



รายงานวิจัยฉบับสมบูรณ์

โครงการ ศึกษาความหลากหลายและการจัดจำแนกเชื้อรา

Hyphomycetes ในเขตร้อน

(Diversity and classification of Hyphomycetes in the tropics)

By

Dr. Saranyaphat Boonmee

October 2020

Contract No. TRG6180001

รายงานวิจัยฉบับสมบูรณ์

โครงการ ศึกษาความหลากหลายและการจัดจำแนกเชื้อรา
Hyphomycetes ในเขตร้อน
(Diversity and classification of Hyphomycetes in the tropics)

Researcher

Dr. Saranyaphat Boonmee

Mae Fah Luang University

สนับสนุนโดยสำนักงานคณะกรรมการการอุดมศึกษา และสำนักงานกองทุนสนับสนุนการวิจัย

(ความเห็นในรายงานนี้เป็นของผู้วิจัย สกอ. และ สกว. ไม่จำเป็นต้องเห็นด้วยเสมอไป)

บทคัดย่อ

ประเทศไทยเป็นประเทศในเขตโซนร้อนและมีสภาพภูมิประเทศตั้งอยู่ในกลุ่มอินโด – เบอร์มีส (Indo-Burma biodiversity hotspot) เป็นบริเวณที่มีความหลากหลายของพันธุ์พืชนานาชนิด ด้วยสภาพภูมิอากาศอบอุ่นถึงร้อนชื้นนี้ส่งผลให้เกิดความหลากหลายของจุลินทรีย์นานาชนิดรวมถึงเชื้อรากลุ่ม Hyphomycetes งานวิจัยนี้ได้ทำการสำรวจและเก็บรวบรวมเชื้อรากลุ่ม Hyphomycetes ตั้งแต่ปี 2561 ถึง 2563 ภายใต้โครงการวิจัย “ศึกษาความหลากหลายและการจัดจำแนกเชื้อรา Hyphomycetes ในเขตร้อน” ได้เก็บเชื้อราจำนวน 185 taxa ซึ่งพบเป็นเชื้อราในคลาส Dothideomycetes และ Sordariomycetes และในจำนวน 100 taxa สามารถแยกเพาะเลี้ยงคัลเจอร์เจริญเติบโต ศึกษาลักษณะสัณฐานวิทยา และวิเคราะห์ข้อมูลลำดับพันธุกรรมเชื้อราแต่ละชนิด โดยข้อมูลลำดับโมเลกุลใช้รหัสบาร์โค้ด ได้แก่ ยีน ITS, SSU, LSU และ TEF1-alpha หรือ RPB2 (กลุ่มยีนโปรตีน) วิเคราะห์ข้อมูลลำดับพันธุกรรมด้วยวิธีการทางสถิติในชีวสารสนเทศศาสตร์ ได้แก่ maximum parsimony (MP), maximum likelihood (ML) และ Bayesian posterior probabilities (BYPP) เชื้อรา Hyphomycetes บางส่วนที่จัดจำแนกสปีชีส์แล้วนั้นได้แก่ เชื้อราสกุลใหม่จำนวน 1 สกุล เชื้อราชนิดใหม่จำนวน 12 สปีชีส์ เชื้อรารวมชื่อสปีชีส์ใหม่จำนวน 1 สปีชีส์ และเชื้อราที่ถูกบันทึกเพิ่มใหม่จำนวน 8 สปีชีส์ (ในโฮสต์ใหม่และมีการกระจายทางภูมิศาสตร์ใหม่) เชื้อราที่พบและแต่งตั้งเป็นสกุลใหม่ คือ *Triseptata* (Latoruaceae) โดยใช้ลักษณะทางสัณฐานวิทยาซึ่งเป็นเอกลักษณ์เฉพาะในเชื้อราสกุลนี้ร่วมกับการวิเคราะห์ข้อมูลพันธุกรรม เชื้อราที่พบเป็นเชื้อราสปีชีส์ใหม่ได้แก่ *Camposporium thailandicum*, *Cladophialophora aquatica*, *Dictyocheiropsora taiwanense*, *Dictyocheiropsora pandanicola*, *Digitodesmium Chiangmaiense*, *Helminthosporium Chiangraiense*, *Mycoenterolobium aquadictyosporium*, *Pleurotheciella dimorphospora*, *Rhexoacrodictys nigrospora*, *Rostriconidium Cangshanense*, *Spegazzinia thailandica* และ *Triseptata sexualis* เชื้อรารวมสปีชีส์ใหม่ได้แก่ *Pseudobactrodesmium stilboideum* และเชื้อราที่ถูกบันทึกในโฮสต์ใหม่หรือมีการกระจายทางภูมิศาสตร์ใหม่ได้แก่ *Dictyocheiropsora aquadulcis*, *Dictyocheiropsora rotunda*, *Hermatomyces sphaericoides*, *Ernakulamia tanakae*, *Megacapitula villosa*, *Cladophialophora abundans*, *Phaeoisaria aquatic* และ *Rostriconidium pandanicola* ได้นำมาเสนอในรายงานนี้ ตลอดระยะเวลาการดำเนินงานวิจัยร่วม 2 ปีมีผลงานวิจัยที่ได้รับการตีพิมพ์ในกลุ่มวารสารระดับนานาชาติจำนวน 6 เรื่อง และผลงานวิจัยที่อยู่ระหว่างดำเนินการจัดเตรียมตีพิมพ์อีกจำนวน 1 เรื่อง

คำสืบค้น ความหลากหลาย, Hyphomycetes, ความสัมพันธ์เชิงวิวัฒนาการ, แซบโพรบ, อนุกรมวิธาน

Abstract

Thailand is a tropical country and constitutes part of the Indo-Burma biodiversity hotspot. With vast variety of tree species and varied vegetation types, this humid and warm belt provides a favorable niche for many taxa of hyphomycetous taxa. A survey on hyphomycetous fungi were carried out from 2018 to 2020 under the project “Diversity and classification of hyphomycetes in the tropics”. In total, 185 taxa from two classes Dothideomycetes and Sordariomycetes were collected and of these, 100 taxa were obtained culture, morphology and sequence data. Microscopic features and cultural characteristics of species were examined. Molecular sequence data used ITS, SSU, LSU and TEF1 α or RPB2 genes. Phylogenetic trees based on combined sequence datasets were performed using statistical methods in Bioinformatics i.e. maximum parsimony (MP), maximum likelihood (ML) and Bayesian posterior probabilities (BYPP). Partial results of this study, hyphomycetous taxa are described and illustrated with its sexual morph include one new genus, 12 new species, one new combination species and eight new records on new hosts and at new geographical distributions. One new genus *Triseptata* (Latoruaceae) is introduced based on their unique morphology and distinct phylogenetic lineages. Newly described species are *Camposporium thailandicum*, *Cladophialophora aquatica*, *Dictyocheiropsora taiwanense*, *Dictyocheiropsora pandanicola*, *Digitodesmium Chiangmaiense*, *Helminthosporium Chiangraiense*, *Mycoenterolobium aquadictyosporium*, *Pleurotheciella dimorphospora*, *Pseudobactrodesmium stilboideum*, *Rhexoacrodictys nigrospora*, *Rostriconidium Cangshanense*, *Spegazzinia thailandica* and *Triseptata sexualis*. New host or new geographical distribution records of *Dictyocheiropsora aquadulcis*, *Dictyocheiropsora rotunda*, *Hermatomyces sphaericoides*, *Ernakulamia tanakae*, *Megacapitula villosa*, *Cladophialophora abundans*, *Phaeoisaria aquatica*, *Rostriconidium pandanicola* are provided. During the two years’ project, six papers were published in SCI journals and one further paper is in preparation.

Keywords: Diversity, Hyphomycetes, Phylogeny, Saprobe, Taxonomy

Executive Summary

The project of “Diversity and classification of Hyphomycetes in the tropics” has been carried out in order to understand the diversity of hyphomycetes fungi in tropical lands. Since, October 2018 to March 2020 of 16 months, the time has been spent on collection, fungal identification, isolation the cultures, and molecular analysis. Hyphomycetous fungal specimens were random collected on non-living plants particularly dead wood, bark, twigs from different parts in Thailand i.e., eastern, northern and southern. Morphological examination and identification of all hyphomycetous fungi were made for the collected specimens of the superficial asexual morph structures. The ability to accurately identify fungi has advanced significantly with the use of molecular data. The phylogenetic analyses were followed in order to validate the taxonomic position of fungal species. Partial results of this study, we introduced six new species have been published in the international journals of six publications by three publications in Phytotaxa, two publications in Fungal Diversity and one publication in Mycological Progress journal. Furthermore, six new species and eight new host or geographical records are in manuscript preparation for publication.

Research content

Objectives

1. Exploring, identifying, describing and naming the poorly studied hyphomycete genera *Acrodictys*, *Dictyocheiropora*, *Dictyosporium*, *Digitodesmium*, *Kirschsteiniothelia*, *Monodictys* and *Moromyces*.
2. Provision of morphological illustration and taxonomy of hyphomycetes and to isolate strains for conservation in the culture collections of MFLU and other.
3. Emphasis on their major morphological characters, molecular study of selected taxa in order to establish their phylogeny, which will result in relatively high impact publications. This will apply in particular to new taxa.
4. Contribution of knowledge of hyphomycetes occurring from different habitats in the tropics.

Research methodology

Collection and isolation of fungi

During October 2018 to March 2020 of 16 months, the time has been spent on fungal collection, morphological identification, culture isolation, deposition of the cultures and molecular sequencing of genera *Acrodictys*, *Dictyosporium*, *Digitodesmium*, *Monodictys* and *Moromyces*. Fresh specimens were collected from various sites throughout Thailand i.e. northern (Chiang Rai, Chiang Mai, Phayao, Phrae, Lampang and Nan), northeastern (Phitsanulok, Loei, Nong Bua Lamphu, Mukdahan and Nakhon Phanom) and southern (Surat Thani, Nakhon Si Thammarat and Krabi). Morphological examination and identification were carried out from the fresh specimens including their sexual morphs. One hundred eighty-five (185) taxa were collected and morphologically examined, of these 100 taxa have been isolated and cultured. Out of 80 culture isolations based on morphologically distinct species were sequenced for phylogenetic identification (Table 1). The fungi were maintained in PDA and MEA for further examination and extraction of DNA for molecular analysis. All fungal materials have been isolated, cultured and deposited in MFLUCC, and dried permanent herbarium specimens were deposited in MFLU (Table 2).

Table 1. Research output

Expected output	Research indicates	Year 1		Year 2	
		1-6	7-12	13-18	10-24
Taxonomy	- Obtained 185 specimens	✓	✓	✓	
	- Isolated 100 taxa and obtained pure cultures	✓	✓	✓	✓
	- Morphological describes	✓	✓	✓	✓
	- Taxa identification				
Molecular analysis	- DNA sequencing of 80 isolates		✓	✓	✓
	- Phylogenetic analyses		✓	✓	✓
	- Taxonomic classification				
Knowledge	- Six papers (as first author, corresponding author and co-authors) were published or are in press in SCI journals and further papers are in preparation		✓	✓	✓

Table 2. Summary of 185 hyphomycetous taxa from various forest sites in Thailand

No.	Original code	Scientific name	Substrate	Ecological habitat	Location
1	LS03	<i>Megacapitula villosa</i>	Dead wood	Terrestrial	Chanthaburi
2	B01	<i>Distoseptispora</i> sp.	Dead wood	Terrestrial	Chiang Rai
3	B02	<i>Arthriniun</i> sp.	Dead wood	Terrestrial	Chiang Rai
4	B03	<i>Torula camporesii</i>	Dead wood	Terrestrial	Chiang Rai
5	NRS01	<i>Monodictys</i> sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
6	NRS03	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
7	NRS04	<i>Rhytidhysterion tectonae</i>	Dead wood	Terrestrial	Nakhon Si Thammarat
8	NRS05	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
9	S2-1	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
10	S2-2	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
11	S2-3	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
12	S4-4	Hyphomycete sp.	Dead wood	Terrestrial	Nakhon Si Thammarat
13	CTU1-1	<i>Zopfiella pilifera</i>	Dead wood	Submerge	Uttaradit
14	CTU10-1	Hyphomycete sp.	Dead wood	Submerge	Uttaradit
15	CTU9	Hyphomycete sp.	Dead wood	Submerge	Uttaradit
16	CTU13	Hyphomycete sp.	Dead wood	Terrestrial	Uttaradit
17	LP1	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
18	RU04	Hyphomycete sp.	Dead wood	Submerge	Chiang Mai
19	Tak1	Hyphomycete sp.	Dead wood	Submerge	Tak
20	TNO10	Hyphomycete sp.	Dead wood	Submerge	Chiang Rai

21	PSL13	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
22	TNM03-4	<i>Sporochisma</i> sp.	Submerged wood	Stream	Southern
23	TNML05-S1-1	<i>Sporochisma</i> sp.	Submerged wood	Stream	Southern
24	NO7(A)-S(PK)-1	<i>Canalisporium</i> cf. <i>caribense</i>	Submerged wood	River	Southern
25	TNM03-3	<i>Canalisporium</i> sp.	Submerged wood	Stream	Southern
26	SB-H6	<i>Canalisporium</i> sp.	Submerged wood	Stream	Southern
27	TNM03-1	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Southern
28	TM05-S1-1	Hyphomycete sp.	Submerged wood	Stream	Southern
29	SB-H5	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
30	SB-H4	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
31	SB-H1	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
32	SB-H2	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
33	MC37	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
34	MC32	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
35	MC26	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Chiang Mai
36	MC1	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
37	MC2	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
38	MC23	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
39	MC4	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
40	PSL 14-1	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
41	PSL 14-2	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
42	PSL 14-3	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
43	PSL 14-4	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
44	PSL 15-3	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
45	PSL 15-4	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
46	PA1	<i>Helicomycetes</i> sp.	Dead wood	Terrestrial	Phrae
47	PA2	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
49	PA3	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
50	PA4	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
51	PA5	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
52	PA6	<i>Monotosporella</i> sp.	Dead wood	Terrestrial	Phrae
53	LP3	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
54	LP4	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
55	LP5	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
56	PY1.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
57	PY2.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
58	PY3.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
59	PY4.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
60	PY5.H	<i>Digitodesmium</i> sp.	Dead wood	Terrestrial	Payao
61	PY6.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
62	PY7.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
63	PY8.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
64	PY9.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
65	PY10.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
66	PY11.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
67	PY12.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao

68	PY13.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
69	PY14.H	Hyphomycete sp.	Dead wood	Terrestrial	Payao
70	PL1	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
71	PL2	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
72	PL3	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
73	Ph1	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
74	B01.B	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
75	B02.B	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
76	B03.B	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
77	B04.B	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
78	DL1	<i>Petriella</i> sp.	Dead wood	Terrestrial	Chiang Rai
79	PR1	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
80	PR2	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
81	PR3	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
82	PR4	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
83	PR5	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
84	PR6	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
85	PR7	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
86	PR8	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
87	PR9	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
88	PR10	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
89	PR11	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
90	PR12	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
91	PR14	Hyphomycete sp.	Dead wood	Terrestrial	Phrae
92	DL2	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
93	DL3	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
94	DL4	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
95	DL5	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
96	DL8	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
97	CRR1	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
98	CRR2	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
99	CRB1	<i>Helminthosporium chiangraiense</i>	Dead wood	Terrestrial	Chiang Rai
100	CRB2	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
101	PL4	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
102	PL5	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
103	PL6	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
104	PL7	Hyphomycete sp.	Dead wood	Terrestrial	Lampang
105	CMM1	<i>Podosporium</i> sp.	Dead wood	Terrestrial	Chiang Mai
106	CMM3	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Mai
107	CMM4	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Mai
108	DL10	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
109	CHM1	<i>Canalisporium</i> sp.	Dead wood	Terrestrial	Chiang Mai
110	CHM2	<i>Berkleasium</i> sp.	Dead wood	Terrestrial	Chiang Mai
111	CBM3	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Mai
112	CBM5	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Mai
113	DL12	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai

114	LSP01	<i>Hermatomyces sphaericoides</i>	Dead wood	Terrestrial	Phetchabun
115	LSP02	<i>Ernakulamia tanakae</i>	Dead wood	Terrestrial	Phetchabun
116	LSP03	<i>Rhexoacrodictys nigrospora</i>	Dead wood	Terrestrial	Phetchabun
117	NKT01	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
118	NKT02	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
119	WNA01	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
120	WNA02	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
121	WNA03	<i>Spegazzinia thailandica</i>	Dead wood	Terrestrial	Phitsanulok
122	WNA04	Hyphomycete sp.	Dead wood	Terrestrial	Phitsanulok
123	DPC1	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
124	DPC2	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
125	DPC3	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
126	BMC1	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
127	BMC2	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
128	BMC3	Hyphomycete sp.	Dead wood	Terrestrial	Chiang Rai
129	ISAN17	<i>Mycoenterolobium aquadictyosporium</i>	Submerged wood	River	Phitsanulok
130	FWHY2	<i>Fuscosporella</i> sp.	Submerged wood	Stream	Phuket
131	FWHY1	<i>Pseudoxylomyces elegans</i>	Submerged wood	Stream	Phuket
132	SBHY1	<i>Monodictys</i> sp.	Submerged wood	Stream	Phuket
133	ISAN01	Hyphomycete sp. 1	Submerged wood	River	Phitsanulok
134	ISAN07	<i>Trichoderma</i> sp.	Submerged wood	River	Phitsanulok
135	ISAN15	<i>Ellisembia</i> sp.	Submerged wood	River	Phitsanulok
136	MCF73	<i>Phaeoisaria</i> sp.	Submerged wood	Stream	Phuket
137	WFW67	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
138	WF11	<i>Eurotiales</i> sp.	Submerged wood	Stream	Chiang Mai
139	WFW01	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
140	WFW05	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
141	WFW06	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
142	WFW08	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
143	WFW09	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
144	WFW10	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Nakhon Si Thammarat
145	WFW11	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
146	WFW12	<i>Xylomyces</i> sp.	Submerged wood	Stream	Nakhon Si Thammarat
147	WFW13	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
148	WFW16	<i>Ellisembia</i> sp.	Submerged wood	Stream	Nakhon Si Thammarat
149	WFW17	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
150	WFW20	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
151	WFW22	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
152	WFW23	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
153	WFW25	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
154	WFW35	Hyphomycete sp.	Submerged wood	Stream	Nakhon Si Thammarat
155	WFW41	Hyphomycete sp.	Submerged wood	Stream	Phuket
156	WFW43	<i>Xylomyces</i> sp.	Submerged wood	Stream	Phuket
157	WFW44	Hyphomycete sp.	Submerged wood	Stream	Phuket
158	WFW45	<i>Canalisporium</i> sp.	Submerged wood	Stream	Phuket
159	WFW46	Hyphomycete sp.	Submerged wood	Stream	Phuket

160	WFW49	Hyphomycete sp.	Submerged wood	Stream	Phuket
161	WFW51	Hyphomycete sp.	Submerged wood	Stream	Phuket
162	WFW54	Hyphomycete sp.	Submerged wood	Stream	Phuket
163	WFW58	Hyphomycete sp.	Submerged wood	Stream	Phuket
164	WFW60	<i>Dictyochaeta</i> sp.	Submerged wood	Stream	Phuket
165	WFW69	<i>Fuscosporella</i> sp.	Submerged wood	Stream	Phuket
166	WFW75	<i>Fuscosporella</i> sp.	Submerged wood	Stream	Phuket
167	WFW57	Hyphomycete sp.	Submerged wood	Stream	Phuket
168	WF-HEL	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Chiang Mai
169	WF65	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Chiang Mai
170	WF64	<i>Helicomycetes</i> sp.	Submerged wood	Stream	Chiang Mai
171	WF65	<i>Fuscosporella</i> sp.	Submerged wood	Stream	Chiang Mai
172	WF62	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
173	WF61	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
174	WF58	Hyphomycete sp.	Submerged wood	Stream	Chiang Mai
175	TFW1	Hyphomycete sp.	Submerged wood	Stream	Phuket
176	TFW2	<i>Canalisporium</i> sp.	Submerged wood	Stream	Phuket
177	MRC01	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
178	MRC02	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
179	MRC07	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
180	MRC10	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
181	MRC11	<i>Xylomyces</i> sp.	Submerged wood	Pond	Chiang Mai
182	MRC16	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
183	MRC18	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
184	MRC22	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai
185	MRC26	Hyphomycete sp.	Submerged wood	Pond	Chiang Mai

Molecular analysis

DNA extraction, PCR amplification, and sequencing

Fungal mycelia from pure cultures grown in MEA for 30 days were scraped using sterilized scalpel and kept in a 1.5 mL microcentrifuge tube. Genomic DNA was extracted using the Biospin Fungus Genomic DNA Extraction kit (BioFlux®, China) following the manufacturer's protocol. Polymerase chain reaction (PCR) was used to amplify five genes: the large subunit (28SrDNA), small subunit (18SrDNA), internal transcribed spacers (ITS1-5.8S-ITS2) translation elongation factor 1-alpha (TEF1- α) and DNA-dependent RNA polymerase II second largest subunit (RPB2). The 28SrDNA was amplified using the primers LROR and LR5 (Vilgalys and Hester, 1990) while 18SrDNA was amplified using the primers NS1 and NS4 (White et al. 1990). For ITS, primers ITS5 and ITS4 were used (White et al. 1990). The TEF1- α was amplified using primers EF1-983F and EF1-2218R (Rehner and Buckley 2005) while RPB2 was amplified using primers fRPB2-5F/fRPB2-7cR (Liu et al. 1999). Polymerase chain reaction was performed in a volume of 25 μ l, which contained 12.5 μ l of 2 $\times$ Power Taq PCR

MasterMix (Bioteke Co., China), 1 µl of each primer (10 µM), 1 µl genomic DNA, and 9.5 µl deionized water. The PCR thermal cycle program for LSU, SSU and TEF1- α amplification were as follows: initial denaturing step of 94 °C for 3 min, followed by 40 cycles of denaturation at 94 °C for 45 seconds, annealing at 56 °C for 50 seconds, elongation at 72 °C for 1 min, and final extension at 72 °C for 10 min. The PCR thermal cycle program for the RPB2 include initial denaturing step of 95 °C for 5 min, followed by 40 cycles of denaturation at 95 °C for 1 min, annealing at 52 °C for 2 min, elongation at 72 °C for 90 seconds, and final extension at 72 °C for 10 min. Agarose gel electrophoresis was done to confirm the presence of amplicons at the expected molecular weight. PCR products were purified and sequenced with the primers mentioned above at a commercial sequencing provider (BGI, Ltd., Shenzhen, China). A BLAST search of the newly generated sequences was carried out to exclude contamination and to search for related taxa in GenBank database (www.ncbi.nlm.nih.gov/blast/).

Phylogenetic analysis

Original sequences will be checked using BioEdit version 7.0.5.3. The homogenous sequences will obtain by BLAST searches from GenBank. Alignments for each locus will be done in MAFFT v7 online version and manually verified in BioEdit. Bayesian inference (BI), maximum parsimony (MP) and maximum likelihood (ML) will be used in this study for phylogenetic analyses. For Bayesian inference analysis, the best model of evolution will be determined. Bayesian inference analysis will be done with MrBayes v 3.2.6. Maximum parsimony analysis will be performed in PAUP*4.0b10. Maximum likelihood analysis will be performed in CIPRES web portal. Phylogenetic trees will be drawn with TreeView 1.6.6 or FigTree v1.4.3.

All new sequences were assembled based on the closest matches from the BLAST search results and from recently published. Sequences generated from the three genes were analyzed along with other sequences retrieved from GenBank. Sequence datasets, one for each gene, were aligned with MAFFT v. 7 using the web server (<http://mafft.cbrc.jp/alignment/server>; Katoh et al. 2019). Alignment was further refined manually using BioEdit v.7.0.9.0 (Hall 1999). The online tool “ALTER” (Glez-Peña et al. 2010) was used to convert the alignment file to Phylip format. Phylogenetic analysis of individual and combined gene data was performed using maximum likelihood (ML) and Bayesian inference (BI). Maximum-parsimony [MP] analyses were performed using the heuristic search option with 1000 random taxa addition and tree bisection and reconnection

(TBR) as the branch-swapping algorithm in PAUP in CIPRES web portal (Swofford 2002, Miller et al. 2010). All characters were unordered and of equal weight and gaps were treated as missing data. Maxtrees were unlimited, branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. Clade stability was assessed using a bootstrap (BS) analysis with 1000 replicates, each with ten replicates of random stepwise addition of taxa (Hillis and Bull 1993). Descriptive tree statistics for parsimony (tree length [TL], consistency index [CI], retention index [RI], relative consistency index [RC], and homoplasy index [HI]) were calculated for trees generated under different optimality criteria.

Maximum likelihood analysis was performed using RAxML v. 8 software on the CIPRES web portal (Stamatakis 2006; Stamatakis et al. 2008, 2014) (<http://www.phylo.org/portal2/>; Miller et al. 2010). The GTR+GAMMA model of nucleotide evolution was used. RAxML rapid bootstrapping of 1000 replicates was performed. Bayesian inference analysis was performed using MrBayes v. 3.2.6 on XSEDE at the CIPRES webportal (Ronquist and Huelsenbeck 2003), using the parameter setting of 2 parallel runs, 4 chains, run for 4000000 generations at which point the standard deviation of split frequencies was below 0.01. Trees were sampled every 1,000 generations and all other parameters were left as default. Newly generated sequences were deposited in GenBank

Phylogenetic analysis and identification of hyphomycetous fungi

The new sequences conducted in this study were blasted to check for related taxa in GenBank database (www.ncbi.nlm.nih.gov/blast/). Hyphomycetous taxa from different families and orders were included in the analyses. Sequences were aligned using MAFFT and alignments were visually checked and manually improved. Phylogenetic analyses were performed by using PAUP v. 4.0b10 for maximum-parsimony (MP), CIPRES web portal for maximum likelihood (ML) via RAxML and Bayesian (BYPP) analyses. Trees rooted to appropriate outgroup taxa. Phylogenetic trees of some hyphomycetous taxa were illustrated and resulted here.

Results of phylogenetic analyses and morphological identifications of hyphomycetes fungi

A part of hyphomycetous taxa from the 185 collections, 100 isolations and 21 species epithets based on are given below in Figures 1–38.

Dictyosporiaceae Boonmee & K.D. Hyde

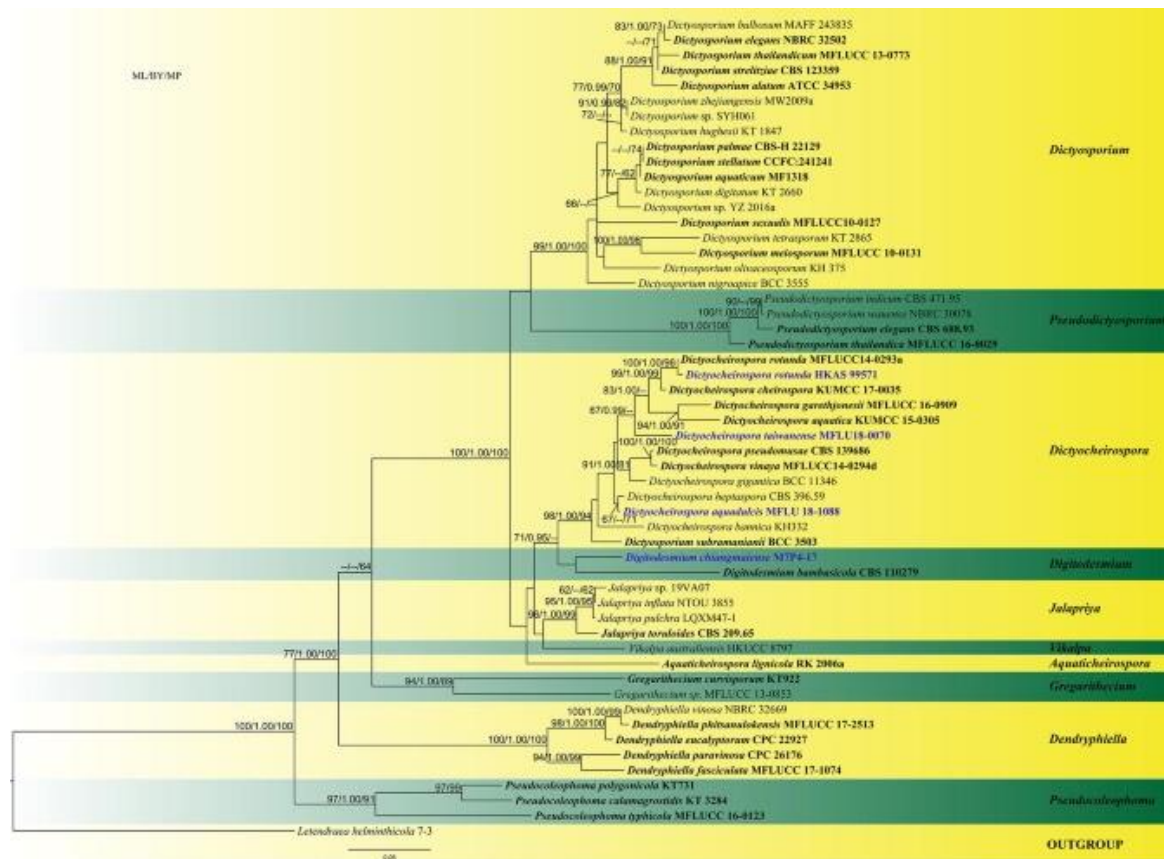


Figure 1. Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequences data in Dictyosporiaceae. Related sequences are taken from Boonmee et al. (2016) and Wang et al. (2016). Fifty-three strains are included in the combined analyses which comprise 1405 characters (553 characters for ITS, 852 characters for LSU) after alignment. *Letendraea helminthicola* (7-3) (Montagnulaceae, Pleosporales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis and the maximum parsimony analysis. The best RAXML tree with a final likelihood value of – 8736.227244 is presented. The matrix had 523 distinct alignment patterns, with 18.97% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241508, C = 0.237486, G = 0.270256, T = 0.250751; substitution rates AC = 2.173342, AG = 3.473225, AT = 3.246966, CG = 0.531302, CT = 36.318285, GT = 1.000000; gamma distribution shape parameter α = 0.567927. Maximum parsimony analysis of 981 constant characters and 292 informative characters resulted in two equally most parsimonious trees of 1392 steps (CI = 0.486, RI = 0.744 RC = 0.361, HI = 0.514). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 60 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or

greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue.

Dictyocheiросpora M.J. D'souza, Boonmee & K.D. Hyde

Dictyocheiросpora aquadulcis Sorvongxay, S. Boonmee & K.D Hyde, Figure 2

Index Fungorum number: IF556308; Facesoffungi number: FoF05963

Etymology: From the Latin *aquadulcis* (aqua = water and dulcis = sweet, in reference to its freshwater habitat.

Holotype: MFLU 18-1088

Saprobic on decaying, submerged wood in freshwater. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate, superficial, scattered. Mycelium immersed, branched, septate, pale brown, smooth-walled. *Conidiomata* 117–412 µm diam., slightly, pulvinate, dark brown. *Conidiophores* micronematous, undifferentiated from vegetative hyphae. *Conidiogenous cells*, holoblastic, integrated, terminal, pale brown. *Conidia* 60–80 µm × 17–29 µm, solitary, cheiroid, ellipsoid to cylindrical, rounded at the apex, consisting of 7 rows of cells, with each row composed of 11–14 cells, with rows digitate, cylindrical, inwardly curved at apex, arising from a basal cell, euseptate, slightly constricted at septa, brown, smooth-walled.

Culture characteristics: Conidia germinated on WA within 24 h. Colonies on MEA reaching 0.2–0.5 cm diam., in 5 days at 25 °C, with wavy margins, initial white and later becoming gray.

Material examined: THAILAND, Pha Yao Province, on decaying wood, in flowing freshwater stream, 11 September 2017, Saranyaphat Boonmee (PK12), (MFLU 18-1088, **holotype**), ex-type living culture (MFLUCC 17-2571).



Figure 2. *Dictyocheirospora aquadulcis* (MFLU 18–1088, **holotype**).

Dictyocheirospora rotunda M.J. D'souza, Bhat & K.D. Hyde, Figure 3

Facesoffungi number: FoF05063;

Saprobic on dead wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiomata* punctiform, sporodochial, velvety, brown to dark brown. *Mycelium* superficial, with brown, smooth, septate, branched hyphae. Conidiophores micronematous, pale brown. *Conidiogenous cells* 5–8 × 6–9 µm, holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* 16–29 × 47–62 µm, solitary, monoblastic, acrogenous, cheiroid, pale brown to brown, consisting of 6–8 rows of cells, rows digitate,

cylindrical, inwardly curved at the tip, arising from a basal cell, each arm composed of 7–9-septated, constricted at septa.

Culture characteristics: Ascospores germinating on PDA (potato dextrose agar) within 1 week at 23 °C. Sporulation after 30 days, colony 1.5 cm diam. Initially, orange from above and reverse, becoming brown, with concentric zonation, with irregular form of margin, filamentous mycelium, with rough surface and raised elevation.

Material examined: CHINA, Yunnan Province, Kunming, Songhuaba Lake, on dead wood, 3 September 2017, S.K. Huang (KUN-HKAS 99571, **new geographical record**), living culture (KUMCC 18-0014).

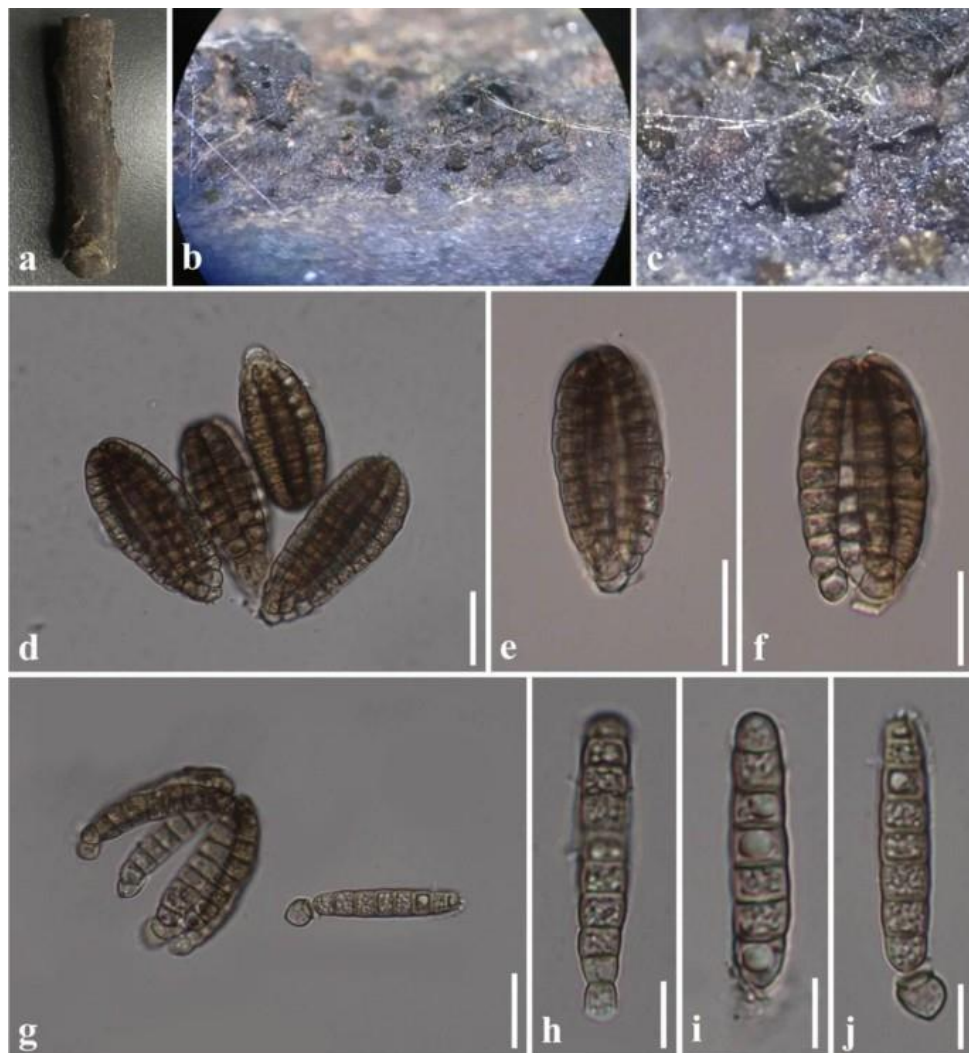


Figure 3. *Dictyocheirospora rotunda* (HKAS 99571, **new geographical record**).

Dictyocheirospora taiwanense Tennakoon, C.H. Kuo & K.D. Hyde, Figure 4

Index Fungorum number: IF556309; Facesoffungi number: FoF05964

Etymology: Named after Taiwan, where this fungus was collected.

Holotype: MFLU 18-0070

Saprobic on decaying wood of *Macaranga tanarius* (L.) Müll.Arg. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiomata* punctiform, sporodochial, 110–230 µm diam., velvety, dark brown to black. *Conidiophores* micronematous, pale brown, smooth, thin-walled. *Conidiogenous cells* holoblastic, cylindrical. *Conidia* (72–)74–84(–86) × 16–20(–24) µm, solitary, brown, ellipsoid to cylindrical, rounded at the apex, cheiroid, not complanate, consisting of 5 rows of cells, rows cylindrical, arising from a basal cell, each composed of 10–13 cells, constricted at septa, without appendages.

Culture characteristics: Conidia germinating on water agar within 24 h, germ tubes appearing from the basal cells of the conidium. Colonies on PDA covering 3 cm diam., in 3 weeks at 27 °C, at first white, colony from above: light orange to yellowish at the margin, yellowish to white at the centre; reverse, orange to yellowish at the margin, orange at the centre; mycelium yellowish to white with tufting; not producing pigments in PDA.

Material examined: TAIWAN, Chiayi, Shihong Forest Area, decaying wood of *Macaranga tanarius* (L.) Müll.Arg. (Euphobiaceae), 25 June 2017, D.S. Tennakoon, DTW013 (MFLU 18-0070, **holotype**), ex-type living culture (MFLUCC 17-2654).

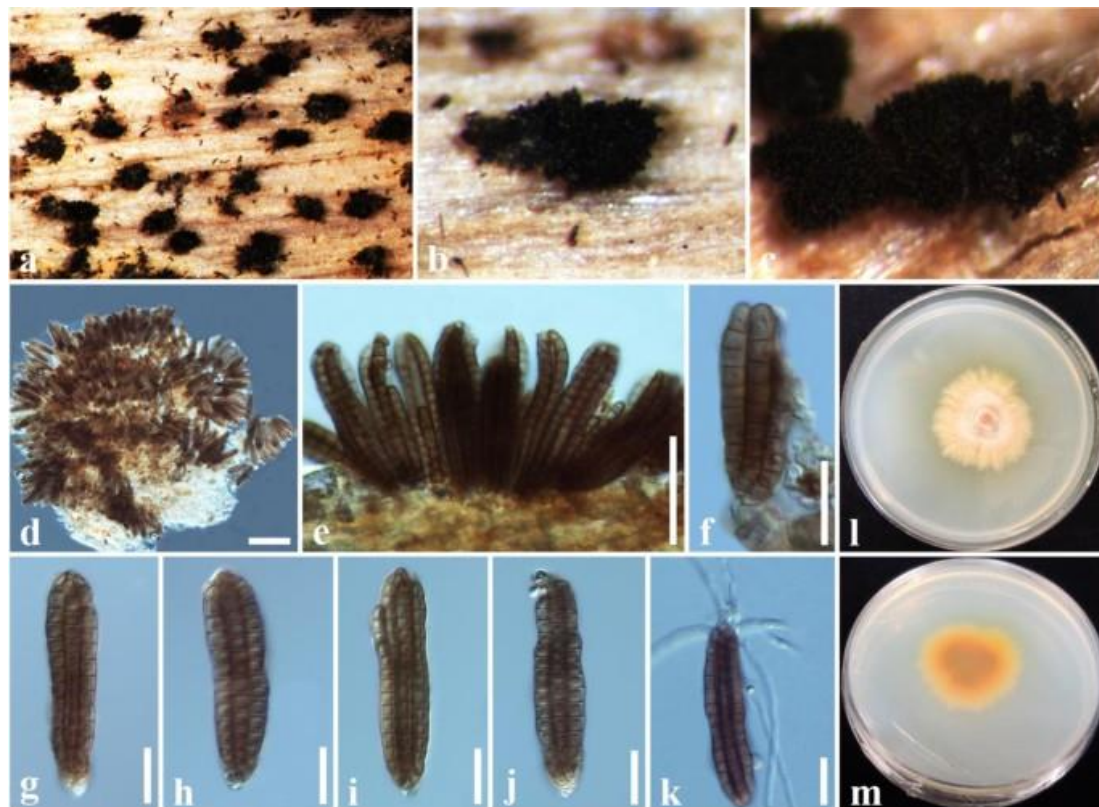


Figure 4. *Dictyocheirospora taiwanense* (MFLU 18–0070, **holotype**).

Digitodesmium Corda, Weitenweber's Beitr.

Digitodesmium Chiangmaiense Q.J. Shang & K.D. Hyde, Figure 5

Indexfungroum number: IF556220; Facesoffungi number: FoF05098

Etymology: Names reflects the province in Thailand, from where the holotype was collected.

Holotype KUN-HKAS 102163

Saprobic on decaying wood submerged in stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* punctiform, sporodochial, scattered, dark brown to black, glistening. *Conidiophores* micronematous, hyaline to pale brown, unbranched, thin-walled, smooth. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, hyaline to pale brown, smooth. *Conidia* acrogenous, solitary, cheiroid, smooth-walled, complanate, brown to dark brown, consisting of three arms closely compact with side arms higher than middle arms, $(24-33-42(-44) \times (13-15-18(-21) \mu\text{m}$, 5-7-euseptate in each arm, without appendages attached at the two outer arms, arms $(20-27-37(-38) \times (4-4-7(-8) \mu\text{m}$, not discrete, unbranched, cylindrical.

Culture characteristics: Conidia germinating on PDA within 24 h. Germ tubes produced from the basal cell. Colonies on PDA reaching 3–5 mm diam. after 7 days at room temperature, colonies circular, with fluffy, dense, white mycelium in the middle and sparse mycelium in the outer ring on the surface with irregular brown margin; in reverse, brown in the middle and pale yellow to brown at the margin.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on dead wood, 27 January 2017, Qiuju Shang, M7P4-17 (KUN-HKAS 102163, **holotype**), ex-type living culture (MFLUCC, ICMP).



Figure 5. *Digitodesmium chiangmaiense* (KUN-HKAS 102163, **holotype**).

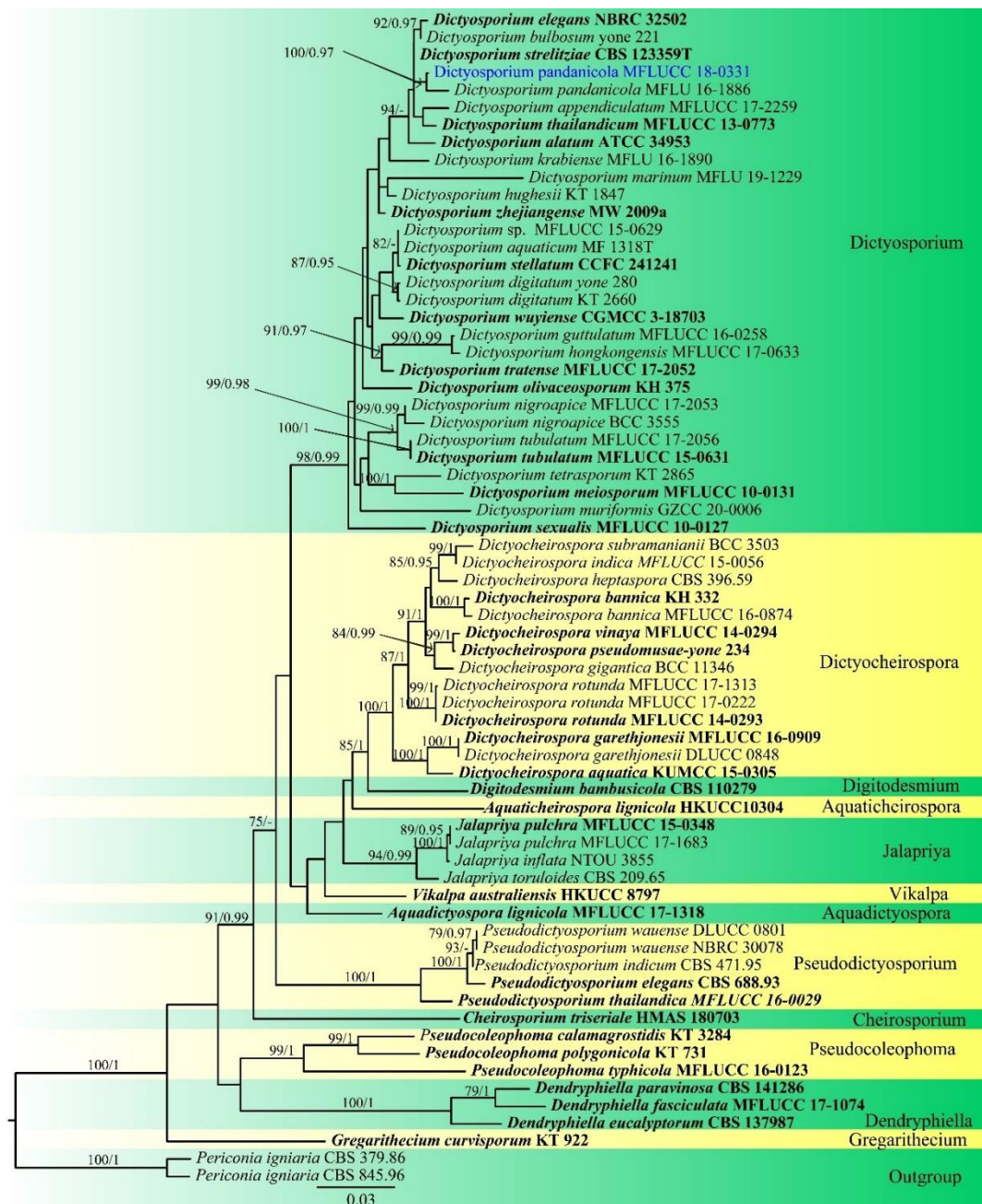


Figure 6. Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU, ITS and TEF1- α sequence data for the species from Melanommataceae. *Periconia igniaria* (CBS 379.86 and CBS 845.96) are used as the outgroup taxa. The dataset comprised 2694 characters after alignment including gaps (LSU = 1245 bp; ITS = 537 bp, TEF1- α = 912 bp and RPB2 = 1006 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of -14912.416315. The matrix had 871 distinct alignment patterns, with 36.52% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239281, C = 0.249660, G = 0.270492, T = 0.240568; substitution rates AC = 1.684833, AG = 3.636355, AT = 2.551537, CG = 0.785971, CT = 9.189334, GT = 1.000000; gamma distribution shape parameter α = 0.180969. Support values

for maximum likelihood (MLBS) above than 75% and Bayesian posterior probabilities (BYPP) greater than 0.95 are given at the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue

Dictyosporium Corda

Dictyosporium pandanicola Tibpromma & K.D. Hyde, Figure 7

Index Fungorum number: IF554481, *Facesoffungi number*: FoF04491

Saprobic on submerged decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies*, punctiform, sporodochial, scattered, dark brown to black, glistening. *Mycelium* mostly immersed, composed of smooth, septate, branched, hyaline to pale brown hyphae. *Conidiomata* sporodochia on the natural substrate in small groups, dark brown. *Conidiophores* 10–20 × 2.5–3 µm, micronematous, mononematous, cylindrical, subhyaline to pale brown, septate, smooth, sometimes reduced to conidiogenous cell. *Conidiogenous cells* holoblastic, integrated, indeterminate, subhyaline to pale brown. *Conidia* 40–48 × 20–25, solitary, oval to ellipsoid, cheiroid, smooth-walled, consisting of 5–6 arms, 9–13-euseptate in each arm, with a basal connecting cell, yellow–brown to brown with age, sometimes with a hyaline, globose, apical appendage.

Culture characters: Conidia germinated on PDA within 24 hours. Colonies on PDA reaching 2.5–3.5 cm diam., after 4 weeks at room temperature, colonies irregular, medium dense, white to yellow in top view. In reverse, yellow in the middle and white at the margin.

Material examined: THAILAND, Surat Thani Province, Sai Daeng, on decaying wood submerged in a small river, 2 October 2017, Z.L. Luo, B77 (MFLU 20-0425, **new record**), living culture (MFLUCC 18-0331).



Figure 7. *Dictyosporium pandanicola* (MFLU 20–0425, **new record**).

Latoruaceae Crous

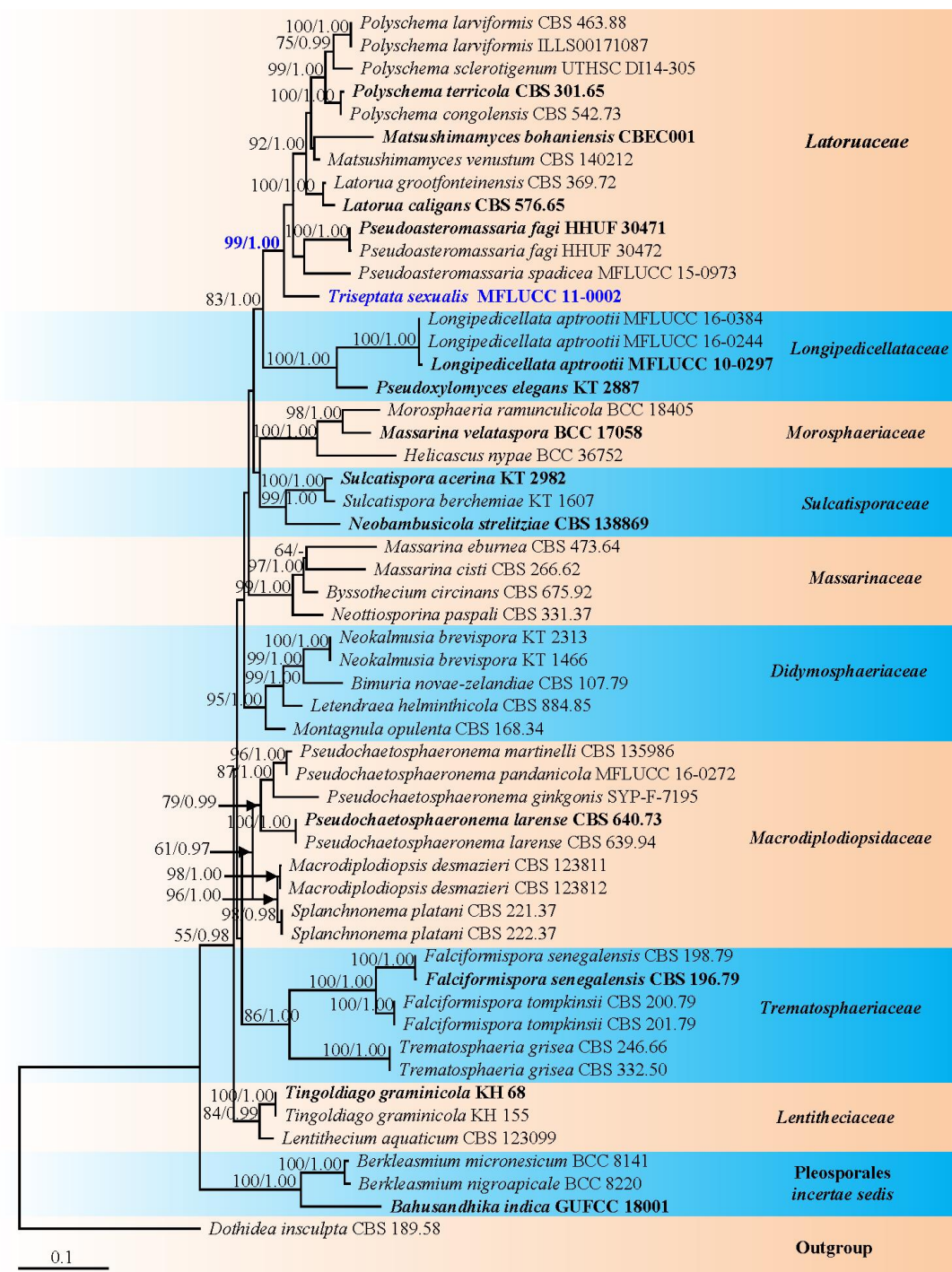


Figure 8. Phylogram obtained from RAxML based on analysis of a combined dataset of LSU, ITS and SSU sequence data. Bootstrap values for RAxML $\geq 55\%$ BS and BYPP ≥ 0.95 are given on the branches. The tree is rooted to *Dothidea inculpta* CBS 189.58 (Dothideaceae, Dothideales). The type species of each genus are in bold and new taxa in blue.

Triseptata Boonmee & Phookamsak

Index Fungorum number: IF557185, Facesoffungi number: FoF07229

Etymology: The generic epithet refers to consistent 3-septate ascospores.

Type species: *Triseptata sexualis* Boonmee & Phookamsak

Saprobic on dried branches of an unidentified plant. Sexual morph: *Ascostromata* immersed to slightly erumpent, visible as black spots, single or clustered, scattered or gregarious, uni- to multi-locular, globose to subglobose, with or without basal stroma, dark brown, obscure ostiole. *Peridium* composing several layers of textura angularis, with compressed of dark brown cells. *Hamathecium* comprising cylindrical, branched, septate, anastomosed, hyaline pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical-clavate, sessile, apically rounded. *Ascospores* 1–2-seriate, partially overlapping, ellipsoid-fusiform, straight or slightly curved, regularly 3-septate, darkened and constricted at the septa, the second cell from the top slightly wider than the others, asymmetrical ends, light brown to brown, smooth-walled. Asexual morph: Hyphomycetous conidia-like structures in culture. Conidiophores and conidiogenous cells absent. *Conidia* superficial, globose to subglobose, multiseptate, brown to dark brown, smooth-walled.

Triseptata sexualis Boonmee & Phookamsak, Figures 9, 10

Index Fungorum number: IF557184, Facesoffungi number: FoF 07230

Etymology: The specific epithet “*sexualis*” referring to sexual morph.

Holotype: MFLU 11-0002

Saprobic on dried branches of an unidentified plant. Sexual morph: *Ascostromata* (108–)148–157 µm high × (120–)157–198 µm diam., immersed to slightly erumpent, visible as black spots, single or clustered, scattered or gregarious, uni- to multi-locular, globose to subglobose, with or without basal stroma, dark brown, obscure ostiole. *Peridium* 16–26 µm wide, composing several layers of textura angularis, with compressed of dark brown cells. *Hamathecium* comprising 1.5–2 µm wide, cylindrical, branched, septate, anastomosed, hyaline pseudoparaphyses. *Asci* 43–60 × 7–9 µm, 8-spored, bitunicate, fissitunicate, cylindrical-clavate, sessile, apically rounded. *Ascospores* 11.5–15 × 4–5 µm, 1–2-seriate, partially overlapping, ellipsoid-fusiform, straight or slightly curved, regularly 3-septate, darkened and constricted at the septa, the second cell from the top slightly wider than the others, asymmetrical ends, light brown to brown, smooth-walled. Asexual morph: Hyphomycetous conidia-like structures in culture. Conidiophores and conidiogenous cells absent. *Conidia* (12–

)16–23 μm diam., superficial, globose to subglobose, multiseptate, brown to dark brown, smooth-walled.

Culture characteristics: Conidia germinating on WA within 12 hrs. Colonies growing on malt extract agar (MEA), reaching 18 mm in 2 weeks at 28°C, effuse, dentate and lobate edges, darkly brown. Mycelium superficial and partly immersed, branched, septate, pale brown to brown, smooth-walled, chlamydospores produced in culture and induced with plant tissues within 90 days.

Material examined: THAILAND, Chiang Mai, Jom Thong, elev. 800–1000 msl., N18°31'E 98°29', on dead branches of an unidentified plant, 16 November 2010, R. Phookamsak, ITN04 (MFLU 11-0002, **holotype**); ex-type living culture, MFLUCC 11-0002 = BBC 52152.

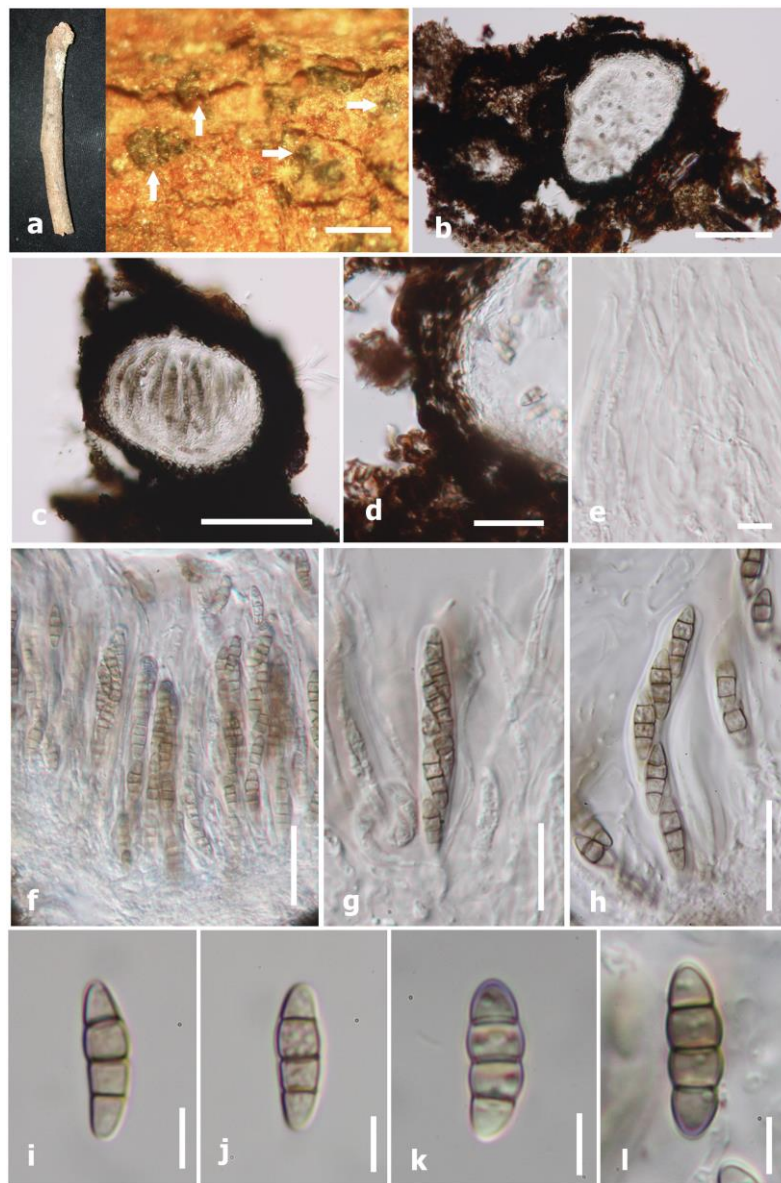


Figure 9. *Triseptata sexualis* (MFLU 11-0002, **holotype**).

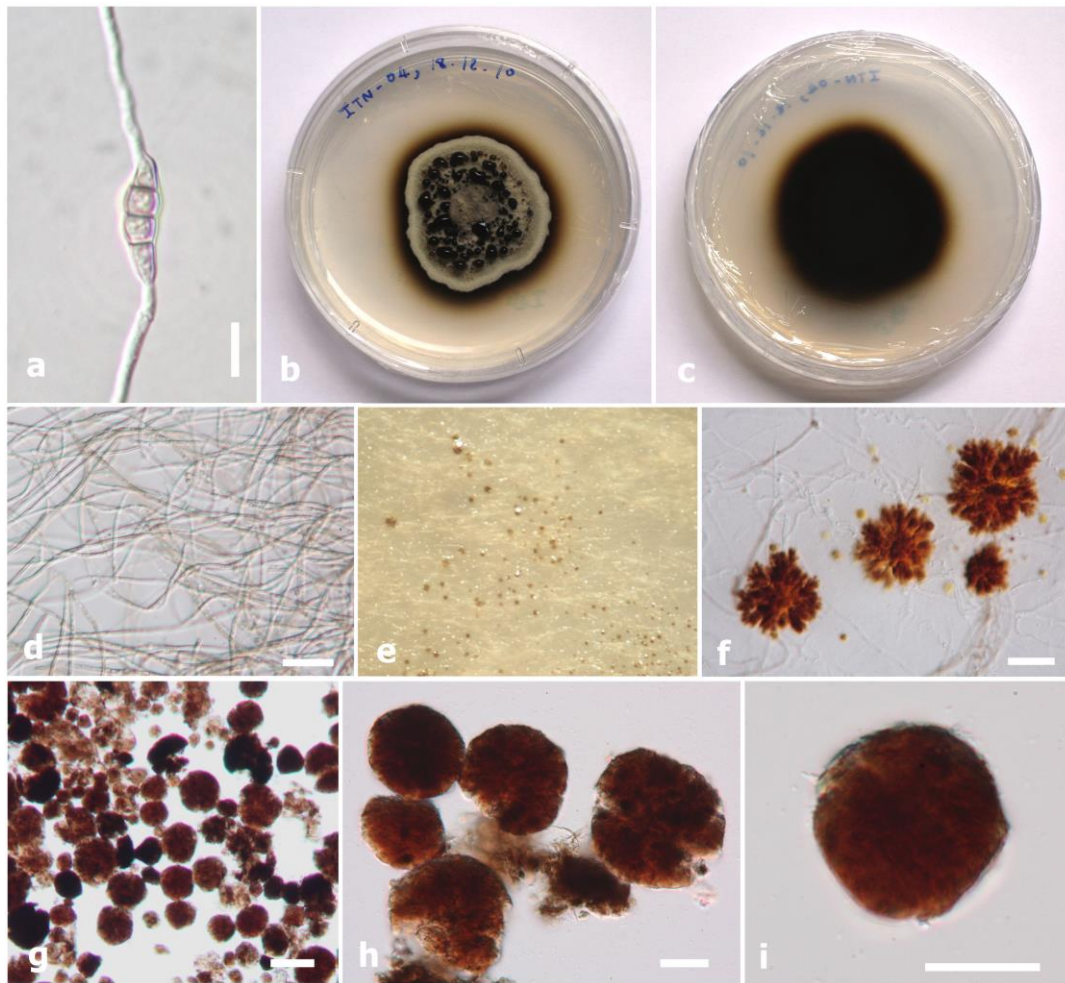


Figure 10. *Triseptata sexualis* (MFLUCC 11-0002, ex-type).

Testudinaceae Arx

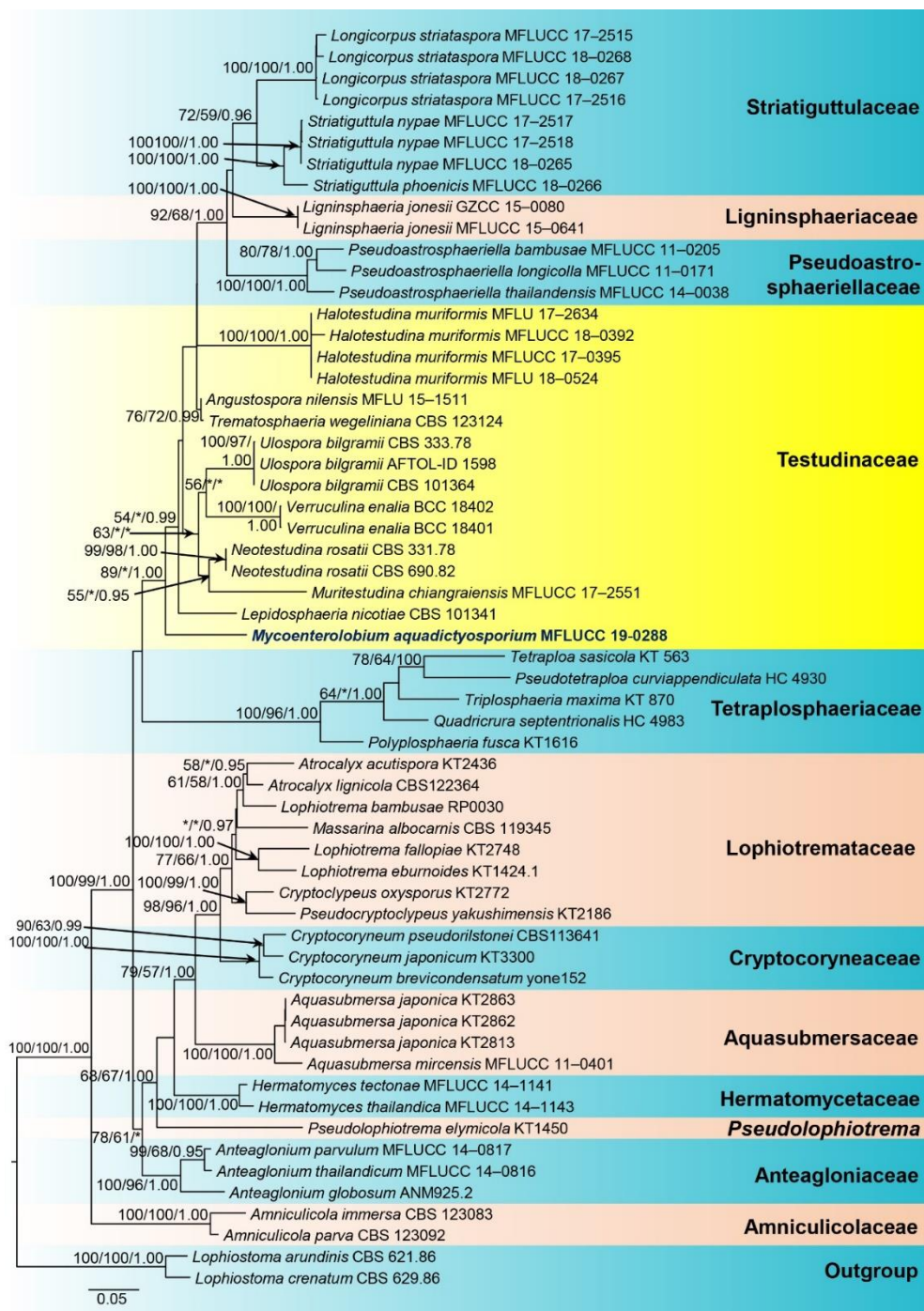


Figure 11. Phylogenetic tree based on RAxML analyses of combined LSU, SSU, ITS, TEF1- α and RPB2 sequence data. Bootstrap support values for maximum likelihood (ML) and maximum parsimony (MP) higher than 50% and Bayesian posterior probabilities (PP) greater than 0.95 are indicated above the nodes as MP/ ML/ PP. The new isolates are represented in blue. The tree is rooted to *Lophiostoma arundinis* (CBS 621.86) and *L. crenatum* (CBS 629.86) (Lophiostomataceae). Bar = 0.05 estimated number of nucleotide substitutions per site per branch.

Mycoenterolobium Goos

Mycoenterolobium aquadictyosporium M.S. Calabon, Boonmee, E.B.G. Jones & K.D. Hyde,
Figures 12, 13

MycoBank number: MB835668; Facesoffungi number: FoF 08423

Etymology: referring to the aquatic habitat and shape of the conidia

Saprobic on decaying wood submerged in freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous, on natural substrate, colonies effuse, black, shiny, uniformly spread, mycelium immersed. *Conidiophores* 7–22 × 2–8 µm, micronematous, inconspicuous, short or absent. *Conidiogenous cells* mono-blastic, integrated, terminal, determinate, oval to irregularly shaped. *Conidia* at immature 19–52 × 138–141 µm, at mature 45–92 × 43–104 µm, and 10–30 µm thick, acrogenous, solitary, dictyosporous, strongly flattened, fan shaped at maturity, composed of 15–25 rows of cells radiating from single cell at the point of attachment, dark brown, smooth-walled.

Culture characteristics: Conidia germinating on MEA within 24 h and germ tubes produce from the basal part of the conidia. On MEA, colony circular with entire margin, reaching 10–15 mm in 25 days at 25°C, dark brown to greyish brown from the above, dark brown to black from below, surface smooth, opaque, dry, raised to becoming umbonate in old cultures, with dense mycelia. Sporulation in culture after 2 weeks of incubation.

Material examined: THAILAND, Phitsanulok Province, Wang Thong District, Kaeng Sopha waterfall stream, on submerged wood, 25 July 2019, S. Boonmee, PSL/WT-17 (MFLU 20-0043, **holotype**), ex-type living culture MFLUCC 19-0288.

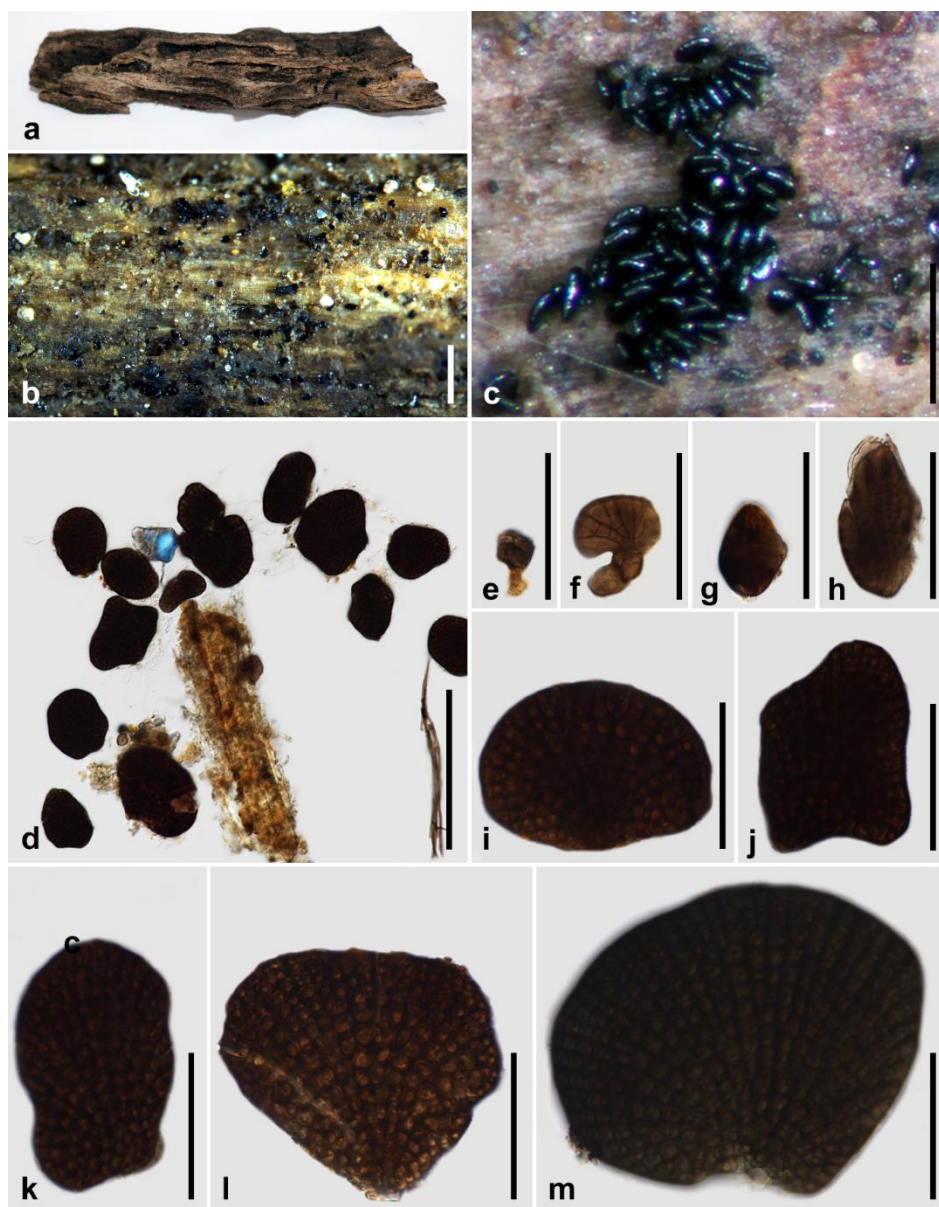


Figure 12. *Mycoenterolobium aquadictyosporium* (MFLUCC 19-0288, **holotype**

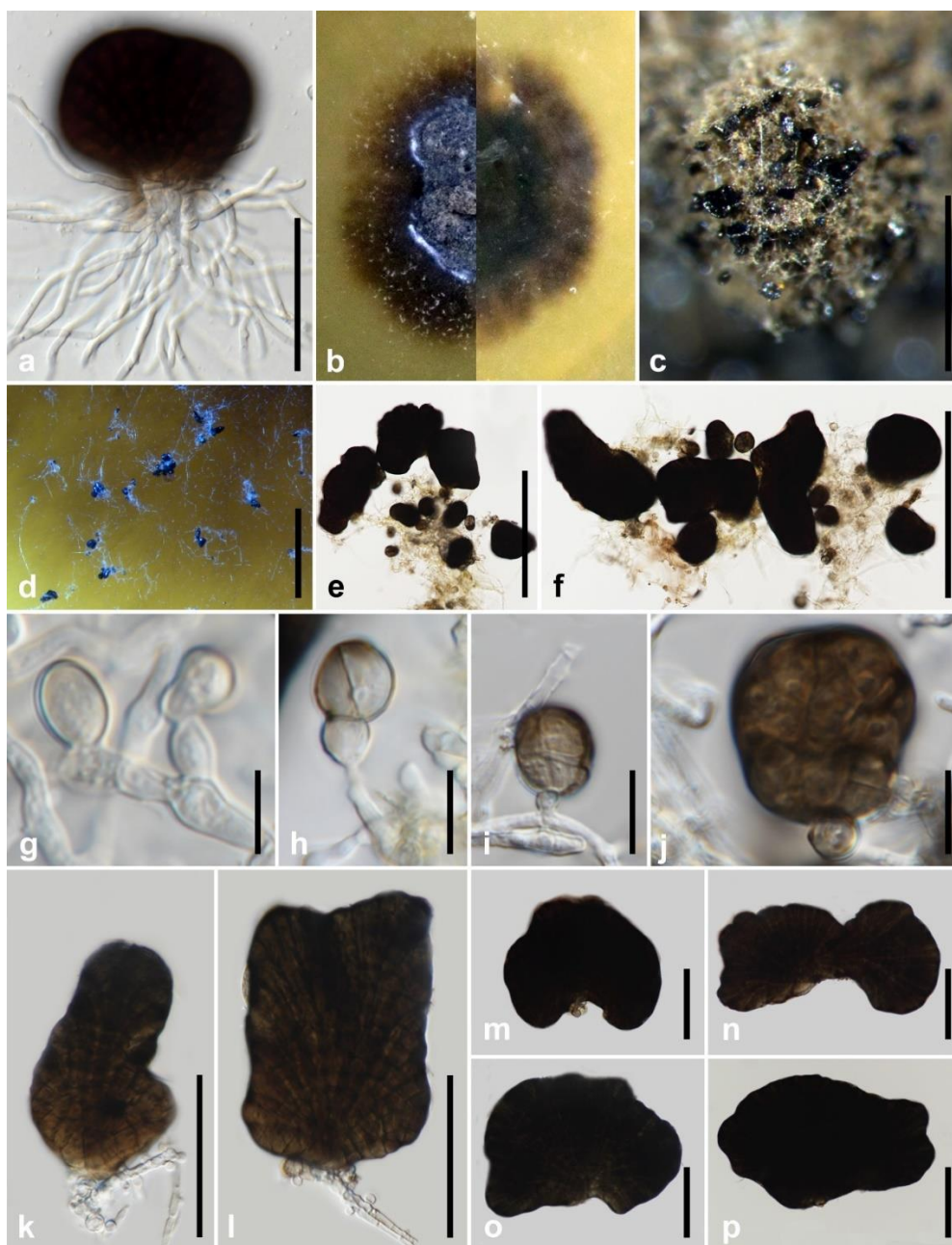


Figure 13. *Mycoenterolobium aquadictyosporium* (MFLUCC 19-0288, **ex-type**).

Didymosphaeriaceae A. Munk

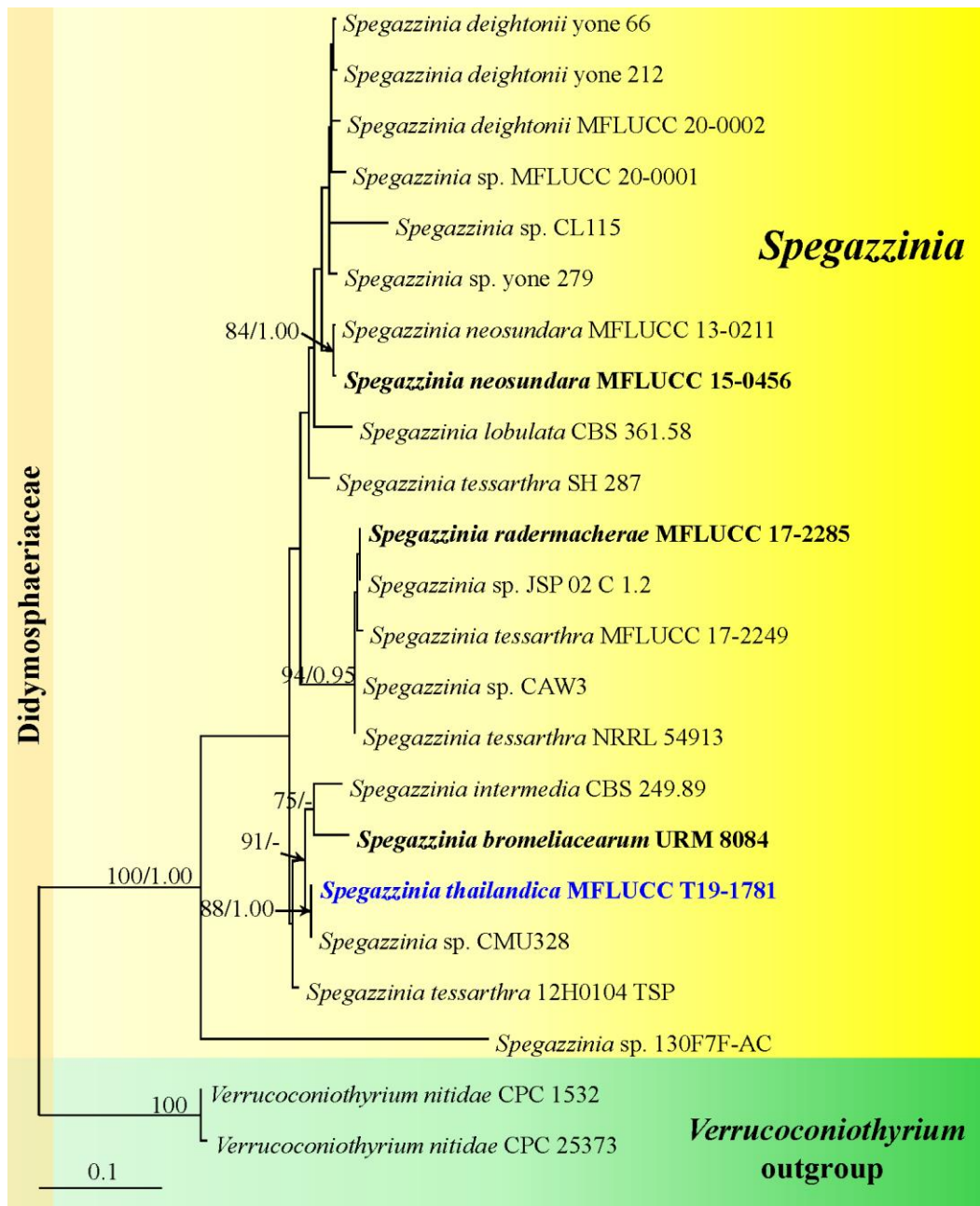


Figure 14. Phylogram generated from the best scoring of the RAxML tree based on combined LSU, ITS and TEF1- α sequence dataset of *Spegazzinia* taxa. Twenty-three strains are included in the combined analyses which comprise a total of 2412 characters. *Verrucoconiothyrium nitidae* (CPC1532 and CPC25373) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of -6489.146269 is presented. RAxML analysis yielded 466 distinct alignment patterns and 43.56% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.227514, C = 0.273092, G = 0.282565, T = 0.216829, with substitution rates AC = 1.859657, AG = 2.236600, AT = 2.355976, CG = 0.905759, CT = 8.747615, GT = 1.000000; gamma distribution shape parameter alpha = 0.145599. Bootstrap

support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue.

***Spegazzinia* Sacc.**

Spegazzinia thailandica Boonmee, Huanraluek & K.D. Hyde, Figure 15

Index Fungorum number: IFxxxxxx, Facesoffungi number: FoF09189

Etymology: Referring to the distribution in Thailand.

Holotype: MFLU xx-xxxx

Saprobic on decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* punctiform, effuse, scattered, dark brown to black on natural wood substrate. *Mycelium* slight raised on host surface, branched, septate, hyaline to pale brown. *Conidiophores* micronematous, mononematous, slight erect, flexuous, simple, unbranched, intercalarily, pale brown. *Conidiogenous cells* indiscrete, indeterminate, terminal. *Conidia* 14–17 diam. µm, holoblastic, globose to subglobose, 4-celled, cruciately septate and constricted at the septa, dentate at the margin, brown to dark brown, darker at the septa, invisible septa at maturity, guttulate when immature, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes arising from terminal end. Colonies on PDA, slow growing, reaching 5 cm diam. after 1 month at room temperature, flat to slightly effuse, surface smooth, circular, radial striations and entire edges, olivaceous brown to dark brown, and sporulated conidia in cultures after 14 days. Mycelium superficial, partly immersed, composed of branched, septate, hyaline to pale brown, smooth-walled. *Conidia* 11–17 µm diam., globose to subglobose, 4-celled cruciate septate and constricted at the septa, dentate at the margin, brown to dark brown, darker at the septa, guttulate, smooth-walled.

Material examined: THAILAND, Phitsanulok Province, Wang Thong, Wang Nok Aen, saprobic on decaying wood, 25 July 2019, S. Boonmee, WNA03 (MFLU xx-xxxx, **holotype**), ex-type living on culture (MFLUCC T19-1781).

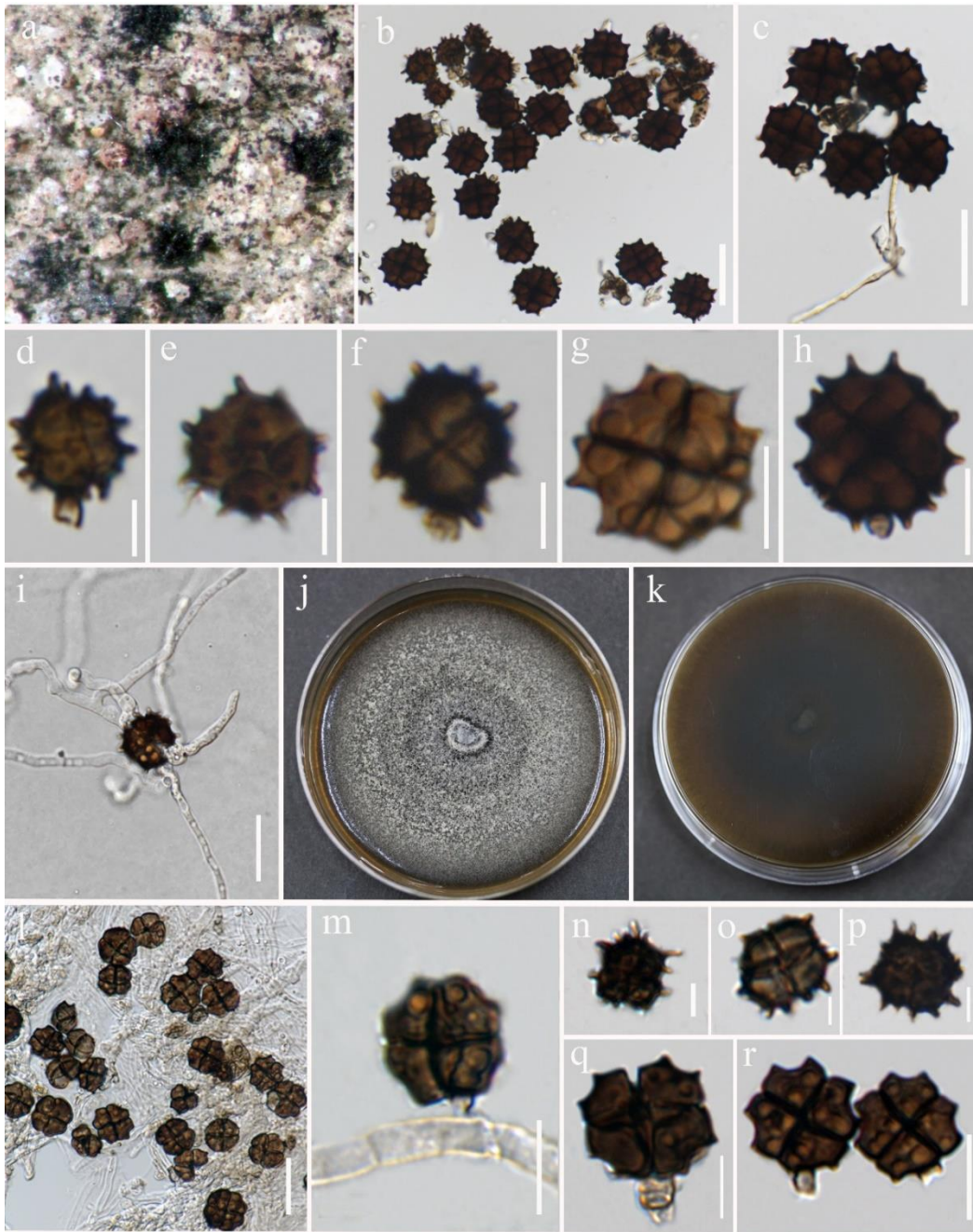


Figure 15. *Spegazzinia thailandica* (MFLU xx-xxxx, holotype).

Hermatomycetaceae Locq.

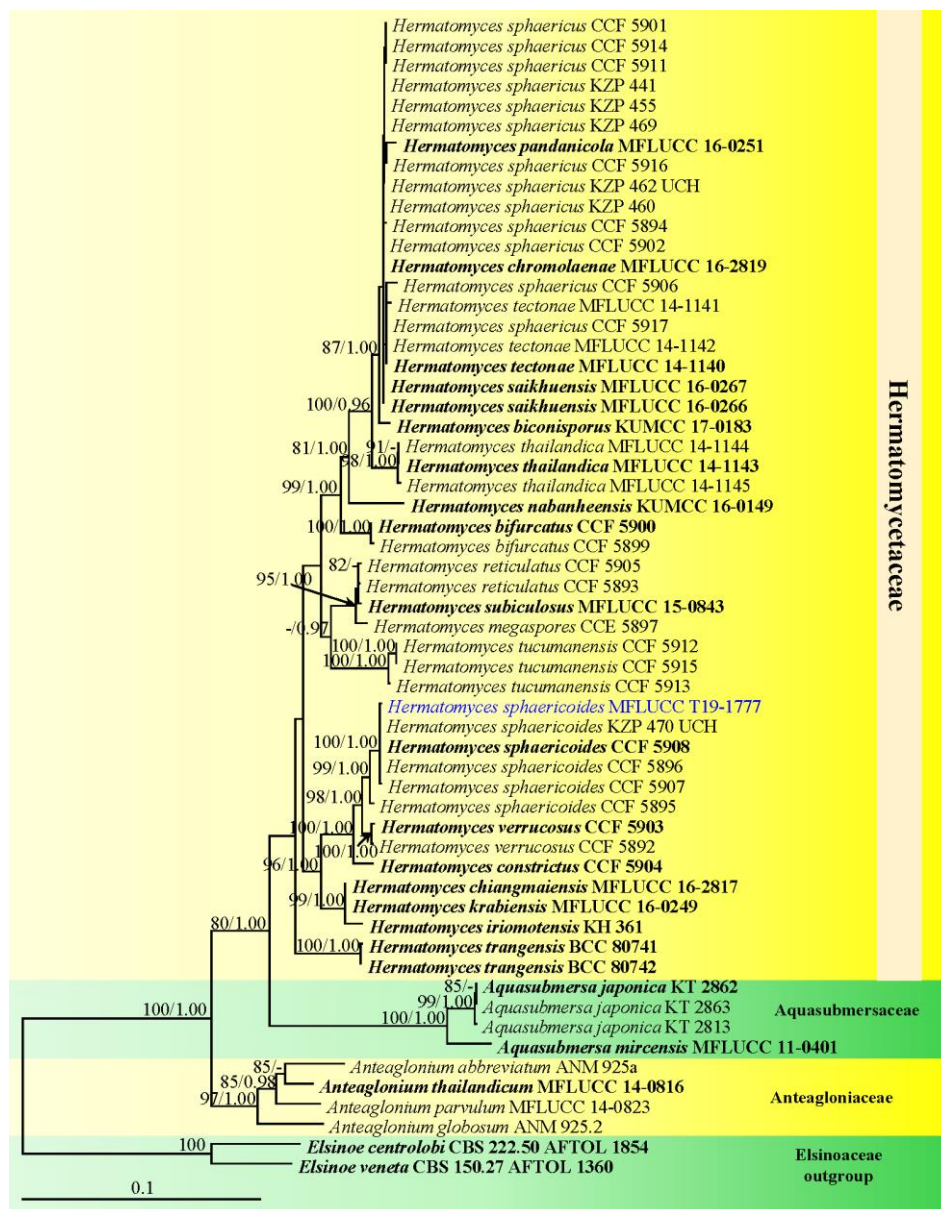


Figure 16. Phylogram generated from the best scoring of the RAxML tree based on combined ITS, LSU and TEF1- α sequence dataset of *Hermatomyces* taxa (Hermatomycetaceae) and closely related families Aquasubmersaceae and Anteagloniaceae. Fifty-eight strains are included in the combined analyses which comprise a total of 2364 characters. *Elsinoe centrolobi* CBS 222.50 and *El. veneta* CBS 150.27 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of -8550.828746 is presented. RAxML analysis yielded 709 distinct alignment patterns and 29.20% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232318, C = 0.270607, G = 0.265308, T = 0.231767, with substitution rates AC = 0.819142, AG = 1.734172, AT = 1.276617, CG = 0.628563, CT = 8.423892, GT = 1.000000; gamma distribution shape parameter alpha =

0.198083. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue.

***Hermatomyces* Speg.**

***Hermatomyces sphaericoides* Koukol & G. Delgado, Figure 17**

Index Fungorum number: IF824248, Facesoffungi number: FoF09190

Saprobic on decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the natural substrate superficial, dry, scattered to partly grouped, black. *Mycelium* 2–3 µm wide, superficial and partly immersed, composed branched, septate, pale brown or brown, sparsely network hyphae. *Conidiophores* micronematous, mononematous, flexuous, inconspicuous, septate, hyaline to pale brown. *Conidiogenous cells* 4–6 × 2–3 µm, holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, pale brown. *Conidia* 25.5–32 × 21–27.5 µm, solitary, acrogenous, cheiroid, globose to subglobose, inwardly curved at the apex, arising from a basal cell, consisting 4–5 rows, row digitate, each row composed of 4–5(–6) cells, multi-septate, constricted at the septa, dark brown to black, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes arising from terminal end of conidium. Colonies on PDA, fast growing, reaching 30 mm diam. after 2 weeks at room temperature, flat, with slightly crenated to radially striated with lobate margin, with white-grey mycelium, pastel grey in middle towards dark brown, greenish brown at margin, dark green to brown in reverse view, not sporulating in cultures after two months.

Material examined: THAILAND, Phetchabun Province, Lom Sak, on decaying wood, 25 July 2019, S. Boonmee, LSP01 (MFLU 20-xxxx, **new record**), living culture (MFLUCC T19-1777).

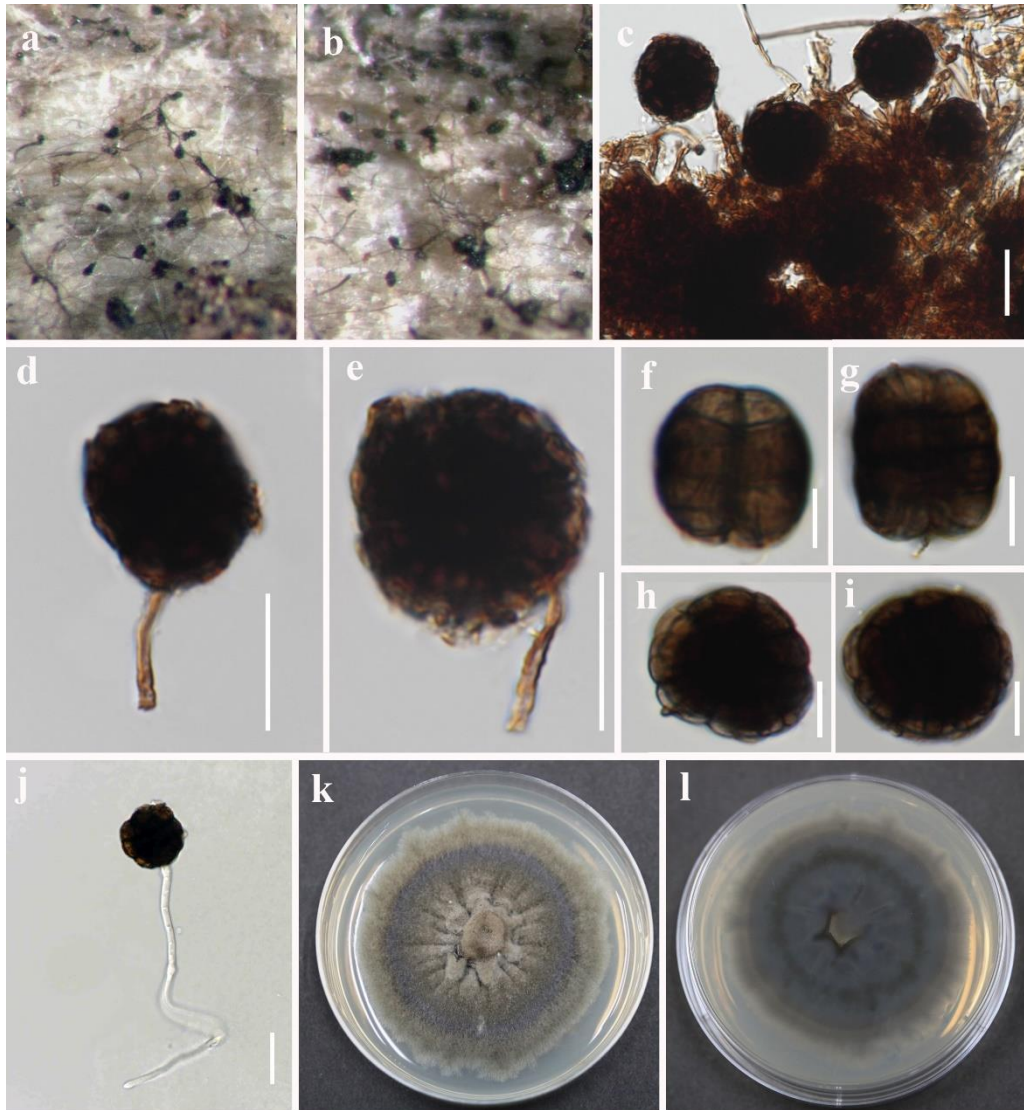


Figure 17. *Hermatomyces sphaericoides* (MFLU xx-xxxx, new record).

Massarinaceae Munk

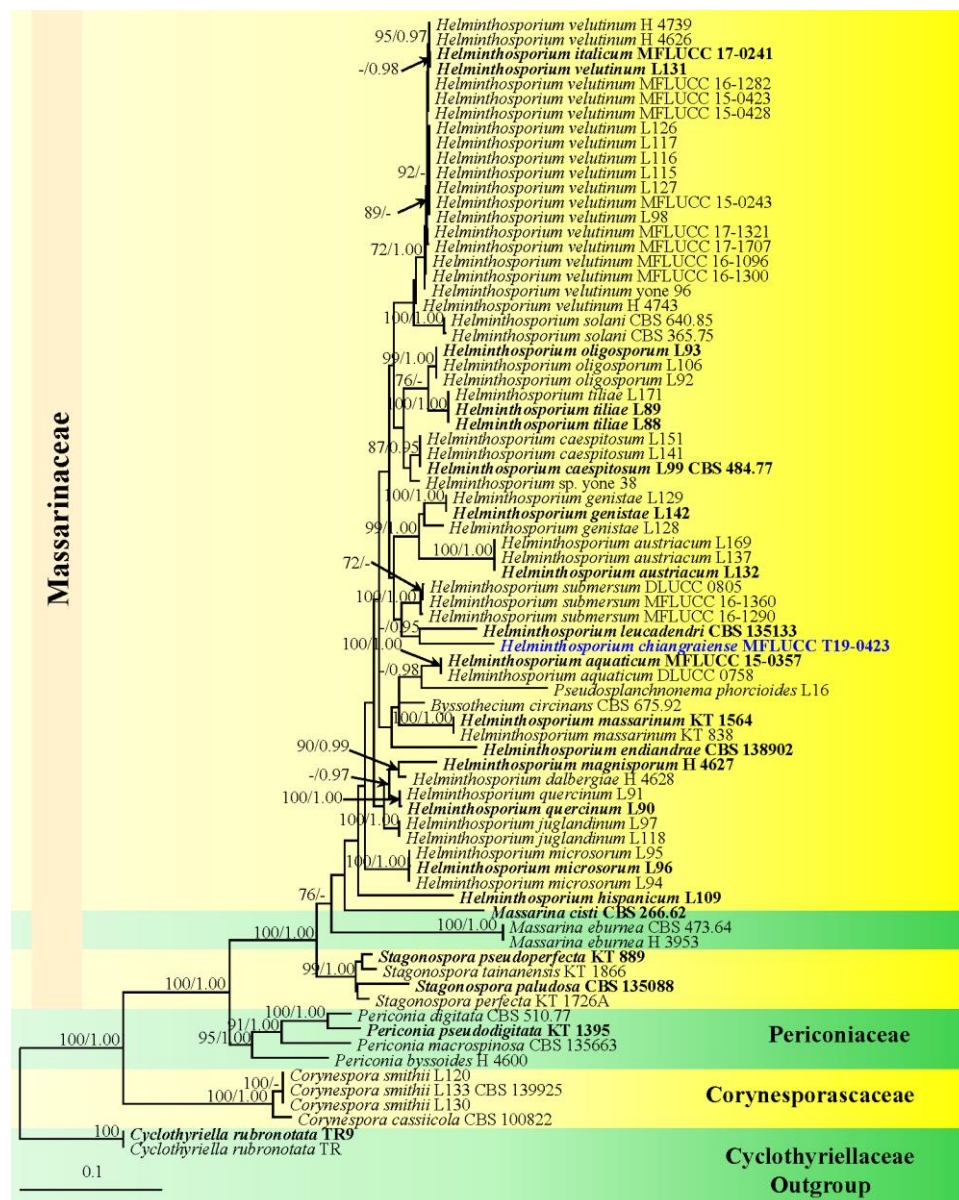


Figure 18. Phylogram generated from the best scoring of the RAxML tree based on combined LSU, SSU and ITS sequence dataset of *Helminthosporium* taxa (Massarinaceae) and related families Corynesporascaceae and Periconiaceae. Seventy-seven strains are included in the combined analyses which comprise a total of 2567 characters. *Cyclothyriella rubronotata* (TR and TR9) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of -11885.302979 is presented. RAxML analysis yielded 713 distinct alignment patterns and 23.08% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246572, C = 0.227244, G = 0.274051, T = 0.252133, with substitution rates AC = 2.645156, AG = 3.449326, AT = 2.077592, CG = 1.025293, CT = 7.769520, GT = 1.000000; gamma distribution shape parameter alpha = 0.143346. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian

posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. The newly generated sequences are indicated in blue.

Helminthosporium Link

Helminthosporium chiangraiense Boonmee & Huanraluek, Figure 19

Index Fungorum number: xxxxxxx, Facesoffungi number: FoF09192

Etymology: In reference to it discover in Chiang Rai Province

Holotype: MFLU 20-xxxx

Saprobic on dead twigs. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* 230–584 µm diam., effuse, dark brown to black, hairy. Mycelium immersed, forming stroma-like aggregations of dark brown pseudoparenchymatous cells. *Conidiophores* 168–304.5 × 5.5–12, mononematous, macronematous, caespitose, erect, cylindrical, straight to slightly flexuous, wide at the base, unbranched, dark brown, with apical pore, multi-septate, with dark scars, smooth-walled. *Conidiogenous cells* mono- to polytretic, integrated, terminal and intercalary, cylindrical, cicatrized, scars often dark, distinct pores. *Conidia* 141–207 × 14–22, solitary, obclavate, straight to slightly curved, wider below than apex, truncate and dark scar at the base, upper cell tapering towards the long apex, cylindrical, apically rostrate and pale brown, 9–13-distoseptate, smooth-walled. *Conidial secession* schizolytic.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes produced from both ends. Colonies on PDA reaching 20 mm diam., in 7 days at room temperature, within a month covering the Petri dish, effuse, hairy, mycelium radiating outwards, fimbriate edge, dense, dark. Mycelium superficial and partly immersed, dark brown.

Material examined: THAILAND, Chiang Rai Province, Muang, Thasud, Mae Fah Lung University, Botanical garden, on dead twigs of unidentified plant, 14 June 2019, N. Huanraluek, CRB1 (MFLU xx-xxxx, **holotype**), ex-type living culture (MFLUCC T19-0423).



Figure 19. *Helminthosporium chiangraiense* (MFLU 20-xxxx, holotype).

Melanommataceae G. Winter (= *Pseudodidymellaceae* A. Hashim. & Kaz. Tanaka)

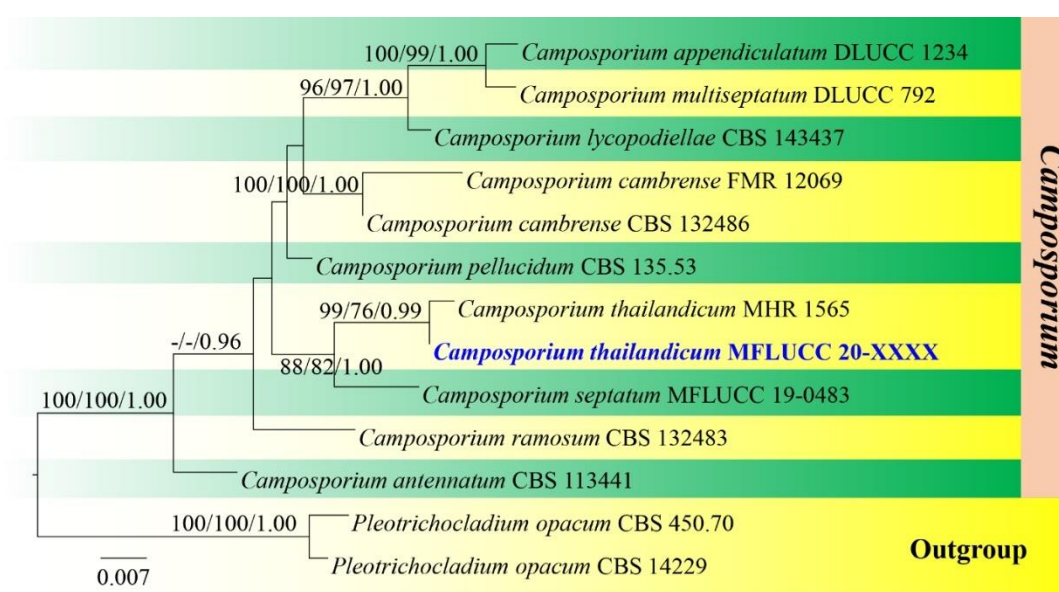


Figure 20. Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing the species of *Camposporium*. Two strains of *Pleotrichocladium opacum* (CBS 450.70 and CBS 14229) are used as the outgroup taxa. Related sequences are taken from Hyde et al. (2020a). Thirteen taxa are included in the combined analyses which comprised 3085 characters (816 characters for LSU and 541 characters for ITS) after alignment. The best scoring RAxML tree with a final likelihood value of -3193.843958 is presented. The matrix had 169 distinct alignment patterns, with 13.79% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244395, C = 0.221122, G = 0.285564, T = 0.248918; substitution rates: AC = 1.875033, AG = 2.327593, AT = 1.577862, CG = 0.477212, CT = 6.322595, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.020000$. The MP analysis resulted a single most parsimonious tree (TL = 225, CI = 0.831, RI = 0.791, RC = 0.658, HI = 0.169). The newly generated sequence is indicated in blue bold.

Camposporium Harkn.

Camposporium thailandicum Calabon, Boonmee, E.B.G. Jones & K.D. Hyde, Figure 21

Index Fungorum number: IF****, Facesoffungi number: FoF09156

Etymology: Name reflects the country from where this species was collected, Thailand.

Holotype: MFLU 20-xxxx

Saprobic on submerged decaying wood in a freshwater. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate, effuse, golden brown, velvety. *Mycelium* mostly immersed, composed of white, septate, branched and guttulate hyphae.

Conidiophores macronematous, mononematous, often procumbent on substrate, light brown to brown, unbranched, irregularly cylindrical, flexuous, septate, thick-walled. *Conidiogenous cells* monoblastic, terminal, integrated, subcylindrical, pale brown. *Conidia* $100\text{--}130 \times 8.5\text{--}13\ \mu\text{m}$ ($\bar{x} = 115 \times 10.7\ \mu\text{m}$, $n = 30$), wide at middle, $4\text{--}9\ \mu\text{m}$ ($\bar{x} = 6.1\ \mu\text{m}$, $n = 30$) wide at base, solitary, dry, cylindrical, elongate, median brown, paler at base, finely verrucose, 8–11-septate, not constricted or slightly constricted at the septa, apex rounded, basal cell truncate, the apical cell gives rise to 2–3 simple appendages; appendage hyaline, aseptate, smooth, tapering from the base to the apex.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 20 mm in 2 weeks at 25°C. Mycelia superficial, circular, with entire edge, flat, rugose, from above mossy gray in the center and pale yellow at the edge, from below brown at the center then becoming yellow orange at the edge. Chlamydospores produced in culture and induced with plant tissues within 60 days. Formation of crystals in the culture was observed.

Material examined: THAILAND, Chiang Mai Province, Mushroom Research Center, on submerged decaying wood in a freshwater stream, 29 January 2019, S. Boonmee, SB14-7 (MFLU 20-xxxx, **holotype**), ex-type living culture (MFLUCC 20-xxxx).



Figure 21. *Camposporium thailandicum* (MFLU 20-xxxx, holotype).

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray

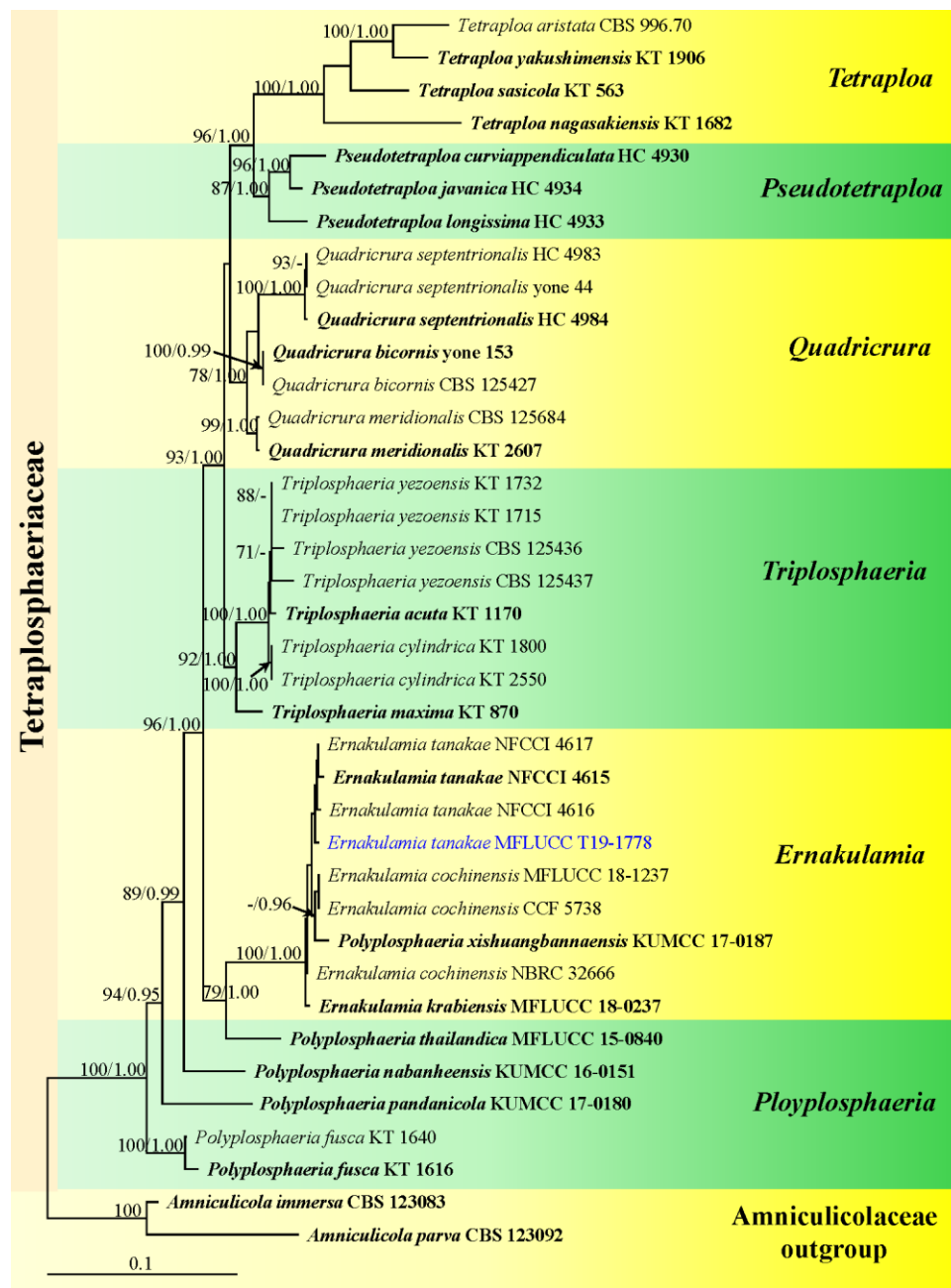


Figure 22. Phylogram generated from the best scoring of the RAxML tree based on combined LSU and ITS sequence dataset of *Ernakulamia* taxa and related genera in Tetraplosphaeriaceae. Thirty-eight strains are included in the combined analyses which comprise a total of 1468 characters. *Amniculicola immersa* (CBS 12308) and *A. parva* (CBS 123092) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of -5624.746373 is presented. RAxML analysis yielded 413 distinct alignment patterns and 15% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.236603, C = 0.245429, G = 0.293755, T = 0.224212, with substitution rates AC = 2.551620, AG = 2.407140, AT = 1.683194, CG = 0.618325, CT = 9.671311, GT = 1.000000; gamma distribution shape

parameter alpha = 0.164106. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue.

Ernakulamia Subram.

Ernakulamia tanakae Rajeshkumar & K.D. Hyde, Figure 23

Index Fungorum number: IF556700, Facesoffungi number: FoF556700

Saprobic on decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse, superficial, dark brown to black, sparsely hyaline hyphal network. *Conidiophores* not seen. *Conidiogenous cells* monotretic, integrated. *Conidia* 35–48 × 22–37 µm, dictyosporous, obconical, obovoid or subglobose, dark brown, multi-septate, thick-walled, with 3–5-appendages per conidium. *Appendages* 24–68 × 4–5 µm, cylindrical stiff, straight, apical or subapical, dark brown, 3–6-septate, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h. Colonies on PDA reaching 3.5 cm diam. after 2 weeks at room temperature, circular, undulate edge, grey to dark-grey, dense and raised on medium surface. Mycelium superficial, velvety, flossy.

Material examined: THAILAND, Phetchabun Province, Lom Sak, saprobic on decaying wood of unidentified host, 25 July 2019, S. Boonmee, LSP02 (MFLU xx-xxxx, **new record**), living culture (MFLUCC T19-1778).

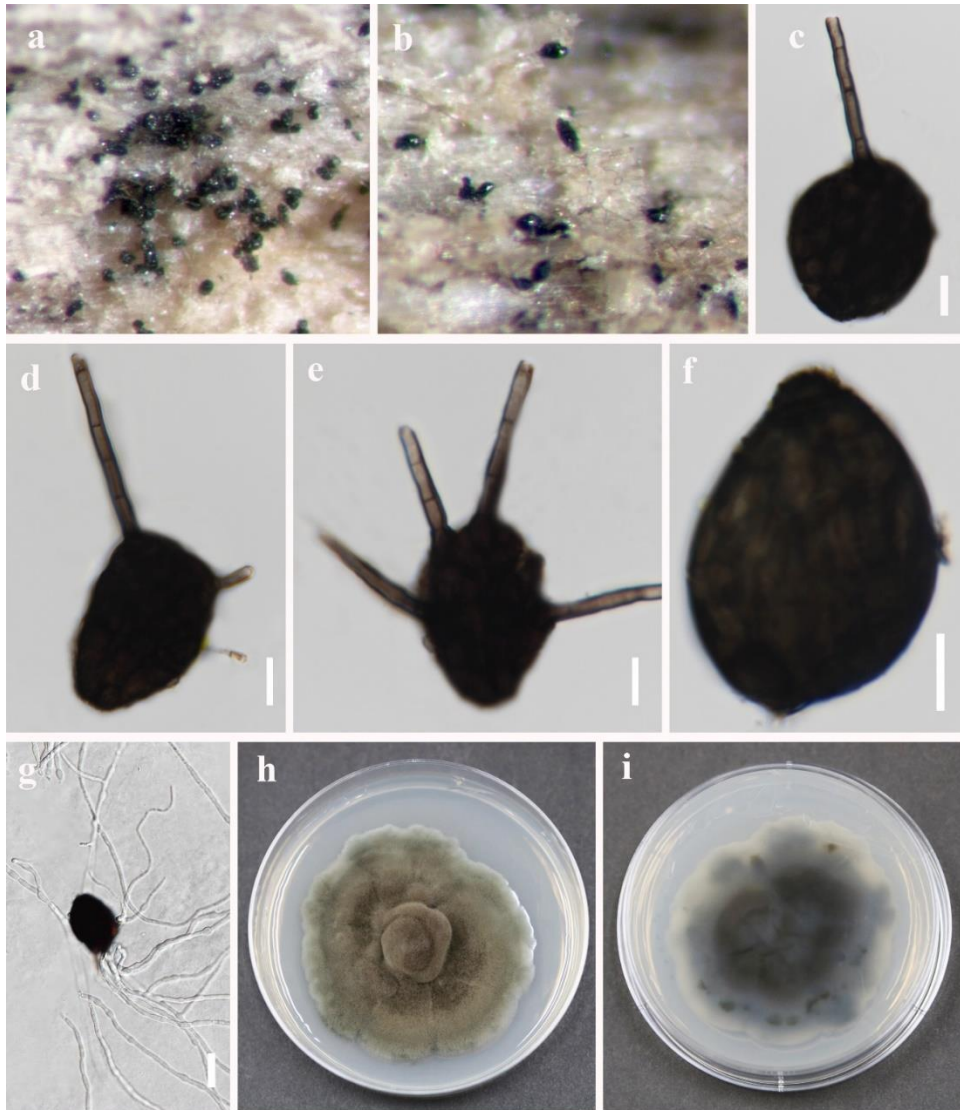


Figure 23. *Ernakulamia tanakae* (MFLU xx-xxxx, **new record**).

Pleosporales, genera *incertae sedis*

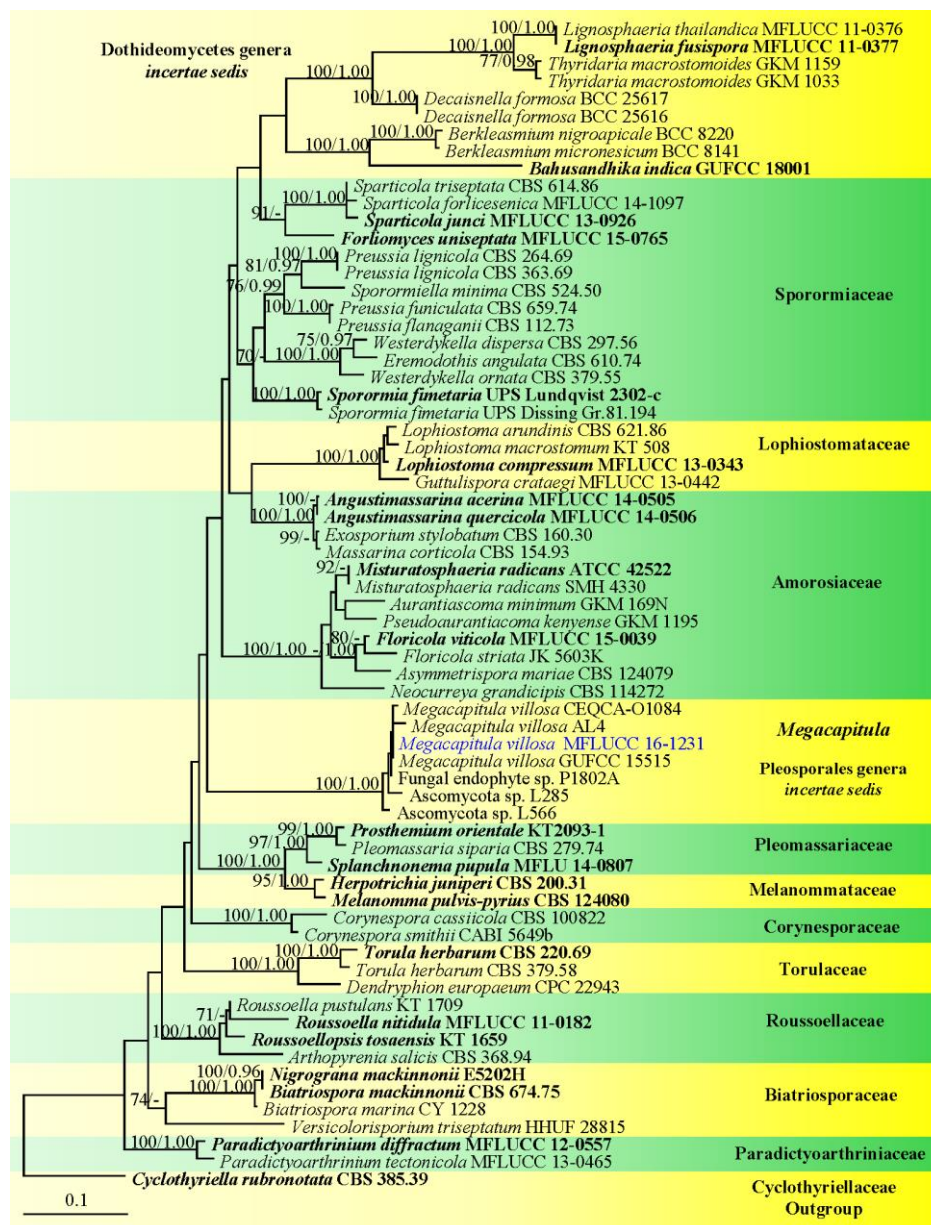


Figure 24. Phylogram generated from the best scoring of the RAxML tree based on combined LSU and ITS sequence dataset of *Megacapitula* taxa and related families in Pleosporales. Sixty-seven strains are included in the combined analyses which comprise a total of 1456 characters. *Cyclothyriella rubronotata* CBS 385.39 is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of -12939.878192 is presented. RAxML analysis yielded 723 distinct alignment patterns and 29.63% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242721, C = 0.238518, G = 0.291320, T = 0.227442, with substitution rates AC = 1.943333, AG = 2.988826, AT = 2.324598, CG = 1.416039, CT = 8.575259, GT = 1.000000; gamma distribution shape parameter alpha = 0.245601. Bootstrap support values for maximum likelihood (ML, left) equal to or greater than

70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in black bold and newly generated sequence are indicated in blue.

Megacapitula J.L. Chen & Tzean

Megacapitula villosa J.L. Chen & Tzean, Figures 25, 26

Index Fungorum number: IF359484; Facesoffungi number: FoF09196

Saprobic on submerged decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* superficial, partly immersed, composed of a loose network of repent, septate, branched, hyaline to light brown hyphae connected with conidia. *Colonies* on natural substrate effuse, solitary, dark brown to black. *Conidiophores* absent. *Conidiogenous cells* monoblastic, semi-macronematous, integrated, terminal or intercalary on mycelial extensions, branched, almost sessile. *Conidia* 139–321.5 × 42.5–94 µm, holoblastic, solitary, scattered, oblong to ovoid, obclavate, ellipsoidal or obpyriform, internally with bundles of narrow of cylindrical hyphae, together emerging as apical appendages towards the top, becoming disappear when dry, invisible septate, dark brow to black, smooth-walled.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 12 h. Colonies growing on MEA, reaching 18 mm in 2 weeks at 28°C, low convex, round with scalloped from middle to margin, radiating, slightly wavy, greyish brown to dark brown in surface, dark brown to black in reverse. Mycelium superficial and partly immersed, branched, septate, with hyaline to dark brown, pigmented verrucose, rough-walled, conidia produced on mycelium in culture at 45 days, 117–314 × 48–91 µm, oblong to ovoid, obclavate, ellipsoidal or obpyriform, muriform, internally with bundles of narrow of cylindrical hyphal appendages towards the top, invisible septate, dark brow to black, smooth-walled.

Material examined: THAILAND, Chanthaburi Province, Laem sing, on submerged decaying wood in a small freshwater stream, 7 July 2015, S. Boonmee, LS03 (MFLU 19-0257, **new record**), living culture (MFLUCC 16-1231).

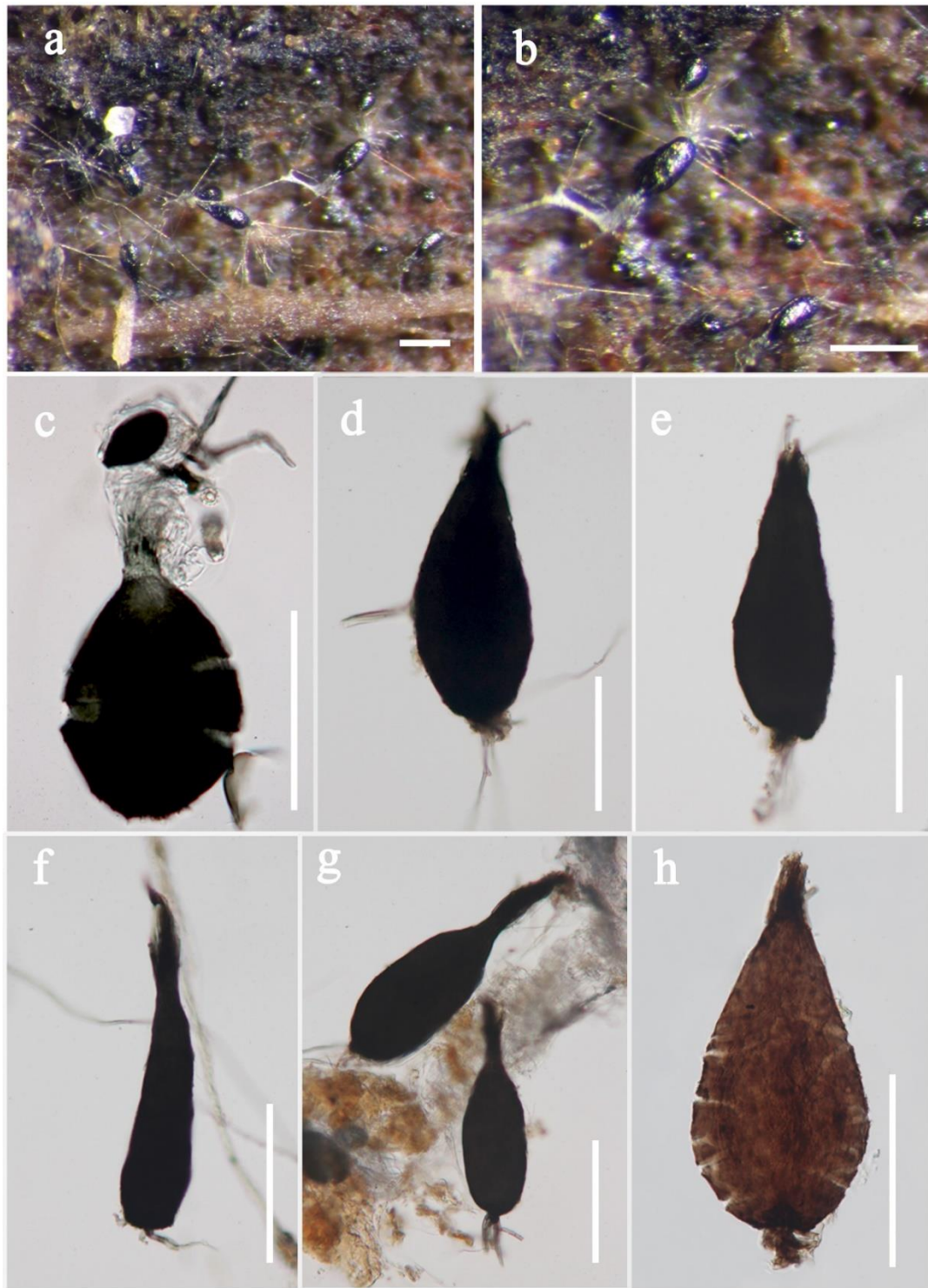


Figure 25. *Megacapitula villosa* (MFLU 19-0257, new record).

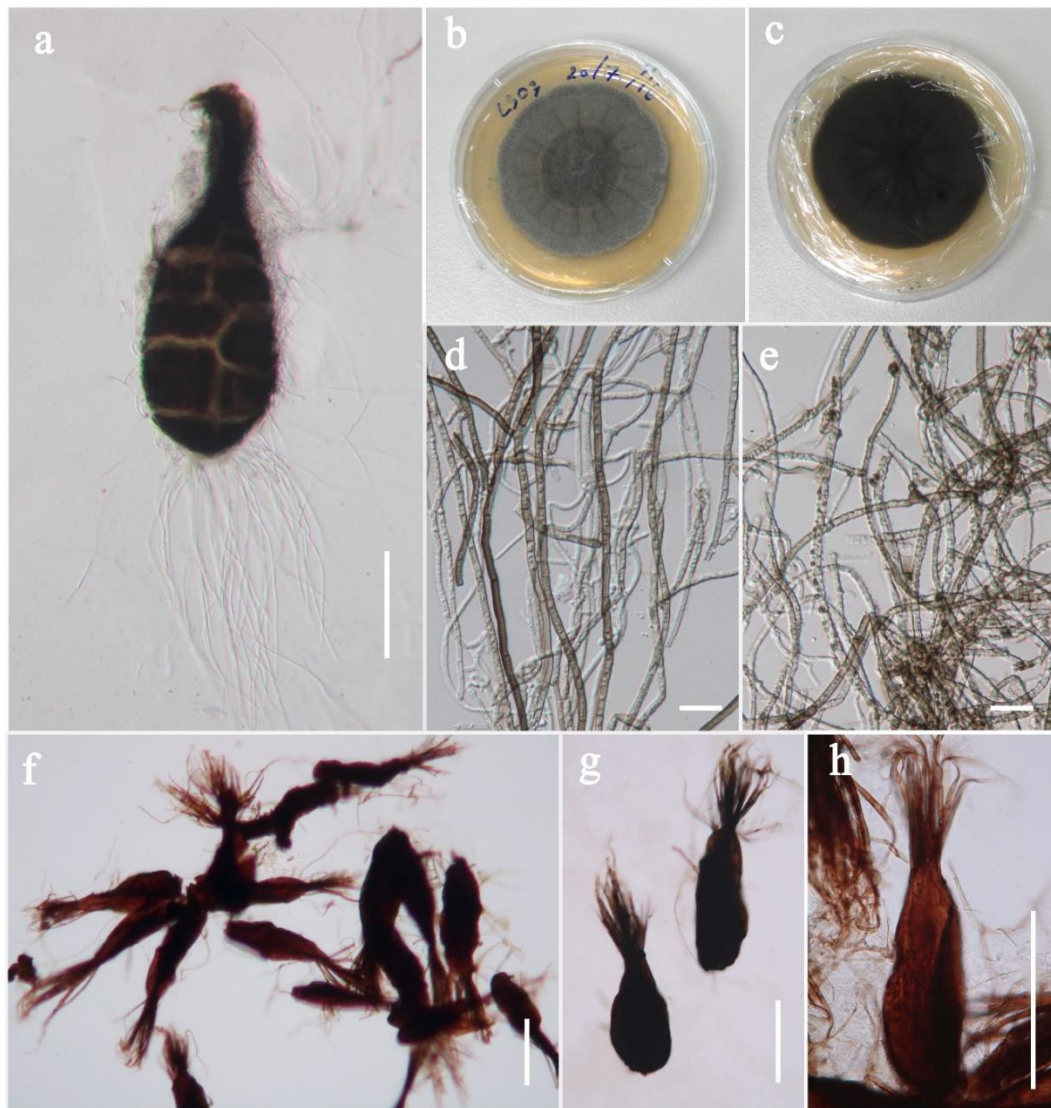


Figure 26. *Megacapitula villosa* sporulated in culture (MFLUCC 16-1231).

Herpotrichiellaceae Munk

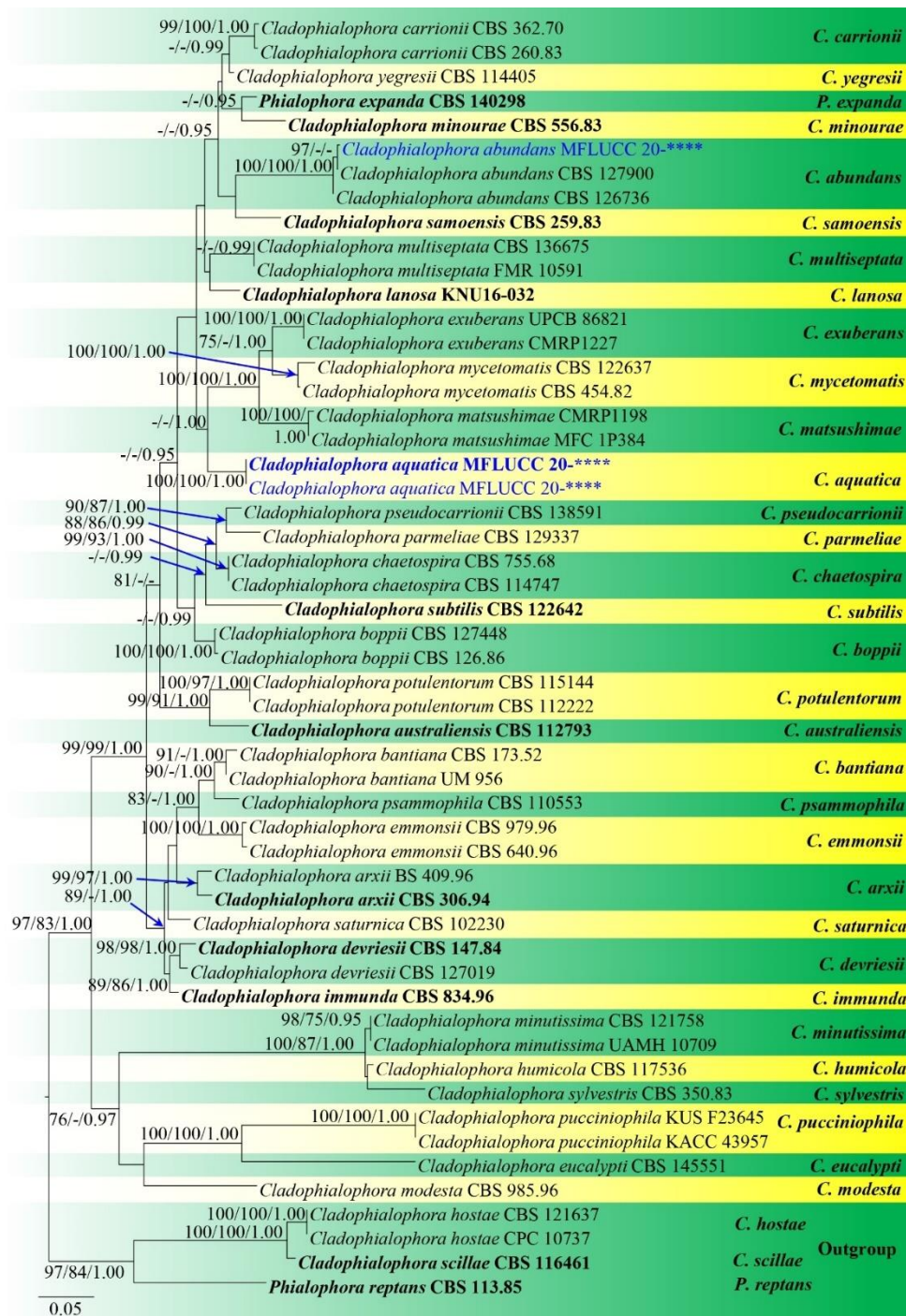


Figure 27. Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing the species of *Cladophialophora*. Related sequences are taken from Kiyuna et al. (2018). *Cladophialophora hostae* (CBS 121637 and CPC 10737), *C. scillae* (CBS 116461) and *Phialophora reptans* (CBS 113.85) were used as the outgroup taxa. Fifty-three taxa are included in the combined analyses which comprised 2163 characters (1668 characters for LSU, 495 characters for ITS) after alignment. The best scoring RAxML tree with a final likelihood value of -11764.771931 is presented. The matrix had 674 distinct alignment

patterns, with 48.87% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243290, C = 0.240717, G = 0.278143, T = 0.237850; substitution rates: AC = 1.885036, AG = 3.116460, AT = 1.481623, CG = 1.074902, CT = 7.751321, GT = 1.000000; gamma distribution shape parameter α = 0.220602. The MP analysis resulted a single most parsimonious tree (TL = 1816, CI = 0.509, RI = 0.708, RC = 0.360, HI = 0.491). Bootstrap support values for ML and MP equal to or greater than 70% and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequences are in blue and ex-type strains are in black bold.

***Cladophialophora* Borelli**

Cladophialophora abundans P. Feng, V.A. Vicente, Najafz., van den Ende, Stielow, Badali, Boeger & de Hoog, Figure 28

Facesoffungi number: FoF09157

Saprobic on submerged decaying wood in a freshwater. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Hyphae* 2.5–4.5 μm wide, irregularly septate, straight or bent, smooth, thin-walled, hyaline to pale brown, guttulate, branched, with formation of hyphal strands, and differentiated ellipsoidal to cylindrical conidiophores with conidial chains. *Conidiophores* semi-macronematous, pale olivaceous to brown, septate, oblong to cylindrical. *Conidial chains* forming laterally or terminally on undifferentiated hyphae, with profuse, strongly coherent conidial chains. *Conidia* 4.5–7.0 $\times$ 3.5–5.5 μm , pale olivaceous to brown, smooth and thin-walled, globose, ovoidal and ellipsoidal, non-septate; conidial scars slightly pigmented. Chlamydospores and yeast cells absent.

Culture characteristics: Colonies growing on MEA, reaching 30–35 mm in 2 weeks at 25°C. Mycelia superficial, irregularly circular, with entire to undulate margin, flat, smooth, from above pale brown, from below dark brown. Sporulation produced in culture within 2 weeks.

Material examined: THAILAND, Phuket Province, Thalang District, Mai Khao, on soil in a mangrove habitat, 5 May 2019, MS Calabon, 0506HY3 (MFLU 20-xxxx, **new record**), living culture (MFLUCC 20-xxxx).

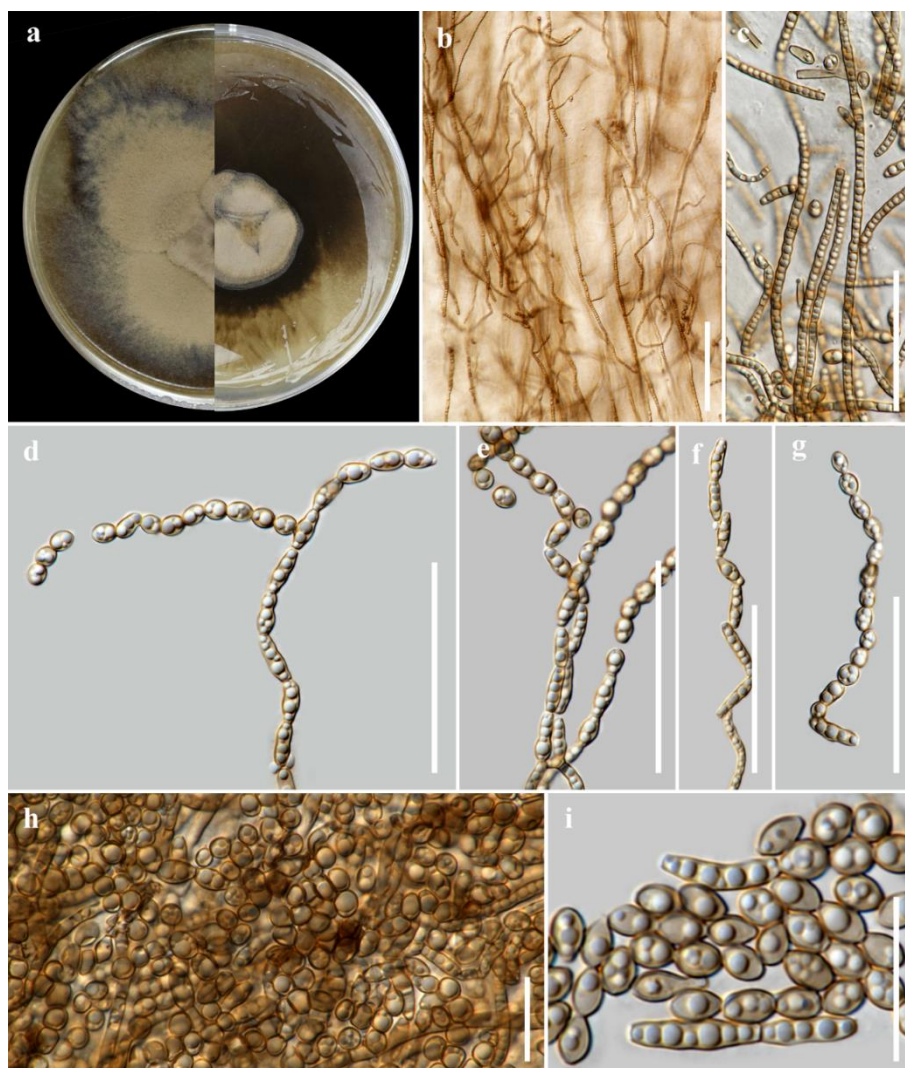


Figure 28. *Cladophialophora abundans* (MFLUCC 20-xxxx, **new record**).

Cladophialophora aquatica Calabon, Boonmee, E.B.G. Jones & K.D. Hyde, Figure 29

Index Fungorum number: IF****; Facesoffungi number: FoF09153

Etymology: Name reflects the aquatic habitat from where this species was collected

Holotype: MFLU 20-xxxx

Saprobic on submerged decaying wood in a freshwater. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous*. *Hyphae* 1.2–4.4 μm wide, septate, hyaline to lightly pigmented. *Chlamydospores* 8.2–13.5 $\times$ 3.5–8.9 μm , numerous, mostly in chain, intercalary or solitary, globose to subglobose, from olivaceous brown to dark brown.

Culture characteristics: Colonies growing on MEA, reaching 20–30 mm in 2 weeks at 25°C. Mycelia superficial, circular, with entire margin, flat, smooth, from above gray, from below dark brown. Chlamydospores produced in culture and induced with plant tissues within 30 days.

Material examined: THAILAND, Chiang Mai Province, Mushroom Research Center, on soil in a freshwater habitat, 11 February 2019, M.S. Calabon, MC03A (MFLU 20-xxxx, **holotype**), ex-type living culture, MFLUCC 20-xxxx; saprobic on decaying wood submerged in lake, 13 September 2019, M.S. Calabon, MRC10-1 (MFLU 20-xxxx, **paratype**), ex-paratype living culture (MFLUCC 20-xxxx).

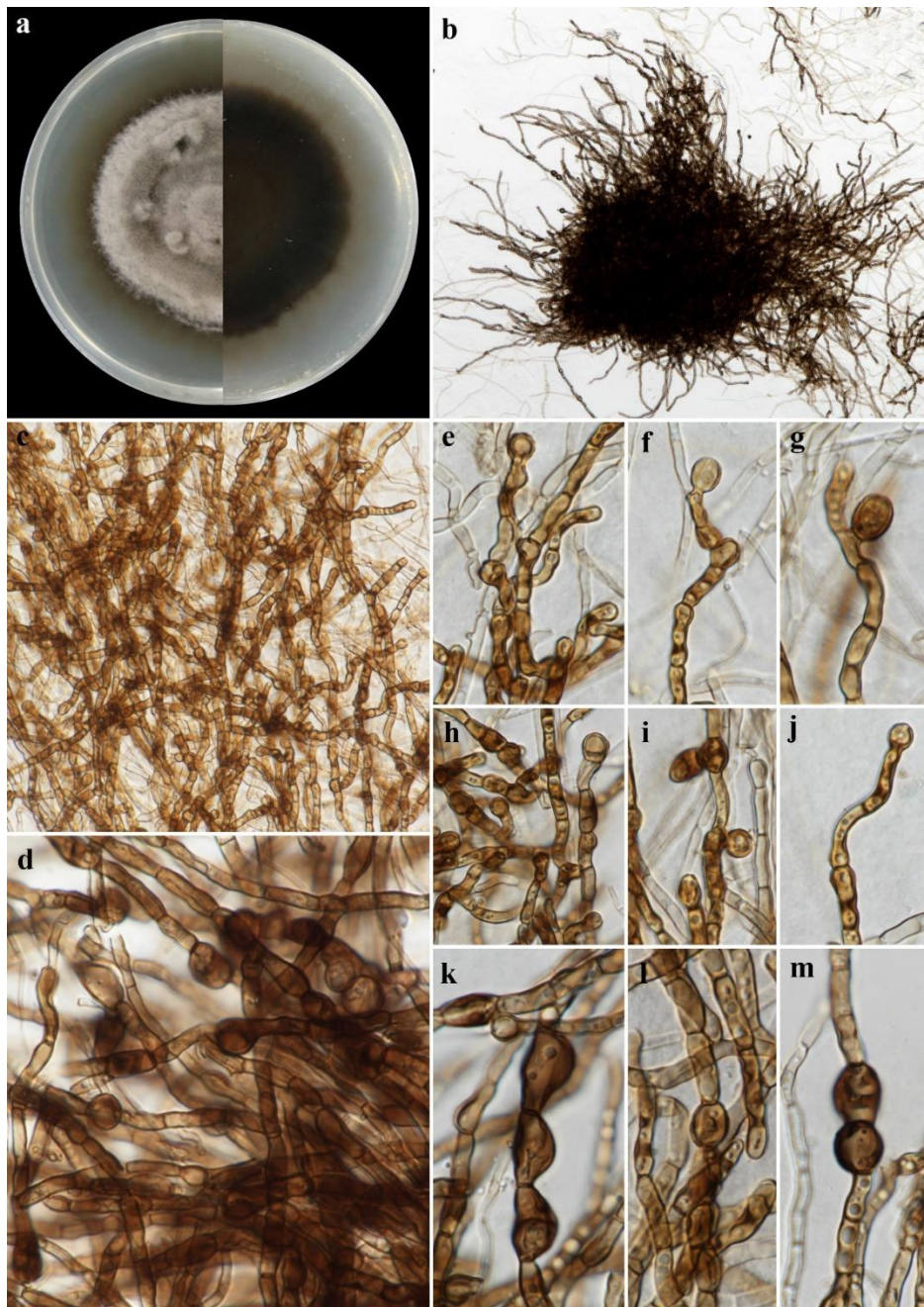


Figure 29. *Cladophialophora aquatica* (MFLUCC 20-***, **ex-type**).

Dactylosporaceae Bellem. & Hafellner (= Sclerococcaceae Réblová, Unter. & W. Gams)

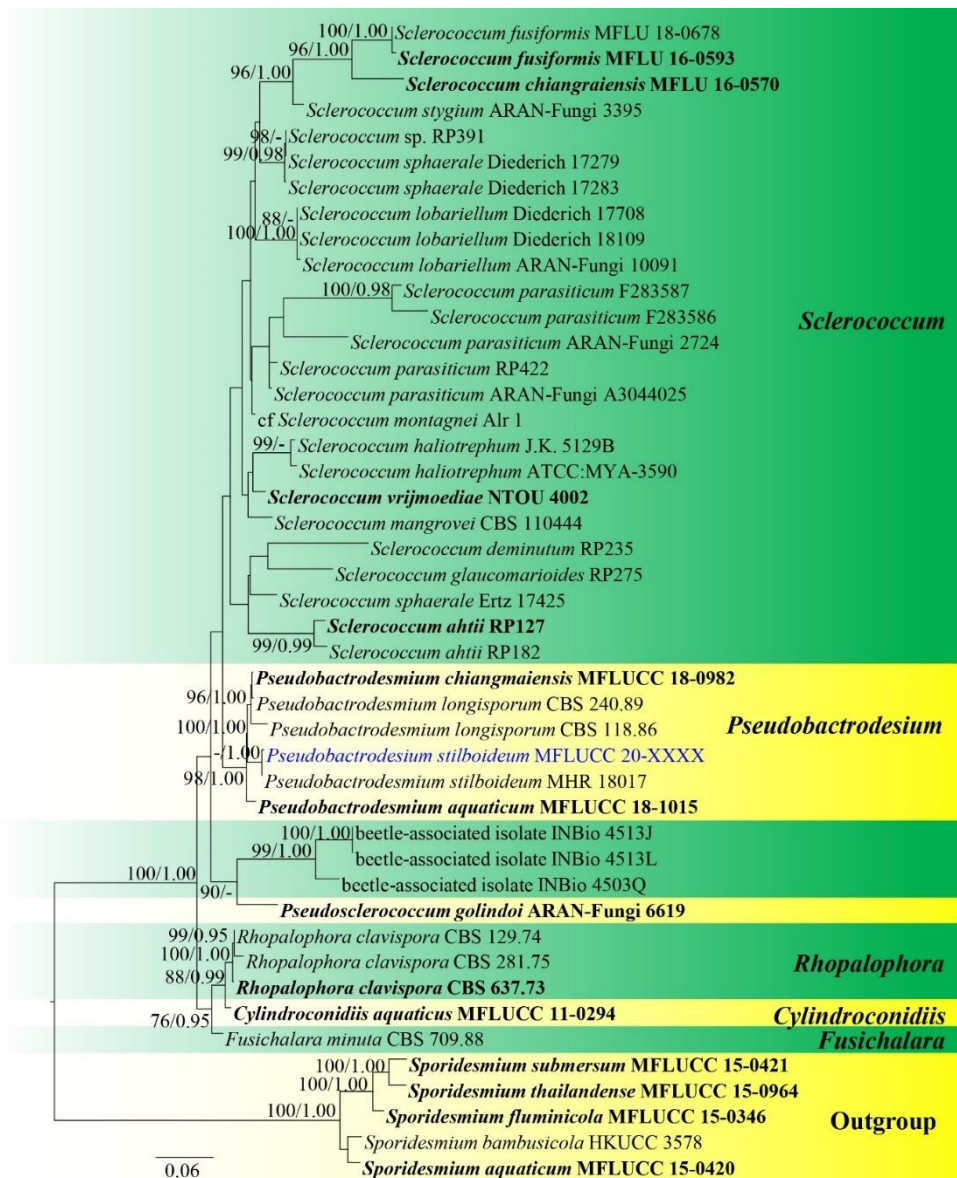


Figure 30. Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU and ITS sequence data for the species from *Dactylosporaceae*. Five species of *Sporidesmium* *aquaticum*, *S. bambusicola*, *S. fluminicola*, *S. submersum* and *S. thailandense* (Sporidesmiaceae) are used as outgroup taxa. The dataset comprised and 1222 characters after alignment including gaps (LSU = 793 bp, ITS = 429 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of -3662.794208. The matrix had 1053 distinct alignment patterns, with 51.86% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.266384, C = 0.211364, G = 0.273019, T = 0.249233; substitution rates AC = 1.261100, AG = 2.304874, AT = 1.337644, CG = 1.220148, CT = 5.907736, GT = 1.000000; gamma distribution shape parameter α = 0.284689. Support values for maximum likelihood (ML) above than 75% and

Bayesian posterior probabilities (BYPP) greater than 0.95 are given at the nodes. Newly generated sequences are in blue and ex-type species are in black bold.

Pseudobactrodesmium H. Zhang, W. Dong & K.D. Hyde

Pseudobactrodesmium stilboideum Calabon, Boonmee, E.B.G. Jones, K.D. Hyde, Figure 31

≡ *Bactrodesmium stilboideum* R. F. Castañeda & G. R. W. Arnold, *Revta Jardín bot. Nac., Univ. Habana* 6(1): 48 (1985)

= *Stigmina longispora* var. *stilboidea* (R.F. Castañeda & G.R.W. Arnold) J. Mena & Mercado, *Reporte de Investigacion del Instituto de Ecología y Sistemática* 17: 10(1987)

Index Fungorum number: IF****, Facesoffungi number: FoF09154

Saprobic on submerged decaying wood in a freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate 415–635 × 14–40.6 µm, synnematus, superficial, effuse, scattered, dark brown to dark olivaceous brown. *Mycelium* mostly immersed, composed of white, septate, branched and guttulate hyphae. *Conidiophores* 14.7–30.4 × 2.3–3.9 µm ($\bar{x}$ = 24.8 × 3.1 µm, n = 15) macronematous, fasciculate, compact, erect, subcylindrical, septate, slightly constricted at the septa, unbranched or branched, brown, smooth. *Conidiogenous cells* monoblastic, terminal, integrated, subcylindrical, pale brown, elongating percurrently. *Conidia* 48.4–65.1 × 7–8, solitary, dry, subcylindrical to narrowly fusiform, usually straight or slightly curved, euseptate, 9–13-phragmoseptate, thin and smooth-walled, slightly constricted and darker at septa, brown, paler towards both ends, obscurely guttulate, wedge-shaped at basal cell, with tapering apical cells, often enveloped by a hyaline, spherical, thin, mucilaginous cap at the apex, 8–10 µm diam. *Apical cells* elongated, up to 12 µm long, tapering gradually toward apex, hyaline to subhyaline, with subglobose tuberculate ends, secession schizolytic.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 20–25 mm in 2 weeks at 25°C. Mycelia superficial, circular, with entire margin, flat, smooth, from above white, from below smoke grey.

Material examined: THAILAND, Tak Province, Tha Sing Yang, Ban Mae Ja Wang, on submerged decaying wood in a freshwater river, 17 October 2019, N. Padaruth, CC44 (MFLU 20-xxxx), ex-type living culture (MFLUCC 20-xxxx).



Figure 31. *Pseudobactrodesmium stilboideum* (MFLU 20-xxx)

Pleurotheciaceae Réblová & Seifert

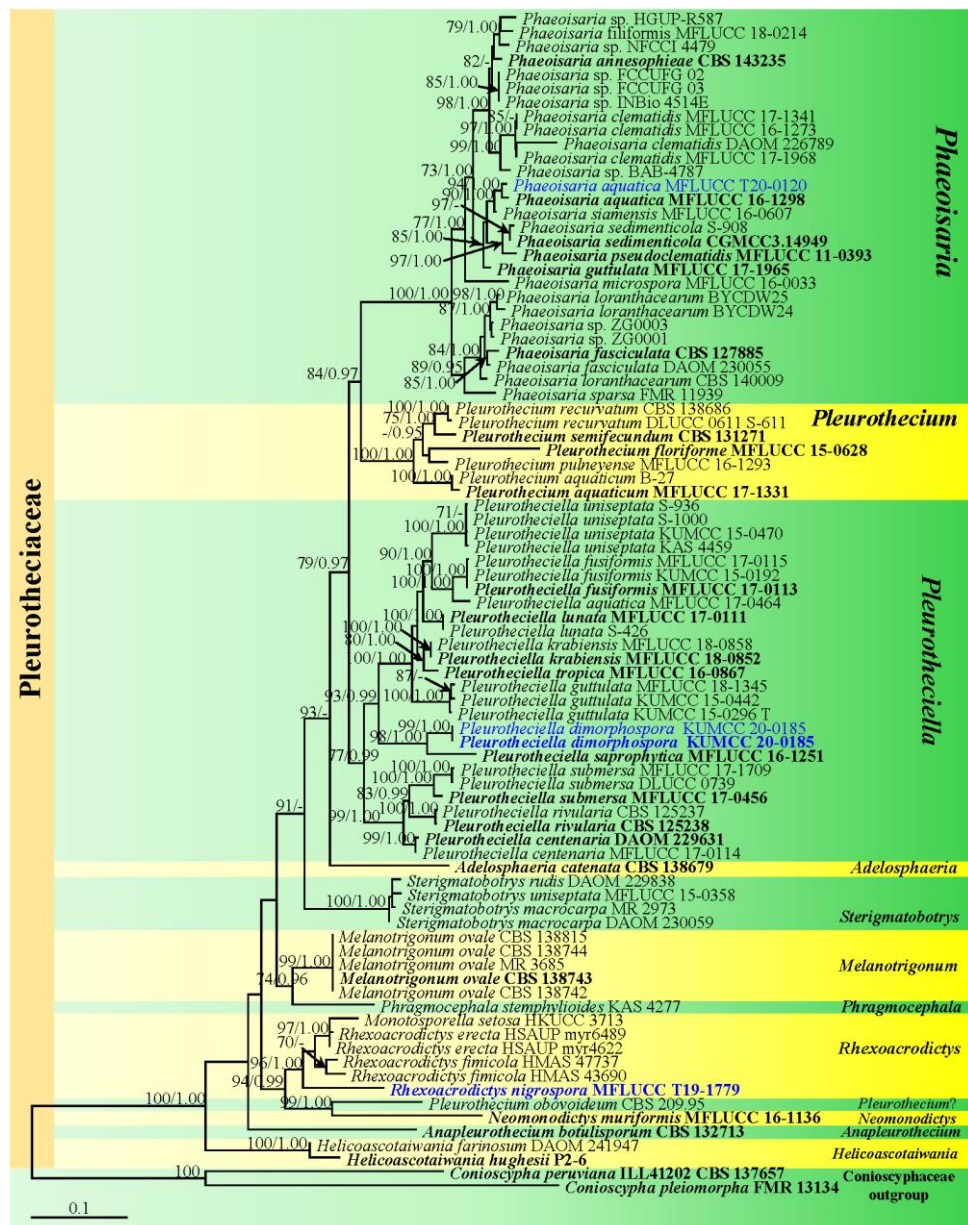


Figure 32. Phylogram generated from the best scoring of the RAxML tree based on the combined LSU, ITS, SSU and RPB2 sequence dataset of genera in Pleurotheciaceae, Pleurotheciales. Eighty-five strains are included in the combined analyses which comprise a total of 3760 characters. *Conioscypha peruviana* CBS 137657 and *Conioscypha pleiomorpha* FMR 13134 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of -22881.013498 is presented. RAxML analysis yielded 1537 distinct alignment patterns and 48.40% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234943, C = 0.258277, G = 0.290939, T = 0.215841, with substitution rates AC = 1.296294, AG = 2.271898, AT = 1.435876, CG = 0.860798, CT = 5.923861, GT = 1.000000; gamma distribution shape parameter alpha = 0.196681. Bootstrap support values for maximum

likelihood (ML, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in black bold and newly generated sequences are indicated in blue.

***Phaeoisaria* Höhn.**

***Phaeoisaria aquatica* Z.L. Luo, X.J. Su & K.D. Hyde, Figure 33**

Index Fungorum number: IF821837, Facesoffungi number: FoF03413

Saprobic on submerged decaying wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse, solitary, dark brown to black, hairy, covered by white conidial mass. *Mycelium* immersed in the substrate. *Synnemata* 313–727 × 11–23 µm, erect, straight to flexuous, dark brown to black, composed of compact parallel conidiophores, wide at the base, wide at the apical fertile region. *Conidiophores* macronematous, synematus, septate, branched, dark brown, smooth. *Conidiogenous cell* 12–21 × 2–5 µm, polyblastic, integrated, terminal and intercalary, sympodial, cylindrical or attenuated towards tip, hyaline to light brown, denticulate, denticle conspicuously cylindrical. *Conidia* 4.5–8 × 2–3 µm, ellipsoid to obovoid or sub-spatulate, straight, aseptate, hyaline, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on malt extract agar (MEA), reaching 2 cm diam. after 2 weeks at room temperature, flat, circular, surface slightly rough with crenated edge, white mist at the middle region, surrounded by greenish brown towards white grey at the margin, olivaceous dark green at the reverse with surrounded by white grey at the margin.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao village, saprobic on submerged decaying wood, 23 September 2019, N. Huanraluek, MY01 (MFLU xx-xxxx, **new record**), living culture (MFLUCC T20-0120).

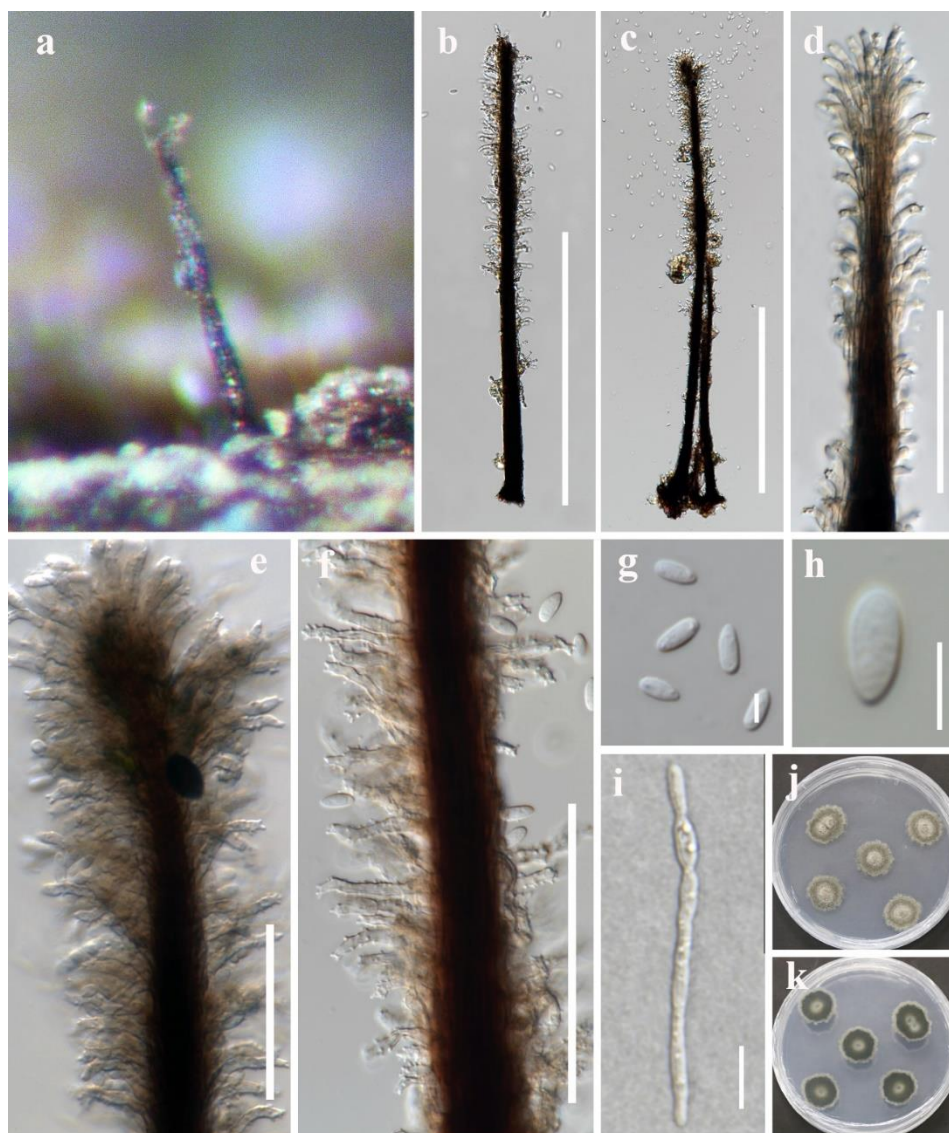


Figure 33. *Phaeoisaria aquatica* (MFLU xx-xxxx, **new record**).

Pleurotheciella Réblová, Seifert & J. Fourn.

Pleurotheciella dimorphospora H.B. Jiang, E.F. Yang & Phookamsak, Figure 34

Index Fungorum number: IFXXXXXX; Facesoffungi number: FoXXXXXX

Etymology: The specific epithet “*dimorphospora*” refers to the fungus forming two types of conidia

Holotype: MFLU 20-0138

Saprobic on a dead branch of *Malus* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *In natural substrate*, visible as small, black, shiny dots on host substrate. *Mycelium* immersed to partly immersed, sparse, brown, septate hyphae. *Conidiophores* 9–15(–21) × 2–4 μm, difficult to observed on host, macronematous, mononematous, subhyaline to brown, septate, unbranched, erect on host surface. *Conidiogenous cells* holoblastic, terminal,

discrete. *Conidia* (16.5–)20–27(–32) × (15–)20–25(–28) µm, dark brown to black, muriform, varied in shapes, ellipsoidal, subglobose, or irregular in shape, sectoried, inconspicuous septate. *In vitro*: Dimorphism, two types of conidial morphology. Type I: *Mycelium* 1.6–2.8 µm wide, superficial to immersed in media, with dark brown, septate, branched, smooth hyphae. *Conidiophores* 4.6–6 × 2.5–3.7 µm, semi-macronematous or macronematous, mononematous, straight or flexuous, hyaline to brown, cylindrical, septate, unbranched. *Conidiogenous cells* holoblastic, terminal or intercalary, integrated, brown. *Conidia* 20–29 × 14–19 µm wide, brown, muriform, varied in shape, subglobose to cordiform, or irregular in shape, with protuberant hilum. Type II: associated with type I, sometimes growing from the conidia. *Mycelium* hyaline, filaments, septate, sometimes compressed, producing brown synnemata. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.9–7.9 × 1.8–2.9 µm, holoblastic, integrated, terminal, hyaline, oblong to cylindrical, aseptate, unbranched. *Conidia* 8.5–10.8 × 3.8–4.8 µm, solitary, acrogenous, hyaline, ellipsoidal, 0–1-septate, smooth-walled, with guttules. *Chlamydospores* brown, phragmosporous or muriform, obovoid to clavate, transversely 2-septate, with longitudinally 1-septate, smooth-walled, with guttules.

Culture characteristics: Conidium germinating on WA within 24 h and germ tubes produced in all directions of cells. *Colonies* on PDA, reaching 20–25 mm diam. after 14 days at room temperature (16–20°C), irregular in shape, flattened to convex, undulate edge, with well-defined margin, medium dense, surface slightly rough, with black, conidial masses, and hyaline, water droplets, colony from above and below, dark brown to black.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany Kunming Institute of Botany (102° 44' 19" E, 25° 8' 27" N; 1951 m ± 3.00 m), on dead branch of *Malus* sp. (*Rosaceae*), 18 August 2018, R. Phookamsak, KIB049 (MFLU 20-0138, **holotype**), ex-type living culture (KUMCC 20-0185H) and isolate KUMCC 20-0185.

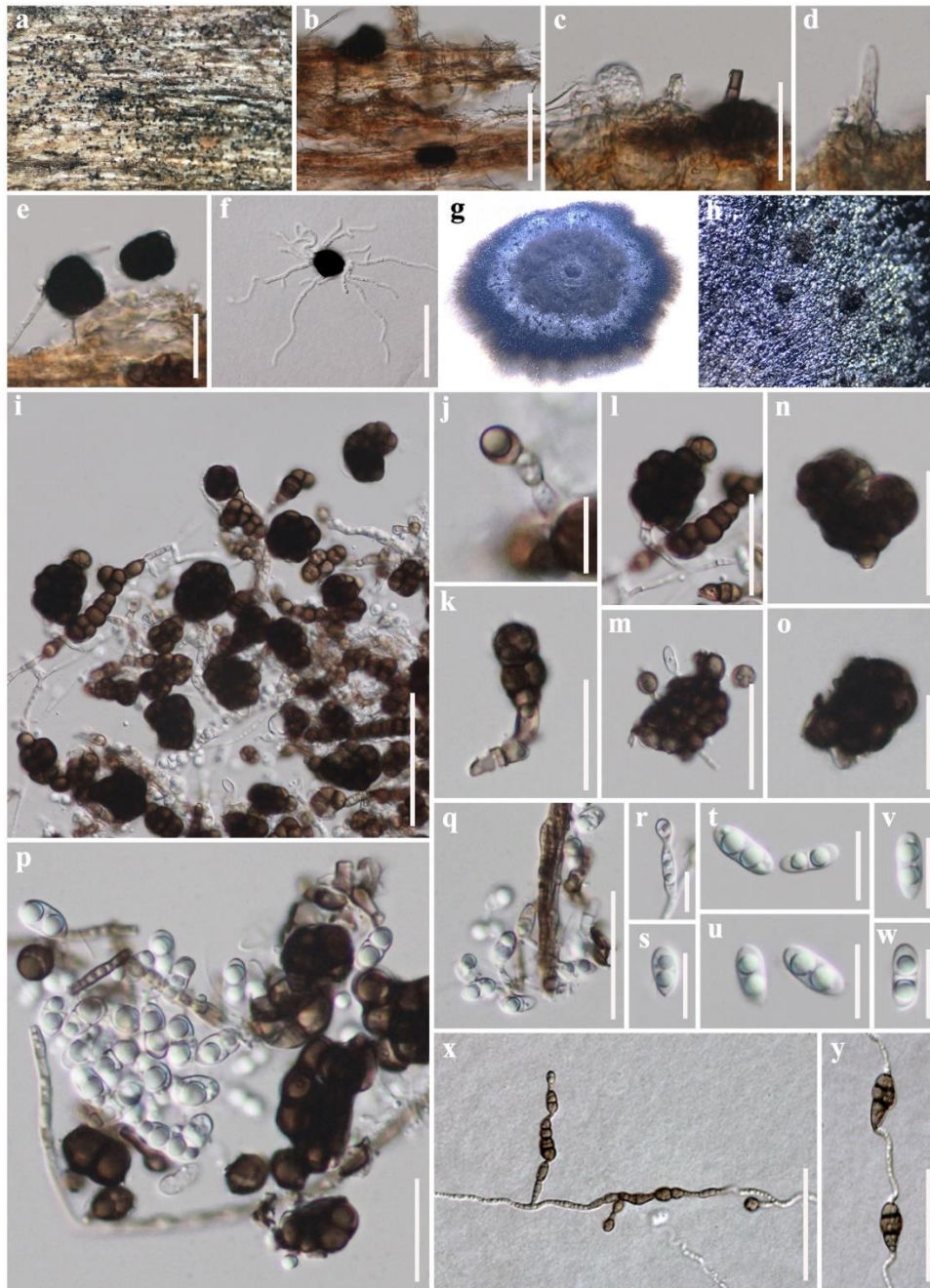


Figure 34. *Pleurotheciella dimorphospora* (MFLU 20–0138, **holotype**)

Rhexoacrodictys W.A. Baker & Morgan-Jones

Rhexoacrodictys nigrospora Boonmee & D.F. Bao, Figure 35

Index Fungorum number: IFxxxxxx; Facesoffungi number: FoF09200

Etymology: The specific epithet “*nigrospora*” refers to the black conidia.

Holotype: MFLU 20-xxxx

Saprobic on decaying bark. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* superficial, dark brown to black. *Mycelium* superficial and

immersed, composed of branched, septate, pale brown to brown hyphae, 1–2 μm wide, verruculose or finely echinulate-walled. *Conidiophores* micronematous or semi-macronematous, mononematous, cylindrical filamentous, flexuous, scattered to grouped, simple, single or a loose cluster brown to dark brown, smooth-walled. *Conidiogenous cells* monoblastic, polyblastic, integrated, terminal and intercalary or discrete, determinate. *Conidia* 15–31 $\times$ 16–33 μm , holoblastic, solitary, dry, acrogenous, simple, globose to subglobose, truncate at the base, multi-septate, dark brown when immature, becoming black and invisible septate at maturity, thick and smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h and germ tubes arising from terminal end cell. Colonies on malt extract agar (MEA), reaching 3.5 cm diam. after 2 weeks at room temperature, colonies circular, low convex, surface slightly rough with entire edge, around the white to greyish brown, dark green to black at the reverse.

Material examined: THAILAND, Phetchabun Province, Lom Sak, saprobic on decaying bark, 25 July 2019, S. Boonmee, LSP03 (MFLU xx-xxxx, **holotype**), ex-type living culture (MFLUCC T19-1779).

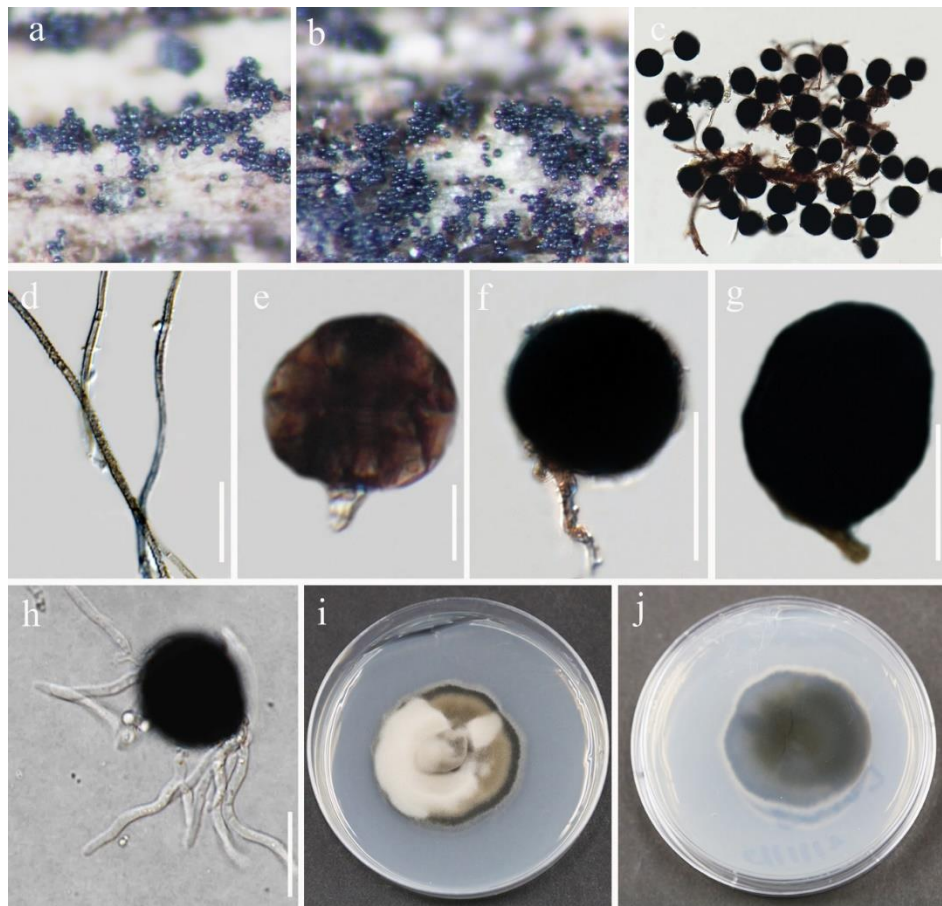


Figure 35. *Rhexoacrodictys nigrospora* (MFLUCC T19-1779, **holotype**)

Torulaceae Corda

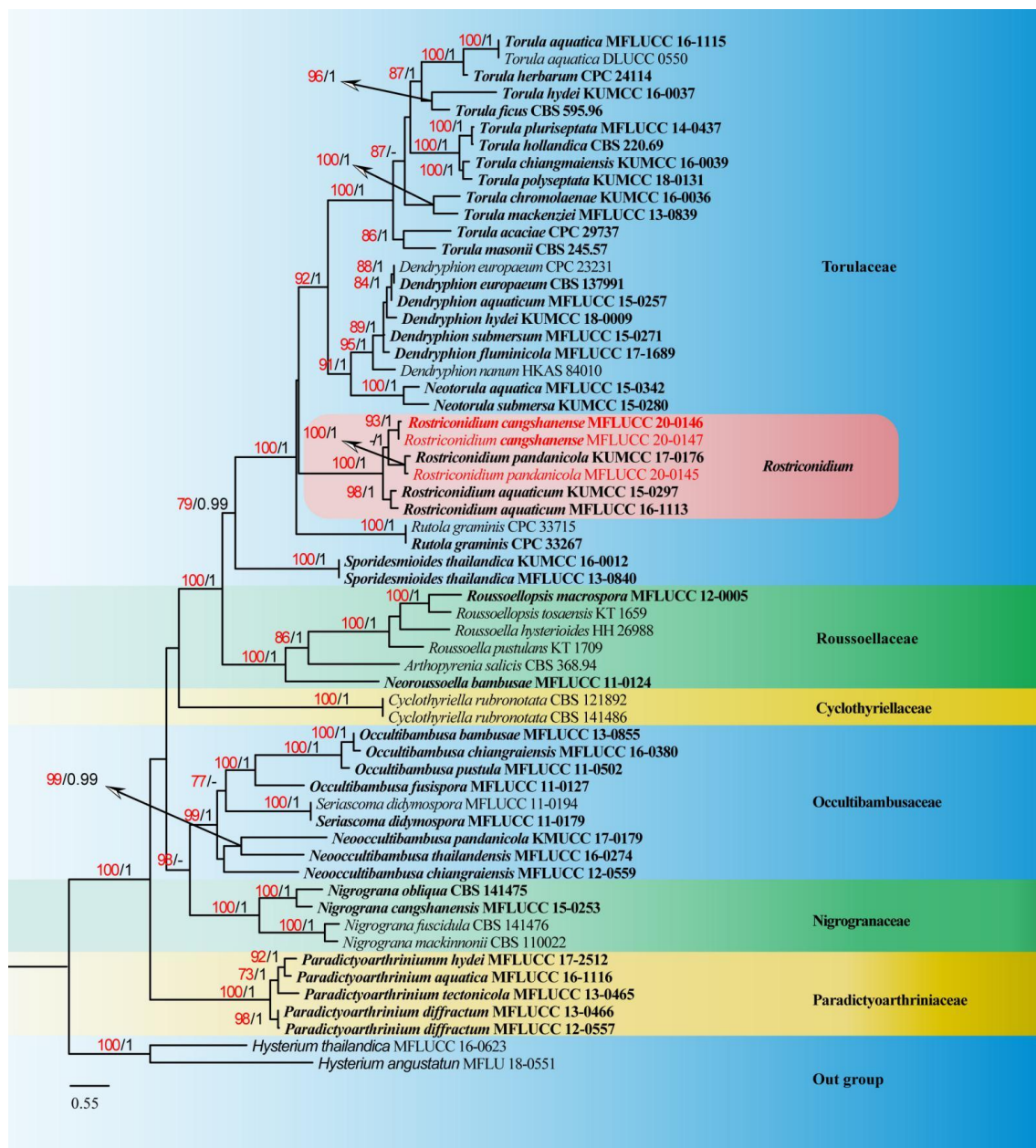


Figure 36. Maximum likelihood (RAxML) tree is based on combined ITS, LSU, RPB2, SSU and TEF1- α sequence data. Bootstrap support values with a maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities (PP) greater than 0.95 is given above the nodes. The tree is rooted with *Hysterium angustatum* (MFLUCC 16-0623) and *H. thailandica* (MFLU 18-0551). Newly generated sequences are indicated in red and ex-type strains are in bold.

Rostriconidium Z.L. Luo, K.D. Hyde & H.Y. Su

Rostriconidium cangshanense H.W. Shen, Z.L. Luo & H.Y. Su, Figure 37

Index Fungorum number: IF 557947, Facesoffungi number: xxx

Etymology: Referring to the collection site from Cangshan Mountain in Yunnan province, China.

Holotype: MFLU 20-0572

Saprobic on submerged rotten wood. Asexual morph: *Colonies* on the natural substrate, scattered, erect, hairy, dark, dry. *Mycelium* is partly immersed in the substrate and partly on the surface, septate, branched, brown hyphae. *Conidiophores* $279\text{--}528 \times 12\text{--}14 \mu\text{m}$ ($\bar{x} = 404 \times 13 \mu\text{m}$, $n = 15$), macronematous, mononematous, single, septate, dark brown to black, smooth or rough-walled, unbranched, straight or slightly flexuous, light-color at the apex. *Conidiogenous cells* polyblastic, integrated, terminal, cylindrical, smooth, dark brown, with black circle-peak shape conidiogenous scars. *Conidia* $94\text{--}109 \times 21\text{--}24 \mu\text{m}$ ($\bar{x} = 101 \times 23 \mu\text{m}$, $n = 20$), dry, solitary, pyriform, fusiform to obclavate, rostrate, with obvious guttulate cells when immature, dark brown to black, 6–8-septate, slightly constricted at some septa, with black truncate, dark structure at the base with a light-colored cell above it, straight or slightly flexuous, smooth-walled, sometimes with hyaline sheath at apex. Sexual morph: Undetermined.

Culture characteristics: Conidia germinating on PDA within 24h. Colonies growing on PDA, after 1 month at room temperature, initially white-grey and later become dark brown, with dense mycelium, circular, with entire edge, black in reverse, with smooth margin.

Material examined: CHINA, Yunnan Province, Nujiang River, on submerged decaying wood in freshwater habitat, 11 October 2016, S.M Tang, S-943 (MFUL 20-0572, holotype), ex-type living culture, MFLUCC 20-0146; Dali City, Cangshan mountain, Heilong stream, on submerged rotten wood in freshwater habitat, 18 November 2016, Z.L Luo, S-270 (MFUL 20-0571), living culture, MFLUCC 20-0147.

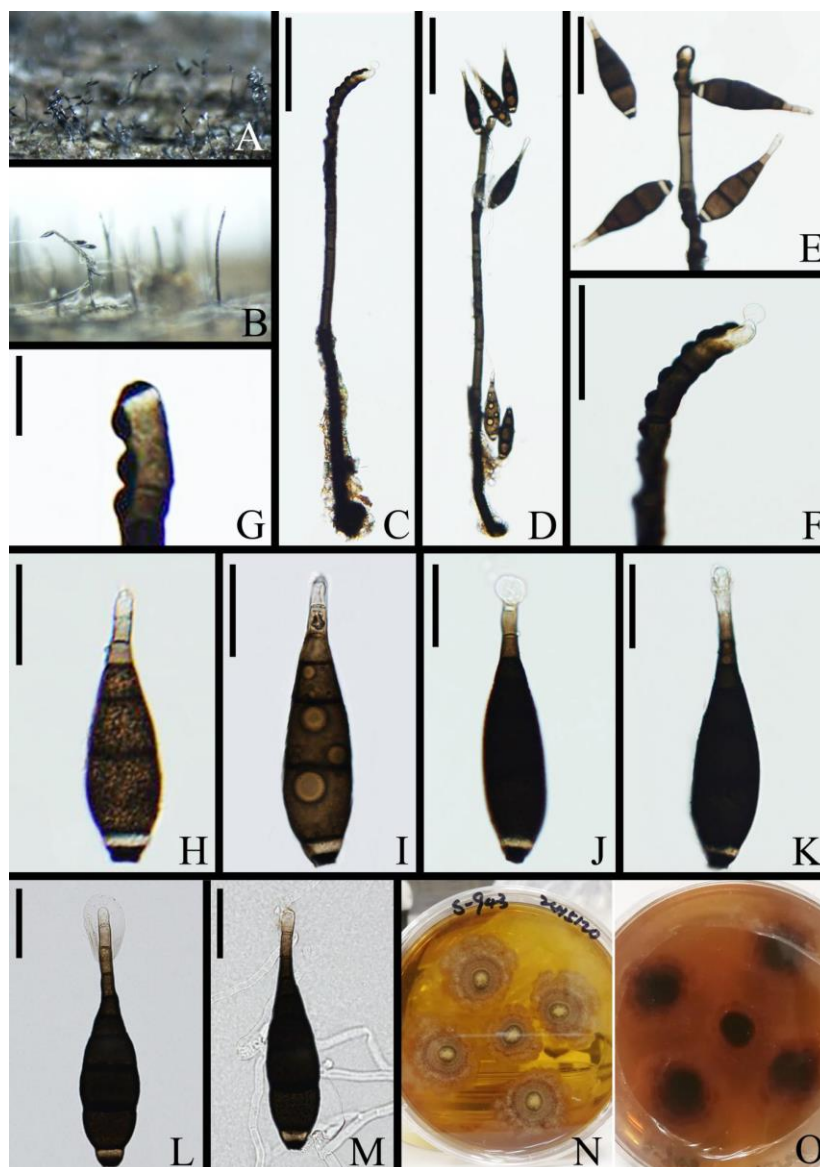


Figure 37. *Rostriconidium cangshanense* (MFLU 20-0572, **holotype**)

Rostriconidium pandanicola Tibpromma & K.D. Hyde, Figure 38

Saprobic on submerged rotten wood. Asexual morph: *Colonies* on the natural substrate, erect hairy, dark. *Mycelium* is partly immersed in the substrate and partly on the surface, septate, branched, white to brown hyphae. *Conidiophores* $171\text{--}211 \times 10\text{--}11 \mu\text{m}$ ($\bar{x} = 196 \times 10 \mu\text{m}$, $n = 10$), macronematous, mononematous, single, septate, smooth or rough-walled, unbranched, straight or slightly flexuous, pale brown to brown, light-color at apex. *Conidiogenous cells* monotretic or polytretic, terminal, sympodial, integrated, cylindrical, dark brown. *Conidia* $90\text{--}111 \times 19\text{--}24 \mu\text{m}$ ($\bar{x} = 101 \times 22 \mu\text{m}$, $n = 20$), solitary, dry, obclavate, rostrate at maturity, with guttulate cells, pale brown to dark brown, 5–8-septate, slightly constricted at septa, with black truncate at the base, dark structure at the base with a light-colored cell above it, straight or slightly flexuous, smooth-walled long rostrate at maturity, with hyaline sheath at apex. Sexual morph: Undetermined.

Culture characteristics: Conidia germinating on PDA within 24h. Colonies growing on PDA, after 1 month of incubation at room temperature, surface white to light brown, with densely mycelium, circular, smooth edges, raised in the middle, brown on back, cracks in the middle.

Material examined: CHINA, Yunnan Province, Lancang River, on submerged rotten wood in freshwater habitat, 28 April 2018, H.W Shen, S-1887 (MFUL 20-0573), living culture, MFLUCC 20-0145.

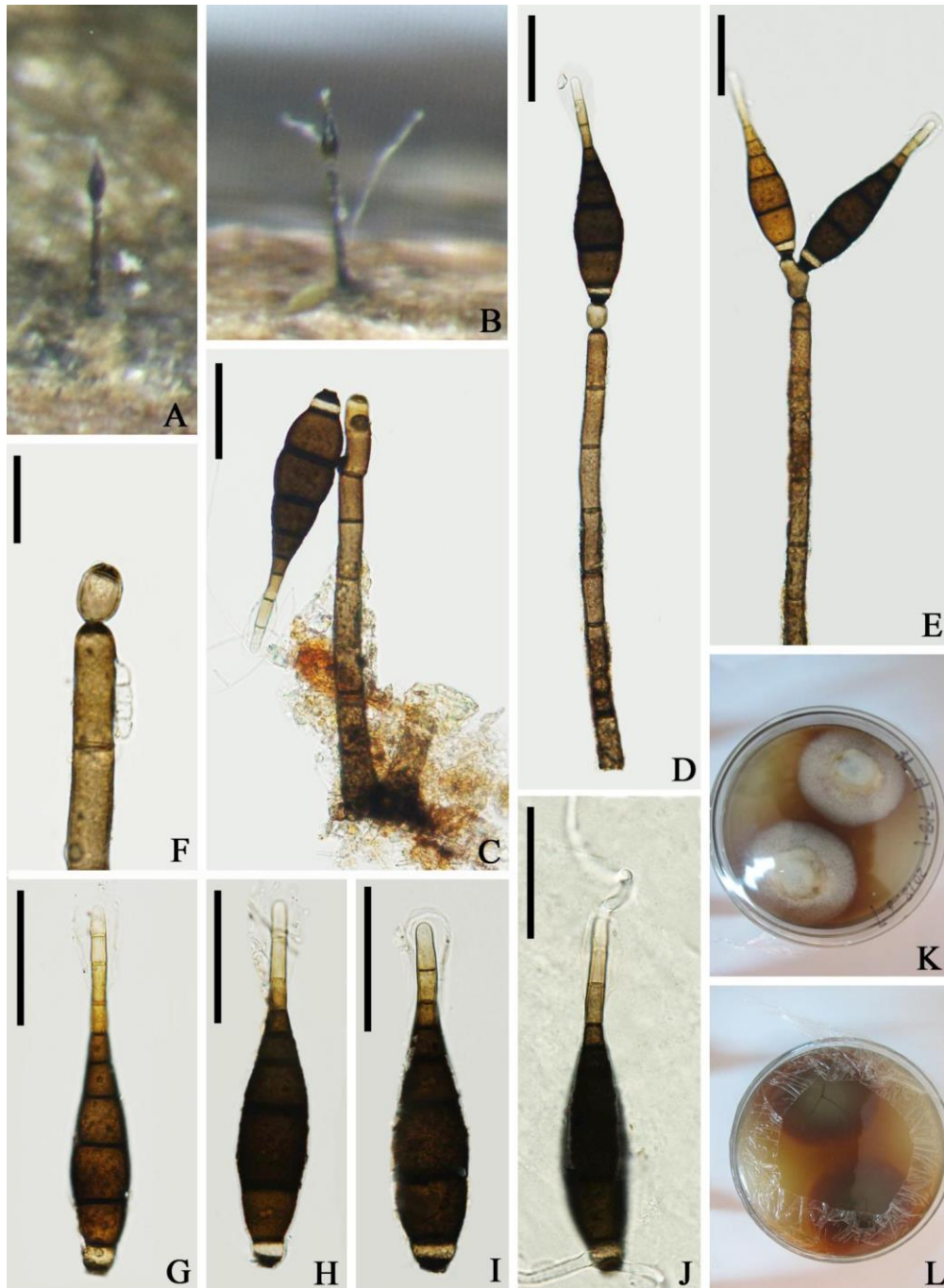


Figure 38. *Rostriconidium pandanicola* (MFLUCC 20-0145)

Conclusion and Discussion

Hyphomycetes are geographically widespread and found in diverse ecological niches. Most taxa are commonly found on plant tissues, wood and bark, lichens, dung, soil, freshwater, marine waters, insects and other arthropods, vertebrates, as well as parasitic on other fungi. The research was conducted to survey hyphomycetous fungi on woody substrates from different terrestrial and aquatic habitats in rainy, dry and winter seasons during October 2018 to March 2020. Hyphomycetes can be recognized in nature on substrate surface by presence of superficial stromata, setae, conidiophores, conidiogenous cells and conidia. Of these 100 taxa obtained cultures and sequences such as species in genera *Dictyocheiropora*, *Dictyosporium*, *Digitodesmium* and other hyphomycetes. Furthermore, we provide a contribution to the knowledge of novel and exists hyphomycetous species in 16 genera i.e. *Camposporium thailandicum*, *Cladophialophora abundans*, *Cladophialophora aquatica*, *Dictyocheiropora aquadulcis*, *Dictyocheiropora rotunda*, *Dictyocheiropora taiwanense*, *Dictyosporium pandanicola*, *Digitodesmium chiangmaiense*, *Ernakulamia tanakae*, *Helminthosporium chiangraiense*, *Hermatomyces sphaericoides*, *Megacapitula villosa*, *Mycoenterolobium aquadictyosporium*, *Phaeoisaria aquatica*, *Pleurotheciella dimorphospora*, *Pseudobactrodesmium stilboideum*, *Rhexoacrodictys nigrospora*, *Rostriconidium cangshanense*, *Rostriconidium pandanicola*, *Spegazzinia thailandica* and *Triseptata sexualis* based on morpho-molecular data identifications.

However, the great majority of hyphomycetes species in other tropical areas include Thailand are still unresolved taxonomy and lacked molecular data. Therefore, fresh collections, epitypifications and sequence data are required further study.

Suggestion for future works

Many of hyphomycetes fungi have never been sequenced include their type species. This study aims to obtain strains of these fungi in culture and multigene sequence data for them. Therefore by studying hyphomycetes fungi in a relatively poorly studied habitat we can establish whether previous estimates of fungal diversity are realistic. As a result of this study we will isolate numerous fungi that will be preserved in MFLU culture collections and dry herbarium specimens will be preserved in MFLU fungarium collections. It is important to carry out studies as stated here to obtain a wide diversity of hyphomycetous fungal isolates across the spectrum of fungi so that screening will use a taxonomically diverse range of fungal taxa.

Output จากโครงการวิจัยที่ได้รับทุนจาก สกว.

1. ผลงานตีพิมพ์ในวารสารวิชาการนานาชาติ (ระบุชื่อผู้แต่ง ชื่อเรื่อง ชื่อวารสาร ปี เล่มที่ เลขที่ และหน้า) หรือผลงานตามที่คาดไว้ในสัญญาโครงการ
2. การนำผลงานวิจัยไปใช้ประโยชน์
 - เชิงพาณิชย์ (มีการนำไปผลิต/ขาย/ก่อให้เกิดรายได้ หรือมีการนำไปประยุกต์ใช้โดยภาคธุรกิจ/บุคคลทั่วไป)
 - เชิงนโยบาย (มีการกำหนดนโยบายอิงงานวิจัย/เกิดมาตรการใหม่/เปลี่ยนแปลงระเบียบข้อบังคับหรือวิธีทำงาน)
 - เชิงสาธารณะ (มีเครือข่ายความร่วมมือ/สร้างกระแสความสนใจในวงกว้าง)
 - เชิงวิชาการ (มีการพัฒนาการเรียนการสอน/สร้างนักวิจัยใหม่)
3. อื่นๆ (เช่น ผลงานตีพิมพ์ในวารสารวิชาการในประเทศ การเสนอผลงานในที่ประชุมวิชาการ หนังสือ การจดสิทธิบัตร)

Appendix

List of publications

1. **Boonmee S**, Wijayawardene NN, Bhat DJ, Tennakoon DS, Hyde KD (2019) *Misturatosphaeria viridibrunnea* sp. nov. (Teichosporaceae, Pleosporales) from Thailand. *Phytotaxa* 388(1): 123-134 (Q2, IF: 1.007).
2. Hyde KD, Danushka S, Tennakoon DS, Jeewon R, Bhat DJ, Maharachchikumbura SSN, Rossi W, Leonardi M, Lee HB, Mun HY, Houbaken J, Nguyen TTT, Jeon SJ, Frisvad JC, Dhanushka N, Wanasinghe DN, Luücking R, Aptroot A, Cáceres MES, Karunarathna SC, Hongsanan S, Phookamsak R, de Silva NI, Thambugala KM, Jayawardena RS, Senanayake IC, **Boonmee S**, Chen J, Luo ZL, Phukhamsakda C, Pereira OL, Abreu VP, Rosado AWC, Bart B, Randrianjohany E, Hofstetter V, Gibertoni TB, da Silva Soares AM, Plautz HL Jr, Sotã o HMP, Xavier WKS, Bezerra JDP, de Oliveira TGL, de SouzaMotta CM, Magalhães OMC, Bundhun D, Harishchandra D, Manawasinghe IS, Dong W, Zhang SN, Bao DF, Samarakoon MC, Pem D, Karunarathna A, Lin CG, Yang J, Perera RH, Kumar V, Huang SK, Dayarathne MC, Ekanayaka AH, Jayasiri SC, Xiao YP, Konta S, Niskanen T, Liimatainen K, Dai YC, Ji XH, Tian XM, Mešić A, Singh SK, Phutthacharoen K, Cai L, Sorvongxay T, Thiagaraja V, Norphanphoun C, Chaiwan N, Lu YZ, Jiang HB, Zhang JF, Abeywickrama PD, Aluthmuhandiram JVS, Brahmanage RS, Zeng M, Chethana T, Wei DP, Réblová M, Fournier J, Nekvindová J, do Nascimento Barbosa R, dos Santos JEF, de Oliveira NT, Li GJ, Ertz D, Shang QJ, Phillips AJL, Kuo CH, Camporesi E, Bulgakov TS, Lumyong S, Jones EBG, Chomnunti P, Gentekaki E, Bungartz F, Zeng XY, Fryar S, Tkalc̃ec Z, Liang J, Li GS, Wen TC, Singh PN, Gafforov Y, Promputtha I, Yasanthika E, Goonasekara ID, Zhao RL, Zhao Q, Kirk PM, Liu JK, Yan JY, Mortimer PE, Xu JC (2019) Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 96: 1-242 (Q1, IF: 15.386).
3. **Boonmee S**, Sorvongxay T, Huanraluek N, Hyde KD (2019) *Wicklowia submersa* sp. nov. (Wicklowiaceae, Pleosporales), a second species in a monotypic family. *Phytotaxa*. 411(1): 73-83 (Q2, IF: 1.007).
4. Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao DF, Li JF, Samarakoon MC,

- Chaiwan N, Lin CG, Phutthacharoen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma s, Brahmanage RS, **Boonmee S**, Huang SK, Thiyagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjana M, Sarma VV, Liimatainen K, Aguirre- Hudson B, Niskanen T, Overall A, Alvarenga RLM, Gibertoni TB, Pfliegler WP, Horváth E, Imre A, Alves AL, da Silva Santos AC, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu JC, Sheng J (2020) Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 100:5-277 (Q1, IF: 15.386).
5. **Boonmee S**, Calabon MS, Phookamsak R, Elgorban AM, Hyde KD (2020) *Triseptata sexualis* gen. et sp. nov. in Latoruaceae (Pleosporales). *Phytotaxa* 447(4): 252-264 (Q2, IF: 1.007).
 6. Calabon MS, Hyde KD, Jones EBG, Doilom M, Liao CF, **Boonmee S*** (2020) *Mycoenterolobium aquadictyosporium* sp. nov. (Pleosporomycetidae, Dothideomycetes) from a freshwater habitat in Thailand. *Mycological Progress* 19:1031–1042 (Q1, IF: 2.149).
 7. **Saranyaphat Boonmee**, Mark S. Calabon, Naruemon Huanraluek, Walter Rossi, Marco Leonardi, Diogo RS Pereira, Alan JL Phillips, María P. Martín, Margarita Dueñas, M. Teresa Telleria, Izabela L. Kałucka, Andrzej M. Jagodziński, Kare Liimatainen, Sanjay K Singh, Shiwali Rana, Paras Nath Singh, Deepak K Maurya, Kunhiraman C. Rajeshkumar, Nikhil Ashtekar, Sneha Lad, Nalin N. Wijayawardene, Darbe J. Bhat, Guo-Jie Li, Wen-Fei Lin, Niranjana M., Sarma V.V., Mohamed A. Abdel-Wahab, Faten A. Abdel-Aziz, Upendra Singh, R.P. Bhatt, Hyang Burm Lee, Thuong T.T. Nguyen, Paul M. Kirk, Arun Kumar Dutta, Krishnendu Acharya, Dan-Feng Bao, Jafar Abdollahzadeh, Isaac Garrido-Benavent, Francesco Dovana, Muhammad Usman, Abdul Nasir Khalid, Rungtiwa Phookamsak, Asha J. Dissanayake, Anusha Telagathoti, Maraike Probst, Ursula Peintner, Lilla Bóna, Zsolt Merényi, et al. (20xx) Fungal diversity notes 1390–1xxx: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* (in preparation).

Misturatosphaeria viridibrunnea sp. nov. (Teichosporaceae, Pleosporales) from Thailand

SARANYAPHAT BOONMEE¹, NALIN N. WIJAYAWARDENE¹, D. JAYARAMA BHAT², DANUSHKA S. TENNAKON¹ & KEVIN D. HYDE^{1*}

¹ Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

² No.128/1-J, Azad Housing Society, Curca, Goa Velha 403108, India

Corresponding author: kdhyde3@gmail.com

Abstract

We introduce a new species, *Misturatosphaeria viridibrunnea*, isolated from dead branches of an unidentified terrestrial dicotyledonous plant in Chiang Rai, Thailand. The new species is characterized by fusiform, 1-septate, olivaceous brown to dark brown, regularly 4-guttulate ascospores with slightly longitudinal striations on surface. *Misturatosphaeria viridibrunnea* is easily distinguishable from other species in the genus by smaller-sized ascomata, asci and ascospores. Phylogenetic analyses using a combined gene analysis of LSU and ITS sequence data indicated that the new species belongs to Teichosporaceae (Pleosporales). A detailed morphological description and illustration of the new species is provided.

Keywords: 1 new species, bitunicate, multi-gene phylogeny, saprobic, taxonomy

Introduction

The genus *Misturatosphaeria* Mugambi & Huhndorf was introduced by Mugambi and Huhndorf (2009) to accommodate nine taxa based on morpho-molecular analyses and accommodated in Lophiostomataceae, Pleosporales. The genus is characterized by immersed to superficial, globose to subglobose or pyriform, darkly pigmented ascomata, bitunicate, cylindric-clavate, stalked asci, pseudoparaphyses, mostly fusiform to oblong elliptical, uni- to multi-septate, hyaline to pigmented ascospores and a coelomycetous asexual morph known only in *Misturatosphaeria radicans* under the basionym *Melanomma radicans* Samuels & E. Müll (Samuels & Müller 1978, Mugambi & Huhndorf 2009, Thambugala *et al.* 2015). Thambugala *et al.* (2015) accepted only three species in the genus i.e., *Misturatosphaeria aurantiacinctata*, *M. radicans* (basionym: *Melanomma radicans* Samuels & E. Müll. and placed *Misturatosphaeria uniseptata* Mugambi, A.N. Mill. & Huhndorf) and an unidentified *Misturatosphaeria* species, in Floricolaceae (= Teichosporaceae), while seven species were transferred to other genera (viz. *Asymmetrispora* Thambug. & K.D. Hyde, *Aurantiascoma* Thambug. & K.D. Hyde, *Magnibotryascoma* Thambugala & K.D. Hyde, *Pseudoaurantiascoma* Thambug. & K.D. Hyde and *Pseudomisturatosphaeria* Thambug. & K.D. Hyde). Jaklitsch *et al.* (2016b) synonymised all genera introduced by Thambugala *et al.* (2015), plus *Misturatosphaeria* introduced by Mugambi & Huhndorf (2009) and three genera of Koblmeier & Volkmann-Koblmeier (2000) i.e., *Floricola*, *Septoriella* and *Stagonospora* under *Teichospora* (Koblmeier & Volkmann-Koblmeier 2000), while synonymising Floricolaceae under Teichosporaceae. Wijayawardene *et al.* (2017) however, did not agree with the synonymies in Jaklitsch *et al.* (2016b) and followed Thambugala *et al.* (2015). Presently, Teichosporaceae comprises 14 genera (Wijayawardene *et al.* 2017, 2018), which we follow here, although the latter publication inadvertently omitted *Asymmetrispora* and *Pseudomisturatosphaeria* (Wijayawardene pers. comm.).

Hyde *et al.* (2018) showed that the novel fungal taxa found in Thailand was between 55–96% and in this study we discovered a new species of *Misturatosphaeria*. *Misturatosphaeria viridibrunnea*, is therefore introduced based on both morphology and phylogeny. Maximum likelihood (ML) and Bayesian analyses (BI) of combined LSU and ITS sequence data evidently showed that this species belongs in *Misturatosphaeria sensu stricto*.



Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa

Kevin D. Hyde^{1,2,3,4,5,6,71} · Danushka S. Tennakoon^{1,2,3,6,7} · Rajesh Jeewon⁸ · D. Jayarama Bhat^{9,10} · Sajeewa S. N. Maharachchikumbura¹¹ · Walter Rossi¹² · Marco Leonardi¹² · Hyang Burm Lee¹³ · Hye Yeon Mun¹⁴ · Jos Houbraken¹⁵ · Thuong T. T. Nguyen¹³ · Sun Jeong Jeon¹³ · Jens Christian Frisvad¹⁶ · Dhanushka N. Wanasinghe^{1,3,4,71} · Robert Lücking¹⁷ · André Aptroot¹⁸ · Marcela E. S. Cáceres¹⁹ · Samantha C. Karunarathna^{1,4,5,71} · Sinang Hongsanant^{3,20} · Rungtiwa Phookamsak^{1,3,4,5,71} · Nimali I. de Silva^{1,3,5} · Kasun M. Thambugala²¹ · Ruvishika S. Jayawardena³ · Indunil C. Senanayake^{3,20} · Saranyaphat Boonmee³ · Jie Chen²² · Zong-Long Luo²³ · Chayanard Phukhamsakda^{2,3} · Olinto L. Pereira²⁴ · Vanessa P. Abreu²⁵ · André Wilson Campos Rosado²⁴ · Buyck Bart²⁶ · Emile Randrianjohany²⁷ · Valérie Hofstetter²⁸ · Tatiana B. Gibertoni²⁹ · Adriene Mayra da Silva Soares³⁰ · Helio Longoni Plautz Jr.³¹ · Helen Maria Pontes Sotão³⁰ · William Kally Silva Xavier³² · Jadson Diogo Pereira Bezerra³³ · Thays Gabrielle Lins de Oliveira³³ · Cristina Maria de Souza-Motta³³ · Olliane Maria Correia Magalhães³³ · Digvijayini Bundhun^{3,34} · Dulanjalee Harishchandra^{2,3,35} · Ishara S. Manawasinghe^{2,3,35} · Wei Dong^{3,6,34,36} · Sheng-Nan Zhang^{3,34} · Dan-Feng Bao^{3,23,34} · Milan C. Samarakoon^{3,5,37} · Dhandevi Pem^{2,3,6,20} · Anuruddha Karunarathna^{1,3,7,34} · Chuan-Gen Lin^{2,3,6} · Jing Yang^{2,3,6,37} · Rekhan H. Perera^{2,3,6,37} · Vinit Kumar^{3,34} · Shi-Ke Huang^{1,2,3,6} · Monika C. Dayaratne^{1,2,3,6} · Anusha H. Ekanayaka^{1,2,3} · Subashini C. Jayasiri^{1,3} · Yuanpin Xiao^{2,3,6,38} · Sirinapa Konta^{1,2,3,6} · Tuula Niskanen³⁹ · Kare Liimatainen³⁹ · Yu-Cheng Dai⁴⁰ · Xiao-Hong Ji⁴⁰ · Xue-Mei Tian⁴¹ · Armin Mešić⁴² · Sanjay K. Singh⁴³ · Kunthida Phutthacharoen^{2,3,6} · Lei Cai⁴ · Touny Sorvongxay³ · Vinodhini Thiagaraja^{1,3,6,34} · Chada Norphanphoun^{2,3,6,7,38} · Napalai Chaiwan^{1,2,3,6} · Yong-Zhong Lu^{3,6,38} · Hong-Bo Jiang^{1,2,3,6} · Jin-Feng Zhang^{3,37} · Pranami D. Abeywickrama^{2,3,35} · Janith V. S. Aluthmuhandiram^{2,3,35} · Rashika S. Brahmanage^{2,3,35} · Ming Zeng^{1,2,3,6} · Thilini Chethana^{2,3,35} · Deping Wei^{1,3,34} · Martina Réblová⁴⁵ · Jacques Fournier⁴⁶ · Jana Nekvindová⁴⁷ · Renan do Nascimento Barbosa⁴⁸ · José Ewerton Felinto dos Santos³³ · Neiva Tinti de Oliveira³³ · Guo-Jie Li⁴⁴ · Damien Ertz^{49,50} · Qiu-Ju Shang^{2,3,37} · Alan J. L. Phillips⁵¹ · Chang-Hsin Kuo⁷ · Erio Camporesi^{52,53,54} · Timur S. Bulgakov⁵⁵ · Saisamorn Lumyong^{3,5,68,69} · E. B. Gareth Jones^{3,56} · Putarak Chomnunt^{2,3} · Eleni Gentekaki^{2,3} · Frank Bungartz^{57,58,59} · Xiang-Yu Zeng^{3,38} · Sally Fryar⁶⁰ · Zdenko Tkalc⁴² · Junmin Liang⁴⁴ · Guangshuo Li^{44,61} · Ting-Chi Wen^{38,62} · Paras Nath Singh⁴³ · Yusufjon Gafforov^{63,64,70} · Itthayakorn Promputtha^{5,72} · Erandi Yasanthika^{2,3} · Ishani D. Goonasekara^{1,2,3} · Rui-Lin Zhao⁴⁴ · Qi Zhao¹ · Paul M. Kirk⁶⁵ · Jian-Kui Liu^{37,66} · JiYe Yan³⁵ · Peter E. Mortimer^{1,71} · Jianchu Xu^{1,4,71} · Mingkwan Doilom^{1,3,4,5,6,7,71}

Received: 28 March 2019 / Accepted: 16 May 2019 / Published online: 24 June 2019
 © School of Science 2019

Abstract

This article is the tenth series of the Fungal Diversity Notes, where 114 taxa distributed in three phyla, ten classes, 30 orders and 53 families are described and illustrated. Taxa described in the present study include one new family (viz. *Pseudoberkleasmiaceae* in *Dothideomycetes*), five new genera (*Caatingomyces*, *Cryptoschizotrema*, *Neoacladium*, *Paramassarina* and *Trochilispora*) and 71 new species, (viz. *Acrogenospora thailandica*, *Ammiculicola aquatica*, *A. guttulata*, *Angustimassarina sylvatica*, *Blackwellomyces lateris*, *Boubovia gelatinosa*, *Buellia viridula*, *Caatingomyces brasiliensis*, *Calophoma humuli*, *Camarosporidiella mori*, *Canalisporium dehongense*, *Cantharellus brunneopallidus*, *C. griseotinctus*, *Castanediella meliponae*, *Coprinopsis psammophila*, *Cordyceps succavus*, *Cortinarius minusculus*, *C. subscotoides*,

Diaporthe italiana, *D. rumicicola*, *Diatrypella delonicis*, *Dictyocheirospora aquadulcis*, *D. taiwanense*, *Digitodesmium Chiangmaiense*, *Distoseptispora dehongensis*, *D. palmarum*, *Dothiorella styphnolobii*, *Ellisembia aurea*,

✉ Mingkwan Doilom
 j_hammochi@hotmail.com

Extended author information available on the last page of the article

***Wicklowia submersa* sp. nov. (Wicklowiaceae, Pleosporales), a second species in a monotypic family**

SARANYAPHAT BOONMEE¹, TOUNY SORVONGXAY^{1,2}, NARUEMON HUANRALUEK¹ & KEVIN D. HYDE^{1,2*}

¹ Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

² Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China

Corresponding author: kdhyde3@gmail.com

Abstract

A new freshwater ascomycetous species, *Wicklowia submersa* was found on submerged wood in a freshwater stream in Krabi Province in southern Thailand. This is a second species in a monotypic family. Morphological examination and phylogenetic analysis of LSU and SSU sequence data support this new species as belonging to *Wicklowia* in the family Wicklowiaceae (Pleosporales). *Wicklowia submersa* possesses ascomata that are immersed, erumpent when mature, raised and visible as dark oval or slit-like structures on host surface. The bitunicate asci have well-developed ocular chambers when immature with a short pedicel. Ascospores are ellipsoidal-oblong, asymmetrical, 1-septate, guttulate when immature, hyaline, with a distinctly mucilaginous sheath. The characteristics of the asci, and ascospores which lack both apical and basal appendages distinguish it from the type species *W. aquatic*. A description, illustration and comparison of the new species is provided. The risk of introducing monotypic families is discussed.

Keywords: 1 new species, bitunicate, monotypic family, phylogeny, submerged wood

Introduction

The family Wicklowiaceae, which was basal to Lindgomycetaceae with strong molecular support, was introduced to accommodate a monotypic genus *Wicklowia* (Ariyawansa *et al.* 2015). From a conservative point of view, it might have been unwise to introduce a new family for a single *Wicklowia* species with two strains (Liu *et al.* 2017). However, the species had always clustered as a distinct lineage with strong support (Liu *et al.* 2017).

The genus *Wicklowia* (Raja *et al.* 2010) was introduced to accommodate a single freshwater ascomycetous species, *W. aquatica* Raja, A. Ferrer & Shearer, which has remained monotypic (Wijayawardene *et al.* 2017). The genus is characterized by a distinct set of characters including immersed to erumpent, dark pigmented ascomata fusing with the host cells, dorsiventrally flattened feature, cellular pseudoparaphyses, broadly clavate bitunicate asci, cylindrical to ellipsoidal, hyaline, 1-septate, thick-walled ascospores with a gelatinous sheath and a basal appendages. The asexual morph is undetermined (Raja *et al.* 2010).

In this paper, a new saprobic freshwater species belonging to *Wicklowia* from submerged wood in Thailand was discovered. Hyde *et al.* (2018) reported that between 55–96% of new taxa were being introduced from Thailand and this adds to the remarkable diversity of the poorly known fungi. We compare the morphological characters of our new taxon with the type species *Wicklowia aquatica* which was introduced based on morphology and only LSU sequence data (Raja *et al.* 2010). In this study, we use LSU and SSU sequence data providing evidence for the new species and justifying its placement in Wicklowiaceae.



Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa

Kevin D. Hyde^{1,5,8,22} · Yang Dong^{2,3} · Rungtiwa Phookamsak^{1,5,6,7} · Rajesh Jeewon⁹ · D. Jayarama Bhat¹⁰ · E. B. Gareth Jones^{11,12} · Ning-Guo Liu^{5,8,14,17} · Pranami D. Abeywickrama^{5,15} · Ausana Mapook^{5,13,16} · Deping Wei^{1,5,8,11} · Rekhani H. Perera^{5,8,17} · Ishara S. Manawasinghe^{5,15} · Dhandevi Pem^{5,8,18} · Digvijayini Bundhun^{5,8,11} · Anuruddha Karunarathna^{5,8,11,19} · Anusha H. Ekanayaka^{1,5} · Dan-Feng Bao^{5,11,20} · Junfu Li^{1,5,8,13} · Milan C. Samarakoon^{5,8,17,22} · Napalai Chaiwan^{4,5,13} · Chuan-Gen Lin^{5,8,13} · Kunthida Phutthacharoen^{1,5,13} · Sheng-Nan Zhang^{5,8,11} · Indunil C. Senanayake¹⁸ · Ishani D. Goonasekara^{5,8,13} · Kasun M. Thambugala²³ · Chayanard Phukhamsakda^{5,13} · Danushka S. Tennakoon^{5,8,13,19} · Hong-Bo Jiang^{1,5,8,13} · Jing Yang^{5,8,13,17} · Ming Zeng^{1,5,8,13} · Naruemon Huanraluek⁵ · Jian-Kui (Jack) Liu⁴¹ · Subodini N. Wijesinghe^{5,8,13,42} · Qing Tian^{5,8,13} · Saowaluck Tibpromma^{1,6,7} · Rashika S. Brahmanage^{5,15} · Saranyaphat Boonmee⁵ · Shi-Ke Huang^{1,5,8,24} · Vinodhini Thiyagaraja^{1,5,8,11} · Yong-Zhong Lu²⁵ · Ruvishika S. Jayawardena⁵ · Wei Dong^{5,8,11,26} · Er-Fu Yang^{1,7} · Sanjay K. Singh²⁷ · Shiv Mohan Singh²⁸ · Shiwal Rana²⁷ · Sneha S. Lad²⁷ · Garima Anand²⁹ · Bandarupalli Devadatha^{5,30} · M. Niranjan³⁰ · V. Venkateswara Sarma³⁰ · Kare Liimatainen³¹ · Begoña Aguirre-Hudson³¹ · Tuula Niskanen³¹ · Andy Overall³² · Renato Lúcio Mendes Alvarenga³³ · Tatiana Baptista Gibertoni³³ · Walter P. Pfliegler³⁴ · Enikő Horváth^{43,47} · Alexandra Imre^{34,44} · Amanda Lucia Alves³⁹ · Ana Carla da Silva Santos³⁹ · Patricia Vieira Tiago³⁹ · Timur S. Bulgakov⁴⁰ · Dhanushaka N. Wanasinghe^{1,6,7} · Ali H. Bahkali^{12,46} · Mingkwan Doilom^{1,6,7} · Abdallah M. Elgorban^{12,46} · Sajeewa S. N. Maharachchikumbura⁴¹ · Kunhiraman C. Rajeshkumar²⁷ · Danny Haelewaters^{35,36,37,38} · Peter E. Mortimer^{1,7} · Qi Zhao¹ · Saisamorn Lumyong^{21,22,45} · Jianchu Xu^{1,6,7} · Jun Sheng^{2,3,4}

Received: 13 November 2019 / Accepted: 20 January 2020 / Published online: 16 March 2020
 © The Author(s) 2020

Abstract

Fungal diversity notes is one of the important journal series of fungal taxonomy that provide detailed descriptions and illustrations of new fungal taxa, as well as providing new information of fungal taxa worldwide. This article is the 11th contribution to the fungal diversity notes series, in which 126 taxa distributed in two phyla, six classes, 24 orders and 55 families are described and illustrated. Taxa in this study were mainly collected from Italy by Erio Camporesi and also collected from China, India and Thailand, as well as in some other European, North American and South American countries. Taxa described in the present study include two new families, 12 new genera, 82 new species, five new combinations and 25 new records on new hosts and new geographical distributions as well as sexual-asexual reports. The two new families are *Eriomycetaceae* (Dothideomycetes, family incertae sedis) and *Fasciatisporaceae* (Xylariales, Sordariomycetes). The twelve new genera comprise *Bhagirathimyces* (Phaeosphaeriaceae), *Camporesiomyces* (Tubeufiaceae), *Eriocamporesia* (Cryphonectriaceae), *Eriomyces* (Eriomycetaceae), *Neomonodictys* (Pleurotheciaceae), *Paraloratospora* (Phaeosphaeriaceae), *Paramonodictys* (Parabambusicolaceae), *Pseudoconularium* (Diaporthomycetidae, genus incertae sedis), *Pseudomurilentitheciium* (Lentitheciaceae), *Setoapiospora* (Muyocopronaceae), *Srinivasanomyces* (Vibrissaceae) and *Xenanthostomella* (Xylariales, genera incertae sedis). The 82 new species comprise *Acremonium chiangraiense*, *Adustochaete nivea*, *Angustimassarina camporesii*, *Bhagirathimyces himalayensis*, *Brunneoclavispora camporesii*, *Camarosporidiella camporesii*, *Camporesiomyces mali*, *Camposporium appendiculatum*, *Camposporium multiseptatum*, *Camposporium septatum*, *Canalisporium aquaticum*, *Clonostachys eriocamporesiana*, *Clonostachys eriocamporesii*, *Colletotrichum hedericola*, *Coniochaeta vineae*, *Conioscypha verrucosa*, *Cortinarius ainsworthii*, *Cortinarius aurae*, *Cortinarius britannicus*, *Cortinarius heatherae*, *Cortinarius scoticus*, *Cortinarius subsanosus*, *Cytospora fusispora*, *Cytospora rosigena*, *Diaporthe camporesii*, *Diaporthe nigra*, *Diatrypella yunnanensis*, *Dictyosporium muriformis*, *Didymella camporesii*, *Diutina bernali*, *Diutina sipiczii*, *Eriocamporesia aurantia*,

Extended author information available on the last page of the article

***Triseptata sexualis* gen. et sp. nov. in *Latoruaceae* (Pleosporales)**

SARANYAPHAT BOONMEE^{1,2,6}, MARK S. CALABON^{1,2,7}, RUNGTIWA PHOOKAMSAK^{3,8}, ABDALLAH M. ELGORBAN^{4,5,9} & KEVIN D. HYDE^{1,3,10*}

¹ Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

² School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

³ Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China

⁴ Center of Excellence in Biotechnology Research, King Saud University P.O. Box. 2455, Riyadh 11451, Saudi Arabia

⁵ Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box: 2455, Riyadh, 1145, Saudi Arabia

⁶  saranyaphat.khag2@gmail.com;  <https://orcid.org/0000-0001-5202-2955>

⁷  mscalabon@up.edu.ph;  <https://orcid.org/0000-0002-6603-1876>

⁸  jonjam.rp2@gmail.com;  <https://orcid.org/0000-0002-6321-8416>

⁹  aelgorban@ksu.edu.sa;  <https://orcid.org/0000-0003-3664-7853>

¹⁰  kahyde3@gmail.com;  <https://orcid.org/0000-0002-2191-0762>

*Corresponding author

Abstract

A survey of lignicolous terrestrial ascomycetes conducted in Thailand yielded a number of novel species. In this paper, we report on a terrestrial collection of a taxon from dead branches of an unidentified plant. *Triseptata* gen. et sp. nov. is characterized by immersed, uni- to multi-loculate ascomata, filamentous pseudoparaphyses, bitunicate, fissitunicate, cylindrical-clavate asci and 3-septate, light brown spores, with asymmetrical ends, in its sexual form. In culture, it produced hyphomycetous, globose to subglobose, multi-septate and darkly pigmented conidia-like structures. Phylogenetic analysis of a combined LSU, ITS and SSU dataset shows *Triseptata* to be a well-separated lineage from all genera in *Latoruaceae*. Based on multigene phylogeny, *Triseptata* gen. nov. is introduced to accommodate a single new species *Triseptata sexualis* and placed in *Latoruaceae*. Illustrations, descriptions and notes are provided for the new genus and species.

Keywords: 2 new taxa, bitunicate, lignicolous fungi, phylogeny, taxonomy

Introduction

Pleosporales is a highly diverse and large order of Dothideomycetes containing 75 families and 52 genera *incertae sedis* (Wijayawardene *et al.* 2018). Wijayawardene *et al.* (2020) recently refined families of Dothideomycetes and included 91 families in Pleosporales and 48 Pleosporales genera *incertae sedis*. Members of Pleosporales can be saprobic on dead material in terrestrial and aquatic habitats, and pathogens on living plants (Zhang *et al.* 2012, Ariyawansa *et al.* 2015, Hyde *et al.* 2017, Wanasinghe *et al.* 2018).

Crous *et al.* (2015) proposed the new genus *Latorua* and *Latoruaceae* to accommodate two hyphomycetous taxa based on morphology and phylogenetic data. *Latorua* is typified by *L. caligans* (= *Bahusandhika caligans* Bat. & H.P. Upadhyay), which was excluded from *Bahusandhika*. *Latorua* comprises the species *L. caligans* (Bat. & H.P. Upadhyay) Crous and *L. grooffonteinensis* Crous, which were isolated from soil and produced conidial structures in culture (Batista & Upadhyay 1965, Crous *et al.* 2015). *Latorua* is characterized by dark brown to black colonies, immersed to superficial mycelium, reduced conidiophores, erect and moniliform conidiogenous cells, and fusoid-ellipsoidal, clavate or ovoid, septate, smooth to warty and pigmented conidia, produced acrogenously in branched chains (Crous *et al.* 2015). Phylogenetic analysis based on combined ITS and LSU sequence data indicated that the two strains of *Latorua* clustered with *Polyschema* and close to the families *Macrodiplodiopsidaceae* and *Lentitheciaceae* (Crous *et al.* 2015). Crane and Miller (2016) synonymized *Latorua* under *Bahusandhika* based on restricted features of conidiogenous cells and conidia characters without molecular evidence. Additionally, Pratibha *et al.* (2014)



Mycoenterolobium aquadictyosporium sp. nov. (Pleosporomycetidae, Dothideomycetes) from a freshwater habitat in Thailand

Mark S. Calabon^{1,2} · Kevin D. Hyde^{1,3} · E. B. Gareth Jones⁴ · Mingkwan Doilom^{5,6} · Chun-Fang Liao^{5,6} · Saranyaphat Boonmee^{1,2}

Received: 25 May 2020 / Revised: 25 July 2020 / Accepted: 28 July 2020
© German Mycological Society and Springer-Verlag GmbH Germany, part of Springer Nature 2020

Abstract

A study of freshwater fungi in Thailand led to the discovery of *Mycoenterolobium aquadictyosporium* sp. nov. Evidence for the novelty and placement in *Mycoenterolobium* is based on comparison of morphological data. The new species differs from the type species, *M. platysporum*, in having shorter and wider conidia, and from *M. flabelliforme* in having much longer and wider conidia. The hyphomycetous genus *Mycoenterolobium* is similar to *Cancellidium* but differs in the arrangement of conidial rows of cells at the attachment point to the conidiophores. The conidia of the former are made up of rows of cells, radiating in a linear pattern from a single cell attached to the conidiophore, while in *Cancellidium*, adherent rows of septate branches radiate from the conidiophore. *Cancellidium* conidia also contain branched chains of blastic monilioid cells arising from the conidia, while these are lacking in *Mycoenterolobium*. At maturity in *Mycoenterolobium*, the two conidial lobes unite and are closely appressed. Phylogenetic analyses based on a combined LSU, SSU, ITS, *TEF1-α*, and *RPB2* loci sequence data support the placement of *Mycoenterolobium aquadictyosporium* close to the family Testudinaceae within Pleosporomycetidae, Dothideomycetes. The novel species *Mycoenterolobium aquadictyosporium* is described and illustrated and is compared with other morphologically similar taxa.

Keywords 1 new taxon · Freshwater hyphomycete · Asian mycology · Multi-locus analysis · Thailand

Section Editor: Gerhard Rambold

✉ Saranyaphat Boonmee
saranyaphat.boonmee@mfu.ac.th

¹ Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

² School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

³ Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, Guangdong Province, People's Republic of China

⁴ Department of Botany and Microbiology, College of Science, King Saud University, P. O. Box 2455, Riyadh 11451, Kingdom of Saudi Arabia

⁵ CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China

⁶ Honghe Innovation Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, People's Republic of China

Introduction

The incorporation of molecular data in phylogenetic and evolutionary studies has revolutionized the current knowledge of fungal systematics (Tanabe et al. 2005; Shenoy et al. 2006; Taylor and Berbee 2006; Choi and Kim 2017; Liu et al. 2017; Tedersoo et al. 2018; Naranjo-Ortiz and Gabaldón 2019; Samarakoon et al. 2019). Natural taxonomic placements of taxa and development of backbone trees based on molecular phylogeny have been possible (Ebersberger et al. 2012; He et al. 2019; Luo et al. 2019; Hongsanan et al. 2020; Hyde et al. 2020a; Wijayawardene et al. 2020). The knowledge of fungal taxonomy and classification are however limited as only approximately 8% (120,000 described taxa) of the 2.2 to 3.8 million estimated global fungal species are described (Hawksworth and Lücking 2017) and even fewer have been sequenced. Several authors have suggested areas as to where to find the “missing fungi,” such as understudied countries and hosts, particularly in tropical regions and biodiversity hot spots, little explored habitats or niches, and cryptic species

Fungal diversity notes 1390–1455: taxonomic and phylogenetic contributions on genera and species of fungal taxa

Saranyaphat Boonmee^{1,2}, Mark S. Calabon^{1,2}, Naruemon Huanraluek^{1,2}, Walter Rossi³, Marco Leonardi³, Diogo RS Pereira⁴, Alan JL Phillips⁴, María P. Martín⁵, Margarita Dueñas⁵, M. Teresa Telleria⁵, Izabela L. Kalucka⁶, Andrzej M. Jagodziński⁷, Kare Liimatainen⁸, Sanjay K Singh⁹, Shiwali Rana⁹, Paras Nath Singh⁹, Deepak K Maurya⁹, Kunhiraman C. Rajeshkumar⁹, Nikhil Ashtekar⁹, Sneha Lad⁹, Nalin N. Wijayawardene¹⁰, Darbe J. Bhat¹¹, Guo-Jie Li¹², Wen-Fei Lin¹³, Niranjana M.^{14,15}, V.V. Sarma¹², Mohamed A. Abdel-Wahab¹⁶, Faten A. Abdel-Aziz¹⁶, Upendra Singh¹⁷, R.P. Bhatt¹⁷, Hyang Burm Lee¹⁸, Thuong T.T. Nguyen¹⁸, Paul M. Kirk¹⁹, Arun Kumar Dutta^{20,21}, Krishnendu Acharya²¹, Dan-Feng Bao^{1,22}, Jafar Abdollahzadeh²³, Isaac Garrido-Benavent²⁴, Francesco Dovana²⁵, Muhammad Usman²⁶, Abdul Nasir Khalid²⁶, Rungtiwa Phookamsak^{27,28,29}, Asha J. Dissanayake³⁰, Anusha Telagathoti³¹, Maraike Probst³¹, Ursula Peintner³¹, Lilla Bóna³², Zsolt Merényi³³, Lajos Boros³⁴, Zoltán Bratek³⁴, J. Benjamin Stielow³⁵, Mingkwan Doilom^{27,28,36}, Chun-Fang Liao^{27,28,36}, Eric H.C. McKenzie³⁷, Ithayakorn Promputtha^{38,39*}, Kevin D. Hyde^{1,2*}

¹ Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

² School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

³ Sect. Environmental Sciences, Dept. MeSVA, University of L'Aquila, 67100 Coppito, AQ, Italy

⁴ Universidade de Lisboa, Faculdade de Ciências, Biosystems and Integrative Sciences Institute (BioISI), Campo Grande, 1749-016 Lisbon, Portugal

⁵ Dept. Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2, 28014, Madrid, Spain

⁶ Department of Algology and Mycology, Faculty of Biology and Environmental Protection, University of Lodz, Banacha 12/16, 90-237 Łódź, Poland

⁷ Institute of Dendrology, Polish Academy of Sciences, Parkowa 5, 62-035 Kórnik, Poland

⁸ Jodrell Laboratory, Royal Botanic Gardens, Kew, Surrey TW9 3AB, United Kingdom

⁹ National Fungal Culture Collection of India (NFCCI), Biodiversity and Palaeobiology Group, MACS Agharkar Research Institute, G.G. Agarkar Road, Pune 411004, India

¹⁰ Center for Yunnan Plateau Biological Resources Protection and Utilization, College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, Yunnan 655011, China

¹¹ No. 128/1-J, Azad Housing Society, Curca, Goa Velha, Goa, India

¹² Key Laboratory of Vegetable Germplasm Innovation and Utilization of Hebei, Collaborative Innovation Center of Vegetable, College of Horticulture, Hebei Agricultural University, No 2596 South Lekai Rd, Lianchi District, Baoding 071001, Hebei, People's Republic of China

¹³ Institute of Edible and Medicinal Fungi, College of Life Science, Zhejiang University, 866 Yuhangtang Rd, Xihu District, Hangzhou 310058, Zhejiang, People's Republic of China

¹⁴ Department of Biotechnology, Pondicherry University, Kalapet, Pondicherry-605014 India

¹⁵ Department of Botany, Rajiv Gandhi University, University Road, Papum Pare, Arunachal Pradesh 791112-India

¹⁶ Department of Botany and Microbiology, Faculty of Science, Sohag University, Sohag 82524 Egypt