Circinotrichum sinense, a new asexual fungus from Hubei, China

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Manuscripts

1 *Circinotrichum sinense*, a new asexual fungus from Hubei, China

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Abstract

A setose hyphomycete was collected as part of a recent expedition for microfungi in the Duheyuan National Nature Reserve in Hubei, China. The conidia are typical of *Circinotrichum*, being curved or falcate, single-celled, colorless, smooth with a setula at the apical end, and similar to *Circinotrichum rigidum*. *Circinotrichum sinense* has a longer setula only at the apical end and verrucose setae, while *C. rigidum* has a setula on both ends and smooth setae. Phylogenetic analysis using ITS and LSU DNA sequence data and examination of morphological characters showed that this fungus cannot be identified as any previously described species of *Circinotrichum*. Thus, a new fungal taxon is described. A key to recognized species of *Circinotrichum* is also provided.

Key Words: Asexual morph, *Gyrothrix*, Hyphomycetes, ITS, LSU, Xylariales.

Introduction

Circinotrichum Nees was typified with *C. maculiforme* Nees (Nees von Esenbeck 1817). *Circinotrichum* was later emended by Pirozynski (1962). It is a foliicolous genus characterized by unbranched, circinate or flexuous setae, and conidiophores reduced to conidiogenous cells, which aggregate around the bases of setae (Pirozynski 1962); in contrast, the similar genus, *Gyrothrix* (Corda) Corda develops repeatedly branched setae (Corda 1842; Pirozynski 1962; Seifert et al. 2011). Twenty six epithets have been proposed in *Circinotrichum* (Index Fungorum 2017; MycoBank 2017). Seifert et al. (2011) accepted 13 species. Later, *Circinotrichum cycadis* Crous & R.G. Shivas was added to the genus (Crous et al. 2014). At present 14 taxa are accepted and in addition to the type species, these taxa are *C. britannicum* P.M. Kirk, *C. chathamense*

49 McKenzie, *C. cochinese* V.G. Rao & Varghese, *C. cycadis* Crous & R.G. Shivas, *C.*
50 *falcatisporum* Piroz., *C. flagelliforme* Zucconi & Onofri, *C. flexuosum* K.G. Karand. et al., *C.*
51 *mediterraneum* Rambelli, *C. olivaceum* (Speg.) Piroz., *C. palmicola* Joanne E. Taylor et al., *C.*
52 *papakurae* S. Hughes & Piroz., *C. poonense* Piroz. & S.D. Patil, *C. rigidum* B. Sutton. Twelve
53 species are questionable or have been reassigned to other genera, including: *Ceratocladium*,
54 *Gyrothrix*, *Hortaea*, *Sarcopodium* or *Selenodriella* (Index Fungorum 2017; Pirozynski 1962). No
55 taxa of *Circinotrichum* have been linked to a sexual morph.

56 Crous et al. (2015a) showed that the genus *Circinotrichum* belongs to Xylariaceae,
57 Xylariales and is paraphyletic based on the phylogenetic study using LSU data of *Circinotrichum*
58 *cycadis*, *C. maculiforme*, and *C. papakurae*; thus, a current revision of this genus is warranted.
59 Several phylogenetic studies on Xylariales have been published (Asgari and Zare 2011;
60 Daranagama et al. 2014; Jaklitsch et al. 2016; Senanayake et al. 2015). Eleven families
61 (Apiosporaceae, Cainiaceae, Coniocessiaceae, Diatrypaceae, Hyponectriaceae, Iodosphaeriaceae,
62 Lopadostomaceae, Melogrammataceae, Pseudomassariaceae, Vialaeaceae and Xylariaceae) were
63 accepted by Senanayake et al. (2015) using ITS and partial nucLSU sequences. Among this
64 group two new families, Lopadostomaceae and Pseudomassariaceae were proposed.
65 Graphostromataceae is doubtful, since it is imbedded in Xylariaceae (Senanayake et al. 2015).
66 Jaklitsch et al. (2016) excluded Iodosphaeriaceae and accepted 16 families in Xylariales
67 including six additional families: Amphisphaeriaceae, Beltraniaceae, Microdochiaceae,
68 Phlogicylindriaceae, Requienellaceae, and Sporocadaceae based on phylogenetic analysis of the
69 same nuclear loci (ITS and LSU). The family Clypeosphaeriaceae (Amphisphaeriales) cannot
70 be maintained since the generic type of *Clypeosphaeria*, *C. mamillana*, belongs to the
71 Xylariaceae (Jaklitsch et al. 2016). However, multiple locus phylogenetic analyses using ITS,

LSU and SSU showed that Xylariaceae could be polyphyletic (unpublished data). Recently, another new family, Castanediellaceae, was proposed (Hernández-Restrepo et al. 2017) and Hypoxylaceae had been resurrected (Wendt et al. 2017). The delineation of Xylariales remains unsettled and further studies are necessary.

A specimen of *Circinotrichum* collected from Hubei, China was determined to be new to science based on its morphological characters and phylogenetic analysis using ITS and LSU sequences data. Thus, it is illustrated and described in this paper and its phylogenetic relationships with allied taxa is discussed.

Materials & Methods

A collecting trip was made to the Duheyuan National Nature Reserve, Guangdu, Zhushan county, Hubei, China in September 2016 to collect saprobic microfungi on plant debris. The specimens were first examined using a stereomicroscope (Olympus SZX7). Microfungi were mounted in 85% lactic acid for further observation. Conidia were picked up from the specimen-using an inoculation needle, transferred to two plates of malt extract medium (MEA) (20 g malt, 20 g agar and 1L distilled water) and incubated at 25°C for two weeks. Since the colonies failed to sporulate, hyphal tips were cut from a colony edge to obtain a pure isolate. Four more MEA plates were prepared from the purified isolate and incubated at 25°C on MEA for two weeks to observe the colony growth and for preparing exatype and molecular work. Each plate was inoculated at three points in a triangle shape with equal distance. To monitor sporulation, Corn meal agar (CMA: 1 L water, 17 g corn meal agar), Oat meal (OA), and Potato dextrose agar (PDA: 1L water, 200g potatoes, 20 g dextrose, 20 g agar) media were also used with the isolate for a two weeks growth period.

All further microscopic observations and measurements of fungal structures were made under a compound microscope Zeiss Imager.M2 with differential interference contrast (DIC) and photomicrographs were taken with Axiocam 506 color camera (Carl Zeiss AG, Oberkochen, Germany). Measurements of the fungal structures were made under a 100× objective lens and statistically analyzed for means and standard deviations (SD) with 95% confidence interval of means.

The type specimen has been deposited in The Connecticut Agricultural Experiment Station (NHES) in the USA, and an extype culture has been deposited in The UAMH Centre for Global Microfungal Biodiversity at University of Toronto (UAMH), Canada.

DNA extraction and sequencing.—DNA was extracted from the fungus grown in a Petri dish of MEA medium according to the procedure in ZR Fungal/Bacterial DNA MicroPrep Kit (Zymo Research, Irvine, California). A combination of primers ITS5 and LR1 were used to amplify a fragment corresponding to the partial small subunit rDNA and internal transcribed spacer 1 and 2 region (ITS) (Vilgalys and Hester 1990; White et al. 1990). The primers 5.8SR and LR7 were similarly used to amplify a portion of the large subunit rDNA region (LSU) (Vilgalys and Hester 1990; White et al. 1990). The primers SR1R and SR6 were used to amplify the small subunit rDNA region (SSU) (White et al., 1990). The parameters for the PCR amplification protocol were 94 °C 3 minutes; 94 °C 30 seconds; 45 °C 30 seconds; 72 °C 2 minutes, repeat 35X, 72 °C 7 minutes. The resulting PCR products were purified using QIA quick PCR Purification columns (Qiagen, Valencia, California) and the DNA concentration determined on a NanoDrop Lite Spectrophotometer (ThermoScientific, Waltham, Massachusetts). The ITS PCR products were sequenced using primers ITS1, ITS2, ITS3 and LR1. The LSU PCR products were sequenced

using primers LROR, LR7, LR5, LR3R, LR16 and LR3B (5' GGTAAAGTTCAGCGGGT 3').

The SSU PCR products were sequenced using primers SR1R, SR1, SR2, SR4, SR6 and SR7R.

All DNA sequencing was performed at the W. M. Keck Biotechnology Resource Laboratory, Yale School of Medicine (New Haven, Connecticut). DNA sequences were deposited to GenBank (ITS KY994106, LSU KY994107, SSU KY994108).

Sequence similarity searches and comparisons were conducted using MegaBLAST (Morgulis et al. 2008; Wheeler et al. 2003) for ITS, LSU, and SSU against the NCBI nucleotide database to choose DNA sequences from allied fungal taxa for phylogenetic analyses. *Circinotrichum*, *Gyrothrix* and 10 additional allied genera (39 taxa/isolates) were chosen for phylogenetic analysis (TABLE 1). *Penicillium chrysogenum* (CBS 306.48) was designated as an outgroup. Since a SSU sequence is available from only three of the allied taxa, SSU sequences are not included in the phylogenetic analysis.

Independently, ITS and LSU DNA sequences were aligned using MUSCLE (Edgar 2004), and the resulting aligned data trimmed and concatenated using FABOX sequence alignment joiner (http://users-birc.au.dk/biopv/php/fabox/alignment_joiner.php#). Phylogenetic analyses were conducted using the neighbor joining and maximum likelihood procedures in MEGA7 (Kumar et al. 2016). A bootstrap test was carried out with 1000 replicates. Bayesian inference was analyzed using MRBAYES3.2.6 (Ronquist et al. 2012). Four Markov chains were executed using 4 runs from random starting trees for 20 million generations. Trees sampling frequency was 1000 generations. The first 10% generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support ($\geq 80\%$) and Bayesian posterior probabilities (BPP) ($\geq 95\%$ (BPP), respectively, were set as significantly supported. Phylogenetic trees were drawn with TREEVIEW 1.6.6 (Page 1996).

Results

Phylogenetic analysis using ITS and LSU showed that *Circinotrichum sinense* UAMH11913 is sister to *C. falcatisporum*, in the same clade as *C. maculiforme* (generic type), and *Gyrothrix circinata*, and subtended by *Lopadostoma* and *Anthostomella*. *Circinotrichum cycadis* and *C. papakurae* are in a different clade with *G. inops*, *G. ramosa*, and *Idriella lunata* (MUCL4103) (FIG. 1).

Taxonomy

Circinotrichum sinense D.W. Li, Neil P. Schultes, Jing Y. Chen, Yi X. Wang & R.F. Castañeda
sp. nov. FIG. 2

MycoBank MB 821257

Typification: China, Hubei, Zhushan county, Guangdu, Bailihe village, Yingzuiyan, Duheyuan National Nature Reserve (31°52'17.81"N, 110°08'56.27"E), dead foliage of *Camellia cuspidata* (Kochs) Wright ex Gard., Sept. 22, 2016, coll. Jing-Yuan Chen et. Yi-Xun Wang, (**Holotype**, NHES L1703; ex-type UAMH 11913).

Etymology: Latin, *sinense*-, referring to China where the holotype was collected.

Asexual morph: Colonies on natural substrate effuse, hairy, blackish brown to black. Mycelium partial immersed and partially superficial, composed of pale brown, smooth, branched, 1.5–3 µm wide, septate hyphae. Setae acicular or subulate, rarely obtuse, erect, straight or flexuous, simple, thick-walled, verrucose, septate, dark brown, occasionally with percurrent extension, 115–260 µm in length, 4–8 µm wide at the base, with most gradually tapering to an acutely pointed or

obtuse apex. Conidiophores reduced to conidiogenous cells. Conidiogenous cells enteroblastic, phialidic, sometimes with several successive inconspicuous annellations, after percurrent extensions, frequently collapsed near the apex, integrated, ampulliform to lageniform, colorless to pale brown, thin-walled, smooth, arising at right angles from the vegetative mycelium, solitary or gregarious at the base of setae, $5-7(-9) \times (2.7-3-4(-4.5)) \mu\text{m}$ (mean $\pm$ SD: $6 \pm 1 \times 3.5 \pm 0.5 \mu\text{m}$, $n=26$). Conidia acrogenous in white masses, curved or falcate, 1-celled, colorless, smooth, $(12-14.5-17(-18.5)) \times (1.6-2-2.5) \mu\text{m}$ (mean $\pm$ SD: $16 \pm 1.5 \times 2 \pm 0.2 \mu\text{m}$, $n=30$), obtuse at the base and abruptly attenuate with a cellular appendage at the apex, $(0.5-1-1.5(-2)) \mu\text{m}$ long ($1.5 \pm 0.5 \mu\text{m}$, $n=30$). Sexual morph: not observed.

Colonies on MEA, effuse, white; retaining 9 mm diam. in two weeks at 25 °C. Mycelium mostly immersed, partially superficial. No sporulation on MEA, CMA, OA and PDA in two weeks.

Comments: Although *Circinotrichum sinense* is morphologically similar to *C. chathamense* and *C. rigidum* it can be differentiated from *C. chathamense* by its smaller, setulate conidia and phialidic conidiogenous cells ($14.5-17 \times 2-2.5 \mu\text{m}$) vs. *C. chathamense* ($20-24 \times 1.5-2 \mu\text{m}$ conidia without setula) (McKenzie 1993). Both *Circinotrichum sinense* and *C. rigidum* develop “phialidic” conidiogenous cells and conidia with similar size and shape. However, *Circinotrichum sinense* has a longer setula only at the apical end and verrucose setae, while *C. rigidum* has a setula on both ends and smooth setae (Sutton 1980). The three specimens -including holotype IMI223850 of *C. rigidum* studied by Sutton (1980) - are no longer available at the Kew Botanic Garden. The two taxa cannot be examined for detailed morphological comparison. Since cultures of the morphologically related species, *C. chathamense* and *C.*

rigidum, are not available, the phylogenetic relationships of *Circinotrichum sinense* with *C. chathamense* and *C. rigidum* remain undetermined.

Discussion

Our phylogenetic analysis confirmed the conclusion of Crouse et al. (2015a) and Hernandez-Restrepo et al. (2017) that *Circinotrichum* belongs to Xylariales (FIG. 1) and the clade of *Circinotrichum sinense*, *C. maculiforme*, *C. falcatisporum*, as well as *Gyrothrix circinata*, a sister to the clade including *Lopadostoma* spp. and *Anthostomella* spp. (FIG. 1). *Circinotrichum*, *Gyrothrix*, and *Idriella*, as currently defined, are polyphyletic. *Circinotrichum sinense* is sister to *C. falcatisporum* in the same clade as *C. maculiforme* and *G. circinata*, and subtended by *Lopadostoma*, including its generic type *L. turgidum* and *Anthostomella*. Crous et al. (2015a) concluded that the genus *Circinotrichum* belongs to Xylariaceae, Xylariales based on their phylogenetic study using LSU data of *Circinotrichum cycadis*, *Circinotrichum maculiforme*, and *Circinotrichum papakurae*, while in their analysis, *Lopadostoma gastrinum* was in the same clade of Xylariaceae, Xylariales. Our analysis is in agreement with the results of Hernández-Restrepo et al. (2017) that the placement of *Circinotrichum* at the family level remains unsolved. However, Lopadostomataceae was proposed and typified with *Lopadostoma* to accommodate *Lopadostoma* spp. and *Creosphaeria* based on ITS and LSU data (Senanayake et al. 2015). Microdochiaceae was established and typified with *Microdochium phragmitis* to accommodate *Idriella*, *Microdochium*, and *Selenodriella* based on LSU sequence data (Hernandez-Restrepo et al. 2016). Delineation of Lopadostomataceae and Microdochiaceae needs to be further studied prior to determine the placement of *Circinotrichum* at family level. Our results showed that

several clades remain uncertain and the phylogeny of Xylariales has not been fully elucidated. Thus, further studies are necessary in the future.

Cunningham (1974) and Pirozynski (1962) considered that *Circinotrichum* and *Gyrothrix* are closely related. Based on their phylogenetic analysis using ITS, LSU and *tef1* α sequence data, Becerra-Hernández et al. (2016) showed that *Gyrothrix* as a polyphyletic genus of Xylariales. However, no culture of the type species of *Gyrothrix*, *G. podosperma* (Corda) Rabenh. ($\equiv$ *Campsotrichum podospermum* Corda) is available. Thus, the phylogenetic placement of the genus *Gyrothrix* at the family level cannot be determined at present.

According to our phylogenetic analysis, *Gyrothrix circinata* is in the same clade with the generic type species, *Circinotrichum maculiforme* (FIG. 1). Thus, *Gyrothrix circinata* belongs in *Circinotrichum*. However, the result showed that the four isolates of *G. circinata* are not conspecific, therefore, no new combination for *G. circinata* is proposed until a further study is conducted to examine its type material and an epitype culture can be designated. Our results suggest that one of the generic characters of *Circinotrichum*, unbranched setae, should be amended and widened to ‘unbranched or branched setae’.

Gyrothrix circinata and *G. podosperma* are morphologically similar in conidial shape and size and subdichotomous branching, rough setae (Pirozynski 1962). The conidia of both taxa are cylindrical to fusoid, straight or slightly curved and similar in size, $8\text{--}16 \times 1.2\text{--}2 \mu\text{m}$ for *G. podosperma* and $12\text{--}15 \times 1.5\text{--}1.8 \mu\text{m}$ for *G. circinata* (Pirozynski 1962). The main difference is setae branching and height. *Gyrothrix podosperma* has setae $120\text{--}260 \mu\text{m}$ long with twisted or loose spiral branching, while *G. circinata* develops setae $80\text{--}140 \mu\text{m}$ long with circinate branching (Pirozynski 1962). *Gyrothrix podosperma* and *G. circinata* share all generic characters of *Circinotrichum* except for one, which is branched circinate or spiral setae (Pirozynski 1962).

A further study is needed to determine the placement of *Gyrothrix podosperma*, the generic type of *Gyrothrix*. The members of *Circinotrichum* that do not develop circinate setae should be further studied. The phylogenetic relationships among *Circinotrichum*, *Gyrothrix* and *Idriella* remain to be determined due to the unavailability of cultures of a number of key taxa.

Circinotrichum sinense, a saprobe on leaf litter of *Camellia cuspidata*, was collected from Duheyuan National Nature Reserve, a transitional area between south temperate and north subtropics (Gao et al. 2012). There is no sign or symptom to indicate that a fungal disease has been caused by *C. sinense* on the leaves *Ca. cuspidata*. Duheyuan National Nature Reserve is very rich in biodiversity and its flora has an ancient origin. The Reserve contains at least 2440 species of vascular plants, belonging to 949 genera, 212 families (Gao et al. 2012) including 39 genera are endemic in China (Gao et al. 2012; Pu et al. 2005). *Camellia cuspidata* is native to forests of south eastern China at (100-)500-1500(-2200) m (Zhang and Ren 1998). No study or survey on microfungi and fungal diversity has been conducted in this area in the past. Clearly more undescribed fungal taxa, especially endemic ones are expected to exist in the area. It is imperative to conduct studies on microfungi, fungal diversity and functions in this ecological sensitive area in the near future.

Key to recognized species of *Circinotrichum*

1. Setae circinate only or both circinate and straight/flexuous	2
1. Setae straight only	8
2. Setae both circinate and straight/flexuous	3
2. Setae circinate only	5

254	3. Setae both circinate and straight; conidia 8–12 μm long	<i>C. poonense</i>
255	3. Setae both circinate and flexuous	4
256	4. Setae 70–153 μm long, conidia 3.5–7 μm long	<i>C. flexuosum</i>
257	4. Setae 120–210 μm long, conidia 15–17 μm long	<i>C. cochinese</i>
258	5. Setae 25–75 μm long	6
259	5. Setae 75–180 μm long	7
260	6. Setae thin-walled, 25–40 μm in length; conidia 9–11 μm long	<i>C. cycadis</i>
261	6. Setae thick-walled, 35–75 μm in length; conidia 8.5–13 μm long	<i>C. olivaceum</i>
262	7. Conidia straight or slightly curved, 9–17 μm long	<i>C. maculiforme</i>
263	7. Conidia falcate, 17.5–21 μm long	<i>C. falcatisporum</i>
264	8. Conidia setulose	9
265	8. Not setulose	10
266	9. Conidia with a setula at both ends, 13–16.5 $\times$ 1.5 μm	<i>C. rigidum</i>
267	9. Conidia with a setula at the apical end, 14.5–17 $\times$ 2–2.5 μm	<i>C. sinense</i>
268	10. Conidia cylindrical, straight	11
269	10. Conidia curved or fusiform	12
270	11. Conidia 12–16 μm long	<i>C. britannicum</i>
271	11. Conidia 12–20 μm long with mucilage drops at one or both ends, developing	
272	two kinds of setae	<i>C. palmicola</i>
273	12. Setae up to 600 μm in height, conidia 16–20 $\times$ 2.3–2.7 μm	<i>C. flagelliforme</i>
274	12. Setae < 600 μm in height	13
275	13. Conidia 11–17 $\times$ 1.5–2 μm	<i>C. papakurae</i>

276 13. Conidia > 20 µm long 14

277 14. Conidia 20–24 × 1.5–2 µm ..... *C. chathamense*

278 14. Conidia 25–28 × 4 µm ..... *C. mediterraneum*

279

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Legends

Fig. 1. Maximum Likelihood analysis of *Circinotrichum sinense* and allied taxa based on concatenated ITS, and LSU sequence data. *Penicillium chrysogenum* is included as outgroup. The bootstrap test was conducted with 1000 replicates. Bootstrap values >80% (before the slash) and Bayesian posterior probabilities (>95%) (behind the slash) were indicated at the nodes. The scale bar indicates the number of expected changes per site. T indicated the ex-types used in the analysis.

Fig. 2. *Circinotrichum sinense* (NHES L1703) A. Seta and conidiogenous cell (arrow), B. Apical portion of seta showing percurrent extension (arrow), C–D. Basal portion of seta and conidiogenous cells (arrows). Scale bars: A = 10 μm , B–E = 5 μm .

Table 1. Taxa and their sequences used in the phylogenetic analysis.

Fig. 2. *Circinotrichum sinense* (NHES L1703) A. Seta and conidiogenous cell (arrow), B. Apical portion of seta showing percurrent extension (arrow), C-D. Basal portion of seta and conidiogenous cells (arrows). Scale bars: A = 10 μm , B-E = 5 μm .

223x279mm (300 x 300 DPI)

1 Table 1. *Circinotrichum sinense* and allied taxa and their sequences used in the phylogenetic analysis.

Taxa	Strain Accession #	Locality	Substrate	Sequence accession #		References	Type (T)/Epit ype (ET) (A) authenti c	Family	Order
				ITS	LSU				
<i>Anthostomella conorum</i>	CBS 119333	South Africa	<i>Protea neriifolia</i> dead leaves	EU552099	EU552099	(Marincowitz et al. 2008)		Xylariaceae	Xylariales
<i>Anthostomella formosa</i>	MFLUCC 14-0170	Italy	on needle of <i>Pinus sylvestris</i>	–	KP340544	(Daranagama et al. 2015)	A	Xylariaceae	Xylariales
<i>Castanediella acaciae</i>	CBS 139896	Malaysia	leaf spots of <i>Acacia mangium</i>	NR_137985	KR47676	(Crous et al. 2015b)	T	Castanediellacea e	Xylariales
<i>Castanediella (Idriella) cagnizarii</i>	CBS 542.96	Cuba	leaf litter	KP859054	KP858991	(Hernandez- Restrepo et al. 2016)	A	Castanediellacea e	Xylariales
<i>Castanediella (Idriella) cagnizarii</i>	MUCL41095	Brazil	–	KC775732	KC775707	(Becerra- Hernández et al. 2016)		Castanediellacea e	Xylariales
<i>Circinotrichum cycadis</i>	CBS 137969	Australia	Leaves of <i>Cycas</i> sp.	KJ869121	KJ869178	(Crous et al. 2014)	T	Incertae sedis	Xylariales
<i>Circinotrichum falcatisporum</i>	NBRC 32658	Japan	dead leaf sheath, <i>Satakentia liukuensis</i>	–	3265801	–		Incertae sedis	Xylariales
<i>Circinotrichum maculiforme</i>	CBS 122758 = FMR 9645	Spain	Plant debris	KR611875	KR611896	(Crous et al. 2015a)		Incertae sedis	Xylariales
<i>Circinotrichum maculiforme</i>	CPC 24566=CBS 140016	Czech Republic	Twig of <i>Loranthus europaeus</i>	KR611874	KR611895	(Crous et al. 2015a)		Incertae sedis	Xylariales
<i>Circinotrichum papakurae</i>	CBS 101373 = INIFAT C98/17-8	Brazil	Rotten leaf	KR611876	KR611897	(Crous et al. 2015a)		Incertae sedis	Xylariales
<i>Circinotrichum sinense</i>	UAMH 11913	China	dead foliage of <i>Camellia cuspidata</i>	KY994106	KY994107	This study	T	Incertae sedis	Xylariales
<i>Gyrophthrix circinata</i>	MUCL 54182	Australia	–	KC775744	KC775719	(Becerra- Hernández et al. 2016)		Incertae sedis	Xylariales
<i>Gyrophthrix circinata</i>	NBRC 32309	Japan	dead leaf of <i>Trachycarpus excelsa</i>	NBRC 32309	NBRC 32309	–		Incertae sedis	Xylariales
<i>Gyrophthrix circinata</i>	NBRC 32310	Japan	dead leaf of <i>Trachycarpus</i>	NBRC 32310	NBRC 32310	–		Incertae sedis	Xylariales

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<i>Gyrophthrix circinata</i>	MUCL54042	Mexico	<i>excelsa</i> Leaf litter	KJ476967	KJ476963	(Becerra-Hernández et al. 2016)		Incertae sedis	Xylariales
<i>Gyrophthrix dichotoma</i>	BE108	México	–	KC775745	KC775720	(Becerra-Hernández et al., 2016)		Incertae sedis	Xylariales
<i>Gyrophthrix inops</i>	BE74	Cuba	–	KC775746	KC775721	(Becerra-Hernández et al., 2016)		Incertae sedis	Xylariales
<i>Gyrophthrix ramosa</i>	MUCL54061	Cuba	–	KC775747	KC775722	(Becerra-Hernández et al., 2016)		Incertae sedis	Xylariales
<i>Gyrophthrix verticiclada</i>	MUCL40992	Venezuela	–	KC775748	KC775723 rcinotr ichum	(Becerra-Hernández et al., 2016)		Castanediellaceae	Xylariales
<i>Gyrophthrix verticilata</i>	NBRC 100032	Spain	Submerged leaf from a stream	10003201	10003201	(Becerra-Hernández et al., 2016)		Microdochiaceae	Xylariales
<i>Hortaea (Circinotrichum) werneckii</i>	ATCC 11717=CBS 410.51 =NBRC4875	Japan	Air	487501	487501	–		Teratosphaeriaceae	Capnodiales
<i>Hortaea werneckii</i>	NBRC6407	–	–	–	640701	–		Teratosphaeriaceae	Capnodiales
<i>Idriella cubensis</i>	MUCL39017	Cuba	–	KC775733	KC775708	(Becerra-Hernández et al., 2016)		Microdochiaceae	Xylariales
<i>Idriella lunata</i>	CBS 204.56	USA	Root of <i>Fragaria chiloensis</i> var. <i>ananassa</i>	KP859044	KP858981	(Hernandez-Restrepo et al. 2016)	T	Microdochiaceae	Xylariales
<i>Idriella lunata</i>	CBS 209.60	The Netherlands		KP859045	KP858982	(Hernandez-Restrepo et al. 2016)		Microdochiaceae	Xylariales
<i>Idriella lunata</i>	MUCL4103	Canada	–	KC775734	KC775709	(Becerra-Hernández et al., 2016)		Incertae sedis	Xylariales
<i>Lopadostoma gastrinum</i>	CBS 133210 = LG2	–	<i>Ulmus glabra</i>	KC774581	KC774581	(Jaklitsch et al., 2014)		Lopadostomataceae	Xylariales
<i>Lopadostoma gastrinum</i>	CBS 134632 = LG4	–	<i>Ulmus minor</i>	KC774584	KC774584	(Jaklitsch et al., 2014)	T	Lopadostomataceae	Xylariales
<i>Lopadostoma turgidum</i>	CBS 133207 = LT2	Austria	<i>Fagus sylvatica</i>	NR_132036	KC774618	(Jaklitsch et al. 2014)	T	Lopadostomataceae	Xylariales
<i>Microdochium phragmitis</i>	CBS 285.71	Poland	<i>Phragmites australis</i>	KP859013	KP858949	(Hernandez-Restrepo et al. 2016)	ET	Microdochiaceae	Xylariales

<i>Penicillium_chrysogenum</i>	CBS 306.48=ATCC 10106	USA	–	JX997093	JQ434684	(Houbraken et al. 2012; Ropars et al. 2012)	T	Trichocomaceae	Eurotiales
<i>Sarcopodium_circinatum</i>	CBS 587.92	–	–	KM231787	HQ232168	(Summerbell et al. 2011)		Nectriaceae	Hypocreales
<i>Sarcopodium_circinosetiferum</i>	CBS 100251/ NBRC 33031	Argentina	garden soil	KM231782	HQ232170	(Summerbell et al., 2011)		Nectriaceae	Hypocreales
<i>Sarcopodium_flavolanatum</i>	CBS 112283	Ecuador	<i>Theobroma gileri</i>	KM231785	KM231649	(Lombard et al. 2015)		Nectriaceae	Hypocreales
<i>Selenodriella_fertilis</i>	CBS 772.83	Australia	<i>Hakea baxteri</i> dead leaf	KP859055	KP858992	(Hernandez-Restrepo et al. 2016)	T	Microdochiaceae	Xylariales
<i>Vermiculariopsiella_immersa</i>	MUCL39135	Cuba	–	KJ476965	KJ476961	(Becerra-Hernández et al., 2016)		Vermiculariopsiellaceae	Microascales
<i>Vermiculariopsiella (Gyrothrix)_microsperma</i>	NBRC 9374	Japan	dead leaf, <i>Castanopsis</i> sp.	937401	937401	(Becerra-Hernández-Restrepo et al. 2017; Hernandez-Restrepo et al. 2016)		Vermiculariopsiellaceae	Xylariales
<i>Xylaria_hypoxylon</i>	ATCC 42768	USA	Wood	AY327477	U47841	(Platas et al. 2004)		Xylariaceae	Xylariales
<i>Xylaria_hypoxylon</i>	CBS 122620	Sweden	old tree stump of <i>Sorbus aucuparia</i>	AM993141	KY610495	(Peršoh et al. 2009; Wendt et al. 2017)	ET	Xylariaceae	Xylariales

ATCC, American Type Culture Collection, Manassas, United States; BCC, BIOTEC Culture Collection, Thailand; CBS, The Westerdijk Fungal Biodiversity Institute (formerly Centraalbureau voor Schimmelcultures), Utrecht, The Netherlands; MFLUCC, Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCL, BCCM Belgian Co-ordinated Collections of Microorganisms, Belgium (formerly The Mycothèque de l’Université catholique de Louvain); NBRC, the NITE Biological Resource Center, Japan; UAMH, The UAMH Centre for Global Microfungal Biodiversity at University of Toronto.