly curved to sinuous, fusiform to filiform. Asexual morph: Mycelium septate, branched, smooth, and hyaline. Conidiophores and conidia not observed.

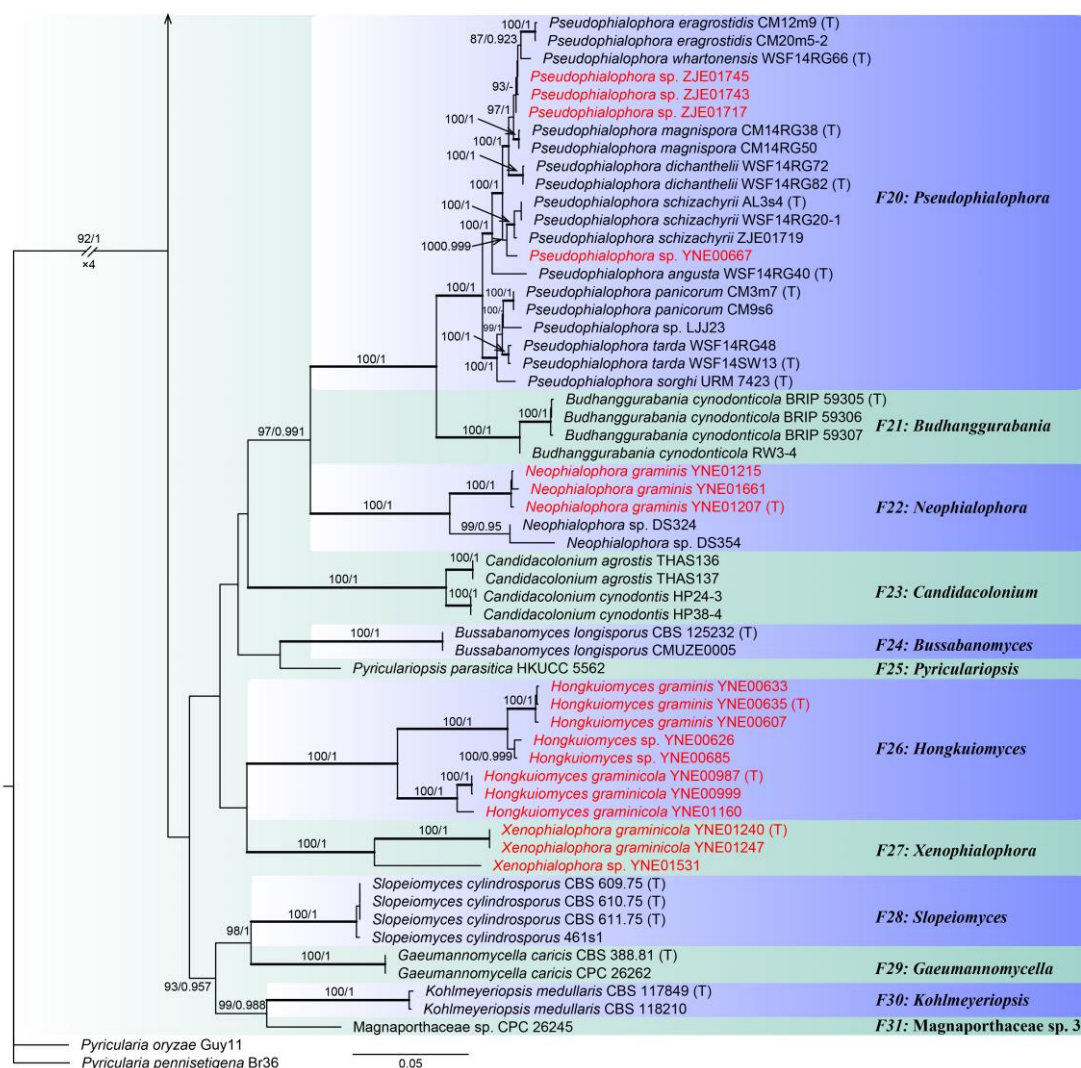


Figure 6 – Continued.

Notes – *Plagiosphaera*, *Muraeriata*, and *Aquafiliformis* are three genera in the family *Plagiosphaeraceae*. *Plagiosphaera* was first described by Petrak (1941) and later placed in the *Magnaporthaceae* family based on phylogenetic analyses conducted by Song et al. (2019). Huhndorf et al. (2008) introduced the genus *Muraeriata* for *Muraeriata africana* and *Muraeriata collapsa* within the *Magnaporthaceae*. Luo et al. (2019) introduced the genus *Aquafiliformis* for *Aquafiliformis lignicola*.

Three endophytic fungal isolates (YNE00682, YNE00705, and YNE00708) were collected from wild rice leaves (*Oryza meyeriana* subsp. *granulata*) in the Naban River Watershed National Nature Reserve, Xishuangbanna, Yunnan, China. Based on the sequence similarity search of NCBI's GenBank nucleotide database, isolate YNE00708 shares high similarities with several species: *Aquafiliformis lignicola* strain MFLUCC 16-1341 (97.68% in ITS [MK828615], 99.87% in LSU [MK835815]), *Sordariomycetes* sp. 6302 (97.51% in ITS [JN998105], 97.51% in LSU [MN727889]), *Plagiosphaera immersa* strain D270 (92.31% in ITS [MN727889], 97.51% in LSU [MN727889]), *Plagiosphaera immersa* strain D266 (92.16% in ITS [MN727888], 97.51% in LSU [MN727888]), *Plagiosphaera*

immersa strain D148 (89.27% in ITS [MN727887], 97.39% in LSU [MN727887]), *Plagiosphaera immersa* strain D98 (88.91% in ITS [MN727886], 97.39% in LSU [MN727886]).

Our phylogenetic analyses (Figs 1–2) strongly support the placement of isolates YNE00682, YNE00705 and YNE00708 in the main clade D of the order *Magnaporthales*, alongside species from *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*. Within this main clade, three well-supported clades were observed: the *Muraeriata* clade consists of *Muraeriata africana* strain GKM1084 and *Muraeriata collapsa* strain SMH4553; the *Plagiosphaera* clade includes *Plagiosphaera immersa* strains D148, D98, D266, and D270; and the *Aquafiliformis* clade comprises of *Aquafiliformis lignicola* strain MFLUCC 16-1341, MFLUCC 18-1338, YNE00682, YNE00708, and YNE00705. Our analysis indicates that YNE00682, YNE00705 and YNE00708 all belong to *Aquafiliformis lignicola*.

Ophioceraeae Klaubauf, M.-H. Lebrun & Crous, Studies in Mycology 79: 103 (2014)

The monotypic family *Ophioceraeae*, consisting solely of the genus *Ophioceras*, was introduced by Klaubauf et al. (2014).

Ophioceras Sacc., Sylloge Fungorum 2: 358 (1883)

Ophioceras is a genus of fungi primarily found on decaying woody substrates in freshwater habitats worldwide (Jiang et al. 2021). However, *Ophioceras freycinetiae* is an exception and is found on leaf spots of *Freycinetia banksii* (*Pandanaceae*) (Crous et al. 2021a). The genus is characterized by globose to elongated-globose ascomata, cylindrical asci, and septate, filiform, narrowly fusoid to cylindrical ascospores. Additionally, it exhibits elongated, curved, or straight phialides with well-developed apical collarette, as well as solitary, aseptate, subcylindrical to falcate conidia. These features have been described in several studies (Crous et al. 2021a, Jiang et al. 2021, Luo et al. 2019, Shearer et al. 1999).

Ophioceras graminis C. L. Zhang, sp. nov.

Fig. 7

Mycobank number: MB842500; Facesoffungi number: FoF16947

Etymology – Named after the grass host from which it was isolated.

Holotype – CGMCC3.20904

Endophytic in the leaves of *Oplismenus undulatifolius* (*Poaceae*). Sexual morph: Undetermined. Asexual morph: Conidiophores single or simple branched. Conidiogenous cells mono- or poly-phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, straight to curve, $6.5\text{--}14.0 \times 2\text{--}3.5 \mu\text{m}$ ($n = 18$). Conidia lunate, allantoid to fusiform, strong to slightly curved, hyaline, $5\text{--}8 \times 1\text{--}2 \mu\text{m}$ ($n = 50$). Hyphopodia elongated clavate, often terminal, first hyaline, late becoming brown, $7.5\text{--}12.5 \times 2.0\text{--}2.5 \mu\text{m}$ ($n = 17$).

Culture characteristics – Colonies growing on PDA reaching 19 mm in 10d at 25 °C, flat, aerial mycelium sparse, pale yellow, reverse brown, margin regular. Colonies growing on MEA reaching 45 mm in 20d at 25 °C, flat, aerial mycelium sparse, white to pale yellow, reverse brown, margin villiform.

Material examined – China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oplismenus undulatifolius*, October 2018, C.L. Zhang YNE00713 (Holotype CGMCC3.20904, stored in a metabolically inactive state), ex-type living culture YNE00713. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oplismenus undulatifolius*, October 2018, C.L. Zhang YNE00717.

GenBank numbers – YNE00713: ITS = MW479093; LSU = OQ891271; ACT = OQ918177; MCM7 = MW482634; RPB1 = MW482855; and TEF1 = MW482742. YNE00717: ITS = MW479094; ACT = OQ918178; MCM7 = MW482635; RPB1 = MW482856; and TEF1 = MW482743.

Notes – *Ophioceras graminis*, an endophytic species, was discovered in the leaves of *Oplismenus undulatifolius*, a gramineous plant in Xishuangbanna, Yunnan Province, China. It

belongs to the genus *Ophioceras* and is closely related to *Ophioceras aquaticus*. The species is characterized by smaller lunate to fusiform and aseptate conidia, as well as darker, globose to lageniform appressoria, in comparison to those of *Ophioceras freycinetiae* (Crous et al. 2021a). The asexual morph of *Ophioceras graminis* is distinct from other *Ophioceras* species that lack an asexual morph, including *Ophioceras aquaticus* (Crous et al. 2021a, Jiang et al. 2021, Luo et al. 2019, Shearer et al. 1999).

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00713, the closest hits include: *Magnaporthaceae* sp. strain SYPF 8345 (95.80% in ITS [MF536887], 99.88% in LSU [MF536885]), uncultured fungus clone OTU573 (90.97% in ITS [MF971531]), an uncultured clone 3183 (97.26% in ITS [MF571451]), *Ophioceras aquaticus* strain MFLUCC 16-0906 (90.99% in ITS [MK828611], 98.42% in LSU [MK835810]), and *Ophioceras aquaticum* IFRDCC 3091 (90.04% in ITS [JQ797440], 98.49% in LSU [NG_067778]).

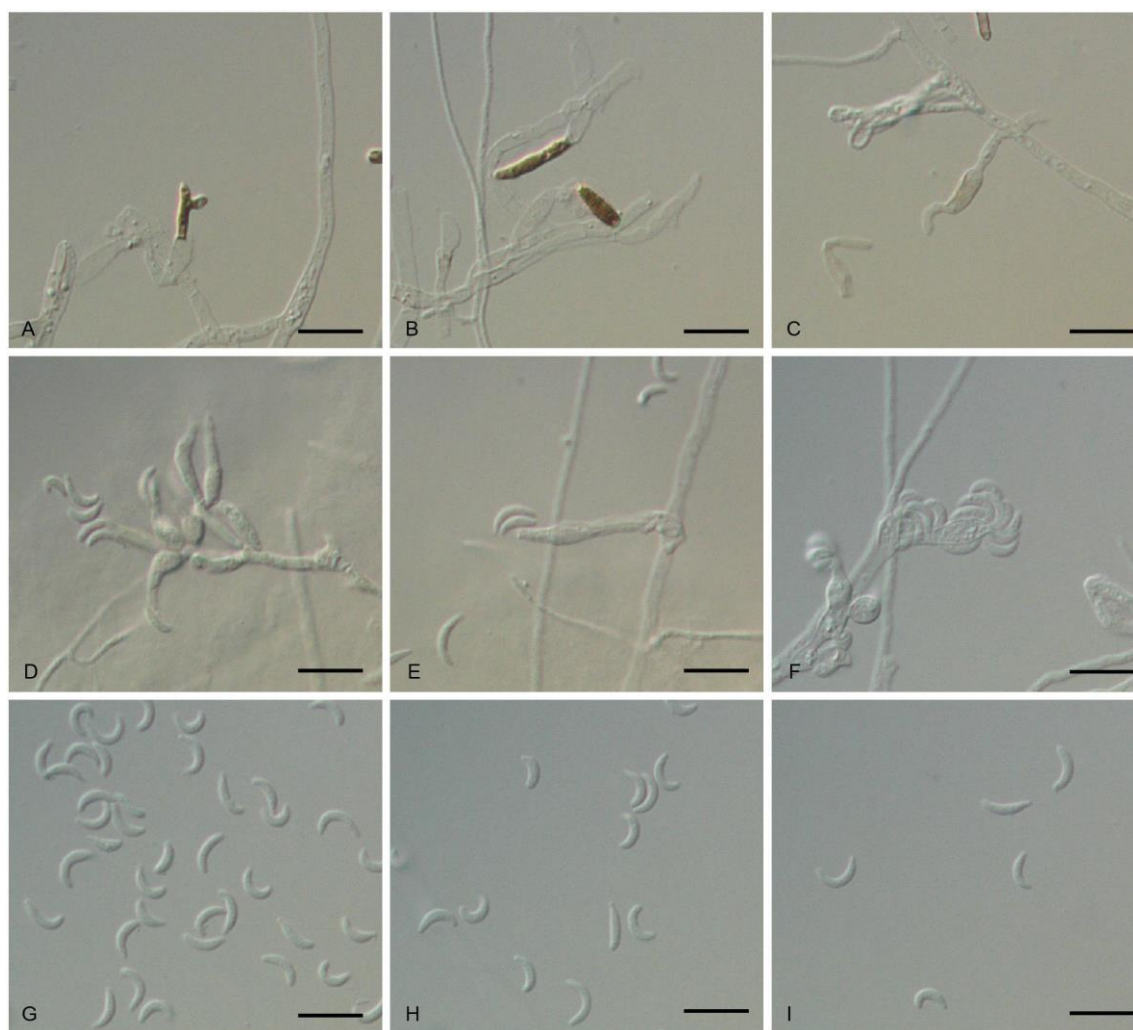


Figure 7 – *Ophioceras graminis* YNE00713. A–B Hyphopodia. C–F Phialides and conidia. G–I Conidia. Scale bars = 10 µm.

Pyriculariaceae Klaubauf, M.-H. Lebrun & Crous, *Studies in Mycology* 79: 104 (2014)

The family *Pyriculariaceae* was introduced by Klaubauf et al. (2014) based on the genus *Pyricularia*. It currently comprises 11 genera, namely *Bambusicularia*, *Barretomyces*, *Macgarvieomyces*, *Neocordana*, *Neopyricularia*, *Proxipyricularia*, *Pseudopyricularia*, *Pyricularia*, *Pyriculariomyces*, *Utrechtiana*, and *Xenopyricularia* (Hernandez Restrepo et al. 2015, Klaubauf et al. 2014, Marin-Felix et al. 2019).

Bipyricularia C.L. Zhang, gen. nov.

Mycobank number: MB842496; Facesoffungi number: FoF16912

Etymology – The name refers to its morphological similarity to *Pyricularia* with dimorphic conidia.

Endophytic in the stems of healthy *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Mycelium consisting of smooth, hyaline, branched, septate hyphae. Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, with a cylindrical collarette. Conidia dimorphic. Macroconidia solitary, pyriform to obclavate, narrowed toward tip, rounded at the base, 2-septate, subhyaline to pale brown, with a distinct protruding basal hilum and minute marginal frill. Microconidia aseptate, lunate, hyaline. Hyphopodia dome-shaped, brown.

Type species – *Bipyricularia graminis* C.L. Zhang

Bipyricularia graminis C.L. Zhang, sp. nov.

Fig. 8

Mycobank number: MB842497; Facesoffungi number: FoF16927

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20906

Endophytic in the stems of healthy *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: on MEA. Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, rare, $25 \times 9 \mu\text{m}$, with a cylindrical collarette. Conidia dimorphic. Microconidia aseptate, lunate, hyaline, $5\text{--}11.5 \times 1\text{--}1.5 \mu\text{m}$ ($n = 50$). Macroconidia solitary, pyriform to obclavate, narrowed toward the tip, rounded at the base, 2-septate, subhyaline to pale brown, with a distinct protruding basal hilum and minute marginal frill, rare, $18\text{--}23.5 \times 8.5\text{--}9.5 \mu\text{m}$. Hyphopodia dome-shaped, brown, rare, $12.5 \times 7.5 \mu\text{m}$.

Culture characteristics – Colonies on PDA reaching 39 mm diam after 7d at 25 °C, flat, aerial mycelium sparse, white to hyaline, regular circular, reverse white. Colonies growing on MEA reaching 71 mm in 14d at 25 °C, flat, aerial mycelium aparse, beige, reverse beige, margin regular.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01013 (Holotype CGMCC3.20906, stored in a metabolically inactive state), ex-type living culture YNE01013. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01016. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01017.

GenBank numbers – YNE01013: ITS = MW479090; LSU = MW478109; ACT = OQ918100; MCM7 = MW482632; RPB1 = MW482852; and TEF1 = MW482739. YNE01016: ITS = MW479091; LSU = MW478110; ACT = OQ918101; MCM7 = MW482633; RPB1 = MW482853; and TEF1 = MW482740. YNE01017: ITS = MW479092; LSU = OQ932795; ACT = OQ918102; MCM7 = MW482631; RPB1 = MW482851; TEF1 = MW482741.

Notes – Phylogenetically, this genus forms a distinct clade within *Pyriculariaceae* and is closely related to *Pyricularia*, *Xenopyricularia*, and *Pyriculariomyces*. Morphologically, it is distinguished from other genera by having two distinct types of conidia. The genus was discovered as an endophytic fungus in *Poaceae* plants in Xishuangbanna, Yunnan Province, China.

A sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01013 revealed the closest hits include '*Xenopyricularia junci*' strain CPC 40968 from dead culm of *Juncus effusus* (OK664720; Identities = 443/476(93%); gaps = 4/476(0%)), *Proxipyricularia zingiberis* CBS 133594 from *Zingiber mioga* (GenBank AB274434; Identities = 422/457(92%), gaps = 13/457(2%)), *Neopyricularia commelinicola* strain CBS 128303 from leaves of *Commelina communis* (GenBank KM484868; Identities = 425/467(91%), gaps = 9/467(1%)), and *Macgarvieomyces borealis* strain CBS 461.65 from leaf spots of *Juncus effusus* (GenBank MH858669; Identities = 418/457(91%), gaps = 10/457(2%)).

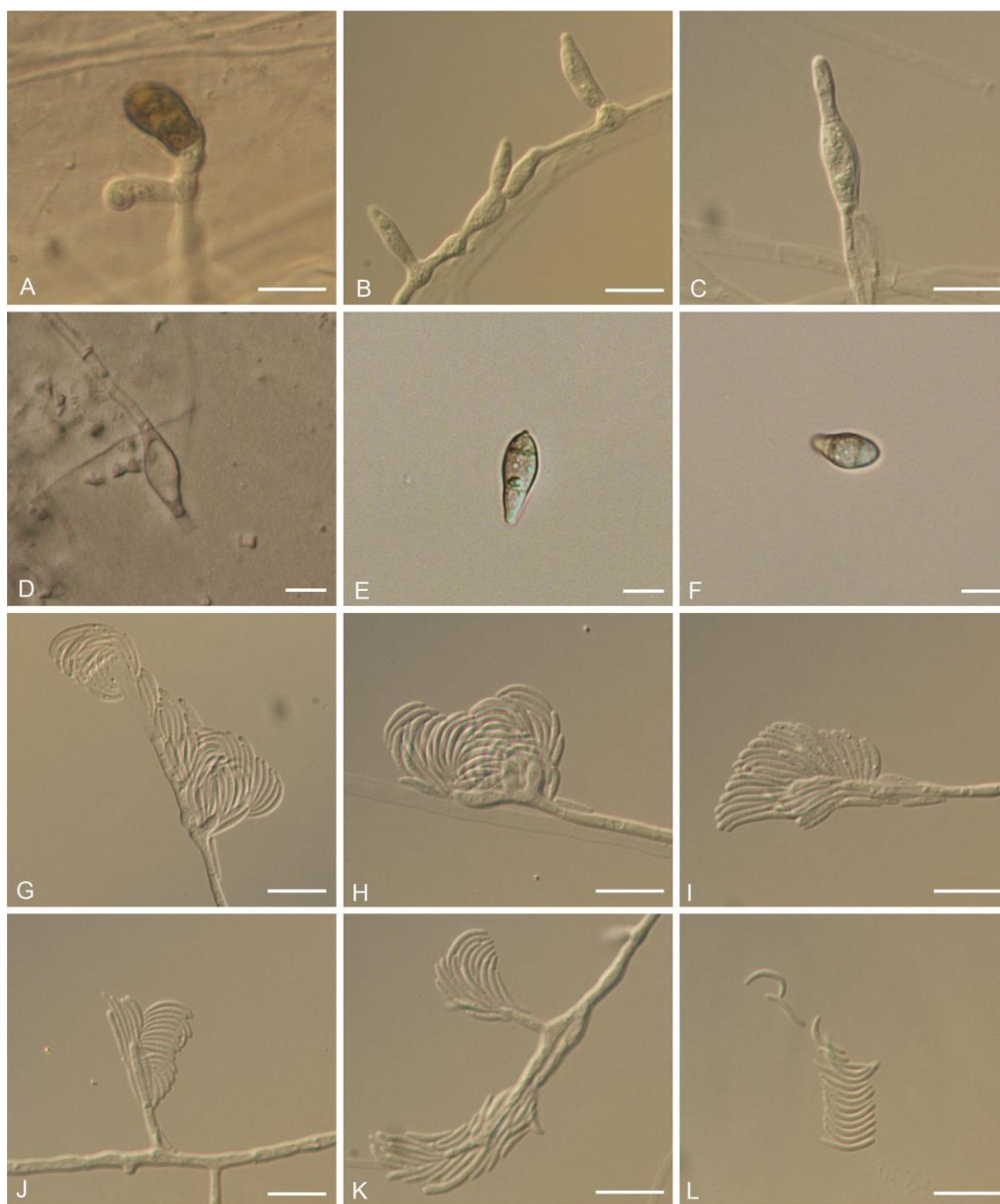


Figure 8 – *Bipyricularia graminis* (YNE01013). A Hyphopodia. B–D Large phialidic conidiogenous cells. E–F Macroconidia. G–K Small phialidic conidiogenous cells and microconidia. L Microconidia. Scale bars = 10 μ m.

Nothopyricularia C.L. Zhang, gen. nov.

MycoBank number: MB849528; Facesoffungi number: FoF16920

Etymology – The generic name refers to its pyriform to narrowly fusoid-ellipsoid shaped conidia and resemblance to the genus *Pyricularia*.

Saprobic on dead culm of *Juncus effusus* (*Juncaceae*). Conidiophores erect, flexuous, dark brown, thick-walled, base somewhat swollen, pale brown, unbranched. Conidiogenous cells integrated, terminal and intercalary, forming a rachis of pimple-like denticles, slightly darkened, pale brown, smooth-walled. Conidia in dry clusters, solitary, pale brown, guttulate, 2-septate, with the middle cell darker brown, pyriform to narrowly fusoid-ellipsoid, apex subobtuse, tapering toward truncate hilum, somewhat darkened. This description is based on Crous et al. (2021b).

Type species – *Nothopyricularia junci* (P.W. Crous & E.R. Osieck) C.L. Zhang.

Nothopyricularia junci (P.W. Crous & E.R. Osieck) C.L. Zhang, comb. nov.

Mycobank number: MB849529; Facesoffungi number: FoF16942

Holotype – CBS H-24847

≡ *Xenopyricularia junci* Crous & Osieck, Persoonia 47, 2021: 223.

Description and illustration – Crous et al. (2021b).

Notes – *Nothopyricularia junci* (synonym. *Xenopyricularia junci*) is the sole member of the monotypic genus *Nothopyricularia*. It is similar to *Bipyricularia* and *Pyricularia* in having denticulate conidiogenous cells and pyriform to narrowly fusoid-ellipsoid conidia (Klaubauf et al. 2014). However, *Nothopyricularia* is distinguished by its narrowly fusiform-ellipsoid conidia (Crous et al. 2021b).

Magnaporthaceae P.F. Cannon, Systema Ascomycetum 13: 26 (1994)

The family *Magnaporthaceae* was proposed by Cannon (1994), defined by Klaubauf et al. (2014), and later accepted by Zhang et al. (2016b), who recognized 12 genera within the family, including *Buergenerula*, *Bussabanomyces*, *Falciphora*, *Gaeumannomyces*, *Kohlmeyeriopsis*, *Magnaporthiopsis*, *Muraeriata*, *Nakataea*, *Omnidemptus*, *Pseudophialophora*, *Pyriculariopsis*, and *Slopeiomyces*. Subsequently, *Budhanggurabania* was introduced by Crous et al. (2015) and *Neogaeumannomyces* by Liu et al. (2015). Hernández-Restrepo et al. (2016) further expanded the family by introducing two new genera, *Falciphoriella* and *Gaeumannomycella*. Luo et al. (2019) introduced *Aquafiliformis*, while Silva et al. (2019) introduced *Bifusisporella*. Hyde et al. (2020) accepted 22 genera within *Magnaporthaceae*, including *Bifusisporella*, *Budhanggurabania*, *Buergenerula*, *Bussabanomyces*, *Ceratosphaerella*, *Clasterosporium*, *Clavatisporella*, *Falciphora*, *Falciphoriella*, *Gaeumannomycella*, *Gaeumannomyces*, *Herbampulla*, *Kohlmeyeriopsis*, *Magnaporthiopsis*, *Muraeriata*, *Mycoleptodiscus*, *Nakataea*, *Neogaeumannomyces*, *Omnidemptus*, *Pseudophialophora*, *Pyriculariopsis*, and *Slopeiomyces*. Additionally, *Plagiosphaera* was placed in *Magnaporthaceae* by Song et al. (2019), and *Atripes* was introduced by Custódio et al. (2021). However, Hernández-Restrepo et al. (2019) reevaluated *Mycoleptodiscus* species and placed them under the order *Muyocoprionales* (*Dothideomycetes*), while Jiang et al. (2021) reevaluated *Ophioceras* species, resulting in the synonymization of *Ceratosphaerella* into *Ophioceras*. In this study, we propose moving the genera *Plagiosphaera*, *Muraeriata*, and *Aquafiliformis* to the family *Plagiosphaeraceae*.

Gaeumannomyces Arx & D.L. Olivier, Transactions of the British Mycological Society 35 (1): 32 (1952)

The genus *Gaeumannomyces* was introduced by Arx & Olivier (1952). Initially, seven species were recognized within this genus by Zhang et al. (2016b). A re-evaluation by Hernández-Restrepo et al. (2016) expanded the genus to include 19 species, grouped into four groups: *Graminis*, *Orzinus*, *Radicicola*, and *Tritici*. Subsequently, *Gaeumannomyces nanograminis* was identified in the roots of diseased bermudagrass in the United States by Vines et al. (2021). Currently, the genus comprises 22 species: *G. amomi*, *G. arxii*, *G. australiensis*, *G. avenae*, *G. californicus*, *G. caricis*, *G. ellisiorum*, *G. floridanus*, *G. fusiformis*, *G. glycinicola*, *G. graminicola*, *G. graminis*, *G. hyphopodioides*, *G. licualae*, *G. nanograminis*, *G. oryzicola*, *G. oryzinus*, *G. radicola*, *G. setariicola*, *G. tritici*, *G. walkeri*, and *G. wongoonoo*.

In this study, four endophytes (YNE00986, YNE01245, YNE01171, and YNE01187) clustered with known *Gaeumannomyces* species, forming a distinct clade F1 within *Magnaporthaceae* with robust bootstrap values. Specifically, YNE01171, YNE01187, and a closely related affinity (1109) formed a well-supported distinct subclade. Consequently, a new species, *G. yunnanensis*, is proposed to accommodate them. Moreover, species of the genus *Gaeumannomyces* are now classified into five groups, with this new species representing the fifth group within the genus, in addition to the four groups previously defined by Hernández-Restrepo et

al. (2016): *Graminis*, *Orzinus*, *Radicicola*, and *Tritici*. Group *Tritici* includes *G. tritici*, *G. avenae*, *G. arxii*, *G. walkeri*, *G. amomi*, *G. glycinicola*, and *G. ellisiorum*. Group *Graminis* includes *G. graminis*, *G. californicus*, *G. australiensis*, and *G. oryzicola*. Group *Oryzinus* includes *G. oryzinus*, *G. floridanus*, *G. fusiformis*, *G. graminicola*, and *G. nanograminis*. Group *Radicicola* includes *G. radicola*, *G. wongoonoo*, *G. hyphopodioides*, and *G. setariicola*.

Gaeumannomyces yunnanensis C.L. Zhang, sp. nov.

Fig. 9

Mycobank number: MB842487; Facesoffungi number: FoF16931

Etymology – The specific epithet refers to its type location.

Holotype – CGMCC3.20898

Endophytic within the stems of healthy *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores reduced to conidiogenous cells. Conidiogenous cells phialidic, hyaline, solitary, terminal or intercalary, cylindrical, straight, $15.5\text{--}17.5 \times 2\text{--}3.5 \mu\text{m}$ ($n = 3$). Conidia aggregated in slimy heads, fusiform, tapering at the base, aseptate, hyaline, smooth, $4.5\text{--}7.5 \times 1\text{--}2 \mu\text{m}$ ($n = 11$). Hyphopodia hyaline when young, turning to very dark desaturated yellow, finally very dark grayish green when mature, lobed, $19\text{--}29.5 \times 11.5\text{--}18 \mu\text{m}$ ($n = 9$).

Culture characteristics – Colonies on PDA reaching 80 mm diam after 7d at 25 °C, flat, cottony, white, abundant aerial mycelium, dense, wheel-like ring in the middle and outward, reverse light gray to black. Colonies on MEA completely filled the 90 mm dish after 14d at 25 °C, cottony, grayish to pale green, abundant aerial mycelium, dense, rich villiform. Reverse dark khaki to black.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01187 (Holotype CGMCC3.20898, stored in a metabolically inactive state), ex-type living culture YNE01187. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01171.

GenBank numbers – YNE01187: ITS = MW478944, LSU = MW478100, ACT = OQ918174, MCM7 = MW482589, RPB1 = MW482768, TEF1 = MW482659. YNE01171: ITS = MW478943, LSU = MW478099, ACT = OQ918173, MCM7 = MW482588, RPB1 = MW482767, TEF1 = MW482658.

Notes – Phylogenetically, *G. yunnanensis* is closely related to *G. ellisiorum*, *G. glycinicola*, *G. amomi*, *G. arxii*, *G. walkeri*, *G. avenae*, and *G. tritici* within the *Tritici* group of *Gaeumannomyces*. Morphologically, *G. ellisiorum* can be differentiated by its clustered phialide and lunate conidia, *G. glycinicola* does not produce conidiophores and conidia, *G. amomi*, *G. tritici*, and *G. avenae* are characterized by sexual structures and the absence of asexual structures, *G. arxii* does not produce hyphopodia, while *G. walkeri* has lunate conidia (Hernández-Restrepo et al. 2016). This species shares similar ecological preferences with *G. amomi* as an endophyte, although the latter is typically found in *Amomum siamense* from the Zingiberaceae family (Bussaban et al. 2001).

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01187, the closest hits include *G. arxii* strain CBS 903.73 from *Pennisetum clandestinum* (GenBank KM484837; Identities = 461/470(98%), gaps = 3/470(0%)), *G. californicus* strain CPC 26044 from *Stenotaphrum secundatum* (GenBank KX306490; Identities = 459/468(98%), gaps = 2/468(0%)), and *G. fusiformis* strain CPC 26068 from *Oryza sativa* (GenBank KX306492; 459/469(98%), gaps = 2/469(0%)).

Magnaporthiopsis J. Luo & N. Zhang, Mycologia 105 (4): 1021 (2013)

The genus *Magnaporthiopsis* was established by Luo & Zhang (2013). This genus is characterized by its globose perithecia with a cylindrical neck, unitunicate asci that are clavate and have a refractive ring, and biseriate, fusiform to fusoid, septate ascospores. The fungus produces simple hyphopodia, and its single or branched conidiophores have phialidic conidiogenous cells. The subglobose to ovoid conidia are aseptate (Luo & Zhang 2013).

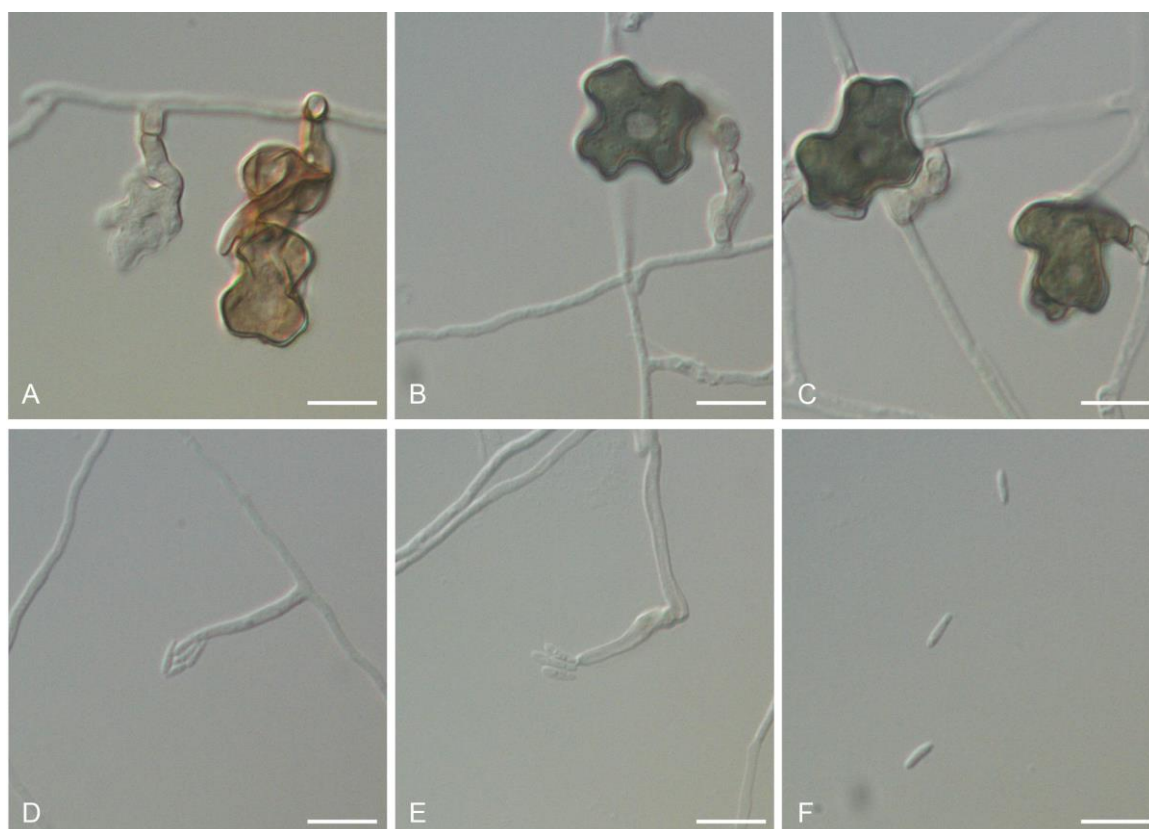


Figure 9 – *Gaeumannomyces yunnanensis* (YNE01187). A–C Hyphopodium. D–E Conidiogenous cells and conidia. F Conidia. Scale bars = 10 μ m.

In this study, four endophyte isolates, namely NME00039, NME00140, NME00191, and NME00142, were found to cluster with known *Magnaporthiopsis* species, forming a distinct clade F2 within *Magnaporthaceae* with robust bootstrap values. Furthermore, species of the genus *Magnaporthiopsis* were classified into three robustly supported groups. The first group consists of *M. poae*, *M. rhizophila*, *M. incrustans*, *M. gubaynggirr*, and *M. gadigal*. The second group comprises only *M. maydis*. The third group consists of the four endophytes from this study, along with *M. panicorum*, *M. meyeri-festuae*, *M. agrostidis*, and *M. cynodontis*. Specifically, NME00039, NME00140, NME00191, and NME00142 formed a robustly supported distinct subclade. Consequently, a new species, *M. stipae*, was proposed to accommodate them. The pairwise homoplasy index (PHI) test revealed that there is no significant recombination ($\Phi_w = 0.9394$) between *M. stipae* and the related taxa: *M. cynodontis* (RS7-2), *M. agrostidis* (BRIP 59300), *M. meyeri-festuae* (CBS 143324) and *M. panicorum* (CM2s8) (Fig. 10). Moreover, phylogenetic analysis revealed that *M. yugambeh* and *M. cynodontis* are conspecific, and thus *M. yugambeh* should be considered a synonym for *M. cynodontis*. Similarly, *M. dharug* and *M. poae* are also conspecific, and *M. dharug* should be regarded as a synonym for *M. poae*.

***Magnaporthiopsis stipae* C.L. Zhang, sp. nov.**

Fig. 11

Mycobank number: MB842488; Facesoffungi number: FoF16935

Etymology – The specific epithet refers to the host genus, *Stipa*, from which it was isolated.

Holotype – CGMCC3.20914

Endophytic within the roots of *Stipa sareptana* var. *krylovii*. Sexual morph: Undetermined. Asexual morph: Conidiophores simple, unbranched, pale brown. Conidiogenous cells phialidic, terminal or intercalary, straight or slightly curved, hyaline to pale brown, $3.5\text{--}8 \times 1.5\text{--}3.5 \mu\text{m}$ ($n = 11$). Conidia present in slimy aggregations, ovoid, pointed in heads, aseptate, hyaline, smooth, $2.5\text{--}4 \times 2\text{--}3 \mu\text{m}$ ($n = 50$).

Culture characteristics – Colonies on PDA reaching 46 mm after 7 d at 25 °C, cottony, with few to moderate aerial mycelium, white, margin rhizoid, reverse white to dark olive green. Colonies on MEA reaching 71 mm after 14d at 25 °C, flat, brownish-black, margin hyaline, reverse white to black.

Material examined – China. Inner Mongolia, Xilinhaote, isolated from the roots of *Stipa sareptana* var. *krylovii* (Poaceae), October 2018, C.L. Zhang NME00039 (Holotype CGMCC3.20914, stored in a metabolically inactive state), ex-type living culture NME00039. China. Inner Mongolia, Xilinhaote, isolated from the roots of *Stipa sareptana* var. *krylovii* (Poaceae), October 2018, C.L. Zhang NME00140.

GenBank numbers – NME00039: ITS = MW479037, LSU = MW478040, ACT = OQ918152, MCM7 = MW482567, RPB1 = OQ918195, TEF1 = MW482662. NME00140: ITS = MW479038.

Notes – Phylogenetically, the species is classified within the *Magnaporthiopsis* clade and forms a robust subclade with *M. panicorum*, *M. meyeri-festuae*, *M. agrostidis*, and *M. cynodontis*. Compared to other species within this subclade, *M. panicorum* has larger conidia (7.5–11.5×3.5–5µm) and is host-specific to *Panicum* (Luo et al. 2014); *M. meyeri-festuae* has more complex and branched conidiophores and is host-specific to *Festuca* (Luo et al. 2017); *M. agrostidis* has more complex branched conidiophores, lunate conidia, and is host-specific to *Agrostis*; while *M. cynodontis* has sparingly branched conidiophores and larger conidia (7–13×2–6.5 µm) and is host-specific to *Agrostis* (Vines et al. 2020). In contrast, this species is most closely related to *M. panicorum* due to their close genetic relationship and shared presence in the roots of Poaceae plants, although the former is an endophyte found in the roots of *Stipa krylovii*.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain NME00039, the closest hits include *M. panicorum* isolate CM2s8 (GenBank KF689643; Identities = 470/482(98%), gaps = 4/482(0%)), *M. cynodontis* isolate RS7-2 from ultradwarf bermudagrass roots (GenBank KJ855508; Identities = 459/481(95%), gaps = 3/481(0%)), and *M. agrostidis* BRIP 59300 from *Agrostis stolonifera* (GenBank KT364753; Identities = 458/479(96%), gaps = 5/479(1%)).

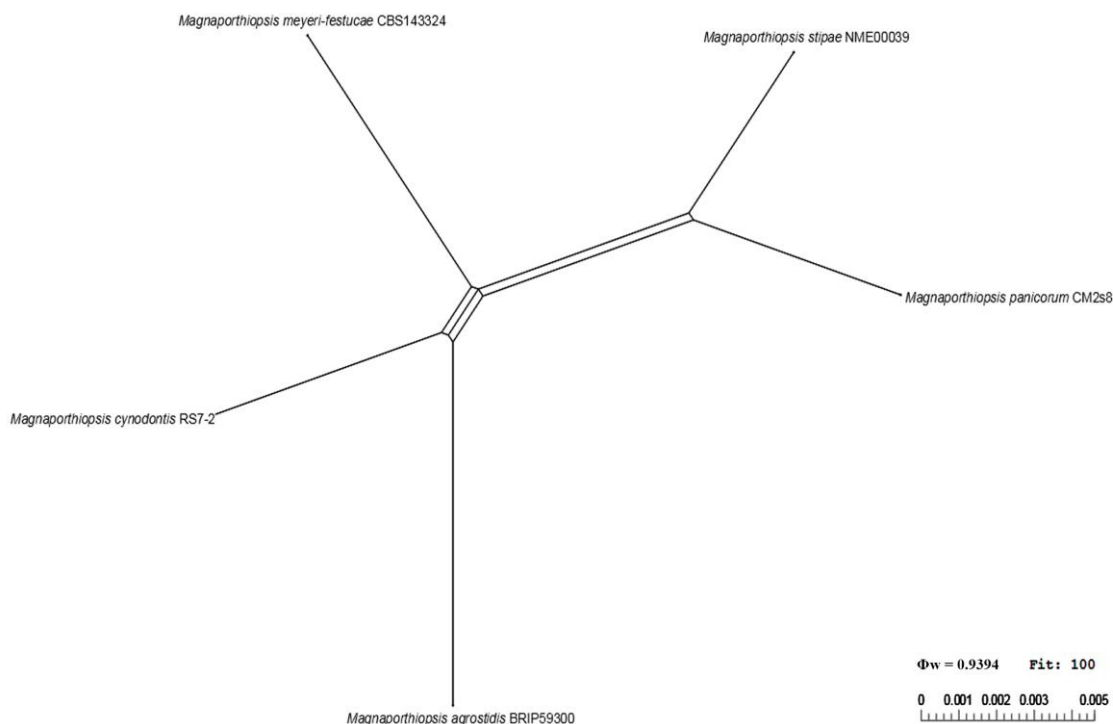


Figure 10 – A split network represents *Magnaporthiopsis stipae* and closely related species based on five loci (ITS, LSU, MCM7, RPB1, and TEF1). The P Distance and Neighbor Net algorithm were applied to infer the split network using SplitsTree CE 6.0.0. The pairwise homoplasy index (PHI) test results ($\Phi_w > 0.05$) indicate no statistically significant recombination within the dataset.



Figure 11 – *Magnaporthiopsis stipae* (NME00039). A–C Conidiogenous cells and conidia. D–F Conidia. Scale bars = 10 µm.

Magnaporthiopsis cynodontis P.L. Vines & Tom.-Pet., Mycologia 112(1): 60 (2020)

= *Magnaporthiopsis yugambah* P. Wong, Y.P. Tan, T.L. Weese & R.G. Shivas, Mycosphere 13(1): 608 (2022)

Notes – Phylogenetically, *M. yugambah* and *M. cynodontis* form a distinct subclade within the first group of *Magnaporthiopsis*. However, *M. yugambah* and *M. cynodontis* clustered as a monophyletic group in the concatenation-based phylogenetic tree, indicating that they are the same species.

Magnaporthiopsis poae (Landsch. & N. Jacks.) J. Luo & N. Zhang, Mycologia 105(4): 1024 (2013)

= *Magnaporthiopsis dharug* P. Wong, Y.P. Tan, T.L. Weese & R.G. Shivas, Mycosphere 13(1): 607 (2022)

Notes – Phylogenetically, *M. dharug* and *M. poae* form a distinct subclade within the third group of *Magnaporthiopsis*. However, *M. dharug* and *M. poae* clustered as a monophyletic group in the concatenation-based phylogenetic tree, indicating that they are the same species.

Xenogaeumannomyces C.L. Zhang, gen. nov.

Mycobank number: MB837630; Facesoffungi number: FoF16922

Etymology – The generic name refers to its morphological similarity to *Gaeumannomyces*.

Endophytic within the stems and roots of healthy Poaceae plants. Sexual morph: Ascomata perithecial, solitary or gregarious, immersed, globose, dark brown, with a cylindrical neck. Asci numerous, unitunicate, cylindrical to elongated clavate, short-stalked, with an apical refringent ring. Ascospores hyaline, vacuolated, slightly curved, rounded ends, septa indistinct. Asexual morph: Mycelium septate, branched, smooth, and hyaline. Conidiophores simple or branched. Conidiogenous cells phialidic, terminal or intercalary, hyaline, lageniform, with a collarette.

Macroconidia lunate, 3-septate. Microconidia aseptate, fusiform, hyaline. Hyphopodia if present, lobed, brown.

Type species – *Xenogaeumannomyces yunnanensis* C. L. Zhang.

Notes – Three endophytes from this study, named YNE01232, YNE01351, and YNE01369, constitute a distinct clade F3 within *Magnaporthaceae* with high bootstrap values. This observation has led to the introduction of a new genus and a new species, *Xenogaeumannomyces yunnanensis*.

Xenogaeumannomyces yunnanensis C.L. Zhang, sp. nov.

Fig. 12

Mycobank number: MB843760; Facesoffungi number: FoF16949

Etymology – The specific epithet refers to the type location.

Holotype – CGMCC3.20201

Endophytic within the stems and roots of healthy Poaceae plants. Sexual morph: Ascomata perithecial, with a long cylindrical neck, submerged, globose, brown, $220\text{--}253 \times 205\text{--}221\ \mu\text{m}$. Asci numerous, unitunicate, cylindrical to elongated clavate, short-stalked, with an apical refringent ring, 8- ascospores, $91\text{--}138 \times 5.3\text{--}15\ \mu\text{m}$. Ascospores hyaline, vacuolated, slightly curved or curved, ends rounded, $76\text{--}95 \times 2.9\text{--}4.4\ \mu\text{m}$, septated, septa indistinct. Asexual morph: Hyphae septate, branched, smooth, and hyaline. Conidiophores simple or branched. Conidiogenous cells phialidic, terminal or intercalary, hyaline, lageniform, $7.3\text{--}9.2 \times 3.2\text{--}3.6\ \mu\text{m}$, with a collarette. Conidia dimorphic. Macroconidia lunate, 3-septate, $19\text{--}30.5 \times 3\text{--}4\ \mu\text{m}$ ($n = 5$). Microconidia aseptate, fusiform, hyaline, $5.9\text{--}8.3 \times 1.7\text{--}2.6\ \mu\text{m}$ ($n = 50$). Hyphopodia lobed, brownish-black, $7\text{--}9.5 \times 7.5\text{--}11.5\ \mu\text{m}$.

Culture characteristics – Colony on PDA cover a 90 mm plate after 14 d at $25\ ^\circ\text{C}$, cottony, with moderate aerial mycelium, dark gray to gray, margin regular, reverse light gray to gray. Colony on MEA cover a 90 mm plate after 14 d at $25\ ^\circ\text{C}$, gray, flat, and reverse gray.

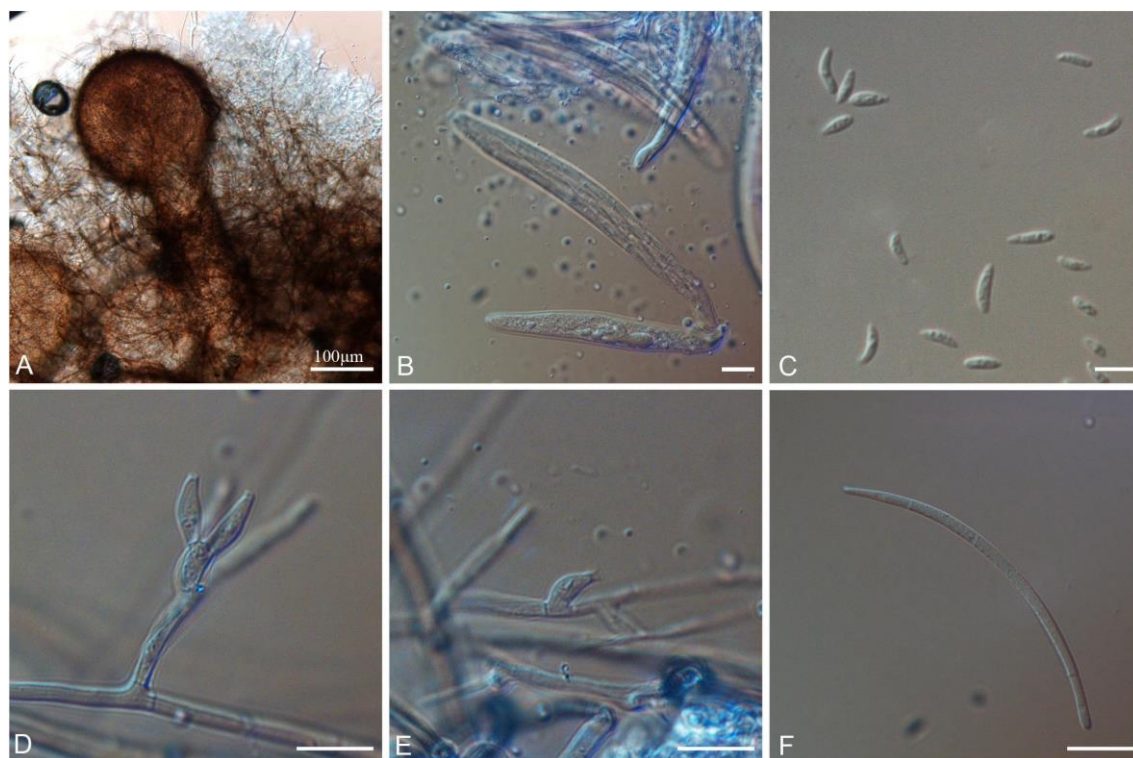


Figure 12 – *Xenogaeumannomyces yunnanensis* (YNE01369). A Perithecia. B Asci. C Conidia. D–E Conidiogenous cells. F Ascospore. Scale bars: A = 100 μm , B–F = 10 μm .

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Poaceae* plants, October 2018, C.L. Zhang YNE01369 (Holotype CGMCC3.20201, stored in a metabolically inactive state), ex-type living

culture YNE01369. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the roots of *Poaceae* plants, October 2018, C.L. Zhang YNE01232. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Poaceae* plants, October 2018, C.L. Zhang YNE01351.

GenBank numbers – YNE01369: ITS = MW055654, LSU = MW478081, ACT = OQ918167, MCM7 = MW056506, RPB1 = MW056509, TEF1 = MW056512. YNE01232: ITS = MW055634, LSU = MW478079, ACT = OQ918165, MCM7 = MW056504, RPB1 = MW056507, TEF1 = MW056510. YNE01351: ITS = MW055650, LSU = MW478080, ACT = OQ918166, MCM7 = MW056505, RPB1 = MW056508, TEF1 = MW056511.

Notes – *Xenogaeumannomyces yunnanensis* is an endophytic fungus that exclusively colonizes *Poaceae* plants found in Yunnan Province, China. Phylogenetically, *Xenogaeumannomyces* is closely related to *Gaeumannomyces* and *Magnaporthiopsis*. Morphologically, it can be distinguished by its fusiform conidia, which are different from the ellipsoidal to sickle-shaped conidia of *Gaeumannomyces* (Hernández-Restrepo et al. 2016) and the subglobose to ovoid conidia of *Magnaporthiopsis* (Luo & Zhang 2013).

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01369, the closest hits include *G. australiensis* CPC 26058 from *Triticum aestivum* (GenBank KX306480; Identities = 437/469 (93%), Gaps = 6/469(1%)), *Falciphoriella solaniterrestris* CBS 117.83 from potato field soil (GenBank KM484842; Identities = 436/471(93%), Gaps = 4/471(0%)), and *Falciphora oryzae* R5-6-1 (GenBank EU636699; Identities = 436/473(92%), gaps = 6/473(1%)).

Falciphora J. Luo & N. Zhang ex Z.L. Yuan, C.L. Zhang & F.C. Lin, gen. nov.

Mycobank number: MB854737; Facesoffungi number: FoF10235

Etymology – The generic name refers to its falcate conidia and its morphological similarity to the genus *Phialophora*.

≡ *Falciphora* J. Luo & N. Zhang, in Luo, Walsh & Zhang, *Mycologia* 170 (3): 643. 2015, nom. inval., Art. 40.1 (Shenzhen)

Endophytic within the roots of healthy *Poaceae* plants. Mycelium septate, branched, smooth, and hyaline. Conidiophores mostly branched. Conidiogenous cells phialidic, collarete, hyaline to brown. Conidia aggregated in slimy heads, sickle-shaped, strongly curved, aseptate, hyaline, smooth. This description is based on Yuan et al. (2010).

Type species – *Falciphora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin ex Z.L. Yuan, C.L. Zhang & F.C. Lin

Notes – The genus *Falciphora* J. Luo & N. Zhang is a nom. inval., Art. 40.1 (Shenzhen), because the type species, *Falciphora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin ex J. Luo & N. Zhang, is invalid (Art. 40.7 (Melbourne); for details see below). Therefore, validation of the genus *Falciphora* is necessary following the validation of its type species, *Falciphora oryzae*, which is done below.

Falciphora oryzae Z.L. Yuan, C.L. Zhang & F.C. Lin ex Z.L. Yuan, C.L. Zhang & F.C. Lin, sp. nov.

Mycobank number: MB854738; Facesoffungi number: FoF16930

Holotype – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the root of wild rice (*Oryza meyeriana* subsp. *granulata*), 27/09/2007, Z.L. Yuan R5-6-1 (CGMCC2737, holotype, stored in a metabolically inactive state), ex-type living culture R5-6-1.

≡ *Harpophora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin, in Yuan, Lin, Zhang & Kubicek, *FEMS Microbiol. Lett.* 307(1): 96. 2010, nom. inval., Art. 40.7 (Melbourne).

≡ *Falciphora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin ex J. Luo & N. Zhang, in Luo, Walsh & Zhang, *Mycologia* 107(3): 644. 2015, nom. inval., Art. 40.7 (Melbourne).

For effectively published description see Yuan et al. (2010: 96–97).

Notes – The first description of the species, *Harpophora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin, is a nom. inval., Art. 40.7 (Melbourne) because for the holotype two repositories (CBS and CGMCC) were cited. The subsequent transfer to the new genus *Falciphora* in Luo et al. (2015c) is invalid as well, as the invalid *Harpophora oryzae* was cited as basionym; therefore, their taxon is formally no new combination but has to be cited as *Falciphora oryzae* Z.L. Yuan, C.L. Zhang & F.C. Lin ex J. Luo & N. Zhang, nom. inval., Art. 40.7 (Melbourne). To validate the species, the lyophilized culture CGMCC2737 is here designated as holotype according the International Code of Nomenclature for algae, fungi, and plants (ICNafp), with reference to the effectively published description in Yuan et al. (2010: 96–97).

Xenofalciphora C.L. Zhang, gen. nov.

Mycobank number: MB849542; Facesoffungi number: FoF16921

Etymology – Named after its morphological similarity to *Falciphora*.

Endophytic within the roots of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores simple branched, hyaline. Conidiogenous cells phialidic, terminal or intercalary, hyaline to light brown, cylindrical to lageniform, with a collarette. Conidia lunate, strong to slightly curved, and some curly, hyaline.

Type species – *Xenofalciphora graminis* C. L. Zhang

Notes – Two endophytes from this study, namely YNE01373 and YNE01584, represent a distinct clade F6 within *Magnaporthaceae* with high bootstrap values, resulting in the introduction of a new genus and a new species (*Xenofalciphora graminis*) to accommodate them. The *Xenofalciphora* lineage was found to be sister to *Falciphora*.

Xenofalciphora graminis C.L. Zhang, sp. nov.

Fig. 13

Mycobank number: MB849543; Facesoffungi number: FoF16948

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20910

Endophytic within the roots of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores simple branched, hyaline. Conidiogenous cells phialidic, terminal or intercalary, hyaline to light brown, cylindrical to lageniform, 10.5–12 × 2–3.5 µm (n = 19), with a collarette. Conidia lunate, strong to slightly curved, and some curly, hyaline, 6–10 × 1.5–2.5 µm (n = 30).

Culture characteristics – Colonies on PDA reaching 33 mm diameter after 7 d at 25 °C, cottony, with few to moderate aerial mycelium, white to pale grayish-white, margin rhizoid, reverse gray to black. Colonies on MEA cover a 90 mm plate after 14 d at 25 °C, cottony, with abundant aerial mycelium, white to smoke gray, reverse gray to black.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the root of *Poaceae* plants, October 2018, C.L. Zhang YNE01373 (Holotype CGMCC3.20910, stored in a metabolically inactive state), ex-type living culture YNE01373. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the root of *Oryza meyeriana* subsp. *granulata* (Poaceae), October 2018, C.L. Zhang YNE01584.

GenBank numbers – YNE01373: ITS = MW478916, LSU = MW478082, *ACT* = OQ918157, *MCM7* = MW482568, *RPB1* = MW482748, *TEF1* = MW482669. YNE01584: ITS = MW478917, LSU = OQ891276, *ACT* = OQ918158, *MCM7* = OQ918179, *RPB1* = OQ918189, *TEF1* = OQ918197.

Notes – Phylogenetically, this species forms a distinct clade within *Magnaporthaceae* and is closely related to *Falciphora oryzae*. Morphologically, this species can be differentiated from *Falciphora oryzae* by its complex, branched conidiophores and relatively smaller conidia measuring 7.5–9 × 0.8–1.2 µm (Yuan et al. 2010).

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01373, the closest hits include *Falciphora oryzae* strain R5-6-1

(GenBank EU636699; Identities = 462/473(98%), gaps = 3/473(0%)), *Falciphoriella solaniterrestris* CBS 117.83 from potato field soil (GenBank KM484842; Identities = 457/471(97%), gaps = 1/471(0%)), *Buergenerula spartinae* strain ATCC 22848 (GenBank JX134666; Identities = 447/473(95%), gaps = 6/473(1%)).

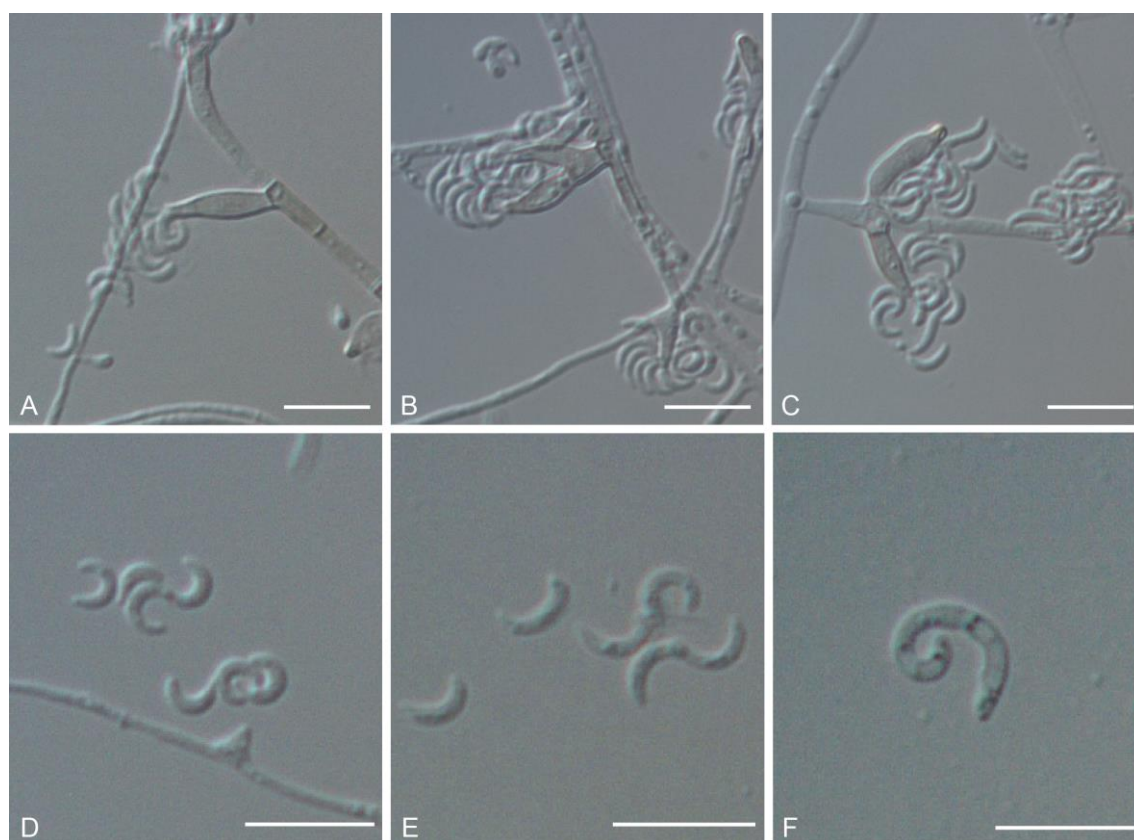


Figure 13 – *Xenofalciphora graminis* (YNE01373). A–C Conidiophores, conidiogenous cells and conidia. D–F Conidia. Scale bar = 10 µm.

Gongchenomyces C. L. Zhang, gen. nov.

Mycobank number: MB849539; Facesoffungi number: FoF16914

Etymology – Named after Prof. Gongchen Wang in recognition of her significant contribution to the fields of mycology and plant pathology in China.

Endophytic in *Poaceae* plants. Mycelium septate, branched, smooth, and hyaline. Conidiophores and Conidia not observed. Hyphopodia lobed, hyaline, becoming brown when mature.

Type species – *Gongchenomyces graminicola* C. L. Zhang

Notes – Five endophytes from this study, namely YNE01096, YNE01382, YNE01394, YNE01186 and YNE01633, form two distinct clades, F9 and F10, within *Magnaporthaceae* with high bootstrap values, constituting a robust lineage. In the *ACT* phylogenetic tree (Supplementary Fig. 10), these two clades were separated, leading to the introduction of two new genera: *Gongchenomyces* and *Neogongchenomyces*. The clade F9 containing YNE01096, YNE01382, and YNE01394 is proposed as *Gongchenomyces graminicola*, while the clade F10 containing YNE01186, and YNE01633 is suggested as *Neogongchenomyces graminis*.

Gongchenomyces graminicola C. L. Zhang, sp. nov.

Mycobank number: MB849540; Facesoffungi number: FoF16932

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.24894

Fig. 14

Endophytic within the stem of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Hyphopodia lobed, hyaline, becoming brown when mature, $13\text{--}21 \times 14.5\text{--}18\ \mu\text{m}$ ($n = 17$).

Culture characteristics – Colonies on PDA reaching 67 mm after 7d at 25 °C, cottony, aerial mycelium abundant, grayish-white, margin rhizoid-like, reverse gray. Colonies on MEA cover a 90 mm plate after 14 d at 25 °C, aerial mycelium abundant, cottony, surface floccus, pale grayish-green, center pale brownish-green, reverse color light gray to gray.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01382 (Holotype CGMCC3.24894, stored in a metabolically inactive state), ex-type living culture YNE01382. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01096. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01394.

GenBank numbers – YNE01382: ITS = MW478994, LSU = ON244714, ACT = OQ918160, MCM7 = MW482594, RPB1 = MW482780, TEF1 = ON367453. YNE01096: ITS = MW478990, LSU = MW478083, ACT = OQ918159, MCM7 = MW482592, RPB1 = OQ942243, TEF1 = MW482665. YNE01394: ITS = MW478989, LSU = MW478085, ACT = OQ918161, MCM7 = MW482593, RPB1 = MW482777, TEF1 = MW482667.

Notes – Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01382, the closest hits include Fungal endophyte isolate GHXL27 from leaves of patchouli (GenBank KY022825; Identities = 400/446(90%), gaps = 15/446(3%)), *Buergenerula spartinae* isolate 14CM2122 from *Spartina maritima* (GenBank KX263857; Identities = 352/377(93%), gaps = 6/377(1%)).

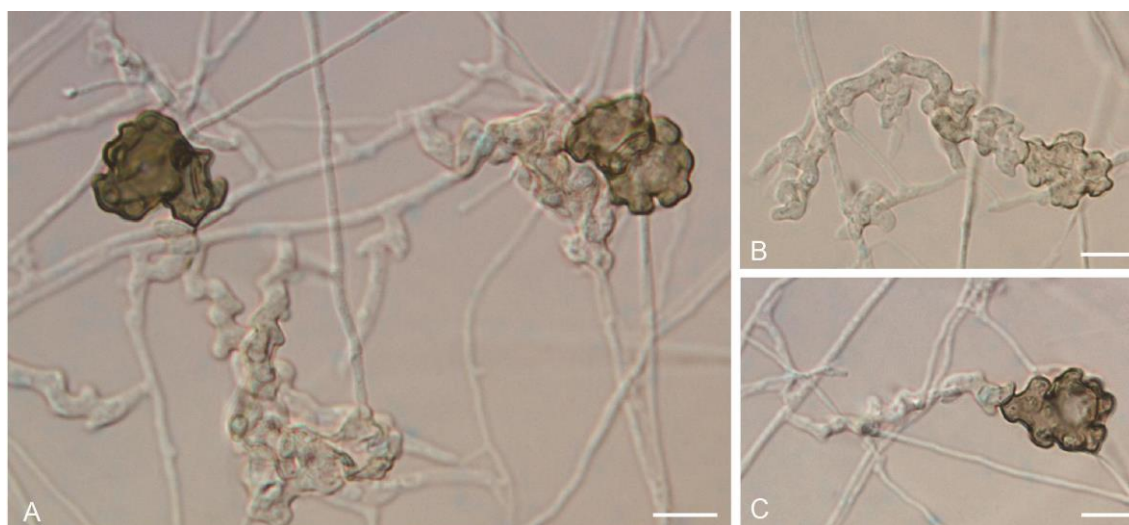


Figure 14 – *Gongchenomyces graminicola* (YNE01382). A–C Hyphopodia. Scale bars = 10 μm .

***Neogongchenomyces* C. L. Zhang, gen. nov.**

Mycobank number: MB854707; Facesoffungi number: FoF16918

Etymology – Named after its morphological similarity to *Gongchenomyces*.

Endophytic in *Poaceae* plants. Mycelium septate, branched, smooth, and hyaline. Conidiophores and Conidia not observed. Hyphopodia lobed, hyaline, becoming brown when mature.

Type species – *Neogongchenomyces graminis* C. L. Zhang

***Neogongchenomyces graminis* C. L. Zhang, sp. nov.**

Mycobank number: MB854709; Facesoffungi number: FoF16940

Etymology – Named after the grass hosts from which it was isolated.

Fig. 15

Holotype – CGMCC3.24893

Endophytic within the stem of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Hyphopodia lobed, hyaline, becoming dark brown when mature, $22.2\text{--}25 \times 18.8\text{--}30 \mu\text{m}$ ($n = 20$).

Culture characteristics – Colonies on PDA cover a 90 mm plate after 7 d at 25°C , aerial mycelium abundant, cottony, center grayish-green, margin light gray, reverse whitesmoke to olive. Colonies on MEA completely cover a 90 mm plate after 14 d at 25°C , cottony, aerial mycelium abundant, grayish-white, reverse olive.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01186 (Holotype CGMCC3.24893, stored in a metabolically inactive state), ex-type living culture YNE01186. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01633.

GenBank numbers – YNE01186: ITS = MW478999, LSU = MW478086, ACT = OQ918162, MCM7 = MW482596, RPB1 = MW482782, TEF1 = MW482670. YNE01633: ITS = MW479001, LSU = OQ891277, ACT = OQ918163, RPB1 = OQ918188, TEF1 = OQ918198.

Notes – Morphologically, this species resembles *Gongchenomyces graminicola* as they do not produce conidiophores or conidia and produce similar lobed hyphopodia.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01186, the closest hits include *Gaeumannomyces californicus* CPC 26044 from *Stenotaphrum secundatum* (GenBank NR_155135.1; Identities = 345/367(94%), gaps = 5/367(1%)), *Gaeumannomyces australiensis* CPC 26058 from *Triticum aestivum* (GenBank NR_155133.1; Identities = 345/367(94%), gaps = 5/367(1%)).

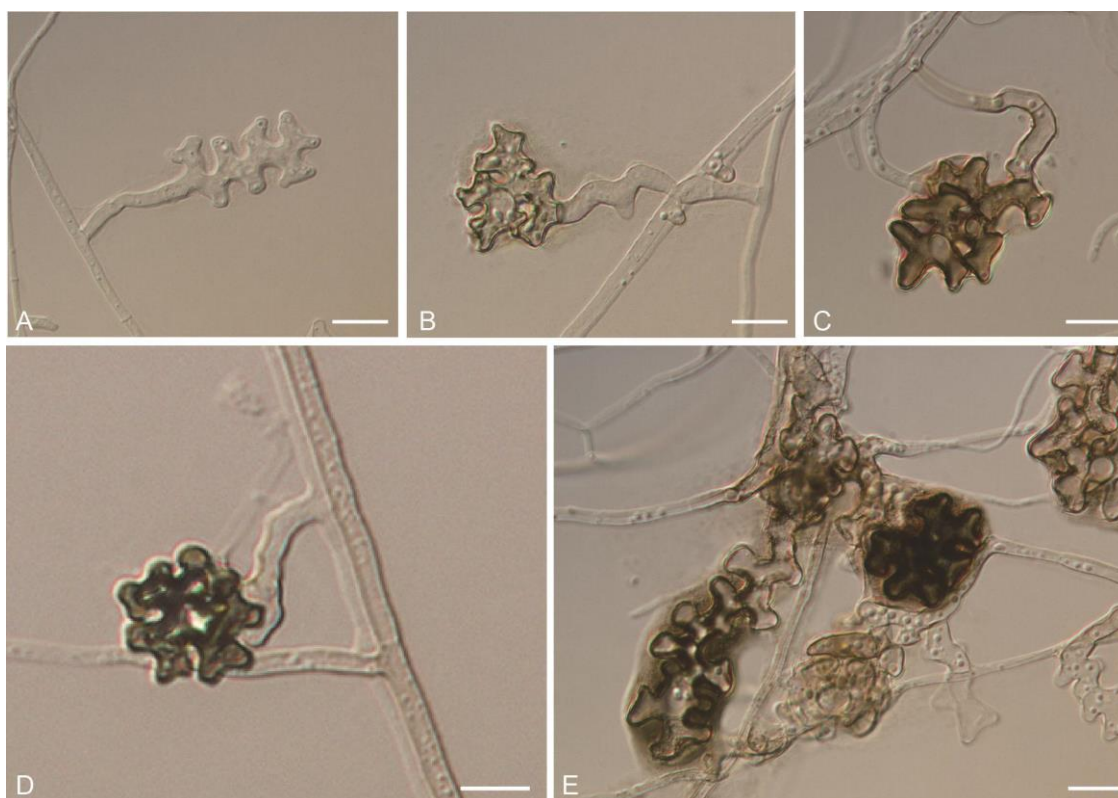


Figure 15 – *Neogongchenomyces graminis* (YNE01186). A–E Hyphopodia. Scale bars = $10 \mu\text{m}$.

Nakataea Hara, Diseases Rice Plant, Edn 2: 185 (1939)

The genus *Nakataea* was introduced by Hara (1939). Luo & Zhang (2013) later reassigned the rice stem rot fungus to this genus as *Nakataea oryzae*. Currently, six morphological species are recognized within this genus, including *N. curvularioides*, *N. multiseptata*, *N. oryzae*, *N. rarissima*,

N. serpens, and *N. setulosa* (Luo & Zhang 2022). However, molecular data is available only for *N. oryzae*.

Three endophytes from this study, namely YNE01084, YNE01094, and YNE01102, were found to cluster with *Nakataea* strains CBS 202.47, CBS 252.34, CBS 253.34, CBS 332.53, ATCC 32149, DAR71531, HK1, M21, and M69 within clade F12, demonstrating high bootstrap values. This clustering supports the identification of three distinct subclades as separate species. The subclade containing YNE01084, YNE01094, and YNE01102 is proposed as a new species *Nakataea graminis*, while the subclade containing ‘*Nakataea oryzae*’ strains ATCC 32149 and CBS 332.53 is suggested to represent an unidentified *Nakataea* species.

Nakataea graminis C. L. Zhang, sp. nov.

Fig. 16

MycoBank number: MB842503; Facesoffungi number: FoF16936

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20913

Endophytic within the stems of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores simple branched. Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, straight to curve, $5\text{--}14.5 \times 2\text{--}3.5\mu\text{m}$ ($n = 4$), with a cylindrical collarette up to $1.5\mu\text{m}$. Conidia lunate, strong to slightly curved, rarely allantoid to fusiform, hyaline, $5\text{--}7 \times 1\text{--}2\mu\text{m}$ ($n = 20$). Hyphopodia hyaline when young and turn pale brown with age, lobed, $16\text{--}27.5 \times 14\text{--}20.5\mu\text{m}$ ($n = 9$).

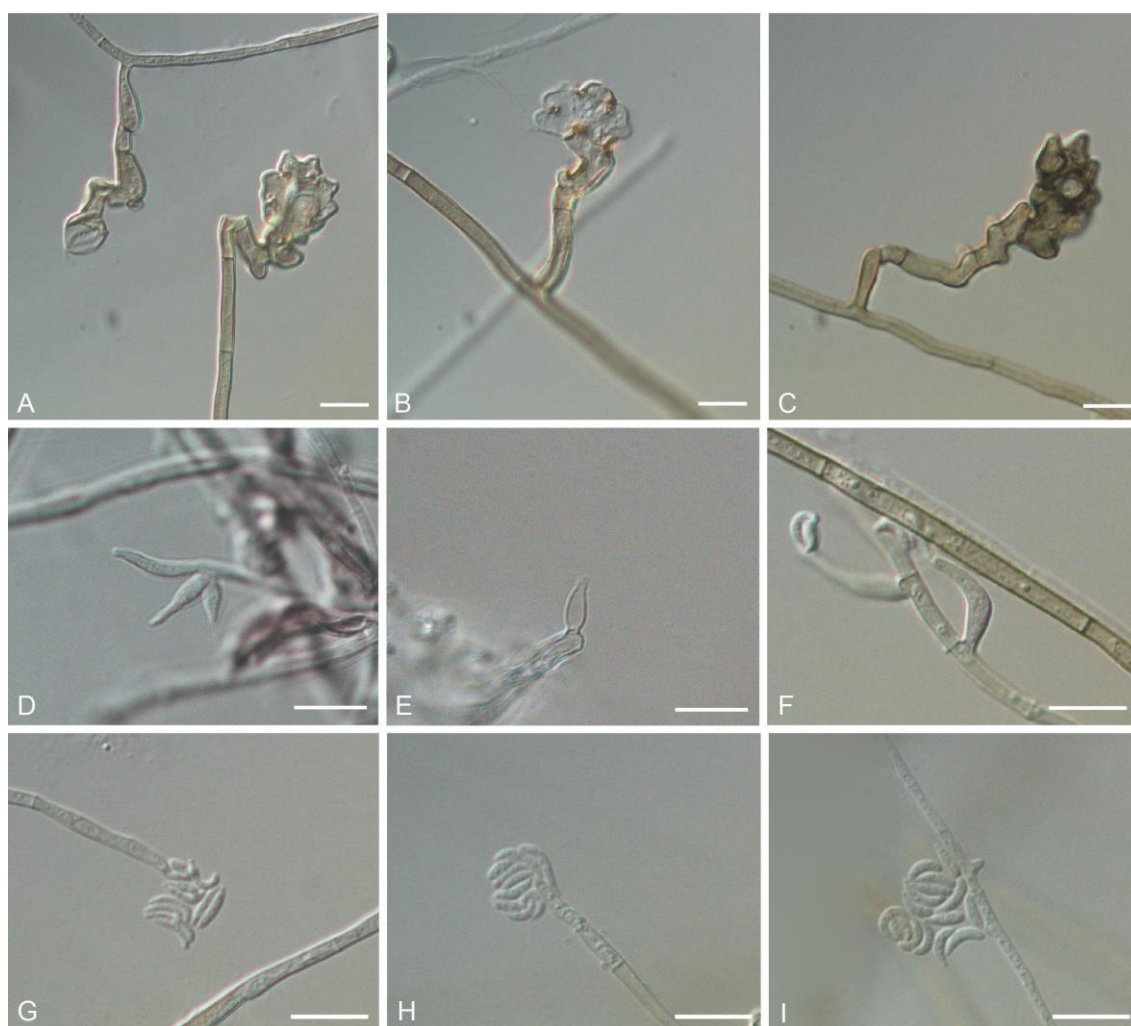


Figure 16 – *Nakataea graminis* (YNE01102). A–C Hyphopodia. D–F Conidiophores and Conidiogenous cells. G–I Conidia. Scale bars = 10 μm .

Culture characteristics – Colonies on PDA reaching 73 mm dish after 7 d at 25 °C, aerial mycelium abundant, dense, villiform in margin, pale greenish-grey, reverse grayish green to very dark grayish cyan. Colonies on MEA completely cover a 90 mm plate after 14 d at 25 °C, cottony, aerial mycelium abundant, dense, dark grayish blue, reverse very dark grayish cyan.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01102 (Holotype CGMCC3.20913, stored in a metabolically inactive state), ex-type living culture YNE01102. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01084. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01094.

GenBank numbers – YNE01102: ITS = MW478920, LSU = MW478078, ACT = OQ918169, MCM7 = MW482590, TEF1 = MW482715. YNE01084: ITS = MW478918, LSU = MW478077, ACT = OQ918168, MCM7 = MW482591, RPB1 = MW482783, TEF1 = MW482714. YNE01094: ITS = MW478919, LSU = OQ891273, ACT = OQ918170, RPB1 = OQ918191, TEF1 = OQ918199.

Notes – Phylogenetically, this species falls within the *Nakataea* clade, with *Nakataea oryzae* as its sister subclade. Morphologically, *N. serpens*, *N. setulosa* and *N. multiseptata* have 3-5 septate fusiform to obclavate conidia with appendages. *N. rarissima* has 3-4 septate, subfusiform to obclavate conidia without appendages. *N. oryzae* and *N. curvularioides* have 3-septate, falcate or sigmoid conidia without appendages (Luo & Zhang 2013, Ma et al. 2014, 2017). This species differs by having aseptate conidia.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01102, the closest hits include *N. oryzae* isolate M21 (GenBank JF414838; Identities = 449/472(95%), gaps = 8/472(1%)), *Falciphoriella solaniterrestris* CBS 117.83 from potato field soil (GenBank KM484842; Identities = 443/469(94%), gaps = 4/469(0%)), and *Falciphora oryzae* isolate R5-6-1 (GenBank EU636699; Identities = 441/471(94%), gaps = 6/471(1%)).

Omnidemptus P.F. Cannon & Alcorn, Mycotaxon 51: 483 (1994)

The genus *Omnidemptus* was introduced by Cannon & Alcorn (1994). Currently, three species have been recorded: *O. affinis*, *O. graminis*, and *O. lunatus* (Hernández-Restrepo et al. 2019). The genus is characterized by the presence of ampulliform or elongated, cylindrical, clavate or ellipsoid phialides, and falcate conidia (Hernández-Restrepo et al. 2019).

Sixteen endophytes from this study, namely YNE01218, ZJE01789, ZJE01773, ZJE01772, YNE00891, YNE00716, YNE00622, YNE00826, YNE01015, YNE01014, ZJE01859, ZJE01860, ZJE01855, ZJE01791, ZJE01803, and ZJE01800, were found to cluster with two known *Omnidemptus* species (*Omnidemptus graminis* CBS 138107, *Omnidemptus affinis* ATCC200212 and CBS141032) and a highly similar affinity GHXL27 within clade F13. This clade received strong support with high bootstrap values and exhibited eight distinct subclades. Four distinct subclades are proposed as four new species. The subclade containing ZJE01789, ZJE01773, and ZJE01772 is proposed as *Omnidemptus zhejiangensis*. The subclade containing YNE01015 and YNE01014 is proposed as *Omnidemptus yunnanensis*. The subclade containing ZJE01859, ZJE01860, and ZJE01855 is suggested as *Omnidemptus graminicola*. The subclade containing ZJE01791, ZJE01803, and ZJE01800 is proposed as *Omnidemptus paragraminis*. YNE00716, YNE00622, YNE00891, and GHXL27 are found clustered with known *Omnidemptus affinis*. Additionally, YNE00826 and YNE01218 represent distinct lineages within *Omnidemptus*, despite being individual singletons. The pairwise homoplasy index (PHI) test revealed no significant recombination ($\Phi_w = 0.9309$) between *Omnidemptus* spp. (Fig. 17).

Omnidemptus paragraminis C. L. Zhang, sp. nov.

Mycobank number: MB849538; Facesoffungi number: FoF16944

Fig. 18

Etymology – Named after its phylogenetic related to *Omnidemptus graminis*.

Holotype – CGMCC3.24900

Endophytic within the shoot of Poaceae plants. Sexual morph: Undetermined. Asexual morph: Hyphopodia lobed, hyaline, becoming dark brown when mature, $17\text{--}23.3 \times 20\text{--}28.8 \mu\text{m}$ ($n = 18$).

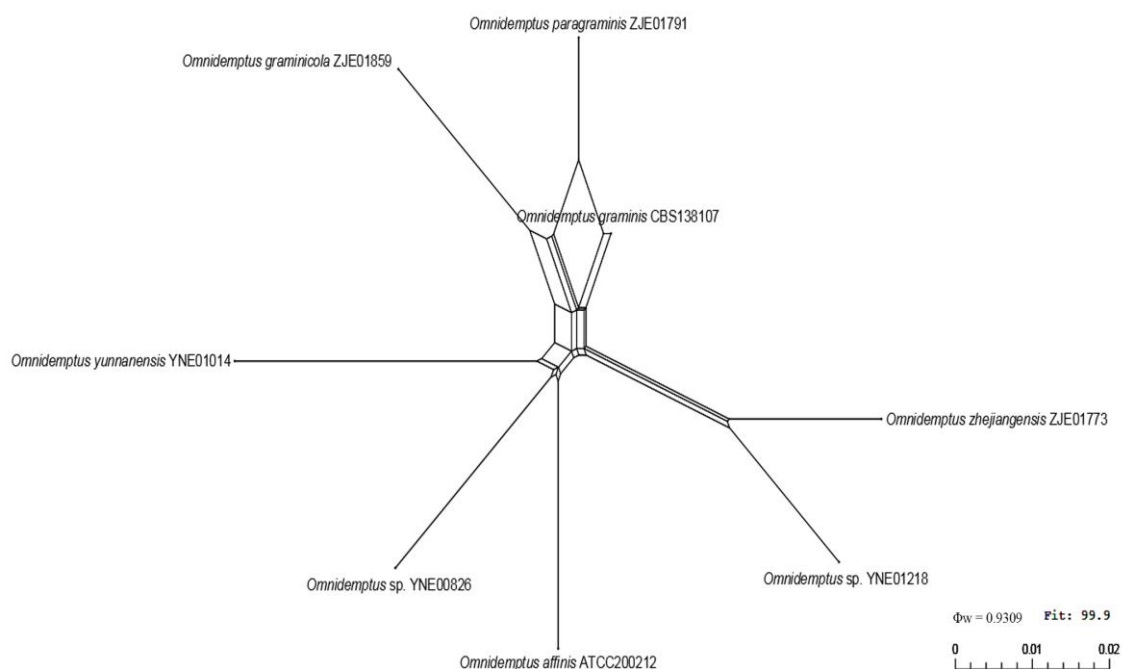


Figure 17 – A split network represents *Omnidemptus* spp. based on six loci (ITS, LSU, ACT, MCM7, RPB1, and TEF1). The P Distance and Neighbor Net algorithm were applied to infer the split network using SplitsTree CE 6.0.0. The pairwise homoplasy index (PHI) test results ($\Phi_W > 0.05$) indicate no statistically significant recombination within the dataset.

Culture characteristics – Colonies on PDA reaching 30 mm after 7 d at 25 °C, cottony, aerial mycelium moderate to abundant, center yellowish-white, margin olive-green. Reverse grayish orange. Colonies on MEA reaching 53 mm after 14 d at 25 °C, cottony, aerial mycelium moderate, white, back gray brown. Reverse center dark grayish blue, margin grayish yellow.

Material examined – China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Paspalum* sp., October 2018, C.L. Zhang ZJE01791 (Holotype CGMCC3.24900, stored in a metabolically inactive state), ex-type living culture ZJE01791. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Phaenosperma* sp., October 2018, C.L. Zhang ZJE01800. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Phaenosperma*, October 2018, C.L. Zhang ZJE01803.

GenBank numbers – ZJE01791: ITS = MW478954, LSU = OQ932800, ACT = OQ918122, MCM7 = OQ942234, RPB1 = OQ942247, TEF1 = OQ918202. ZJE01800: ITS = MW478955, LSU = OQ932801, ACT = OQ918124, MCM7 = OQ942235, RPB1 = OQ942248, TEF1 = OQ918203. ZJE01803: ITS = MW478956, LSU = OQ932802, ACT = OQ918123, MCM7 = OQ942236, RPB1 = OQ942249, TEF1 = OQ918204.

Notes – Phylogenetically, this species forms a cluster with *Omnidemptus graminis*. Morphologically, it differs by the absence of conidia production.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain ZJE01791, the closest hits include Uncultured fungus clone 4248_678 from irrigation water from the pond (GenBank MT236676.1; Identities = 419/431(97%), gaps =

3/431(0%)), *Omnidemptus graminis* FMR 12415 (GenBank NR_164058.1; Identities = 419/431(97%), gaps = 3/431(1%)).

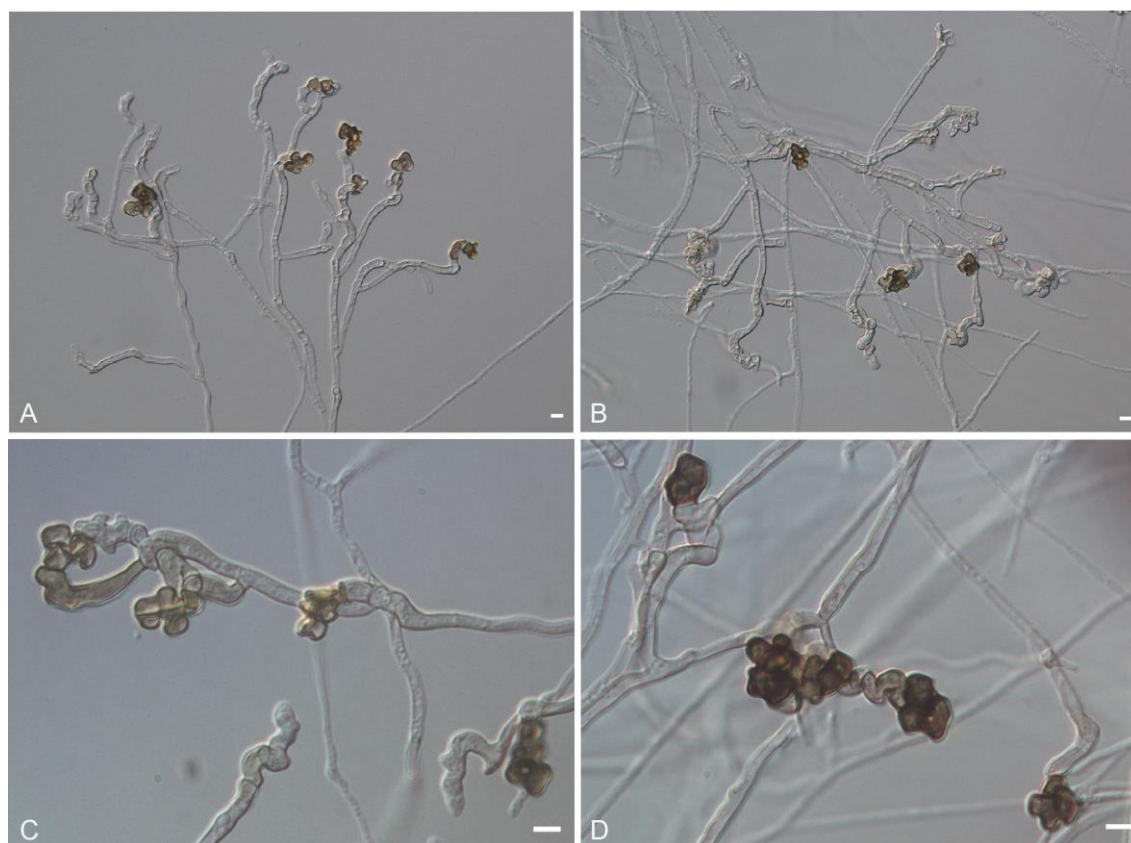


Figure 18 – *Omnidemptus paragraminis* (ZJE01791). A–D Hyphopodia. Scale bars = 10 μ m.

Omnidemptus graminicola C. L. Zhang, sp. nov.

Fig. 19

Mycobank number: MB849537; Facesoffungi number: FoF16943

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.24899

Endophytic within the shoot of *Lophatherum* sp. Sexual morph: Undetermined. Asexual morph: Conidiophores, conidia, and Hyphopodia not observed.

Culture characteristics – Colonies on PDA reaching 37 mm After 14 d at 25 °C, flat, aerial mycelium few to moderate, white, margin rhizoid-like. Reverse dark grayish blue to grayish yellow. Colonies on MEA reaching 50 mm after 14 d at 25 °C, flat, aerial mycelium few to moderate, hyaline to white, margin rhizoid-like. Colonies on SNA reaching 42 mm after 14 d at 25 °C, flat, aerial few, hyaline to white.

Material examined – China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Lophatherum* sp., October 2018, C.L. Zhang ZJE01859 (Holotype CGMCC3.24899, stored in a metabolically inactive state), ex-type living culture ZJE01859. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Lophatherum* sp., October 2018, C.L. Zhang ZJE01855. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Lophatherum* sp., October 2018, C.L. Zhang ZJE01860.

GenBank numbers – ZJE01859: ITS = MW478963, LSU = OQ932806, ACT = OQ918127, MCM7 = OQ942240, RPB1 = OQ942252, TEF1 = OQ918206. ZJE01855: ITS = MW478961, LSU = OQ932805, ACT = OQ918125, MCM7 = OQ942239, RPB1 = OQ942251, TEF1 = OQ918205. ZJE01860: ITS = MW478962, LSU = OQ932807, ACT = OQ918126, MCM7 = OQ942241, TEF1 = OQ918207.

Notes – Phylogenetically, this species falls within the *Omnidemptus* clade with *Omnidemptus paragraminis* and *Omnidemptus graminis* as its sister subclades. Morphologically, this species is distinct from other members of the group as it does produce hyphopodia, conidiophores, or conidia.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain ZJE01859, the closest hits include Uncultured fungus clone 4248_678 from irrigation water from the pond (GenBank MT236676.1; Identities = 423/450(94%), gaps = 14/450(2%)), *Omnidemptus graminis* FMR 12415 (GenBank NR_164058.1; Identities = 423/450(94%), gaps = 14/450(2%)).

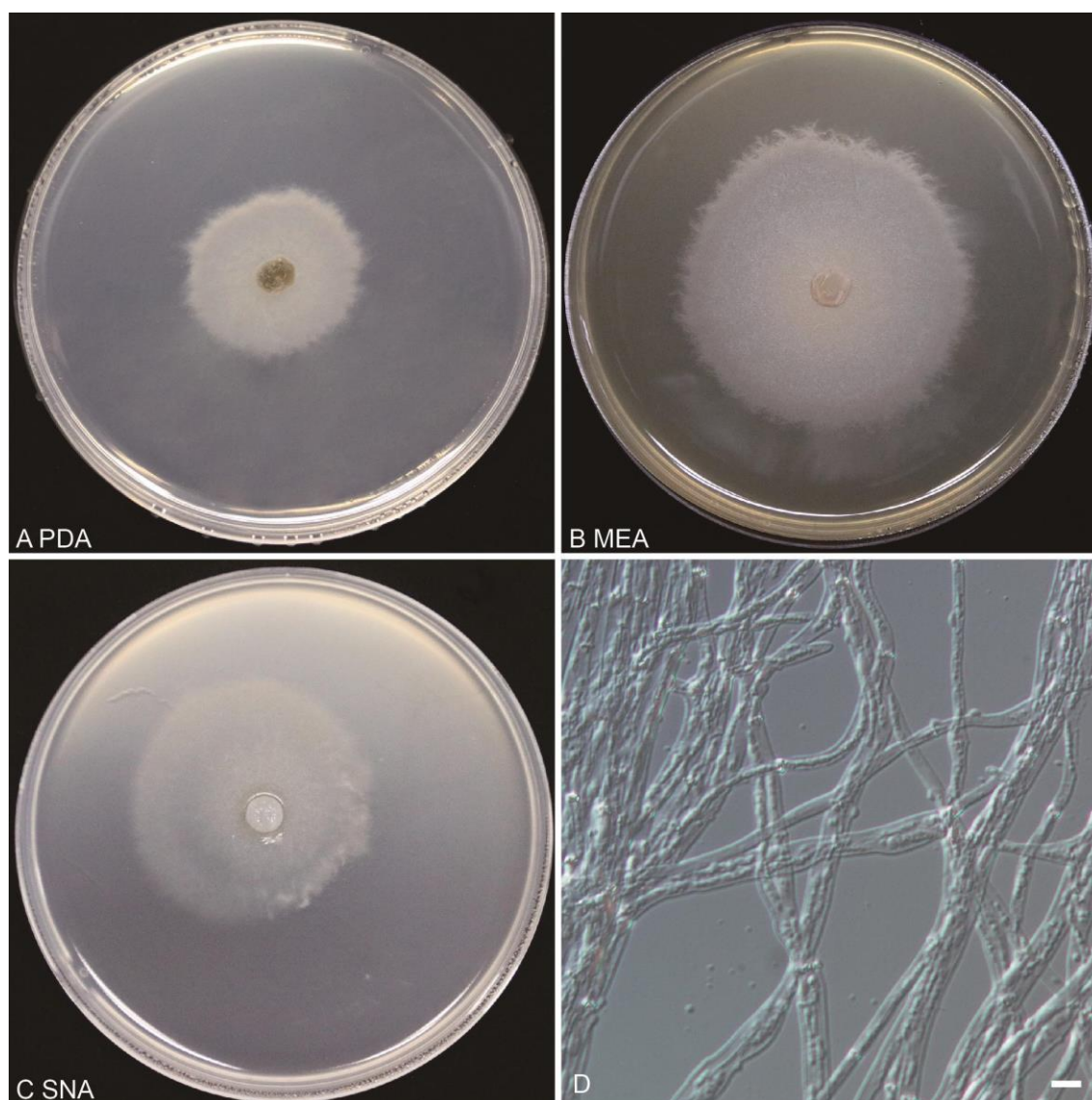


Figure 19 – *Omnidemptus graminicola* (ZJE01859). A–C Colony. D Hyphae. Scale bars = 10 µm.

Omnidemptus yunnanensis C.L. Zhang, sp. nov.

Fig. 20

Mycobank number: MB842504; Facesoffungi number: FoF16945

Etymology – The specific epithet refers to the type location.

Holotype – CGMCC3.20902

Endophytic within the stems of healthy *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores single or branched. Conidiogenous cells phialidic, terminal or intercalary, hyaline to brown, cylindrical to lageniform, straight to curve, $4.5\text{--}9 \times 1.5\text{--}4 \mu\text{m}$ ($n = 13$). Conidia dimorphic, lunate, rarely fusiform, hyaline; microconidia aseptate $5\text{--}10 \times 1\text{--}2 \mu\text{m}$ ($n =$

50); macroconidia, septate indistinct, $24\text{--}40 \times 2\text{--}3 \mu\text{m}$ ($n = 6$). Hyphopodia lobed, brown, $10\text{--}13 \times 9.5\text{--}11.5 \mu\text{m}$ ($n = 20$).

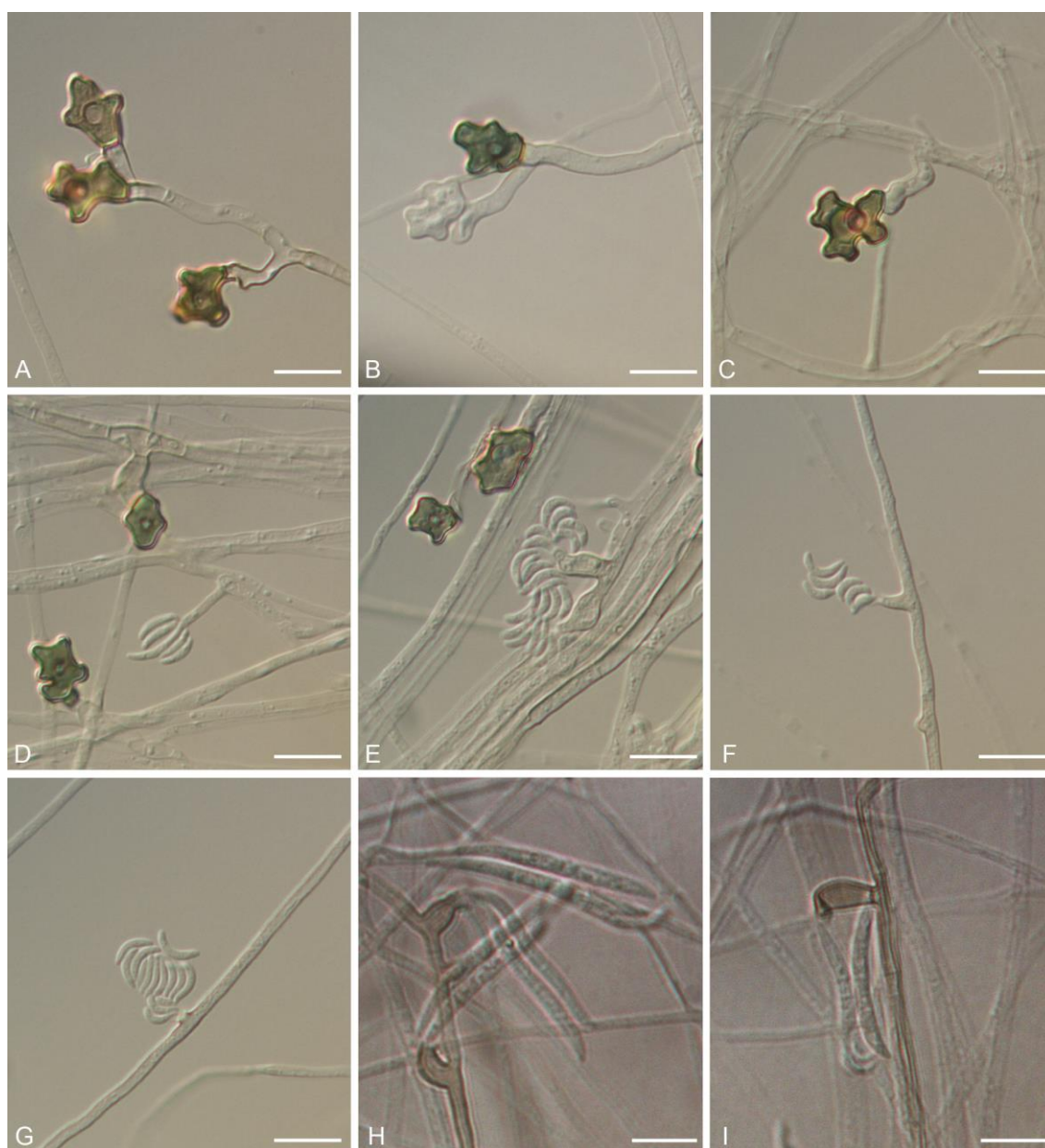


Figure 20 – *Omnidemptus yunnanensis* (YNE01014). A–C Hyphopodia. D–E Hyphopodia, conidiogenous cells and microconidia. F–G Conidiogenous cells and microconidia. H–I Conidiogenous cells and macroconidia. Scale bars = $10 \mu\text{m}$.

Culture characteristics – Colonies on PDA reaching 36 mm after 7 d at 25°C , cottony, aerial mycelium few to moderate, white, shallow from center to margin. Reverse grayish yellow to dark grayish orange. Colonies on MEA reaching 66 mm after 14 d at 25°C , aerial mycelium moderate, grayish-white, cottony, with an irregular ring in the middle and outward. Reverse center very dark grayish blue, margin grayish blue to dark grayish orange.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01014 (Holotype CGMCC3.20902, stored in a metabolically inactive state), ex-type living culture YNE01014. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01015.

GenBank numbers – YNE01014: ITS = MW478964, LSU = MW478073, ACT = OQ918128, MCM7 = OQ942226, RPB1 = MW482813, TEF1 = MW482674. YNE01015: ITS = MW478965, LSU = MW478074, ACT = OQ918129, MCM7 = OQ942227, RPB1 = MW482814, TEF1 = MW482675.

Notes – Phylogenetically, this species falls within the *Omnidemtus* clade with *Omnidemtus paragraminis*, *Omnidemtus graminis*, and *Omnidemtus graminicola* as its sister subclade. Morphologically, this species differs by having fusiform conidia and ampulliform conidiogenous cells. It was isolated from the healthy stems of Poaceae plants from Xishuangbanna, Yunnan Province.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01014, the closest hits include *O. affinis* strain ATCC 200212 (GenBank JX134674; Identities = 402/435(92%), gaps = 19/435(4%)), *O. graminis* strain CBS138107 (GenBank MK487758; Identities = 394/429(92%), gaps = 12/429(2%)).

***Omnidemtus zhejiangensis* C.L. Zhang, sp. nov.**

Fig. 21

MycoBank number: MB842505; Facesoffungi number: FoF16946

Etymology – The specific epithet refers to the type location.

Holotype – CGMCC3.20901

Endophytic within the shoot of healthy *Arthraxon* sp. (*Poaceae*). Sexual morph: Undetermined. Asexual morph: Conidiophores unbranched. Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, straight to curve, $7.5\text{--}24.5 \times 2.5\text{--}3.5 \mu\text{m}$ ($n = 18$). Conidia lunate, allantoid to fusiform, slightly curved, hyaline, $5\text{--}11 \times 1.5\text{--}2 \mu\text{m}$ ($n = 50$). Hyphopodia lobed, brown, $9\text{--}11.5 \times 9\text{--}10.5 \mu\text{m}$ ($n = 20$).

Culture characteristics – Colonies on PDA reaching 34 mm after 7 d at 25 °C, aerial mycelium moderate, cottony, white to pale gray. Upper layer of aerial mycelium white, lower layer pale off-white. Reverse grayish yellow to dark vanilla. Colonies on MEA reaching 79 mm after 14d at 25 °C, aerial mycelium moderate, mycelium sparser in the middle, margin rhizoid-like. Reverse dark grayish yellow.

Material examined – China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Arthraxon* sp. (*Poaceae*), October 2018, C.L. Zhang ZJE01773 (Holotype CGMCC3.20901, stored in a metabolically inactive state), ex-type living culture ZJE01773. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the root of *Arthraxon* sp. (*Poaceae*), October 2018, C.L. Zhang ZJE01789.

GenBank numbers – ZJE01773: ITS = MW478959, LSU = MW478076, ACT = OQ918131, MCM7 = MW482612, RPB1 = MW482815, TEF1 = MW482712. ZJE01789: ITS = MW478960, LSU = ON244716, ACT = OQ918132, MCM7 = OQ942233, RPB1 = ON367461, TEF1 = ON367456.

Notes – Phylogenetically, this species falls within the *Omnidemtus* clade. Morphologically, *Omnidemtus affinis* can be distinguished by its unbranched or sparsely branched brown conidiophores measuring $11\text{--}22 \times 6\text{--}10 \mu\text{m}$, and larger, solitary conidia ($21\text{--}30 \times 3\text{--}4 \mu\text{m}$) with 1-2(-3)-septa along with ascomata. *Omnidemtus graminis* differs in having unbranched brown conidiophores with larger conidia measuring (0-)1-septate ($11\text{--}23 \times 3\text{--}4 \mu\text{m}$). *Omnidemtus lunatus* is differentiated by its larger, pale brown conidiophores ($10.5\text{--}13 \times 6.5\text{--}11 \mu\text{m}$) with larger conidia measuring 1-septate ($24.5\text{--}32 \times 3.5\text{--}4.5 \mu\text{m}$) (Hernández-Restrepo et al. 2019). This species was isolated as an endophyte from the shoot of *Arthraxon* (*Poaceae*) from Baishanzu National Nature Reserve, Zhejiang Province. The main difference between this species and *Omnidemtus yunnanensis* is the longer macroconidia of the latter.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain ZJE01773, the closest hits include *O. graminis* CBS 138107 (GenBank MK487758; Identities = 414/445(93%), gaps = 8/445(1%)), *O. affinis* ATCC 200212 (GenBank NG_059478; Identities = 407/439(93%), gaps = 14/439(3%)).

Dimorphiconidia C. L. Zhang, gen. nov.

Mycobank number: MB842511; Facesoffungi number: FoF16913

Etymology – Name reflects the two types of conidia of this fungus.

Endophytic within Poaceae plants. Sexual morph: Undetermined. Asexual morph: Mycelium septate, branched, smooth, and hyaline to brown. Conidiogenous cells phialidic, terminal or intercalary, cylindrical to lageniform, with a cylindrical to funnel shaped collarette, hyaline to brown. Macroconidia 1~3-septate, falcate, slightly curved, hyaline. Microconidia aseptate, lunate, allantoid to fusiform, strongly to slightly curved, hyaline. Hyphopodia present or absent, if present, lobed and dark brown.

Type species – *Dimorphiconidia yunnanensis* C.L. Zhang.

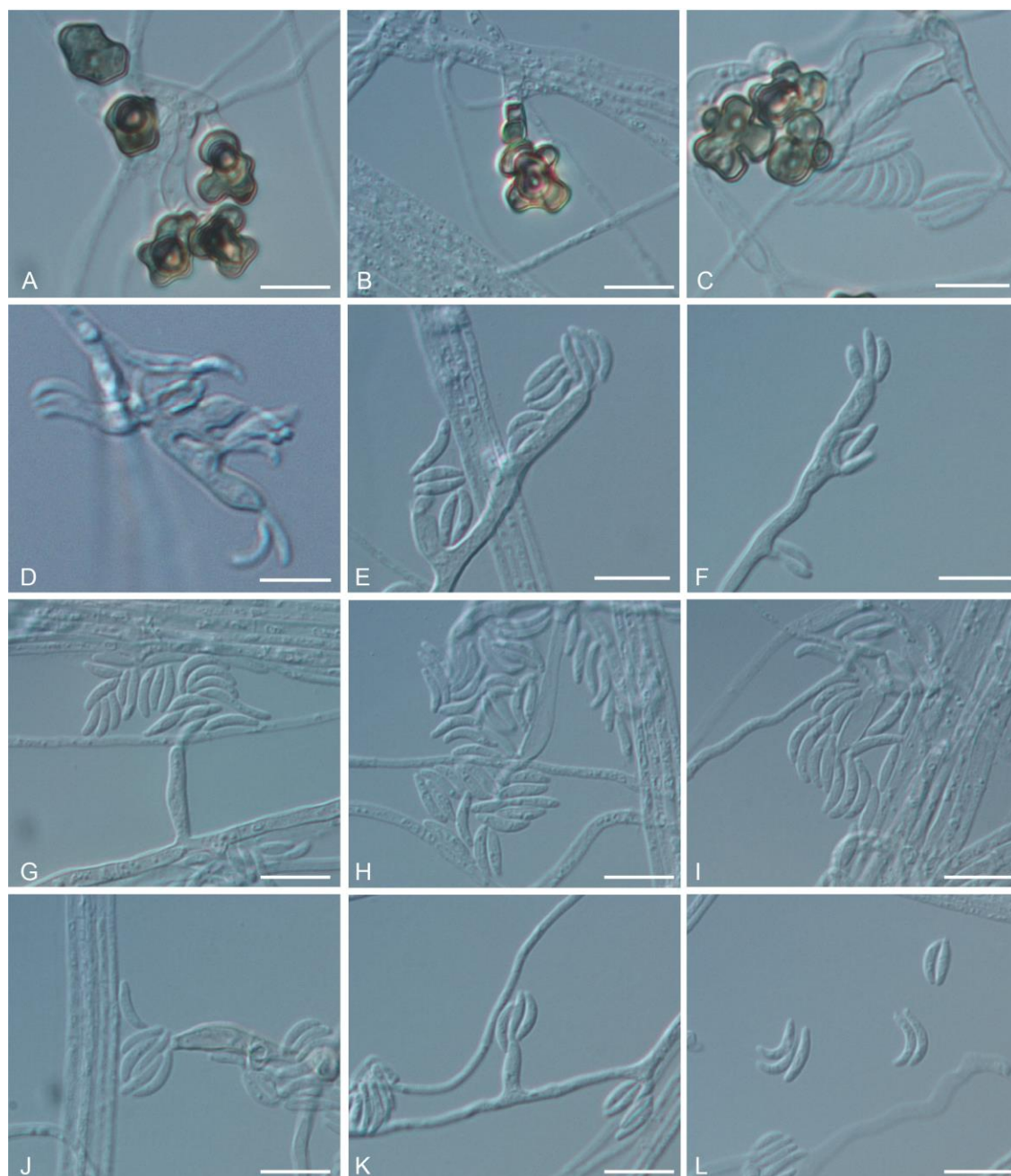


Figure 21 – *Omnidemptus zhejiangensis* (YNE01773). A–C Hyphopodia. D–K Conidiophores, conidiogenous cells, and conidia. L Conidia. Scale bars = 10 μm.

Notes – Seven endophytes from this study, namely YNE00526, YNE00589, YNE00640, YNE01381, YNE01384, YNE01387, and YNE01389, form a distinct clade F14. Among them, two

subclades exhibited high bootstrap values, suggesting the presence of two new species. The first subclade, comprising YNE00526, YNE00589, and YNE00640, is proposed as *Dimorphiconidia graminis*, while the second subclade, containing YNE01381, YNE01384, YNE01387, and YNE01389, is suggested as *Dimorphiconidia yunnanensis*. The *Dimorphiconidia* lineage was found to be sister to *Omnidemptus*.

***Dimorphiconidia yunnanensis* C.L. Zhang, sp. nov.**

Fig. 22

Mycobank number: MB842512; Facesoffungi number: FoF16929

Etymology – The specific epithet refers to the type location.

Holotype – CGMCC3.20909

Endophytic within the stems and leaves of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, terminal or intercalary, cylindrical to lageniform, $16\text{--}17.5 \times 4\text{--}6.5 \mu\text{m}$ ($n = 7$), with a cylindrical to funnel shaped collarette, up to $2\text{--}2.5 \mu\text{m}$ long. Macroconidia 1~3-septate, commonly asymmetrically 2-septate, with the first septum in the median position and the second in the upper half, falcate, slightly curved, hyaline, $30\text{--}50 \times 3.4\text{--}5 \mu\text{m}$ ($n = 50$). Microconidia aseptate lunate, allantoid to fusiform, strongly to slightly curved, hyaline, $5.5\text{--}10 \times 1.5\text{--}3 \mu\text{m}$ ($n = 3$). Hyphopodia present or absent, if present, lobed and dark brown, $12.5\text{--}20 \times 8.5\text{--}13.5 \mu\text{m}$ ($n = 3$).

Culture characteristics – Colonies on PDA reaching 27–28 mm after 7 d at 25 °C, white, cottony, aerial mycelium abundant and dense. Reverse dark grayish orange. Colonies on MEA reaching 67 mm after 14d at 25 °C, aerial mycelium moderate to abundant, cottony, flat, white to pale gray, margin effuse, rhizoid-like. Reverse center very dark grayish blue, margin light grayish yellow.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01381 (Holotype CGMCC3.20909, stored in a metabolically inactive state), ex-type living culture YNE01381. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01384. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01389.

GenBank numbers – YNE01381: ITS = MW478979, LSU = MW478054, ACT = OQ918115, MCM7 = MW482606, RPB1 = MW482820, TEF1 = MW482701. YNE01384: ITS = MW478983, LSU = MW478061, ACT = OQ918117, MCM7 = MW482600, RPB1 = MW482821, TEF1 = MW482702. YNE01389 = ITS = MW478980, LSU = MW478055, ACT = OQ918116, MCM7 = MW482608, RPB1 = MW482822, TEF1 = MW482704.

Notes – Phylogenetically, this genus forms a unique clade within *Magnaporthaceae* and is closely related to *Omnidemptus*. Morphologically, it differs from *Omnidemptus* in that it produces both macroconidia and microconidia simultaneously. This genus was isolated as an endophyte from the stem or leaves of *Poaceae* plants from Xishuangbanna, Yunnan Province.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01381, the closest hits include *O. affinis* ATCC 200212 (GenBank JX134674; Identities = 358/378(95%), gaps = 7/378(1%)), *Falciphora oryzae* isolate R5-6-1 (GenBank EU636699; Identities = 415/453(92%), gaps = 7/453(1%)), and *Falciphoriella solaniterrestris* CBS 117.83 from potato field soil (GenBank KM484842; Identities = 414/453(91%), gaps = 7/453(1%).

***Dimorphiconidia graminis* C.L. Zhang, sp. nov.**

Fig. 23

Mycobank number: MB854764; Facesoffungi number: FoF16928

Etymology – The specific epithet refers to the host isolated.

Holotype – CGMCC3.24892

Endophytic within the stems and leaves of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Mycelium dark brown, Conidiogenous cells phialidic, terminal or intercalary,

cylindrical to lageniform, $14\text{--}18 \times 6\text{--}7.4\text{ }\mu\text{m}$, with a cylindrical to funnel-shaped collarette, $1\text{--}1.5\text{ }\mu\text{m}$ long. Macroconidia usually 3 septate, septate indistinct, sickle-shaped, slightly curved, colorless and transparent, $21\text{--}32 \times 2.7\text{--}5.1\text{ }\mu\text{m}$ ($n = 30$). Microconidia aseptate, lunate, slightly to strongly curved, hyaline, $5\text{--}10.3 \times 1.6\text{--}2.2\text{ }\mu\text{m}$ ($n = 30$). Hyphopodia absent.

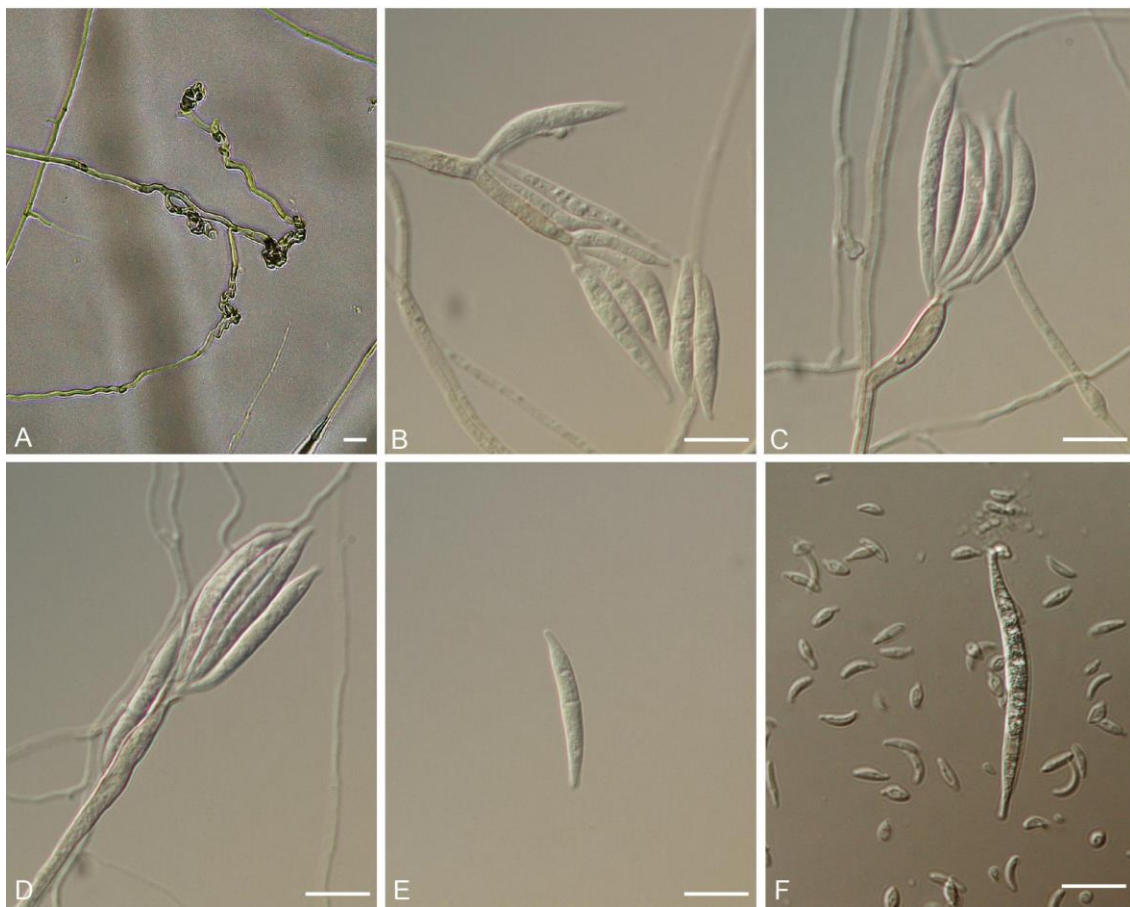


Figure 22 – *Dimorphiconidia yunnanensis* (YNE01381). A Hyphopodia. B–D Conidiogenous cells and macroconidia. E Macroconidia. F Macroconidia and Microconidia. Scale bars = $10\text{ }\mu\text{m}$.

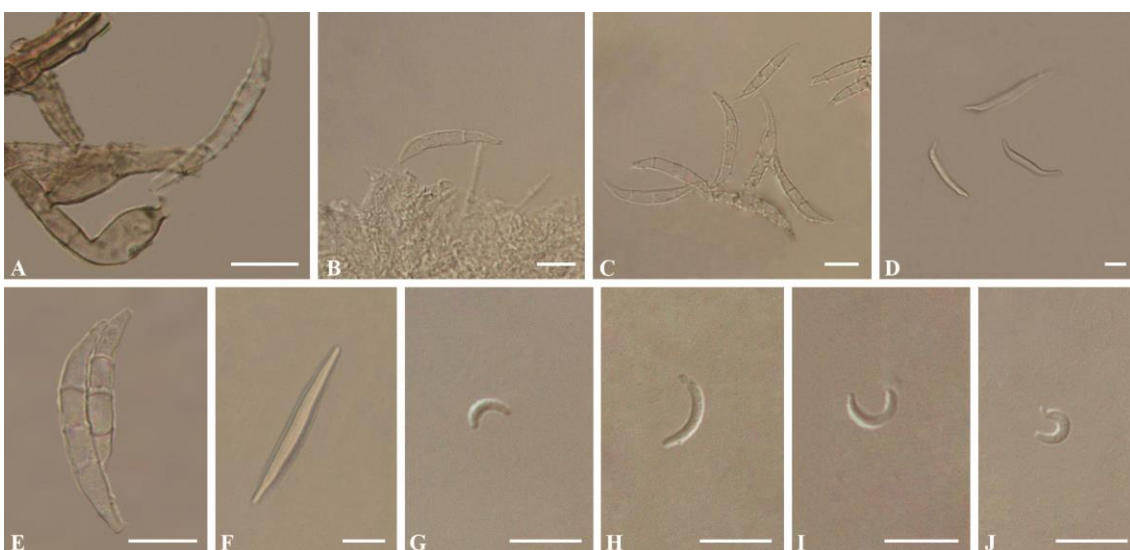


Figure 23 – *Dimorphiconidia graminis* (YNE00589). A Conidiogenous cells and macroconidia. B, C, E Mature macroconidia. D, F Immature macroconidia. G–J Microconidia. Scale bars = $10\text{ }\mu\text{m}$.

Culture characteristics – Colonies on PDA reaching 34.6 mm at 25 °C for 7 days, white, cottony, aerial mycelium moderate. Colonies on MEA reaching 48.7 mm at 25 °C for 14 days, aerial mycelium moderate, cottony, white to light yellowish white, margin effuse.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the living leave of *Oryza meyeriana* subsp. *granulata*, October 2018. C. L. Zhang YNE00589 (Holotype CGMCC3.24892, stored in a metabolically inactive state), ex-type living culture YNE00589. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the living leave of *Oryza meyeriana* subsp. *granulata*, October 2018. C. L. Zhang. YNE00640. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the living leave of *Oryza meyeriana* subsp. *granulata*, October 2018. C. L. Zhang. YNE00526.

GenBank numbers – YNE00589: ITS = MW478967, LSU = MW478051, ACT = OQ918114, MCM7 = MW482605, RPB1 = MW482817, TEF1 = MW482696. YNE00526: ITS = MW478966, MCM7 = MW482604, RPB1 = MW482818, TEF1 = MW482695. YNE00640: ITS = MW478968, MCM7 = MW482603, RPB1 = MW482819, TEF1 = MW482697.

Notes – Phylogenetically, this species is closely related to *Dimorphiconidia yunnanensis*. Morphologically, it differs from *Dimorphiconidia yunnanensis* in that it produces lunate microconidia. Additionally, hyphopodia are absent in this species.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00589, the closest hits include *Harpophora* sp. YQ1-1-1 (GenBank HM008622; Identities = 447/457(97.81%), gaps = 4/457(0%)), *Gaeumannomyces tritici* strain CPC 26281 (GenBank KX306540; Identities = 428/456(93.86%), gaps = 6/456(1%)), and *Gaeumannomyces avenae* strain CPC 26256 (GenBank KX306484; Identities = 428/456(93.86%), gaps = 6/456(1%)).

***Neodimorphiconidia* C. L. Zhang, gen. nov.**

Mycobank number: MB842513; Facesoffungi number: FoF16917

Etymology – Named after its morphological similarity to *Dimorphiconidia*.

Endophytic within the shoot of healthy *Miscanthus* sp. (*Poaceae*). Sexual morph: Undetermined. Asexual morph: Mycelium septate, branched, smooth, and hyaline to pale brown. Conidiogenous cells phialidic, terminal or intercalary, hyaline to pale brown, cylindrical to lageniform, straight or curved. Conidia dimorphic. Microconidia aseptate lunate, slightly to strongly curved, allantoid to fusiform, sinuous, hyaline. Macroconidia lunate, allantoid to fusiform, hyaline. Hyphopodia lobed, dark brown.

Type species – *Neodimorphiconidia zhejiangensis* C.L. Zhang.

Notes – Three endophytes from this study, namely ZJE01842, ZJE01843, and ZJE01844, form a distinct clade F15, resulting in the introduction of a new genus and a new species named *Neodimorphiconidia zhejiangensis* to accommodate them.

***Neodimorphiconidia zhejiangensis* C.L. Zhang, sp. nov.**

Fig. 24

Mycobank number: MB842514; Facesoffungi number: FoF16939

Etymology – The specific epithet refers to the type location.

Holotype – CGMCC3.20912

Endophytic within the shoot of healthy *Miscanthus* sp. (*Poaceae*). Sexual morph: Undetermined. Asexual morph: Small conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, slightness, straight or curved, $89 \times 2 \mu\text{m}$, Microconidia aseptate lunate, slightly to strongly curved, allantoid to fusiform, sinuous, hyaline, $7.5\text{--}11.5 \times 1.5\text{--}2 \mu\text{m}$ ($n = 50$). Large conidiogenous cells phialidic, terminal or intercalary, hyaline to pale brown, cylindrical to lageniform, fat, straight or curved, $81 \times 6.5 \mu\text{m}$. Macroconidia lunate, allantoid to fusiform, slightness, hyaline, $45\text{--}80 \times 2.5\text{--}4.5 \mu\text{m}$ ($n = 7$). Hyphopodia lobed, dark brown, $12\text{--}24 \times 10\text{--}14 \mu\text{m}$ ($n = 20$).

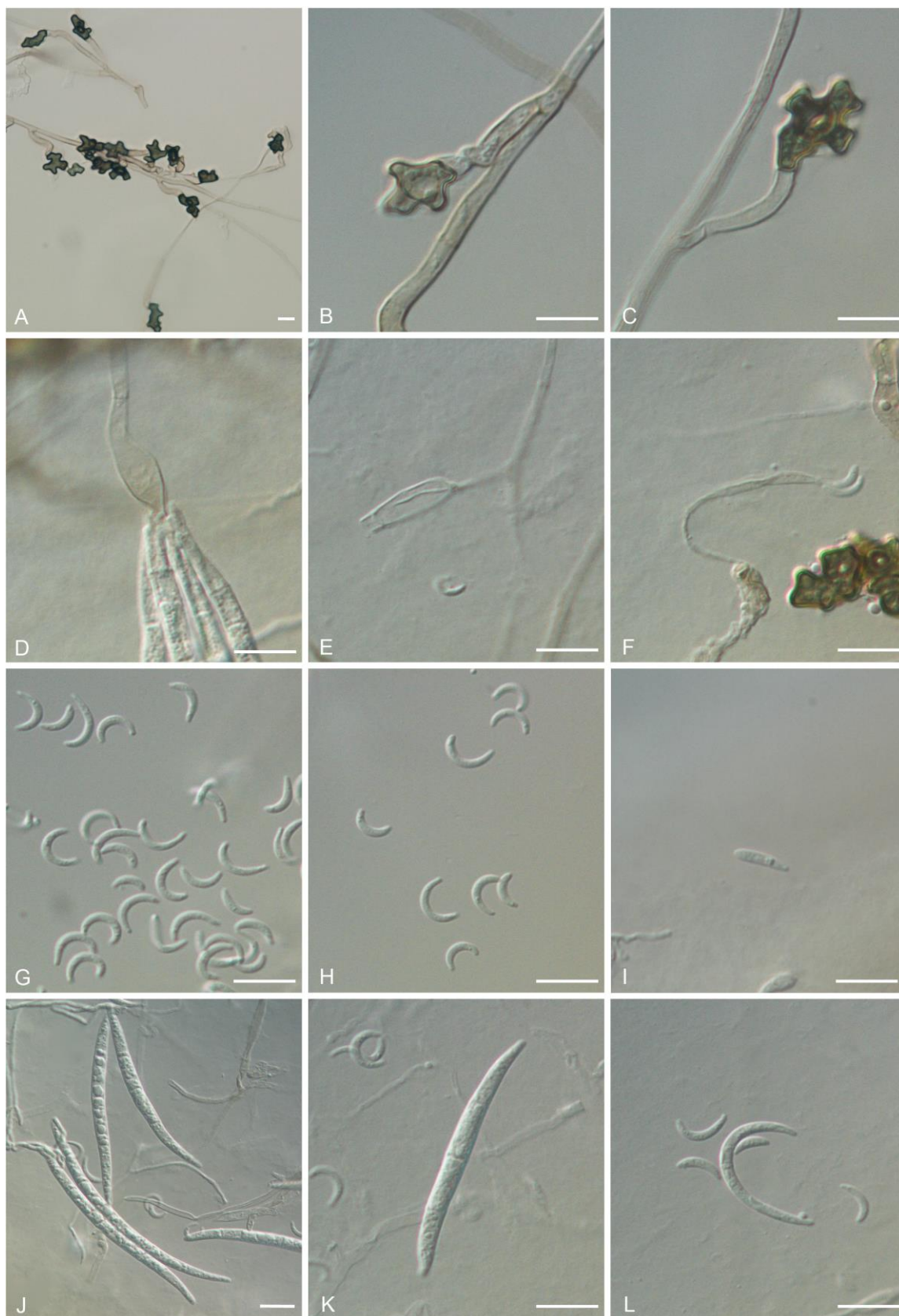


Figure 24 – *Neodimorphiconidia zhejiangensis* (YNE01842). A–C Hyphopodia. D–F Conidiogenous cells. G–I Microconidia. J–L Macroconidia and microconidia. Scale bars = 10 μm.

Culture characteristics – Colonies on PDA reaching 24–32 mm after 7 d at 25 °C, cottony, aerial mycelium moderate to abundant, white, margin foggy, villiform. Reverse grayish yellow to

very dark grayish blue. Colonies on MEA reaching 67–74 mm after 14 d at 25 °C, cottony, flat, aerial mycelium moderate, white to pale gray, margin foggy, effuse, rhizoid. Reverse grayish yellow.

Material examined – China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Miscanthus* sp. (*Poaceae*), October 2018, C.L. Zhang ZJE01842 (Holotype CGMCC3.20912, stored in a metabolically inactive state), ex-type living culture ZJE01842. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Miscanthus* sp. (*Poaceae*), October 2018, C.L. Zhang ZJE01843. China, Zhejiang Province, Baishanzu National Nature Reserve, isolated from the shoot of *Miscanthus* sp. (*Poaceae*), October 2018, C.L. Zhang ZJE01844.

GenBank numbers – ZJE01842: ITS = MW479003, LSU = MW478088, ACT = OQ918133, MCM7 = OQ942237, RPB1 = MW482833, TEF1 = MW482723. ZJE01843: ITS = MW479008, LSU = OQ932803, ACT = OQ918134, MCM7 = OQ942238, RPB1 = OQ942250, TEF1 = OQ918208. ZJE01844: ITS = MW479011, LSU = OQ932804, ACT = OQ918135, MCM7 = MW482615, RPB1 = MW482834, TEF1 = MW482724.

Notes – Phylogenetically, this genus forms a unique clade within *Magnaporthaceae* and is closely related to *Omnidemtus* and *Dimorphiconidia*. Morphologically, it differs from *Dimorphiconidia* by having hyphopodia and slightly larger macroconidia (45–80 × 2.5–4.5 µm). Compared to *Omnidemtus* (Hernández-Restrepo et al. 2019), this genus produces both macroconidia and microconidia simultaneously. This genus was isolated from the shoot of *Miscanthus* sp. from Baishanzu National Nature Reserve, Zhejiang Province.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain ZJE01842, the closest hits include *O. graminis* strain CBS 138107 (MK487734; Identities = 405/441(92%), gaps = 15/441(3%)), *Falciphora oryzae* isolate R5-6-1 (GenBank EU636699; Identities = 412/454(91%), gaps = 20/454(4%)), and *G. californicus* CPC 26044 from *Stenotaphrum secundatum* (GenBank KX306490; Identities = 407/450(90%), gaps = 16/450(3%)).

Bifusisporella R.M.F. Silva, R.J.V. Oliveira, J.D.P. Bezerra, J.L. Bezerra, Souza-Motta & G.A. Silva, Mycological Progress 18 (6): 852 (2019)

Endophytic within the stems and leaves of *Poaceae* plants. Conidiogenous cells phialidic, curvate, elongated, cylindrical or clavate, pale brown, solitary or aggregate. Conidia dimorphic. Macroconidia curved, falcate, hyaline, smooth, aseptate, guttulate, tapering to pointed ends. Microconidia falcate, straight to slightly curved, hyaline, smooth, aseptate. Hyphopodia brown, smooth, elongate, multi-lobulate.

Type species – *Bifusisporella sorghi* R.M.F. Silva, R.J.V. Oliveira, J.D.P. Bezerra, J.L. Bezerra, C.M. Souza-Motta & G.A. Silva.

Notes – The genus *Bifusisporella* was introduced by Silva et al. (2019) to accommodate *Bifusisporella sorghi*. The species *Bifusisporella sichuanensis* was introduced by Zeng et al. (2022) with a sexual morph. Phylogenetically, *Bifusisporella sichuanensis* can be distinguished from *Bifusisporella*, forming a distinct, independent clade F18. It is a sister group to the genera *Bifusisporella* and *Neobifusisporella*. Therefore, we propose transferring *Bifusisporella sichuanensis* to a new combination, *Xenorhytisma sichuanense*. Seven endophytes from this study, namely YNE00934, YNE01000, YNE01170, YNE01150, YNE01004, YNE01143, and YNE00994, cluster with the known species *Bifusisporella sorghi* and a highly similar affinity MJ2014 within clade F16. This clade received robust support and exhibited four subclades. Specifically, MJ2014 forms a distinct subclade, two *Bifusisporella sorghi* strains constitute another distinct subclade, and the strains YNE00934, YNE01000, YNE01170, and YNE01150 form yet another subclade, which is proposed as *Bifusisporella graminicola*. Finally, YNE01004, YNE01143, and YNE00994 constitute the last subclade, which is suggested as *Bifusisporella graminis*.

Bifusisporella graminicola C. L. Zhang, sp. nov.

Fig. 25

Mycobank number: MB849535; Facesoffungi number: FoF16925

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.24891

Endophytic within the leaves of *Panicum bisulcatum*. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, terminal or intercalary, cylindrical to lageniform, $15.5\text{--}17.9 \times 6.4\text{--}7.8 \mu\text{m}$ ($n = 4$). Conidia lunate, slightly curved, hyaline, $25.5\text{--}32.5 \times 3\text{--}3.5 \mu\text{m}$ ($n = 15$), 3-septate, septate indistinct, protoplasm aggregates to form liquid droplets when conidia old and mature. Hyphopodia irregular, dark brown, $9.5\text{--}13 \times 6.5\text{--}9.5 \mu\text{m}$ ($n = 30$).

Culture characteristics – Colonies on PDA reaching 39 mm after 7 d at 25 °C, flat, aerial mycelium moderate, white to yellowish-white in the center, margin hyaline. Reverse dark grayish yellow. Colonies on MEA reaching 39.5 mm after 14 d at 25 °C, aerial mycelium few, flat, white, central villous. Reverse dark grayish blue to grayish yellow.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Panicum bisulcatum*, October 2018, C.L. Zhang YNE00934 (Holotype CGMCC3.24891, stored in a metabolically inactive state), ex-type living culture YNE0934. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01000. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01150. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01170.

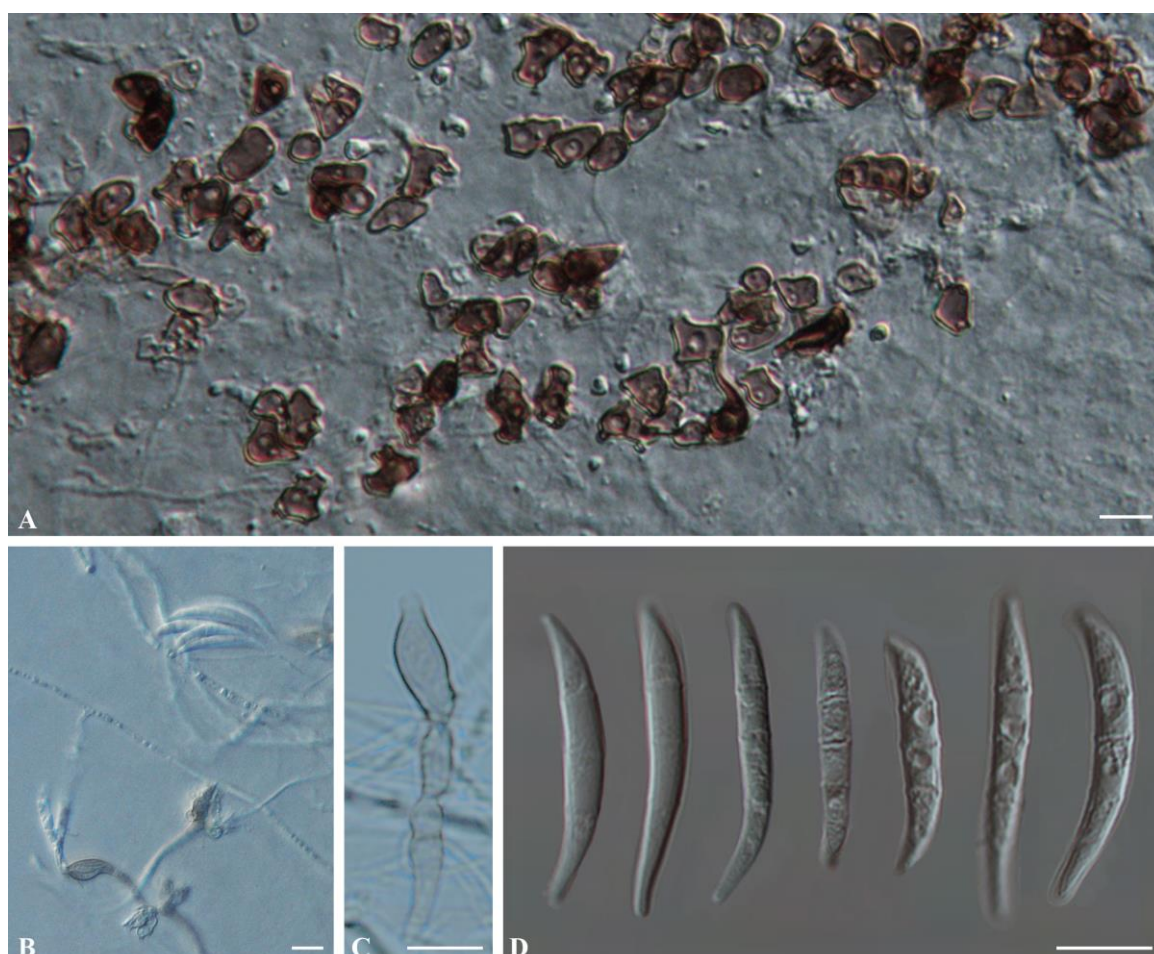


Figure 25 – *Bifusisporella graminicola* (YNE00934). A Hyphopodia. B Conidiogenous cells and conidia. C Conidiogenous cells. D Conidia. Scale bars = 10 μm .

GenBank numbers – YNE00934: ITS = MW479074, LSU = MW478089, ACT = OQ918108, MCM7 = MW482563, RPB1 = MW482801, TEF1 = MW482636. YNE01000: ITS = MW479075, LSU = MW478090, ACT = OQ918110, MCM7 = MW482562, RPB1 = MW482802 and TEF1 = MW482641. YNE01150: ITS = MW479077, LSU = MW478092, MCM7 = MW482561, RPB1 = MW482805, TEF1 = MW482642. YNE01170: ITS = MW479079, LSU = MW478097, ACT = OQ918109, MCM7 = MW482560, RPB1 = MW482803, TEF1 = MW482637.

Notes – Phylogenetically, this species forms a cluster with *Bifusisporrella graminis* and *Bifusisporrella sorghi*. Morphologically, it differs from *Bifusisporrella graminis* by having larger hyphopodia. It differs from *Bifusisporrella sorghi* by having smaller hyphopodia and lacking microconidia, whereas *Bifusisporrella sorghi* has both macro- and microconidia simultaneously.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00934, the closest hits include *Bifusisporrella sorghi* strain URM 7864 from leaves of *Sorghum bicolor* (GenBank MK060156.1; Identities = 414/426(97%), gaps = 5/426(1%)), *Bifusisporrella sorghi* URM 7442 from leaves of *Sorghum bicolor* (GenBank NR_164042.1; Identities = 412/426(97%), gaps = 7/426(1%)).

Bifusisporrella graminis C. L. Zhang, sp. nov.

Fig. 26

Mycobank number: MB842506; Facesoffungi number: FoF16926

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20899

Endophytic within the leaves or stems of Poaceae plants. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, terminal or intercalary, hyaline when young and pale brown when mature, cylindrical to lageniform, straight to curve, $14.5\text{--}20.5 \times 3\text{--}6.5\ \mu\text{m}$ ($n = 3$), with a cylindrical collarette up to $2\text{--}2.5\ \mu\text{m}$. Conidia lunate, slight curved, fat, hyaline, $27\text{--}45 \times 3.5\text{--}4\ \mu\text{m}$ ($n = 20$). Hyphopodia lobed, brown, $10.5 \times 7.5\ \mu\text{m}$ ($n = 5$).

Culture characteristics – Colonies on PDA reaching 33 mm after 7 d at 25 °C, flat, aerial mycelium moderate, pale yellowish-white. Reverse dark grayish blue to grayish yellow. Colonies on MEA reaching 66 mm after 14 d at 25 °C, cottony, aerial mycelium moderate, flat, white, margin effuse, rhizoid, brown. Reverse dark gray.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01143 (Holotype CGMCC3.20899, stored in a metabolically inactive state), ex-type living culture YNE01143. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE00994. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE01004.

GenBank numbers – YNE01143: ITS = MW479087, LSU = MW478068, ACT = OQ918113, MCM7 = OQ942228, RPB1 = MW482809, TEF1 = MW482644. YNE00994: ITS = MW479084, LSU = MW478066, ACT = OQ918111, MCM7 = MW482565, RPB1 = MW482808, TEF1 = MW482643. YNE01004: ITS = MW479085, LSU = MW478067, ACT = OQ918112, MCM7: MW482564, RPB1: MW482807, TEF1: MW482645.

Notes – Phylogenetically, the species is placed within the *Bifusisporrella* clade and is closely related to *Bifusisporrella sorghi*. Morphologically, it differs from *Bifusisporrella sorghi* (Silva et al. 2019) by producing only macroconidia ($27\text{--}45 \times 3.5\text{--}4\ \mu\text{m}$) that are longer than those found in *Bifusisporrella sorghi*. Additionally, it differs by having lobed hyphopodia. This species was isolated as an endophyte from the stem of *Poaceae* plant from Xishuangbanna, Yunnan Province.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01143, the closest hits include *Bifusisporrella sorghi* URM 7442 from leaves of *Sorghum bicolor* (GenBank MK060155; Identities = 402/418(96%), gaps = 7/418(1%)), *O. graminis* strain CBS 138107 (MK487734; Identities = 340/377(90%), gaps = 11/377(2%)), and *Slopeiomyces cylindrosporus* strain CBS 611.75 from grass roots (associated

with *Phialophora graminicola*) (GenBank KM484945; Identities = 244/256(95%), gaps = 4/256(1%).

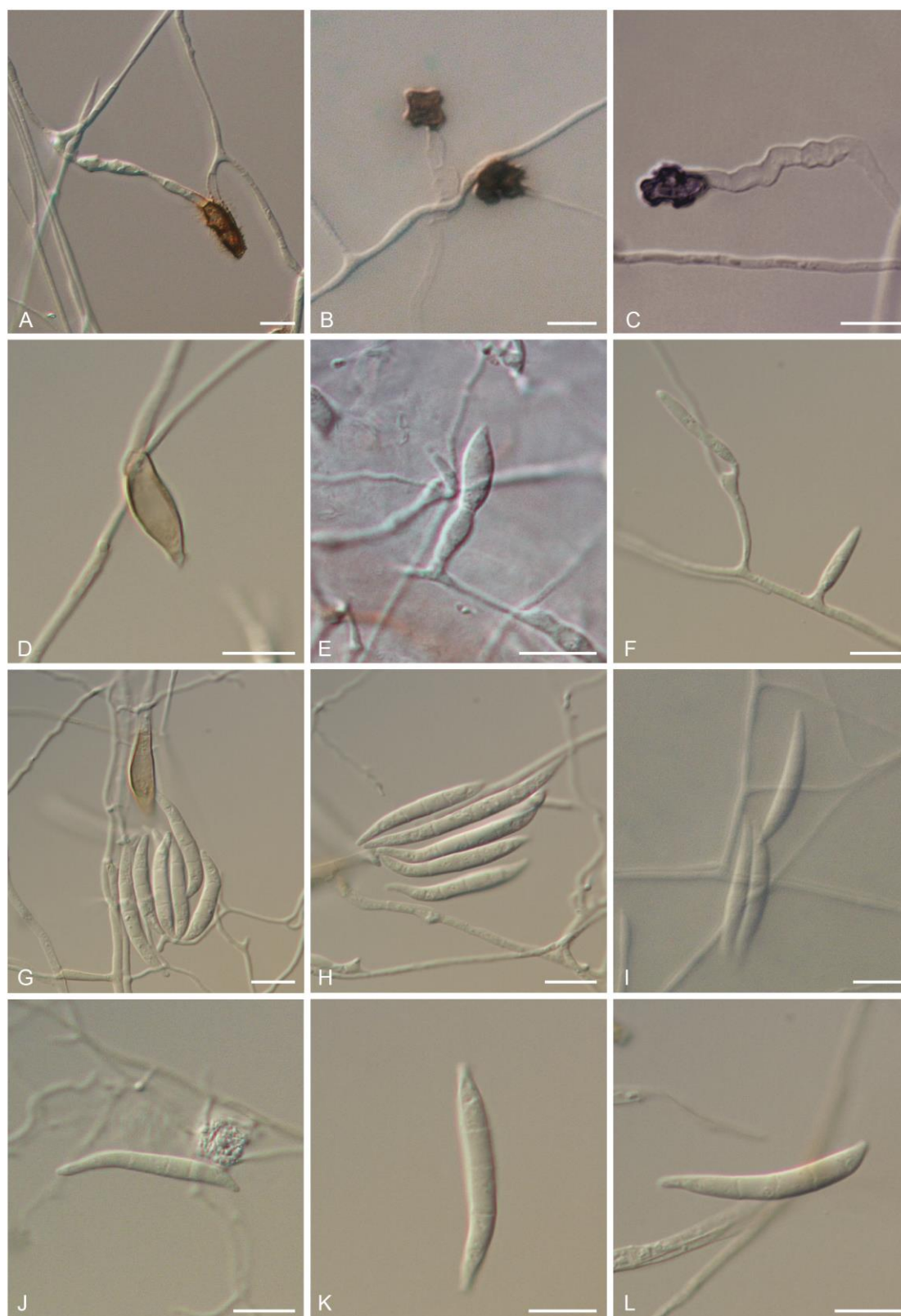


Figure 26 – *Bifusisporella graminis* (YNE01143). A–C Hyphopodia. D–F Conidiogenous cells. G Conidiogenous cells and conidia. H–L Conidia. Scale bars = 10 μm.

Neobifusisporella C. L. Zhang, gen. nov.

Mycobank number: MB842507; Facesoffungi number: FoF16916

Etymology – Named after its morphological similarity to *Bifusisporella*.

Endophytic within the leaves or stems of Poaceae plants. Sexual morph: Undetermined. Asexual morph: Mycelium branched, smooth, hyaline to pale brown, contains bubbles. Conidiogenous cells phialidic, terminal or intercalary, hyaline to pale brown, cylindrical to lageniform, straight or slight curved, with a cylindrical to funnel shaped collarette. Conidia lunate, allantoid to fusiform, slight curved, hyaline. Hyphopodia lobed or chlamydospores-like, dark brown.

Type species – *Neobifusisporella graminis* C. L. Zhang.

Notes – Five endophytes from this study, namely YNE00572, YNE00573, YNE00598, YNE00910, and YNE00998, form a distinct clade within clade F17, resulting in the introduction of a new genus named *Neobifusisporella* to accommodate them. Among them, two subclades exhibited high bootstrap values, indicating the presence of two new species: the first subclade, containing YNE00598, YNE00572, and YNE00573, is proposed as *Neobifusisporella graminis*, while the second subclade, containing YNE00910 and YNE00998, is suggested as *Neobifusisporella graminicola*. *Neobifusisporella* is a sister taxon to *Bifusisporella*.

***Neobifusisporella graminis* C. L. Zhang, sp. nov.**

Fig. 27

Mycobank number: MB842508; Facesoffungi number: FoF16938

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20900

Endophytic within the leaves or stems of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, terminal or intercalary, hyaline to pale brown, cylindrical to lageniform, straight or slight curved, $15\text{--}47.5 \times 3.5\text{--}5.5 \mu\text{m}$ ($n = 10$), with a cylindrical to funnel shaped collarette. Conidia aseptate, lunate or fusiform, slight curved, hyaline, $13.5\text{--}29 \times 4\text{--}5 \mu\text{m}$ ($n = 50$). Hyphopodia lobed, dark brown, $9.5\text{--}11 \times 11 \mu\text{m}$ ($n = 15$).

Culture characteristics – Colonies on PDA reaching 32–35 mm after 7 d at 25 °C, cottony, aerial mycelium moderate to abundant, white, margin foggy. Reverse center grayish yellow to slightly desaturated orange, margin grayish blue. Colonies on MEA reaching 51–66 mm after 14 d at 25 °C, cottony, flat, aerial mycelium few to abundant, pale grayish yellow to hyaline, margin foggy. Reverse dark grayish orange to grayish orange.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00598 (Holotype CGMCC3.20900, stored in a metabolically inactive state), ex-type living culture YNE00598. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00572. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00573.

GenBank numbers – YNE00598: ITS = MW479068, LSU = OQ932793, ACT = OQ918105, MCM7 = MW482547, RPB1 = MW482787, TEF1 = MW482686. YNE00572: ITS = MW479056, LSU = MW478044, ACT = OQ918103, MCM7 = MW482553, RPB1 = MW482794, TEF1 = MW482681. YNE00573: ITS = MW479062, LSU = MW478045, ACT = OQ918104, MCM7 = MW482554, RPB1 = MW482795, TEF1 = MW482690.

Notes – Phylogenetically, this genus forms a unique clade within *Magnaporthaceae*, closely related to *Bifusisporella*. Morphologically, it differs from *Bifusisporella* by having larger phialidic conidiogenous cells and wider conidia (Silva et al. 2019). This genus was discovered as an endophyte within the leaves of *Oryza meyeriana* subsp. *granulata* collected from Xishuangbanna, Yunnan Province, China.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00598, the closest hits include *Bifusisporella sorghi* URM 7442 from the leaves of *Sorghum bicolor* (GenBank MK060155; Identities = 385/418(92%), gaps =

6/418(1%)), and *O. graminis* strain CBS 138107 (MK487734; Identities = 334/374(89%), gaps = 11/374(2%)).

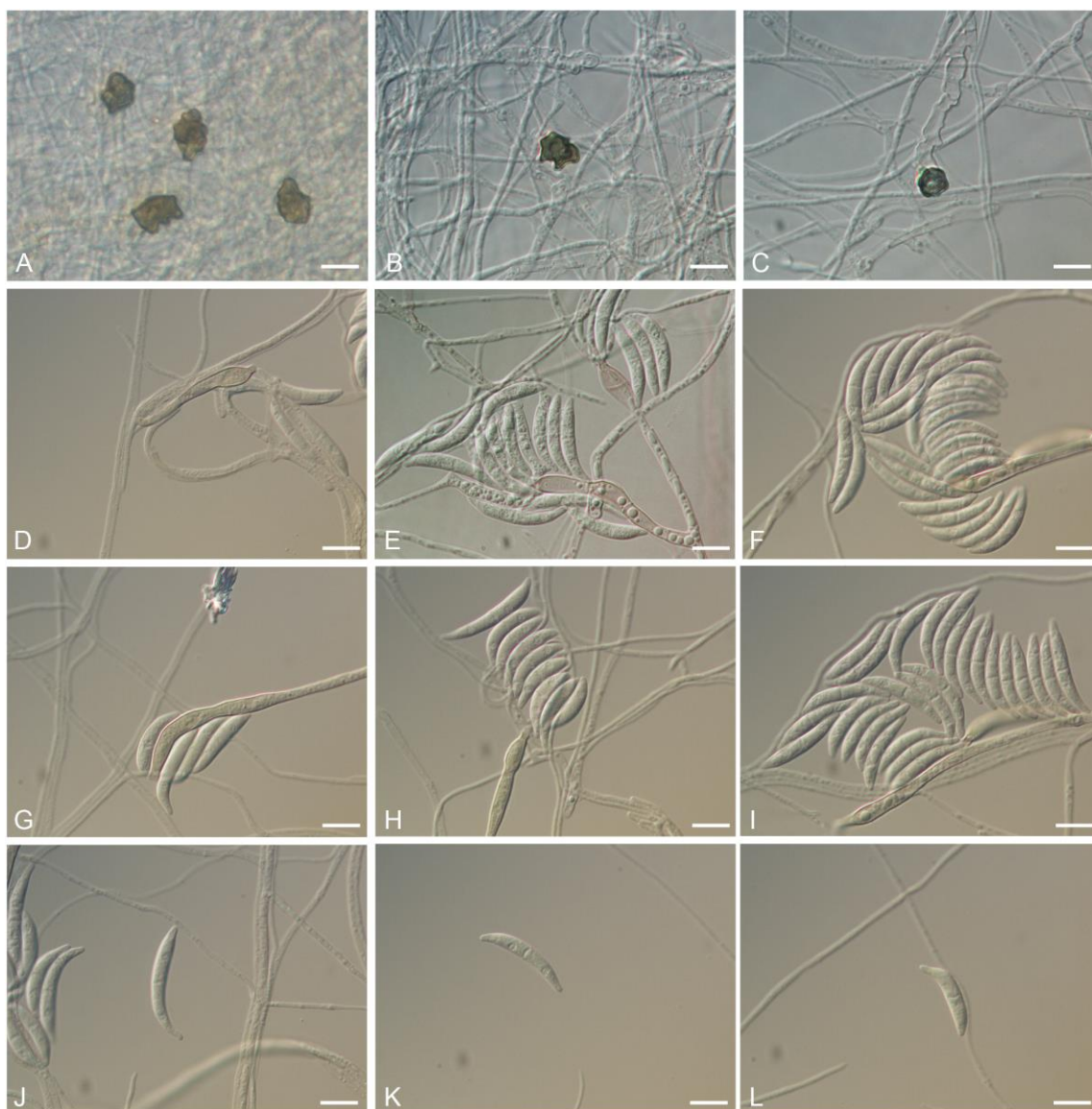


Figure 27 – *Neobifusispora graminis* (YNE00598). A–C Hyphopodia. D–I Conidiogenous cells and conidia. J–L Conidia. Scale bars = 10 µm.

Neobifusispora graminicola C. L. Zhang, sp. nov.

Fig. 28

Mycobank number: MB849534; Facesoffungi number: FoF16937

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.24897

Endophytic within the leaves of *Axonopus compressus*. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, $19.9\text{--}25.9 \times 5\text{--}5.2\mu\text{m}$ ($n = 3$), with a collarette. Conidia lunate, 3-septate, $42.8\text{--}50 \times 3.2\text{--}4.9\mu\text{m}$ ($n = 9$). Hyphopodia subglobose to irregular, brown, $8.5\text{--}15.5 \times 9.5\text{--}12.5\mu\text{m}$ ($n = 12$).

Culture characteristics – Colonies on PDA reaching 39 mm after 7 d at 25 °C, cottony, aerial mycelium dense and abundant, white, dorsal dark, central villous, margin rhizoid. Reverse light grayish yellow. Colonies on MEA reaching 68.5 mm after 14 d at 25 °C, cottony, aerial mycelium dense and abundant, white, central villous, margin rhizoid. Reverse grayish orange.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Axonopus compressus*, October 2018, C.L.

Zhang YNE00910 (Holotype CGMCC3.24897, stored in a metabolically inactive state), ex-type living culture YNE0910. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stem of *Poaceae* plants, October 2018, C.L. Zhang YNE00998.

GenBank numbers – YNE0910: ITS = MW479073, LSU = MW478071, ACT = OQ918106, MCM7 = MW482543, RPB1 = MW482784, TEF1 = MW482693. YNE00998: ITS = MW479072, LSU = MW478072, ACT = OQ918107, MCM7 = MW482542, RPB1 = MW482785, TEF1 = MW482694.

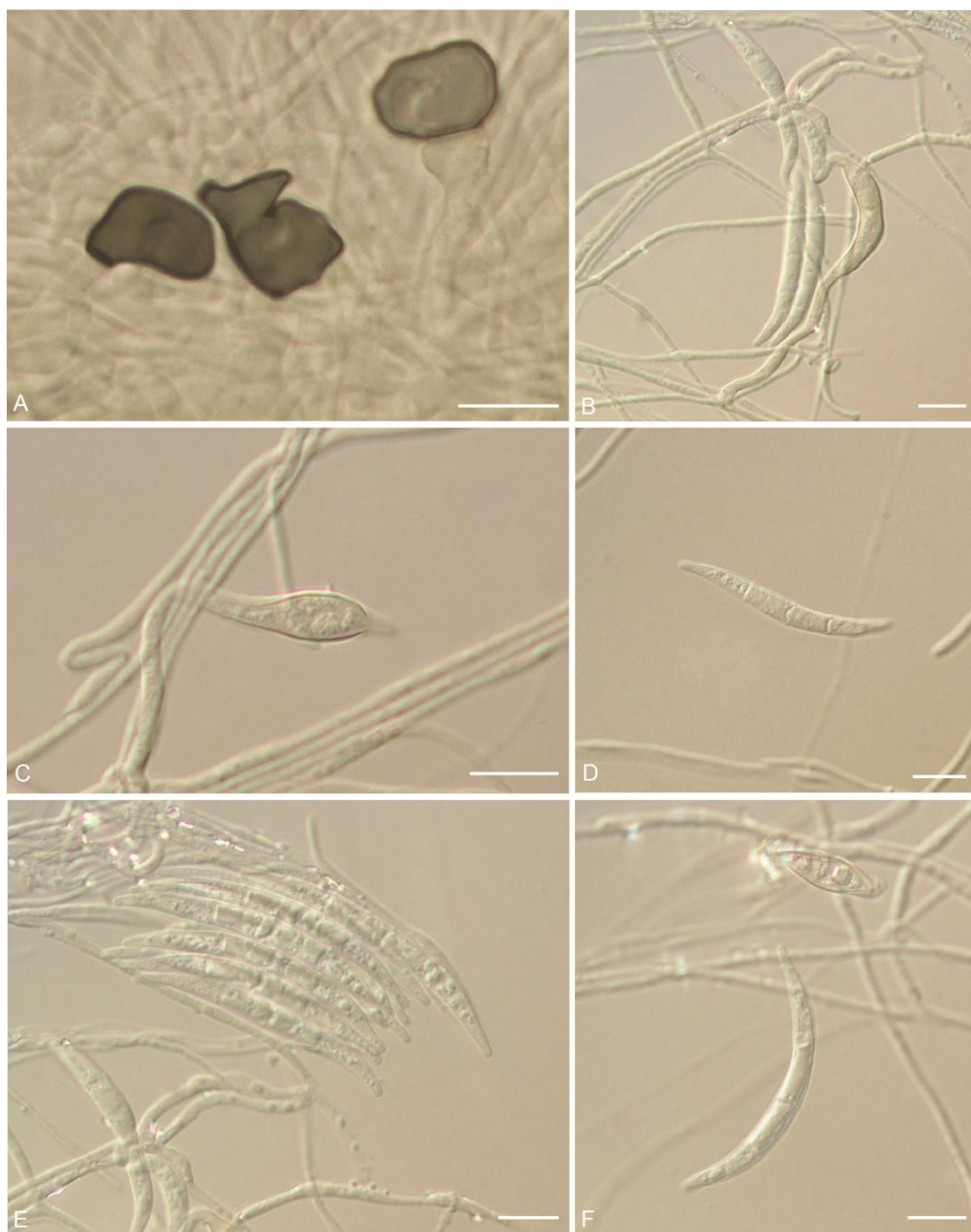


Figure 28 – *Neobifusisporella graminicola* (YNE00910). A Hyphopodia. B Conidiogenous cells and conidia. C Conidiogenous cells. D–F Conidia. Scale bars = 10 μm.

Notes – Phylogenetically, this species belongs to a cluster with *Neobifusispora graminis*. Morphologically, it differs from *Neobifusispora graminis* by having fewer conidia and rod-shaped conidia.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00910, the closest hits include Fungal sp. ZH S8-6-1 from the stem of wild rice (GenBank GQ220333.1; Identities = 383/407(94%), gaps = 5/407(1%)), *Magnaporthaceae* sp. S10-2-1 (GenBank HM008633.1; Identities = 392/427(92%), gaps = 20/427(4%)), and *Bifusispora sorghi* isolate F8831 (GenBank ON332176.1; Identities = 398/436(91%), gaps = 21/436(4%)).

Xenorhytisma C. L. Zhang, gen. nov.

Mycobank number: MB854765; Facesoffungi number: FoF16924

Etymology – The generic name refers to the tar spot forms on host leaves which resemble those caused by the genus *Rhytisma*.

Parasitic on living leaves of *Phyllostachys edulis* (*Poaceae*). Ascstromata separate or gregarious, subglobose, black, coriaceous, semi-immersed, unilocular or multilocular, glabrous. Peridium composed of 3–9 layers, with hyaline to brown cells of textura angularis. Hamathecium, hyaline, cellular, with distinct septa. Asci 8-spored, bitunicate, cylindrical, with an apical chamber and a short pedicel. Ascospores overlapping, biseriate, hyaline, fusiform, 3-septate, rarely constricted at septate, with narrowly rounded ends, smooth-walled, guttules, without gelatinous sheath. This description is based on Zeng et al. (2022).

Type species – *Xenorhytisma sichuanense* (Q. Zeng, Y.C. Lv & C.L. Yang) C.L. Zhang.

Xenorhytisma sichuanense (Q. Zeng, Y.C. Lv & C.L. Yang) C.L. Zhang, com.nov.

Mycobank number: MB854766; Facesoffungi number: FoF16951

Holotype – SICAU 22-0073

≡ *Bifusispora sichuanensis* Q. Zeng, Y.C. Lv & C.L. Yang, in Zeng, Lv, Xu, Deng, Wang, Liu, Liu, Yang & Liu, *Journal of Fungi* 8(no. 702): 14 (2022)

Description and illustration – Zeng et al. (2022).

Notes – Phylogenetically, *Xenorhytisma sichuanense* distinguishes itself from *Bifusispora*, forms a distinct independent clade F18, it is a sister group to the genera *Bifusispora* and *Neobifusispora*; therefore, we propose transferring '*Bifusispora sichuanensis*' to a new combination. Morphologically, *Xenorhytisma sichuanense* produces coriaceous ascstromata, cylindrical asci, fusiform ascospores, as noted by Zeng et al. (2022), while *Bifusispora* (Silva et al. 2019) and *Neobifusispora* does not possess a sexual morph.

Neophialophora C. L. Zhang, gen. nov.

Mycobank number: MB842509; Facesoffungi number: FoF16919

Etymology – Named after its morphological similarity to *Phialophora*.

Endophytic in the living roots of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Hyphae septate, branched, smooth, hyaline. Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, straight or curved. Conidia lunate, allantoid to fusiform, slight curved, hyaline. Hyphopodia not observed.

Type species – *Neophialophora graminis* C. L. Zhang.

Notes – Three endophytes from this study, namely YNE01207, YNE01215, and YNE01661, were found to cluster with two unidentified affinities DS324 and DS354, forming a distinct clade F22. This led to the introduction of a new genus and a new species named *Neophialophora graminis* to accommodate them.

Neophialophora graminis C. L. Zhang, sp. nov.

Mycobank number: MB842510; Facesoffungi number: FoF16941

Etymology – Named after the grass hosts from which it was isolated.

Fig. 29

Holotype – CGMCC3.20907

Endophytic in the roots of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, terminal or intercalary, hyaline, cylindrical to lageniform, straight or curved, $11\text{--}18 \times 2.5\text{--}3.5 \mu\text{m}$ ($n = 16$). Conidia lunate, allantoid to fusiform, slight curved, hyaline, $4\text{--}7 \times 1\text{--}2 \mu\text{m}$ ($n = 50$). Hyphopodia not observed.

Culture characteristics – Colonies on PDA reaching 32 mm after 25 d at 25 °C, cottony, villiform, aerial mycelium abundant, white, margin complete. Reverse grayish orange. Colonies on MEA reaching 47 mm after 14 d at 25 °C, cottony, flat, aerial mycelium few, pale yellow to hyaline, margin foggy. Reverse grayish yellow.

Material examined – China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the roots of *Poaceae* plant in October 2018, C.L. Zhang YNE01207 (Holotype CGMCC3.20907, stored in a metabolically inactive state), ex-type living culture YNE01207. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the roots of *Poaceae* plant in Naban River Watershed, October 2018, C.L. Zhang YNE01215. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the roots of *Poaceae* plant in Naban River Watershed, October 2018, C.L. Zhang YNE01661.

GenBank numbers – YNE01207: ITS = MW479024; LSU = MW478103; *ACT* = OQ918149; *RPB1* = MW482837; and *TEF1* = MW482734. YNE01215: ITS = MW479025; LSU = MW478104; *ACT* = OQ918150; *MCM7* = MW482617; *RPB1* = MW482838; and *TEF1* = MW482735. YNE01661: ITS = MW479029; LSU = ON244715; *RPB1* = ON367460; and *TEF1* = ON367455.

Notes – Phylogenetically, this genus forms a unique clade within *Magnaporthaceae* and is closely related to *Pseudophialophora* and *Budhanggurabania*. Morphologically, *Pseudophialophora* has larger conidia (Crous et al. 2017, Luo et al. 2014, Luo et al. 2015b), while *Budhanggurabania* has distinctive 3-septate ascospores. Compared to other genera in the clade, this genus is characterized by having lunate conidia. The genus was isolated as an endophyte from the roots of healthy *Poaceae* plants collected in Xishuangbanna, Yunnan Province.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01207, the closest hits are *Gaeumannomyces caricicola* CPC33925 from *Carex remota* (GenBank MK442584; Identities = 414/461(90%), gaps = 13/461(2%)), *Pseudophialophora schizachyrii* isolate AL3s4 (GenBank KF689650; Identities = 403/453(89%), gaps = 10/453(2%)), *Budhanggurabania cynodonticola* BRIP 59305 from *Cynodon dactylon* (GenBank KP162134; Identities = 404/456(89%), gaps = 14/456(3%)).

***Hongkuimyces* C.L. Zhang, gen. nov.**

Mycobank number: MB849531; Facesoffungi number: FoF16915

Etymology – Named in honor of Prof. Hongkui Chen, a pioneering figure in the fields of Chinese plant pathologist and mycology.

Endophytic in the living *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores and conidia not observed. Hyphopodia clavate, pointed at the front, or star-shaped, or lobed, hyaline when young, becoming brown when mature.

Type species – *Hongkuimyces graminicola* C. L. Zhang.

Notes – Phylogenetically, a distinct clade F26 with high bootstrap values was formed by eight endophytes from this study, namely YNE00633, YNE00635, YNE00607, YNE00626, YNE0685, YNE00987, YNE00999, and YNE01160, within *Magnaporthaceae*. Therefore, a new genus named *Hongkuimyces* was proposed to accommodate them. Within this clade, three subclades with high bootstrap values were identified, supporting their classification as three new species-level taxa: the subclade containing YNE00987, YNE00999, and YNE01160 is proposed as *Hongkuimyces graminicola*; the subclade containing YNE00633, YNE00635, and YNE00607 is proposed as *Hongkuimyces graminis*; and the subclade containing YNE00626 and YNE0685 is identified as *Hongkuimyces* sp.

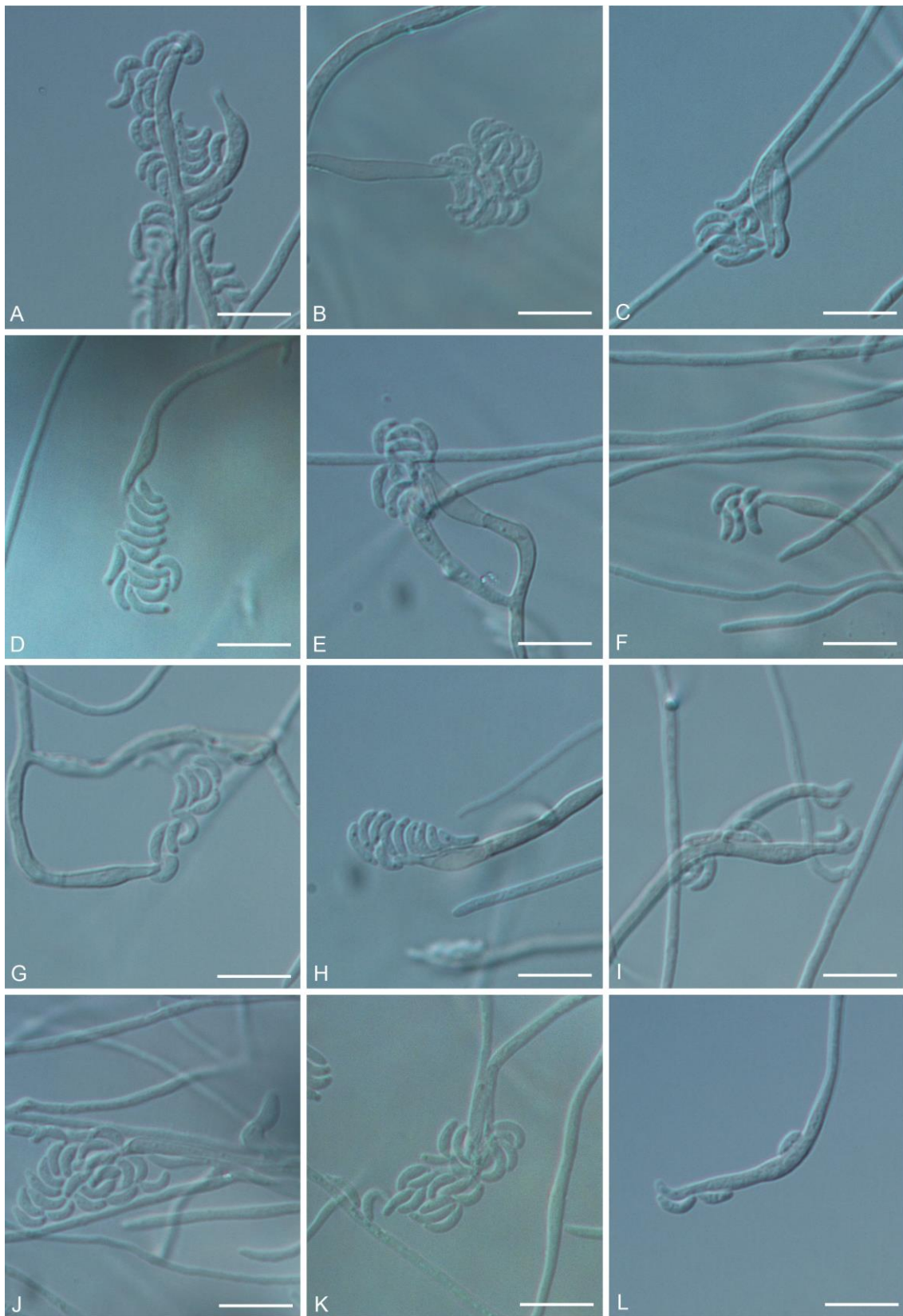


Figure 29 – *Neophialophora graminis* (YNE01207). A–L Phialide and conidia. Scale bars = 10 μ m.

Hongkuiomyces graminicola C. L. Zhang, sp. nov.

Mycobank number: MB849532; Facesoffungi number: FoF16933

Etymology – Named after the grass hosts from which it was isolated.

Fig. 30

Holotype – CGMCC3.24896

Endophytic in the stems of *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Conidiophores and conidia not observed. Hyphopodia dimorphic, mostly clavate and pointed at the front, $30.3\text{--}62.6 \times 7\text{--}12 \mu\text{m}$ ($n = 12$), or few star-shaped, $34.2 \times 25.3 \mu\text{m}$ ($n = 2$), hyaline when young, becoming brown when mature.

Culture characteristics – Colonies on PDA reaching 32.3 mm after 7 d at 25 °C, cottony, aerial mycelium moderate, hyaline to white, margin effuse, foggy. Reverse center mostly desaturated dark blue, margin grayish blue. Colonies on MEA reaching 62.7 mm after 14 d at 25 °C, cottony, aerial mycelium moderate, color changing from brown to white from center to margin. Reverse center very dark grayish yellow, margin light grayish yellow.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Poaceae* plants in Naban River Watershed, October 2018, C.L. Zhang YNE00987 (Holotype CGMCC3.24896, stored in a metabolically inactive state), ex-type living culture YNE00987. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Poaceae* plants in Naban River Watershed, October 2018, C.L. Zhang YNE00999. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Poaceae* plants in Naban River Watershed, October 2018, C.L. Zhang YNE01160.

GenBank numbers – YNE00987: ITS = MW479018, LSU = MW478114, ACT = OQ918139, MCM7 = MW482621, RPB1 = MW482840, and TEF1 = MW482727. YNE00999: ITS = MW479019, LSU = MW478115, ACT = OQ918140, MCM7 = OQ918180, RPB1 = OQ918192, and TEF1 = OQ918210. YNE01160: ITS = MW479020, LSU = MW478116, ACT = OQ918141, MCM7 = MW482619, RPB1 = MW482841, and TEF1 = MW482728.

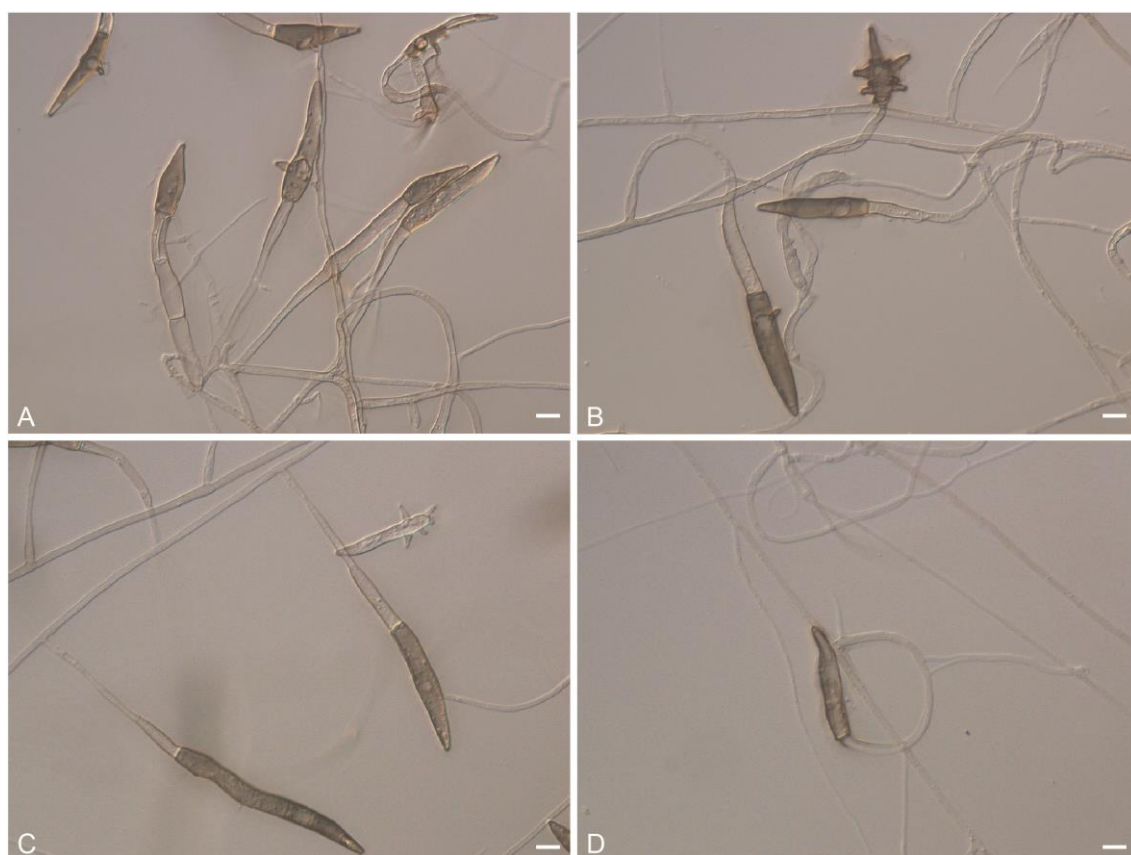


Figure 30 – *Hongkuimyces graminicola* (YNE00987). A–D Hyphopodia. Scale bars = 10 μm .

Notes – Phylogenetically, the genus forms a unique clade within *Magnaporthaceae* and is closely related to *Pseudophialophora*, *Budhanggurabania*, *Neophialophora*, and *Xenophialophora*

(in this study). Morphologically, *Hongkuomyces* differs from its close relatives by lacking conidia and conidiogenesis. Additionally, the main morphological difference between *Hongkuomyces graminicola* and *Hongkuomyces graminis* (in this study) is in their respective Hyphopodia. Specifically, the hyphopodia of *Hongkuomyces graminicola* are clavate, pointed at the front, or star-shaped, while those of *Hongkuomyces graminis* are lobed. Furthermore, these two species were isolated from different sources, with *Hongkuomyces graminicola* isolated from the stems of *Poaceae* plants and *Hongkuomyces graminis* isolated from leaves.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00987, the closest hits include Fungal sp. ZH S50-4-1 from the stem of wild rice (GenBank GQ220335; Identities = 442/481(92%), gaps = 14/481(2%)), *Gaeumannomyces caricicola* CBS145041 from *Carex remota* (GenBank NR_163360; Identities = 420/461(91%), gaps = 9/461(1%)), and Fungal sp. E14709C from the stem of *Renealmia thyrsoides* (GenBank KM265656; Identities = 423/466(91%), gaps = 16/466(3%)).

***Hongkuomyces graminis* C. L. Zhang, sp. nov.**

Fig. 31

Mycobank number: MB849533; Facesoffungi number: FoF16934

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.24895

Endophytic in the leaves of *Oryza meyeriana*. Sexual morph: Undetermined. Asexual morph: Conidiophores and conidia not observed. Hyphopodia lobed and dark brown, $11.5 \times 10.5 \mu\text{m}$ ($n = 3$).

Culture characteristics: Colonies growing on PDA reaching 27.6 mm after 7 d at 25 °C, surface cottony, aerial mycelium moderate, white, margin rhizoid. Reverse grayish blue. Colonies growing on MEA reaching 68.8 mm diam after 14 d at 25 °C, cottony, aerial mycelium few to moderate, color changing from white to hyaline from center to margin, margin effuse, foggy. Reverse dark gray.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00635 (Holotype CGMCC3.24895, stored in a metabolically inactive state), ex-type living culture YNE00635. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00607. China. Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the leaves of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE00633.

GenBank numbers – YNE00635: ITS = MW479015, LSU = MW478113, *ACT* = OQ918137, *MCM7* = MW482624, *RPB1* = MW482844, *TEF1* = MW482731. YNE00607: ITS = MW479013; LSU = MW478111; *ACT* = OQ918136; *MCM7* = MW482622; *RPB1* = MW482842; *TEF1* = MW482729. YNE00633: ITS = MW479014; LSU = MW478112; *ACT* = OQ918138; *MCM7* = MW482623; *RPB1* = MW482843; *TEF1* = MW482730.

Notes – The main morphological difference between *Hongkuomyces graminicola* and *Hongkuomyces graminis* lies in their respective hyphopodia. Specifically, the hyphopodia of *Hongkuomyces graminicola* were clavate, pointed at the front, or star-shaped, while those of *Hongkuomyces graminis* were lobed. Additionally, these two species were isolated from different sources, with *Hongkuomyces graminicola* isolated from the stems of *Poaceae* plants and *Hongkuomyces graminis* isolated from leaves.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE00635, the closest hits include Fungal sp. ZH S50-4-1 from the stem of wild rice (GenBank GQ220335; Identities = 460/482(95%), gaps = 5/482(1%)), *Gaeumannomyces* sp. isolate 15 from *Brachypodium rupestre* (GenBank MW528562; Identities = 427/471(91%), gaps = 14/471(2%)), and *Gaeumannomyces* sp. MH576 (GenBank FJ430719; Identities = 427/473(90%), gaps = 13/473(2%)).

Xenophialophora C.L. Zhang, gen. nov.

Mycobank number: MB842515; Facesoffungi number: FoF16923

Etymology – Named after its morphological similarity to *Phialophora*.

Endophytic in the living *Poaceae* plants. Sexual morph: Undetermined. Asexual morph: Mycelium consisting of septate, branched, smooth, hyaline to brown hyphae. Conidiophores differentiated to some extent, branched. Conidiogenous cells phialidic, hyaline to pale yellow, grouped, terminal or intercalary, lageniform, cylindrical, straight or curved. Conidia lunate, slightly curved, allantoid, hyaline. Hyphopodia chlamydospore-like, globose, hyaline when young, becoming lobed and brown when mature.

Type species – *Xenophialophora graminicola* C.L. Zhang.

Notes – Three endophytes from this study, namely YNE1240, YNE01247, and YNE01531, form a distinct clade F27 within *Magnaporthaceae*, leading to the proposal of a new genus named *Xenophialophora* to accommodate them. Among these, YNE1240 and YNE01247 constitute a distinct subclade, providing support for their classification as a new species, *Xenophialophora graminicola*.

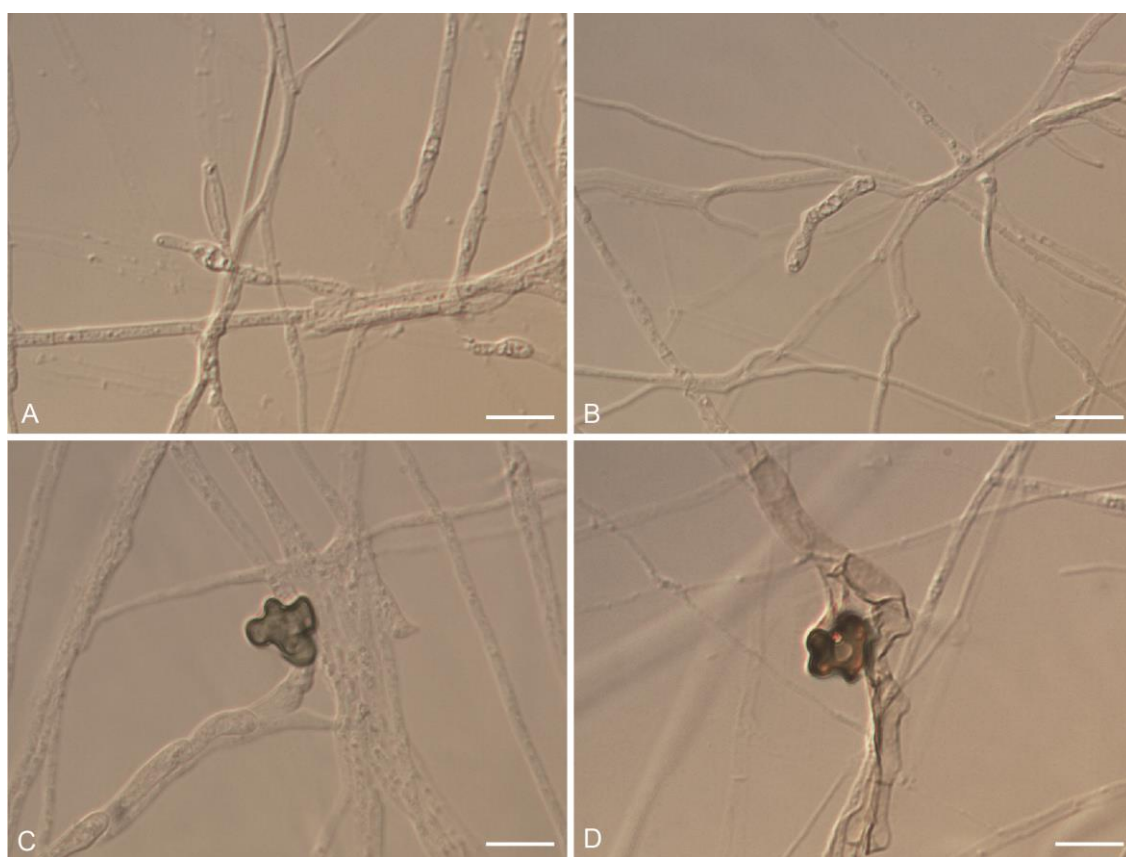


Figure 31 – *Hongkuimyces graminis* YNE00635. A–B Hyphae. C, D Hyphopodia. Scale bars = 10 μ m.

Xenophialophora graminicola C. L. Zhang, sp. nov.

Fig. 32

Mycobank number: MB843759; Facesoffungi number: FoF16950

Etymology – Named after the grass hosts from which it was isolated.

Holotype – CGMCC3.20997

Endophytic in the stems of *Oryza meyeriana*. Sexual morph: Undetermined. Asexual morph: Conidiogenous cells phialidic, hyaline, lageniform, $13.5 \times 5 \mu$ m, with a cylindrical collarette up to 1.5μ m. Conidia allantoid to oval, hyaline, $6\text{--}11.5 \times 2\text{--}3.5 \mu$ m ($n = 50$). Hyphopodia lobed, hyaline at the beginning, become dark brown when mature, $14.5\text{--}15 \times 14.5\text{--}18.5 \mu$ m ($n = 10$).

Culture characteristics – Colonies on PDA reaching 25 mm after 7 d at 25 °C, flat, white, aerial mycelium few. Reverse center dark grayish blue, margin grayish yellow. Colonies on MEA reaching 63 mm after 14 d at 25 °C, flat, white, aerial mycelium few. Reverse dark grayish yellow to mostly desaturated dark orange.

Material examined – China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE01240 (Holotype CGMCC3.20997, stored in a metabolically inactive state), ex-type living culture YNE01240. China, Yunnan Province, Xishuangbanna, Naban River Watershed National Nature Reserve, isolated from the stems of *Oryza meyeriana* subsp. *granulata* (*Poaceae*), October 2018, C.L. Zhang YNE01247.

GenBank number: YNE01240: ITS = MW479021; LSU = MW478108; ACT = OQ918142; MCM7 = MW482618; RPB1 = MW482847; and TEF1 = MW482725. YNE01247: ITS = MW479022; LSU = OQ891275; ACT = OQ918143; TEF1 = OQ918209.

Notes – Phylogenetically, this genus forms a unique clade within *Magnaporthaceae* and is closely related to *Pseudophialophora*, *Budhanggurabania* and *Neophialophora* (in this study). Morphologically, the closely related genus *Pseudophialophora* has shorter and fatter oblong ellipsoidal conidia (Crous et al. 2017, Luo et al. 2014, Luo et al. 2015b), while *Budhanggurabania* has cylindrical conidia and produces teleomorphic spores (Crous et al. 2015), and *Neophialophora* has lunate conidia. In contrast, this genus has hyphopodia and lunate conidia. The species was isolated as an enophytic fungus from the stems of healthy *Oryza meyeriana* subsp. *granulata* from Xishuangbanna, Yunnan Province, China.

Based on a sequence similarity search against the NCBI's GenBank nucleotide database using the ITS sequence of strain YNE01240, the closest hits include *Falciphoriella solaniterrestris* CBS 117.83 from field soil (GenBank KM484842; Identities = 423/472(90%), gaps = 11/472(2%)), *G. australiensis* CPC26058 from *Triticum aestivum* (GenBank KX306480; Identities = 423/472(90%), gaps = 15/472(3%)), and *Gaeumannomyces caricicola* CPC33925 from *Carex remota* (GenBank MK442584; Identities = 419/470(89%), gaps = 9/470(1%)).



Figure 32 – *Xenophialophora graminicola* (YNE01240). A–B Hyphopodia. C Phialide. D–E Conidia. Scale bars = 10 µm.

DISCUSSION

Prior to this study, five families within *Magnaporthales*, viz. *Magnaporthaceae*, *Pyriculariaceae*, *Ophioceraceae*, *Pseudohalonectriaceae*, and *Ceratosphaeriaceae*, were introduced through multi-locus phylogenetic analysis (Hongsanan et al. 2017, Klaubauf et al. 2014, Luo et al. 2019, Thongkantha et al. 2009). Except for species in the families *Ceratosphaeriaceae* and *Pseudohalonectriaceae*, which are reported on decayed wood in aquatic or terrestrial habitats, *Magnaporthales* comprises a diverse array of plant-pathogenic and endophytic fungi, most of which are associated with monocotyledons. A large number of endophytic fungi isolated from *Poaceae* plants, one of the most diverse plant family worldwide, are found in *Magnaporthaceae*, *Pyriculariaceae*, and *Ophioceraceae* (Feng et al. 2021). This study conducted phylogenetic and

taxonomic analyses of *Magnaporthales*, focusing on those endophytic fungi. The analyses resulted in the proposal of 42 new taxa, comprising one new family, 14 new genera, 25 new species, and two new combinations. Consequently, the updated classification of the order *Magnaporthales* now includes six families, 52 genera, and 305 species, as detailed in Supplementary Table 2.

Based on combined multi-locus sequence data, *Aquafiliformis lignicola*, *Muraeriata africana*, *Muraeriata collapsa*, and *Plagiosphaera immersa* form the most basal lineage of the *Magnaporthaceae* family (Luo et al. 2019, Song et al. 2019). However, the phylogenetic position of *Aquafiliformis*, *Plagiosphaera*, and *Muraeriata* was uncertain due to limited sequence information. Our phylogenetic analyses of LSU, MCMC7, RPB1 and TEF1 sequences for species of *Magnaporthales* (Figs 1–2) revealed six distinct main clades. One main clade (D), which includes *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*, is clearly separated from another main clade (F) containing other species of *Magnaporthaceae*. Further phylogenomic analysis confirmed this separation. Therefore, six families corresponding to the six main clades are defined within *Magnaporthales*, and a new family, *Plagiosphaeraceae*, is introduced to accommodate *Aquafiliformis*, *Muraeriata*, and *Plagiosphaera*. Morphologically, members of *Plagiosphaeraceae* have perithecial ascomata with fusiform to filiform ascospores. Ecologically, *Muraeriata* species are saprobic in woody habitats (Huhndorf et al. 2008), *Aquafiliformis lignicola* is saprobic on decaying wood submerged in freshwater (Luo et al. 2019), and *Plagiosphaera immersa*, the only confirmed species of the genus, is found on dead stems of *Urtica dioica* (Urticaceae) and other herbaceous plants. Our study also found endophytic *Aquafiliformis lignicola* in healthy Poaceae plants. Thus, members of *Plagiosphaeraceae* exhibit various nutritional and lifestyle modes, ranging from saprobic to endophytic.

The monotypic family *Ophioceraeae* was introduced by Klaubauf et al. (2014). Ecologically, most species of *Ophioceras* are found on decaying woody substrates and herbaceous plants in aquatic or terrestrial environments (Jiang et al. 2021, Luo et al. 2019, Shearer et al. 1999). *Ophioceras freycinetiae* was recently discovered on leaf spots of *Freycinetia banksii* (Pandanaeae) (Crous et al. 2021a). In this study, *Ophioceras graminis* was identified as endophytic fungus from healthy leaves of Poaceae plants. The strain SYPF 8345 from *Panax notoginseng* (Araliaceae) (GenBank MF536887) and an uncultured clone 3183 from soil (GenBank MF571451) showed closest similarity to *Ophioceras graminis*. Morphologically, *Ophioceras freycinetiae* and *Ophioceras graminis*, as asexual morphs linked to the genus, exhibit *Phialophora*-like asexual states, typically having phialidic structures with apical collarete. They can be distinguished by their asexual morph compared to other sexual *Ophioceras* species (Jiang et al. 2021, Luo et al. 2019, Shearer et al. 1999). *Ophioceras graminis* can further be distinguished by its smaller aseptate lunate to fusiform conidia and brown, globose to lageniform appressoria compared to *Ophioceras freycinetiae* (Crous et al. 2021a).

Pyriculariaceae was introduced by Klaubauf et al. (2014). Prior to this study, *Pyriculariaceae* consisted of 11 genera (Hernandez Restrepo et al. 2015, Klaubauf et al. 2014, Marin-Felix et al. 2019, Wijayawardene et al. 2020). However, this study introduced two new genera in *Pyriculariaceae*. Morphologically, the asexual morphs are hyphomycetous with simple branched conidiophores. Conidiogenous cells are integrated, pigmented, and denticulate, with macroconidia that are hyaline to brown, transversely septate, ellipsoid, obclavate, or pyriform (Klaubauf et al. 2014). However, some members in *Pyriculariaceae*, such as *Pyricularia grisea* and *Pyricularia oryzae*, produce lunate microconidia on SNA (Klaubauf et al. 2014, Zhang et al. 2014). *Bipyricularia graminis* and an unnamed *Pyriculariaceae* sp. YNE00680 were observed to produce pyriform macroconidia in culture, similar to most members of *Pyriculariaceae*, and lunate microconidia on SNA, similar to *Pyricularia*. Ecologically, most members of *Pyriculariaceae* are pathogenic on cereals or turfgrass, such as *Pyricularia oryzae*, the rice blast fungus, and *Pyricularia grisea*, the *Digitaria* blast fungus (Klaubauf et al. 2014, Zhang et al. 2016a). In this study, *Bipyricularia graminis* and an unnamed *Pyriculariaceae* sp. YNE00680 were identified as endophytes in healthy Poaceae plants. The presence of these endophytic *Pyriculariaceae* species in

healthy stems and leaves of *Poaceae* plants indicates that they can live or at least persist for a period of their life cycles, without causing visible damage to their hosts.

Magnaporthaceae is the most diverse family within the order *Magnaporthales*. Based on our phylogenetic analyses of ITS, LSU, ACT, MCM7, RPB1, and TEF1 sequences for species of *Magnaporthaceae* (Fig. 6), the family encompasses 28 genera and three unnamed generic lineages. This study introduced 10 new genera, 25 new species, and one new combination. Morphologically, members of *Magnaporthaceae* typically produce *Phialophora*-like asexual morphs with two types of conidia, one aseptate microconidia and the other septate macroconidia. Genera such as *Omnidemptus*, *Dimorphiconidia*, *Neodimorphiconidia*, *Bifusisporella*, and *Neobifusisporella* illustrate this diversity, indicating not only close phylogenetic relationships but also morphological similarities. Ecologically, *Magnaporthaceae* species are frequently associated with grasses or cereals, acting as pathogens or endophytes. Prior to this study, several endophytic genera and species within the *Magnaporthaceae* family have been recorded. For example, *Bifusisporella sorghi* was isolated from the healthy leaves of *Sorghum bicolor* (*Poaceae*) in Brazil (Silva et al. 2019), *Bussabanomyces longisporus* was found in the healthy leaves of *Amomum siamense* (*Zingiberaceae*) in Thailand (Klaubauf et al. 2014), *Falciphora oryzae* was isolated from the healthy roots of *Oryza meyeriana* subsp. *granulata* (*Poaceae*) in China (Yuan et al. 2010), and *Pseudophialophora* species were isolated from the roots of healthy *Poaceae* plants (Crous et al. 2017, Luo et al. 2014, Luo et al. 2015b). In this study, we identified 9 new endophytic genera and 24 new endophytic species within the *Magnaporthaceae* family. The significant diversity of endophytic *Magnaporthaceae* species in healthy *Poaceae* plants and other monocotyledons indicates potential for discovering additional taxa through further sampling from different regions. On the other hand, most *Gaeumannomyces* species cause take-all disease in *Poaceae* plants (Hernández-Restrepo et al. 2016). However, *Gaeumannomyces amomi* has been reported as an endophyte in the healthy leaves and pseudostems of *Alpinia malaccensis* and *Amomum siamense* (Bussaban et al. 2001). Additionally, species in *Magnaporthiopsis* are necrotrophic parasites infecting roots of grasses (Luo et al. 2017, Luo & Zhang 2013, Vines et al. 2020, Wong et al. 2022). *Nakataea oryzae* causes rice stem rot (Luo & Zhang 2013). *Omnidemptus affinis* and *Omnidemptus lunatus* were isolated from leaf spots on *Panicum effusum* (*Poaceae*) and *Carpobrotus glaucescens* (*Aizoaceae*) (Cannon & Alcorn 1994, Hernández-Restrepo et al. 2019). In this study, *Gaeumannomyces yunnanensis*, *Magnaporthiopsis stipae*, *Nakataea graminis*, *Omnidemptus yunnanensis*, and *Omnidemptus zhejiangensis* were isolated as endophytes. Inoculation experiments have confirmed *Falciphora oryzae* as a dark septate endophyte, promoting the growth and enhancing disease resistance of rice (Su et al. 2013, Yuan et al. 2010), while *Pseudophialophora* spp. have negative effects on the growth of switchgrass (Luo et al. 2015b). In this study (data not shown), we observed no significant difference in the growth of rice treated with *Gaeumannomyces yunnanensis* isolate YNE01171, *Omnidemptus yunnanensis* isolate YNE01014, and *Omnidemptus zhejiangensis* isolate ZJE01773 compared to the control ($p \geq 0.05$). Hyphae were also observed in the roots of the treated rice plants. However, *Magnaporthiopsis stipae* isolate NME00039 was found to be highly pathogenic to rice. These interactions between plants and endophytes suggest that endophytes may exhibit beneficial or neutral effects on plant growth, and some endophytic fungi may also be latent pathogens.

The nutritional and lifestyle characteristics are among the most important features of fungi. Different families of *Magnaporthales* have adapted to various nutritional and lifestyle modes. The basal lineages, includes *Ceratosphaeriaceae* and *Pseudohalonectriaceae*, are saprobic. *Ceratosphaeriaceae* species are commonly found on decayed wood, or dead twigs (Wijayawardene et al. 2020), while *Pseudohalonectriaceae* species are saprobic on wood in aquatic habitats (Hongsan et al. 2017). Most members in *Ophioceraaceae* and *Plagiosphaeraceae* adopt saprobic lifestyles, although some have transitioned to pathogenic or endophytic lifestyles associated with plants. Most species in the *Pyriculariaceae* and *Magnaporthaceae* are either pathogenic or endophytic with monocotyledons. These families display various ecological traits but share a common evolutionary trend of transitioning from saprobic to pathogenic or endophytic lifestyles.

Living as endophytes in healthy plant tissues may play a significant role in their dispersal (Nelson et al. 2020).

Evidence from endophytes, such as the formation of appressoria and the production of cellulose and lignin-degrading enzymes, suggesting that all fungi may have endophytic ancestors (Bhunjun et al. 2024). Appressoria, along with hyphopodia (Emmett & Parbery 1975), are specialized cells or adhesion structures from which a penetration peg emerges to infiltrate host tissues (Chethana et al. 2021b). These structures can be unicellular, forming terminally on germ tubes or laterally or intercalary on hyphae, and include proto-appressoria, hyaline appressoria, and dark/pigmented appressoria (Chethana et al. 2021b). Appressoria are produced not only by pathogens but also by endophytes and saprobes (Chethana et al. 2021a). Most endophytic *Magnaporthales* fungi produce melanized appressoria, similar in form and shape to those in their pathogenic counterparts. For example, the endophytic genus *Bifusisporella* produces brown, elongated to lobed hyphopodia. Similarly, *Gaeumannomyces yunnanense*, an endophytic species, and many pathogenic species of *Gaeumannomyces* produce brown, lobed hyphopodia (Hernández-Restrepo et al. 2016). The pathogenic species in *Pyricularia* (Talbot 2003) and the endophytic species in *Bipyrularia* produce dome-shaped appressoria. Recent studies have shown that melanized appressoria are prevalent among *Magnaporthales*, with such structures found in *Pyricularia*, *Omnidemptus*, and *Kohlmeyeriopsis*, as well as both compound and melanized forms in *Gaeumannomyces* (Chethana et al. 2021a). Many fungi can switch between endophytic, pathogenic, and saprobic lifestyles (Photita et al. 2004, Promputtha et al. 2007, Promputtha et al. 2010). Observations of appressoria formation from germ tubes after conidia germination in saprobes suggest lifestyle shifts from saprobic to pathogenic or endophytic modes (Konta et al. 2016, 2023, Phukhamsakda et al. 2016). Additionally, we observed that most endophytic *Magnaporthales* fungi are capable of producing cellulose and lignin-degrading enzymes (data not shown), which are not necessary for an endophytic lifestyle. The presence of appressoria and degradation enzymes in endophytic *Magnaporthales* species strongly suggests that their lifestyle can shift to saprobic or pathogenic modes under specific nutrient or environmental conditions.

In summary, the discovery of numerous new taxa within *Magnaporthales*, especially within the family *Magnaporthaceae*, has significantly expanded our understanding of the diversity within this order. These findings provide valuable insights into the ecological roles and functional diversity of fungi within *Magnaporthales*.

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Supplementary Table 1 Isolates used in this study and their GenBank accession numbers. Newly generated sequences are indicated in bold, unknown sequences are indicated in ‘–’.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Cryphonectriaceae</i> (outgroup)	<i>Cryphonectria nitschkei</i>	CBS 109758	Russia: Siberia	<i>Quercus mongolica</i>	MN172407	EU255074	genome data	genome data	genome data	genome data	GCA_006503525.1
<i>Cryphonectriaceae</i> (outgroup)	<i>Cryphonectria parasitica</i>	EP155, ATCC 38755	USA	unknown	AY141856	EU199123	genome data	genome data	genome data	genome data	GCA_011745365.1
<i>Ceratosphaeriaceae</i>	<i>Ceratosphaeria aquatica</i>	MFLUCC 18-1337, MFLU 18-2323 (T)	China	Submerged wood	MK828612	MK835812	–	–	–	MN194065	–
<i>Ceratosphaeriaceae</i>	<i>Ceratosphaeria lignicola</i>	MFLUCC 18-0342, MFLU 18-1457 (T)	Thailand	Submerged wood	MK828613	MK835813	–	–	–	MN194066	–
<i>Ceratosphaeriaceae</i>	<i>Ceratosphaeria yunnanensis</i>	KUMCC 21-0013	China	<i>Heteropanax fregans</i>	OP895173	OL473547	–	–	–	OL505597	–
<i>Magnaporthaceae</i>	<i>Atripes paspali</i>	COAD 2959	Brazil	<i>Paspalum guenoarum</i>	MN747361	MN749075	–	–	MN755608	MN698637	–
<i>Magnaporthaceae</i>	<i>Atripes paspali</i>	COAD 2960 (T)	Brazil	<i>Paspalum guenoarum</i>	MN747362	MN749076	–	–	MN755609	MN698638	–
<i>Magnaporthaceae</i>	<i>Atripes paspali</i>	COAD 2961	Brazil	<i>Paspalum guenoarum</i>		MN749077	–	–	MN755610	MN698639	–
<i>Magnaporthaceae</i>	<i>Atripes paspali</i>	COAD 2962	Brazil	<i>Paspalum guenoarum</i>	MN747363	MN749078	–	–	MN755611	MN698640	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminicola</i>	CGMCC3.24891, YNE00934(T)	China: Yunnan	Living leaves of <i>Panicum</i> sp.	MW479074	MW478089	OQ918108	MW482563	MW482801	MW482636	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminicola</i>	YNE01000	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479075	MW478090	OQ918110	MW482562	MW482802	MW482641	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminicola</i>	YNE01150	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479077	MW478092	–	MW482561	MW482805	MW482642	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminicola</i>	YNE01170	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479079	MW478097	OQ918109	MW482560	MW482803	MW482637	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminis</i>	CGMCC3.20899, YNE01143(T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479087	MW478068	OQ918113	OQ942228	MW482809	MW482644	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminis</i>	YNE00994	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479084	MW478066	OQ918111	MW482565	MW482808	MW482643	–
<i>Magnaporthaceae</i>	<i>Bifusisporella graminis</i>	YNE01004	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479085	MW478067	OQ918112	MW482564	MW482807	MW482645	–
<i>Magnaporthaceae</i>	<i>Bifusisporella sorghi</i>	URM 7442 (T)	Brazil: Pernambuco	leaves of <i>Sorghum bicolor</i>	MK060155	MK060153	–	–	MK060159	MK060157	–
<i>Magnaporthaceae</i>	<i>Bifusisporella sorghi</i>	URM 7864	Brazil	Leaves of <i>Sorghum bicolor</i>	MK060156	MK060154	–	–	MK060160	MK060158	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Budhanggurabania cynodonticola</i>	BRIP 59305 (T)	Australia: New South Wales	Roots of <i>Cynodon dactylon</i>	KP162134	KP162140	–	KP162131	KP162143	KP162138	–
<i>Magnaporthaceae</i>	<i>Budhanggurabania cynodonticola</i>	BRIP 59306	Australia: New South Wales	<i>Cynodon dactylon</i>	KP162135	KP162141	–	KP162132	KP162144	–	–
<i>Magnaporthaceae</i>	<i>Budhanggurabania cynodonticola</i>	BRIP 59307	Australia: New South Wales	<i>Cynodon dactylon</i>	KP162136	KP162142	–	KP162133	KP162145	KP162139	–
<i>Magnaporthaceae</i>	<i>Budhanggurabania cynodonticola</i>	RW3-4	unknown	Roots of <i>Cynodon dactylon</i>	KJ855509	KM401649	–	KP007352	KP268931	KP282715	–
<i>Magnaporthaceae</i>	<i>Buergenerula spartinae</i>	14CM2122	unknown	<i>Spartina maritima</i>	KX263857	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Buergenerula spartinae</i>	ATCC 22848	USA	Leaves of <i>Spartina alterniflora</i>	JX134666	DQ341492	–	JX134706	JX134720	JX134692	–
<i>Magnaporthaceae</i>	<i>Buergenerula spartinae</i>	AV4BVC2	Portugal	<i>Spartina maritima</i>	KX263803	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Bussabanomyces longisporus</i>	CBS 125232 (T)	Thailand: Chiang Mai	Leaves of <i>Amomum siamense</i>	KM484832	KM009154	–	KM009178	KM009190	KM009202	–
<i>Magnaporthaceae</i>	<i>Bussabanomyces longisporus</i>	CMUZE0005	Thailand	Leaves of <i>Amomum siamense</i>	AY265319	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Candidacolonium cynodontis</i>	HP24-3	USA	Roots of <i>Cynodon dactylon</i>	KJ855497	KM401637	–	KP007344	KP268919	KP282703	–
<i>Magnaporthaceae</i>	<i>Candidacolonium cynodontis</i>	HP38-4	USA	Roots of <i>Cynodon dactylon</i>	KJ855498	KM401638	–	KP007345	KP268920	KP282704	–
<i>Magnaporthaceae</i>	<i>Candidacolonium agrostidis</i>	THAS136	unknown	unknown	OM910761	OM910782	–	OM938227	OM938229	OM938231	–
<i>Magnaporthaceae</i>	<i>Candidacolonium agrostidis</i>	THAS137	unknown	unknown	OM910762	OM910783	–	OM938228	OM938230	OM938232	–
<i>Magnaporthaceae</i>	<i>Dimorphiconidia graminis</i>	CGMCC3.24892, YNE00589(T)	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478967	MW478051	OQ918114	MW482605	MW482817	MW482696	–
<i>Magnaporthaceae</i>	<i>Dimorphiconidia graminis</i>	YNE00526	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478966	–	–	MW482604	MW482818	MW482695	–
<i>Magnaporthaceae</i>	<i>Dimorphiconidia graminis</i>	YNE00640	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478968	–	–	MW482603	MW482819	MW482697	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
Magnaporthaceae	<i>Dimorphiconidia yunnanensis</i>	CGMCC3.20909, YNE01381(T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478979	MW478054	OQ918115	MW482606	MW482820	MW482701	–
Magnaporthaceae	<i>Dimorphiconidia yunnanensis</i>	YNE01384	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478983	MW478061	OQ918117	MW482600	MW482821	MW482702	–
Magnaporthaceae	<i>Dimorphiconidia yunnanensis</i>	YNE01387	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478982	MW478062	–	–	MW482824	MW482703	–
Magnaporthaceae	<i>Dimorphiconidia yunnanensis</i>	YNE01389	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478980	MW478055	OQ918116	MW482608	MW482822	MW482704	–
Magnaporthaceae	<i>Falciphora oryzae</i>	C3-1	unknown	unknown	FJ752606	–	–	–	–	–	–
Magnaporthaceae	<i>Falciphora oryzae</i>	R5-6-1, CBS 125863 (T)	China: Xishuang–banna	Living roots of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	EU636699	KJ026705	genome data	KJ026709	KJ026706	JN857963	GCA_000733355.1
Magnaporthaceae	<i>Falciphora oryzae</i>	YNE00507	China: Yunnan	Living roots of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478912	–	–	MW482572	MW482746	MW482717	–
Magnaporthaceae	<i>Falciphora oryzae</i>	YNE00525	China: Yunnan	Living roots of <i>Saccharum</i> sp.	MW478913	OQ891270	OQ918155	OQ918181	OQ918194	OQ918196	–
Magnaporthaceae	<i>Falciphora oryzae</i>	YNE00549	China: Yunnan	Living roots of <i>Saccharum</i> sp.	MW478914	–	–	MW482571	MW482745	MW482719	–
Magnaporthaceae	<i>Falciphora oryzae</i>	YNE01374	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW478915	–	–	MW482569	MW482744	–	–
Magnaporthaceae	<i>Falciphoriella solaniterrestris</i>	CBS 117.83 (T)	Netherlands	Soil	KM484842	KM484959	–	–	KM485058	–	–
Magnaporthaceae	<i>Gaeumannomycella caricicola</i>	CPC 33925, CBS 145041 (T)	Germany	<i>Carex remota</i>	MK442584	MK442526	–	–	–	–	–
Magnaporthaceae	<i>Gaeumannomycella caricis</i>	CBS 388.81 (T)	UK	<i>Carex rostrata</i>	KM484843	KM484960	–	–	KM485059	KX306674	–
Magnaporthaceae	<i>Gaeumannomycella caricis</i>	CPC 26262, CBS 141374	UK	<i>Carex rostrata</i>	KX306478	KX306548	–	–	KX306671	KX306675	–
Magnaporthaceae	<i>Gaeumannomycella</i> sp.	15	Spain: Navarra	<i>Brachypodium rupestre</i>	MW528562	–	–	–	–	–	–
Magnaporthaceae	<i>Gaeumannomyces amomi</i>	CMUZE0002, CBS 109354, BCC 4066 (T)	Thailand	Leaves of <i>Amomum</i> sp.	AY265318	DQ341493	–	–	–	KX306679	–
Magnaporthaceae	<i>Gaeumannomyces amomi</i>	YNE00986	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478923	MW478101	–	MW482573	MW482749	MW482646	–
Magnaporthaceae	<i>Gaeumannomyces amomi</i>	YNE01245	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478927	MW478102	–	MW482574	MW482750	MW482649	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Gaeumannomyces arxii</i>	CBS 902.73, DAR 17502	Australia: New South Wales	<i>Stenotaphrum secundatum</i>	KM484836	KM484953	–	–	KM485052	KX306680	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces arxii</i>	CBS 903.73, DAR 23471 (T)	Australia: New South Wales	Stolon of <i>Pennisetum clandestinum</i>	KM484837	KM484954	–	–	KM485053	KX306681	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces arxii</i>	CPC 26054, CBS 141375	USA: California	<i>Stenotaphrum secundatum</i>	KX306479	KX306549	–	–	KX306618	KX306682	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces australiensis</i>	CPC 26058, DAR 32100, CBS 141387 (T)	Australia	<i>Triticum aestivum</i>	KX306480	KX306550	–	–	KX306619	KX306683	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces avenae</i>	CBS 187.65	Netherlands	Roots of <i>Avena sativa</i>	JX134668	JX134680	–	JX134708	JX134722	JX134694	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces avenae</i>	CBS 870.73, DAR 20999	Australia	<i>Avena sativa</i>	KM484833	DQ341495	–	–	KM485048	KX306684	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces avenae</i>	CPC 26258 (T)	Ireland	<i>Avena sativa</i>	KX306486	KX306556	–	–	KX306622	KX306688	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces californicus</i>	CPC 26044, CBS 141377 (T)	USA	<i>Stenotaphrum secundatum</i>	KX306490	KX306560	–	–	KX306625	KX306691	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces ellisiorum</i>	CBS 387.81 (T)	United Kingdom: England	Dead culm and sheath of <i>Deschampsia caespitosa</i>	KM484835	KM484952	–	–	KM485051	KX306692	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces floridanus</i>	CPC 26037, CBS 141378 (T)	USA	<i>Stenotaphrum secundatum</i>	KX306491	KX306561	–	–	KX306626	KX306693	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces fusiformis</i>	CPC 26068, CBS 141379 (T)	USA	<i>Oryza sativa</i>	KX306492	KX306562	–	–	KX306627	KX306694	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces glycinicola</i>	CPC 26057, DAR 28746 (T)	USA	<i>Glycine max</i>	KX306493	KX306563	–	–	KX306628	KX306695	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces glycinicola</i>	CPC 26266, CBS 141380	USA	<i>Glycine max</i>	KX306494	KX306564	–	–	KX306629	KX306696	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces graminicola</i>	CBS 352.93, PD 93/290 (T)	Netherlands	Stems of <i>Ctenanthe</i> sp.	KM484834	DQ341496	–	–	KM485050	KX306697	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces graminicola</i>	CPC 26025, CBS 141381	USA	<i>Stenotaphrum secundatum</i>	KX306495	KX306565	–	–	KX306630	KX306698	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces graminicola</i>	CPC 26036, CBS 141382	USA	<i>Stenotaphrum secundatum</i>	KX306496	KX306566	–	–	KX306631	KX306699	–
<i>Magnaporthaceae</i>	<i>Gaeumannomyces graminicola</i>	CPC 26056, CBS 141383	USA	<i>Eremochloa ophiuroides</i>	KX306497	KX306567	–	–	KX306632	KX306700	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	CPC 26020, CBS 141384	USA	<i>Cynodon dactylon</i> × <i>C. transvaalensis</i>	KX306498	KX306568	–	–	KX306633	KX306701	–
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	CPC 26035, CBS141386	USA	<i>Cynodai dactylcn</i> × <i>C. transvaalensis</i>	KX306502	KX306572	–	–	KX306637	KX306705	–
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	CPC 26039	USA	<i>Cynodai dactylcn</i> × <i>C. transvaalensis</i>	KX306503	KX306573	–	–	KX306638	KX306706	–
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	DR10-3	unknown	Roots of <i>Cynodon dactylon</i>	KJ855488	KM401630	–	KP007337	KP268912	KP282694	–
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	DR6-4	unknown	Roots of <i>Cynodon dactylon</i>	KJ855492	KM401629	–	KP007336	KP268911	KP282698	–
Magnaporthaceae	<i>Gaeumannomyces graminis</i>	RS7-1	unknown	Roots of <i>Cynodon dactylon</i>	KJ855507	KM401647	–	KP007350	KP268929	KP282713	–
Magnaporthaceae	<i>Gaeumannomyces hyphopodioides</i>	CBS 350.77, G6, ATCC 28234, IMI 187786 (T)	UK	Roots of <i>Zea mays</i>	KX306506	KX306576	–	KM009180	KM009192	KM009204	–
Magnaporthaceae	<i>Gaeumannomyces hyphopodioides</i>	CBS 541.86, CPC 26247	Germany	Seedling of <i>Triticum aestivum</i>	KX306507	KX306577	–	–	KX306641	KX306709	–
Magnaporthaceae	<i>Gaeumannomyces hyphopodioides</i>	CPC 26249	UK	<i>Triticum aestivum</i>	KX306510	KX306580	–	–	–	KX306711	–
Magnaporthaceae	<i>Gaeumannomyces nanograminis</i>	GSGC15-3	USA	Roots of <i>Cynodon dactylon</i>	KJ855494	KM401634	–	KP007341	KP268916	KP282700	–
Magnaporthaceae	<i>Gaeumannomyces nanograminis</i>	GSGC15-4, BPI 911226, CBS 147102 (T)	USA	Roots of <i>Cynodon dactylon</i>	KJ855495	KM401635	–	KP007342	KP268917	KP282701	–
Magnaporthaceae	<i>Gaeumannomyces oryzaicola</i>	CPC 26063, CBS 141390 (T)	USA	<i>Oryza sativa</i>	KX306516	KX306586	–	–	KX306646	KX306717	–
Magnaporthaceae	<i>Gaeumannomyces oryzae</i>	CBS 235.32	USA	<i>Oryza sativa</i>	JX134669	JX134681	–	JX134709	JX134723	JX134695	–
Magnaporthaceae	<i>Gaeumannomyces oryzae</i>	CPC 26030, CBS 141391	The Bahamas	<i>Cynodon dactylon</i> × <i>C. transvaalensis</i>	KX306517	KX306587	–	–	KX306647	KX306718	–
Magnaporthaceae	<i>Gaeumannomyces oryzae</i>	CPC 26065	USA	<i>Oryza sativa</i>	KX306521	KX306591	–	–	KX306651	KX306722	–
Magnaporthaceae	<i>Gaeumannomyces radicola</i>	CBS 149.85, PREM 45754	South Africa	<i>Zea mays</i>	KM484844	KM484961	KM485165	KM009181	KM485060	KM009205	–
Magnaporthaceae	<i>Gaeumannomyces radicola</i>	CBS 296.53, MUCL 28970, TRTC 23660 (T)	Canada	Roots of <i>Zea mays</i>	KM484845	KM484962	–	KM009182	KM485061	KM009206	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
Magnaporthaceae	<i>Gaeumannomyces setariicola</i>	CPC 26059, PRRI 4754, CBS 141394 (T)	South Africa	<i>Setaria italica</i>	KX306524	KX306594	–	–	KX306654	KX306725	–
Magnaporthaceae	<i>Gaeumannomyces setariicola</i>	YNE00783	China: Yunnan	Living roots of <i>Setaria</i> sp.	MW478949	MW478098	OQ918175	OQ942223	MW482766	MW482661	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	CBS 186.65	Netherlands	<i>Hordeum vulgare</i>	KM484838	KM484955	KM485164	–	KM485054	KX306726	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	CBS 247.29	Netherlands	<i>Triticum</i> sp.	KM484839	KM484956	–	–	KM485055	KX306727	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	CBS 273.36	Argentina	<i>Triticum aestivum</i>	KX306525	KX306595	–	–	KX306655	KX306729	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	CBS 905.73, DAR 23140	Australia: Western Australia	<i>Triticum aestivum</i>	KM484841	KM484958	–	–	KM485057	KX306730	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	CPC 26273	United Kingdom	<i>Elymus repens</i>	KX306533	KX306603	–	–	KX306661	KX306737	–
Magnaporthaceae	<i>Gaeumannomyces tritici</i>	R3-111a-1	unknown	unknown	FJ541430	–	Genome data	Genome data	Genome data	Genome data	–
Magnaporthaceae	<i>Gaeumannomyces walkeri</i>	CPC 26028, CBS 141400 (T)	USA	<i>Stenotaphrum secundatum</i>	KX306543	KX306613	–	–	KX306670	KX306746	–
Magnaporthaceae	<i>Gaeumannomyces wongoonoo</i>	BRIP 60376	Australia	<i>Buffalo grass</i>	KP162137	KP162146	–	–	–	–	–
Magnaporthaceae	<i>Gaeumannomyces yunnanensis</i>	1109		<i>Nervilia fordii</i>	MZ400525	–	–	–	–	–	–
Magnaporthaceae	<i>Gaeumannomyces yunnanensis</i>	CGMCC3.20898, YNE01187(T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478944	MW478100	OQ918174	MW482589	MW482768	MW482659	–
Magnaporthaceae	<i>Gaeumannomyces yunnanensis</i>	YNE01171	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478943	MW478099	OQ918173	MW482588	MW482767	MW482658	–
Magnaporthaceae	<i>Gongchenomyces graminicola</i>	CGMCC3.24894, YNE01382 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478994	ON244714	OQ918160	MW482594	MW482780	ON367453	–
Magnaporthaceae	<i>Gongchenomyces graminicola</i>	YNE01096	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478990	MW478083	OQ918159	MW482592	OQ942243	MW482665	–
Magnaporthaceae	<i>Gongchenomyces graminicola</i>	YNE01394	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478989	MW478085	OQ918161	MW482593	MW482777	MW482667	–
Magnaporthaceae	<i>Neogongchenomyces graminis</i>	CGMCC3.24893, YNE01186 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478999	MW478086	OQ918162	MW482596	MW482782	MW482670	–
Magnaporthaceae	<i>Neogongchenomyces graminis</i>	YNE01633	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479001	OQ891277	OQ918163	–	OQ918188	OQ918198	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminicola</i>	CGMCC3.24896, YNE00987 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479018	MW478114	OQ918139	MW482621	MW482840	MW482727	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminicola</i>	YNE00999	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479019	MW478115	OQ918140	OQ918180	OQ918192	OQ918210	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminicola</i>	YNE01160	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479020	MW478116	OQ918141	MW482619	MW482841	MW482728	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminis</i>	CGMCC3.24895, YNE00635 (T)	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479015	MW478113	OQ918137	MW482624	MW482844	MW482731	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminis</i>	YNE00607	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479013	MW478111	OQ918136	MW482622	MW482842	MW482729	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces graminis</i>	YNE00633	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479014	MW478112	OQ918138	MW482623	MW482843	MW482730	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces</i> sp.	YNE00626	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479016	–	–	MW482625	MW482846	MW482732	–
<i>Magnaporthaceae</i>	<i>Hongkuiomyces</i> sp.	YNE00685	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479017	–	–	MW482626	MW482845	MW482733	–
<i>Magnaporthaceae</i>	<i>Kohlmeyeriopsis medullaris</i>	CBS 117849, JK5528S (T)	USA: North Carolina	<i>Juncus roemerianus</i>	KM484852	KM484968	–	–	KM485068	–	–
<i>Magnaporthaceae</i>	<i>Kohlmeyeriopsis medullaris</i>	CBS 118210, JK5522N, ATCC MYA-3560	USA: North Carolina	<i>Juncus roemerianus</i>	KM484853	KM484969	–	–	KM485069	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthaceae</i> sp.	CGMCC3.20958, YNE01393	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479012	ON244717	OQ918164	MW482614	ON367459	ON367454	–
<i>Magnaporthaceae</i>	<i>Magnaporthaceae</i> sp.	CPC 26245	United Kingdom	<i>Carex acutiformis</i>	KX306547	KX306617	–	–	KX306673	KX306678	–
<i>Magnaporthaceae</i>	<i>Magnaporthaceae</i> sp.	CPC 26284	United Kingdom	<i>Triticum aestivum</i>	KX306546	KX306616	–	–	–	KX306677	–
<i>Magnaporthaceae</i>	<i>Magnaporthaceae</i> sp.	DS324	USA	Roots of <i>Bouteloua gracilis</i>	MK808693	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthaceae</i> sp.	DS354	USA	Roots of <i>Bouteloua gracilis</i>	MK808723	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis agrostidis</i>	BRIP 59300 (T)	Australia: New South Wales	Roots of <i>Agrostis stolonifera</i>	KT364753	KT364754	–	MF178161	KT364755	KT364756	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	KR10-6	unknown	Roots of <i>Cynodon dactylon</i>	KJ855499	KM401639	–	KP007357	KP268921	KP282705	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	RRFMV10-2	USA	Roots of <i>Cynodon dactylon</i>	KJ855503	KM401643	–	KP007347	KP268925	KP282709	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	RS3-1	USA	Roots of <i>Cynodon dactylon</i>	KJ855505	KM401645	–	KP007348	KP268927	KP282711	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	RS5-5	USA	Roots of <i>Cynodon dactylon</i>	KJ855506	KM401646	–	KP007349	KP268928	KP282712	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	RS7-2 (T)	USA	Roots of <i>Cynodon dactylon</i>	KJ855508	KM401648	–	KP007351	KP268930	KP282714	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i>	TPC5-3	USA	Roots of <i>Cynodon dactylon</i>	KJ855514	KM401654	–	KP007356	KP268936	KP282720	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis cynodontis</i> (as <i>Magnaporthiopsis yugambeh</i>)	BRIP 63074a	Australia: Queensland	unknown	OM890906	–	–	–	OM869947	OM869952	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis gadigal</i>	BRIP 63069a	Australia: New South Wales	<i>Cenchrus clandestinus</i>	OM890904	–	–	–	OM869946	OM869951	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis gumbaynggirr</i>	BRIP 63053a	Australia: New South Wales	<i>Cynodon dactylon</i>	OM890905	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis incrustans</i>	M26 (ATCC64417)	USA: Kansas	<i>Cynodon</i> sp.	JF414842	JF414891	–	JF710385	JF710435	JF710409	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis incrustans</i>	M35	USA	unknown	JF414843	JF414892	genome data	JF710386	JF710437	JF710412	GCA_003049425.1
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis incrustans</i>	M51	USA	Roots of <i>Zoysia matrella</i>	JF414846	JF414895	–	JF710389	JF710440	JF710417	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis maydis</i>	CBS 662.82A (T)	Egypt	<i>Zea mays</i>	KM484856	KM484971	–		KM485072		–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis maydis</i>	M84			KM009160	KM009148	–	KM009172	KM009184	KM009196	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis meyeri-festuca</i>	CBS 143324, FF2 (T)	USA: New Jersey	Roots of <i>Festuca brevipila</i>	MF178146	MF178151	–	MF178156	MF178162	MF178167	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis panicorum</i>	CM10s2	USA: New Jersey		KF689644	KF689634	–	KF689604	KF689614	KF689624	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis panicorum</i>	CM2s8 (T)	USA: New Jersey	Roots of <i>Panicum</i> sp.	KF689643	KF689633	–	KF689603	KF689613	KF689623	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i>	ATCC 64411	USA	<i>Triticum</i> sp.	genome data	genome data	genome data	genome data	genome data	genome data	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i>	Korean	South Korea	Roots of <i>Poa pratensis</i>	–	LC185498	–	–	LC185497	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i>	M47	USA: New Jersey	Roots of <i>Poa pratensis</i>	JF414836	JF414885	–	JF710390	JF710433	JF710415	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i>	M48	USA: New Jersey	<i>Poa pratensis</i>	JF414837	JF414886	–	JF710391	JF710434	JF710416	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i>	TAP35	unknown	Roots of <i>Cynodon dactylon</i>	KJ855511	KM401651	–	KP007358	KP268933	KP282717	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i> (as <i>Magnaporthiopsis dharug</i>)	BRIP 62295a	Australia: New South Wales	<i>Festuca rubra</i> subsp. <i>commuta</i>	OM890902	–	–	–	OM869944	OM869949	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i> (as <i>Magnaporthiopsis dharug</i>)	BRIP 62303a	Australia: New South Wales	<i>Cynodon dactylon</i>	OM890901	–	–	–	–	OM869948	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis poae</i> (as <i>Magnaporthiopsis dharug</i>)	BRIP 62304a	Australia: New South Wales	<i>Poa annua</i>	OM890903	–	–	–	OM869945	OM869950	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis rhizophila</i>	M22	unknown	Roots of <i>Poa pratensis</i>	JF414833	JF414882	–	JF710383	JF710431	JF710407	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis rhizophila</i>	M23	USA	roots of <i>Poa pratensis</i>	JF414834	JF414883	genome data	JF710384	JF710432	JF710408	GCA_003049465.1
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis</i> sp.	CPC 26038	USA	<i>Cynodon dactylon</i> × <i>C. transvaalensis</i>	KX306545	KX306615	–	–	KX306672	KX306676	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis</i> sp.	M46	unknown	<i>Poa pratensis</i>	JF414845	JF414894	–	JN993357	JF710439	JF710414	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis</i> sp. (as <i>Magnaporthiopsis incrustans</i>)	M45	USA: New Jersey	<i>Poa pratensis</i>	JF414844	JF414893	–	JF710387	JF710438	JF710413	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis stipae</i>	CGMCC3.20914, NME00039 (T)	China: Inner Mongolia	Living roots of <i>Stipa sareptana</i> var. <i>krylovii</i>	MW479037	MW478040	OQ918152	MW482567	OQ918195	MW482662	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis stipae</i>	NME00140	China: Inner Mongolia	Living roots of <i>Stipa sareptana</i> var. <i>krylovii</i>	MW479038	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis stipae</i>	NME00142	China: Inner Mongolia	Living roots of <i>Stipa sareptana</i> var. <i>krylovii</i>	MW479039	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Magnaporthiopsis stipae</i>	NME00191	China: Inner Mongolia	Living roots of <i>Stipa sareptana</i> var. <i>krylovii</i>	MW479040	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Nakataea graminis</i>	CGMCC3.20913, YNE01102 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478920	MW478078	OQ918169	MW482590	–	MW482715	–
<i>Magnaporthaceae</i>	<i>Nakataea graminis</i>	YNE01084	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478918	MW478077	OQ918168	MW482591	MW482783	MW482714	–
<i>Magnaporthaceae</i>	<i>Nakataea graminis</i>	YNE01094	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478919	OQ891273	OQ918170	–	OQ918191	OQ918199	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	CBS 202.47	Italy	unknown	KM484860	KM484975	–	–	KM485076	–	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	CBS 252.34	Burma	<i>Oryza sativa</i>	KM484862	KM484976	–	–	KM485078	–	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	CBS 253.34	unknown	unknown	KM484863	KM484977	–	–	KM485079	–	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	DAR71531	Australia	<i>Oryza sativa</i>	MH516052	–	MH516054	–	MH516058	–	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	HK1	Japan: Hiroshima	<i>Oryza sativa</i>	LC203594	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	M21	Japan	<i>Oryza sativa</i>	JF414838	JF414887	–	JF710382	JF710441	JF710406	–
<i>Magnaporthaceae</i>	<i>Nakataea oryzae</i>	M69	USA: California	<i>Oryza</i> sp.	JX134672	JX134684	genome data	JX134712	JX134726	JX134698	GCA_003049435.1
<i>Magnaporthaceae</i>	<i>Nakataea</i> sp.	CBS 332.53	USA: Arkansas	<i>Oryza sativa</i>	MH857230	MH868767	–	–	KM485083	–	–
<i>Magnaporthaceae</i>	<i>Nakataea</i> sp. (as <i>Nakataea oryzae</i>)	ATCC 32149	unknown	unknown	FJ746639	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Neobifusisporella graminicola</i>	CGMCC3.24897, YNE00910 (T)	China: Yunnan	Living leaves of <i>Axonopus</i> sp.	MW479073	MW478071	OQ918106	MW482543	MW482784	MW482693	–
<i>Magnaporthaceae</i>	<i>Neobifusisporella graminicola</i>	YNE00998	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479072	MW478072	OQ918107	MW482542	MW482785	MW482694	–
<i>Magnaporthaceae</i>	<i>Neobifusisporella graminis</i>	CGMCC3.20900, YNE00598 (T)	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479068	OQ932793	OQ918105	MW482547	MW482787	MW482686	–
<i>Magnaporthaceae</i>	<i>Neobifusisporella graminis</i>	YNE00572	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479056	MW478044	OQ918103	MW482553	MW482794	MW482681	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
Magnaporthaceae	<i>Neobifusisporella graminis</i>	YNE00573	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479062	MW478045	OQ918104	MW482554	MW482795	MW482690	–
Magnaporthaceae	<i>Neobifusisporella graminis</i>	YNE00709	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479060	–	–	MW482549	–	MW482692	–
Magnaporthaceae	<i>Neodimorphiconidia zhejiangensis</i>	CGMCC3.20912, ZJE01842(T)	China: Zhejiang	Living shoots of <i>Miscanthus</i> sp.	MW479003	MW478088	OQ918133	OQ942237	MW482833	MW482723	–
Magnaporthaceae	<i>Neodimorphiconidia zhejiangensis</i>	ZJE01843	China: Zhejiang	Living shoots of <i>Miscanthus</i> sp.	MW479008	OQ932803	OQ918134	OQ942238	OQ942250	OQ918208	–
Magnaporthaceae	<i>Neodimorphiconidia zhejiangensis</i>	ZJE01844	China: Zhejiang	Living shoots of <i>Miscanthus</i> sp.	MW479011	OQ932804	OQ918135	MW482615	MW482834	MW482724	–
Magnaporthaceae	<i>Neogaeumannomyces bambusicola</i>	MFLUCC 11-0390 (T)	Thailand	Culms of decaying bamboo	KP744449	KP744492	–	–	–	–	–
Magnaporthaceae	<i>Neophialophora graminis</i>	CGMCC3.20907, YNE01207(T)	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW479024	MW478103	OQ918149	–	MW482837	MW482734	–
Magnaporthaceae	<i>Neophialophora graminis</i>	YNE01215	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW479025	MW478104	OQ918150	MW482617	MW482838	MW482735	–
Magnaporthaceae	<i>Neophialophora graminis</i>	YNE01661	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW479029	ON244715	–	–	ON367460	ON367455	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	ATCC 200212, IMI 353435, CBS 141031 (T)	Australia: Queensland	Leaves of <i>Panicum effusum</i>	JX134674	JX134686	–	JX134714	JX134728	JX134700	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	CBS 141032, BRIP_17195b	Australia	unknown	MK487757	MK487733	–	–	–	–	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	CGMCC3.24898, YNE00622 (T)	China: Yunnan	Living leaves of <i>Hyparrhenia</i> sp.	MW478950	MW478069	OQ918119	MW482599	MW482811	MW482672	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	GHXL27	China	Leaves of patchouli	KY022825	–	–	–	–	–	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	YNE00716	China: Yunnan	Living leaves of <i>Hyparrhenia</i> sp.	MW478951	–	–	MW482598	MW482812	MW482673	–
Magnaporthaceae	<i>Omnidemptus affinis</i>	YNE00891	China: Yunnan	Living leaves of <i>Capillipedium</i> sp.	MW478952	MW478070	OQ918120	MW482597	MW482810	MW482671	–
Magnaporthaceae	<i>Omnidemptus graminicola</i>	CGMCC3.24899, ZJE01859(T)	China: Zhejiang	Living shoots of <i>Lophatherum</i> sp.	MW478963	OQ932806	OQ918127	OQ942240	OQ942252	OQ918206	–
Magnaporthaceae	<i>Omnidemptus graminicola</i>	ZJE01855	China: Zhejiang	Living shoots of <i>Lophatherum</i> sp.	MW478961	OQ932805	OQ918125	OQ942239	OQ942251	OQ918205	–
Magnaporthaceae	<i>Omnidemptus graminicola</i>	ZJE01860	China: Zhejiang	Living shoots of <i>Lophatherum</i> sp.	MW478962	OQ932807	OQ918126	OQ942241	–	OQ918207	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
Magnaporthaceae	<i>Omnidemptus graminis</i>	CBS 138107, FMR 12415 (T)	Spain	Leaves of <i>Poaceae</i> grass	MK487758	MK487734	–	–	–	MK495980	–
Magnaporthaceae	<i>Omnidemptus paragraminis</i>	CGMCC3.24900, ZJE01791 (T)	China: Zhejiang	Living shoots of <i>Paspalum</i> sp.	MW478954	OQ932800	OQ918122	OQ942234	OQ942247	OQ918202	–
Magnaporthaceae	<i>Omnidemptus paragraminis</i>	ZJE01800	China: Zhejiang	Living shoots of <i>Phaenosperma</i> sp.	MW478955	OQ932801	OQ918124	OQ942235	OQ942248	OQ918203	–
Magnaporthaceae	<i>Omnidemptus paragraminis</i>	ZJE01803	China: Zhejiang	Living shoots of <i>Phaenosperma</i> sp.	MW478956	OQ932802	OQ918123	OQ942236	OQ942249	OQ918204	–
Magnaporthaceae	<i>Omnidemptus</i> sp.	YNE00826	China: Yunnan	Living leaves of <i>Thysanolaena</i> sp.	MW478953	MW478087	OQ918121	OQ942224	OQ942242	MW482713	–
Magnaporthaceae	<i>Omnidemptus</i> sp.	YNE01218	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW478957	MW478075	OQ918130	MW482613	MW482816	MW482711	–
Magnaporthaceae	<i>Omnidemptus yunnanensis</i>	CGMCC3.20902, YNE01014 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478964	MW478073	OQ918128	OQ942226	MW482813	MW482674	–
Magnaporthaceae	<i>Omnidemptus yunnanensis</i>	YNE01015	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW478965	MW478074	OQ918129	OQ942227	MW482814	MW482675	–
Magnaporthaceae	<i>Omnidemptus zhejiangensis</i>	CGMCC3.20901, ZJE01773 (T)	China: Zhejiang	Living shoots of <i>Arthraxon</i> sp.	MW478959	MW478076	OQ918131	MW482612	MW482815	MW482712	–
Magnaporthaceae	<i>Omnidemptus zhejiangensis</i>	ZJE01772	China: Zhejiang	Living shoots of <i>Arthraxon</i> sp.	MW478958	–	–	–	–	–	–
Magnaporthaceae	<i>Omnidemptus zhejiangensis</i>	ZJE01789	China: Zhejiang	Living shoots of <i>Arthraxon</i> sp.	MW478960	ON244716	OQ918132	OQ942233	ON367461	ON367456	–
Magnaporthaceae	<i>Pseudophialophora angusta</i>	WSF14RG40 (T)	USA: New Jersey	Roots of <i>Dichanthelium acuminatum</i>	KP769841	KP769833	–	KP784816	KP784824	KP784832	–
Magnaporthaceae	<i>Pseudophialophora dichanthelii</i>	WSF14RG72	USA: New Jersey	Roots of <i>Dichanthelium acuminatum</i>	KP769837	KP769829	–	KP784812	KP784820	KP784828	–
Magnaporthaceae	<i>Pseudophialophora dichanthelii</i>	WSF14RG82 (T)	USA: New Jersey	Roots of <i>Dichanthelium acuminatum</i>	KP769838	KP769830	–	KP784813	KP784821	KP784829	–
Magnaporthaceae	<i>Pseudophialophora eragrostidis</i>	CM12m9 (T)	USA: New Jersey	Roots of <i>Eragrostis</i> sp.	KF689648	KF689638	–	KF689608	KF689618	KF689628	–
Magnaporthaceae	<i>Pseudophialophora eragrostidis</i>	CM20m5-2	USA: New Jersey	Roots of <i>Poaceae</i> sp.	KF689647	KF689637	–	KF689607	KF689617	KF689627	–
Magnaporthaceae	<i>Pseudophialophora magnispora</i>	CM14RG38 (T)	USA: New Jersey	Roots of <i>Dichanthelium acuminatum</i>	KP769835	KP769827	–	KP784810	KP784818	KP784826	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Pseudophialophora magnispora</i>	CM14RG50	USA: New Jersey	Roots of <i>Dichantherium acuminatum</i>	KP769836	KP769828	–	KP784811	KP784819	KP784827	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora panicorum</i>	CM3m7 (T)	USA: New Jersey	<i>Poaceae</i> sp.	KF689652	KF689642	–	KF689612	KF689622	KF689632	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora panicorum</i>	CM9s6	USA: New Jersey	Roots of <i>Poaceae</i> sp.	KF689651	KF689641	–	KF689611	KF689621	KF689631	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora schizachyrii</i>	AL3s4 (T)	USA: New Jersey	<i>Poaceae</i> sp.	KF689650	KF689640	–	KF689610	KF689620	KF689630	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora schizachyrii</i>	WSF14_RG20_1	USA: New Jersey	Soil of <i>Dichantherium acuminatum</i>	KU597372	–	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora schizachyrii</i>	ZJE01719	China: Zhejiang	Living shoots of <i>Arthraxon</i> sp.	MW478910	OQ932797	OQ918148	OQ942230	–	–	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora sorghi</i>	URM7423_RV01	Brazil: Pernambuco	Roots of <i>Sorghum bicolor</i>	KY421938	KY421941	–	–	KY421944	KY421942	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora</i> sp.	LJJ23	unknown	unknown	MT379653	MT379654	–	MZ902036	MZ902037	MZ902038	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora</i> sp.	YNE00667	China: Yunnan	Living roots of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478911	–	–	MW482616	MW482836	MW482738	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora</i> sp.	ZJE01717	China: Zhejiang	Living roots of <i>Miscanthus</i> sp.	MW478907	OQ932796	OQ918145	OQ942229	OQ942245	OQ918211	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora</i> sp.	ZJE01743	China: Zhejiang	Living roots of <i>Miscanthus</i> sp.	MW478909	OQ932798	OQ918146	OQ942231	OQ942246	OQ918212	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora</i> sp.	ZJE01745	China: Zhejiang	Living roots of <i>Miscanthus</i> sp.	MW478908	MW478107	OQ918147	OQ942232	MW482835	MW482737	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora tarda</i>	WSF14RG48	USA: New Jersey	Roots of <i>Panicum virgatum</i>	KP769840	KP769832	–	KP784815	KP784823	KP784831	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora tarda</i>	WSF14SW13-1 (T)	unknown	unknown	KP769839	KP769831	–	KP784814	KP784822	KP784830	–
<i>Magnaporthaceae</i>	<i>Pseudophialophora whartonensis</i>	WSF14RG66 (T)	USA: New Jersey	Roots of <i>Dichantherium acuminatum</i>	KP769834	KP769826	–	KP784809	KP784817	KP784825	–
<i>Magnaporthaceae</i>	<i>Pyriculariopsis parasitica</i>	HKUCC5562, ST68	unknown	unknown	–	DQ341514	–	–	–	–	–
<i>Magnaporthaceae</i>	<i>Slopeiomyces cylindrosporus</i>	461s1	unknown	unknown	KM009171	KM009159	–	KM009183	KM009195	KM009207	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Magnaporthaceae</i>	<i>Slopeiomyces cylindrosporus</i>	CBS 609.75 (T)	UK	Roots of <i>Phialophora graminicola</i>	KM484944	MH872724	–	–	KM485158	–	–
<i>Magnaporthaceae</i>	<i>Slopeiomyces cylindrosporus</i>	CBS 610.75 (T)	UK: England	Roots of <i>Phialophora graminicola</i>	JX134667	DQ341494	–	JX134707	JX134721	JX134693	–
<i>Magnaporthaceae</i>	<i>Slopeiomyces cylindrosporus</i>	CBS 611.75 (T)	UK	Roots of <i>Phialophora graminicola</i>	KM484945	KM485041	–	–	KM485159	–	–
<i>Magnaporthaceae</i>	<i>Xenofalciphora graminis</i>	CGMCC3.20910, YNE01373(T)	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW478916	MW478082	OQ918157	MW482568	MW482748	MW482669	–
<i>Magnaporthaceae</i>	<i>Xenofalciphora graminis</i>	YNE01584	China: Yunnan	Living roots of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478917	OQ891276	OQ918158	OQ918179	OQ918189	OQ918197	–
<i>Magnaporthaceae</i>	<i>Xenogaeumannomyces yunnanensis</i>	CGMCC3.20201, YNE01369 (T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW055654	MW478081	OQ918167	MW056506	MW056509	MW056512	–
<i>Magnaporthaceae</i>	<i>Xenogaeumannomyces yunnanensis</i>	YNE01232	China: Yunnan	Living roots of <i>Poaceae</i> sp.	MW055634	MW478079	OQ918165	MW056504	MW056507	MW056510	–
<i>Magnaporthaceae</i>	<i>Xenogaeumannomyces yunnanensis</i>	YNE01351	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW055650	MW478080	OQ918166	MW056505	MW056508	MW056511	–
<i>Magnaporthaceae</i>	<i>Xenophialophora graminicola</i>	CGMCC3.20997, YNE01240(T)	China: Yunnan	Living stems of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479021	MW478108	OQ918142	MW482618	MW482847	MW482725	–
<i>Magnaporthaceae</i>	<i>Xenophialophora</i> sp.	CGMCC3.20908, YNE01531	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479023	MW478106	OQ918144	–	OQ942244	MW482726	–
<i>Magnaporthaceae</i>	<i>Xenophialophora graminicola</i>	YNE01247	China: Yunnan	Living stems of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW479022	OQ891275	OQ918143	–	–	OQ918209	–
<i>Ophioceraaceae</i>	<i>Ophioceras aquaticum</i>	IFRDCC 3091, IFRD 021-055 (T)	China	unknown	JQ797440	JQ797433	–	–	–	–	–
<i>Ophioceraaceae</i>	<i>Ophioceras aquaticum</i>	MFLUCC 16-0906, S-479	China	unknown	MK828611	MK835810	–	–	–	MN194063	–
<i>Ophioceraaceae</i>	<i>Ophioceras castillense</i>	SMH1865 (T)	Costa Rica	Wood on the ground	–	EU527997	–	–	–	–	–
<i>Ophioceraaceae</i>	<i>Ophioceras Chiangdaoense</i>	CMU 26633 (T)	Thailand: Chiang Mai	Leaves of <i>Dracaena loureiroi</i>	–	EU571272	–	–	–	–	–
<i>Ophioceraaceae</i>	<i>Ophioceras commune</i>	M91	China: Yunnan	Rotten wood	JX134675	JX134687	–	JX134715	JX134729	JX134701	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Ophioceraceae</i>	<i>Ophioceras commune</i>	M92	unknown	unknown	JX134676	JX134688	–	JX134716	JX134730	JX134702	–
<i>Ophioceraceae</i>	<i>Ophioceras dolichostomum</i>	CBS 114926, HKUCC 3936, KM 8	China: Hong Kong	Rotten wood	JX134677	JX134689	–	Genome data	Genome data	Genome data	GCA_003049485.1
<i>Ophioceraceae</i>	<i>Ophioceras ficinum</i>	MFLU 19-2751, GSP045A (T)	China, Taiwan	Leaves of <i>Ficus septica</i>		MW114436	–	–	–	–	–
<i>Ophioceraceae</i>	<i>Ophioceras freycinetiae</i>	CPC 38508, T19_02806E, CBS 146781 (T)	New Zealand	Leaves of <i>Freycinetia banksii</i>	MZ064408	MZ064465	–	–	–	MZ078219	–
<i>Ophioceraceae</i>	<i>Ophioceras graminis</i>	CGMCC3.20904, YNE00713 (T)	China: Yunnan	Living leaves of <i>Oplismenus</i> sp.	MW479093	OQ891271	OQ918177	MW482634	MW482855	MW482742	NMDC60154777
<i>Ophioceraceae</i>	<i>Ophioceras graminis</i>	Clone 3183			MF571451		–	–	–	–	–
<i>Ophioceraceae</i>	<i>Ophioceras graminis</i>	SYPF 8345	China	<i>Panax notoginseng</i>	MF536887	MF536885	–	–	–	MF536886	–
<i>Ophioceraceae</i>	<i>Ophioceras graminis</i>	YNE00717	China: Yunnan	Living leaves of <i>Oplismenus</i> sp.	MW479094	–	OQ918178	MW482635	MW482856	MW482743	–
<i>Ophioceraceae</i>	<i>Ophioceras hongkongense</i>	HKUCC 3624 (T)	China: Hong Kong	Submerged wood		DQ341509	–	–	–	–	–
<i>Ophioceraceae</i>	<i>Ophioceras junci</i>	CPC 42234, CBS 148450, CBS H-24892 (T)	Netherlands: Utrecht	Dead culm of <i>Juncus effusus</i>	OK664750	OK663789	OK651137	–	OK651155	–	–
<i>Ophioceraceae</i>	<i>Ophioceras junci</i>	CPC 42235	Netherlands: Utrecht	Dead culm of <i>Juncus effusus</i>	OK664751	OK663790	OK651138	–	OK651156	–	–
<i>Ophioceraceae</i>	<i>Ophioceras leptosporum</i>	CBS 894.70, ATCC 24161, HME 2955	UK: Exeter	Dead stem of dicot plant (probably <i>Urtica dioica</i>)	JX134678	JX134690	–	JX134718	–	JX134704	–
<i>Ophioceraceae</i>	<i>Ophioceras rhizomorphum</i>	GKM1262 (T)	Kenya	Decaying wood	–	EU527998	–	–	–	–	–
<i>Ophioceraceae</i>	<i>Ophioceras sichuanense</i>	KUN-HKAS 107677, KUMCC 20-0213 (T)	China	Submerged decaying bamboo branches	MW057782	MW057779	–	–	–	MW082017	–
<i>Ophioceraceae</i>	<i>Ophioceras</i> sp.	Clone_FA14	unknown	unknown	HM159457	–	–	–	–	–	–
<i>Ophioceraceae</i>	<i>Ophioceras submersum</i>	MFLUCC 18-0211, MFLU 18-1459 (T)	Thailand	Submerged decaying wood	–	MK835811	–	–	–	MN194064	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Plagiosphaeraceae</i>	<i>Aquafiliiformis lignicola</i>	MFLUCC 16–1341 (T), MFLU 18-2325	China: Yunnan	Submerged decaying wood	MK828615	MK835815	–	–	–	MN194068	–
<i>Plagiosphaeraceae</i>	<i>Aquafiliiformis lignicola</i>	MFLUCC 18–1338, MFLU 18-2324	China: Yunnan	Submerged decaying wood	MK828614	MK835814	–	–	–	MN194067	–
<i>Plagiosphaeraceae</i>	<i>Aquafiliiformis lignicola</i>	YNE00682	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478904	–	–	MW482627	MW482850	–	–
<i>Plagiosphaeraceae</i>	<i>Aquafiliiformis lignicola</i>	YNE00705	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478905	–	–	MW482628	MW482848	–	–
<i>Plagiosphaeraceae</i>	<i>Aquafiliiformis lignicola</i>	YNE00708	China: Yunnan	Living leaves of <i>Oryza meyeriana</i> subsp. <i>granulata</i>	MW478906	OQ932794	OQ918176	MW482629	MW482849	OQ942253	NMDC6015 4778
<i>Plagiosphaeraceae</i>	<i>Muraeriata africana</i>	GKM1084 (T)	Kenya	Bark or wood	–	EU527995	–	–	–	–	–
<i>Plagiosphaeraceae</i>	<i>Muraeriata collapsa</i>	SMH4553 (T)	Costa Rica, Ecuador	Bark or wood	–	EU527996	–	–	–	–	–
<i>Plagiosphaeraceae</i>	<i>Plagiosphaera immersa</i>	D148	Austria	Dead stems of <i>Urtica dioica</i>	MN727887	MN727887	PP996357	PP996361	PP996364	MN720278	–
<i>Plagiosphaeraceae</i>	<i>Plagiosphaera immersa</i>	D266	Austria	Dead stems of <i>Urtica dioica</i>	MN727888	MN727888	PP996358	PP996362	PP996365	MN720279	–
<i>Plagiosphaeraceae</i>	<i>Plagiosphaera immersa</i>	D270	Austria	Dead stems of <i>Urtica dioica</i>	MN727889	MN727889	PP996359	PP996363	MN720276	MN720280	–
<i>Plagiosphaeraceae</i>	<i>Plagiosphaera immersa</i>	D98	Austria	Dead stems of <i>Urtica dioica</i>	MN727886	MN727886	PP996356	PP996360	MN720275	MN720277	–
<i>Pseudohalonectriaceae</i>	<i>Pseudohalonectria fagicola</i>	MFLUCC 15-1117, 177b, MFLU 16-1085 (T)	UK: Hampshire	<i>Fagus sylvatica</i> .		KX426219	–	–	–	KX426226	–
<i>Pseudohalonectriaceae</i>	<i>Pseudohalonectria hampshirensis</i>	MFLUCC 15-0774, MFLU 16-1086, 177 (T)	UK: Hampshire	<i>Fagus sylvatica</i>		KX426218	–	–	–	KX426224	–
<i>Pseudohalonectriaceae</i>	<i>Pseudohalonectria lignicola</i>	M95, YMF1.01288	China: Yunnan	Rotten wood	JX134679	JX134691	genome data	Genome data	Genome data	Genome data	GCA_00304 9395.1
<i>Pyriculariaceae</i>	<i>Bambusicularia brunnea</i>	CBS 133599, MAFF 240225, INA-B-92-45, Ss-1J (T)	Japan: Aichi	<i>Sasa</i> sp.	KM484830	KM484948	AB274449	–	KM485043	–	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Pyriculariaceae</i>	<i>Bambusicularia brunnea</i>	CBS 133600, MAFF 240226, INA-B-93-19, Ph-1J	Japan: Aichi	<i>Phyllostachys bambusoides</i>	AB274436	KM484949	AB274450	–	KM485044	–	–
<i>Pyriculariaceae</i>	<i>Barretomyces calatheae</i>	CBMAI 1060, OF55a (ET)	Brazil: Minas Gerais	<i>Calathea longifolia</i>	GU294490	–	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Barretomyces calatheae</i>	CBS 129274, CPC 18464	Brazil: Minas Gerais	<i>Calathea longifolia</i>	KM484831	MH876639	KM485162	–	KM485045	–	–
<i>Pyriculariaceae</i>	<i>Bipyrularia graminis</i>	CGMCC3.20906, YNE01013(T)	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479090	MW478109	OQ918100	MW482632	MW482852	MW482739	–
<i>Pyriculariaceae</i>	<i>Bipyrularia graminis</i>	YNE01016	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479091	MW478110	OQ918101	MW482633	MW482853	MW482740	–
<i>Pyriculariaceae</i>	<i>Bipyrularia graminis</i>	YNE01017	China: Yunnan	Living stems of <i>Poaceae</i> sp.	MW479092	OQ932795	OQ918102	MW482631	MW482851	MW482741	–
<i>Pyriculariaceae</i>	<i>Bipyrularia graminis</i>	Otu0177			MT908552	–	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Macgarvieomyces borealis</i>	CBS 461.65 (T)	UK: Scotland	Leaves of <i>Juncus effusus</i>	MH858669	DQ341511	KM485170	KM009174	KM485070	KM009198	–
<i>Pyriculariaceae</i>	<i>Macgarvieomyces juncicola</i>	CBS 610.82 (T)	Netherlands	Stems of <i>Juncus effusus</i>	KM009165	KM009153	KM485171	KM009177	–	KM009201	–
<i>Pyriculariaceae</i>	<i>Macgarvieomyces luzulae</i>	CPC 32458, CBS 143401(ET)	Ukraine	Leaves of <i>Luzula</i> sp.	MG934440	–	MG934462	–	MG934469	–	–
<i>Pyriculariaceae</i>	<i>Macgarvieomyces luzulae</i>	CPC 34292	Ukraine	<i>Luzula sylvatica</i>	MK442591	MK442531	MK442635	–	–	–	–
<i>Pyriculariaceae</i>	<i>Neocordana malayensis</i>	CPC 32837, CBS 144604 (T)	Malaysia	<i>Musa</i> sp.	MK442593	MK442533	MK442637	–	–	–	–
<i>Pyriculariaceae</i>	<i>Neocordana musae</i>	CPC 18127, CBS 139318 (ET)	Indonesia, Malaysia	<i>Musa</i> sp.	LN713277	LN713290	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Neocordana musarum</i>	CPC 28529, CBS 142116 (ET)	France: La Reunion	Leaves of <i>Musa</i> sp.	KY173425	KY173516	KY173568	–	KY173577	–	–
<i>Pyriculariaceae</i>	<i>Neocordana musicola</i>	CPC 11225, CBS 139316, S1024 (T)	Mauritius	<i>Musa</i> sp.	LN713285	LN713286	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Neocordana musigena</i>	CPC 29777, CBS 142624 (ET)	Morocco	<i>Musa</i> sp.	KY979749	KY979804	KY979855	–	KY979886	–	–
<i>Pyriculariaceae</i>	<i>Neopyricularia commelinicola</i>	CBS 128303	South Korea: Hongcheon	<i>Commelina communis</i>	KM484868	KM484982	KM485172	KM009175	KM485084	KM009199	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Pyriculariaceae</i>	<i>Neopyricularia commelinicola</i>	CBS 128306, KACC 43869	South Korea: Pocheon	<i>Commelina communis</i>	FJ850123	KM484983	KM485173	–	KM485085	–	–
<i>Pyriculariaceae</i>	<i>Neopyricularia commelinicola</i>	CBS 128307, KACC 44083	South Korea: Hongcheon	Leaves of <i>Commelina communis</i>	FJ850125	KM484984	KM485174	–	KM485086	–	–
<i>Pyriculariaceae</i>	<i>Neopyricularia commelinicola</i>	CBS 128308, KACC 43081 (T)	South Korea: Hongcheon	unknown	FJ850122	KM484985	KM485175	–	KM485087	–	–
<i>Pyriculariaceae</i>	<i>Nothopyricularia junci</i> (as <i>Xenopyricularia junci</i>)	CPC 40968, CBS 148308 (T)	Netherlands: Utrecht	Dead culm of <i>Juncus effusus</i>	OK664720	OK663759	OK651127	–	OK651152	–	–
<i>Pyriculariaceae</i>	<i>Proxipyricularia zingiberis</i>	CBS 132195, HYZiM201-1-1	Japan: Hyogo	<i>Zingiber mioga</i>	KM484869	KM484986	AB274448	–	KM485088	–	–
<i>Pyriculariaceae</i>	<i>Proxipyricularia zingiberis</i>	CBS 132196, HYZiM202-1-2	Japan: Hyogo	<i>Zingiber mioga</i>	KM484870	–	AB274447	–	KM485089	–	–
<i>Pyriculariaceae</i>	<i>Proxipyricularia zingiberis</i>	CBS 132355, MAFF 240221, HYZiM101-1-1 (Z-1J)	Japan: Hyogo	<i>Zingiber mioga</i>	AB274433	KM484987	KM485176	–	KM485090	–	–
<i>Pyriculariaceae</i>	<i>Proxipyricularia zingiberis</i>	CBS 133594, MAFF 240222, HYZiM201-0-1(Z-2J) (ET)	Japan	Leaves of <i>Zingiber mioga</i>	AB274434	KM484988	AB274446	–	KM485091	–	–
<i>Pyriculariaceae</i>	<i>Proxipyricularia zingiberis</i>	CBS 303.39	Japan	<i>Zingiber officinale</i>	KM484871	KM484989	KM485177	–	KM485092	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia bothriochloae</i>	CPC 21650, CPC 21651, CBS 136427 (T)	Thailand	Leaves of <i>Bothriochloa bladhii</i>	KF777186	KF777238	KY905700	–	KY905701	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia cyperi</i>	CBS 133595, MAFF 240229, HYCI201-1-1, Ci-1J (T)	Japan: Hyogo	<i>Cyperus iria</i>	KM484872	KM484990	AB274453	–	AB818013	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia cyperi</i>	CBS 665.79	Israel	<i>Cyperus rotundus</i>	KM484873	DQ341512	KM485178	–	KM485093	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia cyperi</i>	PH0053, CR88383	Philippines	<i>Cyperus rotundus</i>	KM484874	–	KM485179	–	KM485094	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia festucae</i>	CBS H-24352, CPC 37915, CBS 146629 (T)	USA	Leaves of <i>Festuca californica</i>	MW883447	MW883838	–	–	MW890057	–	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Pyriculariaceae</i>	<i>Pseudopyricularia hagahagae</i>	CPC 25635 (T)	South Africa: Eastern Cape	Leaves of unidentified <i>Cyperaceae</i> <i>Cyperus</i> sp.	KT950851	KT950865	KT950873	–	KT950877	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia hedjaroudii</i>	UTFC-PH01 (T)	Iran		MT226734	MT226733	MT468891	–	MT468893	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia higginsii</i>	CBS 121934 (T)	New Zealand: Auckland	Dead leaves of <i>Typha orientalis</i>	KM009164	KM484991	KM485180	KM009176	KM485095	KM009200	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia hyrcaniana</i>	IRAN 2758C, Ck1 (T)	Iran: Golestan	<i>Cyperus alternifolius</i>	KP144447	KP144452	–	–	KY457270	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia iraniana</i>	IRAN 2761C, 17d (T)	Iran: Golestan	<i>Juncus</i> sp.	KY457258	KY457268	–	–	KY457273	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia kyllingae</i>	CBS 133597, MAFF 240227, HYKB202-1-2(K-1J) (T)	Japan: Hyogo	<i>Kyllinga brevifolia</i>	KM484876	KM484992	AB274451	–	KM485096	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia kyllingae</i>	PH0054, CB8959	Philippines	<i>Cyperus brevifolius</i>	KM484877	KM484993	KM485181	–	KM485097	–	–
<i>Pyriculariaceae</i>	<i>Pseudopyricularia persiana</i>	UTFC-PO20 (T)	Iran	<i>Cyperus serotinus</i>	MH780926	MH780974	–	–	MH699975	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia angulata</i>	banana4	China: Yunnan	Banana	OK147749	OK147770	–	OM112330	OK169597	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia angulata</i>	NBRC 9625			AY265322	–	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia ctenantheicola</i>	GR0001, Ct-4, ATCC 200218	Greece: Almyros	<i>Ctenanthe oppenheimiana</i>	KM484878	KM484994	KM485182	–	KM485098	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia ctenantheicola</i>	GR0002, CBS 138601	Greece: Almyros	<i>Ctenanthe oppenheimiana</i>	KM484879	–	KM485183	–	KM485099	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	BR0029	Brazil	<i>Digitaria sanguinalis</i>	KM484880	KM484995	–	–	KM485100	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	CBS 128304	Korea	unknown	MH864859	MH876302	KM485184	–	KM485101	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	CBS 138707, G184, US0043 (T)	USA: Delaware	<i>Digitaria</i> sp.	KM484885	MH877665	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	CR0024	South Korea: Suwon	<i>Lolium perenne</i>	KM484882	KM484997	KM485185	–	KM485102	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	JP0034	Japan	<i>Digitaria eriantha</i>	KM484883	–	KM485186	–	KM485103	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	M82, CG-14			JX134670	JX134682	–	JX134710	JX134724	JX134696	–
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	MT9461a	China: Yunnan	<i>Digitaria sanguinalis</i>	OK147748	OK147769	–	OM112329	OK169595	–	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Pyriculariaceae</i>	<i>Pyricularia grisea</i>	NI907	unknown	<i>Digitaria sanguinalis</i>	AB274429	–	genome data	genome data	genome data	genome data	GCA_004355905.1
<i>Pyriculariaceae</i>	<i>Pyricularia oryzae</i>	70-15, ATCC MYA-4617	unknown	<i>Oryza sativa</i>	genome data	–	genome data	genome data	genome data	genome data	GCA_000002495.2
<i>Pyriculariaceae</i>	<i>Pyricularia oryzae</i>	CBS 255.38	Romania	unknown	KM484889	KM484999	KM485190	–	KM485109	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia oryzae</i>	CBS 365.52, MUCL 9451	Japan: Nagano	unknown	MH857082	MH868617	KM485191	–	KM485110	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia oryzae</i>	Guy11	French: Guiana	<i>Oryza sativa</i>	KM484904	KM485013	KC167438	genome data	Genome data	genome data	GCA_002368485.1
<i>Pyriculariaceae</i>	<i>Pyricularia penniseticola</i>	BF0017	Burkina Faso: Kamboinse	<i>Pennisetum typhoides</i>	KM484925	KM485031	DQ240878	–	KM485144	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia penniseticola</i>	CBS 138603, ML0031 (T)	Mali: Longorola Sikasso	<i>Pennisetum typhoides</i>	KM484929	–	KM485220	–	KM485148	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia penniseticola</i>	CD0086	Cote d'Ivoire: Bouake	<i>Pennisetum typhoides</i>	KM484926	–	DQ240879	–	KM485145	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia penniseticola</i>	ML0048	Mali	<i>Digitaria exilis</i>	KM484930	–	KM485221	–	KM485149	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia pennisetigena</i>	BR0093	Brazil: Primeiro de Maio	<i>Echinochloa colona</i>	KM484932	–	KM485223	–	KM485151	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia pennisetigena</i>	Br36	Brazil	<i>Cenchrus eChinatus</i>	KM484933	KM485033	genome data	genome data	genome data	genome data	–
<i>Pyriculariaceae</i>	<i>Pyricularia pennisetigena</i>	CBS 133596, MAFF 305501, NI981(Cc-1J)	Japan: Kumamoto	<i>Cenchrus ciliaris</i>	KM484934	KM485034	KM485224	–	KM485152	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia pennisetigena</i>	CBS 138604, ML0036 (T)	Mali: Cinzana	<i>Pennisetum</i> sp.	KM484935	–	KM485225	–	KM485153	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia pennisetigena</i>	PH0047, CE88454	Philippines	<i>Cenchrus eChinatus</i>	KM484936	–	KM485226	–	KM485154	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia urashimae</i>	CPC 29414 (T), CBS 142117, CML 3520, URM 7373, isolate 12.0.148, isolate 12.0.149	Brazil, Amambai	Leaves of <i>Urochloa brizantha</i>	KY173437	KY173527	KY173571	–	KY173578	–	–

Supplementary Table 1 Continued.

Family	Species	Strain	Country, Region	Host and Substrate	ITS ⁽¹⁾	LSU	ACT	MCM7	RPB1	TEF1	Genome ⁽²⁾
<i>Pyriculariaceae</i>	<i>Pyricularia urashimae</i>	CPC 29419	Brazil: Aral Moreira	Leaves of <i>Panicum maximum</i>	KY173438	KY173528	KY173572	–	KY173579	–	–
<i>Pyriculariaceae</i>	<i>Pyricularia zingibericola</i>	RN0001, CBS 138605 (T)	Reunion	<i>Zingiber officinale</i>	KM484941	KM485037	KM485229	–	KM485157	–	–
<i>Pyriculariaceae</i>	<i>Pyriculariaceae</i> sp.	CGMCC3.20905, YNE00860	China: Yunnan	Living leaves of <i>Thysanolaena</i> sp.	MW479089	ON244711	OQ918099	OQ942225	ON367457	ON367450	–
<i>Pyriculariaceae</i>	<i>Pyriculariaceae</i> sp. (as <i>Pyricularia occidentalis</i>)	CBS 365.90	Cuba	unknown	MH862217	MH873902	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Pyriculariaceae</i> sp. (as <i>Pyricularia penniseti</i>)	P1604	China: Fuzhou	<i>Pennisetum giganteum</i>	MH619995	MH807632	MH633730	–	MH633733	–	–
<i>Pyriculariaceae</i>	<i>Pyriculariaceae</i> sp. (as <i>Pyricularia penniseti</i>)	P1612	China: Fuzhou	<i>Pennisetum giganteum</i>	MH619997	MH807633	MH633732	–	MH633735	–	–
<i>Pyriculariaceae</i>	<i>Pyriculariomyces asari</i>	CPC 27442	Malaysia: Sabah	Leaves and stems of <i>Asarum</i> sp.	KX228290	KX228341	KX228360	–	MG934472	–	–
<i>Pyriculariaceae</i>	<i>Pyriculariomyces asari</i>	CPC 27444, CBS 141328 (T)	Malaysia: Sabah	Leaves and stems of <i>Asarum</i> sp.	KX228291	KX228342	KX228361	–	KX228368	–	–
<i>Pyriculariaceae</i>	<i>Utrechtiana arundinacea</i>	CPC 33994 (ET)	Netherlands: Utrecht	Leaves of <i>Phragmites</i> sp.	MG934461	–	MG934468	–	MG934473	–	–
<i>Pyriculariaceae</i>	<i>Utrechtiana roumegueri</i>	CBS 128780, CPC 18916 (T)	Netherlands: Utrecht	Leaves of <i>Phragmites australis</i>	JF951153	JF951176	KM485163	–	KM485047	–	–
<i>Pyriculariaceae</i>	<i>Utrechtiana roumegueri</i>	LSU0217	USA: New Jersey	Leaves of <i>Phragmites australis</i>	MT000400	MT000495	–	–	–	–	–
<i>Pyriculariaceae</i>	<i>Xenopyricularia zizaniicola</i>	CBS 132356, MAFF 240220, KYZL201-1-1 (Zz-2J)	Japan: Kyoto	<i>Zizania latifolia</i>	KM484946	KM009155	AB274444	KM009179	KM485160	KM009203	–
<i>Pyriculariaceae</i>	<i>Xenopyricularia zizaniicola</i>	CBS 133593, MAFF 240219, IBZL3-1-1(Zz-1J) (T)	Japan: Ibaraki	<i>Zizania latifolia</i>	KM484947	–	KM485230	–	KM485161	–	–
<i>Magnaporthaceae</i>	<i>Xenorhizisma sichuanense</i>	SICAU 22-0073	China: Sichuan	<i>Phyllostachys edulis</i>	ON227097	ON227101	–	–	ON244428	ON244427	–

Note: (1) Accession numbers deposited in National Center for Biotechnology Information (NCBI) GenBank. (2) Accession numbers “GCA_XXXXXXXXX.X” deposited in NCBI GenBank, Accession numbers “NMDCXXXXXXXXX” deposited in National Microbiology Data Center (NMDC).

Supplementary Table 2 Families, genera, and species of Order *Magnaporthales*.

Family	Genus	Species
<i>Ceratosphaeriaceae</i> Z.L. Luo, H.Y. Su & K.D. Hyde (1)	<i>Ceratosphaeria</i> Niessl (29)	<i>Ceratosphaeria aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su
		<i>Ceratosphaeria lignicola</i> D.F. Bao, Z.L. Luo, H.Y. Su & K.D. Hyde
		<i>Ceratosphaeria yunnanensis</i> C.F. Liao & Doilom
		<i>Ceratosphaeria aparaphysata</i> Feltgen #
		<i>Ceratosphaeria bicellula</i> Panwar & S.J. Kaur #
		<i>Ceratosphaeria caespitosa</i> Lind & Vleugel #
		<i>Ceratosphaeria crossandrae</i> K. Ramakr. #
		<i>Ceratosphaeria emergens</i> Rick #
		<i>Ceratosphaeria ervatamiicola</i> A.K. Kar & Maity #
		<i>Ceratosphaeria flava</i> J. Yang, E.B.G. Jones & K.D. Hyde #
		<i>Ceratosphaeria fragilis</i> Wilberf. #
		<i>Ceratosphaeria grandis</i> Boud. #
		<i>Ceratosphaeria lampadophora</i> (Berk. & Broome) Niessl #
		<i>Ceratosphaeria lanuginosa</i> Maire #
		<i>Ceratosphaeria luculenta</i> Lar.N. Vassiljeva #
		<i>Ceratosphaeria macrorhyncha</i> Gaja #
		<i>Ceratosphaeria moravica</i> Petr. #
		<i>Ceratosphaeria mycophila</i> G. Winter #
		<i>Ceratosphaeria obliquata</i> Feltgen #
		<i>Ceratosphaeria ordinata</i> (Fr.) Kirschst. #
		<i>Ceratosphaeria phialidica</i> (Shearer) Huhndorf, Greif, Mugambi & A.N. Mill. #
		<i>Ceratosphaeria philippinarum</i> Rehm #
		<i>Ceratosphaeria phyllostachydis</i> S. Zhang #
		<i>Ceratosphaeria pusilla</i> (Fuckel) Sacc. #
		<i>Ceratosphaeria quadrinucleata</i> Kirschst. #
		<i>Ceratosphaeria rhenana</i> (Auersw.) Berl. & Voglino #
		<i>Ceratosphaeria silva-nigra</i> (Penz. & Sacc.) Teng #
		<i>Ceratosphaeria subiculosa</i> Sacc. #
		<i>Ceratosphaeria suthemensis</i> (Promp.) J. Yang & K.D. Hyde #
		<i>Atripes paspali</i> F.A. Custódio & O.L. Pereira
<i>Magnaporthaceae</i> P.F. Cannon (33)	<i>Atripes</i> F.A. Custódio & O.L. Pereira (1)	
	<i>Bifusispora</i> R.M.F. Silva, R.J.V. Oliveira, J.D.P. Bezerra, Souza-Motta & G.A. Silva (3)	
		<i>Bifusispora graminicola</i> C. L. Zhang *
		<i>Bifusispora graminis</i> C. L. Zhang *
		<i>Bifusispora sorghi</i> R.M.F. Silva, R.J.V. Oliveira, J.D.P. Bezerra, Souza-Motta & G.A. Silva

Supplementary Table 2 Continued.

Family	Genus	Species
	<i>Budhanggurabania</i> P. Wong, Khemmuk & R.G. Shivas (1)	<i>Budhanggurabania cynodonticola</i> P. Wong, Khemmuk & R.G. Shivas
	<i>Buergenerula</i> Syd. (1)	<i>Buergenerula spartinae</i> Kohlm. & R.V. Gessner
	<i>Bussabanomyces</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Bussabanomyces longisporus</i> (Bussaban) Klaubauf, M.-H. Lebrun & Crous
	<i>Candidacolonium</i> P.L. Vines & M. Tomaso-Peterson (2)	<i>Candidacolonium agrostidis</i> J. Hu & J.M. Geng
		<i>Candidacolonium cynodontis</i> P.L. Vines & M. Tomaso-Peterson
	<i>Clasterosphaeria</i> Sivan. (2)	<i>Clasterosphaeria cyperi</i> Sivan. #
		<i>Clasterosphaeria indica</i> Hosag. & Manojk. #
	<i>Clasterosporium</i> Schwein (41)	<i>Clasterosporium anomalum</i> (Speg.) S. Hughes #
		<i>Clasterosporium asclepiadis</i> Tropova #
		<i>Clasterosporium bambusae</i> Saikia & A.K. Sarbhoy #
		<i>Clasterosporium biseptatum</i> Sacc. #
		<i>Clasterosporium calami</i> Bat. #
		<i>Clasterosporium caricinum</i> Schwein. #
		<i>Clasterosporium caulicola</i> (Corda) Sacc. #
		<i>Clasterosporium clavaeforme</i> (Preuss) Sacc. #
		<i>Clasterosporium coccolobae</i> (F. Stevens & Dalbey) P.M. Kirk #
		<i>Clasterosporium cocoicola</i> M.B. Ellis #
		<i>Clasterosporium coffeanum</i> Av.-Saccá #
		<i>Clasterosporium convolvuli</i> Gonz. Frag. & Cif. #
		<i>Clasterosporium cyperacearum</i> Hosag. #
		<i>Clasterosporium cyperi</i> M.B. Ellis #
		<i>Clasterosporium domus-aliena</i> Cif. & Bat. #
		<i>Clasterosporium elasticae</i> Koord. #
		<i>Clasterosporium flagellatum</i> (Syd. & P. Syd.) M.B. Ellis #
		<i>Clasterosporium flexum</i> (Matsush.) B. Sutton & R.T.A. Cook #
		<i>Clasterosporium glomeratae</i> Overeem #
		<i>Clasterosporium hirudinoides</i> Peyronel #
		<i>Clasterosporium isopyri</i> Bres. #
		<i>Clasterosporium javanicum</i> Koord. #
		<i>Clasterosporium lathyri</i> Verpl. & R. Broecke #
		<i>Clasterosporium lindavianum</i> Reichert #
		<i>Clasterosporium lini</i> Oudem. #
		<i>Clasterosporium longisporum</i> Voorhees #
		<i>Clasterosporium microscopicum</i> Schulzer & Sacc. #
		<i>Clasterosporium mori</i> Syd. & P. Syd. #

Supplementary Table 2 Continued.

Family	Genus	Species
		<i>Clasterosporium ontariense</i> Sacc. #
		<i>Clasterosporium pistaciae</i> M.B. Ellis #
		<i>Clasterosporium polypodii</i> J.A. Stev. #
		<i>Clasterosporium proteae</i> M.B. Ellis #
		<i>Clasterosporium psilosporoides</i> (Schulzer) Sacc. & Traverso #
		<i>Clasterosporium radicola</i> Trotter #
		<i>Clasterosporium resinae</i> Rilstone #
		<i>Clasterosporium roupalae</i> Syd. #
		<i>Clasterosporium scleriae</i> M.B. Ellis #
		<i>Clasterosporium stevensii</i> (G. Arnaud) Toro #
		<i>Clasterosporium tamaricinum</i> Maire #
		<i>Clasterosporium toruloideum</i> Sacc. #
		<i>Clasterosporium traversoanum</i> Peyronel #
	<i>Clavatisporella</i> K.D. Hyde (1)	<i>Clavatisporella musicola</i> K.D. Hyde #
	<i>Dimorphiconidia</i> C. L. Zhang (2) *	<i>Dimorphiconidia graminis</i> C.L. Zhang *
		<i>Dimorphiconidia yunnanensis</i> C.L. Zhang *
	<i>Falciphora</i> J. Luo & N. Zhang ex Z.L. Yuan, C.L. Zhang & F.C. Lin (1) *	<i>Falciphora oryzae</i> Z.L. Yuan, C.L. Zhang & F.C. Lin ex Z.L. Yuan, C.L. Zhang & F.C. Lin *
	<i>Falciphoriella</i> M. Hern.-Restr. & Crous (1)	<i>Falciphoriella solaniterrestris</i> Hern.-Restr. & Crous
	<i>Gaeumannomycella</i> M. Hern.-Restr. & Crous (3)	<i>Gaeumannomycella caricicola</i> Hern.-Restr., Crous & R.K. Schumach. #
		<i>Gaeumannomycella caricis</i> Hern.-Restr. & Crous
		<i>Gaeumannomycella caricigena</i> Crous & Osieck #
	<i>Gaeumannomyces</i> Arx & D.L. Olivier (23)	<i>Gaeumannomyces amomi</i> Bussaban, Lumyong, P. Lumyong, McKenzie & K.D. Hyde
		<i>Gaeumannomyces arxii</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces australiensis</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces avenae</i> (E.M. Turner) Hern.-Restr. & Crous
		<i>Gaeumannomyces californicus</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces caricis</i> J. Walker
		<i>Gaeumannomyces ellisorum</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces floridanus</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces fusiformis</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces glycinicola</i> Hern.-Restr., G. Canning & Crous
		<i>Gaeumannomyces graminicola</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces graminis</i> (Sacc.) Arx & D.L. Olivier
		<i>Gaeumannomyces hyphopodioides</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces licualae</i> J. Fröhl. & K.D. Hyde #
		<i>Gaeumannomyces nanograminis</i> P.L. Vines & M. Tomaso-Peterson

Supplementary Table 2 Continued.

Family	Genus	Species
		<i>Gaeumannomyces oryzae</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces oryzae</i> (Sacc.) Arx & D.L. Olivier
		<i>Gaeumannomyces radicola</i> (Cain) J. Luo & N. Zhang
		<i>Gaeumannomyces setariae</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces tritici</i> (J. Walker) Hern.-Restr. & Crous
		<i>Gaeumannomyces walkeri</i> Hern.-Restr. & Crous
		<i>Gaeumannomyces wongii</i> P. Wong
		<i>Gaeumannomyces yunnanensis</i> C.L. Zhang *
	<i>Gongchenomyces</i> C. L. Zhang (1) *	<i>Gongchenomyces graminicola</i> C.L. Zhang *
	<i>Herbampulla</i> Scheuer & Nograsssek (1)	<i>Herbampulla crassirostris</i> Scheuer & Nograsssek #
	<i>Hongkuomyces</i> C.L. Zhang (2) *	<i>Hongkuomyces graminicola</i> C. L. Zhang *
		<i>Hongkuomyces graminis</i> C. L. Zhang *
	<i>Kohlmeyeriopsis</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Kohlmeyeriopsis medullaris</i> (Kohlm., Volkm.-Kohlm. & O.E. Erikss.) Klaubauf, M.-H. Lebrun & Crous
	<i>Magnaporthiopsis</i> J. Luo & N. Zhang (11)	<i>Magnaporthiopsis agrostidis</i> P. Wong, Khemmuak & R.G. Shivas
		<i>Magnaporthiopsis cynodontis</i> P.L. Vines & Tom.-Pet.
		<i>Magnaporthiopsis gadigal</i> P. Wong, Y.P. Tan, T.L. Weese & R.G. Shivas
		<i>Magnaporthiopsis gumbaynggirr</i> P. Wong, Y.P. Tan, T.L. Weese & R.G. Shivas
		<i>Magnaporthiopsis incrustans</i> (Landsch. & N. Jacks.) J. Luo & N. Zhang
		<i>Magnaporthiopsis maydis</i> (Samra, Sabet & Hing.) Klaubauf, M.-H. Lebrun & Crous
		<i>Magnaporthiopsis meyeri-festuae</i> J. Luo & N. Zhang
		<i>Magnaporthiopsis panicum</i> J. Luo & N. Zhang
		<i>Magnaporthiopsis poae</i> (Landsch. & N. Jacks.) J. Luo & N. Zhang
		<i>Magnaporthiopsis rhizophila</i> (D.B. Scott & Deacon) J. Luo & N. Zhang
		<i>Magnaporthiopsis stipae</i> C. L. Zhang *
	<i>Nakataea</i> Hara (7)	<i>Nakataea curvularioides</i> G.R.W. Arnold #
		<i>Nakataea graminis</i> C. L. Zhang *
		<i>Nakataea multiseptata</i> L.G. Ma & X.G. Zhang #
		<i>Nakataea oryzae</i> (Catt.) J. Luo & N. Zhang
		<i>Nakataea rarissima</i> R.F. Castañeda & W.B. Kendr. #
		<i>Nakataea serpens</i> Shearer & J.L. Crane #
		<i>Nakataea setulosa</i> Jian Ma & X.G. Zhang #
	<i>Neobifusispora</i> C. L. Zhang (2) *	<i>Neobifusispora graminicola</i> C. L. Zhang *
	<i>Neodimorphiconidia</i> C. L. Zhang (1) *	<i>Neodimorphiconidia zhejiangensis</i> C.L.Zhang *
	<i>Neogaeumannomyces</i> D.Q. Dai & K.D. Hyde (1)	<i>Neogaeumannomyces bambusicola</i> D.Q. Dai & K.D. Hyde

Supplementary Table 2 Continued.

Family	Genus	Species
	<i>Neogongchenomyces</i> C. L. Zhang (1) *	<i>Neogongchenomyces graminis</i> C.L. Zhang *
	<i>Neophialophora</i> C. L. Zhang (1) *	<i>Neophialophora graminis</i> C. L. Zhang *
	<i>Omnidemptus</i> P.F. Cannon & Alcorn (7)	<i>Omnidemptus affinis</i> P.F. Cannon & Alcorn
		<i>Omnidemptus graminicola</i> C. L. Zhang *
		<i>Omnidemptus graminis</i> Hern.-Restr., Gené & Guarro
		<i>Omnidemptus lunatus</i> (B. Sutton & Alcorn) Hern.-Restr., J.D.P. Bezerra & Crous
		<i>Omnidemptus paragraminis</i> C. L. Zhang *
		<i>Omnidemptus yunnanensis</i> C. L. Zhang *
		<i>Omnidemptus zhejiangensis</i> C. L. Zhang *
	<i>Pseudophialophora</i> J. Luo & N. Zhang (10)	<i>Pseudophialophora angusta</i> J. Luo & N. Zhang
		<i>Pseudophialophora dichanthelii</i> J. Luo & N. Zhang
		<i>Pseudophialophora eragrostidis</i> J. Luo & N. Zhang
		<i>Pseudophialophora leavittiae</i> Y.P. Tan, Bishop-Hurley & R.G. Shivas
		<i>Pseudophialophora magnispora</i> J. Luo & N. Zhang
		<i>Pseudophialophora panicorum</i> J. Luo & N. Zhang
		<i>Pseudophialophora schizachyrii</i> J. Luo & N. Zhang
		<i>Pseudophialophora sorghi</i> R.J.V. Oliveira, C.M. Gonç., G.A. Silva & J.L. Bezerra
		<i>Pseudophialophora tarda</i> J. Luo & N. Zhang
		<i>Pseudophialophora whartonensis</i> J. Luo & N. Zhang
	<i>Pyriculariopsis</i> M.B. Ellis (8)	<i>Pyriculariopsis amomi</i> (Z.D. Jiang & P.K. Chi) X.H. Lai & H.L. Gao #
		<i>Pyriculariopsis appendiculata</i> Matsush. #
		<i>Pyriculariopsis bicolorata</i> C.R. Silva, Gusmão & R.F. Castañeda #
		<i>Pyriculariopsis breviphora</i> Matsush. #
		<i>Pyriculariopsis formosa</i> Rob. Fernández, R.F. Castañeda & Iturr. #
		<i>Pyriculariopsis miogae</i> Matsush. #
		<i>Pyriculariopsis parasitica</i> (Sacc. & Berl.) M.B. Ellis
		<i>Pyriculariopsis theobromae</i> R.F. Castañeda & W.B. Kendr. #
	<i>Slopeiomyces</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Slopeiomyces cylindrosporus</i> (D. Hornby, Slope, Gutter. & Sivan.) Klaubauf, M.-H. Lebrun & Crous
	<i>Xenofalciphora</i> C. L. Zhang (1) *	<i>Xenofalciphora graminis</i> C.L. Zhang *
	<i>Xenogaeumannomyces</i> C. L. Zhang (1) *	<i>Xenogaeumannomyces yunnanensis</i> C. L. Zhang *
	<i>Xenophialophora</i> C. L. Zhang (1) *	<i>Xenophialophora graminicola</i> C. L. Zhang *
	<i>Xenorhytisma</i> C. L. Zhang (1) *	<i>Xenorhytisma sichuanense</i> (Q. Zeng, Y.C. Lv & C.L. Yang) C.L. Zhang *
<i>Ophioceraeae</i> Klaubauf, E.G. LeBrun & Crous (1)	<i>Ophioceras</i> Sacc. (31)	<i>Ophioceras aquaticum</i> D.M. Hu, L. Cai & K.D. Hyde
		<i>Ophioceras arcuatissporum</i> Shearer, J.L. Crane & W. Chen #

Supplementary Table 2 Continued.

Family	Genus	Species
		<i>Ophioceras bambusae</i> Höhn. #
		<i>Ophioceras castillense</i> (C.L. Sm.) H.B. Jiang, Phookamsak & K.D. Hyde
		<i>Ophioceras cecropiae</i> E. Müll. #
		<i>Ophioceras chiangdaoense</i> Thongk., Lumyong & K.D. Hyde
		<i>Ophioceras commune</i> Shearer, J.L. Crane & W. Chen
		<i>Ophioceras dolichostomum</i> (Berk. & M.A. Curtis) Sacc.
		<i>Ophioceras ficinum</i> Tennakoon, C.H. Kuo & K.D. Hyde
		<i>Ophioceras filiforme</i> (Henn.) Höhn. #
		<i>Ophioceras freycinetiae</i> Crous
		<i>Ophioceras graminis</i> C. L. Zhang *
		<i>Ophioceras guizhouense</i> J.F. Zhang & Jian K. Liu #
		<i>Ophioceras guttulatum</i> C.K.M. Tsui, H.Y.M. Leung, K.D. Hyde & Hodgkiss #
		<i>Ophioceras hongkongense</i> C.K.M. Tsui, H.Y.M. Leung, K.D. Hyde & Hodgkiss
		<i>Ophioceras indicum</i> S.P. Lal #
		<i>Ophioceras junci</i> Crous & Osieck
		<i>Ophioceras leptosporum</i> (S.H. Iqbal) J. Walker
		<i>Ophioceras miyazakiense</i> Matsush. #
		<i>Ophioceras palmae</i> C.K.M. Tsui, H.Y.M. Leung, K.D. Hyde & Hodgkiss #
		<i>Ophioceras parasiticum</i> Teng #
		<i>Ophioceras petrakii</i> Tilak, S.B. Kale & S.V.S. Kale #
		<i>Ophioceras rhizomorphum</i> (Huhndorf & Mugambi) H.B. Jiang, Phookamsak & K.D. Hyde
		<i>Ophioceras sichuanense</i> H.B. Jiang, Phookamsak & K.D. Hyde
		<i>Ophioceras sorghi</i> Saccas #
		<i>Ophioceras submersum</i> D.F. Bao, Z.L. Luo, H.Y. Su & K.D. Hyde
		<i>Ophioceras tambopataense</i> Matsush. #
		<i>Ophioceras tenuisporum</i> Shearer, J.L. Crane & W. Chen #
		<i>Ophioceras thailandense</i> J. Yang, E.B.G. Jones & K.D. Hyde #
		<i>Ophioceras venezuelense</i> Shearer, J.L. Crane & W. Chen #
		<i>Ophioceras zaeae</i> Saccas #
<i>Plagiosphaeraceae</i> C.L. Zhang (3)*	<i>Aquafiliformis</i> Z.L. Luo, K.D. Hyde & H.Y. Su (1)	<i>Aquafiliformis lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su
	<i>Muraeriata</i> Huhndorf, Greif, Mugambi & A.N. Mill. (2)	<i>Muraeriata africana</i> Huhndorf & Mugambi
		<i>Muraeriata collapsa</i> Huhndorf, Greif, Mugambi & A.N. Mill.
	<i>Plagiosphaera</i> Petr. (8)	<i>Plagiosphaera bhargavae</i> E. Müll. #
		<i>Plagiosphaera immersa</i> (Trail) Petr.

Supplementary Table 2 Continued.

Family	Genus	Species
<i>Pseudohalonectriaceae</i> Hongsanan & K.D. Hyde (1)	<i>Pseudohalonectria</i> Minoura & T. Muroi (15)	<i>Plagiosphaera japonica</i> Tak. Kobay. & K. Sasaki #
		<i>Plagiosphaera moravica</i> (Petr.) Petr. #
		<i>Plagiosphaera muroiana</i> (I. Hino & Katum.) J. Walker #
		<i>Plagiosphaera nilotica</i> M. Monod & P.J. Fisher #
		<i>Plagiosphaera platensis</i> (Speg.) J. Walker #
		<i>Plagiosphaera sacchari</i> (Speg.) M. Monod #
		<i>Pseudohalonectria adversaria</i> Shearer #
		<i>Pseudohalonectria aomoriensis</i> Yas. Ono & Tak. Kobay. #
		<i>Pseudohalonectria aurantiaca</i> J. Yang, E.B.G. Jones & K.D. Hyde #
		<i>Pseudohalonectria eubenangeensis</i> K.D. Hyde, Joanne E. Taylor & J. Fröhl. #
		<i>Pseudohalonectria fagicola</i> R.H. Perera, E.B.G. Jones & K.D. Hyde
		<i>Pseudohalonectria falcata</i> Shearer #
		<i>Pseudohalonectria fuxianii</i> L. Cai, C.K.M. Tsui, K.Q. Zhang & K.D. Hyde #
		<i>Pseudohalonectria halophila</i> Kohlm. & Volkm.-Kohlm. #
		<i>Pseudohalonectria hampshirensis</i> R.H. Perera, E.B.G. Jones & K.D. Hyde
		<i>Pseudohalonectria lignicola</i> Minoura & T. Muroi
		<i>Pseudohalonectria longirostrum</i> Shearer #
		<i>Pseudohalonectria lutea</i> Shearer #
		<i>Pseudohalonectria miscanthicola</i> Shenoy, Jeewon & K.D. Hyde #
		<i>Pseudohalonectria palmicola</i> K.D. Hyde, Joanne E. Taylor & J. Fröhl. #
		<i>Pseudohalonectria tayloriae</i> K.D. Hyde & J. Fröhl. #
		<i>Bambusicularia brunnea</i> Klaubauf, M.-H. Lebrun & Crous
<i>Pyriculariaceae</i> Klaubauf, E.G. LeBrun & Crous (13)	<i>Bambusicularia</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Barretomyces calathea</i> (D.J. Soares, F.B. Rocha & R.W. Barreto) Klaubauf, M.-H. Lebrun & Crous
	<i>Barretomyces</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Bipyricularia graminis</i> C.L. Zhang *
	<i>Bipyricularia</i> C. L. Zhang (1) *	<i>Macgarvieomyces borealis</i>
	<i>Macgarvieomyces</i> Klaubauf, M.-H. Lebrun & Crous (3)	<i>Macgarvieomyces juncicola</i>
		<i>Macgarvieomyces luzulae</i>
		<i>Neocordana johnstonii</i> (M.B. Ellis) Hern.-Restr. & Crous #
		<i>Neocordana malayensis</i> Crous
		<i>Neocordana musae</i> (Zimm.) Hern.-Restr. & Crous
		<i>Neocordana musarum</i> Crous
		<i>Neocordana musicola</i> Hern.-Restr. & Crous
		<i>Neocordana musigena</i> Crous

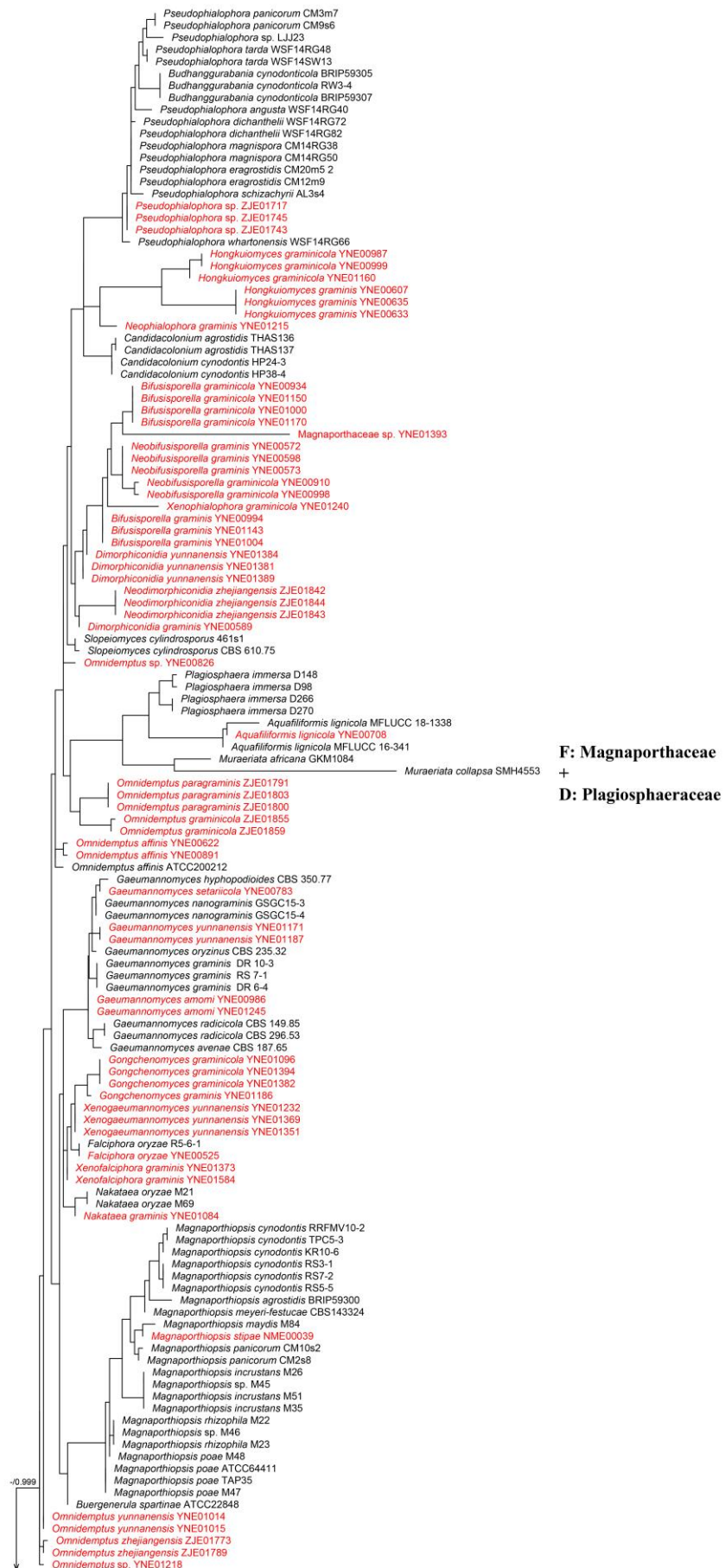
Supplementary Table 2 Continued.

Family	Genus	Species
		<i>Neocordana versicolor</i> (D.J. Soares & R.W. Barreto) Hern.-Restr. & Crous #
	<i>Neopyricularia</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Neopyricularia commelinicola</i> (M.J. Park & H.D. Shin) Klaubauf, M.-H. Lebrun & Crous
	<i>Nothopyricularia</i> C. L. Zhang (1) *	<i>Nothopyricularia junci</i> (P.W. Crous & E.R. Osieck) C.L. Zhang *
	<i>Proxipyricularia</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Proxipyricularia zingiberis</i> (Y. Nisik.) Klaubauf, M.-H. Lebrun & Crous
	<i>Pseudopyricularia</i> Klaubauf, M.-H. Lebrun & Crous (12)	<i>Pseudopyricularia bothriochloae</i> (Crous & Cheew.) Y. Marín & Crous
		<i>Pseudopyricularia caricicola</i> Crous & Osieck #
		<i>Pseudopyricularia cyperi</i> Klaubauf, M.-H. Lebrun & Crous
		<i>Pseudopyricularia festucae</i> Crous
		<i>Pseudopyricularia hagahagae</i> Crous & M.J. Wingf.
		<i>Pseudopyricularia hedjaroudii</i> M. Javan-Nikkhah, A. Pordel & G. Ghorbani
		<i>Pseudopyricularia higginsii</i> (Luttr.) Klaubauf, M.-H. Lebrun & Crous
		<i>Pseudopyricularia hyrcaniana</i> Pordel & Jav.-Nikkh.
		<i>Pseudopyricularia iraniana</i> Pordel & Jav.-Nikkh.
		<i>Pseudopyricularia javanii</i> A. Pordel & G. Ghorbani
		<i>Pseudopyricularia kyllingae</i> Klaubauf, M.-H. Lebrun & Crous
		<i>Pseudopyricularia persiana</i> G. Ghorbani, Pordel & Jav.-Nikkh.
	<i>Pyricularia</i> Sacc. (44)	<i>Pyricularia angulata</i> Hashioka
		<i>Pyricularia apiculata</i> Matsush. #
		<i>Pyricularia buloloensis</i> Matsush. #
		<i>Pyricularia caffra</i> Matsush. #
		<i>Pyricularia cannae</i> Roldan #
		<i>Pyricularia cannicola</i> Hashioka #
		<i>Pyricularia caricis</i> G. Arnaud ex Matsush. #
		<i>Pyricularia contorta</i> Melnik, U. Braun & A.V. Alexandrova #
		<i>Pyricularia cortaderiae</i> McKenzie #
		<i>Pyricularia costii</i> (Sawada) S. Ito #
		<i>Pyricularia ctenantheicola</i> Klaubauf, M.-H. Lebrun & Crous
		<i>Pyricularia curcuma</i> Rathaiah #
		<i>Pyricularia didyma</i> M.B. Ellis #
		<i>Pyricularia distorta</i> Hashioka #
		<i>Pyricularia dubiosa</i> (Speg.) Viégas #
		<i>Pyricularia ebbelsii</i> M.B. Ellis #
		<i>Pyricularia fusispora</i> (Matsush.) Zucconi, Onofri & Persiani #
		<i>Pyricularia graminis-tritici</i> Castroag., S.I. Moreira, Maciel, B.A. McDonald, Crous & Ceresini #

Supplementary Table 2 Continued.

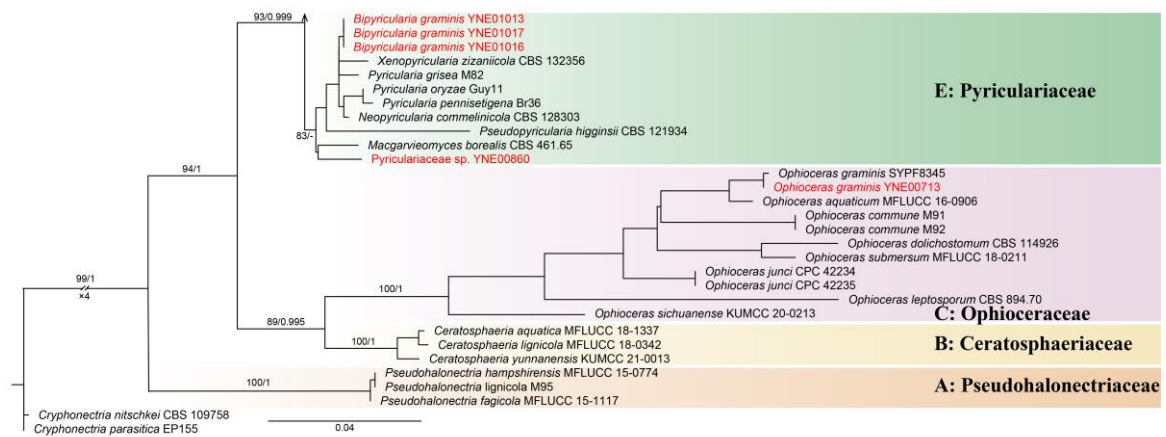
Family	Genus	Species
		<i>Pyricularia grisea</i> Cooke ex Sacc.
		<i>Pyricularia guarumaicola</i> F.C. Albuquerque & M.L. Duarte #
		<i>Pyricularia kookicola</i> Bussaban #
		<i>Pyricularia korlaensis</i> J.H. Kong & T.Y. Zhang #
		<i>Pyricularia lauri</i> P.M. Kirk #
		<i>Pyricularia leersiae</i> (Sawada) S. Ito #
		<i>Pyricularia lourinae</i> F.C. Albuquerque & M.L. Duarte #
		<i>Pyricularia oncosperma</i> Yanna, W.H. Ho & K.D. Hyde #
		<i>Pyricularia oryzae</i> Cavara
		<i>Pyricularia panici-paludosi</i> (Sawada) S. Ito #
		<i>Pyricularia parasitica</i> Ellis & Everh. #
		<i>Pyricularia penniseti</i> Prasada & Goya #
		<i>Pyricularia penniseticola</i> Klaubauf, M.-H. Lebrun & Crous
		<i>Pyricularia pennisetigena</i> Klaubauf, M.-H. Lebrun & Crous
		<i>Pyricularia peruamazonica</i> Matsush. #
		<i>Pyricularia pyricularioides</i> (Matsush.) de Hoog & Oorschot #
		<i>Pyricularia rabaulensis</i> Matsush. #
		<i>Pyricularia sansevieriae</i> Bat., J.L. Bezerra & Cavalc. #
		<i>Pyricularia setariae</i> Y. Nisik. #
		<i>Pyricularia sphaerulata</i> Zucconi & Onofri #
		<i>Pyricularia subsigmoidea</i> R.F. Castañeda & W.B. Kendr. #
		<i>Pyricularia urashimae</i> Castroag., J.L.N. Maciel, Crous & Ceresini
		<i>Pyricularia vandalurensis</i> Subram. & Vittal #
		<i>Pyricularia variabilis</i> Bussaban #
		<i>Pyricularia whetzelii</i> (Chupp) Bat. & R. Garnier #
		<i>Pyricularia zingibericola</i> Klaubauf, M.-H. Lebrun & Crous
	<i>Pyriculariomyces</i> Y. Marín, M.J. Wingf. & Crous (1)	<i>Pyriculariomyces asari</i> (Crous & M.J. Wingf.) Y. Marín, M.J. Wingf. & Crous
	<i>Utrechtiana</i> Crous & Quaedvl. (3)	<i>Utrechtiana arundinacea</i> (Corda) Crous, Quaedvl. & Y. Marín
		<i>Utrechtiana constantinescui</i> (Melnik & Shabunin) Crous & Y. Marín #
		<i>Utrechtiana roumegueri</i> (Cavara) Videira & Crous
	<i>Xenopyricularia</i> Klaubauf, M.-H. Lebrun & Crous (1)	<i>Xenopyricularia zizaniicola</i> (Hashioka) Klaubauf, M.-H. Lebrun & Crous

Note: Numbers in the brackets after the family and genus name indicate the number of the taxon, * indicates a taxon newly introduced in this study, and # indicates that the taxon was not included in the phylogenetic analysis in this study and is based only on the current name of Species Fungorum (Access date 7 September 2024).

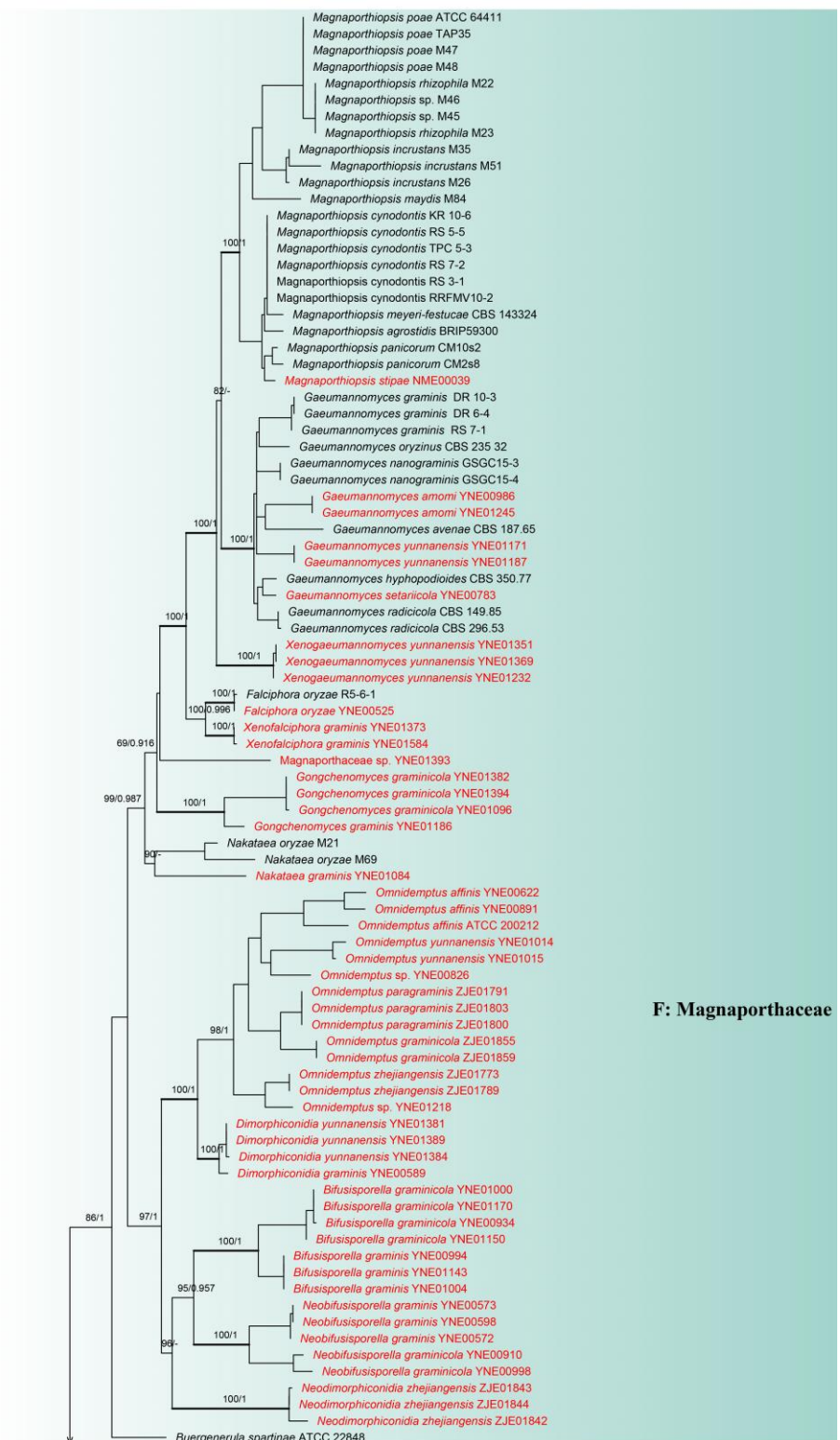


Supplementary Figure 1 – Phylogenetic tree inferred from a maximum likelihood analysis of LSU sequence representing the order *Magnaporthales*. Nodes display corresponding MLBS and BIPP

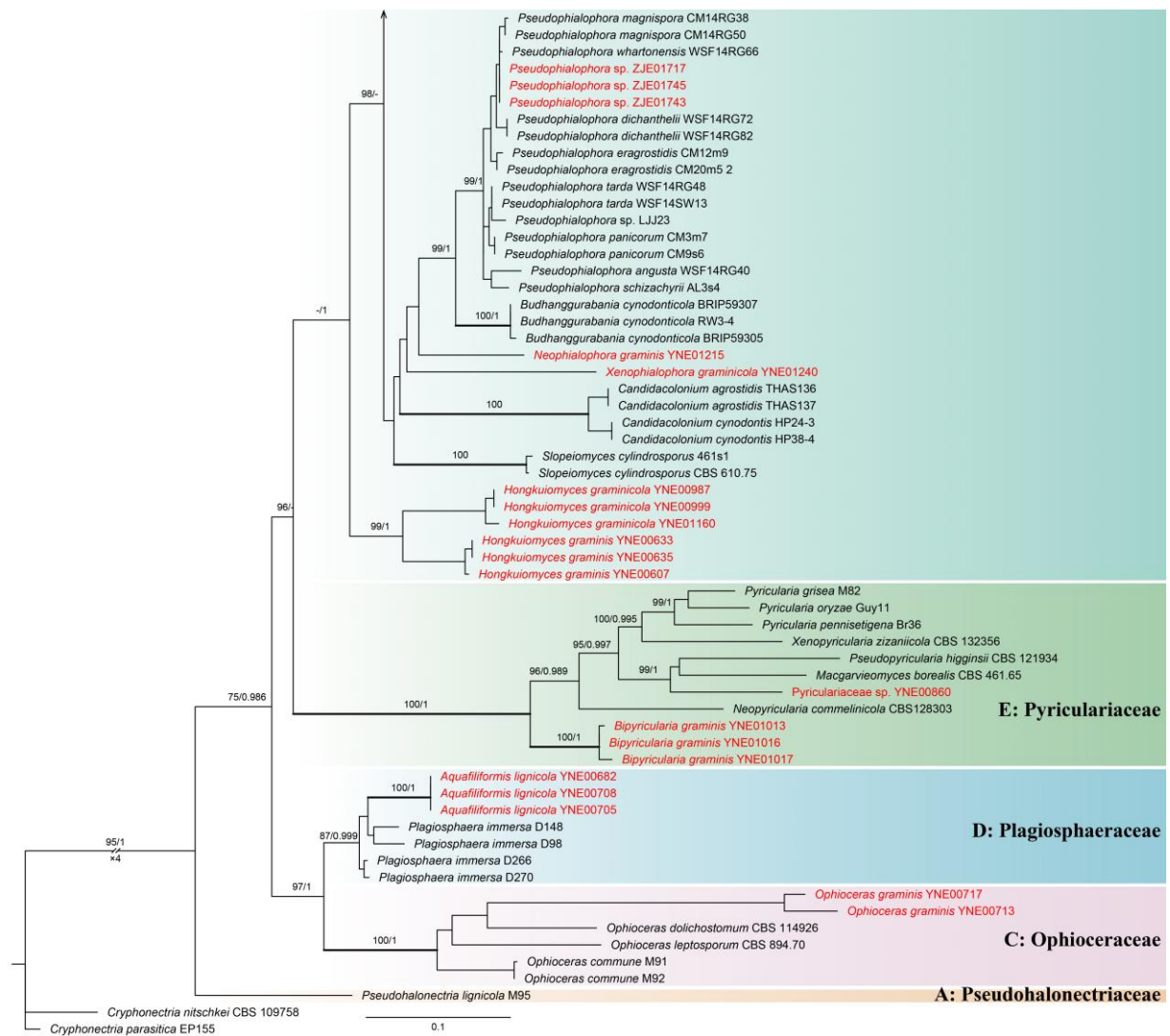
values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . Values for MLBS and BIPP are omitted at nodes of clades below the family level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.



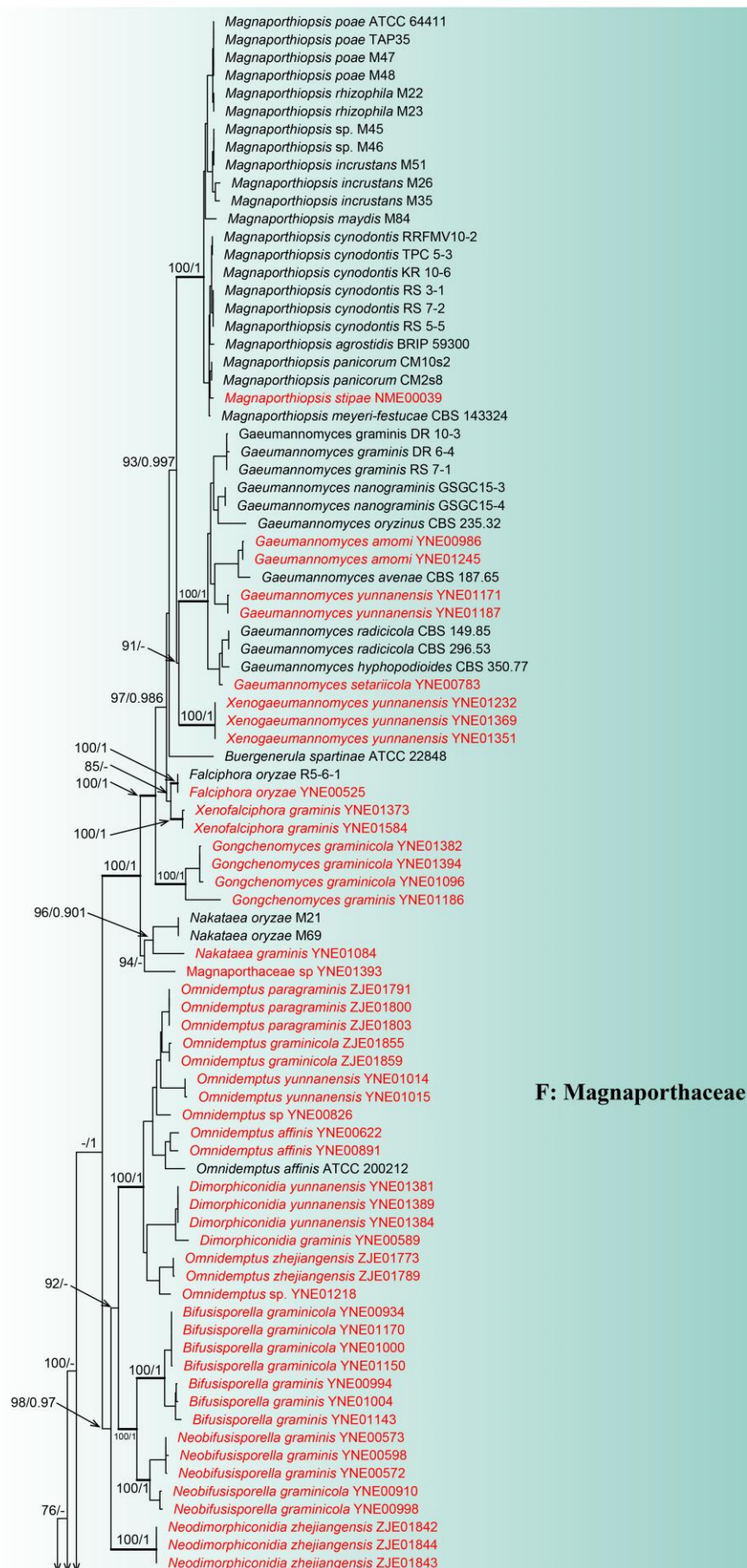
Supplementary Figure 1 – Continued.



Supplementary Figure 2 – Phylogenetic tree inferred from a maximum likelihood analysis of *MCM7* sequence representing the order *Magnaporthales*. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . Values for MLBS and BIPP are omitted at nodes of clades below the genus level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.

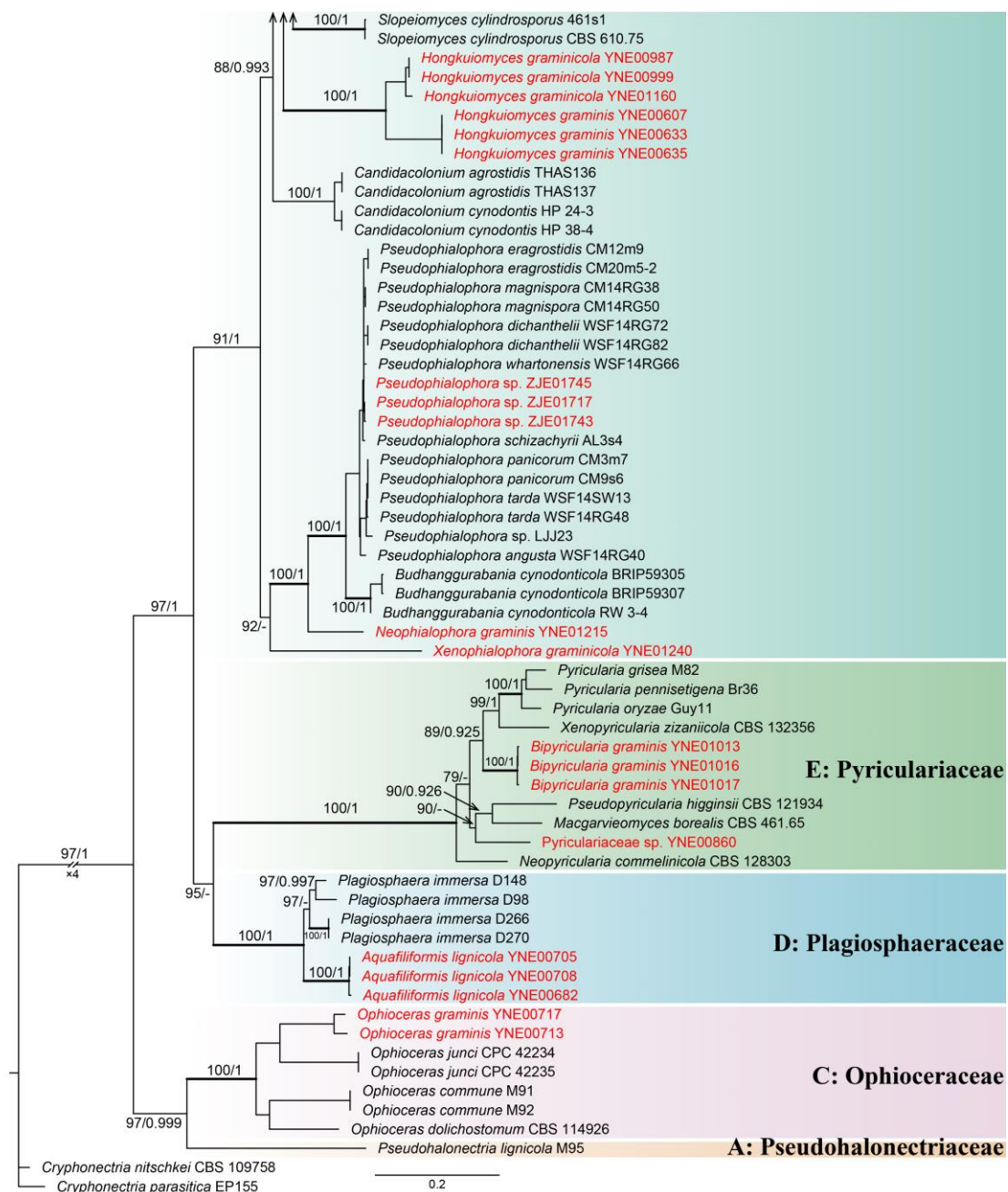


Supplementary Figure 2 – Contitued.

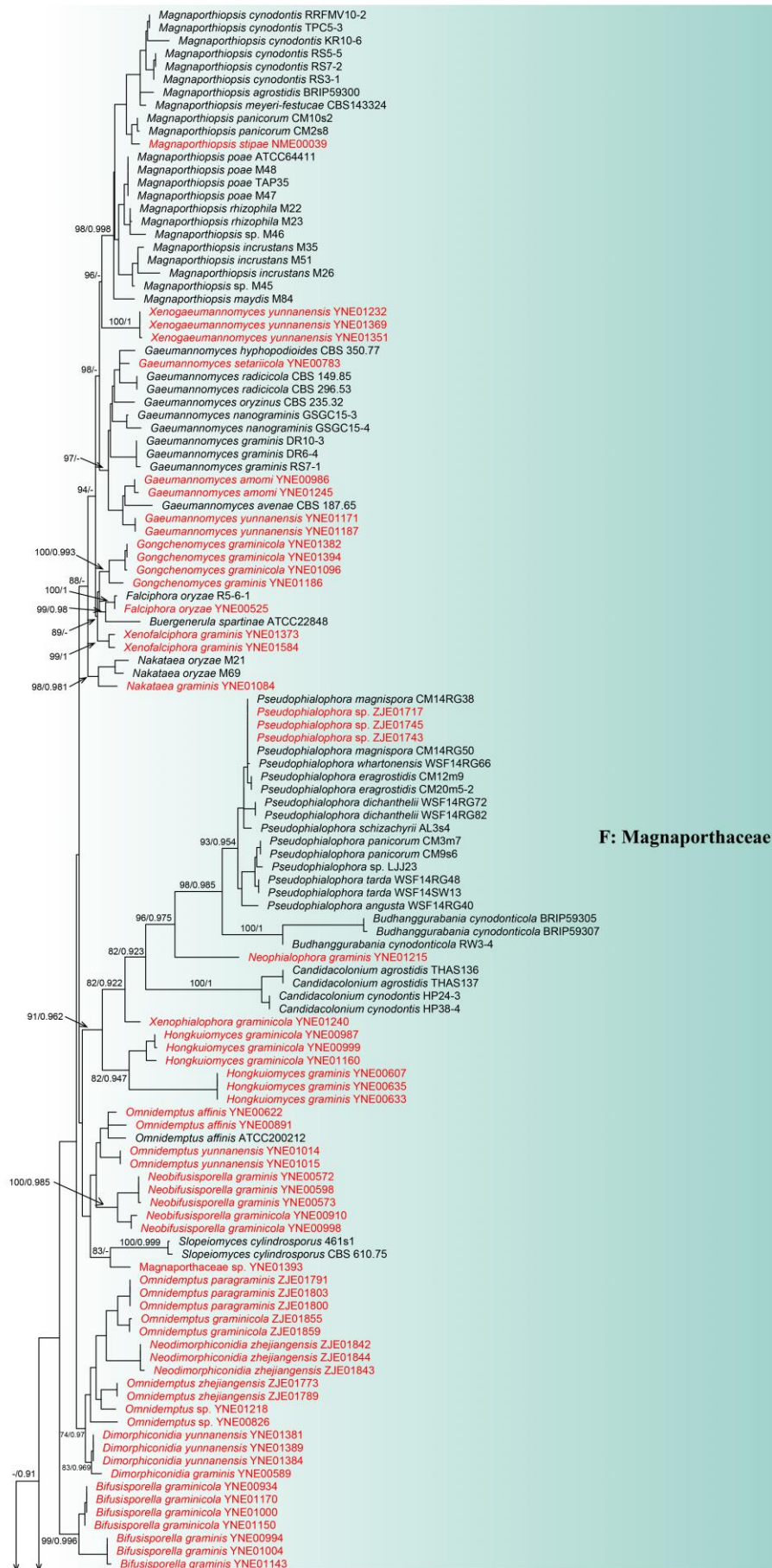


Supplementary Figure 3 – Phylogenetic tree inferred from a maximum likelihood analysis of *RPB1* sequence representing the order *Magnaporthales*. Nodes display corresponding MLBS and

BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . Values for MLBS and BIPP are omitted at nodes of clades below the genus level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.

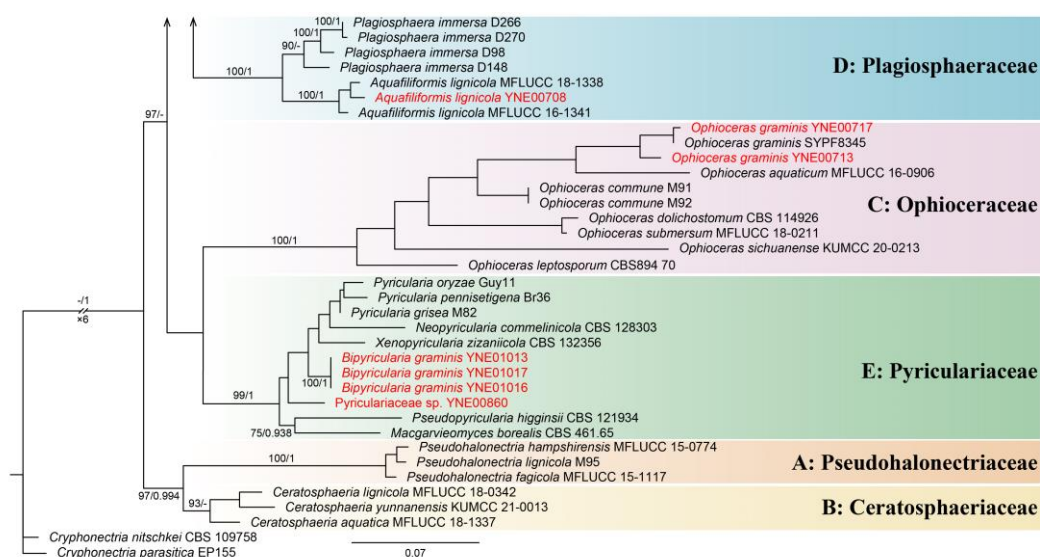


Supplementary Figure 3 – Continued.

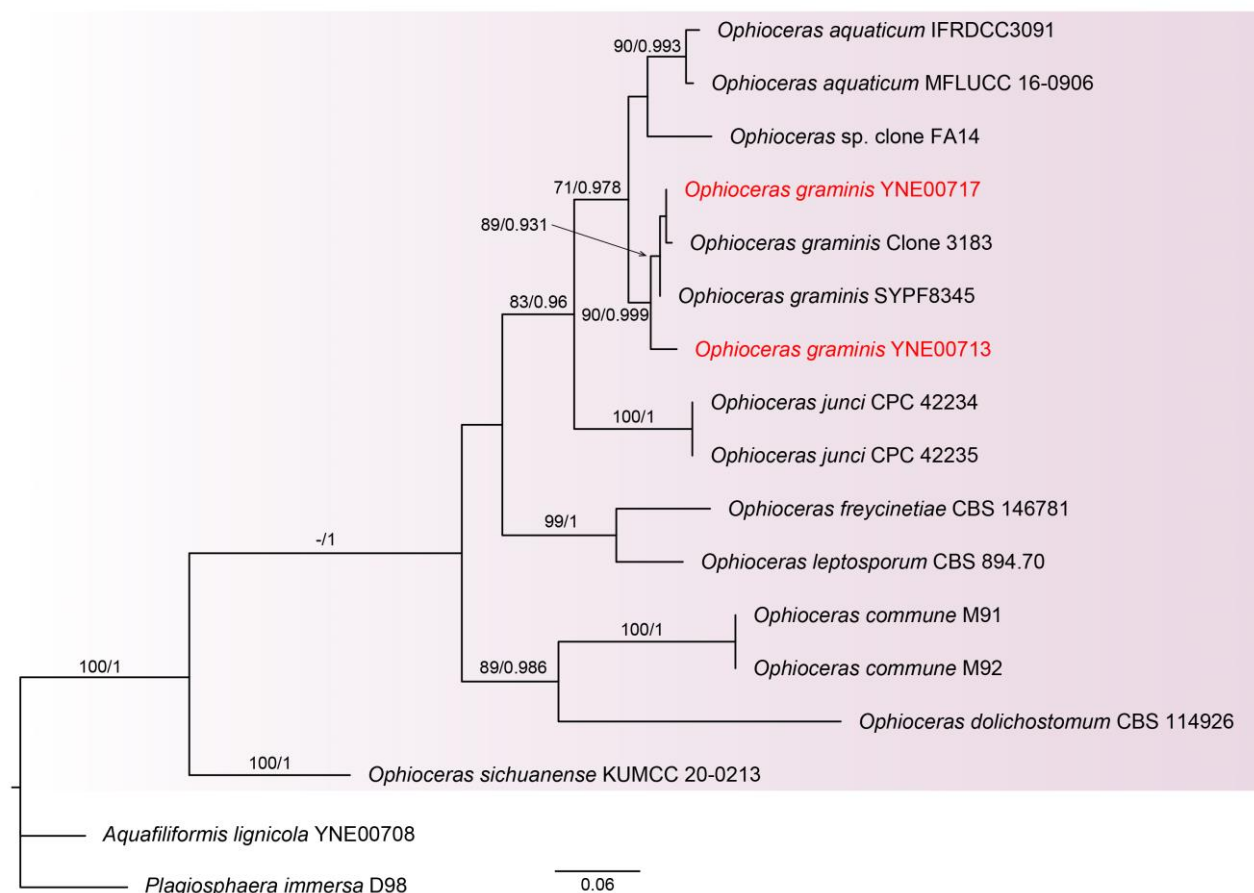


Supplementary Figure 4 – Phylogenetic tree inferred from a maximum likelihood analysis of *TEF1* sequence representing the order *Magnaporthales*. Nodes display corresponding MLBS and

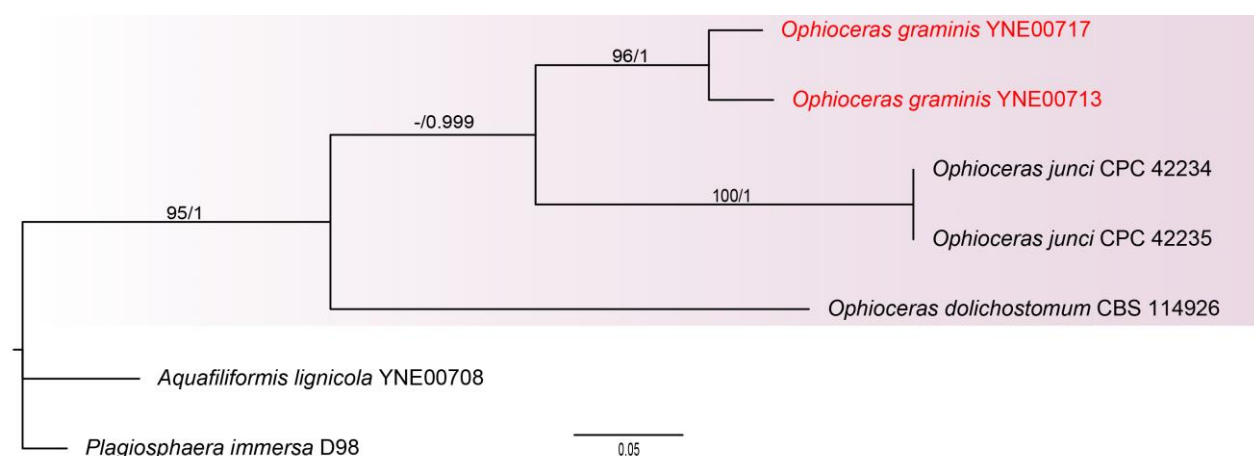
BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . Values for MLBS and BIPP are omitted at nodes of clades below the genus level. The tree is rooted with *Cryphonectria nitschkei* CBS109758 and *Cryphonectria parasitica* EP155.



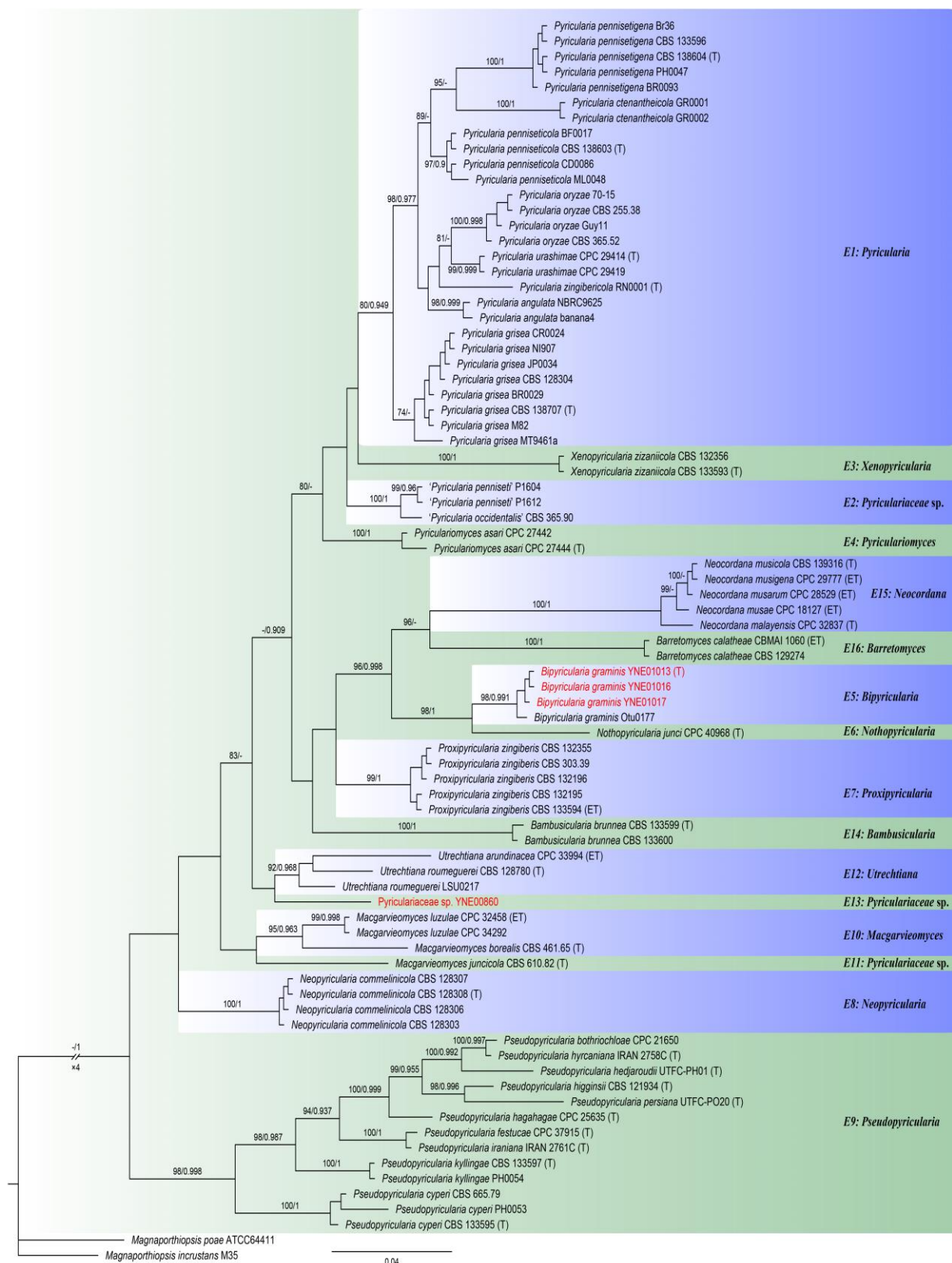
Supplementary Figure 4 – Continued.



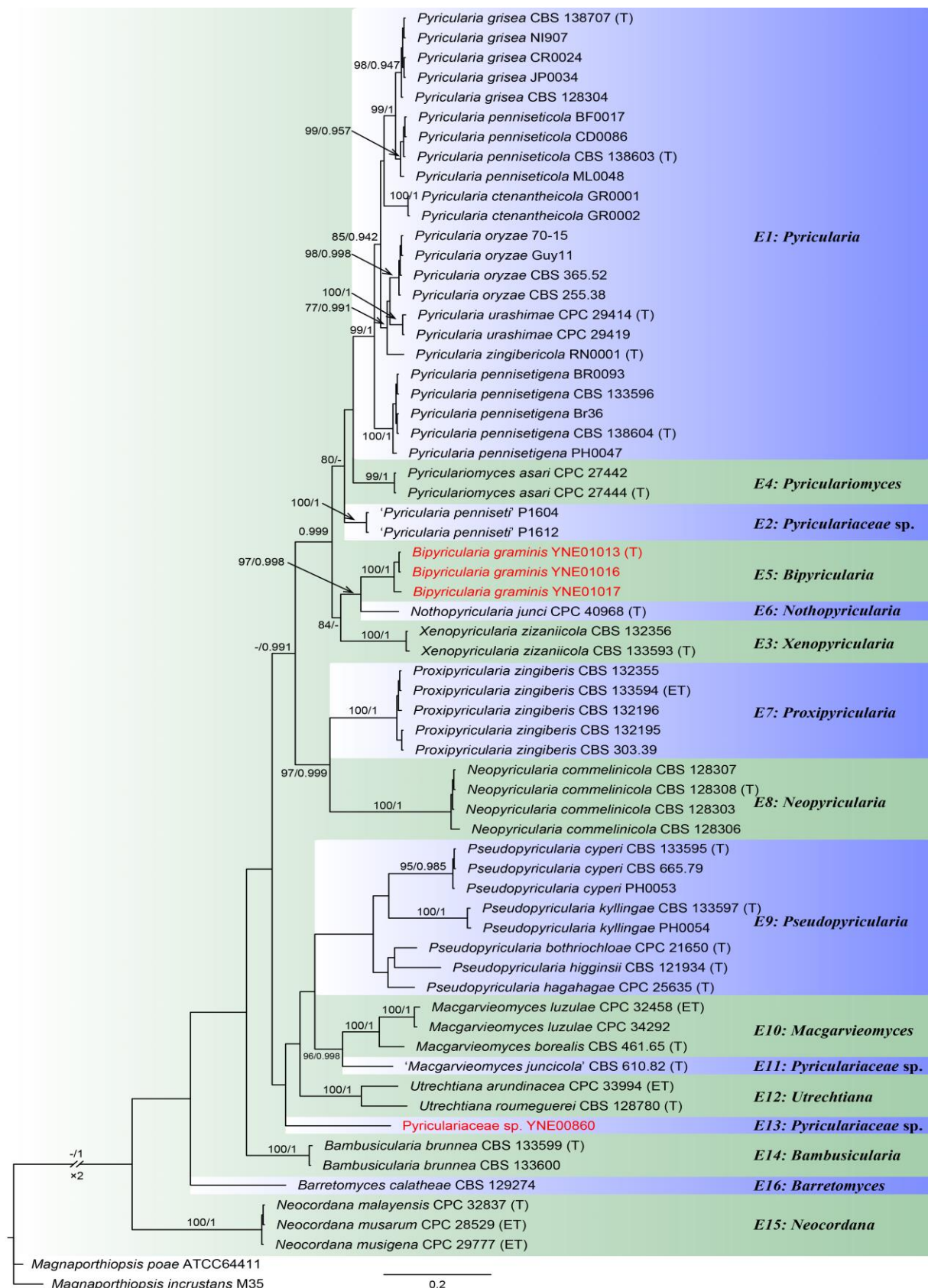
Supplementary Figure 5 – Phylogenetic tree inferred from a maximum likelihood analysis of ITS sequence representing the family Ophioceraaceae. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Aquafiliformis lignicola* YNE00708 and *Plagiosphaera immersa* D98.



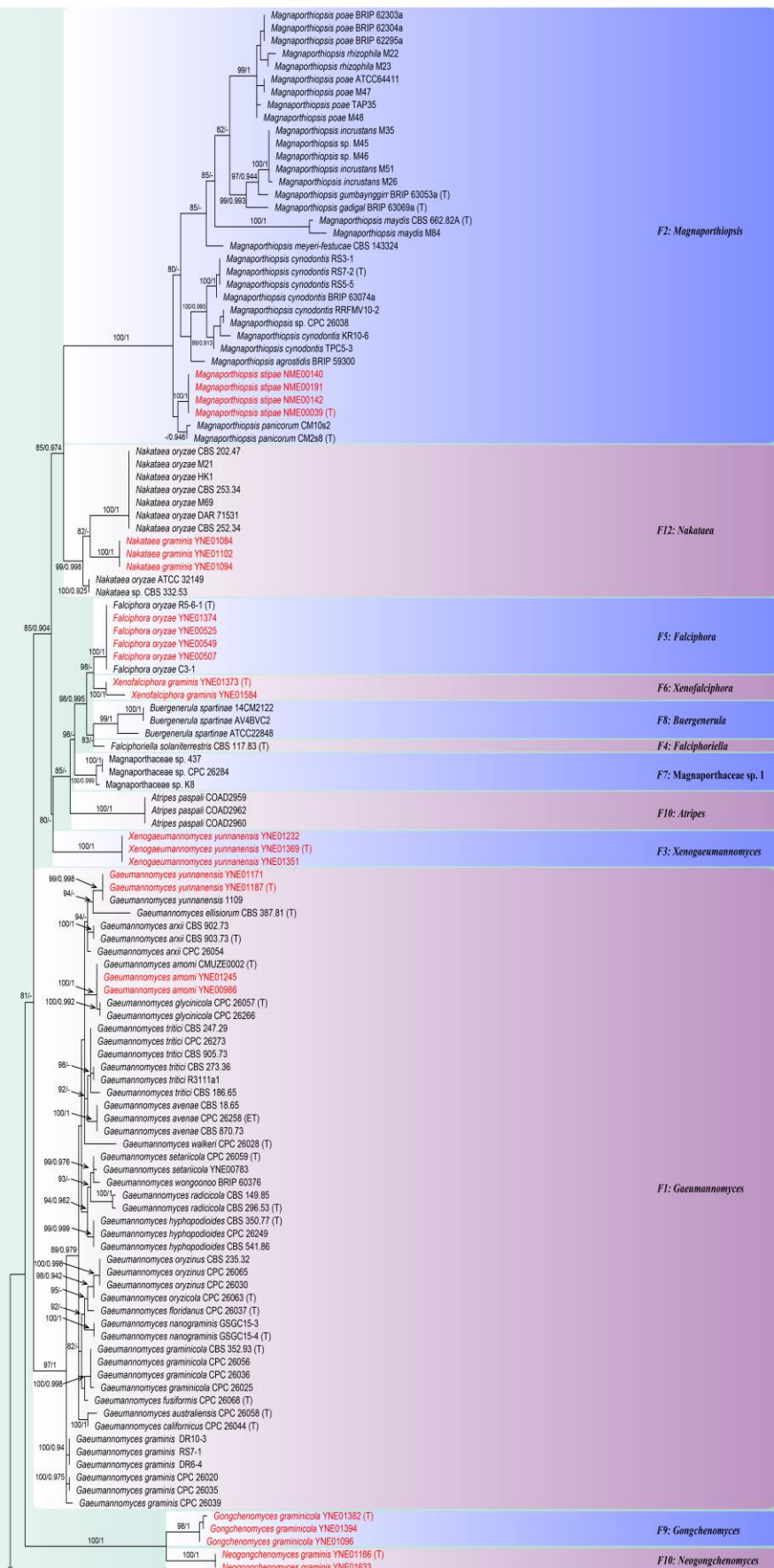
Supplementary Figure 6 – Phylogenetic tree inferred from a maximum likelihood analysis of ACT sequence representing the family Ophioceraaceae. Nodes display corresponding MLBS and BIPP values at nodes when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Aquafiliformis lignicola* YNE00708 and *Plagiosphaera immersa* D98.



Supplementary Figure 7 – Phylogenetic tree inferred from a bayesian inference analysis of the ITS sequence representing the family *Pyriculariaceae*. Nodes display corresponding MLBS and BIPP values when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Magnaporthiopsis incrustans* M35 and *Magnaporthiopsis poae* ATCC 64411.



Supplementary Figure 8 – Phylogenetic tree inferred from a bayesian inference analysis of the ACT sequence representing the family Pyriculariaceae. Nodes display corresponding MLBS and BIPP values at nodes when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Magnaporthiopsis incrustans* M35 and *Magnaporthiopsis poae* ATCC 64411.

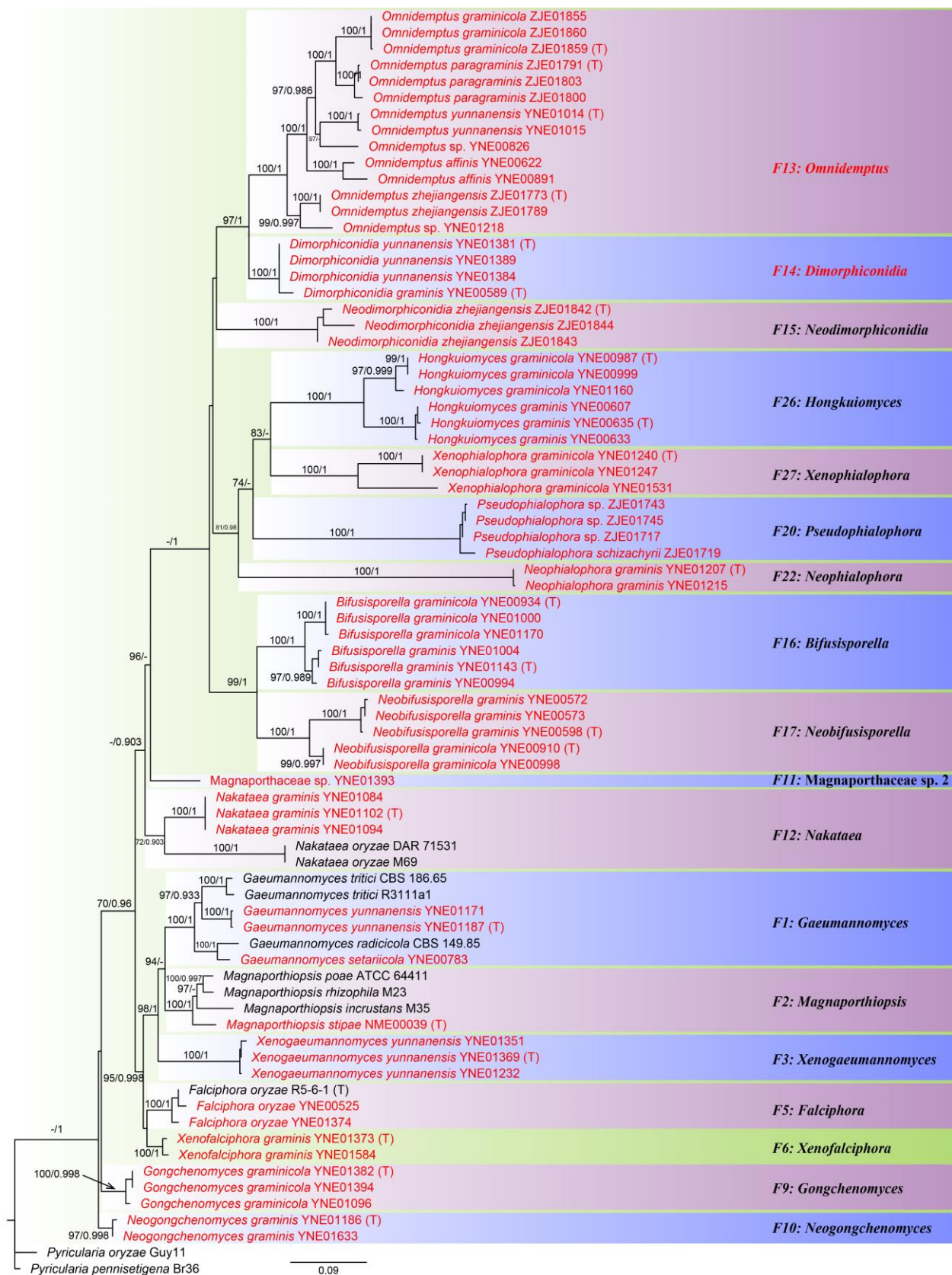


Supplementary Figure 9 – Phylogenetic tree inferred from a maximum likelihood analysis of the ITS sequence representing the family *Magnaporthaceae*. Nodes display corresponding MLBS and

BIPP values at nodes when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Pyricularia oryzae* Guy11 and *Pyricularia pennisetigena* Br36.



Supplementary Figure 9 – Continued.



Supplementary Figure 10 – Phylogenetic tree inferred from a maximum likelihood analysis of the ACT sequence representing the family *Magnaporthaceae*. Nodes display corresponding MLBS and BIPP values at nodes when MLBP is $\geq 70\%$ and BIPP is ≥ 0.9 . The tree is rooted with *Pyricularia oryzae* Guy11 and *Pyricularia pennisetigena* Br36.