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Article

Sexual Morph of *Furcasterigmium furcatum* (Plectosphaerellaceae) from *Magnolia liliifera* Collected in Northern Thailand

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Abstract: We isolated an interesting fungus from dead leaves of *Magnolia liliifera* collected from Chiang Mai, Thailand. The novel strain is related to Plectosphaerellaceae based on the morphology of its asexual morph and the analysis of sequence data. Phylogenetic analyses using a combined gene analysis of LSU and ITS sequence data showed that this strain is clustered in the same clade with *Furcasterigmium furcatum* with high statistical support. The new strains produced the asexual morph in culture which is morphologically similar to *F. furcatum*. Thus, we identified this strain as the sexual morph of *F. furcatum*. This is the first record of sexual morph for the monotypic genus *Furcasterigmium* and the first record of this genus on *Magnolia*.

Keywords: *Acremonium*; phylogeny; sexual morph; sordariomycetes; taxonomy

1 Introduction

The family Plectosphaerellaceae was introduce by Zare et al. [1], with the generic type *Plectosphaerella* [1,2]. Members in this family are found in diverse habitats, and most of them are soil-borne saprobes and plant pathogens [3–5]. Some species are opportunistic animal pathogens: *Gibellulopsis serrae* and *Plectosphaerella oratosquillae* [6–8]. The family Plectosphaerellaceae was placed in the order Glomerellales by Maharachchikumbura et al. [9]. At present, 24 genera are accepted in the family, with two holomorphic genera; *Plectosphaerella* and *Sodiomyces* [10]. However, the asexual morphs are more similar among genera, with simple or verticillate conidiophores, mono- or polyphialidic conidiogenous cells and mostly cylindrical or ellipsoidal one or two celled conidia arranged in slimy heads [1,11]. The sexual morphs are characterised by perithecial or cleistothecial ascomata, superficial, brown to dark brown, with clavate or saccate asci and hyaline to pale brown ascospores [11].

Acremonium represents a polyphyletic genus, with *A. alternatum* as the type species. Most of the species are related to Bionectriaceae (Hypocreales) [12], whereas, other *Acremonium* species belong to either Glomerellales or other Hypocreales [1,4,9,13–17]. *Acremonium furcatum* was established by Moreau et al. [18] with the invalid name; *Cephalosporium furcatum*. Gams et al. [19] validated and transferred the species to *Acremonium*, which grouped in the section Nectrioidea [20]. Glenn et al. [21] showed that

A. furcatum is likely related to *Microascus* and *Ceratocystis* of the order Microascales. However, the taxonomic placement of the species was uncertain [21], until, Zare et al. [1] established the family Plectosphaerellaceae and accommodated *Acremonium furcatum*. Giraldo et al. [11] proposed a new monotypic genus, *Furcasterigmium* with *F. furcatum* as the type species in Plectosphaerellaceae based on their phylogenetic analyses of combined LSU, ITS, TEF1-α and RPB2 sequence data.

During an investigation on diversity of leaf litter fungi in northern Thailand, we isolated an interesting fungus resembling a species of *Plectospharellaceae* collected from *Magnolia liliifera* in Chiang Mai Province. Based on morphological studies and phylogenetic analyses of combined LSU and ITS sequence data, this fungus is referred to *Furcasterigmium furcatum*. The sexual morph of *F. furcatum* is reported for the first time in this study with description and illustrations.

2 Materials and Methods

2.1 Fungal Collection, Isolation and Morphology

Dead leaves of *Magnolia liliifera* was collected from Chiang Mai, Thailand, following the methods outlined by Monkai et al. [22] and taken back to the laboratory using plastic Ziploc bags. Samples were placed in a plastic box with moistened tissue paper and maintained at room temperature (28–32°C) for 1–2 weeks. Morphological characters were observed using a Motic SMZ 168 Series stereomicroscope (Motic Incorporation Ltd., Hong Kong). Microscopy photographs were taken using Nikon ECLIPSE 80i compound microscope equipped with a Canon EOS 600D digital camera. Measurements of fungal structures were calculated using Tarosoft (R) Image Frame Work program. Figures were arranged using Adobe Photoshop CS6 Extended version 10.0 software (Adobe Systems, USA). A pure culture was acquired using the single spore isolation method [23] and sub-cultured onto potatoes dextrose agar (PDA) and sabouraud dextrose agar (SDA) The characteristics of asexual morph were observed on cultures. Culture was deposited in Mae Fah Luang University Culture Collection (MFLUCC) and the type specimen was deposited in the herbarium of Mae Fah Luang University (MFLU). The Faces of Fungi number was issued as described in Jayasiri et al. [24].

2.2 DNA Extraction, PCR Amplification and Sequencing

Fresh mycelium was scraped from the margin of a colony cultivated on PDA for 2 weeks at 28°C. Genomic DNA was extracted from the fresh mycelium using the Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, China) according to the manufacturer protocol. DNA sequence data was processed by the sequences of the internal transcribed spacers region of ribosomal DNA (ITS) using primer pairs ITS5 and ITS4 [25], and partial large subunit nuclear ribosomal DNA (LSU) using primer pairs LR0R and LR5 [26]. The polymerase chain reaction (PCR) amplification included the mixtures of 50 ng template DNA, PCR Master Mix 1 3, 0.5 mM of each primer in a 25 mL volume, 50 U *Taq* DNA polymerase 400 mM of each dNTP, and 3 mM $MgCl_2$. The thermal cycling programme consisted of 95°C for 2 min, followed by 35 cycles of denaturation at 94°C 1 min, annealing at 50°C 1 min, extension at 72°C 1 min and a final extension step of at 72°C for 10 min. PCR products were examined for the quality by staining with red gel on 1% agarose gel electrophoresis. Sequencing were conducted by Shanghai Sangon Biological Engineering Technology & Services Co. Ltd. (Shanghai, China). The obtained nucleotide sequence data was deposited in GenBank (Tab. 1).

2.3 Phylogenetic Analysis

The sequences generated in this study were analysed with the reference sequence data of representative genera in Plectosphaerellaceae which were derived from GenBank, and relevant publications [11,12] (Tab. 1). The alignments of consensus sequences were performed using MAFFT v.7 (http://mafft.cbrc.jp/alignment/server/index.html; [27]), and improved manually using Bioedit v. 7.0.9.1 [28]. The final

Table 1: Details of the taxa used in the analyses and their GenBank accession numbers

Taxa	Culture Accession No.	GenBank Accession No.	
		LSU	ITS
Acrostalagmus annulatus	CBS 121.84	LR025802	LR026673
Acrostalagmus luteoalbus	CBS 112.16	LR025797	LR026668
Acrostalagmus luteoalbus	JW 1001	LR590267	LR590089
Brunneochlamydosporium cibotii	CBS 109240^{IT}	LR025807	LR026678
Brunneochlamydosporium nepalense	CBS 971.72^{IT}	HQ231970	DQ825971
Brunneochlamydosporium terrestre	CBS 112777^{T}	LR025819	LR026690
Brunneomyces brunnescens	CBS 559.73^{T}	HQ231966	LN810520
Brunneomyces europaeus	CBS 652.96^{T}	LN810512	LN810519
Brunneomyces hominis	FMR 10429^{T}	LN810509	KP131517
Chlamydosporiella restricta	CBS 178.40^{T}	LR025822	LR026693
Chlamydosporiella restricta	CBS 443.66	LR025824	LR026695
Chordomyces albus	CBS 987.87^{T}	JX158444	DQ825970
Chordomyces albus	CBS 299.70E	LR025830	LR026701
Chordomyces antarcticus	CBS 120045^{T}	KJ443109	KJ443241
Colletotrichum fructicola	LC0032	JN940418	JN943079
Colletotrichum gloeosporioides	LC0555	JN940412	JN943090
Furcasterigmium furcatum	CBS 299.70C	MH871416	MH859660
Furcasterigmium furcatum	CBS 122.42^{T}	LR025838	LR026709
Furcasterigmium furcatum	CBS 299.70A	LR025839	LR026710
Furcasterigmium furcatum	CBS 116548	LR025842	LR026712
Furcasterigmium furcatum	CBS 116550	LR025843	LR026713
Furcasterigmium furcatum	JW 12002	LR590307	LR590130
Furcasterigmium furcatum	JW 125004	LR590308	LR590131
Furcasterigmium furcatum	JW 170003	LR590309	LR590132
Furcasterigmium furcatum	**MFLUCC 10–0282**	**KC775775**	**KC775774**
Fuscohypha expansa	CBS 418.89^{T}	LR025845	LR026715
Fuscohypha expansa	CBS 103.95	LR025844	LR026714
Gibellulopsis fusca	CBS 560.65^{T}	LR025854	LR026724
Gibellulopsis nigrescens	CBS 120949^{NT}	LR025857	LR026727
Gibellulopsis serrae	CBS 290.30^{T}	LR025872	LR026742
Lectera colletotrichoides	IMI 303685	LR025894	JQ647450
Lectera humicola	IMI 265740^{T}	LR025896	JQ647449
Lectera phaseoli	IMI 366179^{T}	LR025898	JQ693168
Musicillium elettariae	CBS 252.80^{T}	LR025899	LR026765

(Continued)

Table 1 (continued).

Taxa	Culture Accession No.	GenBank Accession No.	
		LSU	ITS
Musicillium theobromae	CBS 968.72^{NT}	LR025907	LR026773
Musicillium tropicale	CBS 120009^{T}	LR025917	LR026783
Musidium stromaticum	CBS 863.73^{T}	MH872546	MH860814
Musidium stromaticum	CBS 132.74	LR025919	LR026785
Nigrocephalum collariferum	CBS 124586^{T}	MH874911	MH863392
Nigrocephalum collariferum	CBS 124585	LR025928	FJ765365
Paragibellulopsis chrysanthemi	MAFF 242621^{T}	KC287230	KC287235
Paragibellulopsis chrysanthemi	MAFF 243429	KC287229	KC287234
Paramusicillium asperulatum	CBS 120158^{T}	LR025930	LR026792
Phialoparvum bifurcatum	CBS 299.70B^{T}	LR025931	LR026793
Phialoparvum maaspleinense	JW 266001^{T}	LR590368	LR590190
Plectosphaerella cucumerina	CBS 137.37^{T}	MH867359	MH855856
Plectosphaerella plurivora	CBS 131742^{T}	LR025967	LR026829
Sayamraella subulata	BCC 78964^{T}	LR025971	LR026833
Sodiomyces alcalophilus	CBS 114.92^{IT}	JX158443	JX158421
Sodiomyces alkalinus	CBS 110278^{T}	JX158427	NR_145378
Sodiomyces tronii	CBS 137618^{T}	KJ443147	KJ443277
Stachylidium bicolor	CBS 121802^{ET}	LR025972	LR026834
Stachylidium pallidum	BCC 79031	LR025973	LR026835
Summerbellia oligotrophica	CBS 657.94^{T}	LR025849	LR026719
Summerbellia oligotrophica	CBS 299.70G	LR025846	LR026716
Theobromium fuscum	CBS 112271^{T}	LR025976	LR026839
Verticillium dahliae	CBS 130341^{ET}	LR026028	LR026889
Verticillium longisporum	CBS 124.64^{T}	LR026040	LR026901
Verticillium tricorpus	CBS 447.54^{T}	LR026083	LR026944

The newly generated sequence is indicated in bold. ^{T}Ex-type, ^{ET}Ex-pitype, ^{IT}Ex-sotype, ^{NT}Ex-eotype. BCC: BIOTEC Culture Collection, Pathumthani, Thailand; CBS: Culture collection of the Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; FMR: Faculty of Medicine of Reus, Reus, Spain; IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, UK; JW: Johanna Westerdijk Collection, Utrecht, The Netherlands; LC: Working collection of Lei Cai, housed at the Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; MAFF: Ministry of Agriculture, Forestry and Fisheries, Ibaraki, Japan; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand.

alignment and tree were deposited in TreeBASE, submission ID 25582 (Study Accession URL: http://purl.org/phylo/treebase/phylows/study/S25582). Phylogenetic analyses of both the individual and combined dataset were carried out using maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI) analyses.

A ML analysis was generated by raxmlGUI v.1.3 [29] using ML + rapid bootstrap setting with 1000 replicates. A MP analysis was conducted in PAUP v.4.0b 10 [30] using the heuristic search option with 1,000 random replicates and maxtrees set as 1000. Alignment gaps were treated as missing characters.

The branches of zero length were collapsed and all equally parsimonious trees were saved. Clade stability was evaluated using a bootstrap (BT) analysis with 1000 replicates, each with 10 replicates of random stepwise addition of taxa [31]. Tree Length [TL], Consistency Index [CI], Retention Index [RI], Relative Consistency Index [RC] and Homoplasy Index [HI] were analyzed for all trees. The Kishino-Hasegawa tests [32] were used to check whether the trees inferred under different optimality criteria were significantly different. The BI analysis was generated by MrBayes v3.1.2 using Markov chain Monte Carlo sampling (BMCMC) to assess posterior probabilities [33,34]. Six simultaneous Markov chains were run for 2000000 generations and trees were sampled every 200th generation. The first 10% generated trees were discarded after checking the effective sampling size (ESS) using the Tracer v. 1.6 [35]. While the remaining 90% of trees were applied for calculating the posterior probability (PP) of the majority rule consensus tree. Phylograms were observed in FigTree v1.4.0 program [36] and reorganized in Adobe Photoshop CS6 software (Adobe Systems, USA).

3 Results

3.1 Phylogenetic Analyses

The combined LSU and ITS sequence dataset including our strain and other related taxa in Plectosphaerellaceae comprised 58 taxa (Fig. 1). Phylogenetic analyses obtained from ML, MP and BI analyses show similar topologies and were not significantly different. The RAxML analysis of the combined dataset yielded a best scoring tree (Fig. 1) with a final ML optimization likelihood value of –8388.191939. The matrix had 453 distinct alignment patterns, with 4.37% of undetermined characters or gaps. Parameters for the GTR + I + G model of the combined LSU and ITS were as follows: Estimated base frequencies; A = 0.231405, C = 0.264478, G = 0.296765, T = 0.207353; substitution rates AC = 1.048443, AG = 1.746751, AT = 2.332002, CG = 0.591076, CT = 5.613633, GT = 1.000000; gamma distribution shape parameter α = 0.198778. The maximum parsimony dataset consists of 1353 characters, including 918 constant characters, 40 variable parsimony-uninformative characters and 395 parsimony-informative characters. The most parsimonious tree showed, TL = 1287, CI = 0.501, RI = 0.777, RC = 0.389, HI = 0.499. The new strain clustered with the type strains (CBS 122.42) and other isolates of *F. furcatum* (100% ML, 100 % MP and 1.00 PP) (Fig. 1).

3.2 Taxonomy

Furcasterigmium furcatum (W. Gams) A. Giraldo & P.W. Crous, Studies in Mycology 92: 227–286 (2019). (Figs. 2 and 3)

Index Fungorum Number: IF 828042; *Facesoffungi Number*: FoF 07081

Holotype: MFLU 12−2222

Saprobic on dead leaves of *Magnolia liliifera*. **Sexual morph:** *Ascomata* solitary, immersed to semi-immersed, becoming erumpent, perithecial, black, papillate. *Papilla* central, black, conical. *Paraphyses* widest at the base up to 8. µm and narrowest at the end up to 3 µm, septate, unbranched. *Asci* 47–61 × 5–10 µm ($\bar{x}$ = 53 × 8 µm), 8-spored, unitunicate, cylindrical, clavate, thin-walled, swollen in the centre in squash mount, with a short pedicel, no apical ring observed in Melzer's reagent. *Ascospores* 8–11 × 2–3 µm ($\bar{x}$ = 3 × 9 µm), uniseriate at the base, overlapping uniseriate to biseriate in the main part, cylindrical with slightly narrowing ends, hyaline, one-celled, with several guttules, rough-walled, surrounded by a gelatinous sheath, 1.5–2.4 thick ($\bar{x}$ = 2 µm). **Asexual morph:** Hyphomycetous. *Conidiophore* hyaline, unbranched, commonly proliferating sympodially. *Conidiogenous cell* 5–42 µm long, 1.5–3 µm wide at the base, with cylindrical collarette, and a conspicuous periclinal thickening at the conidiogenous locus, commonly with a percurrent proliferation, polyphialidic with up to three conidiogenous loci. *Conidia* broadly ellipsoidal, concave in the middle and thickening toward the end, one cell, hyaline, smooth- and thin-walled, 1.8–3.3 × 1.3–2.3 µm ($\bar{x}$ = 2.2 × 1.7 µm), arranged in slimy heads. *Chlamydospore* terminal or intercalary, mostly in chains, ellipsoidal to pyriform, smooth– and thick-walled, 12–23 × 3–5 µm ($\bar{x}$ = 16 × 4 µm).

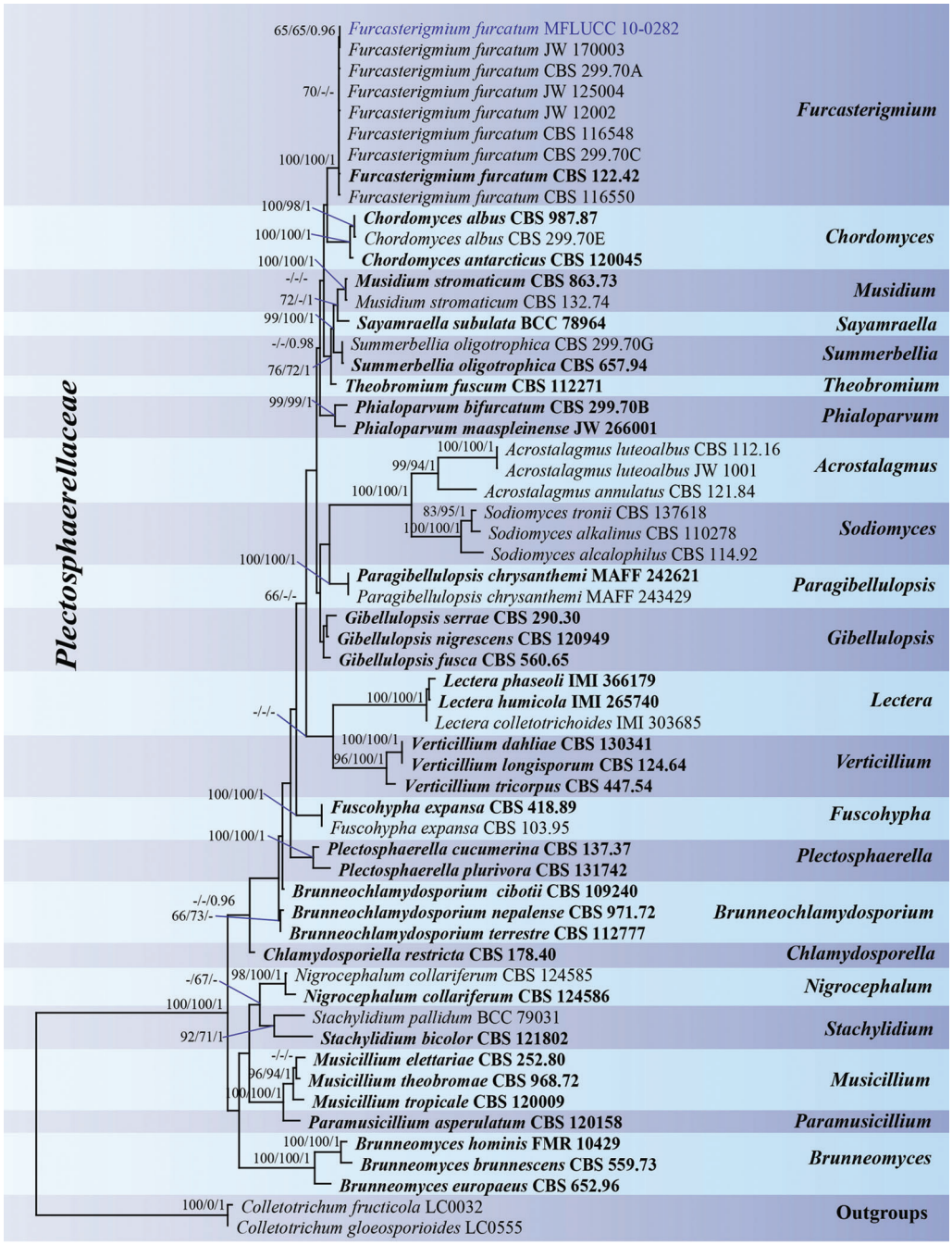

Figure 1: Phylogenetic tree obtained from RAxML analyses of combined LSU and ITS sequence data. Bootstrap support values for ML, MP equal or greater than 65% and PP greater than 0.95 are indicated at the nodes. Ex-epitype, Ex-isotype, Ex-neotype and Ex-type strains are in bold and the new isolate of this study is in dark blue. The tree is rooted to *Colletotrichum fructicola* (LC0032) and *C. gloeosporioides* (LC0555)

Culture characteristics: Colonies on sabouraud dextrose agar (SDA) effuse, mostly superficial, white, 10 mm diam in 15 days at 28°C. Mycelium mucoid, irregular, crenated edge, no pigment diffusing into agar. Asexual morph sporulated after two months.

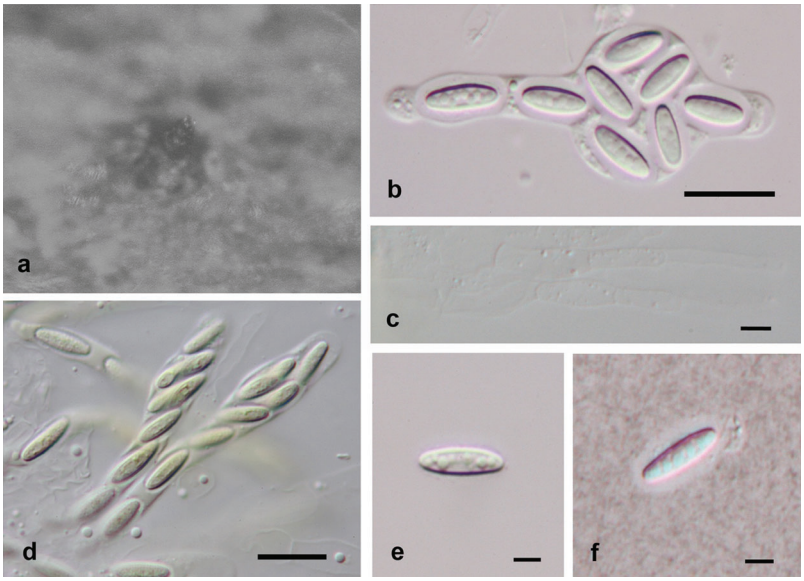

Figure 2: Sexual morph of *Furcasterigmium furcatum* (MFLUCC 12−2222). (a) Ascoma on the host surface. Note the papilla. (b) Ascus in wet mount slide by squashing. (c) Paraphyses. (d) Asci in Melzer's reagent with no visible apical ring. (e) Ascospore. (f) Ascospore in India ink. Scale bars: (b−d) = 10 µm, c = 5 µm, (e−f) = 3 µm

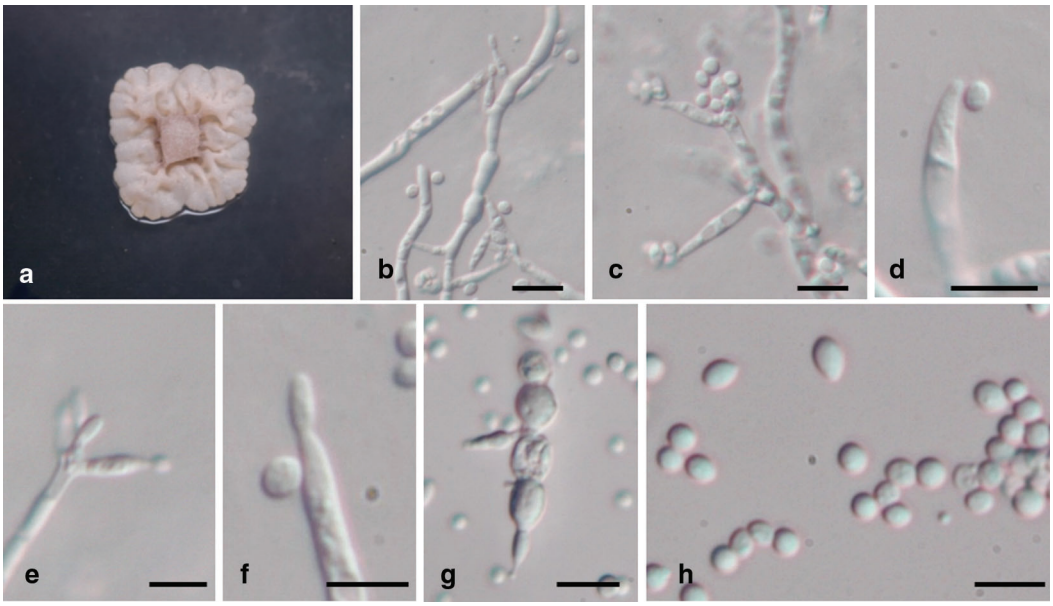

Figure 3: Asexual morph of *Furcasterigmium furcatum* (MFLUCC 10−0282). (a) Colony on SDA after 15 days at 28°C. (b−c) Conidiophores. (d–f) Conidiogenous cells. (g) Chlamydospores. (h) Conidia. Scale bars: (a−h) = 5 µm

Material examined: THAILAND: Chiang Mai, Doi Suthep-Pui forest, on dead leaves of *Magnolia liliifera* (L.) Baill. (Magnoliaceae), 11 January 2010, J. Monkai (MFLU 12−2222), living culture, MFLUCC 10–0282.

Notes: our strain belongs to *F. furcatum* The sexual morph of *F. furcatum* is similar to *Plectosphaerella cucumeris* and *P. plurivora*, but differs in having paraphyses and ascospores with a gelatinous sheath [4,10]. The sexual morph of *F. furcatum* is compared to other related species in Plectosphaerellaceae (Tab. 2). The asexual morph of our strain is similar to the type strains of *F. furcatum* (CBS 122.42) [11]. However, our strain has broadly ellipsoidal conidia with a slightly different size [*F. furcatum* MFLUCC 10–0282, 1.8–3.3 × 1.3–2.3 µm *vs.* 2.7–3.8 × 1.5–2.1 µm, *F. furcatum* CBS 122.42] and the production of chlamydospores in cultures in our strain [11]. However, the asexual characters of the type strain were observed on malt extract agar (MEA). *Chordomyces albus*, *Phialoparvum bifurcatum* and *Theobromium fuscum* were previously identified as *A. furcatum* [5,11]. However, they are phylogenetic distant and these species differ from *F. furcatum* in having polyphialides with up to two conidiogenous loci [11]. The asexual morph of *F. furcatum* is compared to other related species in Plectosphaerellaceae (Tab. 3).

Table 2: Synopsis of the sexual morph species in Plectosphaerellaceae discussed in this study

Species	Ascomata	Paraphyses	Asci	Ascospores	References
Furcasterigmium furcatum	Perithecial solitary, immersed to semi-immersed, becoming erumpent	Septate, unbranched, 8 µm widest at the base and 3 µm narrowest at the end	Cylindrical, clavate, 47–61 × 5–10 µm, swollen in the centre in squash mount, no apical apparatus	Cylindrical with slightly narrowing ends, 1-celled, 8–11 × 2–3 µm, gelatinous sheath present	This study
Plectosphaerella cucumerina	Globose to pyriform, 90–130 µm wide	Absent	Cylindrical 50–80 × 6–9 µm, no apical apparatus	Ellipsoid, both ends rounded, 2-celled, (9–) 10.5–14(–15) × 2.5–3(–4) µm	[4]
P. plurivora	Perithecial solitary or gregarious, superficial, subglobose to pyriform, 100.3–209 × 86–156 µm	Absent	Clavate, 31.4–43 × 6.2–8.2 µm, no apical apparatus	Ellipsoidal, 1– or 2-celled, 6.1–13.2 × 2.4–3.7 µm	[11]
Sodiomyces alkalinus	Cleistothecial, 120–150 µm wide	Absent	Saccate, scattered irregularly in the ascocarp, no apical apparatus	Ellipsoidal or ovoid, 2-celled, 12–15× 5–7 µm	[15]

4 Discussion

This study is the first report of the sexual morph of *Furcasterigmium furcatum* in the family Plectosphaerellaceae and is supported by the molecular evidence. Strains of *F. furcatum* are commonly isolated from soil [11,20]. However, this strain was isolated from moist house and also as an endophyte of *Vitis vinifera* [11]. The distribution of *F. furcatum* was restricted to Europe with reports of this species

Table 3: Synopsis of the asexual morph species in Plectosphaerellaceae discussed in this study

Species	Basionym (previous identification)	Conidiophores	Conidiogenous cell	Conidia	Chlamydospore	References
Furcasterigmium furcatum	*A. furcatum*	Unbranched, proliferating sympodially	Phialides subulate, 18–36 × 2–2.5 µm, cylindrical collarette, polyphialides with up to three conidiogenous loci	Ellipsoidal, 1-celled, 2.7–3.8 × 1.5–2.1 µm, arranged in slimy heads	–	[11]
Brunneochlamydosporium nepalense	*Acremonium nepalense*	Simple or poorly branched	Phialides cylindrical or subulate, 25–55 × 2–2.5 µm, minute cylindrical collarette, polyphialides with up to two conidiogenous loci	Cylindrical with rounded ends to ellipsoidal, 1-celled, 3.2–4.7 × 1.9–2.4 µm, arranged in slimy heads	Lateral, terminal, solitary, in pairs, subglobose or irregularly shaped 4.4–5 × 3.5–3.6 µm	[11]
Chlamydosporiella restricta	*Verticillium dahliae f. restrictum*	Unbranched or basitonously branched	Phialides cylindrical, slightly wavy at the apex, 22.7–45 × 1.5–2 µm, short collarette	Obovoid, widely ellipsoidal with apiculate base, 1-celled, 2.2–4.7 × 1.5–2.3 µm, arranged in slimy heads	Terminal or intercalary, single or branched chains, subglobose, 3–5.6 × 2.3–5.6 µm	[11]
Chordomyces albus	*A. furcatum*	Unbranched, bearing 3–4 phialides	Phialides cylindrical or subulate, 12–22 × 2–2.5 µm, cylindrical collarettes	Ellipsoidal to near cylindrical, 1-celled, 3–4 × 2–2.5 µm, arranged in slimy heads	–	[11]
Musidium stromaticum	*A. stromaticum*	Unbranched or basitonously branched	Phialides subulate, 23–55 × 2–2.5 µm, cylindrical collarette, percurrent proliferation	Cylindrical with rounded ends or ellipsoidal, 1-celled, 4.2–6.2 × 1.4–2.3 µm, arranged in slimy heads	Stromatic hyphae branched	[11]
Nigrocephalum collariferum	*A. collariferum*	Simple or basitonously branched	Phialides sub-cylindrical to subulate, slightly wavy at the apex, 17–51.5 × 1.5–2.5 µm, conspicuous funnel-shaped collarette, percurrent proliferation	Widely ellipsoidal, concave in lateral view, 1-celled, 2.9–5 × 2.1–2.7 µm, pale brown to brown, arranged in slimy heads	–	[11]

(Continued)

Table 3 (continued).

Species	Basionym (previous identification)	Conidiophores	Conidiogenous cell	Conidia	Chlamydospore	References
Phialoparvum bifurcatum	*A. furcatum*	Unbranched or poorly branched	Phialides subulate to ampulliform, 8–15 × 1.5–2.7 µm, cylindrical collarette, polyphialides with up to two conidiogenous loci	Cylindrical, 1-celled, 2.8–4.4 × 1.2–1.8 µm, arranged in slimy heads	–	[11]
Plectosphaerella cucumerina	*Venturia cucumerina*	Unbranched or rarely irregularly branched	Phialides cylindrical, 6–10 × 35–69 µm, cylindrical collarette	Ellipsoidal, tapering gradually to rounded apex and base, widest in the middle, septate or aseptate, aseptate conidia 6.7–7 × 2.7–2.8 µm, septate conidia 8.6–8.9 × 2.8–2.9 µm, arranged in slimy heads	–	[4]
Sayamraella subulata	–	Unbranched or poorly branched, proliferating sympodially	Phialides subulate, 0.3–73.7 × 2.1–3 µm, polyphialides with up to two conidiogenous loci	Ellipsoidal, 1-celled, 3.6–4.7 × 1.7–2.4 µm, arranged in slimy heads	–	[11]
Summerbellia oligotrophica	*Gliocladium cibotii*	Long	Phialides subcylindrical, 13–50 × 1.5–2 µm, minute cylindrical collarette	Ellipsoidal or cylindrical, 1-celled, 2.3–4.3 × 1.2–2 µm, arranged in slimy heads	Terminal or intercalary, mostly in chains, subglobose, 3–4 × 3–4 µm	[11]
Theobromium fuscum	*A. furcatum*	Unbranched or basitonously branched, bearing up to two phialides, proliferating sympodially	Phialides subulate, 23–38 × 2–3 µm, minute cylindrical collarette, polyphialides with up to two conidiogenous loci	Cylindrical or ellipsoidal, 1-celled, 2.7–4.1 × 1.3–2 µm, arranged in slimy heads	–	[11]

from France, Germany Italy, and the Netherlands [8,11,20]. Our study reports the first record of *Furcasterigmium* from dead leaves of *Magnolia liliifera* and the first geographic distribution for Thailand.

The identification of species in Plectosphaerellaceae based on only the asexual morph is difficult as morphological characters in culture can differ in different culture media [11]. Combination of sexual and asexual morph characters together with DNA sequence data can help to improve the taxonomic concept of the species in the family Plectosphaerellaceae. This study provides a good example for the connection of sexual and asexual morphs with supporting phylogenetic analyses.

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