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Insight into the Systematics of Microfungi Colonizing Dead Woody Twigs of *Dodonaea viscosa* in Honghe (China)

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Abstract: Members of *Dodonaea* are broadly distributed across subtropical and tropical areas of southwest and southern China. This host provides multiple substrates that can be richly colonized by numerous undescribed fungal species. There is a severe lack of microfungal studies on *Dodonaea* in China, and consequently, the diversity, phylogeny and taxonomy of these microorganisms are all largely unknown. This paper presents two new genera and four new species in three orders of Dothideomycetes gathered from dead twigs of *Dodonaea viscosa* in Honghe, China. All new collections were made within a selected area in Honghe from a single *Dodonaea* sp. This suggests high fungal diversity in the region and the existence of numerous species awaiting discovery. Multiple gene sequences (non-translated loci and protein-coding regions) were analysed with maximum likelihood and Bayesian analyses. Results from the phylogenetic analyses supported placing *Haniomyces dodonaeae* gen. et sp. in the Teratosphaeriaceae family. Analysis of *Rhytidhysteron* sequences resulted in *Rhytidhysterion hongheense* sp. nov., while analysed Lophiostomataceae sequences revealed *Lophiomurispora hongheensis* gen. et sp. nov. Finally, phylogeny based on a combined dataset of pyrenochaeta-like sequences demonstrates strong statistical support for placing *Quixadomyces hongheensis* sp. nov. in Parapyrenochaetaceae. Morphological and updated phylogenetic circumscriptions of the new discoveries are also discussed.

Keywords: Ascomycota; Asexual morph; Capnodiales; Greater Mekong Subregion; Hysteriales; Pleosporales; Sexual morph; Yunnan

1. Introduction

Fungi are cosmopolitan, featuring a broad geographic distribution and high level of diversity compared to plants and other organisms [1]. 140,000 fungal species have been listed in Kirk [2], and one recent overview of global fungi and fungus-like taxa by Wijayawardene et al. [3] listed approximately 100,000 known taxa. However, both numbers represent less than 5% of global fungal estimates [4,5]. There is a need to bridge the gap between our understanding of these missing fungi and their diversity. Numerous diverse habitats and substrates remain unexplored. It has also been observed that several countries and regions are bountiful repositories of many missing fungi, such as northern Thailand [6]. Despite this, fungi in Asia are relatively understudied [5]. Even though the Greater Mekong Subregion (GMS) hosts a high level of biodiversity and forms an integral part of the Indo-Burma Biodiversity Hotspot, fungi from this region largely remain a mystery. Yunnan Province, China, as part of the GMS, is home to an extremely wide variety of ecosystems. Mycologists working in Yunnan have recently focused their attention on abundant “less-researched habitats” for fungal occurrences, including caves, forests, grasslands, lakes, karst landscapes and mountains; accordingly, there is a rich body of literature documenting novel discoveries across the region [7–19].
The Honghe Hani and Yi Autonomous Prefecture is in south-eastern Yunnan Province. The region features a mountainous topography, numerous limestone deposits and a south-eastward decreasing elevation gradient. Owing to its abundant precipitation and heat as well as its dramatic altitudinal range and varied flora, this region harbours a rich diversity of plant species [20,21]. Along the altitudinal gradient, vegetation from lower to higher elevations range from tropical and montane rain forests to monsoon evergreen, montane mossy evergreen and summit mossy evergreen broad-leaved forests [22]. This complex topography and climatic diversity are both significant contributors to local biodiversity richness [23]. Among publications documenting fungal encounters across Yunnan Province, ascomycetes are critically neglected when compared to the amount of research on basidiomycetes [24]. Regrettably, studies on microfungi in Honghe are virtually non-existent. Except Marasinghe et al. [25], we could not find a single detailed account of microfungi in Honghe based on both morphological and phylogenetic analyses.

*Dodonaea viscosa* is a perennial evergreen woody shrub belonging to the family Sapindaceae. It is drought- and pollution-resistant as well as capable of growing on poor soils and rocky sites. The plant can also easily inhabit open areas and secondary forests [26,27]. A fast-growing plant, it typically grows 1 to 3 m in height but on rare occasions can reach up to 8 m [28]. *Dodonaea viscosa* is believed to have originated from Australia [29], though it grows throughout tropical and subtropical countries, including the African, Asian, Northern American and Southern American continents [30–32]. *Dodonaea viscosa* is effective at performing sand dune fixation and controlling coastal erosion since its roots function as excellent soil binders [33]. It can also be used to reclain marshes. It is also grown as an ornamental plant owing to its shiny foliage and pink–red winged fruit [33]. Moreover, it is a well-known topic in environmental impact studies to determine the growth and yield of crops based on the presence of *D. viscosa* [27,34] as well as study its capacity to increase resilience to pollution [35,36] and drought [37]. In traditional medicine systems, plant parts such as the stem, leaves, seeds, roots, bark and aerial parts are used for various treatments [38]. Hossain [39] reported that extract obtained from *D. viscosa* has shown significant antidiabetic, antimicrobial, insecticidal, antioxidant, cytotoxic, antifertility, anti-inflammatory, analgesic, anti-ulcer, antispasmodic, anti-diarrheal and detoxification properties [27].

This study is the second in a series comprising an exhaustive taxonomic effort to document the microfungi of Yunnan Province [24]. In this study, we collected fresh fungal specimens from dead woody twigs of *Dodonaea* species at the Centre for Mountain Futures (CMF), an applied research centre jointly managed by World Agroforestry (ICRAF) and the Kunming Institute of Botany, Chinese Academy of Sciences (CAS), in Honghe County of the Honghe Hani and Yi Autonomous Prefecture. Using morphology and multi-gene phylogenetic evidence retrieved from the gathered ascomycetes, we characterized two new genera and four new species in the orders Capnodiales, Hysteriales and Pleosporales from dead twigs of *Dodonaea viscosa* in Honghe.

2. Materials and Methods

2.1. Herbarium Material and Fungal Strains

Fresh fungal materials were gathered from dead twigs of *Dodonaea viscosa* at CMF in Honghe County (Yunnan Province, China UTM/WGS84: 48 Q 216849–217075 E, 2592645–2592856 N, 600–750 m above sea level) during the dry season (April 2020). The local environment is characterized by poor eroded soils, steep valleys and a subtropical monsoon climate. Specimens were transported to the laboratory in Ziploc bags. Single spore isolation was conducted in accordance with methods described in Wanasinghe et al. [40]. Germinated spores were individually placed on potato dextrose agar (PDA) plates and grown at 20 °C in daylight. Dry herbarium materials were stored in the herbarium of Cryptogams Kunming Institute of Botany, Academia Sinica (KUN-HKAS). Living cultures were deposited at the Kunming Institute of Botany Culture Collection (KUMCC), Kunming, China and duplicated at China General Microbiological Culture Collection Centre (CGMCC). MycoBank numbers
were registered as outlined in MycoBank (http://www.MycoBank.org accessed on 11 November 2020).

2.2. Morphological Observations

The morphology of external and internal macro-/micro-structures were observed as described in Wanasinghe et al. [24]. Images were captured with a Canon EOS 600D digital camera fitted to a Nikon ECLIPSE Ni compound microscope. Measurements were made with the Tarosoft (R) Image Frame Work program, and images used for figures were processed with Adobe Photoshop CS5 Extended version 10.0 software (Adobe Systems, San José, CA, USA).

2.3. DNA Extraction, PCR Amplifications and Sequencing

The extraction of genomic DNA was performed in accordance with the methods of Wanasinghe et al. [24], using the Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, P.R. China) following the instructions of the manufacturer. The reference DNA for the polymerase chain reaction (PCR) was stored at 4 °C for regular use and duplicated at −20 °C for long-term storage. The primers and protocols used for the amplification are summarized in Table 1. The amplified PCR fragments were then sent to a private company for sequencing (BGI, Ltd. Shenzhen, P.R. China).

Table 1. Genes/loci used in the study with PCR primers, references and protocols.

| Locus | Primers | PCR: Thermal Cycles: (Annealing temp. in Bold) | References |
|-------|---------|-------------------------------------------------|------------|
| act   | ACT-512F ACT2Rd | (96 °C: 120 s, 52 °C: 60 s, 72 °C: 90 s) × 40 cycles | [41,42] |
|       | TUB2Fw TUB4Rd | (94 °C: 30 s, 56 °C: 45 s, 72 °C: 60 s) × 35 cycles | [43] |
| cal   | CAL-235F CAL2Rd | (96 °C: 120 s, 50 °C: 60 s, 72 °C: 90 s) × 40 cycles | [42,44] |
| ITS   | ITS5 ITS4 | (95 °C: 30 s, 55 °C:50 s, 72 °C: 90 s) × 40 cycles | [45] |
| LSU   | LR0R LR5 | (95 °C: 30 s, 55 °C:50 s, 72 °C: 90 s) × 35 cycles | [46,47] |
| rpb2  | fRPB2-5f fRPB2-7cR | (94 °C: 60 s, 58 °C: 60 s, 72 °C: 90 s) × 40 cycles | [48] |
|       | fRPB2-414R | (96 °C: 120 s, 49 °C: 60 s, 72 °C: 90 s) × 40 cycles | [49] |
| SSU   | NS1 NS4 | (95 °C: 30 s, 55 °C:50 s, 72 °C: 90 s) × 35 cycles | [45] |
| tef1  | EF1-983F EF1-2218R | (95 °C: 30 s, 55 °C:50 s, 72 °C: 90 s) × 35 cycles | [50,51] |
|       | EF1-728F EF-2 | (96 °C: 120 s, 52 °C: 60 s, 72 °C: 90 s) × 40 cycles | [41,52] |

*a* act: actin; *btub*: β-tubulin; *cal*: calmodulin; *ITS*: part of rDNA 18S (3’ end), the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, the second ITS region (ITS2), and part of the 28S rRNA (5’ end); *LSU*: large subunit (28S); *rpb2*: RNA polymerase II second largest subunit; *SSU*: small subunit rDNA (18S); *tef1*: translation elongation factor 1-alpha gene. *b* fRPB2-5f and fRPB2-414R were used only for Teratosphaeriaceae analysis. *c* All the PCR thermal cycles include initiation step of 95 °C: 5 min, and final elongation step of 72 °C: 10 min and final hold at 4 °C.

2.4. Molecular Phylogenetic Analyses

2.4.1. Sequence Alignment

Sequences featuring a high degree of similarity were determined from a BLAST search to identify the closest matches with taxa in Dothideomycetes and recently published data [49,53–56]. Initial alignments of the acquired sequence data were first completed using MAFFT v. 7 (http://mafft.cbrc.jp/alignment/server/index.html accessed on 18 January 2021) [57,58] and manually clarified in BioEdit v. 7.0.5.2 when indicated [59].
2.4.2. Phylogenetic Analyses

Single-locus data sets were scanned for topological incongruences between loci for members of the analyses. Conflict-free alignments were concatenated into a multi-locus alignment that underwent maximum-likelihood (ML) and Bayesian (BI) phylogenetic analyses. Evolutionary models for BI and ML were selected independently for every locus using MrModeltest v. 2.3 [60] under the Akaike Information Criterion (AIC) implemented in PAUP v. 4.0b10.

The CIPRES Science Gateway platform [61] was used to perform RAxML and Bayesian analyses. ML analyses were made with RAxML-HPC2 on XSEDE v. 8.2.10 [62] employing the GTR+GAMMA swap model with 1000 bootstrap repetitions.

MrBayes analyses were performed setting GTR+I+GAMMA for 2–5 million generations, sampling every 100 generations and ending the run automatically when standard deviation of split frequencies dropped below 0.01 with a burnin fraction of 0.25. ML bootstrap values equal or greater than 60% and Bayesian posterior probabilities (BYPs) greater than 0.95 were placed above each node of every tree.

Phylograms were visualized with FigTree v1.4.0 program [63] and reassembled in Microsoft PowerPoint (2007) and Adobe Illustrator® CS5 (Version 15.0.0, Adobe®, San Jose, CA, USA). Finalized alignments and trees were deposited in TreeBASE, submission ID: S27699 (http://purl.org/phylo/treebase/phylows/study/TB2: S27699).

3. Results

3.1. Global Checklist of Fungi on Dodonaea Viscosa

Information for the global checklist (Table 2) was retrieved from the Agriculture Research Service Database generated by the United States Department of Agriculture (USDA) [64], related books and research papers. This checklist includes fungal species associated with Dodonaea viscosa and the countries from which they were recorded.

| Phylum and Class | Order | Family | Species | Country | References |
|------------------|-------|--------|---------|---------|------------|
| Ascomycota       | Dothideomycetes | Botryosphaeriales | Lasiodiplodia iranensis | Australia | [65] |
|                  |       |         | Macrohomophora dodonaeae | India | [66] |
|                  |       |         | Macrophomina phaseolina | Arizona | [67] |
| Capnodiaceae     | Capnodiaceae | Mycosphaerellaceae | Cercospora dodonaeae | India | [68] |
|                  |       |         | Pseudocercospora dodonaeae | New Zealand | [73–78] |
|                  |       |         | Pseudocercospora mitteriana | China | [79] |
|                  |       |         | Macrophoma dodonaeae | India | [66] |
|                  |       |         | Macrophomina phaseolina | Arizona | [67] |
|                  |       |         | Cercospora dodonaeae | India | [68] |
|                  |       |         | Pseudocercospora dodonaeae | New Zealand | [73–78] |
|                  |       |         | Pseudocercospora mitteriana | China | [79] |
| Hysteriales      | Hysteriaceae | Teratosphaeriaceae | Hanionyces dodonaeae | China | This study |
| incertae sedis   |       | Pseudoperisporiaceae | Episphaerella dodonaeae | Dominican Republic | This study |
|                  |       |         | incertae sedis | Mycotyphryidium pakistanicum | Pakistan | [80] |
|                  |       |         | incertae sedis | Mycotyphryidium rosselianum | Pakistan | [80] |
|                  |       |         | Tryblidiaria pakistani | Pakistan | [80] |
|                  |       |         | Coniothyriaceae | Coniothyrium sp. | Venezuela | [84] |
|                  |       |         | Corynesporascales | Corynespora cassicola | India | [85] |
|                  |       |         | Didymosphaeriaceae | Didymosphaeria obtisia | Pakistan | [80] |
|                  |       |         | Leptosphaeriaceae | Leptosphaeria dodonaeae | Eritrea | [86] |
|                  |       |         | Lophiostomataceseae | Lophomurispora hongheensis | China | This study |
|                  |       |         | Parapyrenochaetaceae | Quixadomycy pseudolongipes | China | This study |
|                  |       |         | Pleosporascales | Pleospora dodonaeae | Cyprus | [87] |
|                  |       |         | Valsariaceae | Valsaria rubrica | Pakistan | [80] |
| Lecanoromycetes  |        |         | Stictidaeae | Stictis marathwadensis | India | [88,89] |
| Leotiomyces      | Helotiales | Ostropales | Pleospora | Cyprus | [87] |
|                  |       |         | Erysipheaeae | Erysipheaeae | Iraq | [90] |
|                  |       |         | Valarsiaceae | Valarsiaceae | Israel | [90] |
|                  |       |         | Leotiomyces | South Africa | [90] |
Table 2. Cont.

| Phylum and Class | Order | Family | Species | Country | References |
|------------------|-------|--------|---------|---------|------------|
| Sordariomycetes  | Diaporthales | Cytosporaceae | Cytospora sp. | Zimbabwe | [91] |
|                  | Glomerellales | Glomerellaceae | Colletotrichum gloeosporioides | Ethiopia | [92] |
|                  | Meliolales | Meliolaceae | Meliola lyoni | Germany | [93] |
|                  | Hypocreales | Nectriaceae | Calonectria cylinodera | New Zealand | [74,90] |
|                  |              |              | Fusarium solani | South Africa | [94] |
|                  |              | Plectosphaerellaceae | Verticillium dahliae | New Zealand | [74] |
| Coronophorales    | Scortechiniaeae | Pythiaceae | Globisporangium debaryanum | USA | [117] |
| Amphiphausiales   | Sporocadaceae | Schizoporiae | Phaeoacremonium italicum | Australia | [109] |
| Togniniales       | Togniniaceae | Polyporales | Hyphoderma | Hawaii | [73] |
| Basidiomycota     | Agaricales | Marasmiaceae | Campanella junghuhnii | Hawaii | [110] |
|                   | Hymenochaetales | Hymenochaetaceae | Rhizoctonia sp. | Italy | [112] |
|                   | Cantharellales | Ceratobasidiaceae | Arambaria cognata | Uruguay | [113] |
|                   |               | Hymenochaetaceae | Peltigera aurantiaca | Australia | [114] |
|                   |               | Schizoporiae | Phaeoacremonium alvei | Australia | [105-108] |
|                   |               | Hyphoderma | Phaeoacremonium italicum | Australia | [109] |
|                   | Polyporales | Hyphodermaeae | sphaerogedinulatum | Hawaii | [110] |
| Oomycota          | Pucciniales | incertae sedis | Uredio dodonae | Indonesia | [117] |
|                   | Peronosporaceae | Pythiaceae | Phytophthora drechsleri | Australia | [118-120] |
| Peronosporomycetes |               |               | Phytophthora nicotianae | Italy | [121-123] |
|                   |               |               | Phytophthora palmivora | Italy | [123] |
|                   |               |               | Globisporangium debaryanum | New Zealand | [73,74] |
|                   |               |               | Globisporangium irregular | New Zealand | [74] |
|                   |               |               | Globisporangium ultimum | New Zealand | [73] |
|                   |               |               | Pythium inflatum | New Zealand | [73,74] |
|                   |               |               | Pythium sp. | New Zealand | [73] |
|                   |               |               |          | USA | [75] |

3.2. Phylogenetic Analyses

Four phylogenetic analyses were performed using the acquired sequences from GenBank (Table 3). The first is a phylogenetic overview of the genera treated in Teratosphaeriaceae (Figure 1), while the remaining three alignments represent the species in Rhytidiolithteron (Figure 2), an overview of the phylogeny of the genera treated in Lophiostomataceae (Figure 3) and Parapyrenochaeta, and allied genera in Pleosporineae (Figure 4). Other details related to ML and BI analyses from different datasets are presented in Table 4. The acquired phylogenetic results are discussed where applicable in the notes below.
| Species                           | Strain        | SSU   | LSU   | act   | cal   | ITS   | rpb2  | tef1  | btub  | Reference       |
|----------------------------------|---------------|-------|-------|-------|-------|-------|-------|-------|-------|----------------|----------------|
| Acidiella bohemica               | CBS 132720    | -     |       |       |       |       |       |       |       | [49]            |
| Acidiella parva                  | CMW 10189     | -     |       |       |       |       |       |       |       | [49]            |
| Acrodictum crateriforme          | CPC 11509     | -     | GU214682 | GU320413 | KX289011 | GU214682 | KX288404 | GU384425 |       | [124, 125]    |
| Acrodontium pigmentosum          | CBS 111111    | -     | KX286963 | -     | -     | KX287257 | KX288412 | -     |       | [125]           |
| Afloldia vorosii                 | CBS 145501    | MK589346 | MK589354 | -     | -     | JN859336 | -     | MK599320 |       | [126]           |
| Alpestrisphaeria jonesii         | GZCC 16-0021  | KX685775 | KX687753 | -     | -     | KX687757 | -     | KX687759 |       | [128]           |
| Alpestrisphaeria terricola       | Vi0216        | HI160808 | -     | -     | -     | MK703662 | -     |       |       | [127]           |
| Alpestrisphaeria terricola       | SC-12H        | JX885749 | JX885750 | -     | -     | JN629300 | -     |       |       | [128]           |
| Almocolephoma cassiae            | MFLUCC 17-2283 | NG_065775 | NG_066307 | -     | -     | NR_163330 | MK438494 | MK36041 |       | [127]           |
| Angustimassarina actina           | MFLUCC 14-0505 | NG_063573 | KP888637 | -     | -     | NR_138406 | -     | KRO75168 |       | [129]           |
| Angustimassarina quercicola      | MFLUCC 14-0506 | NG_063574 | KP888638 | -     | -     | KP991333 | -     | KRO75169 |       | [129]           |
| Angustimassarina rosarium        | MFLUCC 17-2155 | MT226662 | MT214543 | -     | -     | MT310590 | MT394678 | MT39426 |       | [127]           |
| Aperidiella strumelloidea        | CBS 114484    | -     | KF937229 | -     | -     | -     | KF937266 | -     |       | [49]            |
| Aracuasphearia foliorum           | CPC 33084     | -     | MH327829 | -     | -     | MH327793 | -     |       |       | [131]           |
| Astragalica sasayae              | MFLUCC 17-0832 | MG829098 | MG828986 | -     | -     | NR_157504 | MG829248 | MG829193 |       | [130]           |
| Austrotricana associata          | CPC 13119     | -     | KF901824 | KF903526 | KF902528 | KF901507 | KF902177 | KF903087 |       | [49]            |
| Austrotricana sp.                | CPC 4313      | -     | KF937183 | KF903460 | KF902527 | KF904198 | KF902186 | KF903086 |       | [49]            |
| Austrostigmidium mastodiae        | MA 18215      | NG_057063 | -     | -     | -     | -     |       |       |       | [132]           |
| Austrostigmidium mastodiae        | MA 18213      | -     | KF937262 | -     | -     | -     | KF937252 | -     |       | [49]            |
| Batcheloromyces alistikari       | CPC 12730     | -     | KF937220 | -     | -     | -     | KF937252 | -     |       | [49]            |
| Batcheloromyces leucadendri      | CPC 1838      | -     | KF937221 | -     | -     | -     | KF937252 | -     |       | [49]            |
| Batcheloromyces sedgefeldii      | CPC 3026      | -     | KF937222 | -     | -     | -     | KF937254 | -     |       | [49]            |
| Biappendiculispora japonica      | KT 573        | AB618986 | AB619005 | -     | -     | LC010728 | -     | LC010744 |       | [129, 133]     |
| Biappendiculispora japonica      | KT 686-1      | AB618987 | AB619006 | -     | -     | LC010729 | -     | LC010745 |       | [129, 133]     |
| Camarosporidella caragunicola    | MFLUCC 17-0726 | MF434200 | MF434212 | -     | -     | MF434125 | -     | MF434388 |       | [134]           |
| Camarosporidella elongata        | AFTOL-ID 1568 | DQ678009 | DQ678061 | -     | -     | DQ677957 | DQ677904 | -     |       | [135]           |
| Camarosporidella effimarii       | MFLUCC 17-0207 | MF434321 | MF434233 | -     | -     | MF434145 | MF434488 | -     |       | [134]           |
| Camarosporula perisanensis       | CPC 3350      | JF770460 | -     | -     | -     | KF937255 | -     |       | [49, 136]     |
| Capulatispora sagittiformis       | KT 1934       | AB618693 | AB368267 | -     | -     | AB368268 | LC010756 | -     |       | [129, 133]     |
| Catenulostroma hermanusense      | CPC 18276     | KF902089 | -     | -     | -     | KF902197 | -     |       | [49]            |
| Catenulostroma protearum         | CPC 15370     | KF902090 | -     | -     | -     | KF902198 | -     |       | [49]            |
| Coelodictiosporum pseudopogonii  | MFLUCC 13-0451 | KRO25862 | -     | -     | KRO25858 | -     |       |       | [137]           |
| Coelodictiosporum rosarium       | MFLUCC 17-0776 | NG_063674 | NG_059056 | -     | -     | MG708875 | -     | MG708915 |       | [130]           |
| Conidiomyces palmarum            | CBS 400.71    | EU754054 | JX681084 | -     | -     | MH860184 | KT389592 | -     | KT389792 | [138]           |
| Constantimassarina macranesis    | TRN 440       | -     | KF310005 | -     | -     | NR_164011 | KF310081 | -     |       | [139]           |
| Constantimassarina minimus       | CBS 118766    | -     | KF310003 | -     | -     | NR_144957 | KF310077 | -     |       | [139]           |
| Species                  | Strain     | GenBank Accession Numbers                  | Reference |
|--------------------------|------------|--------------------------------------------|-----------|
| Crassicylpeus aquaticus  | KH 91      | LC312469 LC312527                          | [140]     |
| Crassicylpeus aquaticus  | KH 104     | LC312470 LC312528                          | [140]     |
| Crassicylpeus aquaticus  | KH 185     | LC312471 LC312529                          | [140]     |
| Crassicylpeus aquaticus  | KT 970     | LC312472 LC312530                          | [140]     |
| Desertiserpentica hydei  | SQUCC 15092| MW077163 MW077156                          | [54]      |
| Deversia appanasi        | CPC 19033  | JX069859                                  | -         |
| Deversa strobilae        | X1037      | GL301810                                  | EU436763  |
| Dimorphotis braschiotae  | CPC 22679  | KF777213                                  | -         |
| Elatalcosomyces elastici  | CCFFEE 5513| KJ508994                                  | -         |
| Euteratosphaeria verrucosiafricana | CPC 11167 | -                                         | DQ303056  |
| Flabellascoma aquaticum  | KUMCC 15-0258| MN304832 NG_068307                      | MN328895  |
| Flabellascoma cyanidiola | KT 2034    | LC312473 LC312531                         | LC312589  |
| Flabellascoma fusiforme  | MFLUCC 16-1584| NG_068308                            | MN328898  |
| Flabellascoma minimum    | KT 2013    | LC312474 LC312532                         | LC312589  |
| Flabellascoma minimum    | KT 2040    | LC312475 LC312533                         | LC312589  |
| Flabellascoma unisepitata| MFLUCC 15-0765| NG_061234 NG_059659                        | -         |
| Friedmaniomyces endolithicus | CCFFEE 5199| KF310007                                  | -         |
| Friedmaniomyces endolithicus | CCFFEE 5283| KF310006                                  | -         |
| Glionopsid calami        | MFLUCC 15-0739| NG_063621 NG_059715                      | MN328895  |
| Gloaniopsis calami       | MFLUCC 10-0927| MN577426 MN577415                      | MN328898  |
| Gloaniopsis panreus      | CBS 112415 | FJ161134 FJ161173                         | FJ161133  |
| Guttulispora craetagi    | MFLUCC 13-0442| KF899125 KP888639                    | KP899134  |
| Guttulispora craetagi    | MFLUCC 14-0993| KF899126 KP888640                    | KP899135  |
| Haniomyces dodonaeae     | KUMCC 20-0220| MW264221 MW264192 MW256802              | MW265928  |
| Haniomyces dodonaeae     | KUMCC 20-0221| MW264222 MW264192 MW256803              | MW265928  |
| Hortaea thailandica      | CPC 16651  | KP902125                                  | KP902026  |
| HYperniun angustatum     | MFLUCC 16-0623| MH535885 MH535893                      | MH535875  |
| Hypocondena indica       | NFCC 4146  | -                                         | MN68546   |
| Hypoleurostis queenslandica| BRIP 61322b| NG_059766                                  | KP899134  |
| Incertomyces porrigens   | CCFFEE 5393| KF310009                                  | KF310057  |
| Lapidomyces hispanicus   | TRN126     | KF310016                                  | -         |
| Lentistoma bipolare      | HKUCC 10069| LC312476 LC312534                         | LC312592  |
| Lentistoma bipolare      | HKUCC 10110| LC312477 LC312535                         | LC312592  |
| Lentistoma bipolare      | HKUCC 8277 | LC312478 LC312536                         | LC312594  |
| Lentistoma bipolare      | KT 2415    | LC312483 LC312541                         | LC312599  |
| Lentistoma bipolare      | KT 3056    | LC312484 LC312542                         | LC312600  |

This table continues with similar entries for other species and their associated GenBank Accession Numbers.
### Table 3. Cont.

| Species                  | Strain          | SSU GenBank Accession Numbers | LSU GenBank Accession Numbers | GenBank Accession Numbers | Reference       |
|--------------------------|-----------------|------------------------------|------------------------------|--------------------------|-----------------|
| Leptoparies palmarum     | KT 1653         | LC312485                     | LC312543                     | -                        | LC312514        |
| Leptosphaeria conoida    | CBS 616.75      | JF740099                     | JF740279                     | -                        | JF740201        |
| Leptosphaeria doliciom   | CBS 505.75      | NG_062778                    | NG_068574                    | -                        | NR_155309       |
| Lophiophilchrysum helichrysi | MFLUCC 15-0701 | KT333437                     | KT333436                     | -                        | KT333435        |
| Lophiophaea paramacrostoma | MFLUCC 11-0463 | KF899122                     | KP888636                     | -                        | KF887865        |
| Lophiomurispora hongheensis | KUMCC 20-0217  | MW264225                     | MW264195                     | -                        | MW264216        |
| Lophiomurispora hongheensis | KUMCC 20-0223  | MW264226                     | MW264196                     | -                        | MW264217        |
| Lophiomurispora hongheensis | KUMCC 20-0216  | MW264227                     | MW264197                     | -                        | MW264218        |
| Lophiomurispora hongheensis | KUMCC 20-0219  | MW264228                     | MW264198                     | -                        | MW264219        |
| Lophiomurispora hongheensis | KUMCC 20-0224  | MW264229                     | MW264199                     | -                        | MW264220        |
| Lophiophacus winterti    | KT 740          | AB613699                     | AB619017                     | -                        | AB619018        |
| Lophiophacus winterti    | KT 764          | AB618700                     | AB619018                     | -                        | AB619018        |
| Lophiostoma caulium      | CBS 623.86      | GU296163                     | GU301833                     | -                        | GU301833        |
| Lophiostoma macrostomum  | KT 635          | AB521731                     | AB433273                     | -                        | AB433273        |
| Lophiostoma multiseptatum | JCM 17668     | AB616864                     | AB619003                     | -                        | AB619003        |
| Lophiostoma multiseptatum | MAFF 239451    | AB616855                     | AB619004                     | -                        | AB619004        |
| Lophiostoma roae         | TASM 6115       | NG_065145                    | NG_069558                    | -                        | NG_069558       |
| Lophiostoma semilibersum | KT 828          | AB616966                     | AB619014                     | -                        | AB619014        |
| Massearina cistii        | CBS 266.62      | AB797249                     | AB807539                     | -                        | AB807539        |
| Massearia eburnea        | CBS 473.64      | GU296170                     | GU301840                     | -                        | GU301840        |
| Meristemomyces frigidum  | CCFEE 5457     | GU250389                     | GU371791                     | -                        | GU371791        |
| Meristemomyces frigidum  | CCFEE 5507     | GU250389                     | GU371791                     | -                        | GU371791        |
| Meristemomyces frigidum  | CCFEE 5492     | -                            | -                            | -                        | -               |
| Myrgetopodella corymbia  | CCFEE 14640    | -                            | -                            | -                        | -               |
| Neocatenulostroma albus  | CBS 110038     | -                            | -                            | -                        | -               |
| Neocatenulostroma microporum | CPC 1960     | -                            | -                            | -                        | -               |
| Neocatulostroma frigidus  | CCFEE 10202    | -                            | -                            | -                        | -               |
| Neophaeothecoidea proteae | CPC 2831      | -                            | -                            | -                        | -               |
| Neopyrenochaeta acicola  | CBS 812.95     | GQ387603                     | GQ387603                     | -                        | GQ387603        |
| Neopyrenochaeta asiatica | CBS 80134      | GQ387542                     | GQ387542                     | -                        | GQ387542        |
| Neopyrenochaeta fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |
| Neopyrenochaeta fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |
| Neopyrenochaeta fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |
| Neopyrenochaeta macrospora | CPC 14640    | -                            | -                            | -                        | -               |
| Neopyrenochaeta phragmidica | CPC 11922    | -                            | -                            | -                        | -               |
| Neowalbertia radicata    | CPC 1836       | -                            | -                            | -                        | -               |
| Neowalbertiidena phragmidica | CPC 1460     | -                            | -                            | -                        | -               |
| Neophytophthora acicola  | CBS 812.95     | GQ387603                     | GQ387603                     | -                        | GQ387603        |
| Neophytophthora asiatica | CBS 80134      | GQ387542                     | GQ387542                     | -                        | GQ387542        |
| Neophytophthora fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |
| Neophytophthora fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |
| Neophytophthora fragariae | CBS 142394    | MF795840                     | MF795875                     | -                        | MF795875        |

**Reference**
- [140]
- [153]
- [154]
- [139]
- [130]
- [157]
- [151]
- [143]
- [130]
- [153]
- [154]
- [155]
- [139]
- [162]
- [163]
- [164]
- [165]
Table 3. Cont.

| Species                        | Strain          | GenBank Accession Numbers | Reference |
|--------------------------------|-----------------|---------------------------|-----------|
| Neopyrenochaeta maesuayensis   | MFLUCC 14-0043  | -                         | -         |
| Neopyrenochaeta telephoni      | CBS 139022      | -                         | -         |
| Neotrematosphaeria biappendiculata | KT 1124       | GU205256 GU205227         | -         |
| Neotrematosphaeria biappendiculata | KT 975        | GU205254 GU205228         | -         |
| Neotrematosphaeria excentricum | CPC 13092       | KF901840 KF903534 KF902562 KF901518 KF902236 KF903123 | -         |
| Neocoxypilispora clematidis    | MFLUCC 17-2149  | MT226676 MT214559         | -         |
| Neocoxypilispora fukelii       | CBS 101952      | FJ95496 DQ99531           | -         |
| Neocoxypilispora fukelii       | KH 161          | AB618689 AB619008         | -         |
| Neocoxypilispora fukelii       | KT 634          | AB618690 AB619009         | -         |
| Oleoguttula mirabilis          | CCFEE 5522      | KF310019                  | -         |
| Parapaucispora pseudaromatica  | KT 2237         | LC100018                 | -         |
| Parapaucispora tasmaniensis    | CPC 12400       | KF901844 KF903562 KF902589 KF901522 KF902265 KF903152 | -         |
| Parapaucispora tasmaniensis    | CPC 1555        | KF901843 KF903541 KF902587 KF901521 KF902263 KF903150 | -         |
| Parapaucispora tasmaniensis    | CPC 25527       | KX228316                  | -         |
| Parapaucispora tereuterum      | CBS 131315      | JQ044453                  | -         |
| Pancospora kammingense         | MFLUCC 17-0932  | MF173430 NG_059829        | -         |
| Pancospora quadriquorpus       | KH 448          | LCO01720 LCO01722         | -         |
| Pancospora quadriquorpus       | KT 843          | AB618692 AB619011         | -         |
| Pancospora versicolor          | KH 110          | LCO01721 AB918732         | -         |
| Pediella colombiana            | CBS 486.80      | KF901865 KF903587 KF902594 KF901630 KF902272 KF903158 | -         |
| Penicillium aggregatum         | CBS 128277      | NG_057905 #                | -         |
| Penicillium crispum            | CPC 19778       | KF901843 KF903541 KF902587 KF901521 KF902263 KF903150 | -         |
| Penicillium radiculare         | CBS 131976      | KU216314 KU216292         | -         |
| Penicillium ramosum            | CBMA1 1937      | KU216317 KU216295         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MT240624 MT240623         | -         |
| Phaeoseptum fluidi             | MFLUCC 17-0801  | MT240624 MT240623         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MT240624 MT240623         | -         |
| Phaeoseptum manglicola         | NFCCI-4666      | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Phaeosporangiculinae           | MFLUCC 17-0801  | MK307817 MK307814         | -         |
| Species                     | Strain            | SSU      | LSU      | act | cal | ITS   | rpb2 | tef1 | btau | Reference          |
|----------------------------|-------------------|----------|----------|-----|-----|-------|------|------|------|--------------------|
| Platystomum rosei         | MFLUCC 15-0633    | KT026115 | KT026111 |    |    | KT026119 |    |      |      | [129]              |
| Platystomum salicicola    | MFLUCC 15-0632    | KT026114 | KT026110 |    |    | KT026118 |    |      |      | [129]              |
| Pseudolophiostoma cornisporum | KH 322        | LC312486 | LC312544 |    |    | LC312515 | LC312602 | LC312573 | - | [140]              |
| Pseudolophiostoma obtusisporum | KT 2838      | LC312489 | LC312547 |    |    | LC312518 | LC312605 | LC312576 | - | [140]              |
| Pseudolophiostoma obtusisporum | KT 3119      | LC312491 | LC312549 |    |    | LC312520 | LC312607 | LC312578 | - | [140]              |
| Pseudolophiostoma tropicum | KH 352        | LC312492 | LC312550 |    |    | LC312521 | LC312608 | LC312579 | - | [140]              |
| Pseudolophiostoma tropicum | KT 3134       | LC312493 | LC312551 |    |    | LC312522 | LC312609 | LC312580 | - | [140]              |
| Pseudolophiostoma tropicum | KH 227        | LC312494 | LC312552 |    |    | LC312523 | LC312610 | LC312581 | - | [140]              |
| Pseudolophiostoma tropicum | BCC 22835     | GQ925831 | GQ925844 |    |    | -      | -      | GL479830 | GU479857 | [174]              |
| Pseudolophiostoma tropicum | BCC 22836     | GQ925832 | GQ925845 |    |    | -      | -      | GL479829 | GU479856 | [174]              |
| Pseudopyrenochaeta lycopersici | CBS 306.65  | MB870217 | MB870216 |    |    | NR_103581 | LT717680 | - | LT717674 | [154]              |
| Pseudopyrenochaeta terrestris | CBS 282.72   | LT623216 | LT623216 |    |    | LT623228 | LT623227 | LT623246 | - | [16]               |
| Pseudoteratosphaeria flexuosa | CPC 673     | KP002698 | KP003403 | KP002653 |    | KP001745 | KP002345 | KP003282 | - | [18]               |
| Pseudoteratosphaeria flexuosa | CPC 1109    | KP002110 | KP003421 | KP002654 |    | KP001755 | KP002345 | - | - | [18]               |
| Pyrenochaeta nobilis       | CBS 407.76    | DQ898287 | EU754206 |    |    | -      | -      | DQ677991 | DQ677936 | MI75916 | [176]              |
| Pyrenochaeta pinicola      | CBS 137997    | KJ669152 | LT717684 |    |    | -      | -      | KJ669249 | - | - | [177]              |
| Pyrenochaeta sp.           | DTO 305-C6    | KX171361 | KX147606 |    |    | -      | -      | - | - | [176]              |
| Pyrenochaetopsis betulinipora | CBS 142458  | LN907440 | LT939245 | LT939084 | LT939035 | LT939024 | LT939033 | LT939266 | [53]               |
| Pyrenochaetopsis globosa   | CBS 143034    | LN907418 | LT939243 | LT939072 | LT939035 | LT939024 | LT939033 | LT939266 | [53]               |
| Pyrenochaetopsis paucisetosa | CBS 142460  | LN907336 | LT939246 | LT939072 | LT939035 | LT939024 | LT939033 | LT939266 | [53]               |
| Quixadomyces terrestrisiae | CPC 13333     | KP001860 | KP003538 | KP002663 | KP001538 | KP003536 | KP003282 | - | [14]               |
| Quixadomyces terrestrisiae | CPC 282.72    | LT623216 | LT623216 | LT623228 | LT623227 | LT623246 | LT623246 | LT623246 | [16]               |
| Recurvomyces mirabilis     | CCCF 896823    | MN017930 | MN017930 | MN017930 | MN017930 | MN017930 | MN017930 | MN017930 | [19]               |
Table 3. Cont.

| Species                  | Strain      | GenBank Accession Numbers                  | Reference |
|--------------------------|-------------|---------------------------------------------|-----------|
| Rhytidhysteron camporesii | HKAS 104277 | MN429072 - MN429071 - MN429069 - MN442087 | [148]     |
| Rhytidhysteron chromolaenae | MFLUCC 17-1516 | NG_070139 - NG_086675 - MN632461 - MN635663 | [55]     |
| Rhytidhysteron erioi      | MFLU 16-0584 | MN429071 - MN429068 - MN442086 - MN442087 | [148]     |
| Rhytidhysteron hongheense | KUMCC 20-0222 | MW264224 - MW264194 - MW264215 - MW256807 | This study |
| Rhytidhysteron hongheense | HAKAS1122348 | MW541831 - MW541820 - MW541824 - MW556132 | This study |
| Rhytidhysteron hongheense | HAKAS1122349 | MW541832 - MW541821 - MW541825 - MW556133 | This study |
| Rhytidhysteron hysterinum | EB 0351 | GL397350 - GL397350 - GL397340 | [149]     |
| Rhytidhysteron hystrix | MFLUCC 18-0719 | MN989382 - MN989384 - MN997309 | [177]     |
| Rhytidhysteron mangarei | MFLUCC 18-1113 | NG_082668 - NR_165548 - MK350300 | [178]     |
| Rhytidhysteron neorufulum | MFLUCC 13-0216 | KU377571 - KU377566 - KU377561 - KU377560 | [179]     |
| Rhytidhysteron neorufulum | GKM 361A | GU296192 - GQ221893 - GQ221893 - GQ221893 | [179]     |
| Rhytidhysteron neorufulum | MFLUCC 12-0528 | KJ418119 - KJ418117 - KJ418117 - KJ418117 | [181]     |
| Rhytidhysteron neorufulum | CBS 306-38 | AI164375 - FJ469672 - FJ469672 - FJ469672 | [181]     |
| Rhytidhysteron neorufulum | MFLUCC 12-0011 | KJ418110 - KJ418109 - KJ418109 - KJ418109 | [181]     |
| Rhytidhysteron neorufulum | MFLUCC 12-0567 | KJ546129 - KJ546126 - KJ546126 - KJ546126 | [181]     |
| Rhytidhysteron neorufulum | MFLUCC 14-0577 | KU377570 - KU377565 - KU377560 | [179]     |
| Rhytidhysteron neorufulum | EB 0384 | GU397368 - GU397368 - GU397368 | [182]     |
| Rhytidhysteron neorufulum | EB 0382 | GU397367 - GU397367 - GU397367 | [182]     |
| Rhytidhysteron neorufulum | EB 0383 | GU397353 - GU397353 - GU397353 | [182]     |
| Rhytidhysteron neutrofulum | MFLUCC 12-0013 | KJ418113 - KJ418113 - KJ418113 | [181]     |
| Rhytidhysteron neutrofulum | MFLUCC 13-0710 | KL746698 - KL746698 - KL746698 | [183]     |
| Rhytidhysteron neutrofulum | MFLUCC 13-0051 | MN594343 - MN594343 - MN594343 | [56]     |
| Rhytidhysteron thailandicum | MFLUCC 12-0530 | KJ546128 - KJ546126 - KJ546126 | [172]     |
| Rhytidhysteron thailandicum | MFLUCC 14-0503 | KJ546128 - KJ546126 - KJ546126 | [172]     |
| Sigarispora arundinis       | KT 651 | AB618680 - AB618680 - AB618680 | [129,133] |
| Sigarispora caudata         | MAFF 239453 | AB618681 - AB619000 - AB619000 | [129,133] |
| Sigarispora caudata         | MAFF 239450 | AB618682 - AB619001 - AB619001 | [129,133] |
| Sigarispora caudata         | ICM 17649 | AB618683 - AB618683 - AB618683 | [129,133] |
| Sigarispora ononidis        | MFLUCC 15-2667 | KU243126 - KU243125 - KU243125 | [169]     |
| Sigarispora rosicola        | MFLU 15-1888 | M028160 - M028160 - M028160 | [130]     |
| Simplicidiella nigra        | CMB 1939 | KL216313 - KL216313 - KL216313 | [171]     |
| Sparticola junce           | MFLUCC 15-0030 | KJ721765 - KJ721765 - KJ721765 | [46]     |
| Stiltsmania ulmi           | CPC 13055 | KF01874 - KF01874 - KF01874 | [49]     |
Table 3. Cont.

| Species                     | Strain      | GenBank Accession Numbers         | Reference |
|-----------------------------|-------------|-----------------------------------|-----------|
|                             |             | SSU | LSU | act | cal | ITS | rpb2 | tef1 | btub |           |
| Staurosphaeria lycii        | MFLUCC 17-0210 | MF434372 | MF434284 | -   | -   | MF434196 | -   | MF434458 | -   | [134]        |
| Staurosphaeria lycii        | MFLUCC 17-0211 | MF434373 | MF434285 | -   | -   | MF434197 | -   | MF434459 | -   | [134]        |
| Stereilia araguta           | FMC 245     | KF902168 | -   | -   | -   | -   | -   | -   | -   | [49]         |
| Suberoteratosphaeria        | CPC 12085   | KF902144 | KP903508 | -   | KF901786 | -   | KP903275 | -   |     |
| pseudosuberosa              |             |       |       |     |     |     |     |     |     |              |
| Suberoteratosphaeria        | CPC 13093   | KF901879 | KP903584 | -   | KF901557 | -   | KP903280 | -   |     |
| xenosuberosa                | CPC 13093   | KF901879 | KP903584 | -   | KF901557 | -   | KP903280 | -   |     |
| Telichorospora mariae       | CI36        | KU601581 | -   | -   | -   | -   | KU601581 | KU601595 | KU601611 | [184]       |
| Telichorospora rubriostiolata| TR 7        | KU601590 | -   | -   | -   | -   | KU601590 | KU601599 | KU601609 | [184]       |
| Telichorospora thailandica  | MFLUCC 17-2093 | MT226708 | MT214597 | -   | -   | KF902393 | -   | -   | -   | [167]       |
| Teratosphaeria aurantia     | MFLUCC 17-0210 | MF434372 | MF434284 | -   | -   | MF434196 | -   | MF434458 | -   | [134]        |
| Teratosphaeria blakeyi      | CPC 12837   | KF901888 | KP903518 | -   | KF902704 | KF901561 | KF902413 | KF903288 | -   | [49]         |
| Teratosphaeria destructans  | CPC 1324    | KF901901 | KP903529 | -   | KF902720 | KF901574 | KF902427 | KF903301 | -   | [49]         |
| Teratosphaeria fimbriata    | CPC 1324    | KF901901 | KP903529 | -   | KF902720 | KF901574 | KF902427 | KF903301 | -   | [49]         |
| Teratosphaeria gauchensis   | CMW 17331   | KF902148 | KP903521 | -   | KF902729 | KF901579 | KF902439 | KF903315 | -   | [49]         |
| Teratosphaeria mareebensis  | CPC 1272    | KF901906 | KP903581 | -   | KF902734 | KF901582 | KF902444 | KF903320 | -   | [49]         |
| Teratosphaeria pseudocryptica| CPC 11267   | KF902032 | KP903598 | -   | KF902760 | KF901687 | KF902472 | KF903348 | -   | [49]         |
| Teratosphaeriaceae sp.      | CPC 13680   | KF901921 | KP903657 | -   | KF902765 | KF901597 | KF902477 | KF903353 | -   | [49]         |
| Teratosphaeriaceae sp.      | CCFEE 5569  | KF310015 | -   | -   | -   | -   | KF310071 | -   | -   | [139]       |
| Teratosphaeriola pseudofricans| CPC 1231   | KF902045 | KP903435 | -   | KF902782 | KF901699 | KF902499 | KF903370 | -   | [49]         |
| Teratosphaeriola pseudofricans| CPC 1230   | KF902084 | KP903473 | -   | KF902783 | KF901737 | KF902500 | KF903071 | -   | [49]         |
| Teratosphaeriopsis pseudofricans| CPC 1261   | KF902085 | KP903436 | -   | KF902784 | KF901738 | KF902501 | KF903732 | -   | [49]         |
| Vaginatispora amgdali       | KT 2248     | LC312495 | LC312553 | -   | LC312524 | LC312611 | LC312582 | -   | -   | [140]       |
| Vaginatispora appendiculata | MFLUCC 16-0314 | KU743219 | KU743218 | -   | KU743217 | KU743220 | -   | -   | -   | [140]       |
| Vaginatispora armatospora   | MFLUCC 16-0314 | KU743219 | KU743218 | -   | KU743217 | KU743220 | -   | -   | -   | [140]       |
| Vaginatispora neoapinae     | MFLUCC 16-0314 | KU743219 | KU743218 | -   | KU743217 | KU743220 | -   | -   | -   | [140]       |
| Vaginatispora pseudocatenata| CPC 18472   | KF902508 | -   | -   | -   | -   | -   | -   | -   | [49]         |
| Xenopenidiella inflata      | CBS 379.55  | GU296208 | GU301880 | -   | -   | AY943045 | -   | GU349021 | -   | [142]       |
| Xenopenidiella tarda        | CBCAI 1940  | KL216312 | KL216303 | -   | KL216303 | KT831171 | -   | KU2116359 | -   | [171]       |
| Xenopenidiella tarda        | CBCAI 1940  | KL216312 | KL216303 | -   | KL216303 | KT831171 | -   | KU2116359 | -   | [171]       |

GenBank accession numbers with * are resulting from EF1-728F and EF-2 primers and – means missing data or not used in the phylogenetic analyses. The newly generated sequences are indicated in bold.
Figure 1. RAxML tree based on a combined dataset of partial LSU, ITS, rpb2, act, cal and tef1 DNA sequence analysis in Teratosphaeriaceae. The tree is rooted to Staninwardia suttonii (CPC 13055). Bootstrap support values for ML equal to or greater than 60%, Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are presented as ML/BI above nodes. Known genera are indicated with coloured blocks. Blue represents new isolates. The ex-type strains are indicated in **bold**. The scale bar presents the expected number of nucleotide substitutions per site.
Table 4. Maximum-likelihood (ML) and Bayesian (BI) analyses results for each sequenced dataset.

| Analyses                  | Teratosphaeriaceae | Rhytidhysteron | Lophiostomataceae | Parapyrenochaeta |
|---------------------------|-------------------|----------------|-------------------|-----------------|
| Number of Taxa            | 106               | 34             | 106               | 37              |
| Gene regions              | LSU, ITS, rpβ2, act, cal and tef1 | LSU, ITS and tef1 | LSU, ITS, tef1 and rpβ2 | LSU, ITS, rpβ2, tef1 and btub |
| Number of character positions | 3517              | 3667           | 4649              | 5510            |
| ML optimization likelihood value | −50604.86449     | −10386.988691 | −42280.12689     | −27947.901235  |
| Distinct alignment patterns in the matrix | 1973              | 739            | 2082              | 1710            |
| Number of undetermined characters or gaps (%) | 48.76%            | 30.69%         | 27.07%            | 38.18%          |
| Estimated base frequencies |                   |                |                   |                 |
| A                         | 0.23693           | 0.241388       | 0.24893           | 0.245506        |
| C                         | 0.26813           | 0.244526       | 0.24732           | 0.244909        |
| G                         | 0.283733          | 0.277859       | 0.267917          | 0.265204        |
| T                         | 0.211207          | 0.256427       | 0.235833          | 0.244381        |
| AC                        | 1.498833          | 1.533268       | 1.549406          | 1.619926        |
| AG                        | 2.784366          | 2.507774       | 4.37387           | 4.391077        |
| AT                        | 1.662835          | 1.340621       | 1.462392          | 1.995039        |
| Substitution rates        |                   |                |                   |                 |
| CG                        | 1.129905          | 1.029121       | 1.453674          | 1.225921        |
| CT                        | 6.210175          | 6.529612       | 8.808274          | 8.980921        |
| GT                        | 1.0               | 1.0            | 1.0               | 1.0             |
| Proportion of invariant sites (I) | 0.416989         | 0.610823       | 0.453545          | 0.55191         |
| Gamma distribution shape parameter (α) | 0.626612        | 0.475911       | 0.51454           | 0.443538        |
| Number of trees sampled in BI after 25% were discarded as burn-in | 29861            | 3451           | 9001              | 951             |
| Number of generated trees in BI | 22396            | 2589           | 6751              | 714             |
| Final split frequency     | 0.009999         | 0.009261       | 0.009977          | 0.007923        |
| The total of unique site patterns | 1974             | 740            | 2084              | 1711            |

Figure 2. RAxML tree based on a combined dataset of partial SSU, LSU, ITS and tef1 DNA sequence analysis in Rhytidhyster. The tree is rooted to Gloniopsis calami (MFLUCC 15-0739, MFLUCC 10-0927). Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are shown as ML/BI above the nodes. Known species are indicated with coloured blocks. Blue represents new isolates. The ex-type strains are indicated in bold. The scale bar represents the expected number of nucleotide substitutions per site.
Figure 3. RAxML tree based on a combined dataset of partial SSU, LSU, ITS, tef1 and rpb2 DNA sequence analysis in Lophiostomataceae. The tree is rooted to Gloniopsis praelonga (CBS 112415) and Hysterium angustatum (MFLUCC 16-0623). Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are shown as ML/BI above the nodes. Known families and selected genera are indicated with coloured blocks. Blue represents new isolates. The ex-type strains are indicated in bold. The scale bar represents the expected number of nucleotide substitutions per site.
3.3. Taxonomy of Fungi Colonising Dodonaea Viscosa Twigs

In the current study, two new genera and four novel species were found. These taxa are subsequently described below.

Class Dothideomycetes O.E. Erikss. and Winka, Myconet 1: 5 (1997)
Capnodiales Woron., Annales Mycologici 23: 177 (1925)
Teratosphaeriaceae Crous and U. Braun, Studies in Mycology 58: 8 (2007)

Haniomyces J.C. Xu gen. nov.
MycoBank: MB837991

Etymology: The generic epithet refers to the “Hani” ethnic group in Honghe County, Yunnan Province, China.

It is saprobic on dead twigs and branches in terrestrial habitats. Sexual morph: the ascomata is a scattered, immersed to semi-immersed, subglobose to conical or shaped irregularly, glabrous, brown to dark brown ostiolute. The ostiole is a short papillate, black, smooth periphysate. The peridium comprises cells of textura angularis. The hamathecium
comprises numerous, filamentous, branched, septate, pseudoparaphyses. The *asci* are eight-spored, bitunicate, fissitunicate, clavate, with a pedicel, apically rounded with or without an ocular chamber. The *ascospores* overlap the biseriate, are ellipsoidal to sub-fusiform, hyaline, one-septate, with small to large guttules in each cell, with the ends remaining rounded, surrounded by a distinct mucilaginous sheath. Asexual morph: Coelomycetous. The *conidiomata* are sporodochial on PDA, globose, solitary or aggregated, semi-immersed, black, exuding yellow conidial masses. *Conidiophores* and conidiogenous cells were not observed in vitro. The *conidia* are solitary, aseptate, globose to ellipsoid, with the hyaline becoming medium to golden brown, and finely verruculose.

**Type species:** Haniomyces dodonaeae

*Haniomyces dodonaeae* Wanas. and Mortimer sp. nov. (Figure 5)

Figure 5. The sexual (HKAS110128, holotype) and asexual (KUMCC 20-0220, ex-type) morphs of *Haniomyces dodonaeae*. (a,b) ascomata on the dead woody twigs of *Dodonaea viscosa*; (c,d) vertical section of ascoma; (e) periphyses; (f) peridium; (g) pseudoparaphyses; (h–j) asci; (k–p) ascospores (p in Indian Ink); (q,r) colony on potato dextrose agar (PDA) (r from the bottom); (s) squashed pycnidia which were produced on PDA; (t) pycnidia wall; (u–w) conidia. Scale bars, (c,d) 100 µm; (e,h–j,l,u) 20 µm; (f,k–p,v,w) 10 µm; (s) 200 µm.

MycoBank: MB837997

**Etymology:** The specific epithet reflects the host genus *Dodonaea*.

**Holotype:** HKAS110128

It is saprobic on dead twigs of *Dodonaea viscosa* Jacq. (Sapindaceae). Sexual morph: the *ascomata* is a 150–200 µm high, 350–450 µm diam. (M = 165.4 × 390.3 µm, n = 5), scattered,
semi-immersed to erumpent, subglobose to conical or shaped irregularly, flattened base, glabrous, brown to dark brown ostiolar, fused with host tissues. The ostiole is a short papillate, black and smooth, with hyaline periphyses (15–25 µm long, 1.5–2 µm wide). The peridium 5–10 µm wide at the base, 10–20 µm wide at sides, comprising 2–4 layers, outer layer pigmented, comprising reddish brown to dark brown, with thin-walled cells of textura angularis, and an inner layer composed of hyaline, loose, cells of textura angularis. The hamatheicum comprises numerous, 2–3 µm wide, filamentous, branched, septate, pseudoparaphyses. The asci are 110–130 × 25–35 µm (M = 118.5 × 31.2 µm, n = 20), eight-spored, bitunicate, fissitunicate, clavate, with a short pedicel (10–15 µm long), apically rounded with an ocular chamber. The ascospores 25–35 × 12–15 µm (M = 32.2 × 14.3 µm, n = 30), overlap the biseriate, are ellipsoidal to sub-fusiform, hyaline, one-septate, with the septum almost median, densely constricted at the middle septum, with the upper cell wider than the lower cell, and are smooth-walled with small to large guttules in each cell, rounded at both ends and covered by a distinct mucilaginous sheath (30–50 µm, diam.). Asexual morph: Coelomycetous. The conidiumata are up to 250 µm diam., sporodochial on PDA, globose, solitary or aggregated, semi-immersed, black, exuding yellow conidial masses. Conidiophores and conidiogenous cells were not observed in vitro. The conidia are 5.5–7.5 × 4.5–5.5 µm (M = 6.4 × 5.4 µm, n = 30), solitary, aseptate, globose or ellipsoid, with the hyphae becoming medium to golden brown, and finely verruculose.

Culture characteristics: the colonies on PDA reached a 3 cm diameter after 2 weeks at 20 °C. They were circular has a serrate margin, whitish at the beginning, becoming brown at the centre and brownish green towards the margin after 4 weeks. They were slightly raised, and reverse blackish brown. The hyphae septate were branched, hyaline, thin, and smooth-walled.

Known distribution: Yunnan, China, on Dodonaea viscosa.

Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Honghe County, 23.421068 N, 102.229128 E, 735 m, on dead twigs of Dodonaea viscosa, 22 April 2020, D.N. Wanasinghe, Honghe 005 (HKAS110128, holotype), ex-type living culture, KUMCC 20-0220, ibid. 23.419206 N, 102.231375 E, 618 m, Honghe 010 (HKAS110125, paratype), ex-paratype living culture, KUMCC 20-0221.

Hysteriales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 265 (1897)

Hysteriaceae Chevall., Flore Générale des Environ de Paris 1: 432 (1826)

Rhytidhysterion Spec., Annales de la Sociedad Científica Argentina 12 (4): 188 (1881)

Rhytidhysterion hongheense Wanjas. sp. nov. (Figure 6)

Mycobank: MB837992

Etymology: The specific epithet is derived from Honghe County, Yunnan Province, China.

Holotype: HKAS110133

It is aerobic on dead twigs of Dodonaeai Mill. (Sapindaceae). Sexual morph: The hysterothecia is 1200–2000 µm long × 350–500 high × 600–1000 µm diam. (M = 1590 × 410 × 840 µm, n = 10), arising singly or in small groups, sessile, and slightly erumpent from the substrate. The receptacle is cupulate, black, flat or slightly concave, with a slightly dentate margin. The excipulum are 70–100 µm wide, with the ectal excipulum narrow layered, deep, and thick-walled, with black cells of textura globulosa to textura angularis; the medullary excipulum is composed of narrow, long, thin-walled, hyaline to brown cells of textura angularis. The hamatheicum are 2.5–4 µm wide, numerous, propoloid, pseudoparaphyses, exceeding asci in length, apically swollen, branched and reddish-orange pigmented. The branched apices form a layer on hymenium to develop pseudo-epitheciun. The asci are 140–180 × 12–16 µm (M = 163.3 × 13.8 µm, n = 20), eight-spored, long cylindrical, short pedicellate, and is rounded at apex. The ascospores 20–33 × 9–13 µm (M = 28.2 × 11.2 µm, n = 30), overlap the uniseriate, are hyaline to light brown, one-septate, with wrinkled walls when young, becoming dark brown at maturity. They are ellipsoid with conical ends, regularly three-septate, and rarely muriform with one longitudinal septum, smooth walled, guttulate. Asexual morph: Undetermined.
Figure 6. Rhytidhysteron hongheensis (HKAS110133, holotype). (a,b) Appearance of hysterothecia on the dead woody twigs of Dodonaea viscosa; (c,d) horizontal section of hysteriothecium; (e) vertical section of hysteriothecium; (f) cells of peridium; (g,h) pseudoparaphyses; (i,j) asci; (k–p) ascospores; (q,r) colony on PDA (r from the bottom). Scale bars, (d,e) 200 µm; (f,i,j) 50 µm; (g,h,k–p) 10 µm.

Culture characteristics: Colonies on PDA reached a 4 cm diameter after 2 weeks at 20 °C. The colony was dense, circular, slightly raised, and the surface was smooth, with an undulated edge, with floccose which were greenish grey at the centre and brown towards margin from the top and reverse dark brown. The hyphae septate were branched, hyaline, thin, and smooth-walled.

Known distribution: Yunnan, China, on Dodonaea.

Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Honghe County, 23.421068 N, 102.229128 E, 735 m, on dead twigs of Dodonaea, 22 April 2020, D.N. Wanasinghe, Honghe 006 (HKAS110133, holotype), ex-type culture, KUMCC 20-0222. ibid. on dead twigs of Dodonaea viscosa, 08 December 2020, DWH6-1 (HKAS112348). ibid. 07 December 2020, DWH7-2 (HKAS112349).

Pleosporales Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)
Lophiostomataceae Sacc., Sylloge Fungorum 2: 672 (1883)
Lophiomurispora Wanas. and Mortimer, gen. nov.
MycoBank: MB837993
Etymology: The generic epithet stems from the combined two words “lophio” and “murispora”, referring to muriform ascospores in Lophiostomataceae.

It is saprobic on woody substrates in terrestrial habitats. Sexual morph: The ascomata is a solitary or gregarious, semi-immersed, erumpent through the host surface, coriaceous to carbonaceous, dark brown to black, globose to subglobose or conical ostiolate. The ostiole is a slit-like, central papillate, with or without a crest, opening by an apical, lysiogenous pore or dehiscence, comprising hyaline periphyses or hyaline to lightly pigmented, pseudoparenchymatous cells. The peridium is broad at the apex and thinner at the base,
comprising two strata with several layers of brown or lightly pigmented to hyaline cells of *textura angularis* to *textura prismatica*, fusing and indistinguishable from the host tissues. The hamathecium comprises many branched, septate, cellular pseudoparaphyses, located between and above the asci, embedded in a gelatinous matrix. The asci are eight-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, and apically rounded, with an ocular chamber. The ascospores are uni- to bi-seriate, partially overlapping, and are hyaline when immature, becoming brown to dark brown when mature. They are ellipsoidal to fusiform, muriform, two-to-eight-transversely septate, with one-to-two-longitudinal septa, constricted at the central septum, with or without a mucilaginous sheath. Asexual morph: Coelomycetous. The conidiomata is pycnidial, phoma-like, solitary, gregarious, dark brown to black, immersed or slightly erumpent, coriaceous to carbonaceous, papillate or apapillate. The conidiomata wall is multi-layered, with three to four outer layers of brown-walled pseudoparenchymatous cells, with the innermost layer being thin and hyaline. The conidiphores are long, septate, and sparsely branched, which are formed from the innermost layer of the pycnidium wall. The conidiogenous cells are phialidic, cylindrical, hyaline, flexuous and smooth, with a short collarette. The conidia are hyaline, aseptate, straight to curved, ellipsoidal with rounded ends, thin-walled, smooth, and numerous.

Type species: *Lophiomurispora hongheensis*

*Lophiomurispora hongheensis* Wanas. sp. nov. (Figures 7 and 8)

**Figure 7.** Sexual morph of *Lophiomurispora hongheensis* (HKAS110127, holotype). (a–c) Ascomata on the dead woody twigs of *Dodonaea viscosa*; (d) cross section of ascomata; (e) vertical section of ascoma; (f) closeup of ostiole; (g,h) peridium; (i) pseudoparaphyses; (j–l) asci; (m–s) ascospores (s in Indian Ink); Scale bars, (e) 100 µm; (f–h,j–l) 20 µm; (i,m–s) 10 µm.
Figure 8. Asexual morph of *Lophiomurispora hongheensis* (KUMCC 20-0217, ex-type culture). (a,b) colony on PDA (b from the bottom); (c,d) immersed pycnidia in PDA (from the bottom); (e) pycnidia wall; (f–i) conidiophore; (j) conidia. Scale bars, (e–i) 10 µm; (j) 5 µm.

MycoBank: MB 837998

*Etymology:* The specific epithet is derived from Honghe County, the region of Yunnan Province in which this species was gathered.

*Holotype:* HKAS110127

It is *saprobic* on dead twigs of *Dodonaea viscosa* Jacq. (Sapindaceae) in terrestrial habitats. Sexual morph: The *ascomata* is a 280–360 µm high, 200–250 µm diam. (M = 318.6 × 232.7 µm, n = 5), scattered to gregarious, immersed, coriaceous, dark brown to black, globose to subglobose ostiolate. The *ostiole* is a 70–100 µm long, 40–80 µm diam. (M = 82.1 × 64.8 µm, n = 5), crest-like, central papillate, with a pore-like opening, comprising hyaline periphyses. The *peridium* is 20–30 µm wide at the base, 30–60 µm wide at the sides, broad at the apex, comprising two strata, with outer stratum composed of small, pale brown to brown, slightly flattened, thick-walled cells of *textura angularis*, fusing and indistinguishable from the host tissues. The inner stratum is composed of several layers with lightly pigmented to hyaline cells of *textura angularis* to *textura prismatica*. The *hamathecium* comprises 1–2 µm wide, branched, septate, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. The *asci* are 120–160 × 17–22 µm (M = 135.2 × 18.5 µm, n = 15), eight-spored, bitunicate, fissitunicate, cylindric-clavate, with a short pedicel, and is rounded at the apex, with an ocellar chamber. The *ascospores* are 25–30 × 11–13 µm (M = 27.8 × 12 µm, n = 30), uni- to bi-seriate, overlapping, and are initially hyaline, turning brown at maturity. They are ellipsoid to fusiform, muriform, four-to-eight-transversely septate, with one-to-two-longitudinal septa. They are slightly curved, deeply constricted at
the central septum, slightly constricted at the remaining septa, conically rounded at the ends, and smooth-walled, with a distinct mucilaginous sheath. Asexual morph: Coelomycetous. The conidiomata is 1–1.5 mm diam. pycnidial, phoma-like, solitary, gregarious, dark brown to black, and immersed, with a sphaerical mass of slimy conidia oozing out at ostiolar apex. The conidiomata wall is multi-layered, with brown-walled pseudoparenchymatous cells, with a hyaline inner most layer. The conidiomata are 10–15 × 1.5–2.5 µm long (M = 12.4 × 2.1 µm, n = 15), septate and sparsely branched, which are formed from the inner most layer of the pycnidium wall. The conidiogenous cells are phialidic, cylindrical, hyaline, flexuous and smooth, with a short collarette. The conidia are 2.5–4 × 1.5–2 µm (M = 3 × 1.7 µm, n = 50), hyaline, aseptate, straight to curved, ellipsoidal with rounded ends, and are thin-walled, smooth-walled, and numerous.

Culture characteristics: the colonies on PDA reached a 4 cm diameter after 2 weeks at 20 °C. They were circular, had a serrate margin, and were whitish at the beginning, becoming greenish-brown 4 weeks later. They were slightly raised, and reverse dark brown. The hyphae septate were branched, hyaline, thin, and smooth-walled.

Known distribution: Yunnan, China, on Dodonaea viscosa. Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Honghe County, 23.421068 N, 102.229128 E, 735 m, on dead twigs of Dodonaea viscosa, 22 April 2020, D.N. Wanasinghe, Honghe 003 (HKAS110127, holotype), ex-type culture, KUMCC 20-0217, ibid. 23.419206 N, 102.231375 E, 618 m, Honghe 008 (HKAS110129, paratype), ex-paratype living culture, KUMCC 20-0223, ibid. 23 April 2020, ibid. DWHH07-1 (HKAS110130), living culture, KUMCC 20-0224, DWHH01 (HKAS110132), living culture, KUMCC 20-0216, ibid. DWHH04 3 (HKAS110131), living culture, KUMCC 20-0219.

Parapyrenochaetaceae Valenz-Lopez, Crous, Stchigel, Guarro and J.F. Cano, Studies in Mycology 90: 64 (2017)

Quixadomyces Cantillo and Gusmão, Persoonia 40: 317 (2018)

Quixadomyces hongheensis Wanas. sp. nov. (Figure 9)

MycoBank: MB837994

Etymology: The specific epithet is derived from Honghe County, Yunnan Province, China. Holotype: HKAS110126

It is saprobic on dead twigs of Dodonaea viscosa Jacq. (Sapindaceae) in terrestrial habitats. Sexual morph: Undetermined. Asexual morph: Coelomycetous. The conidiomata is immersed to erumpent, solitary, globose, brown, from 200–300 µm diam, with a central ostiole, exuding a hyaline conidial mass. It has a wall of two to three layers of brown textura angularis. The paraphyses are 20–100 µm long, 2–3 µm wide, cylindrical, hyaline, septate, and smooth. The conidiophores are mostly reduced to conidiogenous cells. The conidiogenous cells are 5–8 × 3.5–5 µm (M = 6.4 × 3.1 µm, n = 15), lining the inner cavity, hyaline, smooth, are ampulliform to subcylindrical, and are phialidic with periclinal thickening. The conidia are 3–4.7 × 1.2–2 (M = 3.7 × 1.7 µm, n = 60) µm, solitary, hyaline, smooth, aseptate, and allantoid with obtuse ends.

Culture characteristics: The colonies on PDA reached a 4 cm diameter after 2 weeks at 20 °C. They were circular, had a serrate margin, and were greenish brown after 4 weeks. They were slightly raised, and reverse dark brown. The hyphae septate were branched, hyaline, thin, and smooth-walled.

Known distribution: Yunnan, China, on Dodonaea viscosa. Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Honghe County, 23.421068 N, 102.229128 E, 735 m, on dead twigs of Dodonaea viscosa, 22 April 2020, D.N. Wanasinghe, Honghe 01-N (HKAS110126, holotype), ex-type living culture, KUMCC 20-0215. 08 December 2020, HDW4-1 (HKAS112347). ibid. HDW4-3 (HKAS112346).
4. Discussion

Teratosphaeriaceae was introduced by Crous et al. [187]. Given that it is composed of 61 genera, it is regarded as one of the largest families in Dothideomycetes [188]. Members of this family are adapted to a broad range of life modes and can be saprobic, plant and human pathogenic, rock-inhabiting and endophytic; accordingly, they are widely distributed across varied terrain [49,136,139,188,189]. We have included representative sequence data of all available genera listed in Hongsanan et al. [188] for the phylogenetic analyses (except Davisoniella, Pachysacca and Placocrea, which lack DNA-based sequence data). Among them, Aulographina was grouped in Venturiales, and Leptomelanconium was related to Helotiales in the initial analysis. Therefore, they were excluded from the final analysis (Figure 1). In addition, representative taxa for Piedraia were included in the final dataset that were phylogenetically closely related to Teratosphaeriaceae. However, this genus is still considered a member in Piedraiaeae. The phylogeny generated herein (Figure 1) is congruent with those of other published studies to resolve intergeneric relationships in Teratosphaeriaceae [49,188]. In the combined LSU, ITS, rpb2, act, cal and tef1 data analysis, 58 clades are recognized from the ingroup taxa. Two strains from our new collections...
constitute a distinct monophyletic lineage (subclade 17, Figure 1) within the genera in Teratosphaeriaceae, which we introduce as a new genus.

The phylogeny (Figure 1) reveals a close relationship between two strains of the newly collected fungus (*Haniomyces dodonaeae*) to *Camarosporula persooniae*, *Lapidotheca hispanicus*, *Neophaeothecoidea proteae*, Teratosphaeriaceae sp. (CCFEE 5569), *Xenocoelomyces catenata* and *Xenophacidiella pseudocatenata*, with 87% ML and 1.00 BYPP support values. Among them, only *Camarosporula persooniae* is reported from the sexual morph, and despite the high degree of phylogenetic similarity, these two species are morphologically dissimilar [136]. *Neophaeothecoidea* is more closely related to *Haniomyces* in the phylogenetic results, but this relationship lacks statistical support. In addition, *Neophaeothecoidea* is reported as a hyphomycete [188], whereas *Haniomyces* produces a coelomycetous asexual morph.

Out of the 61 genera listed in Teratosphaeriaceae, only 24 genera are described with sexual morphs. We suggest that the sexual morphs of these genera require further examination with increased collections to verify the accurate treatment of and relationships to remaining species. During asexual stages of Teratosphaeriaceae, most members are pathogenic, whereas they are non-pathogenic during sexual stages. This is an important distinction for identifying opportunistic pathogens, as members of this family can easily spread diseases between locations. The new taxon, *Haniomyces dodonaeae*, fits morphologically well into Teratosphaeriaceae by its periphysate ostiole and hyaline ascospores with a single septum in each. However, the dimensions of the asci and ascospores are significantly larger than the existing sexual reports of this family. The golden brown, ellipsoidal conidia of *Haniomyces dodonaeae* are similar to those in *Neophaeothecoidea* and *Readeriella*. Phylogenetically, *Haniomyces dodonaeae* has a close proximity to *Neophaeothecoidea proteae*. This relationship, however, is not strongly supported in the ML and BI analyses (Figure 1). *Neophaeothecoidea proteae* was originally isolated as a coelomycete (*Phaeothecoidea proteae*) based on its yeast-like growth in culture [190]; however, it is currently accounted for in a hyphomycetous genus. Comparison of the 805 base pairs (bp) across the LSU gene region of *Haniomyces dodonaeae* shows 17 bp (2.1%) differences exist in comparison with *Neophaeothecoidea proteae*. Similarly, comparison of the 356 bp of the rpb2 gene region shows 56 bp (15.73%) differences in comparison with *Neophaeothecoidea proteae*.

*Rhytidhysteron* was introduced by Spegazzini [191] to account for *R. brasiliense* and *R. viride* collected from southern Brazil in 1877 and 1880, respectively. Spegazzini [56] did not designate any type; therefore, Clements and Shear [192] designated *R. brasiliense* as the type species. Subsequently, few species were introduced to this genus based on morphological evidence [193–196]. In recent studies, more species have been introduced based on both morphology and DNA-based sequence data [55,56,172,177,178,183]. Presently, there are 23 species mentioned in *Species Fungorum* [197], including saprobic to weakly pathogenic taxa that grow on woody plants in terrestrial habitats [56,181]. Species of *Rhytidhysteron* are typically involved in wood degradation and occur primarily on the woody parts of a broad range of hosts [64,188].

We introduce a new species into *Rhytidhysteron* from a dead twig of *Dodonaea* sp. in Honghe, China, and its relationships with other species are presented based on multigene phylogenetic analyses (Figure 2). Our analysed molecular data generated phylogenies consistent with those of Mapook et al. [55] and Hyde et al. [56]. The novel species, *Rhytidhysteron hongheense*, is phylogenetically closely related to *R. camporesii* (KUN-HKAS 104277) and *Rhytidhysteron chromolaenae* (MFLUCC 17-1516), and these three constitute a strongly supported monophyletic clade. The ascospore and asc charactistics between the three species are similar, but the colour of hysterotheca in *R. chromolaenae* (green) is different from the other two (black). The pseudo-epithecium of *R. camporesii* is brown to purple, whereas it is reddish orange in *R. hongheense*. The significance of these morphological characteristics in species delineation should be further investigated in terms of phylogenetic signals. A pairwise comparison of 521 ITS (+5.8S) sequence data showed 31 (5.95%) bp differences between *R. hongheense* and *R. camporesii* as well 28 (5.37%) bp differences between *R. hongheense* and *R. chromolaenae*. Currently, there are only two *Rhytidhysteron* species,
viz. *Rhytidhysteron magnoliae* and *Rhytidhysteron thailandicum*, reported from China [56,198], making this report the third of its kind from China and first from Honghe Prefecture.

Lophiostomataceae species are usually characterized by a slot-like ostiole on the top of the flattened neck, occurring mainly on twigs, stems or the bark of different woody and herbaceous plants in terrestrial, freshwater and marine environments as saprobes [129,140,188]. Thambugala et al. [129] undertook a comprehensive study of this family and accepted 16 genera. Subsequently, 12 new genera have been introduced by recent publications, and currently the family comprises 28 accepted genera [188]. The most recent multi-locus phylogenetic backbone tree to the family is presented in this study, including a novel genus (*Lophiomurispora*) found in Honghe County, Yunnan Province, China.

*Lophiomurispora* morphologically resembles *Coelodictyosporium*, *Platystomum* and *Sigarispora* with its crest-like ostiole and brown, multi-septate ascospores. However, these genera are re-rounded to treat our isolate as a new species in *Quixadomyces* potentially be reclassified as a synonym of *Parapyrenochaeta*. Very few of these taxa are confirmed by both morphological and phylogenetic evidence. Lophiomurispora revealed as phylogenetically distant in multi-gene phylogenetic analysis (Figure 3). *Rhytidhysteron magnoliae* and *R. thailandicum* are widely distributed across southwest and southern China, e.g., Fujian, Guangdong, Guangxi, Hainan, making this report the third of its kind from China and first from Honghe Prefecture.

Parapyrenochaetaceae was proposed by Valenzuela-Lopez et al. [53] to accommodate three isolates which were previously recognized in *Pyrenochaeta*. They introduced the novel genus *Parapyrenochaeta* for *P. acaciae* (*Pyrenochaeta acaciae*), *P. protearum* (*Pyrenochaeta protearum*) and for the strain CBS 137997, formerly misidentified as *Pyrenochaeta pinicola* (re-identified as *Parapyrenochaeta protearum*). Later, Crous et al. [131] introduced *Quixadomyces* as another genus in *Parapyrenochaetaceae* to accommodate *Quixadomyces cearensis*. Therefore, there are currently two accepted genera in *Parapyrenochaetaceae* [3,188].

Crous et al. [131] introduced *Quixadomyces* for a fungus that was collected from Brazil on decaying bark. However, they did not observe the development of any internal structures. This fungus slightly resembles species in *Pleosporales* with its setose pycnidia [131,188]. In a multi-gene (concatenated LSU, SSU, ITS, *rpb1*, *tef1* and *rpb2*) phylogenetic analysis, the ex-type strain of *Quixadomyces cearensis* (HUEFS 238438) clustered with two of our new strains as a monophyletic clade with poor bootstrap support (Figure 4). We introduce this isolate as a novel species belonging to this genus, *Q. hongheensis*. Based on the features of conidiogenous cells and conidia of *Quixadomyces hongheensis*, no substantial morphological differences exist to warrant two generic ranks. Therefore, this genus could potentially be reclassified as a synonym of *Parapyrenochaeta* in future studies. Because we did not perform extensive taxonomic reassessment using multiple fresh collections (especially sexual morphs of both genera), we will not attempt to synonymize any extant taxa.

Owing to lack of details on the internal structures of *Quixadomyces cearensis*, it is difficult to compare morphological characteristics such as conidiogenous cells and conidia between the new collection and this species. Lacking sufficient morphological evidence to perform accurate comparisons, we analysed nucleotide differences between these two strains. Comparing the 544 ITS (+5.8S) nucleotides of the two strains (HUEFS 238438 and KUMCC 20 0215) revealed 32 (5.88%) nucleotide differences. Therefore, it would seem prudent to treat our isolate as a new species in *Quixadomyces* as *Q. hongheensis*.

Nearly a century’s worth of taxonomic investigation into *Dodonaea viscosa* has yielded only 58 fungal records [Table 2]. These are mainly reported as saprobes or pathogens, but very few of these taxa are confirmed by both morphological and phylogenetic evidence. Many of these published records lack illustrations, descriptions or DNA sequence data, resulting in unclear taxonomic relationships. Even though *Dodonaea viscosa* is widely distributed across southwest and southern China, e.g., Fujian, Guangdong, Guangxi, Hainan, Honghe.
Sichuan and Yunnan [199], there is only one report for the fungus *Pseudocercospora mitteriana* on this host from China [124]. Previous taxonomic studies have suggested that increased collections might lead to the discovery of many new fungal species, and we, too, believe that *Dodonaea* is likely teeming with fungal diversity. More *Dodonaea* collections across different geographic regions are urgently needed, along with accompanying work in culture isolation, morphological description, DNA sequence analyses, phylogenetic relationship investigation, and accurate identification and classification. This study provides a case study for *Dodonaea viscosa* as a worthwhile host for the further study of microfungal associations and hints that it may potentially host numerous unknown fungal species.

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