TAXONOMY AND PHYLOGENY OF MICROFUNGI ASSOCIATED WITH *AMOMUM VILLOSUM* IN SOUTHERN CHINA

CHUNFANG LIAO

DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE

SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY

2025

©COPYRIGHT BY MAE FAH LUANG UNIVERSITY

TAXONOMY AND PHYLOGENY OF MICROFUNGI ASSOCIATED WITH *AMOMUM VILLOSUM* IN SOUTHERN CHINA

CHUNFANG LIAO

THIS DISSERTATION IS A PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY IN BIOLOGICAL SCIENCE

SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY

2025

©COPYRIGHT BY MAE FAH LUANG UNIVERSITY

DISSERTATION APPROVAL

MAE FAH LUANG UNIVERSITY

FOR

DOCTOR OF PHILOSOPHY IN BIOLOGICAL SCIENCE

Dissertation Title: Taxonomy and Phylogeny of Microfungi Associated with *Amomum Villosum* in Southern China

Author: Chunfang Liao

Examination Committee:

Ishara Sandeepani Manawasinghe, Ph. D.	Chairperson
Assistant Professor Khanobporn Tangtrakulwanich, Ph. D.	Member
Adjunct Professor Kevin David Hyde, Ph. D.	Member
Thilini Chethana Kandawatte Wedaralalage, Ph. D.	Member
Chitrabhanu Sharma Bhunjun, Ph. D.	Member
Mingkwan Doilom, Ph. D.	Member

Advisors:

Khanobporn Tangtrakulwanich .....Advisor

(Assistant Professor Khanobporn Tangtrakulwanich, Ph. D.)

.....Co-Advisor

(Adjunct Professor Kevin David Hyde, Ph. D.)

.....Co-Advisor

(Thilini Chethana Kandawatte Wedaralalage, Ph. D.)

Dean:

.....

(Professor Surat Laphookhieo, Ph. D.)

ACKNOWLEDGEMENTS

Over the course of the five years from my enrollment to graduation, I have encountered numerous individuals and experienced a wide range of events, some joyful, others more challenging. Notably, more than two of these years coincided with the COVID-19 pandemic, a period that posed significant difficulties for all of us. Nevertheless, I was fortunate to have met an exceptional supervisor and many inspiring individuals whose support and encouragement sustained me through moments of adversity. Their presence played a crucial role in helping me persevere during times when I felt close to giving up. Therefore, I extend my sincere gratitude to all those who have contributed in various ways throughout this journey.

First and foremost, I would like to express my deepest gratitude to Dr. Mingkwan Doilom, my supervisor at the Innovative Institute for Plant Health / Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou, China. Dr. Doilom provided me with the rare and valuable opportunity to conduct my doctoral research at the Center of Excellence in Fungal Research, Mae Fah Luang University, one of the world's foremost laboratories in this field. Her expert guidance, encouragement, and consistent support were vital to the successful completion of this dissertation. She has been both an outstanding academic mentor and a trusted source of personal support. I am deeply grateful to Prof. Dr. Kevin David Hyde, Director of the Center of Excellence in Fungal Research at Mae Fah Luang University, for his exceptional guidance, thoughtful feedback, and constructive suggestions throughout this project. His leadership and the collaborative environment he fostered were instrumental to the successful completion of our research.

I am also deeply grateful to my main advisor, Asst. Prof. Dr. Khanobporn Tangtrakulwanich, and co-advisor Dr. Kandawatte Wedaralalage Thilini Chethana for their valuable feedback on my research proposal and publications. When I first arrived in Thailand, it was them who offered me help and support. No matter what difficulties or problems I faced, they were always the first people I could turn to, and they never hesitated to assist me. Their continued guidance and care, both academically and

personally, have meant a great deal to me. They have become not only my academic mentors but also my friends in daily life. I would also like to express my sincere gratitude to Dr. Ishara Sandeepani Manawasinghe for her thoughtful guidance and support when I first arrived at Zhongkai University of Agriculture and Engineering. I still clearly remember the many challenges I faced during that time, insufficient equipment, unstable salary, and an undefined research direction. Fortunately, I met Dr. Ishara, who not only helped resolve each of these difficulties but also took the initiative to organize regular learning sessions, monthly progress meetings, and English practice activities. She taught me so much, and I truly believe that without her support, I would not have reached where I am today in my PhD journey.

Meanwhiles, I would also like to express my sincere appreciation to Prof. Dr. Dongqing Dai, Dr. Dhanushka N. Wanasinghe, Dr. Ishara S. Manawasinghe, Dr. Rungtiwa Phookamsak, Prof. Dr. Samantha C. Karunarathna, and Prof. Dr. Saowaluck Tibpromma for their invaluable guidance and support. I am deeply grateful to Dr. Ishara Sandeepani Manawasinghe, Asst. Prof. Dr. Khanobporn Tangtrakulwanich, Dr. Kandawatte Wedaralalage Thilini Chethana, Prof. Dr. Kevin D. Hyde, Dr. Mingkwan Doilom, and Dr. Chitrabhanu Sharma Bhunjun for their valuable time, expertise, and constructive feedback during my defense examination. Their instruction in fundamental laboratory techniques and foundational knowledge in biological systematics and phylogenetics has been instrumental to the development of my research skills. Beyond their academic mentorship, their encouragement and support have been a source of great strength throughout my academic journey.

I sincerely appreciate Mae Fah Luang University for provide the for providing the tuition-fee scholarship and dissertation writing grant. Additionally, most of the research work during my Ph.D. was conducted at the Innovative Institute for Plant Health / Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou, China. Moreover, I would also like to express my sincere gratitude to all the staff members at the Center of Excellence in Fungal Research and the CAS Key Laboratory for Plant Diversity and Biogeography of East Asia for their support in providing laboratory facilities, specimen preservation, and facilitating the preparation and submission of numerous essential documents. I am

truly grateful to the many dedicated faculty members I had the chance to work with during my time there. They not only provided crucial support in laboratory procedures and field sampling but also offered mentorship and encouragement in my academic and daily life. My heartfelt thanks go to all those who patiently guided me in basic lab skills and ensured the availability of necessary equipment and resources throughout the research process.

I am deeply grateful for the financial support provided by the Guangzhou Municipal Science and Technology Bureau (Grant Nos. 2023A04J1425 and 2023A04J1426), the Guangdong Provincial College Key Laboratory of Green Prevention and Control of Fruit and Vegetable Pests and Diseases (Grant No. KA21031C502), and the National Natural Science Foundation of China (Grant No. 32200015). Additional funding was generously provided by the High-level Talents Program of Zhongkai University of Agriculture and Engineering (Grant No. J2201080102) and the Starting Research Fund of Zhongkai University of Agriculture and Engineering (Grant No. KA22016B746). Special thanks are extended to Dr. Shaun Pennycook (Landcare Research, New Zealand) for his invaluable contribution in reviewing the fungal nomenclature.

My heartfelt thanks go to my family, whose steadfast encouragement and unconditional support have accompanied me through every step of my personal and scholarly journey. I would also like to sincerely thank Ms. Yunhui Yang for her quiet dedication and help, particularly with specimen collection and molecular analysis, both of which were instrumental in bringing this research to completion.

Chunfang Liao

Dissertation Title	Taxonomy and Phylogeny of Microfungi Associated with *Amomum Villosum* in Southern China
Author	Chunfang Liao
Degree	Doctor of Philosophy (Biological Science)
Advisor	Assistant Professor Khanobporn Tangtrakulwanich, Ph. D.
Co-Advisor	Adjunct Professor Kevin David Hyde, Ph. D. Thilini Chethana Kandawatte Wedaralalage, Ph. D.

ABSTRACT

Wurfbainia villosa (=*Amomum villosum*), commonly known as "Sharen or Chunsharen" in Chinese, is a perennial, evergreen herb, known as one of the "four great southern medicines" in China. *Wurfbainia villosa* is extensively cultivated in Yunnan and Guangdong provinces, China, owing to its crucial medicinal properties and its essential role as a culinary spice. However, the taxonomic and phylogenetic research on microfungi associated with *W. villosa* remains highly limited. To date, only 18 fungal species have been documented on *W. villosa*, which significantly constrains our understanding of its fungal diversity. Thus, our objective is to conduct extensive, long-term surveys to comprehensively investigate the microfungi on *W. villosa* in southern China and to establish a global checklist of fungi associated with this plant. Based on the morphological and phylogenetic evidence (ITS, LSU, SSU, *act*, *chs-1*, *gapbh*, *rpb1*, *rpb*2, *tub*2, *tef1-α*), a total of 77 species were identified, which are distributed across 32 families in Sordariomycetes, Dothideomycetes, Eurotiomycetes, Agaricomycetes, and Mucoromycetes. Fungal taxa were discovered from 41 genera, including two new genera, 47 new species, and 30 new host and geographical records, and a species pending confirmation. Two new genera are *Bulbopyricularia*, and *Nigrosynnema*. A new combination, *Nigrosynnema natarajanensis*, is proposed for the previously described *Virgatospora natarajanensis*. In this study, we found several species, *Bussabanomyces wurfbainiae*, *Corynespora cassiicola*, *Curvularia geniculate*, *Musicillium tropicale*, *Muyocopron laterale*, *Musidium wurfbainiae*, *Sarocladium wurfbainiae*, in all three life forms, namely endophytic, saprobic, and pathogenic, from

Wurfbainia villosa. We also discovered numerous fungi that were restricted to specific plant tissues such as leaves, stems, roots, or fruits. However, some fungi, including *Bulbopyricularia guangdongensis*, *Corynespora wurfbainiae*, and *Musidium wurfbainiae*, were reported from multiple plant tissue types, occurring across all examined tissues. Hence, we suggest that the lifestyle of the same fungus within a plant may shift rather than remaining fixed. Meantime, we also observed that some endophytic fungal species produce appressoria, the specialized infection structures typical of pathogens, such as *Colletotrichum*, *Fusarium*, and *Bulbopyricularia*. This strongly supports the possibility that endophytes may shift to a pathogen lifestyle. Furthermore, we provided a global checklist of fungi associated with *Amomum villosum*, revealing that most species have been reported from China, with endophytic fungi representing the majority.

Furthermore, we evaluated and compared three isolation methods, plant tissue isolation, tissue maceration, and intercellular fluid culture, for their effectiveness in isolating endophytic fungi from various tissues of *Wurfbainia villosa*. Our results demonstrated that plant tissue isolation is the most effective method for recovering endophytic fungi across all tissue types. However, we are not sure whether tissue maceration showed potential for isolating slow-growing fungi, and intercellular fluid culture is suitable for root endophyte isolation of *Wurfbainia villosa*. We further tested a range of sporulation culture media and identified that plant tissue + pine needle-enriched medium and fruit juice medium yielded the highest sporulation rates. These findings offer valuable methodological insights for the effective isolation and cultivation of endophytic fungi from *W. villosa*.

In addition to the experimental results, we provide a comprehensive review of the diversity and ecological roles of endophytic fungi, and propose a refined definition that incorporates their colonization behavior, potential pathogenicity, host benefits, and lifestyle diversity. The integrative approach combining morphological analysis and multi-gene phylogenetic study has led to more accurate taxonomic placements, significantly enhancing our understanding of fungal diversity associated with *Wurfbainia villosa* in southern China, an area and host that have been largely understudied. This study not only reveals the rich fungal biodiversity linked to *W. villosa* but also provides insights into fungal lifestyle changes. Furthermore, the fungal

specimens collected have been deposited in herbarium and culture collections, serving as valuable resources for future research in fungal taxonomy and the exploration of their biomaterial properties.

Keywords: Ascomycota, Dothideomycetes, Sordariomycetes, Fungal Lifestyle Change, Chunsharen Plant, Zingiberaceae, Taxonomy, Multi-locus Phylogeny

TABLE OF CONTENTS

CHAPTER	Page
1 INTRODUCTION	**1**
1.1 *Wurfbainia villosa*	1
1.2 Microfungi	3
1.3 Microfungi Associated with *Wurfbainia villosa*	4
1.4 Research Objectives	5
1.5 Research Contents	5
2 MATERIALS AND METHODS	**7**
2.1 Sample Collection, Morphological Study, and Isolation	7
2.2 Fungal Sporulation Inducing Methods	9
2.3 DNA Extraction, PCR Amplification, and Sequencing	10
2.4 Sequence Alignment and Phylogenetic Analyses	10
2.5 Checklist Preparation	11
3 OPTIMIZATION OF THE ISOLATION AND SPORULATION TECHNIQUES FOR FUNGAL ENDOPHYTES	**13**
3.1 Introduction	13
3.2 Definition of Endophytes	14
3.3 Endophytic Fungi Colonization Mechanism	16
3.4 How Do Fungal Endophytes Evade Plant Defenses?	16
3.5 Endophyte Isolation Techniques and Induce Sporulation	18
3.6 Results and Discussion	19
4 FUNGAL LIFESTYLE TRANSITION	**24**
4.1 Introduction	24
4.2 How Does Evolution Drive The Endophytic Lifestyle?	27
4.3 Fungi Isolated from *Wurfbainia villosa* and Their Lifestyle Transitions	28

TABLE OF CONTENTS

CHAPTER	Page
5 TAXONOMY AND PHYLOGENY OF FUNGI FROM *WURFBAINIA VILLOSA* IN CHINA	**34**
5.1 Introduction	34
5.2 Results	35
5.3 Global Checklist	309
5.4 Discussion	315
6 OVERALL CONCLUSIONS	**321**
6.1 Conclusions	321
6.2 Research Advances	324
6.3 Future Work	326
6.4 Publications	327
REFERENCES	**382**
APPENDIX A CHEMICAL REAGENTS AND MEDIA	382
APPENDIX B ABSTRACT OF PUBLICATIONS	386
APPENDIX C TAXA ISOLATED FROM NON *WURFBAINIA VILLOSA* HOSTS	393
CURRICULUM VITAE	**411**

LIST OF TABLES

Table	**Page**
2.1 Gene regions, primers, and PCR conditions used in this study	12
3.1 The genera suggest those media to induce sporulation	23
4.1 List of fungal taxa with overlapping lifestyles (endophytic, saprobic, and potentially pathogenic) isolated from *Wurfbainia villosa*	31
4.2 List of microfungi associated with overlapping plant tissues of *Wurfbainia villosa* in globally	33
5.1 Global checklist of fungal taxa associated with *Wurfbainia villosa* (species name, country, life mode, climate) do analysis, like fungi from different country, life model, climate, order	309

LIST OF FIGURES

Figure	Page
1.1 *Wurfbainia villosa*	3
3.3 The different isolation methods results	21
3.4 The sporulation methods evaluation	23
4.1 Venn diagrams show microfungi lifestyle and tissue part overlapping	31
5.1 Maximum likelihood phylogeny based on combined LSU, ITS, SSU, and *tef1-α* sequences data of *Muyocopron*	38
5.2 *Muyocopron laterale* (MHZU 24-0370, new host and geographical record)	39
5.3 Maximum likelihood phylogeny based on combined ITS, LSU, and SSU sequences data of *Acrocalymma*	42
5.4 *Acrocalymma guangdongensis* (MHZU 24-0210, holotype)	43
5.5 *Acrocalymma* sp. (MHZU 24-0212)	45
5.6 *Acrocalymma wurfbainiae* (MHZU 24-0135, holotype)	47
5.7 Maximum likelihood phylogeny based on combined LSU, ITS, SSU, *rpb2*, and *tef1-α* sequences data of *Corynespora*	50
5.8 *Corynespora cassiicola* (MHZU 24-0177, new host record)	51
5.9 Sexual morph of *Corynespora wurfbainiae* (MHZU 24-0180, holotype)	54
5.10 Asexual morph of *Corynespora wurfbainiae* (MHZU 24-0218, holotype)	55
5.11 Maximum likelihood phylogeny based on combined ITS, LSU, *rpb2*, and *tub2* sequences data of *Pyrenochaetopsis*	58
5.12 *Pyrenochaetopsis endophytica* (MHZU 24-0193, holotype)	59
5.13 *Pyrenochaetopsis guangdongensis* (MHZU 24-0040, holotype)	61
5.14 *Pyrenochaetopsis wurfbainiae* (MHZU 24-0320, holotype)	63
5.15 Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and *tef1-α* sequences data of *Dictyoarthrinium*	66
5.16 *Dictyoarthrinium wurfbainiae* (MHZU 24-0101, holotype)	67

LIST OF FIGURES

Figure		Page
5.17	Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and *tef1-α* sequences data of *Periconia*	70
5.18	*Periconia endophytica* (MHZU 23-0245, holotype)	72
5.19	*Periconia epilithographicola* (MHZU 24-0408, new host and geographical record)	75
5.20	*Periconia neoyangjiangensis* (MHZU 24-0071, holotype)	77
5.21	*Periconia wurfbainiae* sexual morph (MHZU 23-0248)	80
5.22	*Periconia wurfbainiae* asexual morph (MHZU 23-0247, holotype)	81
5.23	*Periconia yangjiangensis* (MHZU 23-0246, holotype)	84
5.24	Maximum likelihood phylogeny based on the combined ITS, LSU, and *tub2* sequences data of *Setophoma*	87
5.25	*Setophoma wurfbainiae* (MHZU 24-0215, holotype)	88
5.26	Maximum likelihood phylogeny based on the combined ITS, LSU, SSU, *tef1-α*, *rpb2*, *gapdh*, and *Alt-a1* sequences data of *Alternaria*	91
5.27	*Alternaria pogostemonis* (MHZU 24-0234, new host record)	92
5.28	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *gapdh* sequences data of *Bipolaris*	95
5.29	*Bipolaris bicolor* (MHZU 24-0176, new host)	97
5.30	*Bipolaris wurfbainiae* (MHZU 24-0175, Holotype)	99
5.31	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *gapdh* sequences data of *Curvularia*	101
5.32	*Curvularia geniculata* (MHZU 24-0218, new host record)	104
5.33	*Curvularia plantarum* (MHZU 24-0296, new host record)	106
5.34	*Curvularia wurfbainiae* (MHZU 24-0225, holotype)	108
5.35	Maximum likelihood phylogeny based on the combined LSU, ITS, SSU, *tef1-α*, and *rpb2* sequences data of *Neoroussoella*	111
5.36	*Neoroussoella leucaenae* (MHZU 24-0195)	113
5.37	*Roussoella wurfbainiae* (MHZU 24-0110, holotype)	116

LIST OF FIGURES

Figure		Page
5.38	Maximum likelihood phylogeny based on the combined LSU, SSU, ITS, *tef1-α*, and *tub2* sequences data of *Tetraploa*	119
5.39	*Tetraploa wurfbainiae* (MHZU 23-0231, holotype)	120
5.40	Maximum likelihood phylogeny based on the combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequences data of *Torula*	123
5.41	*Torula wurfbainiae* (MHZU 24-0112, holotype)	124
5.42	Maximum likelihood phylogeny based on combined ITS, *tef1-α*, and *tub2* sequences data of *Lasiodiplodia*	128
5.43	*Lasiodiplodia wurfbainiae* (MHZU 24-0048, holotype)	130
5.44	Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and tef1-α sequences data of *Neodeightonia*	133
5.45	*Neodeightonia wurfbainiae* (MHZU 24-0179, holotype)	134
5.46	Maximum likelihood phylogeny based on combined ITS, *tef1-α*, *tub2*, and *rpb2* sequence data of *Neofusicoccum*	137
5.47	*Neofusicoccum wurfbainiae* (MHZU 24-0259, holotype)	139
5.48	Maximum likelihood phylogeny based on combined ITS, LSU, *tef1-α*, *act*, and *gapdh* sequences data of *Phyllosticta*	143
5.49	*Phyllosticta capitalensis* (MHZU 24-0181, new host record)	145
5.50	Maximum likelihood phylogeny based on the combined ITS, *rpb2*, *tub2*, and CaM sequences data of *Penicillium*	148
5.51	*Penicillium allaniae* (MHZU 24-0290, new host record)	149
5.52	*Penicillium guangdongensis* (MHZU 24-0255, holotype)	151
5.53	*Penicillium meleagrinum* (MHZU 24-0257, new host and geographical record)	153
5.54	*Penicillium polonicum* (MHZU 24-0293, new host record)	155
5.55	*Penicillium wurfbainiae* (MHZU 24-0256, holotype)	157
5.56	Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tub2* sequences data of *Talaromyces*	160

LIST OF FIGURES

Figure		Page
5.57	*Talaromyces dimorphus* (MHZU 24-0238, new host record)	161
5.58	*Talaromyces wurfbainiae* (MHZU 24-0237, holotype)	163
5.59	Maximum likelihood phylogeny based on the combined ITS, LSU, *tef1-α*, and *tub2* sequences data of *Talaromyces*	167
5.60	*Apiospora endophytica* (ZHKU 23-0002, holotype)	169
5.61	*Apiospora guangdongensis* (ZHKU 23-0001, holotype)	171
5.62	*Apiospora phyllostachydis* (MHZU 23-0010, a new host record)	173
5.63	*Apiospora wurfbainiae* (ZHKU 23-0003, holotype)	175
5.64	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *tub2* sequences data of *Nigrospora*	178
5.65	*Nigrospora camelliae-sinensis* (MHZU 24-0323, new host record)	179
5.66	*Nigrospora chinensis* (MHZU 24-0300, new host record)	181
5.67	*Nigrospora guangdongense* (MHZU 24-0242, holotype)	183
5.68	*Nigrospora sphaerica* (MHZU 23-0230, new host record)	185
5.69	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *tub2* sequences data of *Pseudopestalotiopsis*	188
5.70	*Pseudopestalotiopsis avicenniae* (MHZU 24-0233, new host and geographical record)	189
5.71	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, *tub2*, *cal*, and *his3* sequences data of *Diaporthe arecae* species complex	192
5.72	*Diaporthe neoceratozamiae* (MHZU 24-0299, Holotype)	194
5.73	*Diaporthe neohongkongensis* (MHZU 24-0302, Holotype)	196
5.74	Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, *tub2*, *cal*, and *his3* sequences data of *Diaporthe sojae* section	198
5.75	*Diaporthe kochmanii* (MHZU 24-0148, new host record)	201
5.76	*Diaporthe loculata* (MHZU 24-0146, holotype)	204
5.77	*Diaporthe neosiamensis* (MHZU 24-0247, holotype)	206

LIST OF FIGURES

Figure		Page
5.78	*Diaporthe wurfbainiae* (MHZU 24-0317, holotype)	208
5.79	*Diaporthe yangjiangensis* (MHZU 24-0147, holotype)	211
5.80	Maximum likelihood phylogeny based on the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequences data of *Colletotrichum gloeosporioides* species complex	215
5.81	*Colletotrichum fructicola* (MHZU 24-0161, record)	217
5.82	*Colletotrichum siamense* (MHZU 24-0411, new host record)	220
5.83	Maximum likelihood phylogeny based on the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequences data of *Colletotrichum orchidearum* species complex	223
5.84	*Colletotrichum plurivorum* (MHZU 24-0304, new host record)	224
5.85	Maximum likelihood phylogeny based on the combined ITS and LSU sequence data of *Acrostalagmus*	227
5.86	*Acrostalagmus annulatu* (MHZU 24-0202, new host and geographical record)	228
5.87	Maximum likelihood phylogeny based on the combined LSU, ITS, *tef1-α*, and *rpb2* sequences data of Plectosphaerellaceae	231
5.88	*Musicillium tropicale* on the substrate (MHZU 24-0073, new host record)	233
5.89	*Musicillium tropicale* on the culture (MHZU 24-0073, new host record)	234
5.90	*Musidium wurfbainiae* (MHZU 24-0339, holotype)	237
5.91	Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tef1-α* sequences data of *Trichocoma*	240
5.92	*Trichoderma guangdongensis* (MHZU 24-0235, holotype)	242
5.93	*Trichoderma wurfbainiae* (MHZU 24-0236, holotype)	244
5.94	Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Purpureocillium*	247

LIST OF FIGURES

Figure	Page
5.95 *Purpureocillium lilacinum* (MHZU 24-0261, new host record)	248
5.96 Maximum likelihood phylogeny based on the combined ITS, LSU, and act sequences data of *Sarocladium*	252
5.97 *Sarocladium wurfbainiae* on the substrate (MHZU 24-0077, new host record)	253
5.98 *Sarocladium wurfbainiae* on the culture (MHZU 24-0077, new host record)	254
5.99 Maximum likelihood phylogeny based on the combined *cmdA*, ITS, LSU, *rpb2*, *tef1-α*, and *tub2* sequences data of Stachybotryaceae	257
5.100 *Brevistachys wurfbainiae* (MHZU 23-0254, holotype)	259
5.101 *Nigrosynnema guangdongense* on the substrate (MHZU 23-0255, holotype)	262
5.102 *Nigrosynnema guangdongense* on the culture (MHZU 23-0255)	263
5.103 Maximum likelihood phylogeny based on the combined ITS, LSU, *rpb1*, and *tef1-α* sequences data of c	266
5.104 *Bussabanomyces wurfbainiae* (MHZU 24-0045, holotype)	268
5.105 Maximum likelihood phylogeny based on the combined LSU, ITS, *rpb1*, *cal*, and *act* sequences data of *Bulbopyricularia*	273
5.106 *Bulbopyricularia guangdongensis* (MHZU 24-0306, holotype)	275
5.107 *Bulbopyricularia wurfbainiae* (MHZU 24-0173, holotype)	277
5.108 Maximum likelihood phylogeny based on the combined LSU, ITS, SSU, *rpb2*, and *tef1-α* sequences data of Pleurotheciales	280
5.109 *Dematipyriforma wurfbainiae* (MHZU 23-0249, holotype)	281
5.110 Maximum likelihood phylogeny based on the combined ITS, LSU, *rpb2*, and *tub2* sequences data of Chaetomiaceae	285
5.111 *Chaetomium globosum* (MHZU 24-0298, new host record)	287
5.112 *Humicola wurfbainiae* (MHZU 24-0155, new host and geographical record)	290

LIST OF FIGURES

Figure		Page
5.113	Maximum likelihood phylogeny based on the combined ITS and *tub2* sequences data of *Peroneutypa*	293
5.114	*Peroneutypa wurfbainiae* (MHZU 24-0226, holotype)	294
5.115	Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tub2* sequences data of *Astrocystis*	296
5.116	*Astrocystis heterocyclae* (MHZU 24-0169, new host record)	297
5.117	Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Phanerochaete*	300
5.118	*Phanerochaete chrysosporium* (MHZU 24-0231, new host record)	302
5.119	Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Mucor*	305
5.120	*Mucor nidicola* (MHZU 24-0125, new host record)	306
5.121	*Mucor wurfbainiae* (MHZU 24-0126, holotype)	308
5.122	a Fungal lifestyle in global distribution; b Fungal isolation frequence in global distribution	315
6.1	Total 503 microfungi strains isolated from *Wurfbainia villosa*	324

ABBREVIATIONS AND SYMBOLS

cm	centimeter
diam.	diameter
e.g.	for example
et al.	and others
gen.	genus (singular) and genera (plural)
h	hour
i.e.	that is
m	meter
mm	millimeter
nov.	novum (Latin for new thing)
sp.	species
spp.	species (plural)
$\bar{x}$	average
$°C$	degree centigrade
µm	micrometer
ml	milliliter
L	Liter
%	percent

CHAPTER 1

INTRODUCTION

1.1 *Wurfbainia villosa*

Wurfbainia villosa, commonly known as *Villous Amomum* or hairy cardamom, is a perennial herbaceous plant belonging to the Zingiberaceae family. This is an evergreen shrub that grows at 600–800 m elevations, often in the mountain area and under the shade of trees of 1.5–3 m high (Zheng et al., 2001; Boer et al., 2018; Tropical Plants Database, 2022). *Wurfbainia villosa* is characterized by rhizomes procumbent above ground, clothed with brown and scalelike sheaths. Leaf blade lanceolate to linear, glabrous, base subrounded, apex caudate. The capsule is purple, green, or brownish when mature and fresh, however, when older, it gets brown, elliptical, or oval shape with three unobvious ridges. The apex has remnants of the perianth. Seeds are bound together in a cluster; the center has a white membrane that splits seeds into three sections. They are externally brownish-red or dark brown, with thin wrinkles and densely spiny protrusions, hard texture, and the endosperm is milky-white. Potent aromatic odour, acrid and cool, slightly bitter taste (Zeng et al., 2022; Wu et al., 2023) (Figure 1.1).

Wurfbainia villosa is mainly distributed in southeast and east Asia (e.g., China, Vietnam, Thailand, Myanmar, Laos, Cambodia, India, and Indonesia) (Zeng et al., 2021). In China, it is distributed in Guangdong, Guangxi, Fujian, and Yunnan provinces (Lai et al., 2016) (Figure 1.1). Interestingly, different regions have different names for this plant. In China, it is known as “Sha Ren” or “Amomi fructus”, whereas the English name is “*Amomum*” or “*Villous amomum*”. In Thailand, it is known as “Bustard cardamom”; in Laos, it is known as “Chinese cardamom”; in India, it is known as “Indian Cardamom or Java Cardamom”.

The city of Yangchun, Guangdong province, has been considered the birthplace of *Wurfbainia villosa* in China (Xu et al., 2022). The *W. villosa* produced in Yangchun city has a special name, “Chunsharen”, reflecting its long cultivating history and high

medicinal value (Lai et al., 2016). In 1963, *W. villosa* was introduced to Xishuangbanna Prefecture of Yunnan Province (Zhou, 1993), which was also largely planted in Xishuangbanna City, Lincang City, Dehong City, and Honghe City. Nowadays, the main producing areas of *W. villosa* are Yunnan and Guangdong provinces (Huang et al., 2014; Zeng et al., 2022), yet it is mostly valued for its medicinal properties in Guangdong (Huang et al., 2014; Liu et al., 2020). However, due to the low pollination rate of *W. villosa*, the high amount of fruit drop rate leads to its output being far below the market demand (Yang et al., 2021).

Wurfbainia villosa is an important traditional Chinese medicinal plant and is recognized as one of the "Four Great Southern Medicines" in China (Lin et al., 2023). The fruit of *W. villosa* is aromatic and rich in essential oils, making it an important spice and medicinal ingredient (Gu et al., 2025). In traditional Chinese medicine (TCM), it is widely used to treat digestive disorders, such as bloating, indigestion, and abdominal pain (Ao et al., 2019). The dried fruits are also utilized as a flavoring agent in various cuisines, adding a distinctive aroma and taste to soups, stews, and herbal teas. Studies have shown that its bioactive compounds, including flavonoids and terpenoids, contribute to its therapeutic effects, such as anti-inflammatory, antioxidant, and antimicrobial activities (Liao et al., 2024).

In recent years, *Wurfbainia villosa* has attracted significant scientific interest due to its potential applications in modern pharmacology and functional foods (Gu et al., 2025). Research has explored its role in improving gastrointestinal health, modulating the immune system, and even exhibiting anti-cancer properties (Tran-Trung et al., 2024; Yang et al., 2021). As a result, it is increasingly used in the development of natural health products. With growing demand for plant-based therapeutics and natural spices, *W. villosa* continues to be a valuable botanical resource in both traditional and contemporary medicine (Yang, Zhao et al., 2022).

Note a, b Living *W. villosa* plant. c, Leaves. d, Rhizome. e, Rhizome with inflorescence. f, Rhizome with fruits. g, h, Fruits. i, Section fruit with inside seeds.

Figure 1.1 *Wurfbainia villosa*

1.2 Microfungi

Microfungi, also known as micromycetes, are a diverse group of fungi characterized by their microscopic structures, including molds, mildews, and rusts (Sahay et al., 2021). They are distinguished from macrofungi by the absence of large fruiting bodies, making them invisible to the naked eye. Ubiquitous in nature,

microfungi inhabit various environments, such as soil, water, plant surfaces, and even extreme habitats like high-radiation caves (Martin-Pozas et al., 2022). Their microscopic hyphae infiltrate substrates, remaining asymptomatically within plant tissues, triggering disease in some cases, or decomposing organic matter to recycle nutrients, all of which contribute to essential ecosystem functions (Liao et al., 2025).

Beyond their ecological roles, microfungi have significant economic and medical importance. Species like *Penicillium* are renowned for producing antibiotics such as penicillin, revolutionizing modern medicine (Correia et al., 2023). Additionally, microfungi are employed in the food industry for the production of bread, beer, and cheese (Lim et al., 2022). However, some microfungi pose challenges; for instance, *Botrytis cinerea* causes gray mold in crops, leading to substantial agricultural losses (Williamson et al., 2007). Conversely, certain microfungi contribute positively to agriculture by enhancing soil fertility and aiding plant growth (Yadav et al., 2010).

The diversity of microfungi is vast, with estimates suggesting that many species remain undocumented, especially in underexplored regions (Bhunjun et al., 2024). Research continues to uncover new species and understand their roles within various ecosystems. For example, studies in the Greater Mekong Subregion have revealed a rich variety of microfungi associated with different substrates, highlighting the need for further exploration and classification (Chaiwan et al., 2021). Understanding the full spectrum of microfungal diversity is essential, as they hold potential for novel biotechnological applications, including enzyme production and bioremediation (Dinakarkumar et al., 2024).

1.3 Microfungi Associated with *Wurfbainia villosa*

Wurfbainia villosa is associated with a wide range of fungi, though historical records have been limited and biased toward pathogens. According to published data, the majority are pathogens (13 species), while only three are epiphyllous fungi, one is an endophyte, and no saprobes have been reported (Jiang & Qi, 1994; Zhang, 2001, 2003; Zeng et al., 2019; Liao et al., 2023). Sixteen fungal species have been reported on *W. villosa* up to 2023 from China, Thailand and India (Farr & Rossman, 2022; Jiang

& Qi, 1994; Zhang, 2001, 2003; Li et al., 2010; Zeng et al., 2019; Song et al., 2021). Among these, 14 species were recorded in China, including *Cladosporium oxysporum*, *C. variabile*, *Colletotrichum capsici*, *Co. fructicola*, *Co. gloeosporioides*, *Co. zingiberis*, *Fusarium solani*, *Gonatopyricularia amomi*, *Pyricularia costina*, *Rhizoctonia solani*, *Scolecopeltidium menglaense*, *S. wangtianshuiense* and *Septoria amomi*. In addition, *Epicoccum thailandicum* and *Micropeltis amomi* have been reported from Thailand, while *Pseudocercospora amomi* has been recorded in India.

Despite this pathogen-focused history, culture-based work indicates a rich and largely unexplored endophytic community. Zhang et al. (2010) isolated approximately 301 endophytic fungal strains from leaves, stems, and roots in South China, finding significant differences among plant tissues: leaves yielded the most abundant endophytic fungi, followed by roots and stems. However, most isolates were not identified to species level. Later, Zhang et al. (2021) reported one endophytic fungus, *Letendraea helminthicola*, from *W. villosa* that produces secondary metabolites.

1.4 Research Objectives

1.4.1 To study the taxonomy and phylogeny of microfungi associated with *Wurfbainia villosa* based on morphology and multi-gene phylogenetic analyses.

1.4.2 To evaluate different endophytic fungi isolation method(s).

1.4.3 To understand the diversity of endophytic fungi with relation to other life modes.

1.5 Research Contents

This thesis is divided into 6 chapters.

Chapter 1 provides a general introduction, covering the research background on *Wurfbainia villosa*, microfungi, microfungi-associated with *W. villosa*, and fungal lifestyle changes.

Chapter 2 describes the materials and methods utilized in the study, covering the sampling approach, laboratory methodologies, and analytical procedures applied to investigate fungal communities.

Chapter 3 includes a review on endophytic fungi, focusing on the optimization of isolation and sporulation techniques, as well as an evaluation of different methods used for isolating and inducing sporulation in endophytic fungi.

Chapter 4 discusses fungal lifestyle transitions, aiming to enhance our understanding of how fungal lifestyles change and to explore the evolutionary factors that drive the endophytic lifestyle.

Chapter 5 describes microfungi isolated from *Wurfbainia villosa* in China and Thailand, supplemented with complete morphological descriptions, illustrations, phylogenetic analyses, and a global checklist.

Chapter 6 presents the overall conclusions, summarizing the key findings of the study and discussing the significance of fungal diversity associated with *Wurfbainia villosa*, as well as the implications of fungal lifestyle transitions for future research and applications.

CHAPTER 2

MATERIALS AND METHODS

2.1 Sample Collection, Morphological Study, and Isolation

Asymptomatic, symptomatic, and dead leaves, stems, roots, and fruits of *Wurfbainia villosa* were collected in Guangdong and Yunnan provinces from 2021 to 2024 (Figure 1.1). Samples were taken to laboratory and placed into zip-lock plastic bags at room temperature. Asymptomatic and symptomatic plant tissues were kept at 4°C if the samples could not be proceeded on the collection date.

2.1.1 Plant Tissue Culture Method

Fresh and healthy leaf, stem, and root were chosen and washed in tap water (75% ethanol clean surface, absorb the water with tissue paper). Each part of the sample had five replicates. The leaf piece was surface sterilized in 2.5% sodium hypochlorite for 1 minute, for 2 minutes (the stem and root both were sterilized in 2.5% sodium hypochlorite and 75% ethanol, while the sterilized time extended to 3–5 minutes), sterilized water for 3 minutes each time, and finally dried on tissue filter paper. Surface-disinfected the leaf piece were cut into 5 × 5 cm with scissors, and the leaf fragments were picked up with tweezers, placed in the PDA medium, and grown in an incubator at 25°C. The hyphae were observed every day for up to seven days (it is preferable to obtain a single hypha under a stereoscope) and then purified three to four times to obtain a pure hyphae culture. All fungal isolates were grown on PDA slants and stored at 4°C. All fungal structures were measured using Tarosoft (R) Image Frame Work program v. 0.9.7. and NIS-Elements BR 5.30.03.

2.1.2 Plant Tissue Maceration Method

This method is preferred for isolating endophytic bacteria, but has also been used to isolate endophytic fungi, especially the slowly growing ones (Sieber, 2002). After surface sterilization, plant tissues were macerated using a mortar and pestle or other mechanical devices, such as Klecco tissue pulveriser (Mahaffee & Kloepper, 1997), depending on the sample size and hardness of the plant tissue. As enzymes and

toxins released during maceration can inactivate or kill endophytic microorganisms, the sample should be diluted immediately to reduce the concentration of toxic compounds to ineffective levels. After the maceration of the surface sterilized tissues, the suspension is streaked onto a selected medium in aseptic condition (Schulz et al., 2006; Hardoim et al., 2015; Senanayake et al., 2020). Each part of the sample had five replicates. Pure culture was obtained for further studies.

2.1.3 Plant Intercellular Fluid Culture Method

This method uses centrifugation to collect intercellular (apoplastic) microorganisms, especially used for isolating endophytes from root tissues (Schulz et al., 2006; Senanayake et al., 2020). Initially, the plant tissue was washed in tap water and then in distilled water for 1 minute and dried in air. After surface sterilization and grind, the plant fragments were centrifuged at 3000G, for 1–20 minutes to collect the apoplastic fluid (Dong et al. 1994). Each part of the sample had five replicates. The fluid was transferred to the media for endophytic isolation (Senanayake et al., 2020).

2.1.4 Pathogenic Fungi Isolation Method

The disease leaf, stem, and root were collected from filed. Firstly, observed the fruit bodies are present or not, if found fruit bodies can isolation based on the single spore isolation (Senanayake et al., 2020); if no fruiting bodies present, tissue isolation proceeds from other infected material. Samples are treated sequentially in 2% NaOCl for 1–2 minutes and then 75% ethanol for 30 seconds, followed by rinsing three times with sterilized water. The sterilized tissue or spores are then dried on sterilized filter paper and finally placed on Potato Dextrose Agar (PDA) plates for incubation and growth. Plates were incubated at 25 °C and monitored daily for 1–7 days. Emerging fungal colonies were subcultured onto fresh PDA medium through three to four times successive transfers to ensure pure culture.

2.1.5 Saprobic Fungi Isolation and Morphological Study

Fungal isolation from dead specimens was performed using single spore isolation, following the methods described by Senanayake et al. (2020). Fungal isolation from asymptomatic and symptomatic plant tissues was carried out using plant tissue isolation method (Liao et al., 2025). Macroscopic morphologies were observed using SZ650 (Chongqing Auto Optical Instrument Co., Ltd., Chongqing, China) stereo microscope. The microscopic morphologies (e.g., ascomata, conidiomata, conidiophores,

hamathecium, appressoria, asci, conidiogenous cells, ascospores, and conidia) were photographed using Nikon Eclipse 80i compound microscope (Tokyo, Japan) equipped with a Digital Sight DS-Fi1 high-definition camera. The photo plates were processed using Adobe Photoshop 2020 (Adobe Systems, USA), and fungal structure were measured using NIS-Elements BR 5.30.03 and Tarosoft (R) Image Frame Work program v. 0.9.7.

Dry specimens of fungal cultures were prepared from one-month-old colonies and dried specimens were deposited in the Mycological Herbarium of Zhongkai University of Agriculture and Engineering (MHZU), Guangzhou, China. The living cultures were preserved both on PDA slants and in 15% glycerol (2 mL cryotubes) and deposited in the Zhongkai University of Agriculture and Engineering Culture Collection (ZHKUCC), Guangdong, China. All newly described fungal species were registered in the Faces of Fungi (FoF) (http://www.facesoffungi.org) and Index Fungorum (IF) databases (http://www.indexfungorum. org/names/names.asp), while other known species in this study were registered in Faces of Fungi (FoF).

2.2 Fungal Sporulation Inducing Methods

The fungi strains selected for inducing sporulation were isolated from the fruits, leaves, stems, and roots of *Wurfbainia villosa* in southern China. Ninety-one strains were selected for sporulation and five sporulation methods were used: oatmeal Agar medium (OA), synthetic low-nutrient agar (SNA), soil medium, carnation leaf agar (CLA), and 1/4 malt extract agar (MEA) + host tissue (leaf, stem and root) + pine needle. The isolates from the leaf were sporulated on 1/4 MEA+ host tissue and 1/4 MEA+ pine needle media; The isolated from roots were sporulated on 1/4 MEA + pine needle medium. Additionally, a specialized sporulation-inducing medium, referred to as the *Wurfbainia villosa* fruit juice medium, was developed for the endophytic fungi isolated from the fruit of *W. villosa*. This medium was prepared by boiling 200 g of fresh *W. villosa* fruit to extract the juice, which was then combined with 20 g of agar. This method was designed specifically to mimic the natural host environment and

stimulate sporulation in fruit-associated endophytes. The culture medium formula should follow Appendix C: Chemical Reagents and Media.

2.3 DNA Extraction, PCR Amplification, and Sequencing

Mycelium covering 60–80% of the plate can be prioritized for scraping and collected into 2 mL centrifuge tubes for Genomic DNA extraction using the MagPure Plant DNA Kit (Guangzhou Magen Biotechnology Co., Ltd., Guangzhou, China), following the manufacturer's instructions. Extracted DNA were kept 4 ℃ and -20℃ for further experiment and future long-term storage, respectively. The thermal cycler conditions and the primers used for Polymerase Chain Reactions (PCR) for each locus are given in Table 2.1. The PCR reaction was prepared in a final volume of 25 μl, comprising 12.5 μl of 2× PCR Master Mix (containing buffer, dNTPs, and Taq DNA polymerase; Nanjing Vazyme Biotech Co., Ltd., Nanjing, China), 9.5 μl of dd water, 1 μl of each primer (forward and reverse), and 1 μl of DNA template.

2.4 Sequence Alignment and Phylogenetic Analyses

All of the sequences used in phylogenetic analyses were obtained from GenBank based on the Blastn search of ITS in GenBank and the latest relevant literature. The download sequences were aligned using MAFFT (Katoh & Toh, 2010), adjusted using BioEdit v.5 (Hall, 1999), and generated consensus sequences by OFPT (Zeng et al., 2023). The dataset was trimmed with TrimAl v.1.3 using the Gappyout option (Capella-Gutiérrez et al., 2009) and format transferred using ALignment Transformation EnviRonment online platform (http://www.sing-group.org/ALTER/).

The combined sequence dataset was used to perform maximum likelihood (ML) and Bayesian inference (BI) analyses in the CIPRES Science Gateway online platform (https://www.phylo.org/portal2/home.action). The GTR + I + G model of evolution and 1000 rapid bootstrap inferences were used in the ML analyses. All free model parameters were estimated using RAxML with 25 per-site rate categories, and the final tree likelihood was optimized under the GAMMA distribution. The ML analysis was

using RAxMLHPC v.8.2.12 on XSEDE (Stamatakis, 2014), and the BI analysis was conducted with the Markov Chain Monte Carlo (MCMC) method using MrBayes on ACCESS (3.2.7a) on XSEDE in the CIPRES portal. Six Markov chains were run concurrently for 5,000,000 generations, with phylogenetic trees sampled at every 100th generation. The phylogenetic trees were visualized using FigTree v. 1.4.0 (Rambaut, 2009) and formatted and edited by PowerPoint 2010 (Microsoft Corporation, Redmond, WA, USA).

2.5 Checklist Preparation

This checklist was compiled using data from the present study, relevant publications, Index Fungorum, reference books, and online databases, including annual reports on *Wurfbainia villosa* and the USDA Fungus–Host Distributions database (https://nt.ars-grin.gov/fungaldatabases/fungushost/fungushost.cfm). For each fungal record, the ecological lifestyle—pathogen, endophyte, or saprotroph—is specified. The checklist provides information on fungal species names, geographic distribution (country and province), host tissue type, lifestyle category, climatic zone, and associated references. Species names are updated in accordance with Index Fungorum (2025), and taxonomic classification follows the system proposed by Wijayawardene et al. (2020). Fungal genera and species are organized alphabetically. In some instances, host names from the original sources were revised to align with current taxonomic standards. Where a cited name could not be matched with a current species or known synonym, the original name was retained as published.

Table 2.1 Gene regions, primers, and PCR conditions used in this study

Gene Regions	Primer	PCR condition					Reference
		Initial Denaturation	Denaturation	Annealing	Extension	Final extension	
ITS	ITS5/ ITS4	94°C, 3 min, 1 cycle	94°C, 30 secs,	52°C, 30 sec	72°C, 1 min	72°C, 10 min,	White et al. (1990)
	ITS1/ITS4		35 cycles	53°C, 30 sec		1 cycle	White et al. (1990)
LSU	LR0R/LR5			52°C, 30 sec			White et al. (1990)
SSU	NS1/NS4						Vilgalys and Hester (1990)
ACT	512F/783R			58°C, 30 sec			White et al. (1990)
CAL	228F/737R			58°C, 30 sec			Carbone and Kohn (1999)
CHS-1	354F/79R			58°C, 30 sec			Carbone and Kohn (1999)
GAPDH	GDF/GDR	94°C, 3 min, 1 cycle	94°C, 30 sec,	59°C, 30 sec	72°C, 1 min	72°C, 10 min,	Templeton et al. (1992)
			35 cycles			1 cycle	
HIS	CYLH3F/CYLH3R			56°C, 30 sec			Crous et al. (2004)
tef1-α	728F/986R			55°C, 50 sec			Carbone and Kohn (1999)
	728F/EF2			53°C, 30 sec			Carbone and Kohn (1999) and
				50°C, 45 sec			O'Donnell et al. (1998)
	EF1/EF2			53°C, 30 sec			O'Donnell et al. (1998)
	688F/1251R			59°C, 30 sec			Alves et al. (2008)
	983F/2218R			55°C, 50 sec			Rehner (2001)
rpb2	fRPB2-5f/fRPB2-7cR	95°C, 3 min, 1 cycle	94°C, 1 min,	52°C, 2 min	72°C, 1.5 min		Liu et al. (1999)
tub2	Bt2a/ Bt2b		35 cycles	55°C, 50 sec			Glass and Donaldson (1995)
	T1/T22			58°C, 55 sec			Glass and Donaldson (1995)
	T1/2b			55°C, 50 sec			O'Donnell and Cigelnik (1997)

CHAPTER 3

OPTIMIZATION OF THE ISOLATION AND SPORULATION TECHNIQUES FOR FUNGAL ENDOPHYTES

3.1 Introduction

Endophytes, pathogens, and saprobes are the three primary lifestyles that fungi adopt in most ecological strategies. Among them, the endophytic lifestyle is one of the highly debated and controversial life modes. Endophytes are well known to cohabit with their hosts over a long period. Mycologists are continually attempting to understand the roles and relationships of endophytes with their hosts in their natural ecosystems. Most endophytic fungi belong to Ascomycota (Arnold, 2007; Senanayake et al., 2022), while a few belong to Basidiomycota (Eo et al., 2022). The number of fungal endophytes has been estimated to exceed 1 million (Strobel & Daisy, 2003; Sun & Guo, 2012), and this could represent one-fifth of the actual estimate of 2.2 to 3.8 million fungal species as proposed by Hawksworth and Lücking (2017). Even an estimate of over 1 million endophytes seems plausible if we assume that for every one plant there are about six fungal endophytes as previously postulated. Previously, the exclusive reliance on cultured samples resulted in a plant-fungus ratio of 1:6 (Hawksworth, 2001). If there are six species of endophytic fungi in each plant and a minimum of 270,000 plant species, this leads to an estimate of over 1.5 million (Hawksworth 2001; Gunatilaka, 2006; Guo et al., 2008; Bhunjun et al., 2022).

The concept of endophytes has evolved since its initial definition in 1809 (Link 1809), necessitating periodic re-evaluation based on new research findings. With the extensive knowledge accumulated from published studies, it is necessary to revisit and update the definition of a fungal endophyte. However, the definition of what is an endophytic fungus is challenged by different lifestyles of fungi, lifestyle shifts, and a wide range of host associations depending upon the plant growth stages (Bhunjun et al., 2022; Norphanphoun et al., 2022; Liao et al., 2023; Dissanayake et al., 2024). In addition, it is necessary to understand how life mode appeared first, especially in

economically important crops. Pathogens may exist as an endophyte while the plant remains symptomless and appears healthy. Another important aspect is to re-evaluate the fungal endophytic association with plants, focusing on host preferences and their coevolutionary dynamics (Delaye et al., 2013; Hardoim et al., 2015; DeMers, 2022).

The difficulties in isolating endophytes have been recognized as contributing to the complexity of theoretical approaches to study endophytes. Traditional isolation methods, such as tissue isolation followed by cultural studies and microscopy, are the most widely and commonly used approach (Senanayake et al., 2020). However, in recent years, microbiome analysis with High Throughput Sequencing (HTS)/ Next-Generation Sequencing (NGS) has also been employed (Dissanayake et al., 2018; Baldrian et al., 2022). Both traditional and culture-independent approaches have their pros and cons, thus, making it necessary to reevaluate these techniques for better species diversity and taxonomy (Jeewon et al., 2018). This paper on fungal endophytes will provide a collation of scattered knowledge on endophytes and the necessary platform for further discussion on fungal endophytes.

3.2 Definition of Endophytes

The definition of endophytes goes back to 1809 when the German botanist Heinrich Friedrich Link described them as “entophytae”, by which he meant partial parasitic fungi in plants (Link, 1809; Hardoim et al., 2015; Swamy et al., 2021). Later, the term “endophyte” was adopted by de Bary (1866). The most common definition used at present is derived from Petrini (1991), who stated that “endophytes are all organisms inhabiting plant organs at some time in their life, which can colonize internal plant tissues without causing apparent harm to their host”. An additional definition is provided by Hallmann et al. (1997), who stated that “endophytes are those (bacterial) that can be isolated from surface-disinfested plant tissue or extracted from within the plant, and that do not visibly harm the plant”. The dictionary of the fungi defined endophytes as; “in its widest sense the term has been used to include organisms ranging from bacteria to parasitic angiosperms (e.g., mistletoes) that exist completely or partially within any plant-like organism” (Kirk et al., 2008). Many previous

publications accepted the definition “fungal endophytes are microorganisms that reside in internal tissues of living plants without causing any immediate overt negative effects” (Bacon & White, 2000; Guo et al., 2008; Meenatchi et al., 2016). Following many fungal studies related to recovery of endophytes (e.g., Wei et al. 2006; An et al., 2020), many definitions of endophytes have surfaced, but these have also led to much confusion and debate. To date there is not any universally accepted definition and several queries with regards to the boundary of an endophyte, and whether mycorrhizal fungi are actually endophytes remain largely unanswered. Bills (1996) and Bayman et al. (1997) went a step further in identifying mycorrhizal fungi as endophytes. The mycorrhizal associations with plants are considered as mutualistic relationships in which both plant and the fungus share benefits (Lanfranco et al., 2016). Almost all living plants in the world are associated with mycorrhizal endophytes, and in an estimate, only about 10% of land plants are non-mycorrhizal species (Wang et al., 2022). It is to be noted that while mycorrhizal fungi are confined only to the rhizosphere, endophytes could be found in association with all above-ground plant tissues. Bearing this in mind, we reckon that mycorrhizae have an independent fungal lifestyle different from endophytes, and there is a need to set clear boundaries between mycorrhizae and endophytes. Therefore, when it comes to root endophytes it is important to establish whether the fungal group has been reported as a mycorrhiza earlier, before defining it as an endophyte. With reference to plant epiphytes, they are those fungi that live on the surface of plants, while endophytes are able to penetrate into the host tissues (Hardoim et al., 2015). Here we propose a new definition taking into account updated scientific evidence from published studies with regards colonization, disease causing potential, benefits to hosts and their lifestyle. We propose that fungal endophytes can be defined as “asymptomatic microbial partners that are intimately associated and co-inhabit within healthy internal plant tissues with the ability to confer benefits, co-evolve and alter their lifestyle depending upon plant life stages and adverse conditions”.

3.3 Endophytic Fungi Colonization Mechanism

As discussed previously in this paper, endophytic fungi colonize plant tissues inter- and intra-cellularly (Barrow, 2003). In contrast to endophytic bacteria, the mode of ingress into plant tissues by endophytic fungi is active and occurs via stomata, cell walls or wounds (Schulz & Boyle, 2006). Endophytic fungal diversity and colonization density occur in different plant tissues at varying levels, and they vary with the habitat and host (Schulz & Boyle, 2006). For example, fungal growth within roots was extensive compared to that of the above-ground parts (Schulz & Boyle, 2005).

Fungal colonization also varies depending on the class to which the endophyte belongs (Rodriguez et al., 2009). The clavicipitaceous endophytes (C-endophytes or Class 1 endophytes) with a narrow host range, extensively and systematically colonize plant shoots and rhizomes (Saikkonen et al., 2002; Rodriguez et al., 2009). Plants colonized by C-endophytes usually comprise one dominant fungal isolate or genotype (Wille et al., 1999). Non-clavicipitaceous endophytes (NC-endophytes) have a broad host range, including non-vascular plants, ferns and allies, conifers, and angiosperms and are found in all terrestrial ecosystems from the tropics to the tundras. These NC-endophytes can be further categorized into functional classes based on host colonization patterns and the transmission mechanism among hosts (Rodriguez et al., 2009). Class 2 NC-endophytes colonize both above-ground as well as below-ground tissues (roots and rhizomes). In contrast to Class 2, Class 3 NC-endophytes show highly localized shoot colonization and can also be isolated from above-ground parts of conifers, herbaceous angiosperms, non-vascular plants, vascular plants, and woody plants (Tejesvi et al., 2005; Rodriguez et al., 2009). Class 4 endophytes colonize the root part of conifers, pine tree roots, and shrubs worldwide (Jumpponen, 2001; Rodriguez et al., 2009).

3.4 How Do Fungal Endophytes Evade Plant Defenses?

Upon recognition, plants initiate defense signaling cascades to prevent intrusions from endophytic fungi. Endophytic fungi must circumvent these plant

defense mechanisms by evading microbe-associated molecular pattern recognition by suppressing or avoiding microbe-associated molecular pattern-triggered responses to initiate colonization (Sarsaiya et al., 2019; Waqar et al., 2023). Endophytic fungi exist in different forms, such as mycelial, yeast-like or mycosomes (Atsatt & Whiteside, 2014). Their morphology changes during plant colonization, facilitating them to evade recognition by plant defenses. Mycorrhizal fungi form arbuscules as interfaces between plant and cells to transfer compounds while avoiding plant detection, whereas other endophytes achieve this by relatively unspecialized hyphae (Brundrett, 2002, 2006). Furthermore, they evolve divergent microbe-associated molecular patterns and modify cell wall components to evade recognition and overcome plant immunity (Lu et al., 2021). Similar to plant-pathogen interactions, plants induce symbiotic signals upon detection of endophytes through their recognition receptors. They evade plant immune signals by secreting effectors, such as apoplastic effectors and eATPs, and symbiotically colonize plant parts (Lu et al., 2021). Zipfel and Oldroyd (2017) stated that the plant receptors for the pathogenic and symbiotic invaders are similar but act distinctly by triggering entirely different responses for pathogens and endophytes. Upon recognition of lipo-chitooligosaccharide signals produced from microbial cell wall components, and exudates and short-chain chitin oligomers produced by mycorrhizal fungi via lysinmotif receptors, common symbiosis signaling pathways are activated (Gough & Cullimore, 2011; Genre et al., 2013). In addition to the microbial cell wall surface polysaccharides, microbe-to-plant signal compounds are important for microbial interactions in plants (Lu et al., 2021). For example, the endophyte *Piriformospora indica* produces fungal-specific β-glucan-binding lectin, responsible for changing fungal cell wall composition and properties, thus suppressing theβ-glucan-triggered immunity in their hosts (Wawra et al., 2016, 2019).

In addition to the efforts by fungi to evade host defense, plant genotypes also influence endophytes favorably (Devers et al., 2011; Lu et al., 2021). Several studies have shown that plant miRNAs play an important role in regulating the symbiosis interactions in plants (Devers et al., 2011; Bologna & Voinnet, 2014). It was found that plant miRNAs respond distinctly and oppositely against endophytes and pathogens. These responses suggest the involvement of plants in facilitating endophytes to evade

their own defenses (Bologna & Voinnet, 2014). Further, plants also secrete chemical metabolites to attract and establish beneficial interactions with endophytes, such as tryptophan-derived metabolites by Brassicaceae plants (Lu et al., 2021). However, further studies are required to understand these immune evasion mechanisms by fungi to clarify the communication between the endophytic fungi colonization and the plant.

3.5 Endophyte Isolation Techniques and Induce Sporulation

The isolation technique of fungal endophytes is mostly known as the tissue isolation method which includes several key steps including surface sterilization of plant tissues, cultivation in appropriate media and purification of endophytic isolates under suitable conditions to obtain pure cultures of endophytes. Once the pure cultures are obtained, DNA based molecular identification, together with morphological approaches are used to identify the fungal species as well as in diversity-related studies. This approach is commonly known as the culture-dependent or traditional method.

With the development of next-generation sequencing techniques, metagenomic approaches are also highly utilized in endophytic characterization, which was called culture-independent methods. Thus, culture-dependent methods and culture-independent methods are mostly used to identification of endophytic fungi (Pereira et al., 2011; Vaz-Moreira et al., 2011; Wijayawardene et al., 2021). However, culture-dependent methods have several limitations as follows: (1) slow-growing endophytes may not be obtained due to their inhibition by fast-growing species or unsuitable conditions; (2) obligate endophytes are difficult to maintain and identify in laboratory conditions on artificial media; (3) culture conditions used (aeration, nutrition, temperature), tissue size and numbers of plant samples can affect number and growth for observed fungal diversity and community composition; and (4) some endophytic taxa may not produce reproductive structures on artificial media which is insufficient to identify species based on culture-dependent methods solely. The culture-independent methods are mostly used for fungal diversity studies. However, this method does not allow identifying species at the species level, which will greatly hinder the identification of fungi. In addition, it can be used as a complement to the culture-

dependent methods, as many fungi cannot grow on artificial medium. Hence, this method is suitable for exploring fungal diversity.

One of the common problems concerning the identification of endophytic fungi is that some endophytes possess sterile mycelia, which makes species identification difficult due to the unavailability of morphological characters (Gamboa & Bayman, 2001; Promputtha et al., 2005). Up to 54% of the total endophytic isolates do not sporulate on commonly used media, e.g., PDA and MEA (Sun & Guo, 2012). In view of this, various methods have been employed to promote sporulation. These include growing of sterile mycelia on sterilized host substrates, and exposure to alternating UV at wavelength of 300 nm (Guo et al., 1998; Abbo et al., 2015); incubation of non-sporulating isolates on different natural media such as cornmeal agar, oatmeal agar, V8 juice agar, or chemically defined media including Czapek's agar, including medium containing extracts of the host plant (e.g., Cucurbita pepo) (Eevers et al., 2015). Guo et al. (1998) promoted sporulation of mycelia sterilia of palm endophytic fungi in flasks containing MEA with sterilized host substrates and incubating for 12 h alternating near UV-light and darkness conditions, which resulted in 83.5% of mycelia sterilia forming fruiting bodies on the surface of petioles, after three months. Zhou et al. (2020) found that adding vitamin B in the culture medium can increase the diversities of isolated fungi, as high as 207% and 81% at the genus level, under 4°C and 25°C, respectively. In this study, we comparison and tested different endophytes sporulation methods based on different sporulation culture media and added different plant tissues.

3.6 Results and Discussion

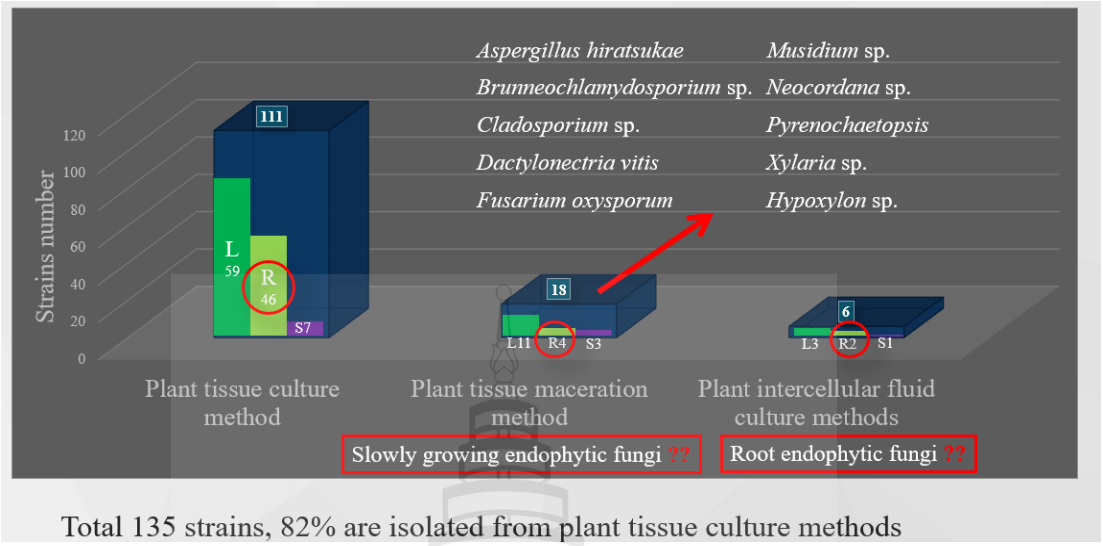
3.6.1 Results of Culture-Dependent Methods and Discussion

A total of 135 endophytic strains were isolated using three different methods: plant tissue culture, plant tissue maceration, and plant intercellular fluid culture. Among these, the plant tissue culture method proved to be the most effective, yielding 111 strains, which accounts for 82% of the total. Specifically, this method isolated 59 strains from leaves, 46 from roots, and 7 from stems. In comparison, the plant tissue maceration method produced 18 strains (11 from leaves, 4 from roots, 3 from stems), while the

plant intercellular fluid culture method resulted in only 6 strains (3 from leaves, 2 from roots, 1 from stems) (Figure 3.3). Overall, the highest number of isolates was consistently obtained from leaf tissues across all methods, followed by roots and stems.

In this study, the plant tissue maceration method yielded 18 strains, including *Aspergillus hiratsukae*, *Brunneochlamydosporium* sp., *Cladosporium* sp., *Dactylonectria vitis*, *Fusarium oxysporum*, *Hypoxylon* sp., *Musidium* sp., *Neocordana* sp., *Pyrenochaetopsis*, and *Xylaria* sp. These genera are generally characterized by rapid growth. Therefore, it remains uncertain whether the plant tissue maceration method is truly suitable for isolating slow-growing fungi from *Wurfbainia villosa*. Further experiments are required to clarify this. In addition, the isolation results showed that only two root endophytic strains were obtained using the plant intercellular fluid culture method. In contrast, the plant tissue culture and plant tissue maceration methods yielded 46 and 4 strains from roots, respectively, both considerably more than the intercellular fluid culture method. Therefore, in this study, it remains uncertain whether the plant intercellular fluid culture method is truly effective for isolating root endophytes from *Wurfbainia villosa*. Further experiments are needed to confirm this.

These findings indicate that the plant tissue culture method is significantly more efficient for isolating endophytic microorganisms, particularly from leaf and root tissues. The results also suggest that leaves are a more favorable tissue source for endophyte recovery. Therefore, for future studies aiming to isolate endophytes, especially in large-scale or biodiversity-oriented surveys, the use of the plant tissue culture method is strongly recommended due to its superior isolation efficiency and broader applicability across plant organs.



Note L: Leaf, R: Root, S: Stem

Figure 3.3 The different isolation methods results

3.6.2 Results of Sporulation Methods and Discussion

In this study, a total of 301 endophytic fungal strains were obtained. After applying various sporulation-inducing methods—such as carnation leaf agar (CLA), Oatmeal agar (OA), Synthetic nutrient-poor agar (SNA), host plant tissue, and fruit juice media, 212 strains (approximately 84%) successfully produced spores, while the remaining 16% did not sporulate (Figure 3.4b). Among the most challenging genera to induce sporulation were *Xylaria*, *Cercospora*, *Pseudocercospora*, and *Ceratobasidium.* Based on experimental observations, specific media are recommended for certain genera to enhance sporulation, as summarized in the accompanying table 3.1. The following section presents and discusses the results obtained from testing various sporulation-inducing media in this study.

A total of 91 endophytic fungal strains were tested under various sporulation-inducing culture conditions, including Soil media, SNA, OA, 1/4 MEA + host tissue, 1/4 MEA + pine needle, and a combination of plant tissue + 1/4 MEA + pine needle. Among these, 63 strains (approximately 69%) successfully sporulated, while 28 strains (31%) remained non-sporulating despite being exposed to these enriched conditions. The medium composed of plant tissue + 1/4 MEA + pine needle yielded the highest sporulation efficiency, supporting sporulation in 28 strains, followed by 1/4 MEA + pine needle (12 strains), and SNA (14 strains) (Figure 3.4a). The basic Soil media

supported only 11 sporulating strains, indicating its relatively poor efficacy in inducing sporulation. Genera such as *Pyricularia*, *Colletotrichum*, *Cercospora*, and *Neodeightonia* appeared across multiple media, suggesting their higher responsiveness to environmental cues. Additionally, the results of the sporulation assay using the *Wurfbainia villosa* fruit juice medium demonstrated a remarkably high success rate, with up to 84% of the endophytic isolates producing spores. Only a few genera, such as *Cercospora*, *Pseudocercospora*, and *Xylaria*, failed to sporulate under these conditions. These findings indicate that the fruit juice medium is highly effective in promoting sporulation of endophytic fungi isolated from *W. villosa* fruits and represents a highly efficient medium for inducing sporulation in fruit-derived endophytes.

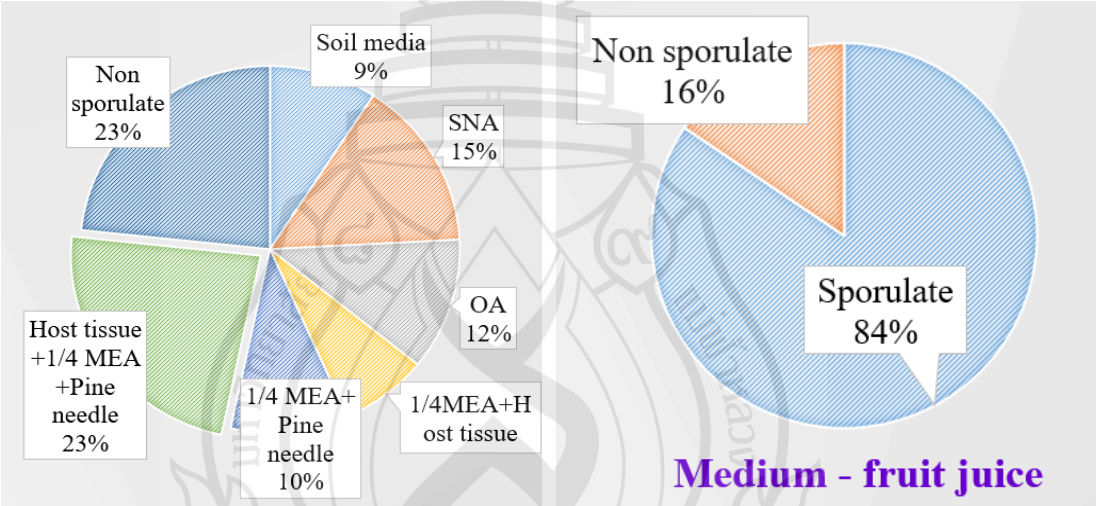
In this study, some strains sporulated only on the Host tissue + ¼ MEA + Pine needle medium, including *Arcopilus aureus*, *Bipolaris wurfbainiae*, *Idriella lunata*, *Neoroussoella leucaenae*, and *Pyrenochaetopsis microspora*. *Leptosphaeria* sp. sporulated exclusively on OA, while *Coprinellus disseminatus* produced spores only on ¼ MEA + Host tissue. In contrast, certain fungi sporulated on both SNA and OA, such as *Annulohypoxylon* sp., *Humicola wurfbainiae*, *Letendraea eurotioides*, and *Setophoma wurfbainiae*. Additionally, some genera were able to sporulate on multiple media, including Host tissue + ¼ MEA + Pine needle, OA, and SNA, such as *Bulbopyricularia*, *Colletotrichum*, *Trichoderma*, *Neodeightonia*, and *Corynespora*.

This study highlights the critical role of medium composition in stimulating fungal sporulation, with the plant tissue + pine needle-enriched medium and fruit juice medium being the most effective overall. However, the fact that nearly one-third of strains did not sporulate, even under enriched conditions, underscores a key limitation: some endophytic fungi are inherently reluctant to sporulate in artificial media, possibly due to specific, unknown host-derived signals or developmental constraints. For future work, a two-pronged strategy is recommended: (1) employ complex, host-mimicking media early in isolation protocols to improve morphological identification; and (2) continue integrating molecular identification for non-sporulating isolates. Additionally, exploring co-culture systems or adding chemical inducers (e.g., plant hormones, epigenetic modifiers) could further enhance sporulation success in recalcitrant strains.

Table 3.1 The genera suggest those media to induce sporulation

Genera	Media
Corynespora/Nigrospora	SNA
Hypoxylon/Hypomontagnella	OA
Diaporthe/Gaeumannomyces	¼ MEA + Host tissue
Dactylonectria/Musidium Fusarium (Nectriaceae)	CLA/SNA
Acrocalymma/Bulbopyricularia	¼ MEA + Host tissue

Note CLA = carnation leaf agar; OA = Oatmeal agar; SNA = Synthetic nutrient-poor agar



a The sporulation methods evaluation b The sporulation methods results for fruit juice methods

Figure 3.4 The sporulation methods evaluation

CHAPTER 4

FUNGAL LIFESTYLE TRANSITION

4.1 Introduction

Fungi exhibit remarkable adaptability in their lifestyles, transitioning between different ecological niches to survive and thrive in diverse environments. This ability to shift lifestyles is crucial for their evolutionary success and ecological functions. Fungal lifestyle changes refer to the transition between saprotrophic, pathogenic, endophytic, and symbiotic modes of existence, influenced by environmental pressures, host interactions, and genetic regulation (Liao et al., 2025a). Some fungi, such as *Colletotrichum* species, can exist as endophytes in asymptomatic hosts but become pathogenic under specific environmental conditions (Chang et al., 2014; Carneiro & Baric, 2021). Similarly, *Fusarium* species are known to switch between saprotrophic and pathogenic lifestyles depending on nutrient availability and host susceptibility (Rodriguez et al., 2009; Orr et al., 2018).

Several factors contribute to fungal lifestyle transitions, including genetic, epigenetic, and environmental influences. Horizontal gene transfer, gene duplications, and mutations play significant roles in acquiring new metabolic pathways that facilitate adaptation (Redman et al., 1999; Redman et al., 2001; Rodriguez & Redman, 2008). For example, *Magnaporthe oryzae*, the rice blast fungus, has undergone gene duplication events that enhance its pathogenicity by improving its ability to infect host tissues (Hyun Khang & Valent, 2010). Epigenetic modifications, such as DNA methylation and histone modifications, enable fungi to regulate gene expression dynamically in response to environmental cues. For instance, histone acetylation in *Botrytis cinerea* modulates its ability to shift between necrotrophic and saprotrophic lifestyles (Keller et al., 2003).

Environmental factors, such as temperature, humidity, and host immune responses, also play a crucial role in lifestyle transitions. *Alternaria alternata*, a common plant pathogen, may remain as an endophyte in favorable conditions but

become virulent when the host experiences stress (DeMers, 2022). Under specific environmental or physiological stresses, endophytes can transition from beneficial symbionts to pathogens or saprobes (Fisher & Petrini, 1992; Promputtha et al., 2007; Hilário & Gonçalves, 2023; Wang et al., 2024). As saprobes, they begin decomposing dead or decaying organic matter, particularly when plant tissues die, thereby recycling nutrients back into the ecosystem (Promputtha et al., 2007; Rodriguez & Redman, 2008). On the other hand, endophytes may adopt a pathogenic role when the host plant experiences stresses, such as nutrient deficiency or drought, allowing them to proliferate within plant tissues and potentially cause disease symptoms (Newsham, 2011). This shift is driven by a combination of environmental factors and genetic interactions between the host and the endophyte (Photita et al., 2004; Promputtha et al., 2007; Hardoim et al., 2015). For example, *Epichloe* (formerly known as *Neotyphodium*) species typically have a mutualistic relationship with grasses, but can become harmful under stressful conditions (Lee et al., 2021). This remarkable adaptability enables endophytes to navigate between beneficial and harmful states, allowing them to occupy diverse ecological niches and respond flexibly to changes in their environment.

Several studies have postulated intimate relationships between endophytes and saprobes (Promputtha et al., 2007; Promputtha et al., 2010; Hu et al., 2024). Promputtha et al. (2010) proposed that during the endophytic life stage, fungi live in healthy plant tissues, suppressing the production of these enzymes until they start living in a nutrient-deficient condition of the host tissue due to senescence, to become saprobes. The production of degrading enzymes by endophytic fungi in decomposing leaves and artificial media is proof of the ability of that particular endophyte to produce degrading enzymes once leaves reach the senescing stage in order to survive as saprobes. When endophytes switch to saprobes, they activate genes responsible for degrading enzymes such as ligninolytic enzymes, β-mannanase, and cellulase to acquire nutrients (Promputtha et al., 2010). Purahong and Hyde (2011) suggested that certain fungal endophytes may switch their ecological roles and adopt a new lifestyle as saprotrophs based on evidence derived from the combination of classical morphology, molecular approaches, and digestion enzyme studies. Nelson et al. (2020) revealed a novel finding that foliar endophytes can colonize woody substrates through direct contact with leaves, thus demonstrating their ability to transition between endophytic and saprotrophic life

stages. Based on these findings, the fact that endophytes can transform into saprobic mode upon host decay has been confirmed while opening the platform for discoveries and further discussion.

The pathogenic potential of several endophytes has been duly reported. In a previous study, Fisher and Petrini (1992) identified that the transition of life mode from one to another might be induced by a weakening of host resistance due to factors such as excessive humidity, drought, or poor nutrient supply. The potential for some endophytes to switch into pathogens can arise through genetic mutations. For instance, Young et al. (2020) found that the upregulation of Zn(II)-Cys6 genes in the early colonization process of soybean may play a role in enhancing the pathogenicity of *Fusarium virguliforme* in soybean by comparing the endophytic lifestyle of *F. virguliforme* in corn and its transition to a pathogenic lifestyle in soybean. In terms of genes and heredity, the lifestyle changes of endophytes depend on slight alterations in fungal gene expression in response to the host, as well as the host's recognition and reaction to the fungi (Aly et al., 2011; Bhunjun et al., 2023). When endophytes switch to pathogens, they activate additional genes, such as effectors, cell wall-degrading enzymes, transposons, transporters, and toxins (Aylward et al., 2017). For example, the high diversity of membrane transporters in the genomes of *Fusarium oxysporum* and *Pyrenochaeta lycopersici* suggests a strong implication in their pathogenicity ability (Aragona et al., 2014). Endophytic fungi can transition to pathogens due to environmental changes, such as light conditions. For instance, *Botryosphaeria stevensii* (Current name: *Diplodia mutila*) associated with the plant *Iriartea deltoidea* is in the endophytic state in the shaded and low light, whereas it turns into a pathogen under high light (Álvarez-Loayza et al., 2011). There is also evidence that certain endophytes can become pathogenic when the host plant is under stress (Kulik, 1984; Photita et al., 2004). For example, Eydoux and Farrer (2020) reported that high salinity stress can lead to a lifestyle change of *Fusarium solani* in *Oryza sativa* (rice) from endophytic to pathogenic.

The ability of fungi to modify their lifestyles has profound ecological implications, influencing nutrient cycling, plant health, and disease outbreaks. Endophytic fungi, for instance, may become opportunistic pathogens when host conditions deteriorate, whereas some saprotrophs can acquire pathogenic traits under

favorable conditions (Liao et al., 2025a). *Armillaria* species, known as root rot fungi, can exist as saprotrophs decomposing dead wood but transition to aggressive pathogens when infecting living trees (Kim et al., 2022). Understanding these transitions provides insights into fungal evolution, host-pathogen dynamics, and potential applications in agriculture and biotechnology. For example, utilizing endophytic fungi like *Trichoderma* species for biocontrol can help suppress plant diseases while maintaining beneficial symbiosis (Siddaiah et al., 2017).

4.2 How Does Evolution Drive the Endophytic Lifestyle?

Like other fungus-host interactions, endophyte-plant interactions depend on the morphological, physiological and historical traits of the fungus, such as pattern of infection, genotypic variation, ecological factors and fungal reproduction (Saikkonen et al., 1998, 2004). Moreover, the evolutionary history of fungi and plants also determines their interactions (Saikkonen et al., 2004). Endophytes may have evolved from pathogenic fungi and therefore, are closely related to each other (Saikkonen et al., 1998; Carroll, 1986, 1992), and this have been supported from views on latency periods and virulence in endophytes (Carroll, 1986, 1992; Petrini et al., 1992; White et al., 1993). Recent evidence from banana plants also indicates that *Deightoniella torulosa* can be isolated as an endophyte as well as a pathogen, and hence the endophytic stage may be important in the life cycles of pathogens (Photita et al., 2016). DeMers (2022) also proposed that *Alternaria alternata* is a common fungus capable of both endophytism and at least mild pathogenicity. Bhunjun et al. (2023) postulated that an endophytic lifestyle represents the ancestral state for many fungi, evidence being the presence of appressoria in endophytes. Appressoria, which are prominent infection structures in pathogens, have persisted throughout evolutionary history and can also be found in endophytes and saprobes (Chethana et al., 2021; Bhunjun et al., 2023). Moreover, the presence of appressoria within the same genus across different lifestyles provides compelling evidence for the transition of fungi between different lifestyles. For example, *Colletotrichum* is one of the top ten plant pathogenic species worldwide, and has been reported to produce appressoria across its endophytic, pathogenic and

saprobic lifestyles (Jayawardena et al., 2021; Zhang et al., 2023b). Samarakoon et al. (2022) stated that stromatic, clypeate ascomata with aseptate, hyaline ascospores lacking a germ slit likely represent the ancestral Xylariomycetidae, which evolved through plant-fungal endophytic associations. Based on 5.8S rRNA and ITS sequences of 163 fungal strains, Delaye et al. (2013) proposed that endophytic and necrotrophic lifestyles can arise due to frequent evolutionary and even ecological changes, whereas once biotrophy has evolved, there is no easy return to the other lifestyles. Several studies have also hypothesized that fungal endophytes can become saprobes. Generally, fungal switch between different lifestyles is due to their flexible genomes, which can rapidly evolve through mechanisms such as mutation, gene duplication, and horizontal gene transfer. Hill et al. (2022) provided evidence of multiple and frequent lifestyle transitions based on phylogenetic reconstruction and demonstrated that *Fusarium* has frequently undergone lifestyle changes due to the highly diverse and dynamic genome. In addition, fungal lifestyles also change depending on changes in their nutritional modes and are influenced by multiple factors, including mutualistic relationships, host tolerance and immune evasion, and ecological factors (Dickinson, 1976; Hyde & Soytong, 2008; Croll & McDonald, 2012; Hu et al., 2024). During senescence, endophytic fungi may gain the ability to penetrate and colonize host tissues (Dickinson, 1976; Wilson, 2000). Promputtha et al. (2010) agreed with the hypothesis that "endophytes can change lifestyles to saprobes" with evidence of enzyme-producing ability of endophytes as their saprobic counterparts.

4.3 Fungi Isolated from *Wurfbainia Villosa* and Their Lifestyle Transitions

This study investigates three primary scenarios of fungal lifestyle transitions among isolates from *Wurfbainia villosa*: (1) lifestyle shifts among fungal species isolated from *Wurfbainia villosa*, transitioning between different ecological roles (e.g., endophytic, saprobic and potentially pathogenic); (2) tissue-specific shifts within the same plant across different organs (e.g., leaves, stems, fruits, and roots); and (3) cross-host transitions between different host plants. Through integrated morphological and multi-locus phylogenetic analyses, we identified 197 fungal strains representing 65

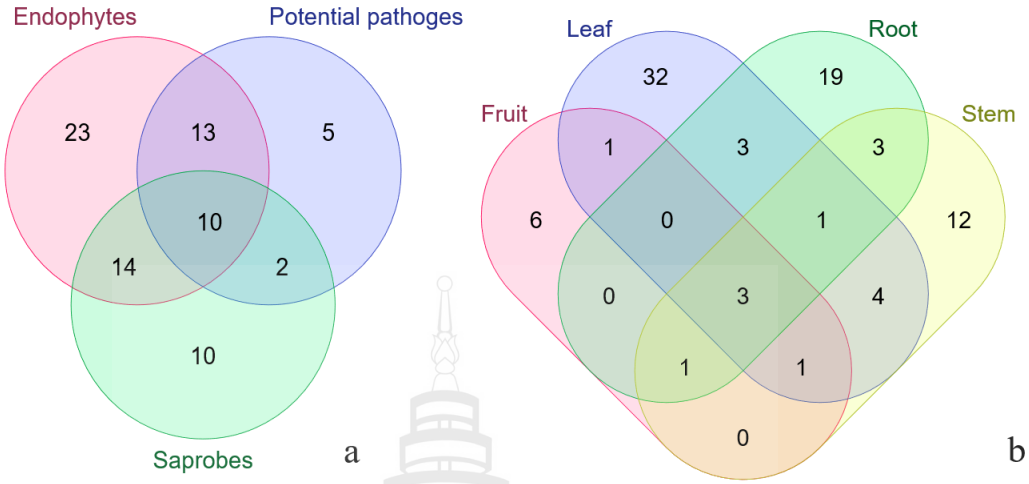
species from 44 genera. We found that nine fungal species exhibited transitions among all three lifestyles (endophytic, saprophytic, and potentially pathogenic) in *Wurfbainia villosa*. These ten fungal species are *Bulbopyricularia guangdongensis*, *Bussabanomyces wurfbainiae*, *Corynespora cassiicola*, *Curvularia geniculata*, *Musicillium tropicale*, *Muyocopron laterale*, *Musidium wurfbainiae*, *Nigrospora camelliae-sinensis*, *Nigrospora oryzae*, and *Nigrospora sphaerica* (Figure 4.1, Table 4.1). While 14 fungal species displayed both endophytic and saprobic lifestyles (Figure 4.1, Table 4.1), 13 fungal species displayed both endophytic and potential pathogenic lifestyles, and two species, *Chaetomium globosum* and *Pyrenochaetopsis guangdongensis* exhibited saprobic and potentially pathogenic lifestyles.

Regarding tissue-specific shifts within the same plant across different tissues, we found that 32 species were found exclusively in leaf tissue, making leaves the most colonized organ. This high frequency may be attributed to the leaf's large surface area, exposure to airborne spores, and variable microenvironments that favor fungal settlement. In contrast, 19 species were restricted to roots, suggesting active interactions with soil and root-associated niches, possibly including endophytic or rhizosphere-adapted fungi. Stem-specific colonizers were less common, with only 12 species found exclusively in this tissue, while fruit-exclusive fungi were the least frequent, represented by just six species, likely due to the seasonal and chemically defensive nature of fruits.

Notably, several fungal species demonstrated the ability to colonize multiple tissue types, indicating ecological flexibility and low host tissue specificity. *Bulbopyricularia guangdongensis*, *Corynespora wurfbainiae*, and *Musidium wurfbainiae* were found in all four tissues, leaf, root, stem, and fruit, highlighting their broad tissue adaptability and potential for diverse ecological roles. Other species, such as *Colletotrichum fructicola*, *Curvularia plantarum*, and *Sarocladium wurfbainiae*, were present in three different tissues, further supporting the presence of generalist colonizers within the fungal community. These findings suggest a dynamic fungal assemblage where both tissue-specialist and tissue-generalist species coexist, potentially contributing to different aspects of plant health, decomposition, and disease under varying environmental conditions.

Notably, several fungal species exhibited host-dependent lifestyle transitions, functioning as endophytes in *Wurfbainia villosa* while adopting pathogenic or saprobic roles in other hosts. For example, *Curvularia geniculata* was isolated as an endophyte from the root of *W. villosa*, but has been reported as a pathogen of coffee, maize, and human cutaneous infections (Revankar & Sutton, 2010; Manzar et al., 2021; Nam et al., 2024), and as a saprobe on wild bananas (Manamgoda et al., 2011; Absalan et al., 2024). *Phyllosticta capitalensis*, isolated here as an endophyte from the leaf of *Wurfbainia villosa*, has been reported as a pathogen causing leaf spot disease in castor bean, oil palm, and tea plants (*Camellia sinensis*) (Cheng et al., 2019; Nasehi et al., 2020; Tang et al., 2020).

Interestingly, we observed appressoria formation in fungal isolates obtained from asymptomatic tissues of *Wurfbainia villosa* when cultured on PDA. While these specialized infection structures are typically associated with pathogenic fungi for host tissue penetration, recent studies indicate their dual role in endophytic colonization and nutrient acquisition from living hosts (Chethana et al., 2021). Notably, we observed appressoria formation in several endophytic fungal genera, including *Colletotrichum* and *Pyricularia*. We found that two *Colletotrichum* species, *Colletotrichum siamense*, and *C. plurivorum*, and *Bulbopyricularia wurfbainiae* isolated from symptomatic and asymptomatic tissues of *Wurfbainia villosa* produced appressoria. This finding aligns with emerging perspectives that appressorial formation capability in fungi with multiple ecological roles may facilitate lifestyle transitions (Bhunjun et al., 2023). Supporting this hypothesis, many studies have reported appressoria production across genera exhibiting diverse lifestyles (Hyde et al., 2007; Marasinghe et al., 2023; Bhunjun et al., 2023), suggesting these structures represent an evolutionarily conserved adaptation with functional plasticity depending on ecological context.



Note a, Venn diagrams show the species number of endophytes, saprobes, and pathogens associated with *Wurfbainia villosa*; b Venn diagrams show the numbers of microfungi in different plant tissues of leaves, stems, fruits, and roots.

Figure 4.1 Venn diagrams show microfungi lifestyle and tissue part overlapping

Table 4.1 List of fungal taxa with overlapping lifestyles (endophytic, saprobic, and potentially pathogenic) isolated from *Wurfbainia villosa*

EN ∩ S	EN ∩ P	EN ∩ P ∩ S	P ∩ S
Acrostalagmus annulatu	*Alternaria pogostemonis*	*Bulbopyricularia guangdongensis*	*Chaetomium globosum*
Apiospora phyllostachydis	*Bipolaris bicolor*	*Bussabanomyces wurfbainiae*	*Pyrenochaetopsis guangdongensis*
Astrocystis heterocyclae	*Bulbopyricularia wurfbainiae*	*Corynespora cassiicola*	
Lasiodiplodia wurfbainiae	*Colletotrichum fructicola*	*Curvularia geniculata*	
Mucor nidicola	*Colletotrichum plurivorum*	*Muyocopron laterale*	
Neoroussoella leucaenae	*Colletotrichum siamense*	*Neomusidium wurfbainiae*	
Penicillium allaniae	*Corynespora wurfbainiae*	*Nigrospora camelliae-sinensis*	

Table 4.1 (continued)

EN ∩ S	EN ∩ P	EN ∩ P ∩ S	P ∩ S
Penicillium meleagrinum	*Diaporthe kochmanii*	*Nigrospora oryzae*	
Penicillium polonicum	*Diaporthe neosiamensis*	*Nigrospora sphaerica*	
Periconia epilithographicola	*Nigrospora chinensis*	*Bulbopyricularia guangdongensis*	
Phanerochaete chrysosporium	*Phyllosticta capitalensis*		
Sarocladium wurfbainiae	*Pseudopestalotiops is avicenniae*		
Talaromyces dimorphus	*Pyrenochaetopsis endophytica*		
Tetraploa wurfbainiae	*Xylaria* sp.		

Note EN=endophytes, P= associated with lesion, S=saprobes

Table 4.2 List of microfungi associated with overlapping plant tissues of *Wurfbainia villosa* globally

Fruit ∩ Leaf ∩ Stem	**Leaf ∩ Stem**	**Fruit ∩ Root ∩ Stem**	**Fruit ∩ Root ∩ Leaf ∩ Stem**	**Leaf ∩ Root ∩ Stem**	**Root ∩ Stem**	**Leaf ∩ Root**	**Fruit ∩ Leaf**
Colletotrichum fructicola. *Xylaria* sp.	*Pyrenochaetopsis guangdongensis* *Pyrenochaetopsis wurfbainiae*	*Sarocladium wurfbainiae*	*Bulbopyricularia guangdongensis* *Corynespora wurfbainiae* *Musidium wurfbainiae*	*Colletotrichum siamense*	*Acrocalymma* sp. *Phanerochaete chrysosporium* *Tetraploa wurfbainiae*	*Bipolaris wurfbainiae* *Corynespora cassiicola*	*Colletotrichum plurivorum*

CHAPTER 5

TAXONOMY AND PHYLOGENY OF FUNGI FROM *WURFBAINIA VILLOSA* IN CHINA

5.1 Introduction

Fungi are a remarkably diverse group of organisms found in almost every ecological niche, including soil, freshwater, marine, air, plant surfaces, and within living hosts (Wijayawardene et al., 2024). They serve fundamental roles in ecosystems as decomposers, symbionts, and pathogens, influencing nutrient cycling, plant health, and ecosystem stability (Hyde et al., 2019; Chethana et al., 2021; Viret & Gindro, 2024). The ecological versatility of fungi enables them to colonize a vast array of substrates, including economically significant crops and medicinal plants (Hyde et al., 2024). One of the major fungal lineages, Ascomycota, is especially dominant across diverse habitats and is well-known for its morphological complexity and ecological adaptability (Kirk et al., 2008; Lumbsch & Huhndorf, 2010; Hyde et al., 2024; Tian et al., 2024).

Numerous studies have documented the fungal communities associated with various plant hosts (Rashmi et al., 2019; Pem et al., 2024; Hyde et al., 2024; Wijayawardene et al., 2024). However, the microfungi of medicinal plants have received comparatively less attention, despite the increasing interest in these plants due to their pharmaceutical potential and ethnobotanical value (Liao et al., 2024). *Wurfbainia villosa*, a tropical medicinal plant in the Zingiberaceae family, is widely cultivated in southern China and Southeast Asia for its aromatic seeds, which are used in traditional Chinese medicine (Wu & Larsen, 2000; Zhao et al., 2023). As a perennial understory plant, *W. villosa* grows in humid, shaded forest environments that provide ideal microhabitats for a wide variety of fungal taxa. The interactions between fungi and *W. villosa* may range from mutualistic associations such as endophytes and mycorrhizae, to pathogenic relationships that can affect the plant's growth or yield. Despite its ecological and medicinal importance, the fungal diversity associated with *W. villosa* remains poorly understood, with limited studies integrating both morphological and molecular approaches for species identification and

phylogenetic placement. Furthermore, transitions between different fungal lifestyles (e.g., endophytic, pathogenic, or saprobic) are common yet underexplored from this important medicinal plant, raising questions about the ecological flexibility and evolutionary drivers of these associations.

China's subtropical regions, particularly Yunnan and Guangxi provinces, are centers of plant and fungal biodiversity, yet comprehensive surveys of fungi on medicinal plants in these regions are still scarce (Lau & Long, 2021; Phookamsak et al., 2024). To address this knowledge gap, we investigated the taxonomy and phylogeny of fungi associated with *W. villosa* in China, employing both morphological examinations and multigene phylogenetic analyses to accurately characterizing the fungal taxa. In this study, we aimed to: (1) systematically identify and classify fungi associated with *Wurfbainia villosa* from Guangdong and Yunnan provinces using morphological and molecular approaches; (2) investigate their lifestyle adaptations and potential transitions between symbiotic states; and (3) compile a global checklist of fungi associated with *W. villosa* to facilitate future research. By integrating taxonomic, phylogenetic, and ecological perspectives, this work provides a foundation for understanding fungal diversity in this host system while contributing to broader knowledge of plant-fungal interactions in tropical and subtropical ecosystems. The findings will not only contribute to mycological knowledge but also hold significant implications for the further potential discovery of bioactive fungal metabolites. The global checklist will serve as a key reference for researchers studying fungal biodiversity, host specificity, and ecological adaptation in related plant systems.

5.2 Results

Ascomycota Caval.-Sm., Biol. Rev. 73: 247 (1998)

Dothideomycetes P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1045 (2007)

The taxonomic treatments are detailed in Hongsanan et al. (2020a, b) and Pem et al. (2024).

Muyocopronales Mapook, Boonmee & K.D. Hyde, in Mapook, Hyde, Dai, Li, Gareth Jones, Bahkali & Boonmee, Phytotaxa 265(3): 230 (2016)

Notes – Muyocopronales, along with its sole family Muyocopronaceae, was introduced by Mapook et al. (2016). The morphological characteristics followed Mapook et al. (2016).

Muyocopronaceae K.D. Hyde, in Hyde et al., Fungal Diversity 63: 164 (2013)

Notes – Muyocopronaceae was introduced by Luttrell (1951), without a Latin diagnosis, until Hyde et al. (2013) provided a Latin diagnosis and accepted it as a distinct family. Ten genera are accepted in Muyocopronaceae: *Arxiella*, *Leptodiscella*, *Muyocopron*, *Mycoleptodiscus*, *Neocochlearomyces*, *Neomycoleptodiscus*, *Paramycoleptodiscus*, *Pseudopalawania*, *Quadrisporella*, and *Setoapiospora*, with *Muyocopron* as the type genus (Hyde et al. 2024).

Muyocopron Speg., Anal. Soc. cient. argent. 12(3): 113 (1881)

Notes – *Muyocopron* was commonly reported as a saprobic and pathogenic fungus in tropical and temperate regions (Mapook & Hyde, 2023). The asexual morph is characterized by irregular sporodochium-like conidiomata, globose or broadly ellipsoidal to ampulliform conidiogenous cells, and fusiform to fusoid-ellipsoidal conidia, with or without brown appressoria (Hernãndez-Restrepo et al., 2019). Up to now, 83 epithets are listed in the Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we report *M. laterale* as a new host record on *Wurfbainia villosa* and provide the first geographical record of this species in China based on phylogenetic analyses and morphological characteristics.

Muyocopron laterale (Alcorn & B. Sutton) Hern.-Restr., J.D.P. Bezerra & Crous, in Hernández-Restrepo, Persoonia 42: 216 (2019) Figure 5.2

Index Fungorum number: IF828986; Facesoffungi number: FoF 17902

Associated with diseased stems of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Conidiophores, conidiogenous cells, and conidia not observed. *Appressoria* 11–36 × 5–15 μm ($\overline{x}$ = 18.5 × 11 μm, n = 30), gregarious, subglobose, ellipsoidal to pyriform, obovoid to clavate, or irregular, dark brown, straight to uncinate, multi-guttulate, septate, thick-walled.

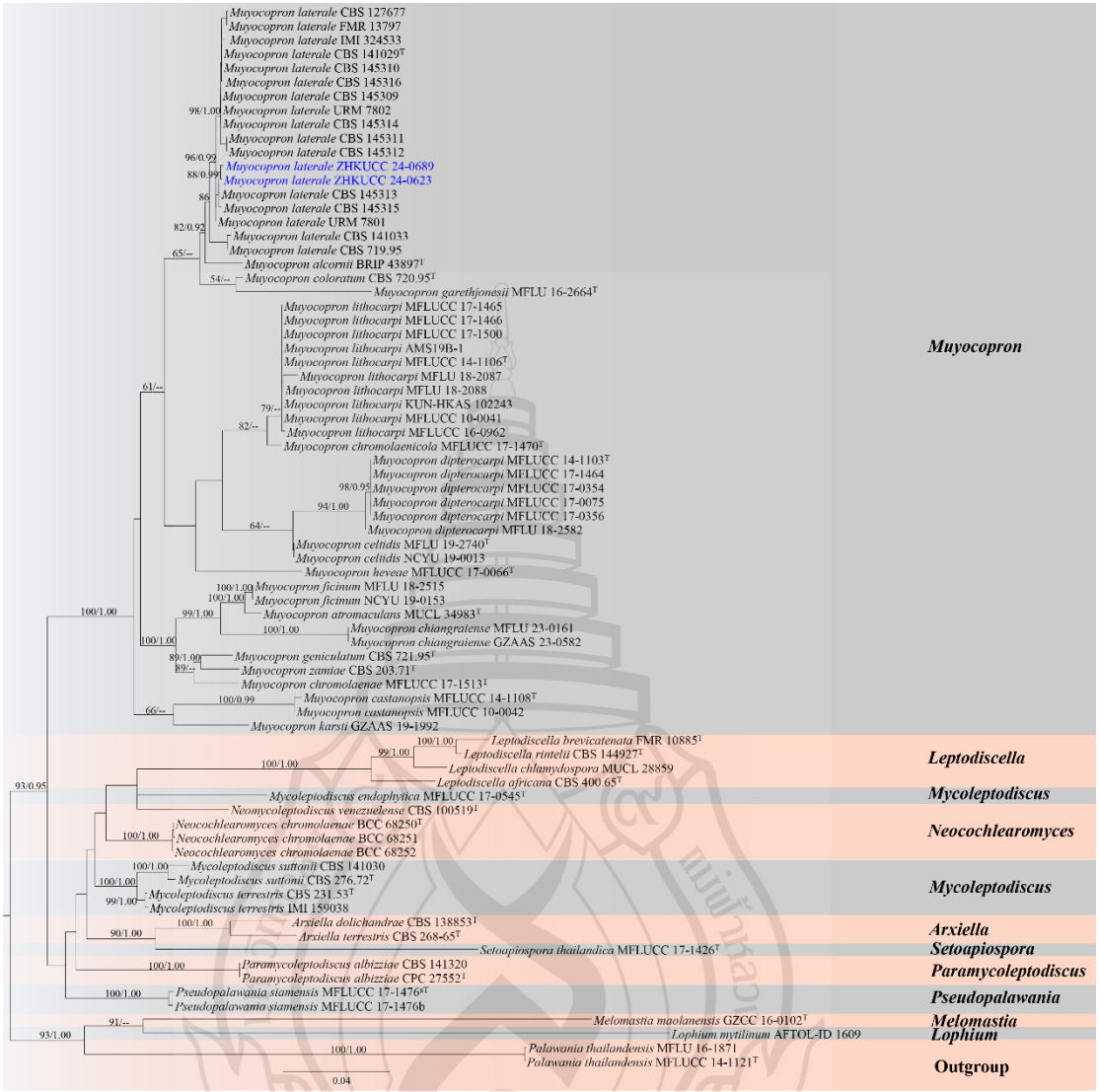
Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 1 month at 28 ± 2°C, medium sparse, flat, gray to dark brown at center and pale brown to cream white at edge from above and reverse, without pigmentation.

Known hosts (based on molecular data) – Aspirate ex joint from *Homo sapiens*, Canis lupus subsp. familiaris, endophyte from *Poincianella pyramidalis*, *Felis catus* (Hernández-Restrepo et al., 2019), freshwater foam (Ramesh & Vijaykumar, 2005), leaves of monocotyledonous plants (*Alloteropsis semialata*, *Chlorophytum capense*, and *Dianella congesta*) (Sutton & Alcorn, 1990; Alcorn, 1994), endophyte from *Banksia verticillata* (Andrioli et al., 2012, as *Muyocopron indicus*) and *Opuntia ficus-indica* (Bezerra et al., 2012), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Australia, Brazil, Canada, India, USA (Hernández-Restrepo et al., 2019), China (this study).

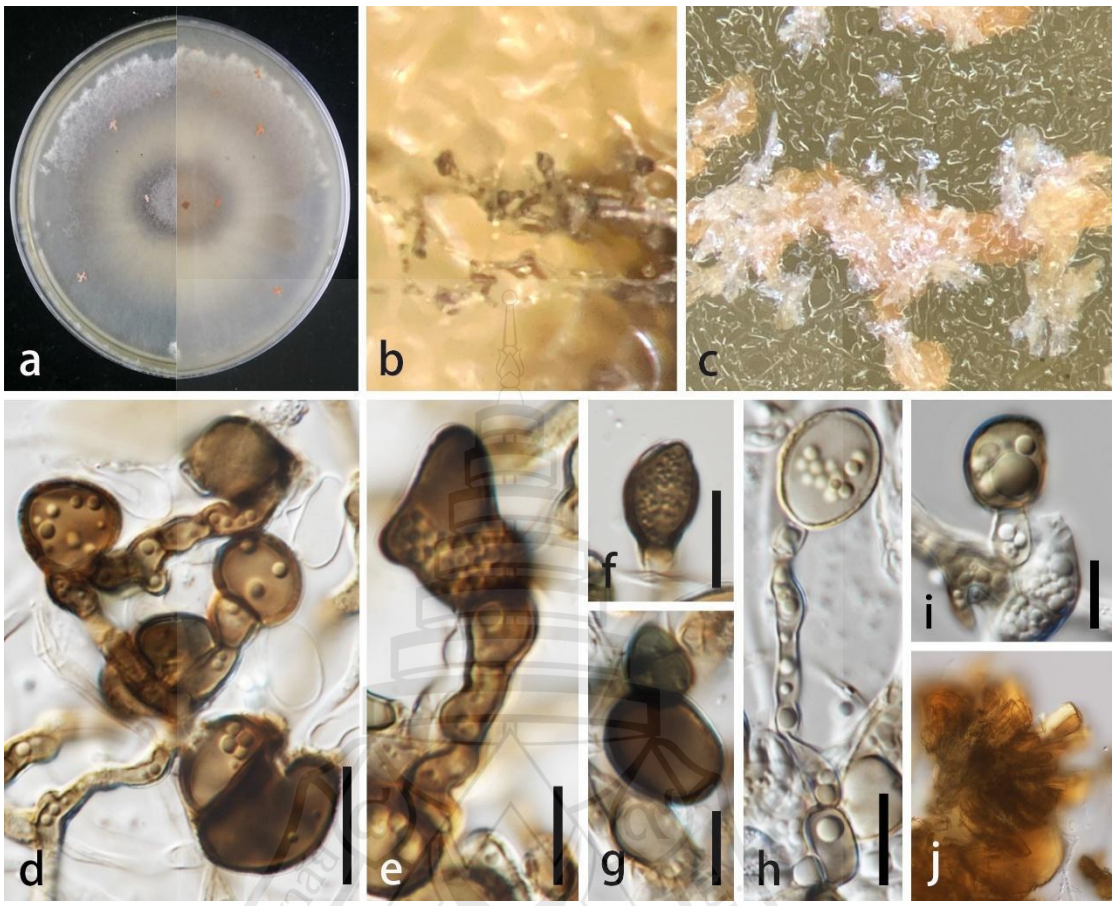
Material examined – China, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), on diseased stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP51A3 (MHZU 24-0370); living culture, ZHKUCC 24-0689; *ibid*., Yangchun City, Heshui Town (22.19027 N, 111.91027 E), on symptomatic stem of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP12B2, living culture, ZHKUCC 24-0623.

Notes – In the phylogenetic analyses, our strains (ZHKUCC 24-0689 and ZHKUCC 24-0623) clustered within the *Muyocopron* clade and clustered separately from *Muyocopron laterale* (CBS 145313 and CBS 145315) with 89 ML/0.99 PP support (Figure 5.1). *Muyocopron laterale* was originally described as *Mycoleptodiscus lateralis* by Alcorn and Sutton (1990) from leaf spots of *Alloteropsis semialata* in Australia. Hernández-Restrepo et al. (2019) transferred most *Mycoleptodiscus* species to *Muyocopron* based on phylogenetic reassessment. Our isolates only produced the appressoria, which showed most similarity to *M. laterale* in having obovoid to clavate, irregular in shape, straight to uncinate, and septate. Hence, we introduce our isolates as a new host and geographical record of *M. laterale*.



Note Tree rooted as *Palawania thailandensis* (MFLU 16-1871, MFLUCC 14-1121). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.1 Maximum likelihood phylogeny based on combined LSU, ITS, SSU, and *tef1-α* sequences data of *Muyocopron*



Note a Culture characteristic on PDA. b Appressoria on aerial mycelia on PDA. c Solid produce by culture. d–i Appressoria. j Photo of solid from culture. Scale bars: d–i = 10 μm.

Figure 5.2 *Muyocopron laterale* (MHZU 24-0370, new host and geographical record)

Pleosporales Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

Notes – Pleosporales, the largest order in Dothideomycetes, comprises a diverse range of fungi with varying ecological roles, including plant pathogens, endophytes, saprobes, and lichenized fungi (Brahmanage et al., 2020). Members of Pleosporales are characterized by bitunicate asci within pseudothecial ascomata (Zhang et al., 2012). The order includes 94 families, such as Pleosporaceae, Didymellaceae, Leptosphaeriaceae, and Massarinaceae, among others (Wijayawardene et al., 2022).

Acrocalymmaceae Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

Notes – Acrocalymmaceae was proposed only a single genus of *Acrocalymma*, which was typified by *A. medicaginis*. Species of Acrocalymmaceae have been recorded in various habitats, from tropical to temperate regions, and are typically associated with wood, plant stems, and leaves. Calabon et al. (2023) and Manawasinghe et al. (2025) provided the phylogenetic analyses of *Acrocalymma* based on combined ITS, LSU, and SSU sequences.

Acrocalymma Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

Notes – *Acrocalymma* was introduced by Alcorn and Irwin (1987), with *A. medicaginis* designated as the type species. *Acrocalymma* species are found in various habitats, with many species occurring as saprobes associated with decaying plant material, including fallen leaves, stems, and wood (Liu & Zeng, 2022). The sexual morph of *Acrocalymma* species typically produces bitunicate asci that distinctive ascospores discharge (Liu & Zeng, 2022). The asexual morph is characterized by cylindrical, hyaline conidia, with a helmet-shaped mucilaginous appendages at each end (Jayasiri et al., 2019). Currently, 19 species are listed in Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we introduce two novel species in *Acrocalymma, A. guangdongensis* and *A. wurfbainiae*, and another *Acrocalymma* sp. with only chlamydospores, which has the potential to be a new species, based on the phylogenetic analyses and morphological characteristics.

Acrocalymma guangdongensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.4

Index Fungorum number: IF904007; Facesoffungi number: FoF 17903

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China, where the holotype was collected

Holotype – MHZU 24-0210

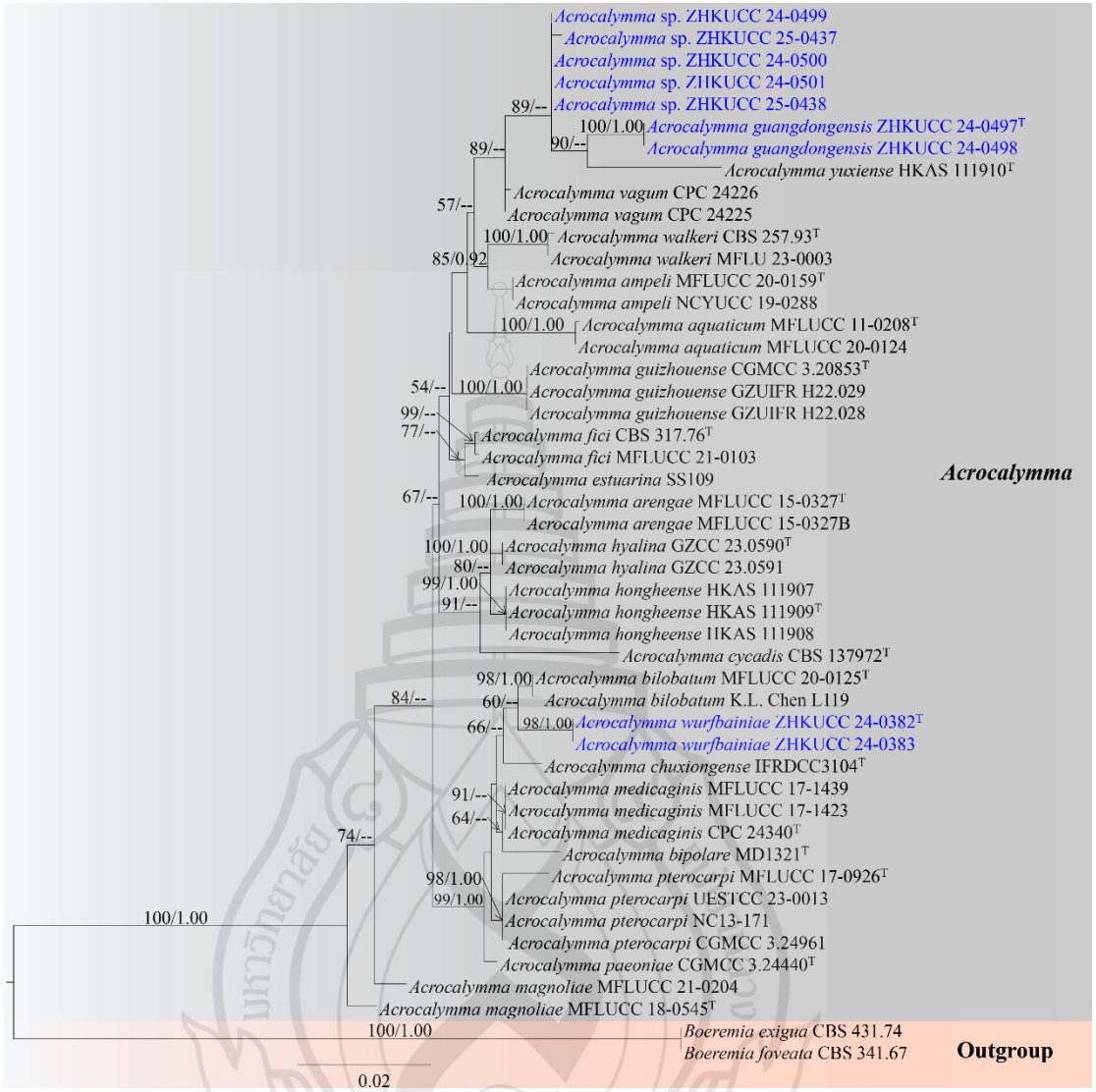
Endophytic in the asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 1 month, *Conidiomata* 161–343 × 138–294 μm ($\overline{x}$ = 229 × 202 μm, n = 20), pycnidial, solitary to gregarious, unilocular to bilocular, coriaceous, immersed to erumpent, globose to subglobose, brown to black. *Peridium* 5–18 μm wide ($\overline{x}$ = 9.5 μm, n = 20), composed of 5–8 layers, thick-walled, hyaline inner cells and thin-walled, brown outer cells of *textura angularis*.

Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 9–25 × 3–7 μm ($\overline{x}$ = 16.5 × 5 μm, n = 30), phialidic, cylindrical, subglobose, cone-shaped, hyaline, smooth-walled. *Conidia* 13–19 × 4–5.5 μm ($\overline{x}$ = 16 × 4.5 μm, n = 30), ovoid to fusiform, hyaline, 1–3-septate, straight to slightly curved, with obtusely rounded or truncate apices and base, truncate at base, bearing a flaring mucoid appendage at both ends, smooth-walled.

Culture characteristics – Colonies on PDA reaching 7.0–7.5 cm diameter in 1 month at 28 ± 2°C, moderately sparse, flat at the center, sparse and raised at the edge, undulate, pale brown from above, pale brown to cream-white from reverse, without pigmentation.

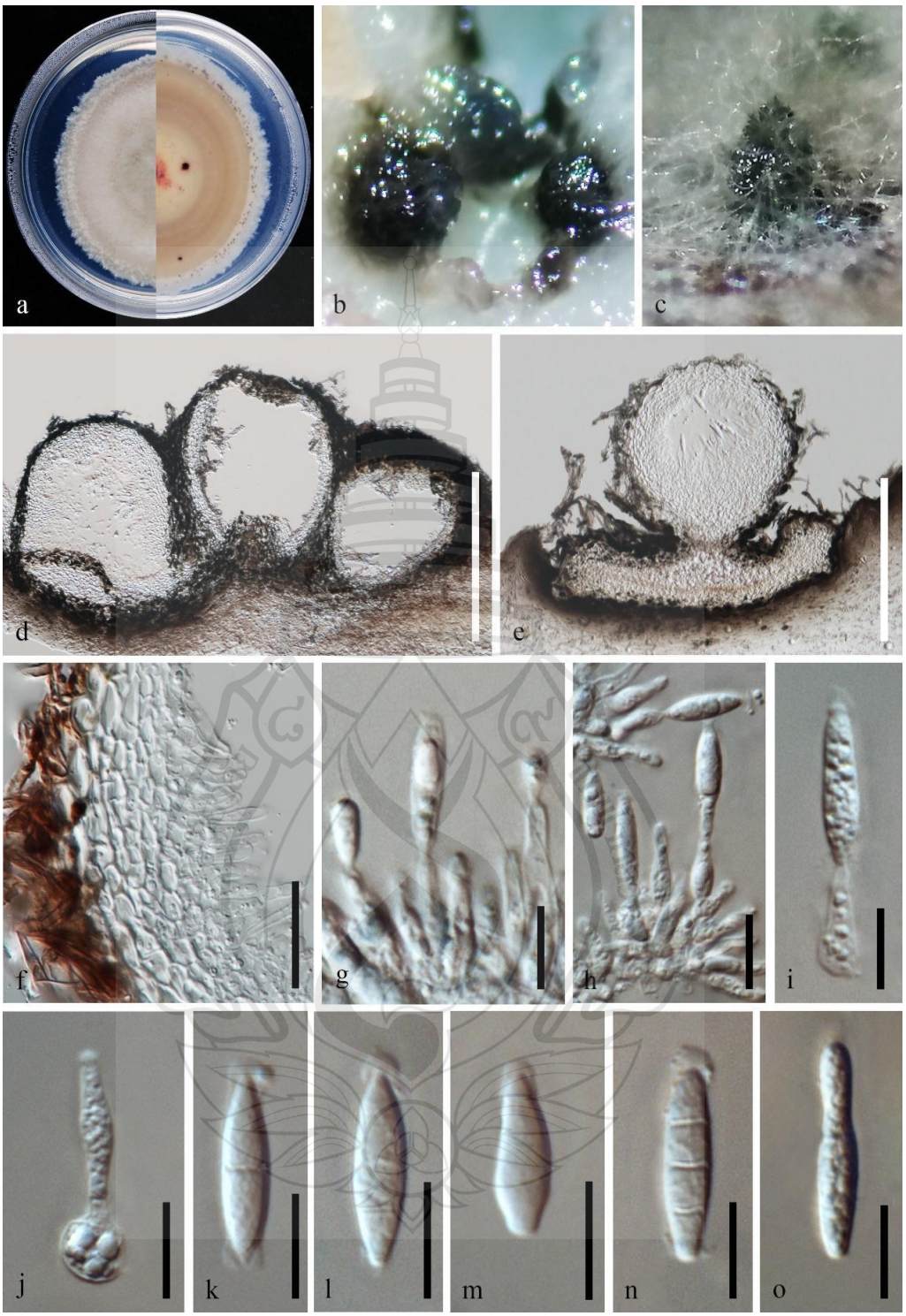
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR03C-3 (MHZU 24-0210, holotype); ex-type culture, ZHKUCC 24-0497, *ibid*., living culture ZHKUCC 24-0498.

Notes – Multi-gene phylogenetic analysis indicated that *Acrocalymma guangdongensis* was clustered sister to *A. yuxiense* with (Figure 5.3). *Acrocalymma guangdongensis* was similar to *A. fici* and *A. yuxiense* in having semi-erumpent to erumpent, globose, dark brown conidiomata, hyaline, smooth conidiogenous cells and conidia (Trakunyingcharoen et al., 2014; Mortimer et al., 2021). However, *A. guangdongensis* has larger conidiomata than *A. fici* (161–343 × 138–294 μm vs. up to 200 μm diam). Additionally, the conidiogenous cells of *A. guangdongensis* are larger (9–25 × 3–7 μm vs. 5–12 × 3–5 μm), with cylindrical, phialidic, subglobose, cone-shaped, while those of *A. fici* are ampulliform to doliiform. Furthermore, the conidia of *A. guangdongensis* are ovoid, fusiform, 1–3-septate, contrasting with the cylindrical and medianly 1-septate conidia of *A. fici*. *Acrocalymma guangdongensis* can be distinguished from *A. yuxiense* by its larger conidiomata (161–343 × 138–294 μm vs. 130–170 × 220–260 μm) and larger asci (9–25 × 3–7 μm vs. 4–8 × 2.5–4.5 μm). Moreover, the conidiomata of *A. guangdongensis* are unilocular to bilocular and lacking an ostiole, but *A. yuxiense* are unilocular with a central ostiole. The conidiogenous cells of *A. guangdongensis* are cylindrical, phialidic, subglobose, and cone-shaped, without guttules, while *A. yuxiense* are cylindrical to subcylindrical, percurrently proliferating 1–2 times at the apex, multi-gutttulate. We introduce *A. guangdongensis* as a novel species.



Note Tree rooted as *Boeremia exigua* (CBS 431.74, CBS 341.67). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.3 Maximum likelihood phylogeny based on combined ITS, LSU, and SSU sequences data of *Acrocalymma*



Note *Acrocalymma guangdongensis* (MHZU 24-0210, holotype). a Culture characteristic on PDA for one month. b, c Appearance of conidiomata on PDA after 1 month. d, e Section through conidiomata. f Peridium. g–j Conidiogenous cells with conidia. k–o Conidia. Scale bars: d, e = 200 μm, f = 20 μm, g–o = 10 μm.

Figure 5.4 *Acrocalymma guangdongensis* (MHZU 24-0210, holotype)

***Acrocalymma* sp.** C.F. Liao, Doilom & K.D. Hyde Figure 5.5

Index Fungorum number: IF904008; Facesoffungi number: FoF 17904

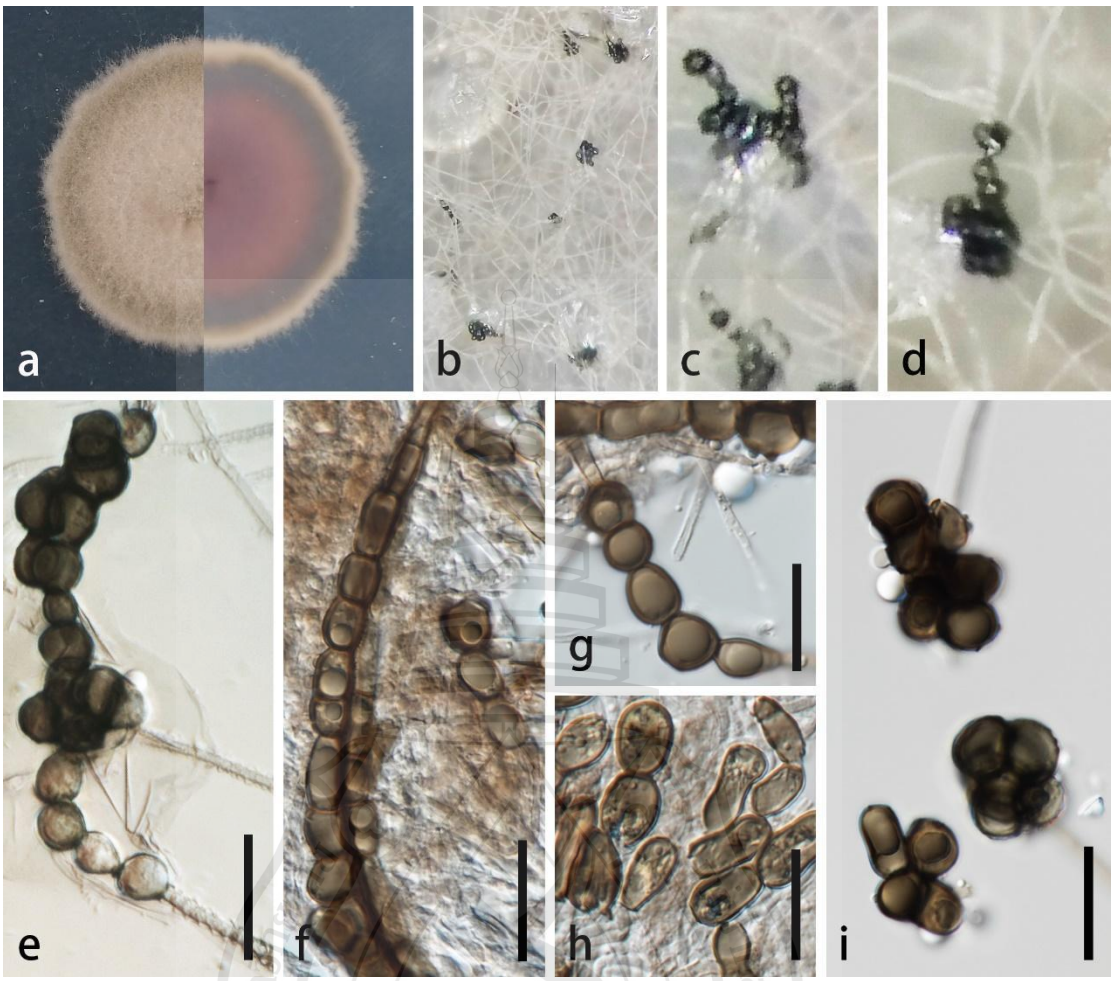
Holotype – MHZU 24-0212

Endophytic associated with roots and stems of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Chlamydospores* 7–15 × 5–10 μm ($\overline{x}$ = 11 × 7 μm, n = 30), catenate, variable in shape, subglobose to globose, ellipsoidal to oblong, cuboid to doliiform, or cruciform, sometimes with two chains of chlamydospores are fused into form a single, broader chain, guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 2.0–5.5 cm diameter in 10 days at 28 ± 2°C, moderately medium dense, flat, with an entire edge, pale brown from above, pale brown to black-brown from reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR03B-6 (MHZU 24-0212); living culture, ZHKUCC 24-0501; *ibid*., living culture, AMR18A-1, AMR18A-2, AMR20C-2, ZHKUCC 24-0499, ZHKUCC 24-0500, ZHKUCC 25-0437; *ibid*., from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS11A-2, ZHKUCC 25-0438.

Notes – *Acrocalymma* sp. produced only chlamydospores on PDA after 2 months, which are subglobose to globose, ellipsoidal to oblong, cuboid to doliiform, or cruciform. Chlamydospores in *Acrocalymma* have also been observed in *A. vagum*, and they are black, irregular, and often concatenated into chains (Jin et al., 2018). In the phylogenetic analyses, *A. neovagum* strains ZHKUCC 24-0499, ZHKUCC 24-0500, and ZHKUCC 24-0501 formed a distinct branch separate from *A. vagum* and grouped as a sister branch to *A. guangdongensis* and *A. yuxiense* (Figure 5.3), supporting *A. neovagum* as a distinct species within *Acrocalymma*. Morphologically, our isolates produced only chlamydospores of various shapes (subglobose to globose, ellipsoidal to oblong, cuboid to doliiform, or cruciform). However, chlamydospores in *Acrocalymma* have only been observed in *A. vagum*, and they are structurally black, irregular, and plurality of chlamydospores concatenated into a chain. Although this taxon may represent a new species, the absence of additional diagnostic characters beyond chlamydospores and insufficient supporting evidence led us to provisionally identify it as *Acrocalymma* sp.



Note a Culture characteristic on PDA for 10 days. b–d Chlamydospores on aerial mycelia on PDA after 2 months. e–i Chlamydospores. Scale bars: e–i = 20 μm.

Figure 5.5 *Acrocalymma* sp. (MHZU 24-0212)

Acrocalymma wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.6

Index Fungorum number: IF904009; Facesoffungi number: FoF 17905

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0135

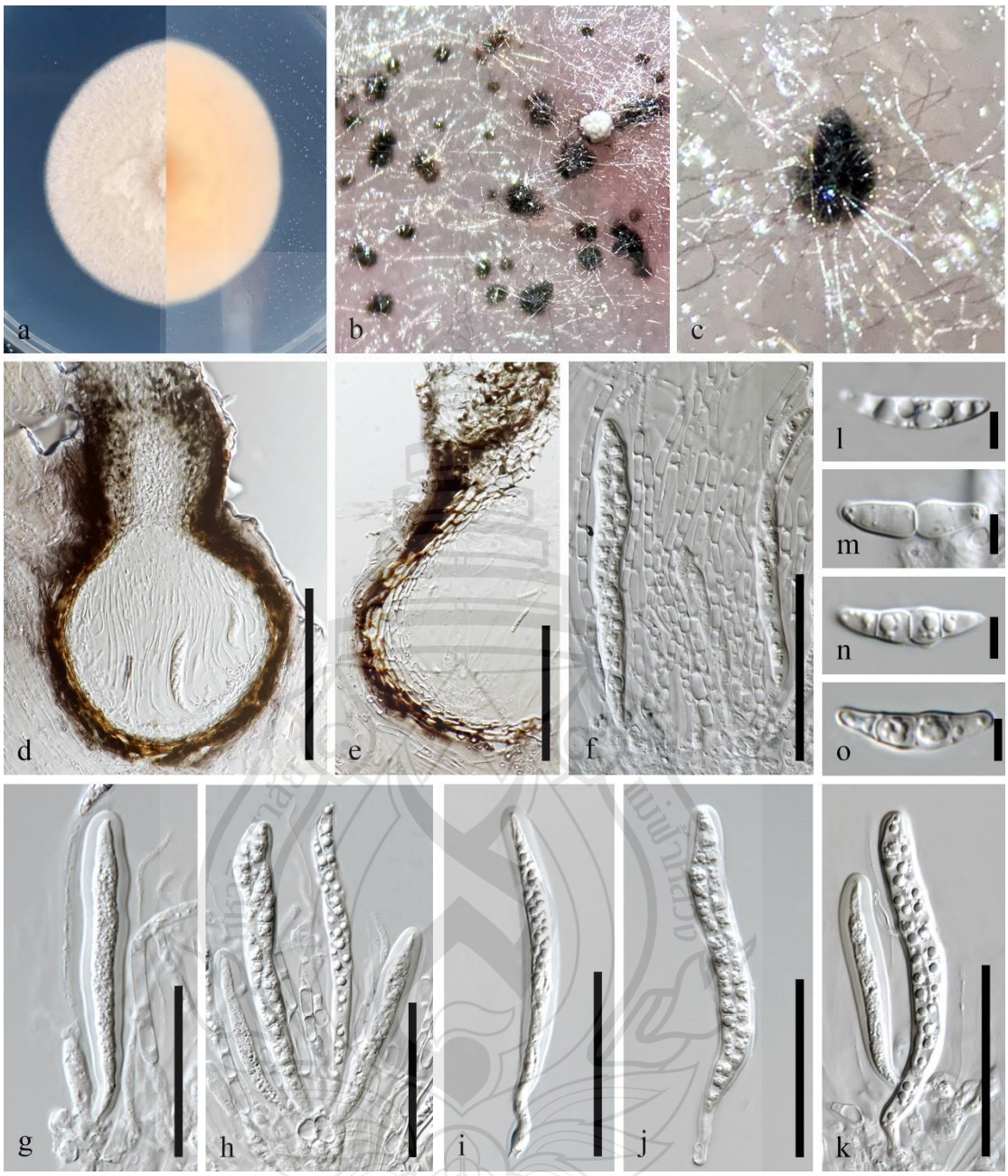
Endophytic associated with fruits of *Wurfbainia villosa*. Sexual morph: On PDA after 2 months, *Ascomata* 463–762 × 331–545 μm ($\bar{x}$ = 601 × 439 μm, n = 20), solitary to gregarious, unilocular, coriaceous, immersed to erumpent, globose to subglobose, brown to black, ostiolate. *Peridium* 51–127 μm wide ($\bar{x}$ = 85 μm, n = 20), composed of 3–6 layers of hyaline to dark brown, thin-walled cells of *textura angularis*.

Hamathecium 2.5–4.5 μm wide ($\overline{x}$ = 3.5 μm, n = 30), comprising numerous, hyaline, unbranched or branched, septate, smooth-walled paraphyses. *Asci* 70–93 × 8–11 μm ($\overline{x}$ = 82.5 × 9.5 μm, n = 30), 8-spored, bitunicate, cylindrical, slightly curved, apically rounded, short pedicellate, with an ocular chamber. *Ascospores* 18–23 × 5–6 μm ($\overline{x}$ = 20 × 5.5 μm, n = 30), biseriate, fusiform to broadly fusiform, mostly widest at the center, tapering towards at both ends, curved, (1–)3-septate, constricted at the septum, hyaline, guttulate, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 4.0–4.5 cm diameter in 3 weeks at 28 ± 2°C, moderately dense, flat, with an entire edge, cream-white from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), asymptomatic fruit of *Wurfbainia villosa*, 29 October 2023, C.F. Liao, AMF31B (MHZU 24-0135, holotype); ex-type culture, ZHKUCC 24-0382; *ibid*., living culture, ZHKUCC 24-0383.

Notes – Multi-gene phylogenetic analyses indicated that *Acrocalymma wurfbainiae* formed a sister branch with *A. bilobatum* (Figure 5.3). However, morphological comparison with *A. bilobatum* was not possible as only its asexual morph has been described (Calabon et al., 2023). *Acrocalymma wurfbainiae* also formed a sister branch with *A. chuxiongense* in the phylogenetic analyses. Morphologically, it differs from *A. chuxiongense* by its fusiform to broadly fusiform, curved, (1–)3-septate, larger ascomata (463–762 × 331–545 μm vs. 50–80 × 270–320 μm), while *A. chuxiongense* produced obovoid to ellipsoidal, 1-septate ascospores. *Acrocalymma wurfbainiae* is similar to *A. pterocarpi* by its immersed to erumpent, globose or subglobose ascomata, *textura angularis* peridium, 8-spored, bitunicate, cylindrical asci, and hyaline, fusiform ascospores (Jayasiri et al. 2019). However, it can be distinguished from *A. pterocarpi* by having larger ascomata (463–762 × 331–545 μm vs. 140–150 × 130–145 μm) with ostioles (vs. non-ostiiolate), thicker peridium (51–127 μm vs. 15–25 μm), longer asci (70–93 × 8–11 μm vs. 65–75 × 7–12 μm). Although different substrates may contribute to variations in morphological characteristics, phylogenetic analyses distinguish *A. wurfbainiae* from other described *Acrocalymma* species, and we therefore propose it as a novel species. However, as the molecular support is insufficient, further collections are needed to confirm its status.



Note a Culture characteristic on PDA for 1 month. b, c Appearance of ascomata on PDA after 2 months. d Section through ascoma. e Peridium. f Paraphyses and asci. g–k Asci. l–o Ascospores. Scale bars: d = 300 µm, e = 200 µm, f–k = 50 µm, l–o = 10 µm.

Figure 5.6 *Acrocalymma wurfbainiae* (MHZU 24-0135, holotype)

Corynesporascaceae Sivan., Mycol. Res. 100(7): 786 (1996)

Notes – Corynesporascaceae was introduced by Sivanesan (1996) and currently comprises two genera *Corynespora* (as the type genus) and *Corynesporasca* (Liu et al., 2023). This family included both the sexual (*Corynesporasca caryotae*) and asexual (*Corynespora*) morphs. The members of Corynesporascaceae are commonly found as pathogenic and saprobic fungi on leaves and wood litter in tropical and subtropical regions (Zou et al., 2022). Morphological characteristics followed Sivanesan (1996), Hyde et al. (2013), and Faces of Fungi (https://www.facesoffungi.org/corynesporascaceae/).

Corynespora Güssow, J. Royal Agric. Soc. England 65: 272 (1905) [1904]

Notes – Güssow (1905) established *Corynespora* and designated *C. mazei* as the type species. *Corynespora* species are mainly reported as pathogens, with *C. cassiicola* being one of the most common pathogenic species. *Corynespora cassiicola* causes target spot on a wide range of hosts, including over 690 plant species across 53 families, such as cowpea, cucumber, papaya, rubber, soybean, and tomato (Dixon et al., 2009; Sierra-Orozco et al., 2023; USDA 2025). To date, 214 epithets have been listed in Species Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we report the occurrence of *C. cassiicola* on *Wurfbainia villosa* as a new host record and introduce a novel species, *Corynespora wurfbainiae*, based on the phylogenetic analyses and morphological characteristics.

Corynespora cassiicola (Berk. & M.A. Curtis) C.T. Wei, Mycol. Pap. 34: 5 (1950) Figure 5.8

Index Fungorum number: IF296024; Facesoffungi number: FoF 06663

Endophytic in asymptomatic leaves, roots and stems of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on SNA after 1 month of incubation at 28 ± 2°C. *Mycelium* 2–7 µm wide ($\bar{x}$ = 4 µm, n = 30), superficial, composed of hyaline to pale brown, septate, branched, with smooth-walled hyphae. *Conidiophores* 34–695 × 6–15 µm ($\bar{x}$ = 258 × 9 µm, n = 30), macronematous, mononematous, solitary or gregarious, cylindrical, straight to flexuous, unbranched, brown, up to 18- distoseptate, verruculose. *Conidiogenous cells* monotretic, integrated, lateral, cylindrical, tapering towards the apex, with a rounded apex, straight or slightly flexuous, unbranched, pale brown, septate, smooth-walled. *Conidia* 46–283 × 8–13 µm ($\bar{x}$ = 155 × 10 µm, n = 30), acrogenous, solitary or in short chains developing through

a wide apical pore on conidiophores and proliferate through the pore, forming new conidia at the tip, with darker pore, filiform, obclavate to cylindrical, straight to slightly flexuous, up to 13-distoseptate, mostly 3–8-distoseptate, hyaline to pale brown, thick-walled, smooth-walled, with truncate base and rounded apex.

Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 1 month at 28 ± 2°C, medium dense, flat, circular, filiform, pale brown to brown from above, pale brown with a black central region reverse, without pigmentation.

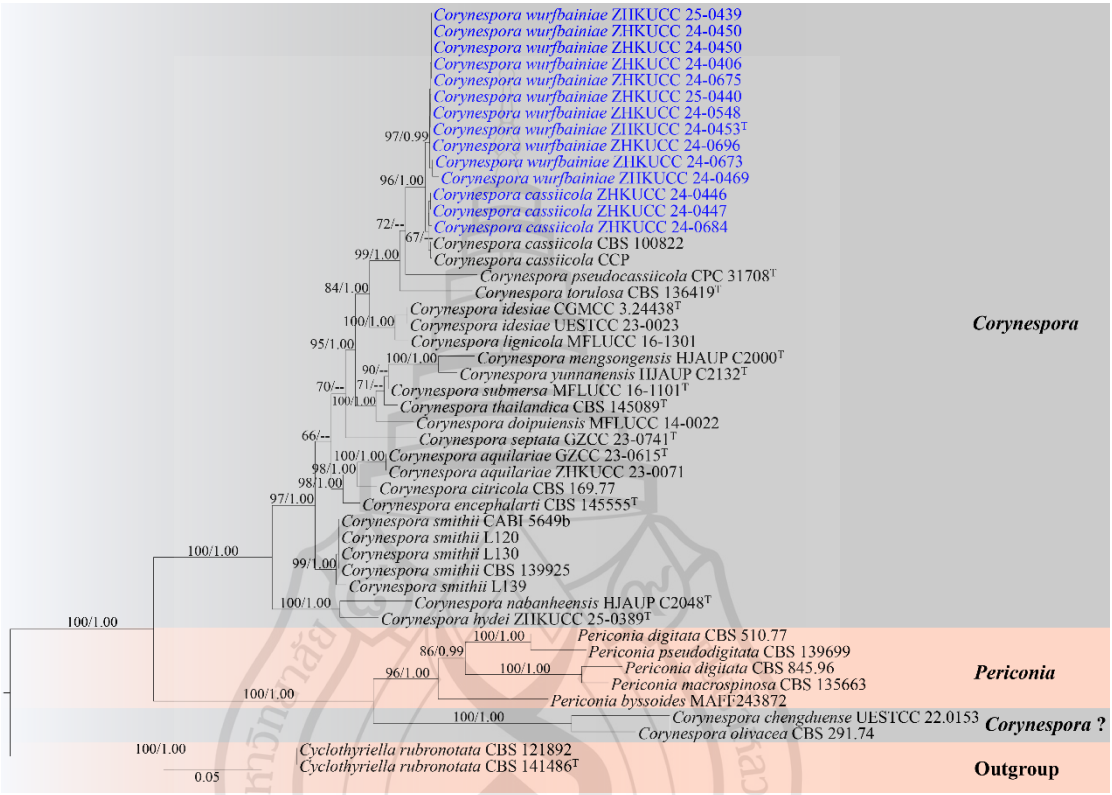
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic leaf and root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML11A-1, AMR23C-4 (MHZU 24-0177; living culture, ZHKUCC 24-0446, ZHKUCC 24-0447; *ibid*., Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from asymptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP48B2, living culture, ZHKUCC 24-0684.

Known hosts (based on molecular data) – *Bidens alba*, *Carica papaya*, *Catharanthus roseus*, *Chromolaena odorata*, *Cucumis sativus*, *Cucurbita pepo*, *Hevea brasiliensis*, *Hibiscus rosa-sinensis*, *Ipomoea batatas*, *Ipomoea cairica*, *Lagerstroemia* spp., *Lantana camara*, *Manihot esculenta*, *Mikania micrantha*, *Momordica charantia*, *Ocimum basilicum*, *Phaseolus vulgaris*, *Plumeria* spp., *Saintpaulia ionantha*, *Solanum lycopersicum*, *Solanum melongena*, *Tabebuia pallida*, *Vigna unguiculata* (Dixon et al., 2009), cotton (Sain et al., 2024), *Nanhaia speciosa* (Pan et al. 2024), *Pogostemon cablin* (Liao et al., 2025c), *Senna obtusifolia* (Patel et al., 2025), soybean (Edwards Molina et al., 2022), tobacco (Feng et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Americas (Edwards Molina et al., 2022), Brazil, Florida, Guam, Hawaii, Italy, Japan, Malaysia, Mississippi, Netherlands, New Zealand, Palau, Pohnpei, Saipan, Tennessee, Yap (Dixon et al., 2009), India (Sain et al., 2024), China (Feng et al., 2024; Pan et al., 2024; Liao et al., 2025; this study), USA (Patel et al., 2025).

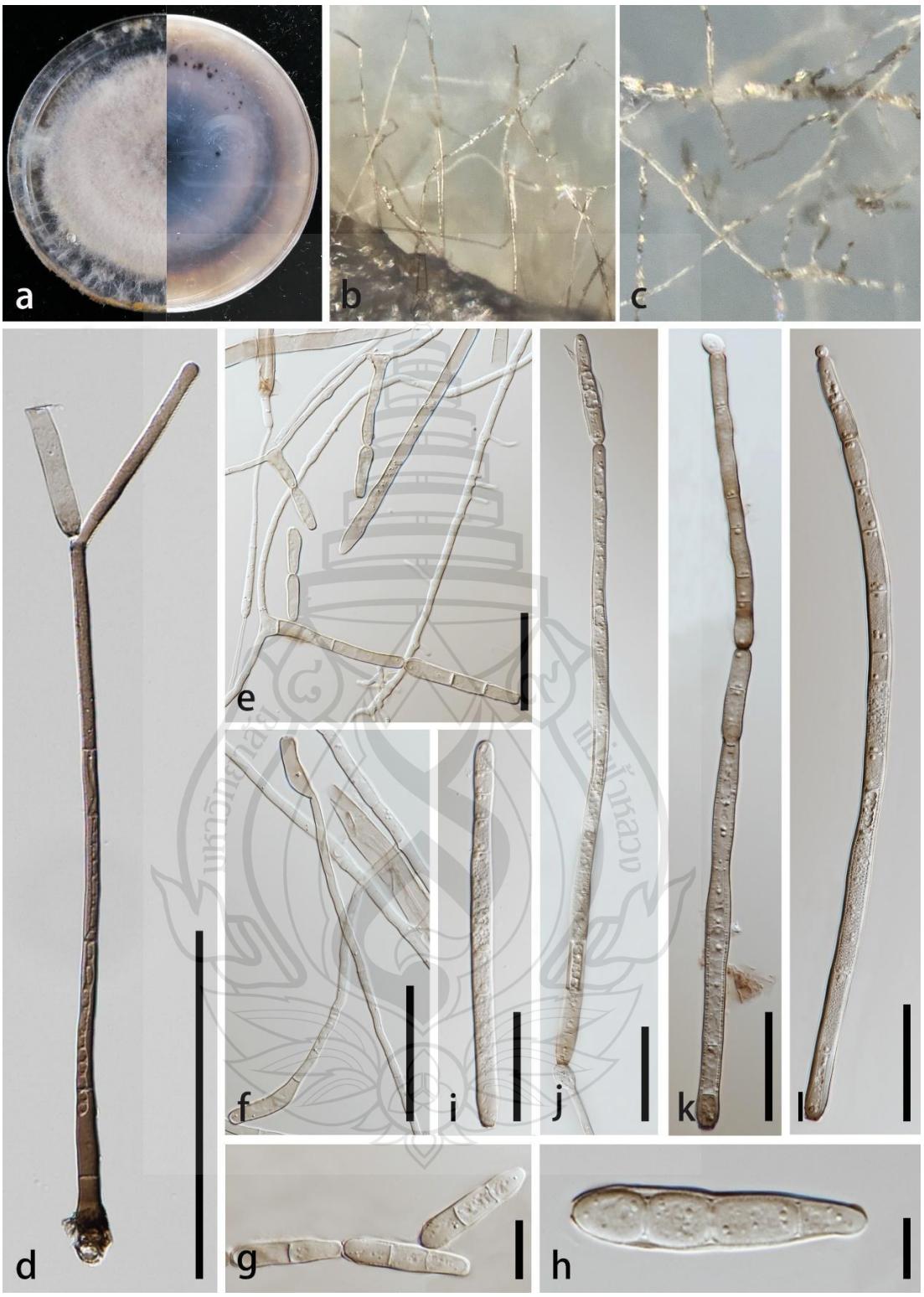
Notes – Phylogenetically, ZHKUCC 24-0446, ZHKUCC 24-0447, and ZHKUCC 24-0684 showed affinity with *Corynespora cassiicola* CBS 100822 and CCP (Figure 5.7). Morphologically, MHZU 24-0177 resemble *C. cassiicola* in having simple, straight, septate, thick-walled conidiophores, and obclavate to cylindrical, multi-septate, straight or slightly flexuous conidia (Wen, 1950). Additionally, it has

overlapping sizes of conidiophores (34–695 × 6–15 µm vs. up to 600 × 3.8–11.3 µm) and conidia (46–283 × 8–13 µm vs. 32–220 × 8.4–22.4). The concordance between molecular phylogenetic position and morphological characteristics confirms our isolates as *C. cassiicola*, representing a new host record for *Wurfbainia villosa*.



Note Tree rooted as *Cyclothyriella rubronotata* (CBS 121892, CBS 141486). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.7 Maximum likelihood phylogeny based on combined LSU, ITS, SSU, *rpb2*, and *tef1-α* sequences data of *Corynespora*



Note a Culture characteristic on PDA for 4 weeks. b, c Conidia on aerial mycelia on SNA after 1 month. d Conidiophores with conidiogenous cells. e, f Conidiogenous cells with conidia. g–l Conidia. Scale bars: d = 200 µm, e, f = 20 µm, i–l = 50 µm, g, h = 10 µm.

Figure 5.8 *Corynespora cassiicola* (MHZU 24-0177, new host record)

Corynespora wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.9, 5.10

Index Fungorum number: IF904010; Facesoffungi number: FoF 17906

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0180

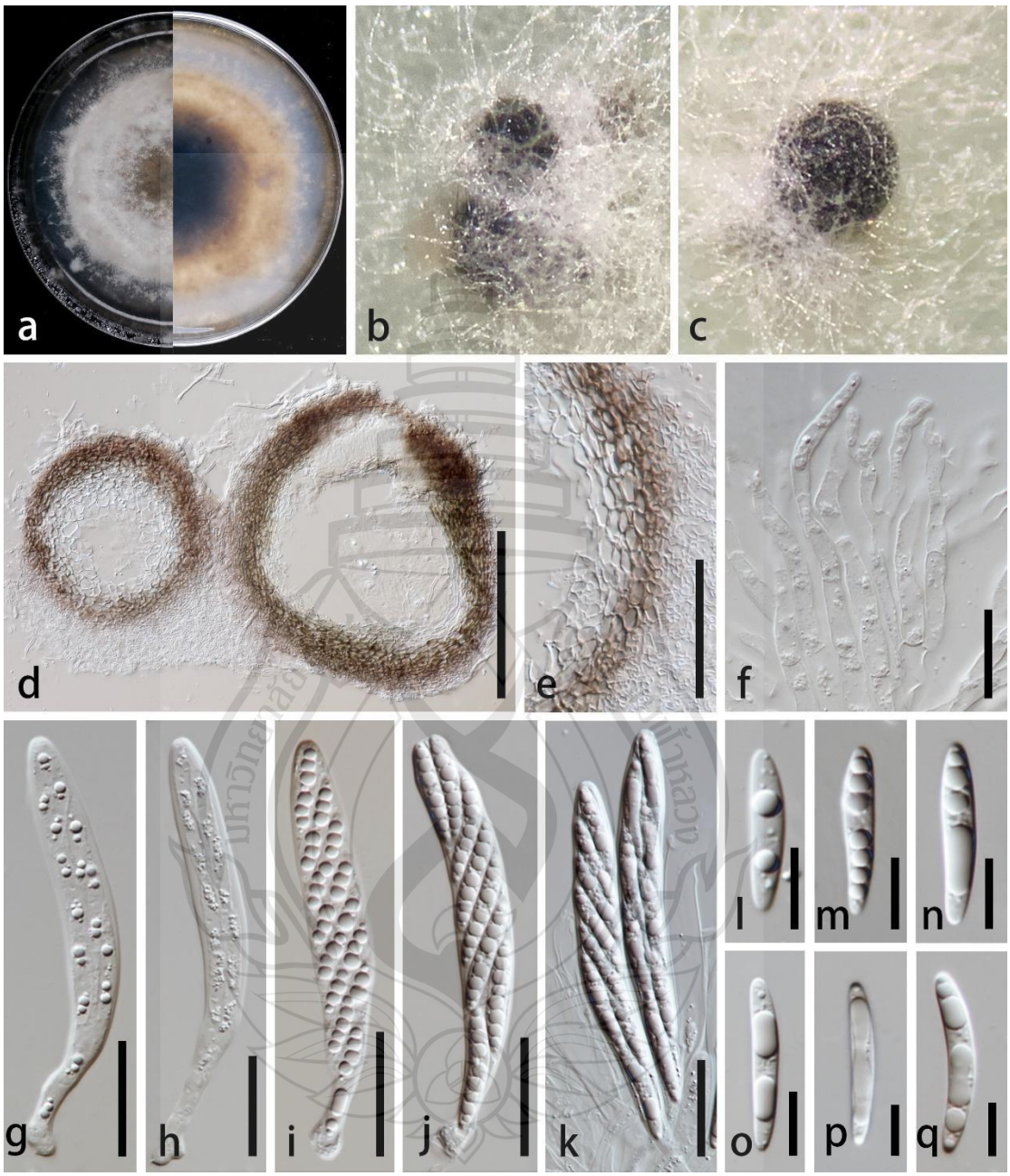
Endophytic in stem, leaf, root, and fruit, and associated with the symptomatic stem of *Wurfbainia villosa*. Sexual morph: On SNA after 3 weeks: *Ascomata* 148–226 × 134–206 μm ($\bar{x}$ = 199 × 182 μm, n = 10), solitary to gregarious, unilocular, coriaceous, superficial, globose to subglobose, brown to black. *Peridium* 30–70 μm wide ($\bar{x}$ = 42.5 μm, n = 20), composed of 4–11 layers of hyaline to brown, thick-walled cells of *textura angularis*. *Hamathecium* 3.5–7 μm wide ($\bar{x}$ = 5.5 μm, n = 30), comprising numerous, hyaline, branched, septate, smooth-walled paraphyses, with lengths similar to asci. *Asci* 68–105 × 8.5–11 μm ($\bar{x}$ = 90 × 9.5 μm, n = 30), 8-spored, unitunicate, cylindrical, slightly curved, apically rounded, with a short, furcate pedicel. *Ascospores* 18–25 × 3–5 μm ($\bar{x}$ = 22 × 4.5 μm, n = 30), biseriate or overlapping uniseriate, allantoid, cylindrical to fusiform, straight or slightly curved, hyaline, aseptate, multi-guttulate, smooth-walled. Asexual morph: sporulating on SNA after three weeks of incubation (28 ± 2°C). *Mycelium* 2–5.5 μm wide ($\bar{x}$ = 3 μm, n = 30), superficial, composed of hyaline to pale brown, septate, branched, with smooth-walled hyphae. *Conidiophores* 15–298 × 5–10 μm ($\bar{x}$ = 98 × 7 μm, n = 30), micronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, unbranched, pale brown, septate, smooth-walled. *Conidiogenous cells* monotretic, integrated, terminal or lateral, cylindrical, with a rounded apex, straight or slightly flexuous, unbranched, pale brown, 1–5-septate, smooth-walled. *Conidia* 65–210 × 8–19 μm ($\bar{x}$ = 121 × 12.5 μm, n = 30) acrogenous, solitary or in short chains, developing through a wide pore at the conidiophore tip and proliferating sympodially to form new conidia, obclavate to cylindrical, straight or curved, up to 10-distoseptate, mostly 4–8-distoseptate, the conidia inside forming a single square, cuneiform, or cuboid structure connect together in a chain, hyaline to pale brown, truncate at base, with rounded or obtuse at tip, mostly tapering towards the apex, thick- and smooth-walled.

Culture characteristics – Colonies on PDA reaching 6.0–6.5 cm diameter in two weeks at 28 ± 2°C, moderately dense, raised, circular, filiform, wooly, pale brown from above, black at the center, brown to pale brown at the edge from reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML19C-3, (MHZU 24-0180, holotype); ex-type living culture, ZHKUCC 24-0453; *ibid*., AML04B-1, living culture, ZHKUCC 24-0450; *ibid*., AML10A-6, living culture, ZHKUCC 25-0440; *ibid*., AML15B-4, living culture, ZHKUCC 25-0439; *ibid*., AML12A-2, living culture, ZHKUCC 24-0548; *ibid*., from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR02B-1, living culture, ZHKUCC 24-0469; *ibid*., from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, ZHKUCC 24-0448; *ibid*., Chunwan Town (22.436461 N, 111.938281 E), from asymptomatic fruit of *Wurfbainia villosa*, 29 October 2023, C.F. Liao AMF70B, living culture, ZHKUCC 24-0406; *ibid*., Xinyi City, Qianpai Town, (22.41410 N, 111.27459 E), from symptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP60A1, living culture, ZHKUCC 24-0696; China, Yunnan Province, Jinghong City, Manmo Xinzhai, (21.91825 N, 101.14701 E), from symptomatic stem of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YP40B1, YP44A1, living culture, ZHKUCC 24-0673, ZHKUCC 24-0675.

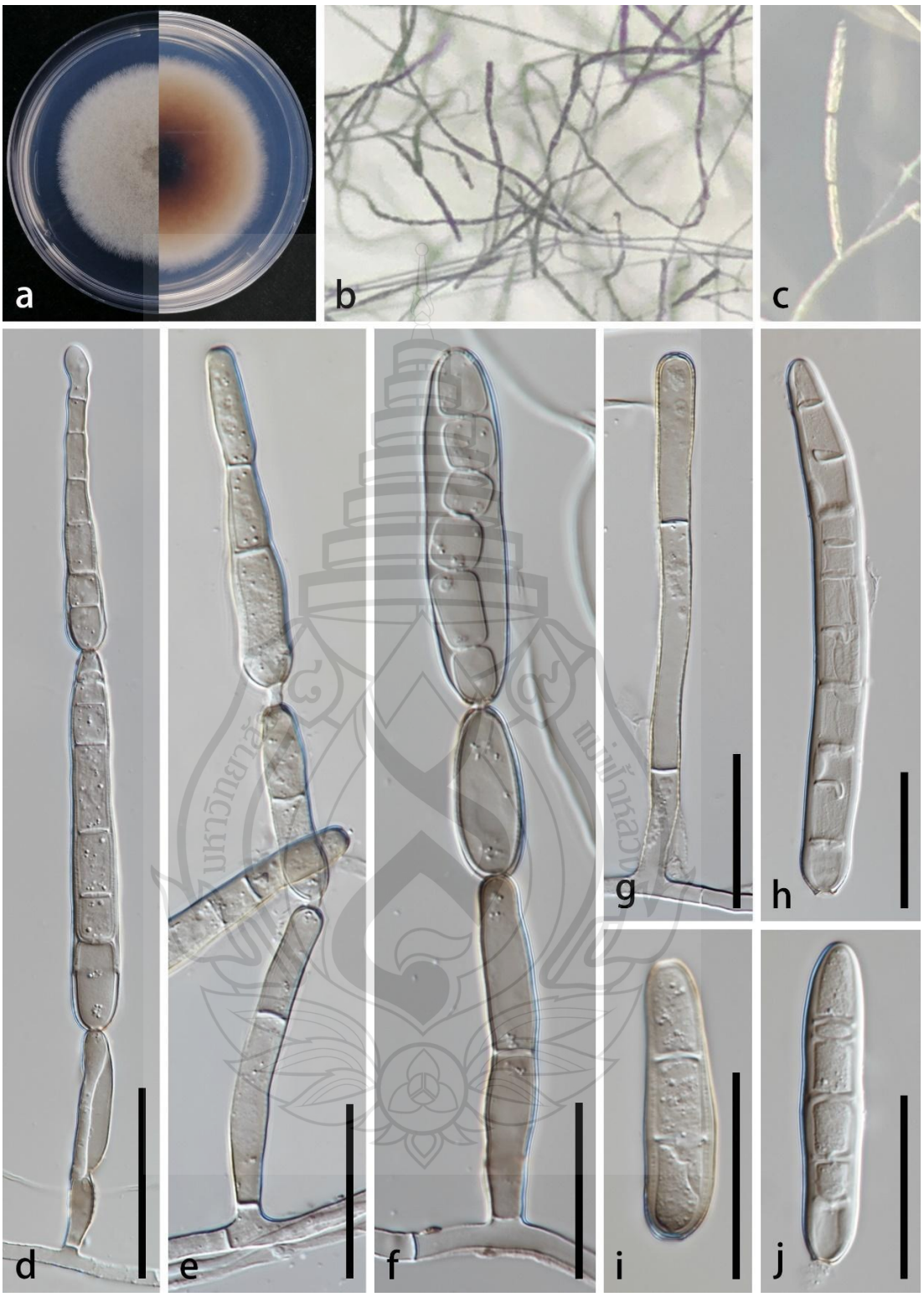
Notes – In the phylogenetic analysis, our strains (ZHKUCC 24-0406, ZHKUCC 24-0448, ZHKUCC 24-0450, ZHKUCC 24-0453, ZHKUCC 24-0469, ZHKUCC 24-0673, ZHKUCC 24-0675, and ZHKUCC 24-0696) formed a sister branch with *Corynespora cassiicola* (CBS 100822, CCP, ZHKUCC 24-0446, ZHKUCC 24-0447, and ZHKUCC 24-0684) with 96% ML/1.00 PP support (Figure 5.7). *Corynespora cassiicola*, originally described by Berkeley and Curtis (1868) as *Helminthosporium cassiicola*, was transferred by Wen (1950) based on morphological characteristics. Morphologically, *C. wurfbainiae* can be distinguished from *C. cassiicola* due to its thin-walled, shorter conidiophores (15–298 × 5–10 μm vs. up to 600 × 3.8–11.3 μm). The conidia of *C. wurfbainiae* form a single square, cuneiform, or cuboid in a chain, a character not found in *C. cassiicola*. We propose *C. wurfbainiae* as a novel species

based on the phylogenetic analyses and unique morphology. This represents the first record of both the sexual and asexual morphs of this species.



Note a Culture characteristic on PDA for 2 weeks. b, c Appearance of ascomata on SNA after 3 weeks. d Section through ascomata. e Peridium. f Paraphyses. g–k Asci. i–q Ascospores. Scale bars: d = 100 µm, e = 500 µm, f–k = 20 µm, l–q = 10 µm.

Figure 5.9 Sexual morph of *Corynespora wurfbainiae* (MHZU 24-0180, holotype)



Note a Culture characteristic on SNA for 3 weeks. b, c Conidia on aerial mycelia on SNA. d–g Conidiogenous cells with conidia. h–j Conidia. Scale bars: d, e = 500 μm, f–h = 30 μm, i, j = 20 μm.

Figure 5.10 Asexual morph of *Corynespora wurfbainiae* (MHZU 24-0218, holotype)

Cucurbitariaceae Luerss., Handbuch der systematischen Botanik mit besonderer Berücksichtigung der Arzneipflanzen 1: 154 (1879)

Notes – Cucurbitariaceae was introduced by Winter (1885) with *Cucurbitaria* designated as the type genus. The sexual morph of Cucurbitariaceae is characterized by scattered or clustered ascomata on basal hypostroma, aggregated ostiolate, fissitunicate and cylindrical asci and phragmosporous or muriform ascospores (Doilom et al., 2013; Pem et al., 2024). Asexual morphs are coelomycetous or hyphomycetous, resembling coniothyrium-like, or phaeoseptoria-like (Hyde et al., 2013). Currently, this family comprises 13 accepted genera (Hyde et al., 2024).

Pyrenochaetopsis de Gruyter et al., Mycologia 102(5): 1076 (2010)

Notes – *Pyrenochaetopsis* was introduced by de Gruyter (2010) and typified by *Py. leptospora*. *Pyrenochaetopsis* species are characterized by setose pycnidia and phoma-like conidiogenesis. They are commonly found in soil, terrestrial, and marine environments (Fan et al., 2020). The genus *Pyrenochaetopsis* remains underexplored regarding its bioactive compounds (Fan et al., 2020). Up to now, 28 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we introduce three novel species, *Pyrenochaetopsis endophytica*, *Py. guangdongensis*, and *Py. wurfbainiae*, based on the phylogenetic analyses and morphological characteristics.

Pyrenochaetopsis endophytica C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.12

Index Fungorum number: IF904011; Facesoffungi number: FoF 17907

Etymology – The epithet "*endophytica*" refers to its endophytic lifestyle

Holotype – MHZU 24-0193

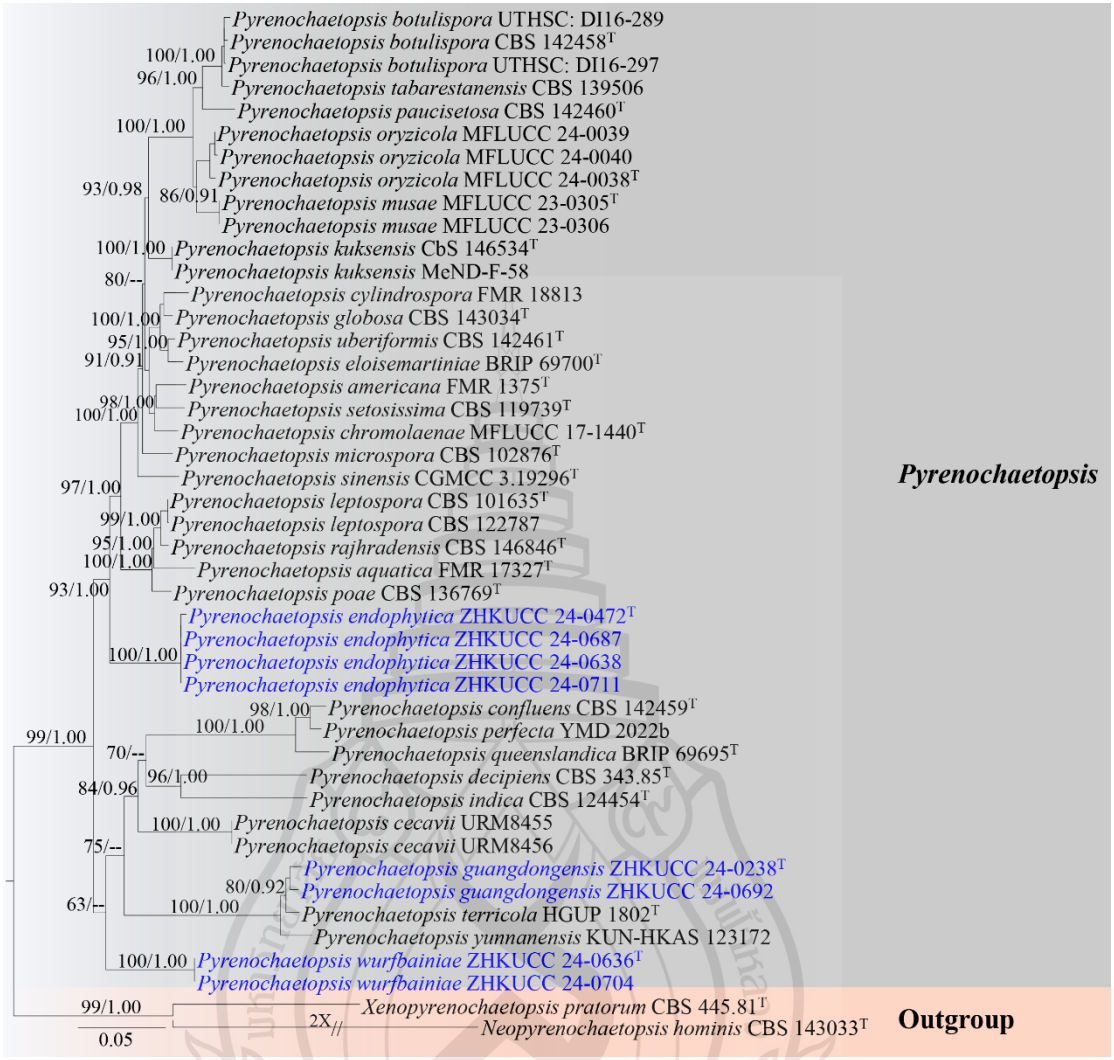
Endophytic in the asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Coelomycetous, sporulated on PDA after 1 month at 28 ± 2°C, appearing as large masses of white slimy conidial exudates, superficial or immersed in PDA, numerous, with abundant surface hyphae. *Conidiomata* 94–190 × 78–115 μm ($\overline{x}$ = 122 × 93 μm, n = 10), scattered to gregarious, uniloculate, erumpent to superficial, subglobose to obpyriform. *Conidiomata walls* 10–20 μm wide ($\overline{x}$ = 14 μm, n = 20), 3–6 layered, composed of brown and flattened polygonal, thick-walled cells of *textura angularis* or *textura prismatica*. *Setae* 3–5 μm wide ($\overline{x}$ = 4 μm, n = 20),

pale brown, septate, curved, thick-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–8 × 2–5 μm ($\bar{x}$ = 6 × 4 μm, n = 30), phialidic, gregarious, hyaline, aseptate, subglobose to ampulliform, angular to variously shaped, arising directly from the inner conidiomata wall, confusing with conidiomata wall. *Conidia* 11–15 × 7–10 μm ($\bar{x}$ = 13 × 9 μm, n = 30), subglobose to ellipsoidal, oblong, hyaline, aseptate, 1–2-guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 3.0–3.5 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, flat, rhizoid, filiform, pale brown from above and reverse, without pigmentation.

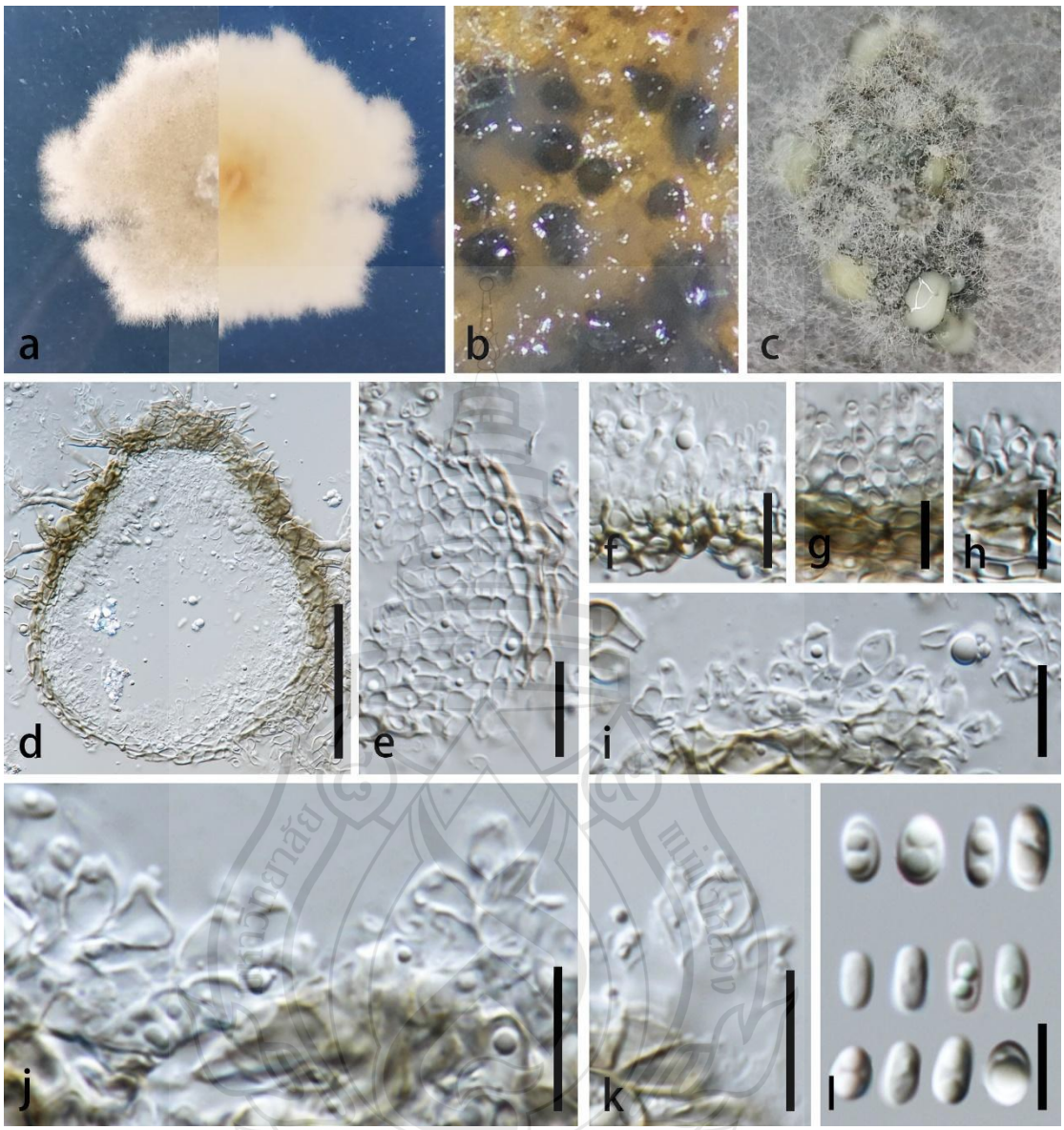
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS11C-3 (MHZU 24-0193, holotype); ex-type culture, ZHKUCC 24-0472; *ibid*., Heshui Town (22.29861 N, 111.98444 E), from symptomatic leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP20B3, living culture, ZHKUCC 24-0638; *ibid*., Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), diseased leaf of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP50B1, YP66B2; ZHKUCC 24-0687, ZHKUCC 24-0711.

Notes – In the phylogenetic analysis, ZHKUCC 24-0638, ZHKUCC 24-0472, ZHKUCC 24-0687, and ZHKUCC 24-0711 formed a distinct lineage separate from other *Pyrenochaetopsis* species, including *Py. Poae*, *Py. aquatica*, and *Py. confluens* formed a distinct lineage with 93% ML/1.00 PP support (Figure 5.19). Morphologically, *Py. endophytica* can be distinguished from *Py. poae* by having subglobose to obpyriform conidiomata, subglobose to ampulliform, angular to variously shaped conidiogenous cells, and subglobose to ellipsoidal or oblong conidia, in contrast to the globose conidiomata, subcylindrical to ampulliform conidiogenous cells, and cylindrical conidia of *Py. poae*. Furthermore, *Py. endophytica* differs from *Py. poae* in having smaller conidiomata (94–190 × 78–115 μm vs. up to 250 μm diam), thicker conidiomata walls (3–6 layers vs. 2–3 layers), larger conidiogenous cells (4–8 × 2–5 μm vs. 4–5 × 3–4 μm), and larger conidia (11–15 × 7–10 μm vs. (3–)4–5(–7) × 1.5(–2) μm). Hence, based on the morphological differences and multi-gene phylogeny, we propose *Py. endophytica* as a new species.



Note Tree rooted as *Neopyrenochaetopsis hominis* (CBS 143033) and *Xenopyrenochaetopsis pratorum* (CBS 445.81). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.11 Maximum likelihood phylogeny based on combined ITS, LSU, *rpb2*, and *tub2* sequences data of *Pyrenochaetopsis*



Note a Culture characteristic on PDA for 2 weeks. b, c Appearance of conidiomata on PAD after 1 month. d Section through conidioma. e Peridium. f–k Conidiogenous cells. l Conidia. Scale bars: d = 50 μm, e–k = 10 μm, l = 20 μm.

Figure 5.12 *Pyrenochaetopsis endophytica* (MHZU 24-0193, holotype)

Pyrenochaetopsis guangdongensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.13

Index Fungorum number: IF904012; Facesoffungi number: FoF 17908

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China where the holotype was collected

Holotype – MHZU 24-0040

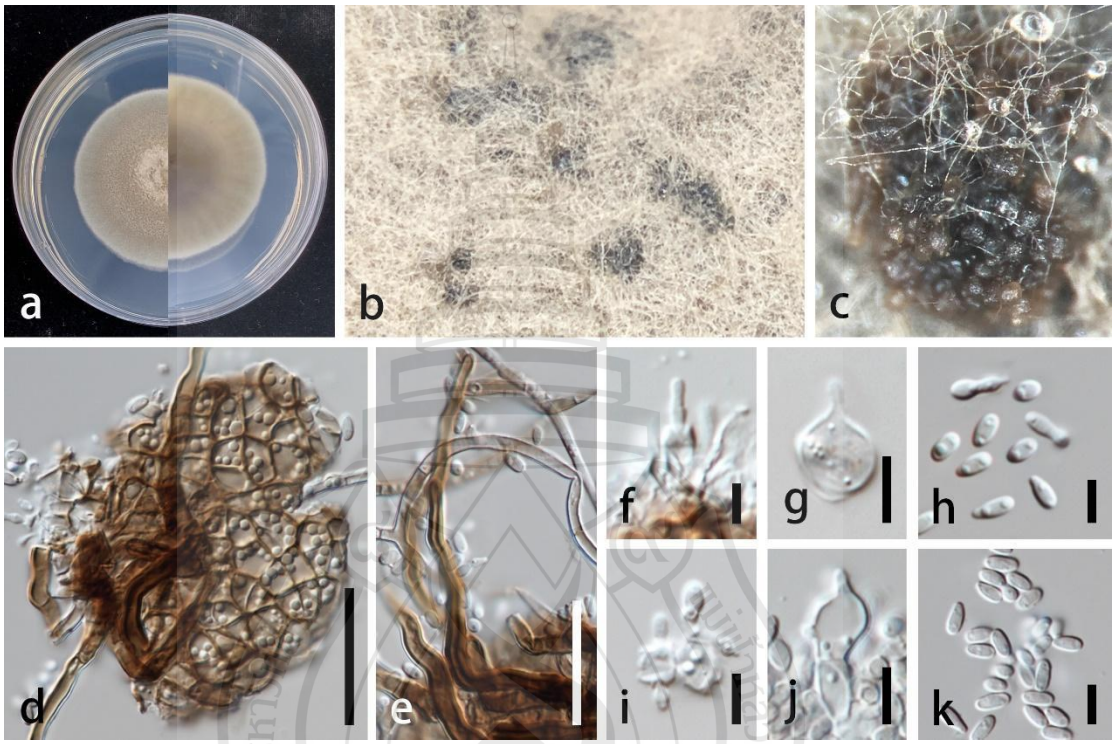
Saprobic on dead stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Coelomycetous, sporulating on PDA after three months at 28 ± 2°C, appearing as black dots, superficial or immersed, surface covered by abundant hyphae. *Conidiomata* scattered, multi-loculate, erumpent to superficial, subglobose. *Setae* 3–5 μm wide ($\overline{x}$ = 4 μm, n = 20), brown to dark brown, septate or aseptate, curved, tapering towards the apex, apical rounded, thick-walled. *Conidiomata walls* composed of brown, flattened, polygonal, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.5–8.5 × 2.5–6 μm ($\overline{x}$ = 6.5 × 4 μm, n = 30), phialidic, gregarious, hyaline, aseptate, subglobose, cylindrical to ampulliform, sometimes directly arising from the inner conidiomata wall, barely distinguishable with conidiomata wall. *Conidia* 3.5–5 × 2–2.5 μm ($\overline{x}$ = 4 × 2.2 μm, n = 30), ellipsoidal to subglobose, oblong to obovoid, hyaline, aseptate, 1–2-guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 5.0–5.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, umbonate, with entire edge, pale brown to olivaceous green from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Jinghuaken (22.19027 N, 111.91027 E), from dead stem of *Wurfbainia villosa*, 10 April 2023, C.F. Liao, YAM38 (MHZU 24-0040, holotype); ex-type culture, ZHKUCC 24-0238; *ibid*., Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from symptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP51B3, living culture, ZHKUCC 24-0692.

Notes – In the phylogenetic analyses, two strains (ZHKU 24-0238 and ZHKUCC 24-0692) formed clade separated from *Pyrenochaetopsis terricola* (HGUP1802) with 80% ML/0.92 PP support (Figure 5.11). Morphologically, the setae of *Py. guangdongensis* are septate or aseptate, curved setae, in contrast to aseptate, erect ones in *Py. terricola*. Additionally, conidia of *P. guangdongensis* are ellipsoidal to

subglobose, oblong to obovoid and larger (3.5–5 × 2–2.5 μm vs. 2–3 × 1–2μm), while the conidia of the latter are ovoid to cylindrical (Wang et al., 2019). Additionally, *Py. terricola* was collected from soil in China, while *Py. guangdongensis* was obtained from dead and symptomatic stems of *Wurfbainia villosa* in China. Thus, we propose *Py. guangdongensis* as a novel species based on morphology and phylogenetic evidence.



Note a Culture characteristic on PDA for 3 months. b, c Appearance of conidiomata on PDA. d Peridium. e Setae. f, g, i, j Conidiogenous cells with conidia. h, k Conidia. Scale bars: d, e = 20 μm, f–k = 5 μm.

Figure 5.13 *Pyrenochaetopsis guangdongensis* (MHZU 24-0040, holotype)

Pyrenochaetopsis wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.14

Index Fungorum number: IF904013; Facesoffungi number: FoF 17909

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0320

Associated with symptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Coelomycetous, sporulating on sterile leaf segments of

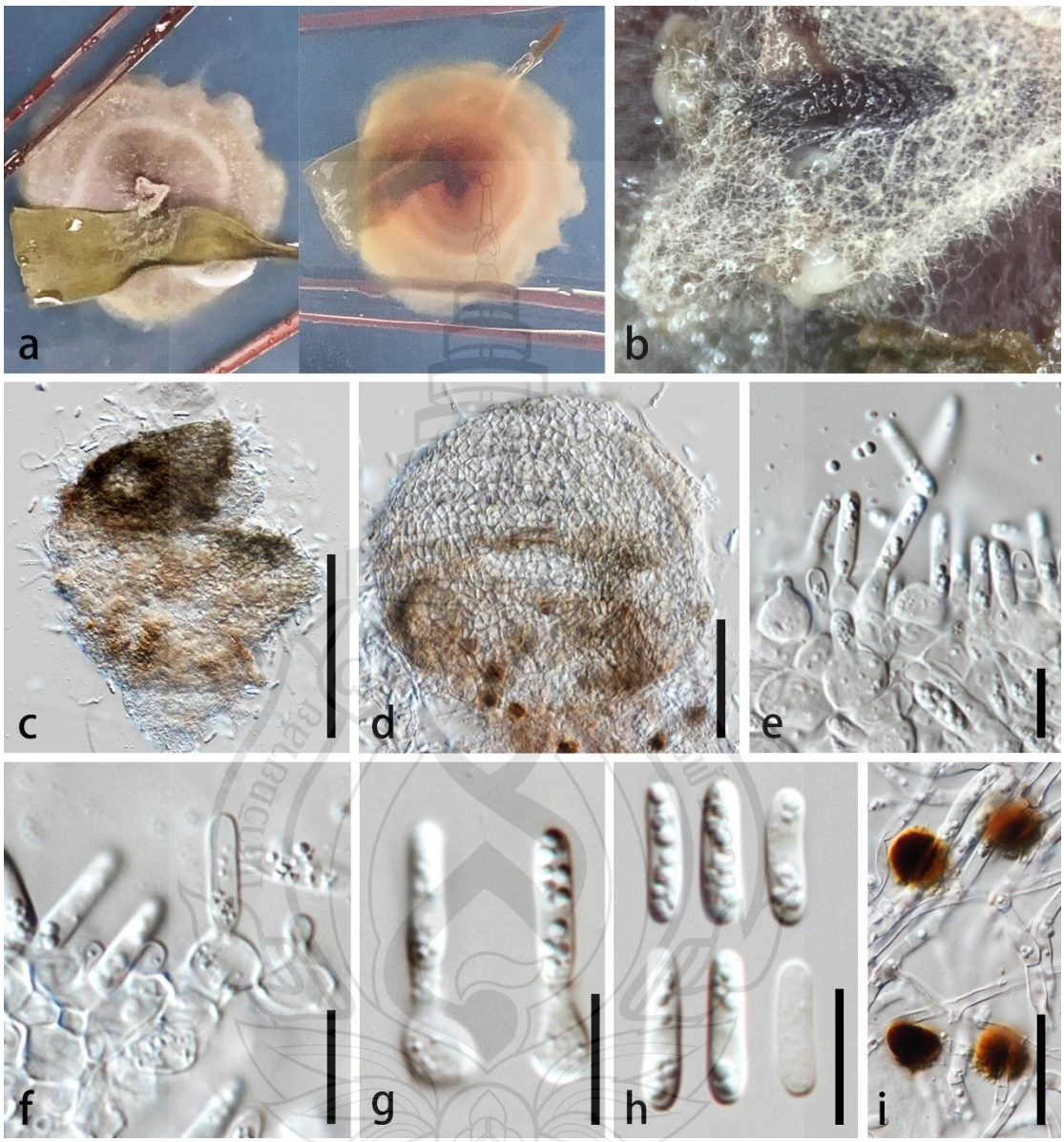
Wurfbainia villosa placed on PDA after 2 weeks at 28 ± 2°C, appearing as large masses of white slimy conidial exudates, superficial or immersed, many hyphae covered on the surface. *Conidiomata* 102–188 × 93–162 μm ($\overline{x}$ = 149 × 137 μm, n = 10), scattered, uniloculate, erumpent to superficial, subglobose, ostiolate. *Ostiole* center, opening, pale brown. *Conidiomata walls* composed of brown, thick-walled, flattened polygonal cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 24.5–44 × 20–38 μm ($\overline{x}$ = 33 × 29 μm, n = 30), phialidic, gregarious, hyaline, aseptate, subglobose to ampulliform, arising directly from the inner conidiomata wall, barely distinguishable from the conidiomatal wall cells. *Conidia* 48–62.5 × 12.5–19 μm ($\overline{x}$ = 56 × 15 μm, n = 30), oblong, hyaline, aseptate, multi-guttulate, smooth-walled. *Chlamydospores* 8–20 × 4–15 μm ($\overline{x}$ = 13 × 10 μm, n = 30), globose to subglobose, orange-red to dark reddish.

Culture characteristics – Colonies on PDA reaching 2.0–2.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, undulate, irregular, pale purple to pale brown from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.19027 N, 111.91027 E), on symptomatic leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP19A3 (MHZU 24-0320, holotype); ex-type culture, ZHKUCC 24-0636; *ibid*., Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), on symptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP64A3, living culture, ZHKUCC 24-0704.

Notes – In the phylogenetic analysis, ZHKUCC 24-0636 and ZHKUCC 24-0704 formed a distinct lineage basal to all other *Pyrenochaetopsis* species (Figure 5.11). Morphologically, *Py. wurfbainiae* is characterized by setose pycnidia, oblong to cylindrical, hyaline, aseptate conidia with guttules, which align with the generic concept of *Pyrenochaetopsis*. When compared to *Py. yunnanensis*, one of the closest to our isolate, *Py. wurfbainiae* has larger conidiomata (102–188 × 93–162 μm vs. 50–100 × 68–105 μm), larger conidiogenous cells (24.5–44 × 20–38 μm vs. 2–4 × (1.8–)2–3.5 μm), and larger conidia (48–62.5 × 12.5–19 μm vs. (2.8–)3–4 × 1–2(–2.5) μm) (Phookamsak et al., 2022). Additionally, *Py. wurfbainiae* produces globose to subglobose, orange-red to dark reddish chlamydospores, which are not observed in

other species of this genus. Hence, we introduce *Py. wurfbainiae* as a new species based on morphology and phylogenetic analyses.



Note a Culture characteristic on PDA after 2 weeks. b Appearance of conidiomata on sterilized leaf of *Wurfbainia villosa*. c, d Conidiomata. e–g Conidiogenous cells with conidia. h Conidia. i Sclerotia. Scale bars: c, d = 100 µm, e–h = 50 µm, i = 20 µm.

Figure 5.14 *Pyrenochaetopsis wurfbainiae* (MHZU 24-0320, holotype)

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953)

Notes – Didymosphaeriaceae is a large family placed in Pleurotheciales, with *Didymosphaeria* introduced by Munk (1953) as the type genus. Species of Didymosphaeriaceae have a wide host range and are distributed globally. They have been reported as saprobes on woody substrate pods, and soil, as well as endophytes, plant pathogens (Samarakoon et al., 2020). Didymosphaeriaceae are characterized by sexual morphs with globose to sub-globose, central ostiolate ascomata, cellular or trabeculate pseudoparaphyses, septate or muriform ascospores (Hyde et al., 2013; Ariyawansa et al., 2014). Their asexual morphs are diverse, including camarosporium-like, square shape and spegazzinia-like (Ren et al., 2022).

Dictyoarthrinium S. Hughes, Mycol. Pap. 48: 29 (1952)

Notes – *Dictyoarthrinium* was described by Hughes (1952) with *D. quadratum* designated as the type species. The *Dictyoarthrinium*, *Endocalyx*, *Arthrinium* and *Spegazzinia* have been placed in Apiosporaceae (Xylariales, Sordariomycetes) based on basauxic conidiogenous cells (Hyde et al., 1998; Crous & Groenewald, 2013; Tanaka et al., 2015; Hyde et al., 2020; Wijayawardene et al., 2020). Later, Samarakoon et al. (2020) resolved the generic placements and transferred *Dictyoarthrinium* to Didymosphaeriaceae based on the morphological characters and multi-gene phylogenetic analyses. To date, numerous studies have confirmed and supported this placement (Maharachchikumbura et al., 2021; Ren et al., 2022; Manawasinghe et al., 2024; Wijayawardene et al., 2024).

Dictyoarthrinium wurfbainiae C.F. Liao & Doilom, sp. nov. Figure 5.16

Index Fungorum number: ####; Facesofungi number: FoF ###

Etymology – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*, from which the holotype was collected.

Holotype – MHZU 24-0101

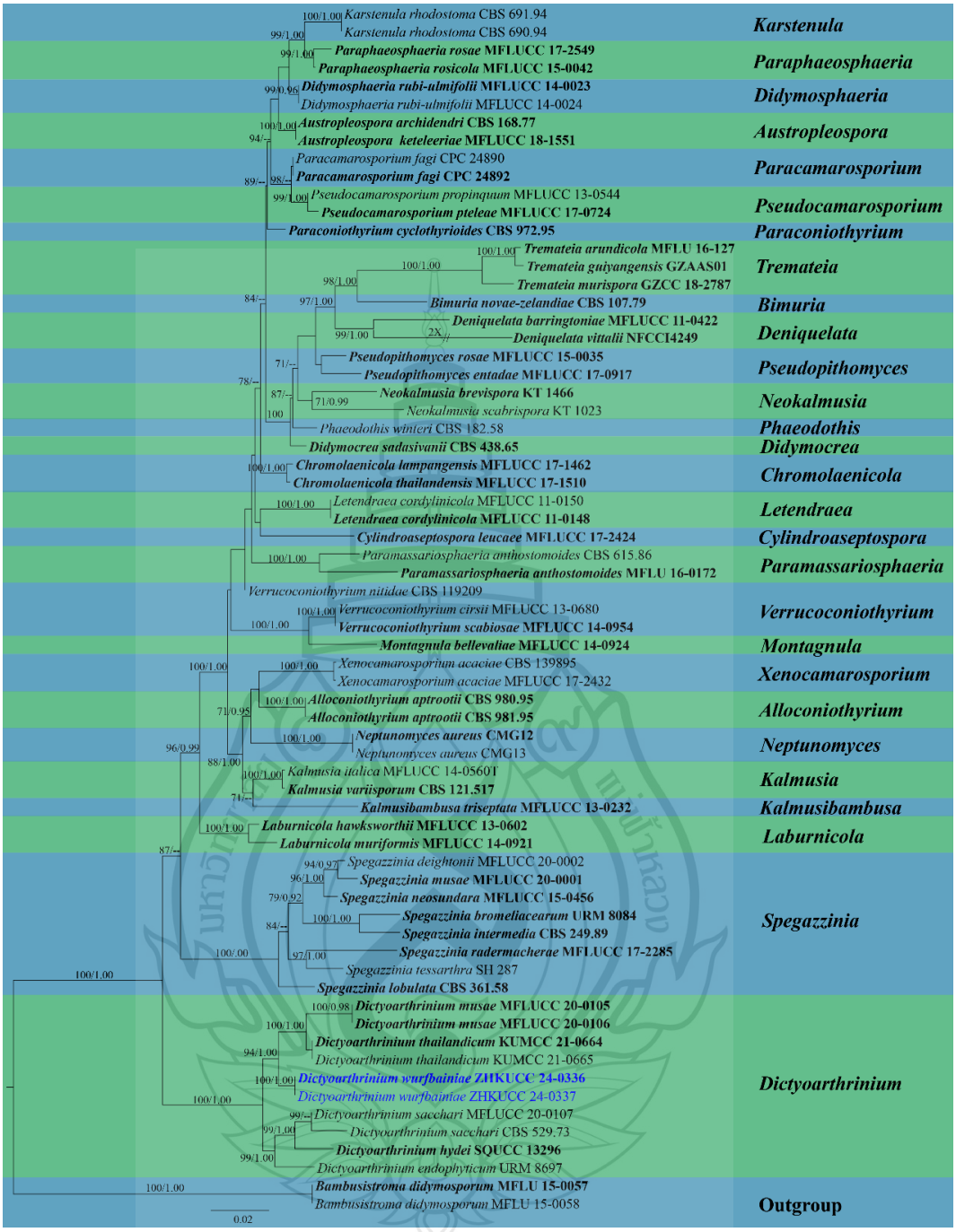
Saprobic on decaying stems of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: hyphomycetes. Colonies on natural substrate, solitary, scattered, superficial, powdery, black patch, irregular. *Conidiophores* 131–238 × 3–5 μm, ($\bar{x}$ = 168.5 × 4 μm n = 30), macronematous, basauxic, flexuous, cylindrical, hyaline to pale brown, smooth to finely rough-walled, with dark brown transverse septa. *Conidiogenous cells* 1–2 × 1.5–2.2 μm, ($\bar{x}$ = 1.5 × 1.75 μm n = 20), integrated,

basauxic, cylindrical, hyaline to pale brown, terminal and intercalary, smooth-walled, very small and sometimes not observed. *Conidia* 10–13 × 9–12 μm, ($\overline{x}$ = 11 × 11 μm, n = 30), holoblastic, subglobose, hyaline to pale brown, smooth-walled when young; becoming four cells by septa, slightly constricted at the septa, globose to subglobose in face view, ellipsoidal in side view, verrucose, dark brown when mature.

Culture characteristics – Conidia germinate on PDA at room temperature (25±2°C) within 24 hours, and produce germ tubes from the center of the bottom septa. Colonies after two weeks at 28°C reach 75–80 mm in diam., sparse, flat, circular, cream white to brownish gray from front view and reverse view.

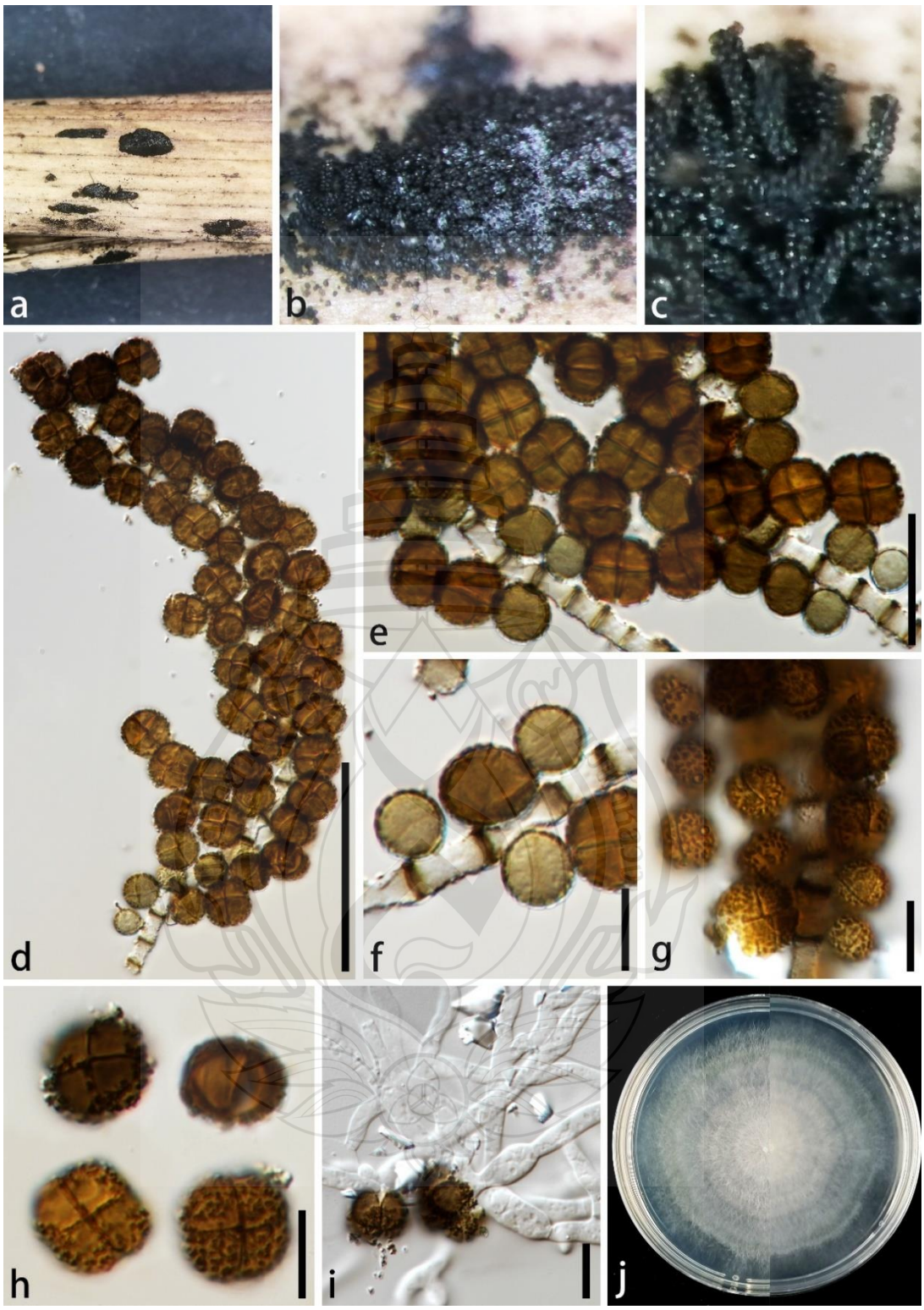
Material examined – China, Yunnan Province, Jinghong City, Mengla County, Menglun Town, Manzhang, from decaying stems of *Wurfbainia villosa* (Zingiberaceae), 16 January 2024, C.F. Liao, MHZU 24-0101, holotype; ex-type culture ZHKUCC 24-0336; *ibid*., ZHKUCC 24-0337.

Notes – The phylogenetic analyses show that our strains (ZHKUCC 24-0336 and ZHKUCC 24-0337) form clustered separately from *Dictyoarthrinium thailandicum* (KUMCC 21-0664, KUMCC 21-0665) and D. musae with 94% ML and 1.00 BYPP (Figure 5.15). *Dictyoarthrinium wurfbainiae* has some similar characters with *D. thailandicum* by having macronematous, cylindrical, straight or flexuous conidiophores and holoblastic, spherical, 1-celled when young, cruciate-septate with four cells when mature. However, *D. wurfbainiae* are unique from *D. thailandicum* by not having conidiophore mother cells, having smaller conidiogenous cells (1–2 × 1.5–2.2 μm vs. 3–7 × 3–5 μm) (Ren et al. 2022). Further, the mature conidia of *D. thailandicum* split along a septum, but *D. wurfbainiae* does not follow such pattern. Additionally, the *D. wurfbainia* also differ from *D. musae* by having larger conidiophores (131–238 × 3–5 μm vs. 30–140 × 1–2 μm) and smaller conidiogenous cells (1–2 × 1.5–2.2 μm vs. 4.1–4.5 × 4.3–4.7 μm) (Samarakoon et al. 2022). Therefore, we propose *D. wurfbainiae* as a novel species based on unique morphological characteristics and molecular evidence.



Note The tree is rooted with *Bambusistroma didymosporum* (MFLU 15-0057, MFLU 15-0058). Bootstrap support values with an ML greater than 70% and Bayesian posterior probabilities (PP) greater than 0.90 are given above the nodes, shown as "ML/PP". Isolates of the current study are indicated in blue and type strains are bold.

Figure 5.15 Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and *tef1-α* sequences data of *Dictyoarthrinium*



Note (a–c) colonies on wood substrate. d–g conidiophores, conidiogenous cell, and conidia. h conidia. i A germinated conidium. j colony on PDA (left-front, right-reverse). Scale bars: d 50 µm, e 20 µm, f–i 10 µm.

Figure 5.16 *Dictyoarthrinium wurfbainiae* (MHZU 24-0101, holotype)

Periconiaceae Nann., Repert. mic. uomo: 482 (1934)

Notes – Periconiaceae was resurrected by Tanaka et al. (2015) to accommodate four genera, *Bambusistroma*, *Flavomyces*, *Noosia*, and *Periconia*. Yang et al. (2022) synonymized *Bambusistroma* and *Noosia* under *Periconia*. Currently, the family includes two genera, *Flavomyces* and *Periconia*. However, Liao et al. (2024b) demonstrated that *Flavomyces fulophazii* (the type species of *Flavomyces*) clusters in *Periconia* clade and forms a distinct lineage with *Periconia endophytica*, *P. yangjiangensis*, and *P. wurfbainiae* based on the phylogenetic analyses of the combined ITS, LSU, SSU, and *tef1-α* sequence data. Nevertheless, Knapp et al. (2015) did not provide a detailed morphological description of *F. fulophazii*. Therefore, its classification requires re-examination supported by additional morphological evidence and molecular analyses.

Periconia Tode, Fung. mecklenb. sel. (Lüneburg) 2: 2 (1791)

Notes – *Periconia* was introduced by Tode (1791), with the type species *P. lichenoides*. Most *Periconia* species are reported as saprobes, and some species are also found as endophytes and plant pathogens (Pem et al., 2024; Liao et al., 2024b). They are widely distributed in terrestrial habitats, less so in aquatic and marine environments (Liao et al., 2024b). The morphological characteristics are detailed in Tanaka et al. (2015), Yang et al. (2022), and Su et al. (2023). *Periconia* is an important source of bioactive compounds, with over 100 compounds isolated from this genus (Azhari et al. 2021). According to Index Fungorum, the genus includes 234 epithets (https://www.indexfungorum.org/names/Names.asp). In this study, we reported a new host and geographical record, *Periconia epilithographicola*, and a novel species, *P. neoyangjiangensis*, based on phylogenetic analyses and morphological characteristics.

Periconia endophytica C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.18

Index Fungorum number: IF851407; Facesoffungi number: FoF15276

Etymology – The epithet "*endophytica*" refers to the endophytic lifestyle of the species. Holotype. MHZU 23-0245

Endophytic associated with leaves of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: sporulation on the sterile plant tissue in PDA after a month of incubation, spore masses visible as black spot, scattered on colonies. *Hyphae* 1.5–3.5 µm wide (x = 2.5 µm, n = 30), branched, hyaline, septate, smooth to slightly

verruculose. *Conidiophores* 15–110 × 2.5–5.5 µm (x = 45 × 4 µm, n = 30), micro to semi macronematous, mononematous, erect, flexuous or straight, branched, sparsely septate, slightly constricted at septa, rough-walled, verruculose, thin-walled, hyaline, pale brown to yellowish brown in the upper portion. *Conidiogenous cells* 5–20 × 2.5–5.5 µm (x = 9 × 4 µm, n = 30), holoblastic, mono- and polyblastic, integrated, determinate, terminal, subcylindrical, obovoid, ellipsoidal with truncated ends, pale brown to yellowish brown, verruculose. *Conidia* 4–6 × 3–5 µm (x = 5 × 4 µm, n = 30), globose to subglobose, aseptate, catenate, with 4–10 conidia in a chain, hyaline when young, becoming pale brown, yellowish brown and reddish brown when mature, verruculose.

Culture characteristics – Colonies on PDA reaching 4.2 cm in two weeks at 28 ± 2°C, medium dense, center umbonate, circular, floccose to fluffy, velvety, filiform edge, golden brown at the center, pale brown at the margin from above; orange-brown to golden brown at the center, pale brown at the margin from reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning Town (22.256185 N, 111.609037 E), from healthy leaves of *Wurfbainia villosa*, 10 April 2022, C.F. Liao & Y.H. Yang, AML04C-3 (MHZU 23-0245, holotype); ex-type culture, ZHKUCC 23-0995; *ibid*., living culture ZHKUCC 23-0996.

Notes – Phylogenetically, *P. endophytica* formed a distinct linage and clustered with other sister *Periconia* species with 95% ML and 1.00 BYPP (Figure 5.25). *Periconia endophytica* differs from its phylogenetically close species *P. wurfbainiae* and *P. yangjiangensis* by having smaller conidiophores (15–110 × 2.5–5.5 µm vs. 225–315 × 8–14 µm vs. 275–420 × 5–15 µm), smaller conidiogenous cells (5–20 × 2.5–5.5 µm vs. 7–11 × 5–9 µm vs. 15–25 × 8–10 µm), and smaller conidia (4–6 × 3–5 µm vs. 3.5–7 µm diam vs. 6–10 µm). Conidiophores of *Periconia endophytica* are micro to semi macronematous, branched, and pale brown to yellowish brown in the upper portion, compared to macronematous, unbranched, black conidiophores in *P. wurfbainiae* and macronematous, branched conidiophores that are dark brown to black in the lower portion, brown in the upper portion, 1–4 times of enteroblastically percurrent proliferating, forming 1–4 swollen in *P. yangjiangensis*. In addition, our species differs by having subcylindrical conidiogenous cells, 4–10 catenated conidia in a chain, in contrast to obovoid, ellipsoidal conidiogenous cells and 6–8 conidia in a chain in

P. *wurfbainiae* and oblong conidiogenous cells and 3 conidia in a chain in *P*. *yangjiangensis*. Based on the morphological differences and molecular support, *Periconia endophytica* is introduced as a new species.

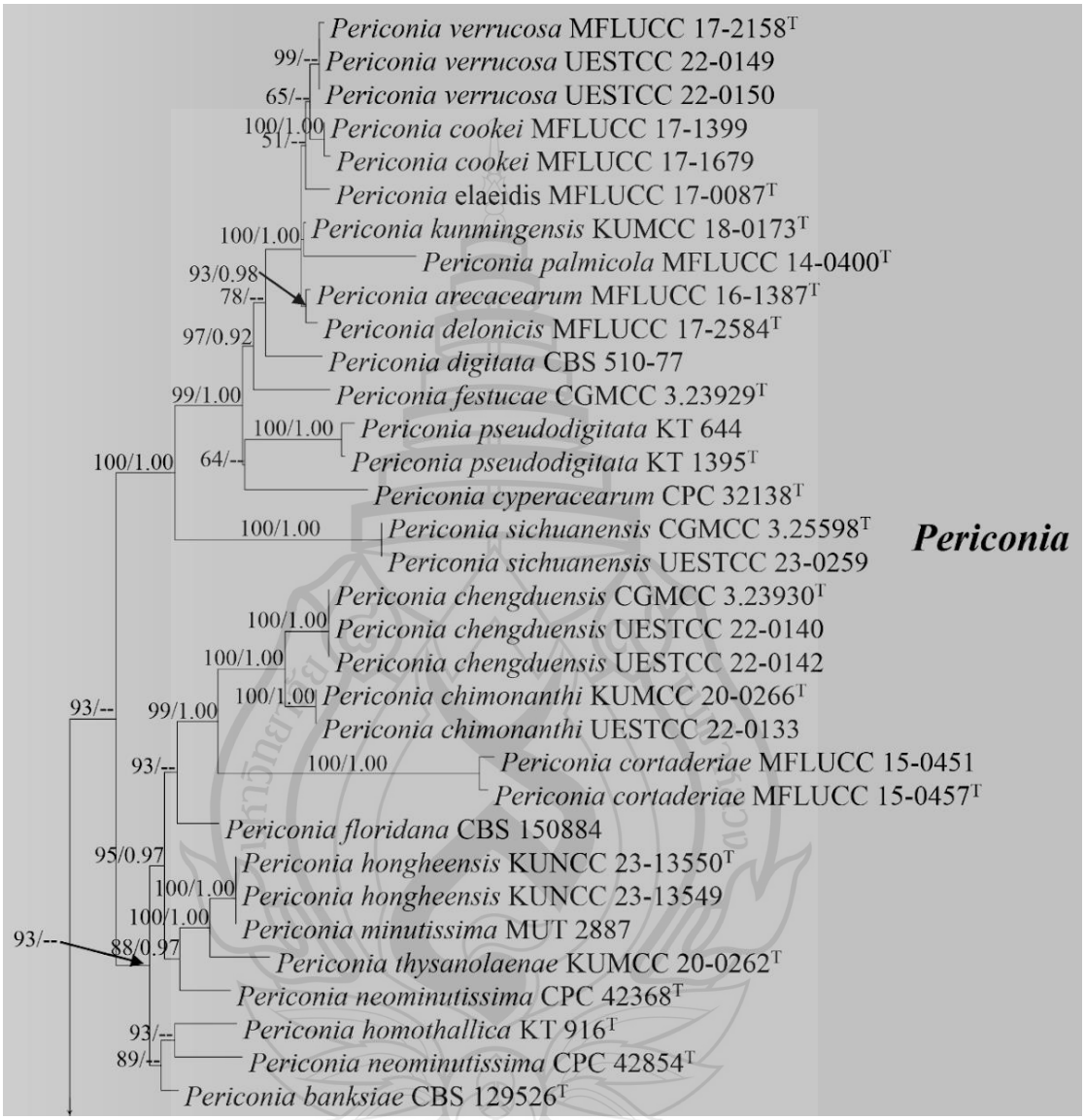
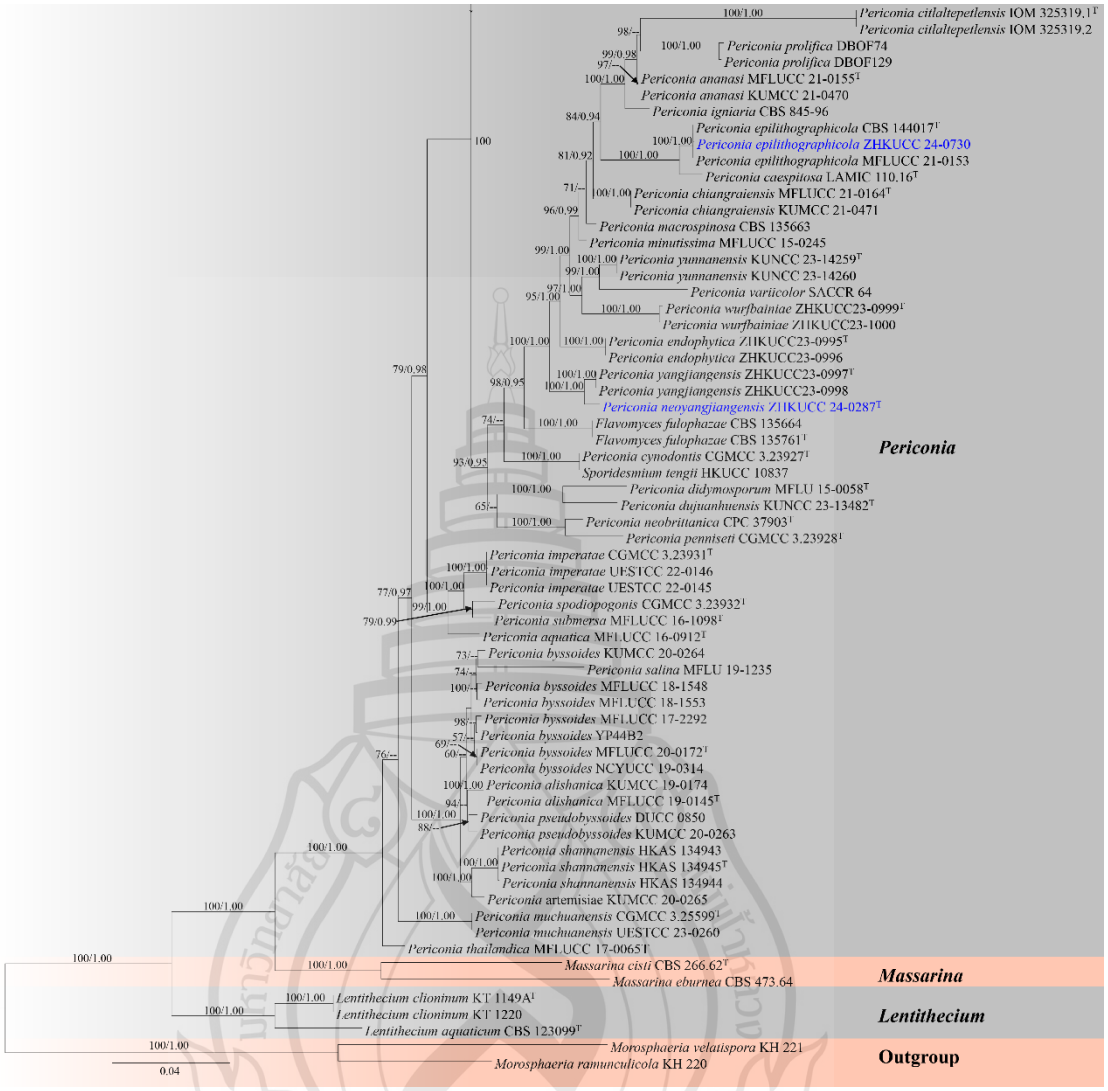
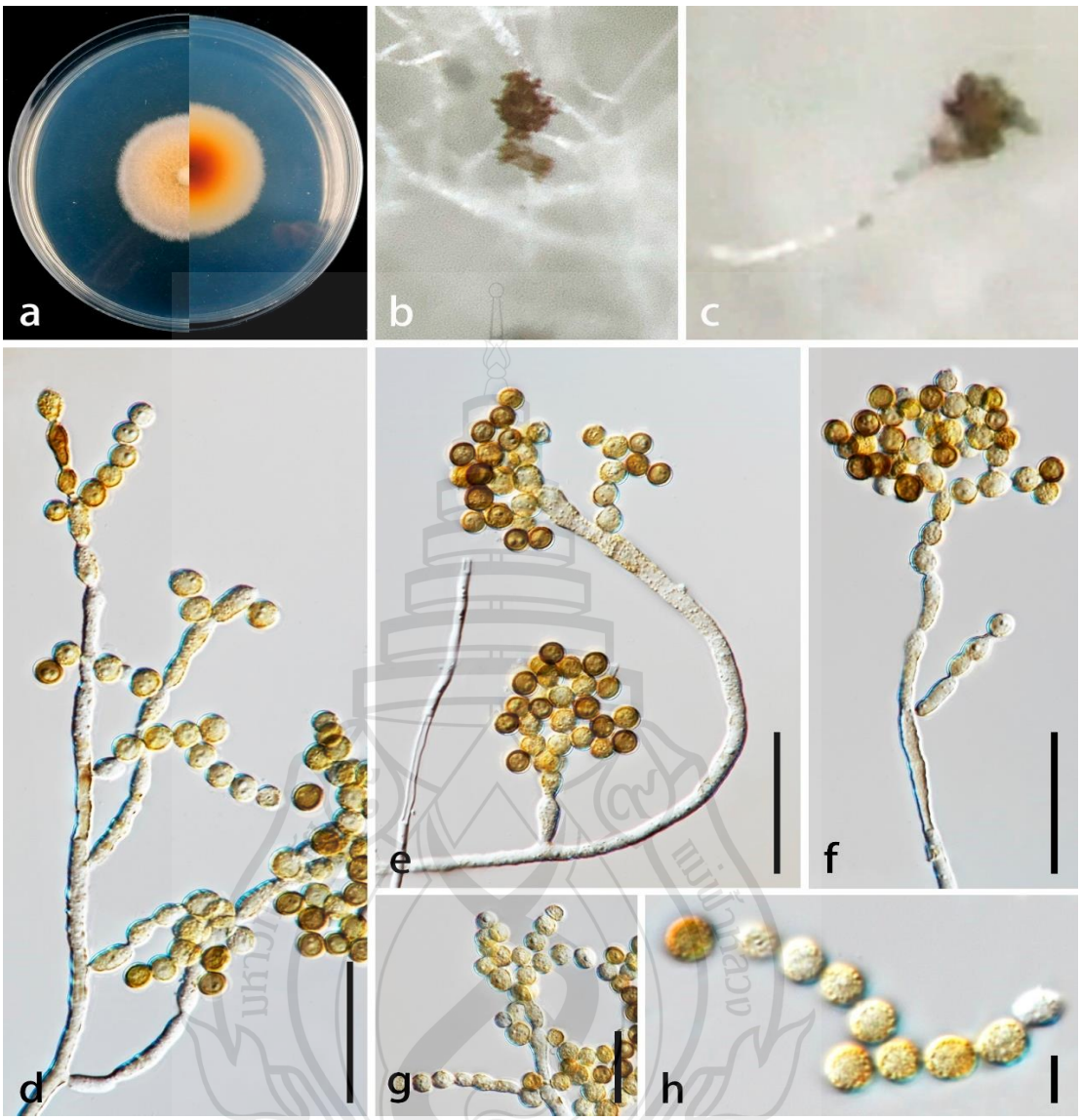


Figure 5.17 Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and *tef1-α* sequences data of *Periconia*



Note Tree rooted with *Morosphaeria ramunculicola* (KH 220) and *Morosphaeria velatispora* (KH 221). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.17 (continued)



Note a Upper view and reverse view of culture on PDA. b, c) Close-up of mycelia and conidia on the sterile plant tissue in PDA after a month of incubation. d–g Conidiophores, conidiogenous cells with conidia. h Conidia. Scale bars: d–f = 50 µm, g = 20 µm, h = 5 µm.

Figure 5.18 *Periconia endophytica* (MHZU 23-0245, holotype)

Periconia epilithographicola Coronado-Ruiz, Avendaño, Escudero-Leyva, Conejo-Barboza, P. Chaverri & Chavarría, Scientific Reports 8 (no. 7492): 3 (2018). Figure 5.19

Index Fungorum number: IF825093; Facesoffungi number: FoF 10660

Endophytic in asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on the sterile pine needles on PDA after six weeks of incubation. *Hyphae* 1.5–3 μm wide ($\overline{x}$ = 2.5 μm, n = 30), hyaline, septate, branched, smooth-walled. *Conidiophores* 23–353 × 4–15.5 μm ($\overline{x}$ = 173 × 8 μm, n = 30), macronematous, mononematous, erect, flexuous, branched, septate, slightly constricted at septa, smooth- and thick-walled, hyaline apically, with olivaceous green to yellowish brown at the base. *Conidiogenous cells* 5.5–34 × 2.5–8 μm ($\overline{x}$ = 10 × 6 μm, n = 30), holoblastic, mono- and poly- blastic, integrated, determinate, terminal, subglobose, subcylindrical, obovoid, ellipsoidal with truncated ends, hyaline, pale brown to yellowish brown, verruculose. *Conidia* 9–16 μm diam ($\overline{x}$ = 13 μm, n = 30), globose to subglobose, aseptate, catenate, with 3–8 conidia in a chain, hyaline when young, becoming pale brown, yellowish brown to pinkish brown when mature, verrucose.

Culture characteristics – Colonies on PDA reaching 7.0–7.5 cm diameter in 2 weeks at 28 ± 2°C, medium sparse, loose, flat, circular with entire edge, granular, cream-white from above, yellowish gray at center, and cream-white towards the edge from reverse, pink pigmentation.

Material examined – China, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from asymptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, ST28A (MHZU 24-0408); living culture, ZHKUCC 24-0730.

Known hosts (based on molecular data) – University of Costa Rica (Coronado-Ruiz et al. 2018), dead leaves of *Ananas comosus* (Tian et al., 2022), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Central America (Coronado-Ruiz et al., 2018), Thailand (Tian et al., 2022), China (this study).

Notes – In the phylogenetic analyses, our isolate (ZHKUCC 24-0730) clustered with *Periconia epilithographicola* (MFLUCC 21-0153 and CBS 144017) with 100 ML/1.00 PP support (Figure 5.25). The conidiophores of our strain are olivaceous green to yellowish brown at the base and larger than *P. epilithographicola* (23–353 × 4–15.5 μm vs.

251.6–270 × 3.6–6.1 μm) (Coronado-Ruiz et al., 2018). Moreover, the conidia color of our isolate is hyaline when young, becoming pale brown, yellowish brown, and pinkish brown when mature, but they are golden to brown in *P. epilithographicola* (CBS 144017). In addition, our isolate differs from *P. epilithographicola* (CBS 144017) in having longer and shorter conidiogenous cells (5.5–34 × 2.5–8 μm vs. (5.1−) 7 × 10 (−11.5) μm) and larger conidia (9–16 μm diam vs. (7.8−) 9.2 (−10.7) μm diam). Despite these morphological differences, phylogenetic analyses confirm their congeneric relationship between our strain (ZHKUCC 24-0730) and the holotype of *P. epilithographicola* (CBS 144017). Hence, we introduce our isolate as *P. epilithographicola*, representing a new host from *Wurfbainia villosa* and a new geographical record in China.

Note a Culture characteristic on PDA after 1 month. b–d Conidia on aerial mycelia on sterile pine needles on PDA. e–h Conidiophores, conidiogenous cells with conidia. i Conidia. Scale bars: e = 100 μm, f–i = 20 μm.

Figure 5.19 *Periconia epilithographicola* (MHZU 24-0408, new host and geographical record)

Periconia neoyangjiangensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.20

Index Fungorum number: IF904014; Facesoffungi number: FoF 17910

Etymology – The epithet "*neoyangjiangensis*" indicates its morphological resemblance to *Periconia yangjiangensis*

Holotype – MHZU 24-0071

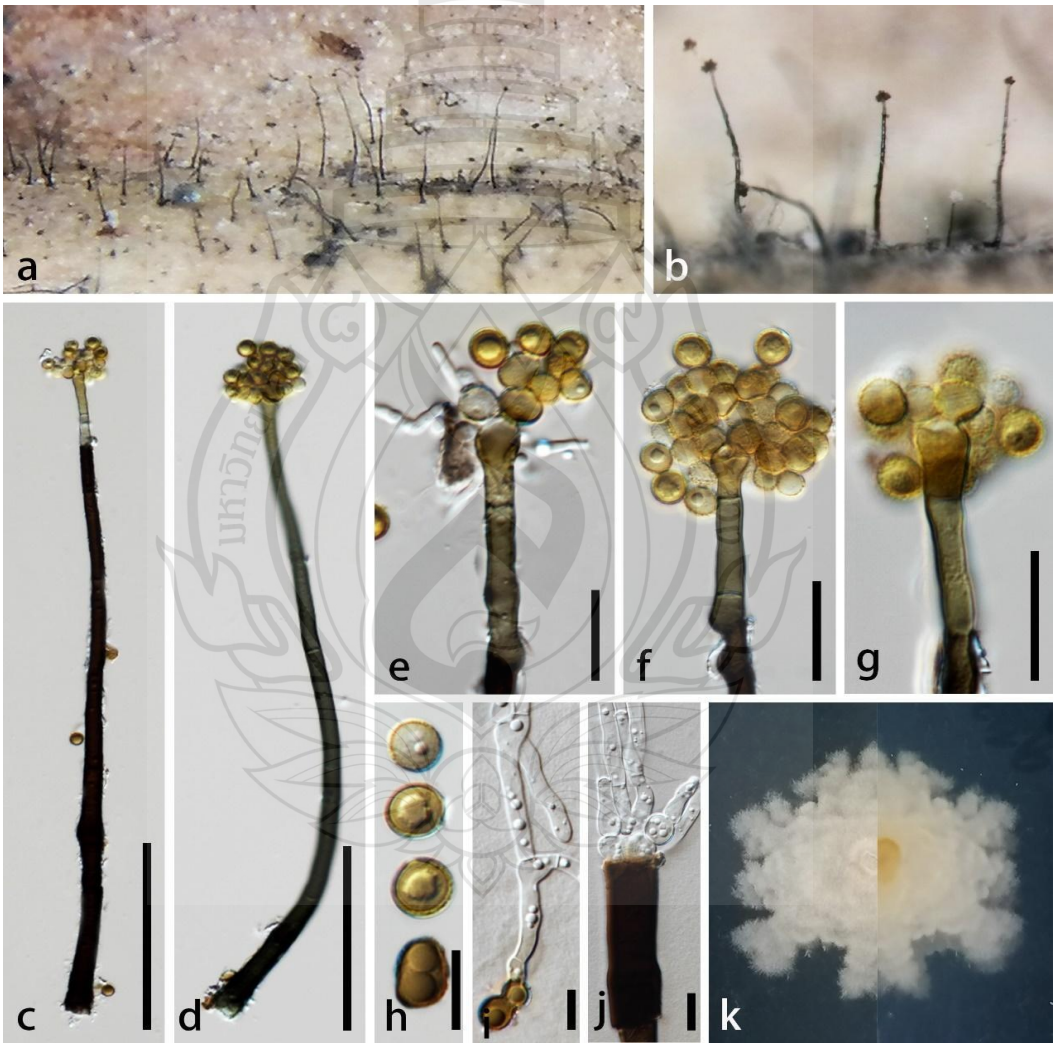
Saprobic on decaying leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Colonies superficial on the host substrate, hairy, gregarious, brown to dark brown. *Conidiophores* 156–323 × 9–17.5 μm ($\bar{x}$ = 260 × 13.5 μm, n = 10), macronematous, mononematous, erect, flexuous, unbranched, septate, slightly constricted at septa, smooth- and thick-walled, hyaline at the apex, tapering toward the apex, olivaceous green to yellowish brown at the base, with 0–2-enteroblastic percurrent proliferating, forming 0–2 swollen, dumbbell-shaped. *Conidiogenous cells* 6–10 × 6.5–9 μm ($\bar{x}$ = 8 × 7.5 μm, n = 20), holoblastic, polyblastic, integrated, determinate, terminal, subglobose, wider than the conidiophores, apex rounded, base truncate, pale brown to yellowish brown, smooth- and thin-walled. *Conidia* 6–8 μm diam ($\bar{x}$ = 7.5 μm, n = 30), globose to amygdaliform, sparse, aseptate, initially hyaline, becoming golden brown at maturity, thick-walled, verruculose.

Culture characteristics – Colonies on PDA reaching 2.8–3.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, raised, curled, undulate, irregular, filiform, cream-white from above, center yellowish brown toward to cream-white at the edge from reverse, without pigmentation.

Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), on decaying leaves of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YAM82 (MHZU 24-0071, holotype); ex-type culture, ZHKUCC 24-0287.

Notes – In the phylogenetic analysis, ZHKUCC 24-0287 clustered closely related to *Periconia yangjiangensis* with 100 ML/1.00 PP support (Figure 5.17). Morphologically, *Periconia neoyangjiangensis* has enteroblastic conidiophores that are olivaceous green to yellowish brown at the base, with 0–2 times of percurrent proliferation, forming 0–2 swollen conidiophores. In contrast, conidiophores of *P. yangjiangensis* are dark brown to black in the lower portion, with 1–4 times of

enteroblastic percurrent proliferation, forming 1–4 swollen conidiophores (Liao et al., 2024b). Furthermore, the conidiogenous cells of *P. neoyangjiangensis* are subglobose, pale brown to yellowish brown and its conidia are globose to amygdaliform. Conversely, *P. yangjiangensis* has oblong, brown conidiogenous cells and its conidia are globose. Additionally, *P. neoyangjiangensis* can be distinguished from *P. yangjiangensis* by its shorter conidiophores (156–323 × 9–17.5 µm vs. 275–420 × 5–15 µm) and smaller conidiogenous cells (6–10 × 6.5–9 µm vs. 15–25 × 8–10 µm). Based on phylogenetic analyses and distinct morphological characteristics, we propose *P. neoyangjiangensis* as a novel species.



Note a, b Colonies on the host substrate. c, d Conidiophores, conidiogenous cells with conidia. e–g Conidiogenous cells with conidia. h Conidia. i Germinated conidium. j Germinated conidia. Scale bars: c, d = 100 µm, e–g = 20 µm, h–j = 10 µm.

Figure 5.20 *Periconia neoyangjiangensis* (MHZU 24-0071, holotype)

Periconia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.21, 5.22

Index Fungorum number: IF851409; Facesoffungi number: FoF 15277

Etymology – In reference to the host genus "*wurfbainiae*" from which it was isolated.

Holotype– MHZU 23-0247

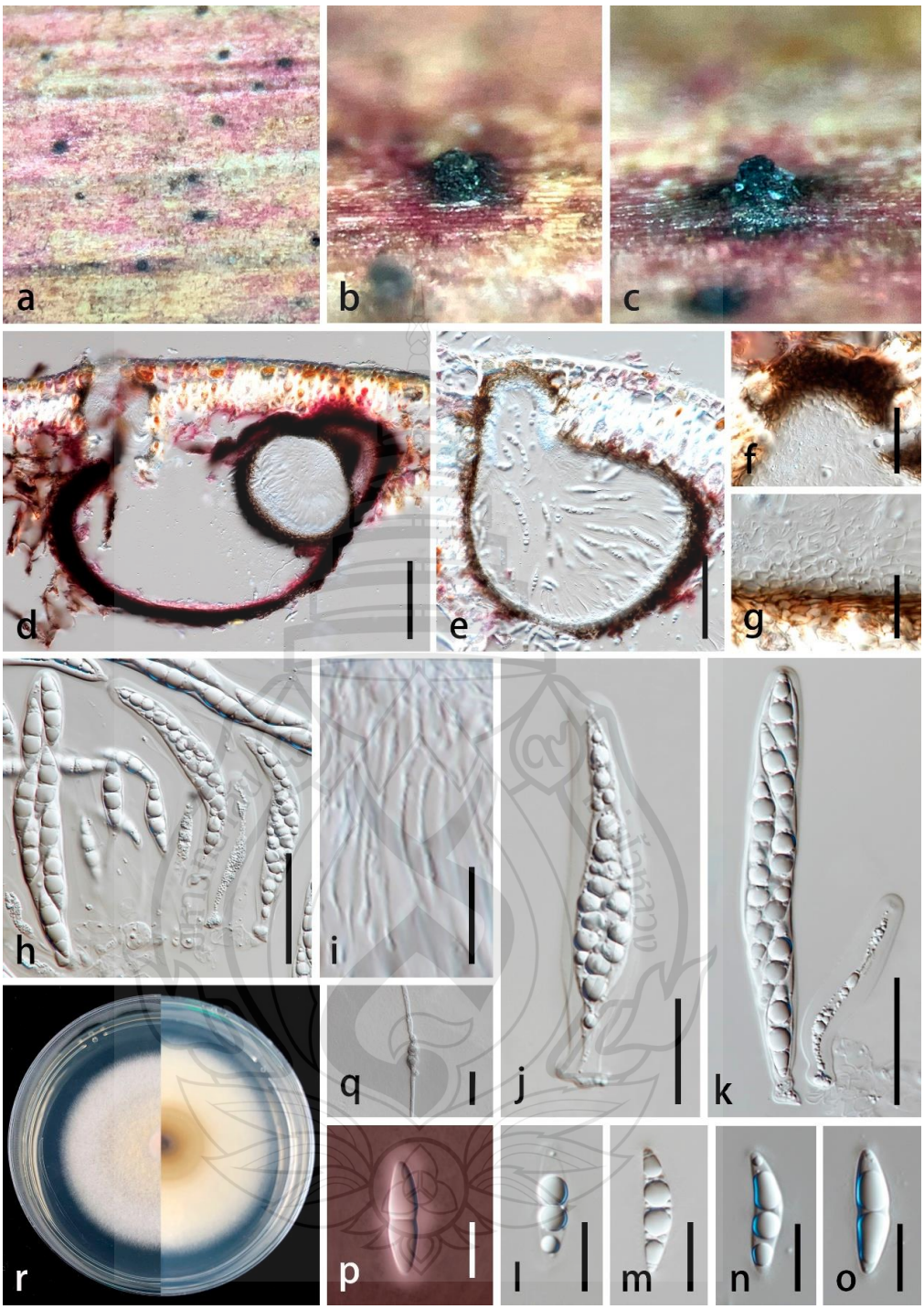
Saprobic on dead stems of *Wurfbainia villosa*. Sexual morph: from MHZU 23-0248: *Ascomata* 220–300 × 150–220 µm, solitary to scattered, immersed to semi-immersed, pyriform, black, papillate, stain the substrate purple, visible as black dots on the host surface. *Peridium* 13–30 µm thick ($\bar{x}$ = 19 µm, n = 20), composed of 6–12 layers, hyaline to brown cells of *textura angularis*. *Hamathecium* 1.5–4 µm wide ($\bar{x}$ = 3 µm, n = 30), comprises of dense, trabeculate, filiform, septate, branching pseudoparaphyses. *Asci* 65–100 × 9.5–15 µm ($\bar{x}$ = 81 × 12 µm, n = 20), 8-spored, bitunicate, cylindrical, with a rounded apex and narrower, short pedicellate, with an obscured ocular chamber. *Ascospores* 20–26 × 5–8 µm ($\bar{x}$ = 23.5 × 7 µm, n = 30), overlapping uniseriate, biseriate in the middle portion, fusiform, slightly curved, 1-septate, slightly constricted at the septum, narrowly rounded at both ends, hyaline, guttulate, smooth-walled, sur rounded by a mucilaginous sheath. Asexual morph from MHZU 23-0247: colonies superficial on the host substrate, hairy, solitary, gregarious, dark brown. *Conidiophores* 225–315 × 8–14 µm ($\bar{x}$ = 265 × 10 µm, n = 20), macronematous, mononematous, sometimes 1–2 cluster together on the stroma, erect, subcylindrical, with robust and swollen base, straight or slightly curved, 5–7-septate, black, unbranched, smooth-walled to slightly rough. *Conidiogenous cells* 7–11 × 5–9 µm ($\bar{x}$ = 8 × 6 µm, n = 10), holoblastic, polyblastic, with several prominent conidiogenous loci at the apex, integrated, determinate, terminal and intercalary, reddish brown to black, subcylindrical, verruculose. *Conidia* 3.5–7 µm diam. ($\bar{x}$ = 5 µm, n = 15), globose, aseptate, catenate, usually 6–8 conidia in a chain, initially hyaline, becoming yellowish brown and greenish brown, and reddish brown to dark brown at maturity, thick-walled and verruculose.

Culture characteristics – Ascospores from specimen number MHZU 23-0248 germinated on PDA within 24h, germ tubes produced from both ends. Colonies on PDA reaching 5.5 cm diam. after two weeks at room temperature (25 ± 2°C), medium dense, center umbonate, circular, center zone forming a clear bound with margin zone, floccose to fluffy, velvety, filiform edge, white from above, brown at the center, cream

at the margin from reverse. Conidia from specimen number MHZU 23-0247 germinated on PDA within 12–24 h, germ tubes produced from both ends. Colonies on PDA reaching 4.5 cm diam. after two weeks at room temperature (25 ± 2°C), medium dense, center umbonate, circular, floccose to fluffy, velvety, filiform edge, cream white from above, brown at the center, pale luteous at the margin from reverse. No reproduction structures of asexual morph or fruit bodies of a sexual morph on PDA.

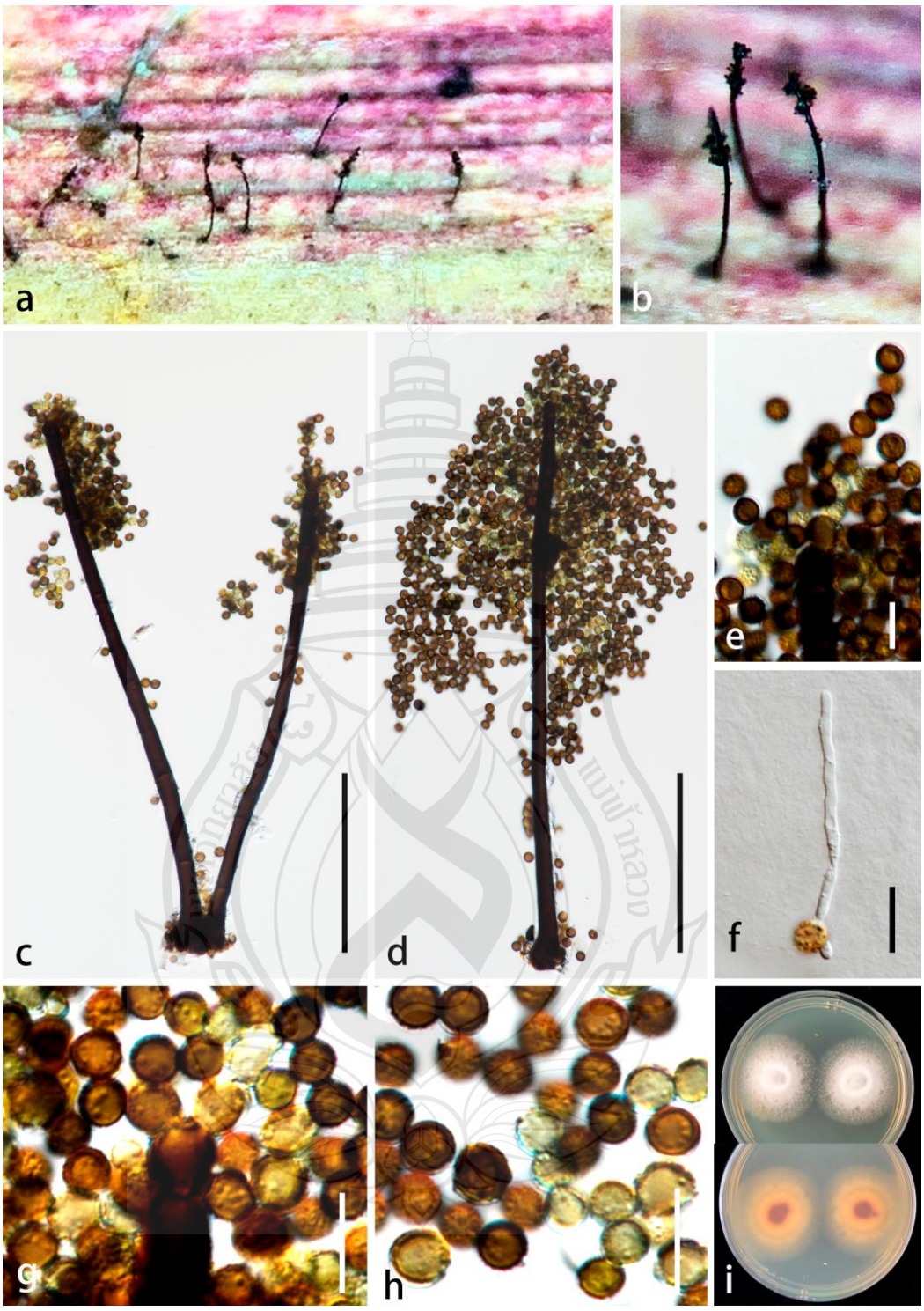
Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.32718988 N, 111.89251818 E), on dead stems of *Wurfbainia villosa*, 10 April 2022, C.F. Liao & Y.H. Yang, YAM28 (MHZU 23-0247, holotype); ex-type culture, ZHKUCC 23-0999; *ibid*., YAM29 (MHZU 23-0248), living culture ZHKUCC 23-1000.

Notes – In the phylogenetic analyses, *P. wurfbainiae* formed a distinct lineage from other *Periconia* species with 62% ML and 0.94 BYPP (Figure 5.17). *Periconia wurfbainiae* differs from its phylogenetically related species *P. variicolor* by having longer conidiophores (225–315 × 8–14 µm vs. 20–271 × 3–8 µm) and smaller conidia (3.5–7 µm vs. 7.5–9.5 µm). The conidiophores with a stipe and swollen apex is absent in *P. wurfbainiae*, whereas they are observed in *P. variicolor* (Cantrell et al., 2007). Moreover, the conidiophores of *P. wurfbainiae* are macronematous, dark brown to black, and smooth to slightly rough-walled. In contrast, *P. variicolor* has macronematous and micronematous conidiophores, initially subhyaline, becoming pale to dark brown at maturity, and smooth-walled (Crous et al., 2018). Based on the distinct morphological characteristics and phylogenetic support, we introduce *P. wurfbainiae* as a new species.



Note a–c Ascomata developing on *Wurfbainia villosa* stem. d, e Vertical section of an ascoma. f, g Section through the peridium. h, j, k Immature and mature asci. i Paraphyses. l–o Ascospores. p Ascospore in Indian ink. q Germinated ascospore. r Colony on PDA (front and below). Scale bars: d, h, i = 50 µm, e = 100 µm, f, g, j, k, q = 20 µm, (l–p) = 10 µm.

Figure 5.21 *Periconia wurfbainiae* sexual morph (MHZU 23-0248)



Note a, b Colonies on the host substrate. c, d Conidiophores with conidia. e, g Conidiogenous cell with conidia. f Germinated conidium. h Conidia. i Colony on PDA (front and below). Scale bars: c, d = 100 µm, e–h = 10 µm.

Figure 5.32 *Periconia wurfbainiae* asexual morph (MHZU 23-0247, holotype)

Periconia yangjiangensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.23

Index Fungorum number: IF851410; Facesoffungi number: FoF 15278

Etymology – In reference to the collection location, Yangjiang City, Guangdong Province of China.

Holotype – MHZU 23-0246

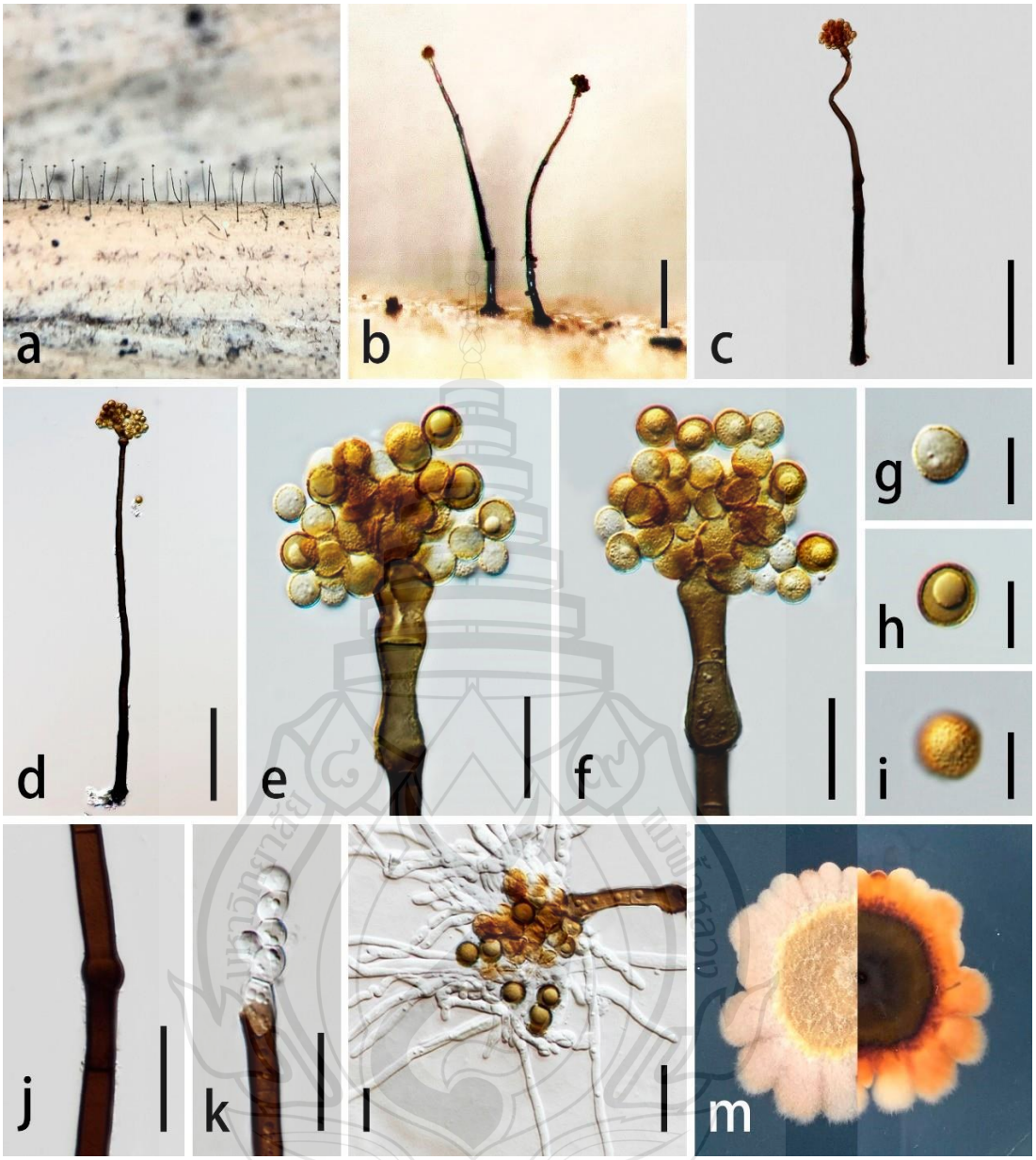
Saprobic on dead stems of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: colonies superficial on the host substrate, hairy, gregarious, dark brown. *Conidiophores* 275–420 × 5–15 µm ($\bar{x}$ = 355 × 10 µm, n = 20), macronematous, mononematous, erect, subcylindrical, tapering towards the apex, with robust base, straight or slightly flexuous, dark brown to black in the lower portion, brown in the upper portion, with 1–4 times of enteroblastic percurrent proliferating, forming 1–4 swollen, pyriform or dumbbell-shaped, dark brown or paler cells from a collar cell, unbranched, sparsely septate, smooth-walled, thick-walled. *Conidiogenous cells* 15–25 × 8–10 µm ($\bar{x}$ = 18 × 9 µm, n = 10), holoblastic, polyblastic, integrated, determinate, terminal, oblong, with a rounded apex, wider than conidiophores, brown, smooth-walled, thin-walled. *Conidia* 6–10 µm diam. ($\bar{x}$ = 7.5 µm, n = 30), globose, catenate, mostly with three conidia in a chain, aseptate, initially hyaline, becoming golden brown at maturity, thick-walled, verruculose.

Culture characteristics – Conidia germinating on PDA within 24h, germ tube produced from both ends. Colonies on PDA reaching 35–45 diam., after two weeks at room temperature (25 ± 2°C), medium dense, center raised, irregular, floccose to fluffy, velvety, lobate edge, golden brown at the center, pale brown at the margin from above and reverse.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.32718988 N, 111.89251818 E), on dead stems of *Wurfbainia villosa*, 10 April 2022, C.F. Liao & Y.H. Yang, YAM04 (MHZU 23-0246, holotype); ex-type culture, ZHKUCC 23-0997; *ibid*., living culture ZHKUCC 23- 23-0998.

Notes – *Periconia yangjiangensis* resembles *P. pseudobyssoides* in the morphologies of conidiophores and conidia on the natural substrate (Markovskaja & Kačergius, 2014; Su et al., 2023). However, conidia of *P. yangjiangensis* are initially hyaline, globose, becoming golden brown at maturity, and verruculose but they are golden yellow to golden brown or reddish brown, spherical, verruculose when young,

mature conidia with specific ornamentation consisting of irregular lobate crests in *P. pseudobyssoides* (Markovskaja & Kačergius, 2014; Su et al., 2023). The morphological characteristics of *P. yangjiangensis* were also compared with those of *P. endophytica* and *P. wurfbainiae*, which were isolated from the same host plant, *Wurfbainia villosa*. The conidiophores of *P. yangjiangensis* are macronematous, dark brown to black, and unbranched, while they are micro and semi macronematous, hyaline, and branched in *P. endophytica*. The conidia of *P. yangjiangensis* are golden brown with typically three conidia found in a chain while they are pale brown to golden brown and typically form a long chain consisting of 4 to 10 conidia in *P. endophytica*. However, morphological differences could occur as *P. yangjiangensis* were directly observed on a dead host plant while *P. endophytica* were observed in PDA. *Periconia yangjiangensis* differs from *P. wurfbainiae*, in having conidiophores mostly 1–4 times of enteroblastic percurrent proliferating, forming 1–4 swollen, dark brown to black, paler towards the apex, terminal conidiogenous cells, with mostly three conidia in a chain. In contrast, *P. wurfbainiae* has conidiophores that are not swollen at the terminal cells, dark brown to black, with both terminal and intercalary conidiogenous cells, usually 6–8 conidia in a chain. In addition, *P. yangjiangensis* can be distinguished from *P. wurfbainiae* by its longer conidiophores (275–420 × 5–15 µm vs. 225–315 × 8–14 µm) and larger conidiogenous cells (15–25 × 8–10 µm vs. 7–11 × 5–9 µm). In the phylogenetic analyses, *P. yangjiangensis* formed a distinct branch separated from other *Periconia* species with 95% ML, and 1.00 BYPP (Figure 5.17) indicating that *P. yangjiangensis* is distinct from other *Periconia* species. Based on morphological and phylogenetic support, we introduce *P. yangjiangensis* as a new species.



Note a, b Colonies on host substrate. c, d Conidiophore with conidia. e, f Swollen conidiophore, conidiogenous cell with conidia. g–i Conidia. j Swollen conidiophore. k Germinated conidiophore. l Germinated conidia. m Colony on PDA (front and below). Scale bars: b–d = 100 µm, e, f, j–l = 20 µm, g–i = 10 µm.

Figure 5.23 *Periconia yangjiangensis* (MHZU 23-0246, holotype)

Phaeosphaeriaceae M.E. Barr, Mycologia 71(5): 948 (1979)

Notes – Phaeosphaeriaceae (Pleosporales) comprises 87 genera and 801 species, though many species remain undescribed or poorly characterized (Wanasinghe et al., 2023; Hyde et al., 2024). This family was introduced by Barr (1979a) with *Phaeosphaeria* as the type genus. Members of Phaeosphaeriaceae have a cosmopolitan distribution and are frequently associated with monocotyledons, occurring as nectrotrophic or saprobic lifestyles. Many species in this family produce pycnidial coelomycetous asexual morphs, and detailed morphological descriptions are provided by Pem et al. (2024).

Setophoma Gruyter, Aveskamp & Verkley, in de Gruyter, Woudenberg, Aveskamp, Verkley, Groenewald & Crous, Mycologia 102(5): 1077 (2010)

Notes – *Setophoma* was introduced by de Gruyter (2010) to accommodate phoma-like species with setose conidiomata, with *S. terrestris* as the type species. Members of *Setophoma* are an important plant pathogens and endophytes (Liu et al., 2019b). The well-known species, *S. terrestris*, causes pink root rot and leaf spots in various crops, including onions, sugarcane (*Saccharum officinarum*), tea, and bamboo (Phookamsak et al., 2014; Yoshida, 2022). *Setophoma* typically produces pycnidial coelomycetous asexual morphs, characterized by setose conidiomata, phialidic conidiogenous cells and hyaline, ellipsoidal to subcylindrical conidia (de Gruyter, 2010; Liu et al., 2019). Currently, 17 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we describe a novel species, *Setophoma wurfbainiae*, isolated from roots of *Wurfbainia villosa*.

Setophoma wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.25

Index Fungorum number: IF904015; Facesoffungi number: FoF 17911

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0215

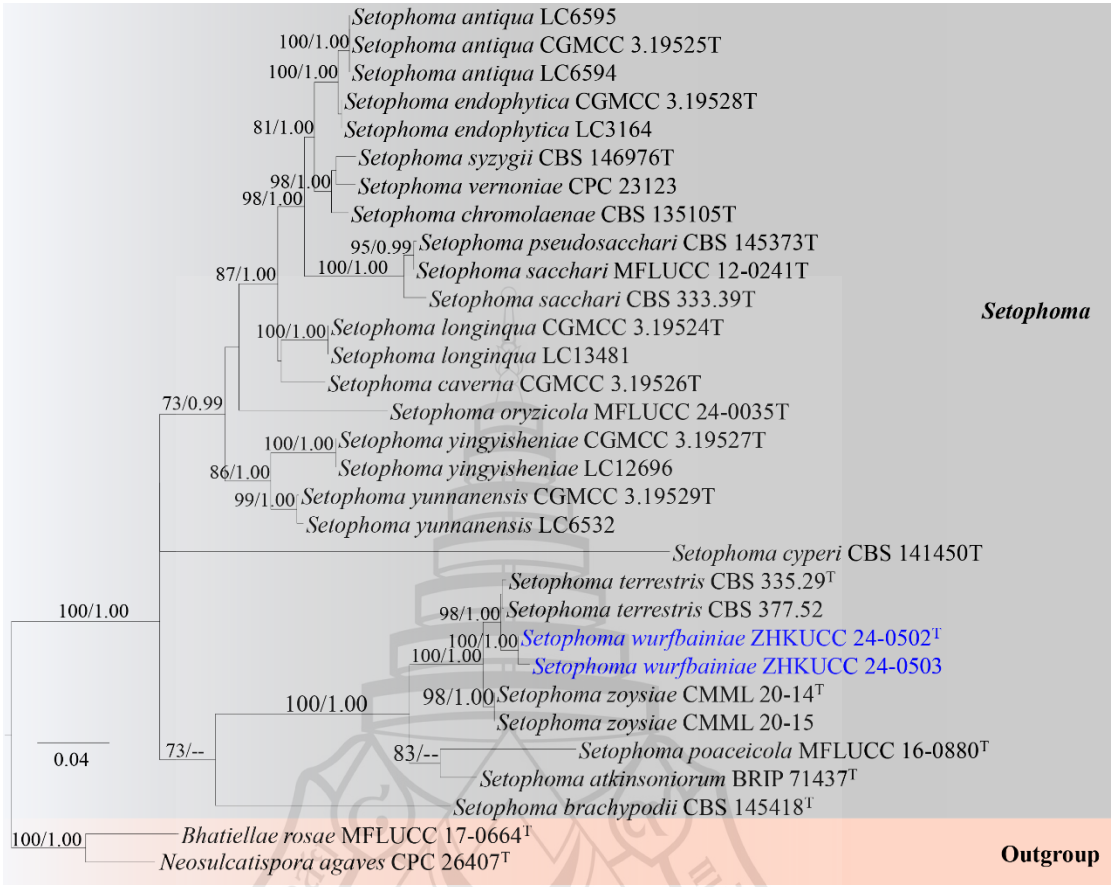
Endophytic in asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 2 months: *Conidiomata* 65–183 × 70–166 μm ($\overline{x}$ = 164 × 116 μm, n = 20), pycnidial, solitary, multi-locular, coriaceous, immersed to erumpent, subglobose to ellipsoidal, irregular, pale brown to dark brown. *Peridium* 11–27 μm wide ($\overline{x}$ = 17 μm, n = 20), composed of 5–12 layers of thin, hyaline

inner cells to thick, brown to dark outside cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 3.5–7 μm ($\overline{x}$ = 7 × 5.5 μm, n = 30), acute to papillate, cylindrical or irregular, hyaline, guttulate, smooth-walled. *Conidia* 4–5.5 × 2–3 μm ($\overline{x}$ = 5 × 2.5 μm, n = 30), globose to subglobose or oblong, hyaline, aseptate, 2–4-guttulate, apex rounded, straight to curved, smooth-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 4 weeks at 28 ± 2°C, moderately dense, flat, filiform, with white spots, pale purplish to pale brown from above, pale purplish to purplish with numerous dark purplish spots from reverse, with pink pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic roots of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR27A-1 (MHZU 24-0215, holotype); ex-type culture, ZHKUCC 24-0502; *ibid*., living culture ZHKUCC 24-0503.

Notes – In the phylogenetic analysis, ZHKUCC 24-0503 formed a sister branch with *Setophoma terrestris* (CBS 335.87 and CBS 377.52) with 98 ML/1.00 PP support (Figure 5.24). However, our isolate differs from *S. terrestris* in having smaller conidiomata (65–183 × 70–166 μm vs. 130–250 μm diam.). Moreover, the conidiomata of our strain are solitary, multi-locular, subglobose to ellipsoidal, irregular, without setae, but *S. terrestris* has globose and usually unilocular conidiomata, with setae (Boerema et al., 2004). The peridium of our strain consists of 5–12 layers, and lacks pigmentation, but *S. terrestris* comprises up to 2–5 layers, with pigmented outer layers. Furthermore, the conidia of our strain are globose to subglobose or oblong, more various, 2–4-guttulate, but *S. terrestris* are ellipsoidal to subcylindrical with usually 2 guttules. In additional, the culture characters of our isolate are pale purplish to pale brown with white spots from above, pale purplish to purplish with numerous dark purplish spots from reverse, while *S. terrestris* are pale olivaceous grey/grey olivaceous to dark herbage green/dull green from above, reverse dull green/olivaceous to leaden grey/leaden black from reverse. Hence, we introduce *S. wurfbainiae* as a novel species.



Note Tree rooted as *Bhatiellae rosae* (MFLUCC 17-0664) and *Neosulcatispora agaves* (CPC 26407). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.24 Maximum likelihood phylogeny based on the combined ITS, LSU, and *tub2* sequences data of *Setophoma*

Note a Culture characteristic on PDA for 4 weeks. b Appearance of conidiomata on PDA after 2 months. c, d Section through conidiomata. e Peridium. f–i Conidiogenous cells with conidia. j, k Conidia. Scale bars: d = 50 μm, e, f = 20 μm, g–i = 10 μm. j, k = 5 μm.

Figure 5.25 *Setophoma wurfbainiae* (MHZU 24-0215, holotype)

Pleosporaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 74 (1869)

Notes – Pleosporaceae was introduced by Nitschke (1869) with *Pleospora* as the type genus. Pleosporaceae represents a loculoascomycete family that usually comprises asexual morphs (Hyde et al., 2013). This family comprises a wide range of fungal species with diverse ecological roles, including plant pathogens, endophytes, saprophytes, and lichen associates (Zhang et al., 2022). Twenty-three genera and over 1000 species are accepted in Pleosporaceae (Wijayawardene et al., 2022). They have a cosmopolitan distribution, and some species produce secondary metabolites with potential pharmaceutical applications, such as antibiotics and anticancer compounds (Masi et al., 2022).

Alternaria Nees, Syst. Pilze (Würzburg): 72 (1816) [1816–17]

Notes – *Alternaria* is a major plant pathogen and a common allergen in humans. For example, *Alternaria alternata* can cause hay fever or hypersensitivity reactions, sometimes leading to asthma (Hernandez-Ramirez et al., 2021). Additionally, *Alternaria* species can be saprophytes and endophytes and are widely distributed in soil, plant debris, food storage, and indoor environments (Sánchez et al., 2022). *Alternaria* causes at least 20% of agricultural spoilage by producing potent toxic metabolites, which reduce the quantity and quality of fruit (Meena et al., 2017). *Alternaria* is characterized by pigmented (brown to dark green), multicellular, muriform conidia, typically borne in chains (Zhang et al., 2013). As of now, 858 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we report *Alternaria pogostemonis* as a new host record from *Wurfbainia villosa*, as detailed below.

Alternaria pogostemonis M. Luo, M.P. Zhao & Z.Y. Dong, in Luo et al. Pathogens 11(no. 1105): 5 (2022) Figure 5.27

Index Fungorum number: IF554928; Facesoffungi number: FoF 17912

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Colonies superficial, hairy, gregarious, black. *Conidiophores* 25–82 × 4–6 μm ($\bar{x}$ = 52 × 4.5 μm, n = 20), macronematous, mononematous, straight to slightly curved, filiform to cylindrical, terminal or intercalary, septate, branched, hyaline, smooth-walled. *Conidiogenous cells* 3–12 × 3–5 μm ($\bar{x}$ = 7 × 4 μm, n = 20), monoblastic or polyblastic, integrated, determinate, terminal, phialidic, oblong to cylindrical, straight to

slightly curved, mostly sympodially proliferating, geniculate-sinuous, hyaline to brown, smooth- and thick-walled, conidiogenous loci protuberant, thickened, bearing up to six conidiogenous loci. *Conidia* 16–28 × 8–13 µm ($\bar{x}$ = 20.5 × 11 µm, n = 30), catenate, ellipsoidal to ovoid, or cylindrical to subcylindrical, 3–5-conidia in a chain, usually with 1–4 transverse septa when young, becoming 1–4 transverse septa and 0–3 longitudinal septa when mature, sometimes forming V-shape or inverted V-shape, hyaline to pale brown, smooth-walled.

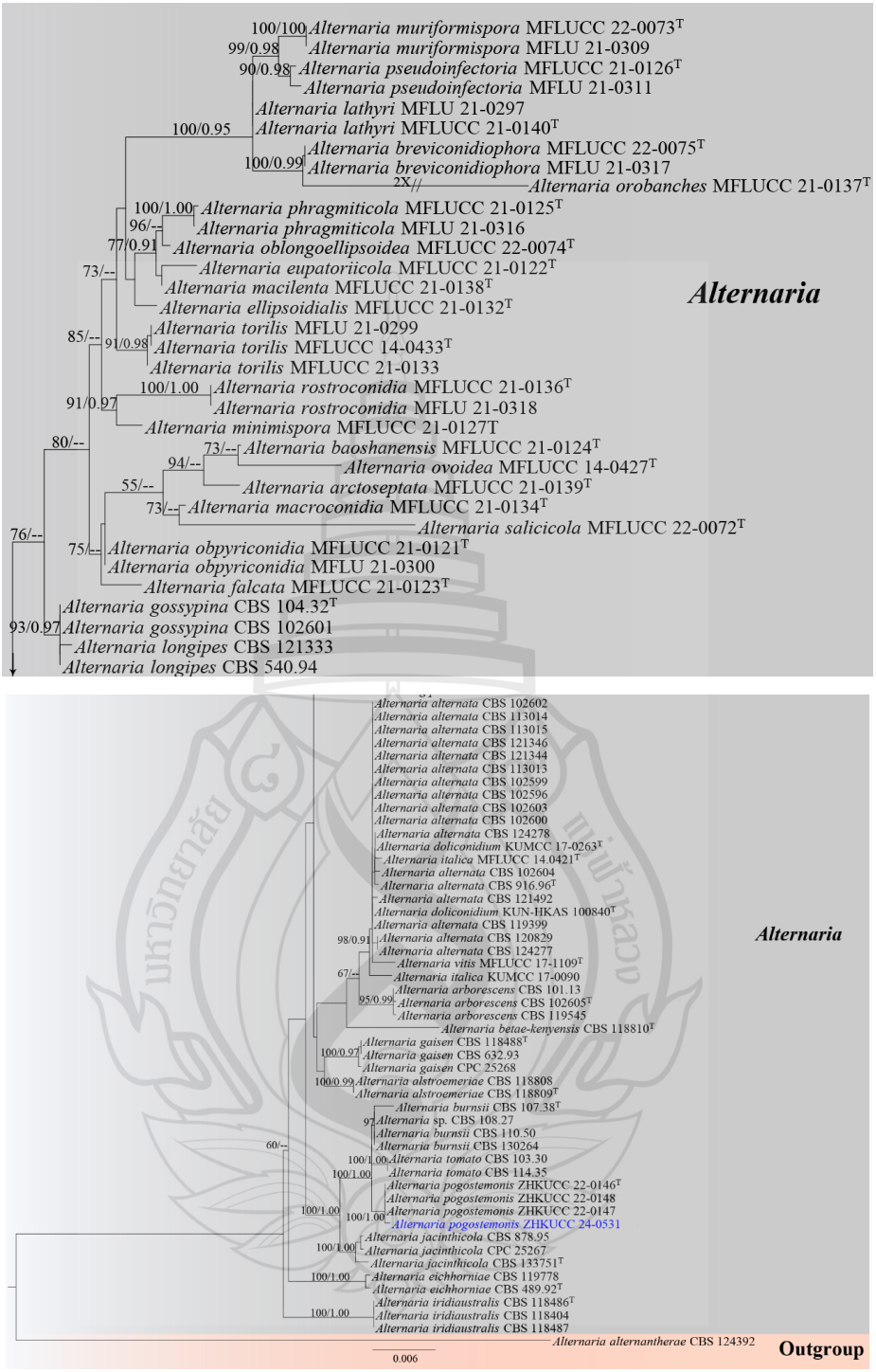
Culture characteristics – Colonies on PDA reaching 4.0–4.5 cm diameter in 1 week at 28 ± 2°C, medium dense, flat in center and undulating edges, circular, filiform, brown to pale brown from reverse, no pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR06A-4 (MHZU 24-0234); living culture, ZHKUCC 24-0531.

Known hosts (based on molecular data) – diseased leaves of *Pogostemon cablin* (Luo et al. 2022), *Wurfbainia villosa* (this study).

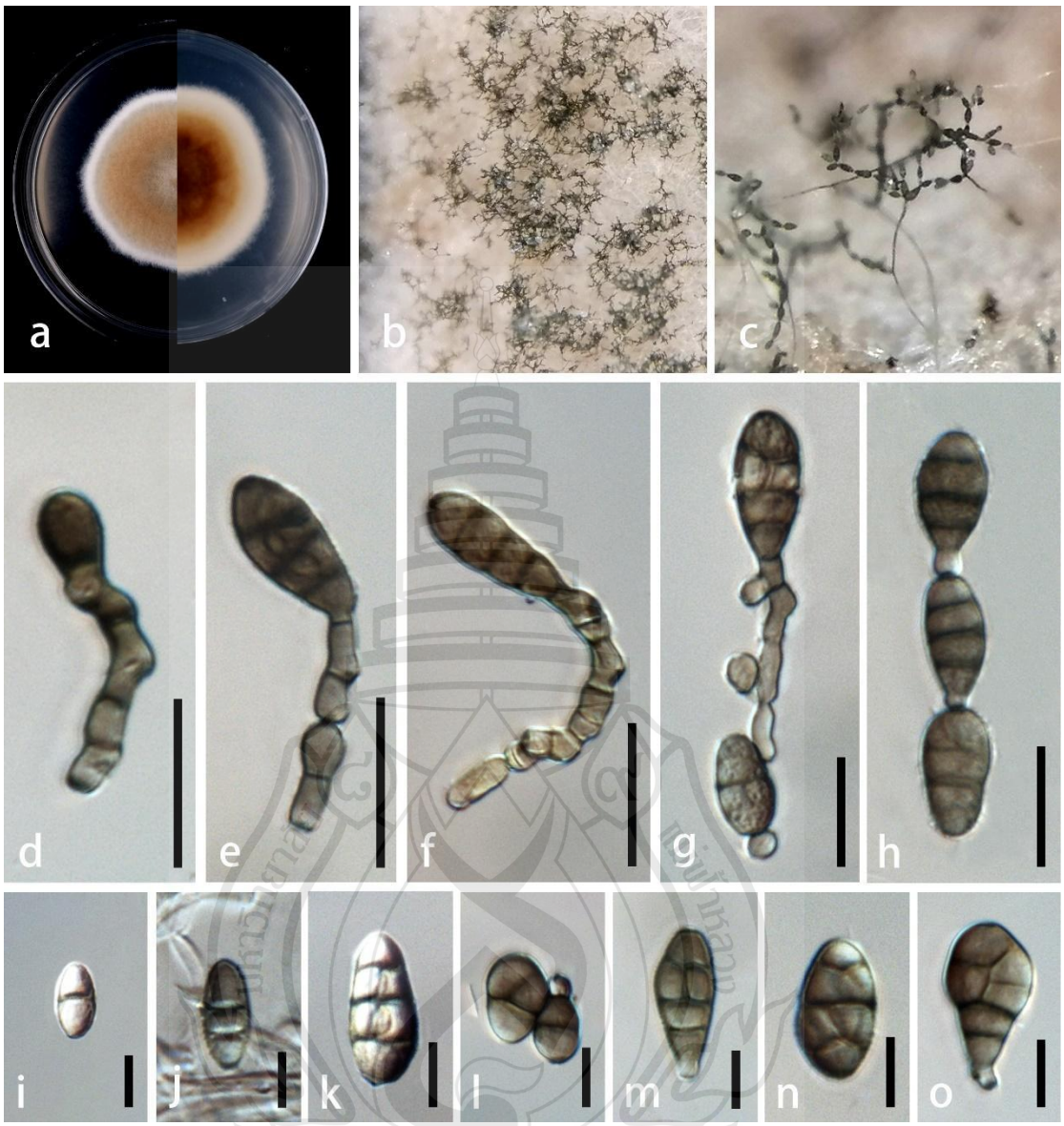
Known distribution (based on molecular data) – China (Luo et al., 2022; this study).

Notes – Phylogenetic analyses revealed that strain ZHKUCC 24-0531 clustered closely with *Alternaria pogostemonis* with 100% ML/1.00 PP support (Figure 5.26). Morphological comparison showed that our isolate resembles *A. pogostemonis* in having septate, branched conidiophores, and ovoid, cylindrical conidia, but has smaller conidia than *A. pogostemonis* (16–28 × 8–13 µm vs. 17–77 × 9–22 µm) (Luo et al. 2022). While *A. pogostemonis* was originally described from diseased leaves of *Pogostemon cablin*, our strain represents its first endophytic isolation from the asymptomatic root of *Wurfbainia villosa*.



Note Tree rooted as *Alternaria alternantherae* (CBS 124392). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strain from this study is shown in blue.

Figure 5.26 Maximum likelihood phylogeny based on the combined ITS, LSU, SSU, *tef1-α*, *rpb2*, *gapdh*, and *Alt-a1* sequences data of *Alternaria*



Note a Culture characteristic on PDA for 1 week. b, c Conidia on aerial mycelia on PDA after 1 month. d–g Conidiogenous cells with conidia. h–o Conidia. Scale bars: d–h = 20 μm, i–o = 10 μm.

Figure 5.27 *Alternaria pogostemonis* (MHZU 24-0234, new host record)

Bipolaris Shoemaker, Can. J. Bot. 37(5): 882 (1959)

Notes – *Bipolaris* was introduced by Shoemaker (1959) and typified by *B. maydis*. Many species in this genus are important plant pathogens causing leaf blights, leaf spots, melting outs, root rots, and fruit rots in various host plants (Manamgoda et al., 2014; Sun et al., 2020). Additionally, some species are saprobes, endophytes, or human

pathogens, such as *B. australiensis*, *B. hawaiiensis*, and *B. spicifera*, which are well-known causative agents of human diseases (Shoff & Perfect, 2021). *Bipolaris* is a dematiaceous hyphomycete and its asexual morph is known as *Cochliobolus* (Hyde et al., 2013). Phylogenetic analyses rely on the combined ITS, *gapdh*, and *tef1-α* sequences to distinguish the species within *Curvularia* (Manamgoda et al., 2014). Currently, 146 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we propose one new species *Bipolaris wurfbainiae* and one new host record *B. bicolor* from *Wurfbainia villosa*.

Bipolaris bicolor (Mitra) Shoemaker, Can. J. Bot. 37(5): 884 (1959) Figure 5.29

Index Fungorum number: IF293671; Facesoffungi number: FoF 17913

Endophytic in asymptomatic leaves and roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 2 months: *Colonies* superficial, erect, gregarious, with white and dark brown patches. *Conidiophores* 255–532 × 7–22 μm ($\overline{x}$ = 374 × 11.5 μm, n = 30), macronematous, mononematous, straight to curved, mostly geniculate at upper part, filiform, terminal or intercalary, septate, rarely branched, hyaline to brown, multi-guttulate, smooth-walled. *Conidiogenous cells* sympodially proliferating, polytretic, terminal or intercalary, with indistinct nodes, brown. *Conidia* 19–53 × 6–24 μm ($\overline{x}$ = 39 × 17 μm, n = 30), oblong to cylindrical, obclavate, with obtuse ends, usually two end cells narrower than middle cells, 2–6-distoseptate, multi-guttulate, pale brown to brown, smooth-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 1 month at 28 ± 2°C, moderately dense, raised, pulvinate, pale brown with scattered white and dark brown patches from the above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML22B-2 (MHZU 24-0176); living culture, ZHKUCC 24-0445.

Known hosts (based on molecular data) – *Andropogon aciculatus*, *Apluda aristata*, *Brachiaria ruziziensis*, *Eleusine coracana*, *Eragrostis japonica*, *Melanocenchris abyssinica*, *Oryza sativa*, *Panicum maximum*, *Pennisetum* sp., *P. glaucum*, *P. typhoides*, *Pennisetum clandestinum*, *Setaria* sp., *Sorghum* sp., *S. vulgare*, *Triticum aestivum*, *Urochloa panicoides*, Zea mays, *Zizania aquatica* (Poaceae), non-Poaceae hosts: *Quercus* sp.

(Fagaceae) (Manamgoda et al., 2014), *Eleusine indica* (Marin-Felix et al., 2017), Rubber tree (Liang et al., 2019), Tea plants (*Camellia sinensis* cv. *Fenghuang Dancong*) (Zhong et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Africa, Australia, Brazil, Canada, Cote d'Ivoire, Denmark, India, New Zealand, Nigeria, Swaziland, Zimbabwe (Manamgoda et al., 2014), China (Liang et al., 2019; Zhong et al., 2024; this study), Thailand (Marin-Felix et al., 2017).

Notes – The ZHKUCC 24-0445 is phylogenetically grouped in a cluster with *Bipolaris bicolor* (CBS 690.96, CPC 28811) with 100% ML/1.00 PP support (Figure 5.28). Morphologically, our isolate is similar to *B. bicolor*, characterized by simple or branched, septate, straight or curved conidiophores, and cylindrical to obclavate, brown conidia (Manamgoda et al., 2014). Hence, we identify our isolate as a new host on *Wurfbainia villosa* of *B. bicolor*.

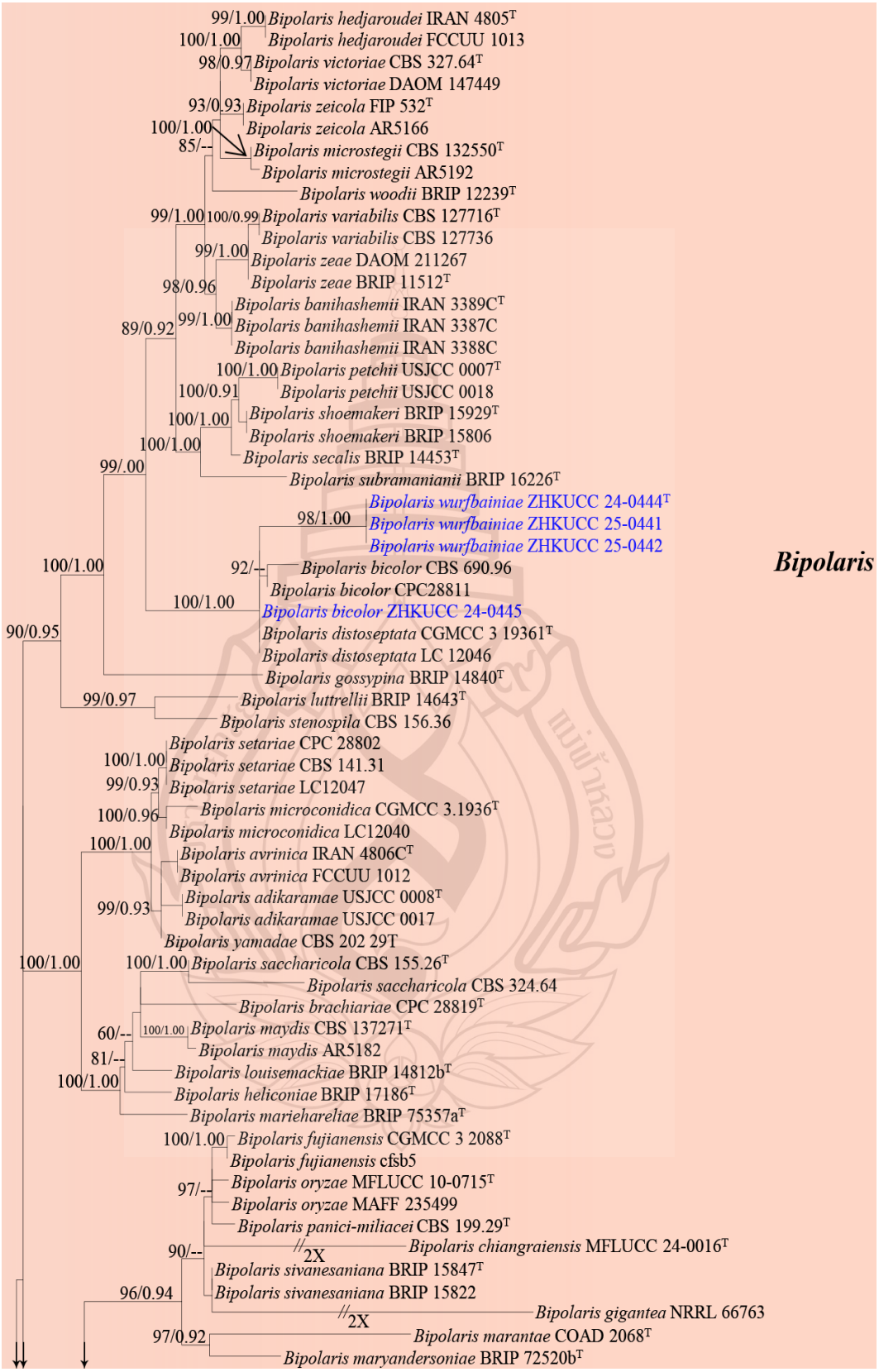
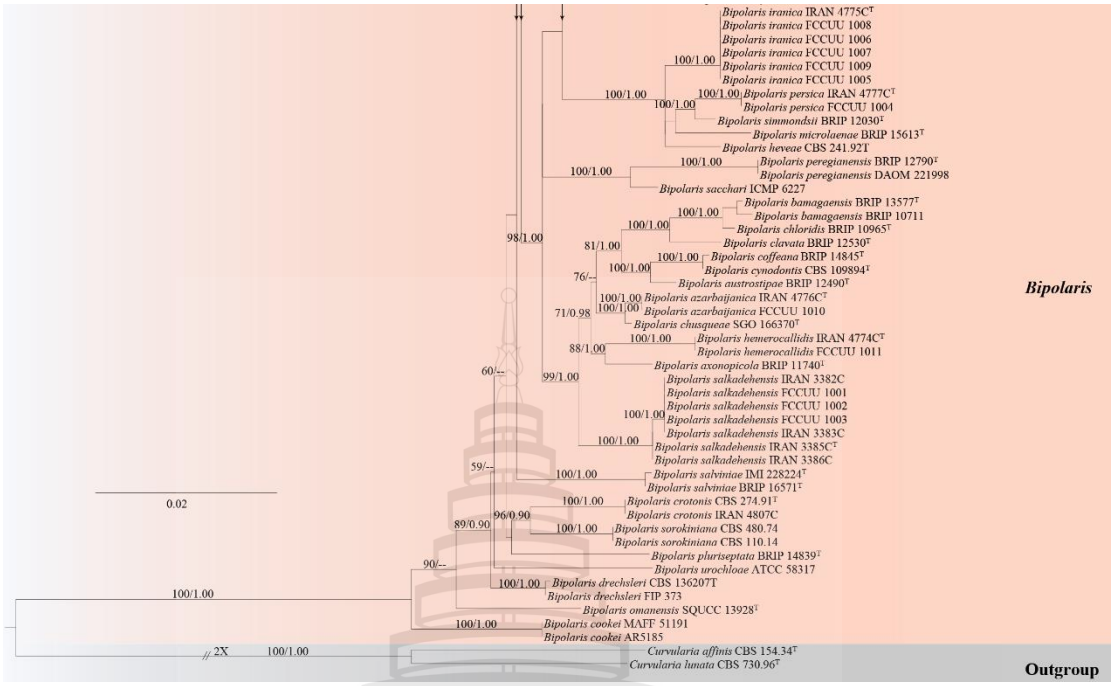


Figure 5.28 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *gapdh* sequences data of *Bipolaris*



Note Tree rooted with *Curvularia affinis* (CBS 154.34) and *C. lunata* (CBS 730.96). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.28 (continued)

Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d–g Conidiophores, conidiogenous cells with conidia. h Conidia. Scale bars: d–g = 50 μm, h = 20 μm.

Figure 5.29 *Bipolaris bicolor* (MHZU 24-0176)

Bipolaris wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.30

Index Fungorum number: IF904016; Facesoffungi number: FoF 17914

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

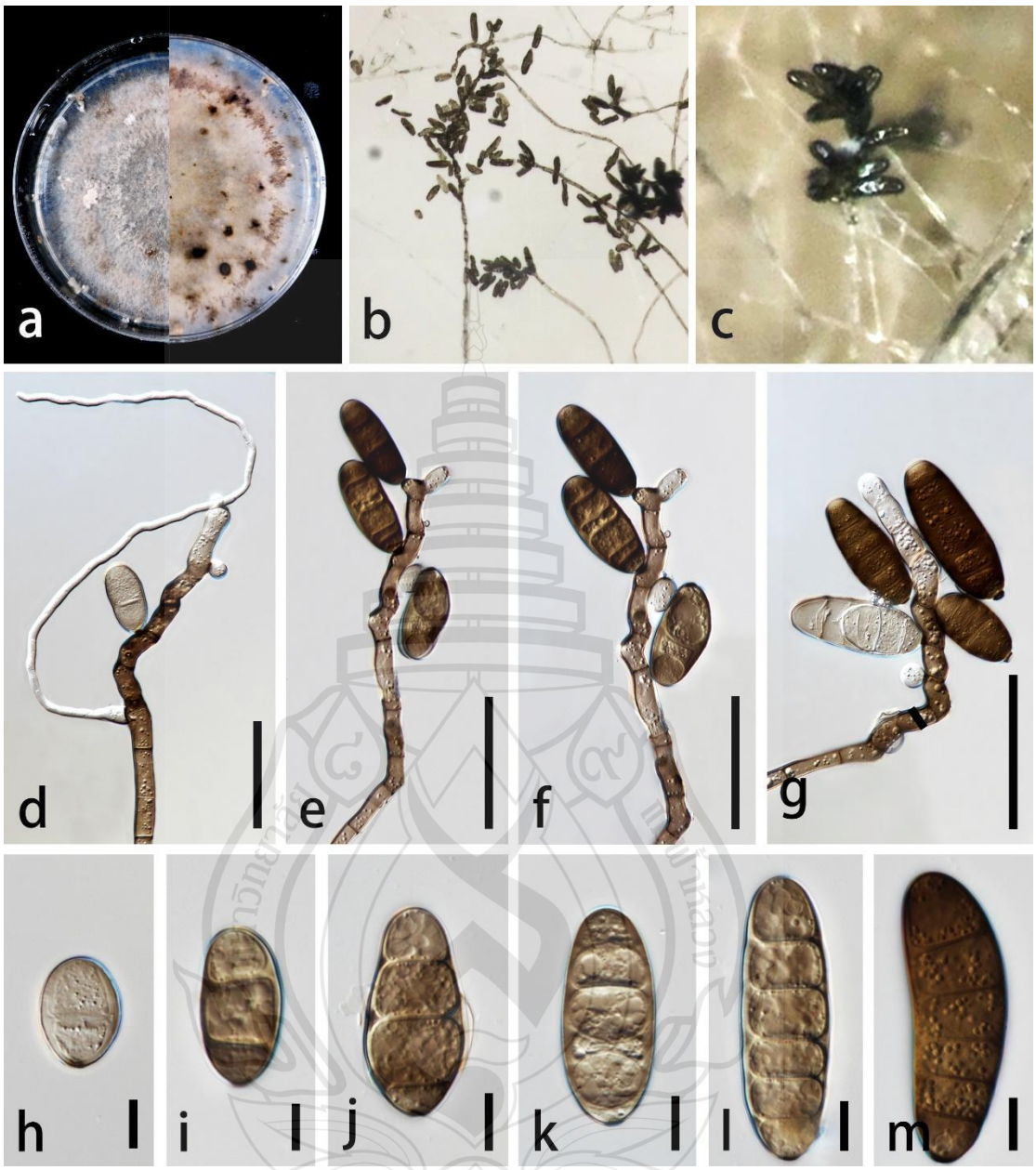
Holotype – MHZU 24-0175

Endophytic in asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Colonies superficial on the mycelium, solitary to gregarious, with black patches. *Conidiophores* 151–424 × 8.5–12.5 μm ($\bar{x}$ = 221 × 10.5 μm, n = 30), macronematous, mononematous, straight to curved, usually geniculate in the upper part, rarely straight, filiform, constricted at the upper part, septate, branched, hyaline to brown, smooth- and thick-walled. *Conidiogenous cells* sympodially proliferating, polytretic, terminal or intercalary, black node. *Conidia* 56–94 × 14–25 μm ($\bar{x}$ = 69 × 20 μm, n = 30), subglobose, oblong or cylindrical, obclavate to fusiform with obtuse ends, 2–8-distoseptate, multi-guttulate, pale brown to brown, smooth-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, flat, convex or umbonate, often pulvinate, velutinous, forming four radially and concentrically circular, gray to pale pink to pale brown to mouse gray from the above, pale brown to brown from the reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML08B-2 (MHZU 24-0175); living culture, ZHKUCC 24-0444; *ibid*., on asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, living culture AMR17A-2, AMR19A-3, ZHKUCC 25-0441, ZHKUCC 25-0442.

Notes – The strain (ZHKUCC 24-0444) is phylogenetically formed a sister clade with *Bipolaris distoseptata* (CGMCC 3.19361, LC12046) with 99% ML/0.99 PP support (Figure 5.28). Morphologically, *B. wurfbainiae* differs from *B. distoseptata* by having filiform, larger conidiophores (151–424 × 8.5–12.5 μm vs. 40–80 × 5–8 μm), constricted at the upper part, in contrast to elongate-ampulliform conidiophores, constricted at the base, lighter towards apex of the latter (Raza et al., 2019). The conidia of *B. wurfbainiae* are subglobose, oblong or cylindrical, obclavate to fusiform, pale brown to brown, and bigger (56–94 × 14–25 μm vs. 22–65 × 8.5–18.5 μm), however, *B. distoseptata* are ellipsoid, oblong or cylindrical, pale brown to dark brown, hyaline when young. Hence, we introduce *B. wurfbainiae* as a novel species.



Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on PDA after 2 months. d–g Conidiogenous cells with conidia. h–m Conidia. Scale bars: d–g = 50 μm, h–m = 10 μm.

Figure 5.30 *Bipolaris wurfbainiae* (MHZU 24-0175, Holotype)

Curvularia Boedijn, Bull. Jard. bot. Buitenz, 3 Sér. 13(1): 123 (1933)

Notes – *Curvularia* comprises species with diverse ecological roles, including plant pathogens, opportunistic human pathogens, saprophytes, endophytes, or soil-inhabiting fungi (Manamgoda et al., 2014). *Curvularia* species are mostly reported as

filamentous fungi with *Cochliobolus* sexual morphs. *Curvularia* and *Bipolaris* have various host ranges and mainly infect Poaceae, especially rice (Manamgoda et al., 2011). Although *Bipolaris* and *Curvularia* share many morphological similarities, they can be distinguished through phylogenetic analysis using the combined ITS, GAPDH, and *tef1-α* sequences. Currently, 248 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we report two new host records of *C. geniculata* and *C. plantarum* and one new species *Curvularia wurfbainiae* from *Wurfbainia villosa*, as detailed below.

Curvularia geniculata (Tracy & Earle) Boedijn, Bull. Jard. bot. Buitenz, 3 Sér. 13(1): 129 (1933) Figure 5.32

Index Fungorum number: IF265873; Facesoffungi number: FoF 16747

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on the sterile pine needles on PDA after 6 weeks of incubation. *Hyphae* 2.5–6 µm wide ($\bar{x}$ = 4.5 µm, n = 20), pale brown, septate, branched, smooth-walled. *Conidiophores* 75–345 × 4–8 µm ($\bar{x}$ = 198 × 6 µm, n = 20), macronematous, mononematous, solitary or gregarious, flexuous, branched, brown, septate, smooth-walled. *Conidiogenous cells* 3.5–11 × 3–6.5 µm ($\bar{x}$ = 7 × 5 µm, n = 30), polyblastic, integrated, terminal or lateral, subcylindrical, truncate at the apex, hyaline to pale brown, smooth-walled. *Conidia* 20–34 × 10–22 µm ($\bar{x}$ = 26 × 14 µm, n = 30), reniform, straight or curved, hyaline to pale brown in terminal cells, and pale brown to dark brown in median cells, 2–4-septate, middle cells enlarged, smooth- and thick-walled.

Culture characteristics – Colonies on PDA reaching 8.0–8.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, flat, circular, filiform, velutinous, granular, large droplets of water exuded from the mycelial surface, pale brown from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR02B-4 (MHZU 24-0218); living culture, ZHKUCC 24-0514.

Known hosts (based on molecular data) – *Amomum corynostachyum* (Thaung 2008), *Bletilla striata* (Xie et al. 2023), coffee leaf (Nam et al. 2024), *Costus igneus*

(Somasekhara et al. 2024), *Oryza australiensis*, *Oryza sativa* (Pak et al. 2017), *Vitis* sp. (Jayawardena et al. 2018), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Australia (Pak et al., 2017), Burma, Myanmar (Thaung, 2008), India (Somasekhara et al., 2024), South Korea (Nam et al., 2024), China (Xie et al., 2023, this study).

Notes – The phylogenetic analyses revealed that our strain ZHKUCC 24-0514 clusters with *Curvularia geniculata* with 100 ML/1.00 PP support (Figure 5.31). Morphologically, our isolate resembles *Cu. geniculata*, characterized by flexuous, septate conidiophores and straight or curved conidia, which are usually 4-septate and abruptly geniculate at the enlarged central cell. *Curvularia geniculata* (originally described as *Helminthosporium geniculatum*) was first isolated from spikelets of *Eragrostis rachitricha* in Mississippi, USA (Tracy & Earle, 1896). This species has later been reported from various hosts (see Known hosts). In this study, our strain was isolated from *Wurfbainia villosa*, which represents a new host record.

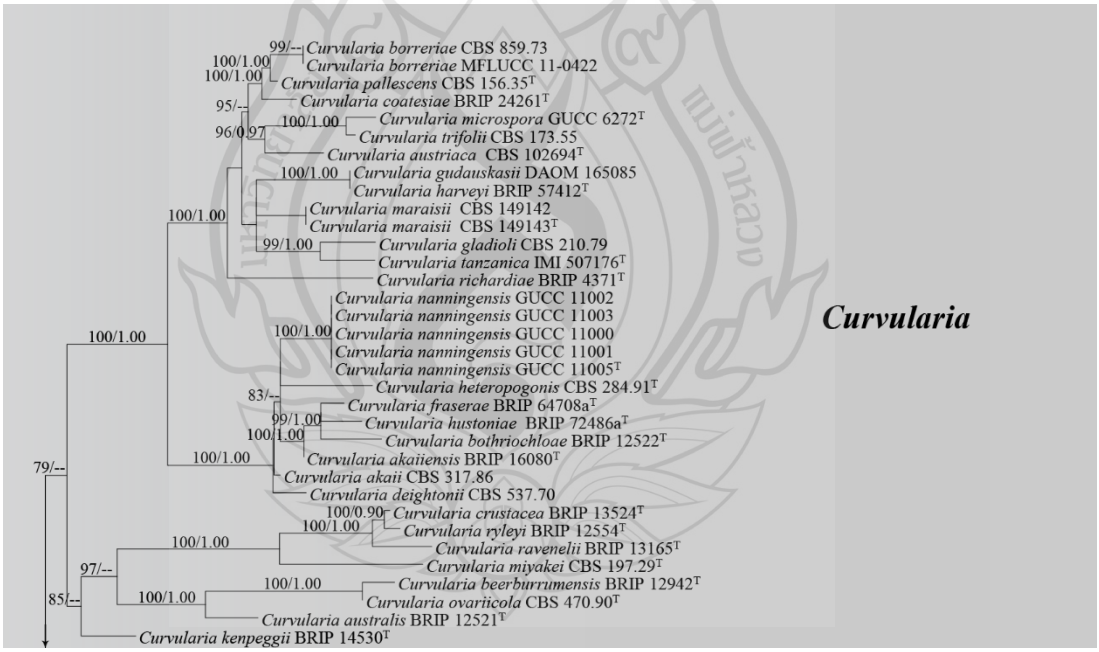


Figure 5.31 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *gapdh* sequences data of *Curvularia*

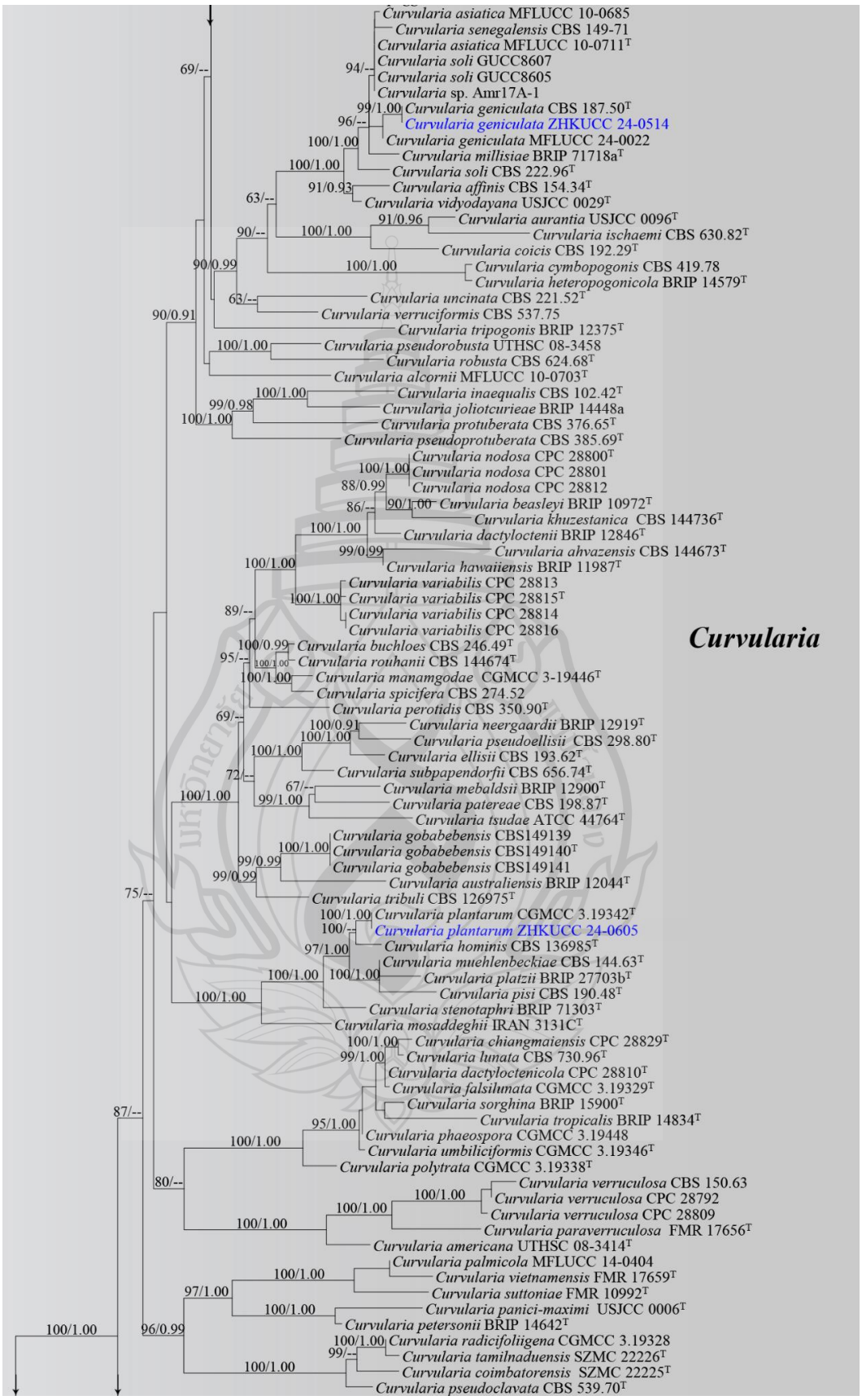
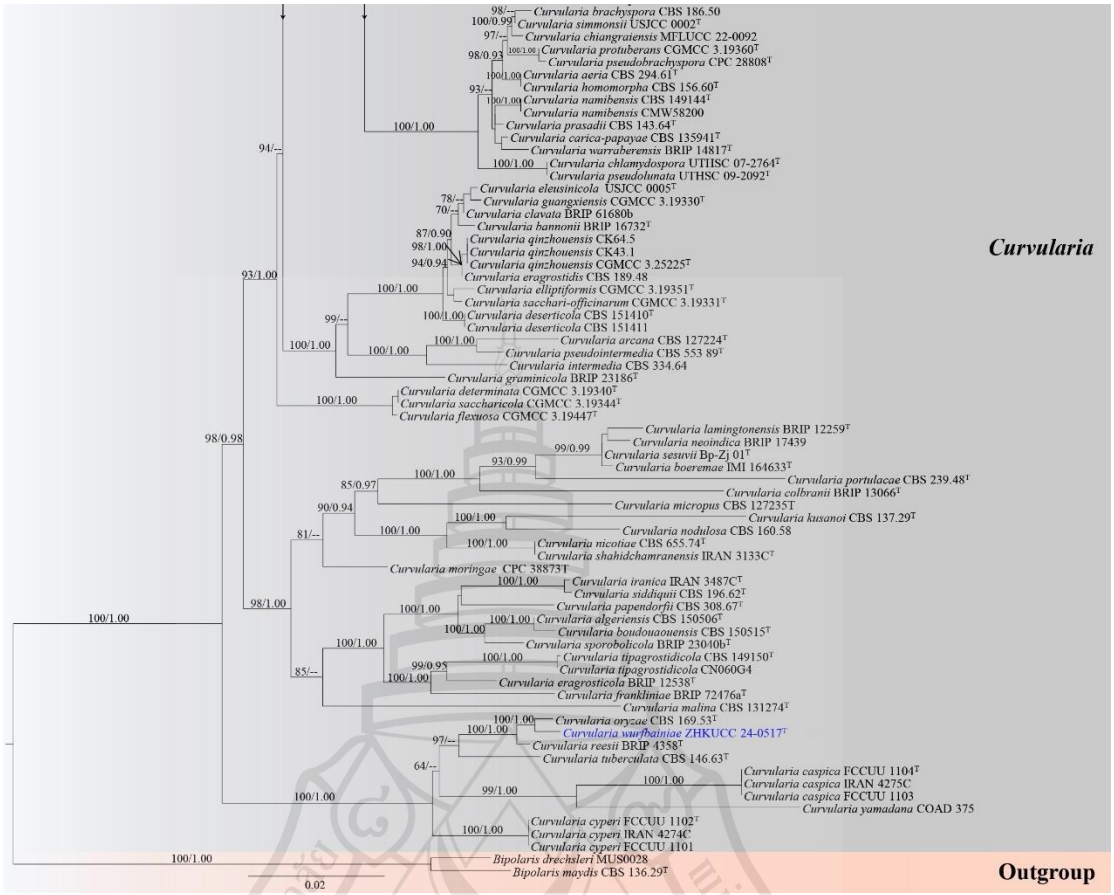
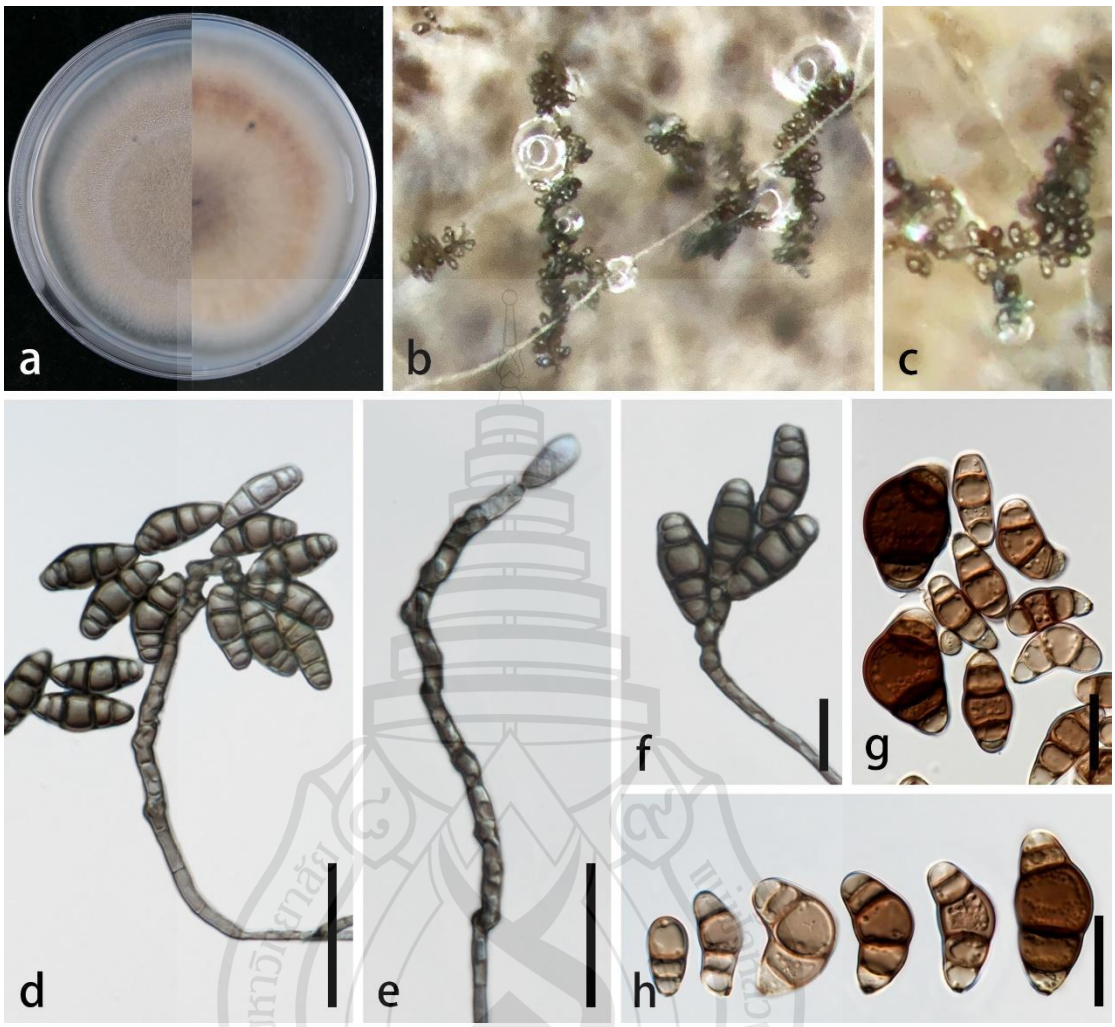


Figure 5.31 (continued)



Note Tree rooted as *Bipolaris drechsleri* (MUS0028) and *Bipolaris maydis* (CBS 136.29). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.31 (continued)



Note a Culture characteristic on PDA for 2 weeks. b, c Conidia on aerial mycelia on PDA after 6 weeks. d–f Conidiogenous cells with conidia. g, h Conidia. Scale bars: d, e = 50 µm, f–h = 20 µm.

Figure 5.32 *Curvularia geniculata* (MHZU 24-0218, new host record)

Curvularia plantarum Raza, K.D. Hyde & L. Cai, in Raza et al., Fungal Diversity 99: 61 (2019) Figure 5.33

Index Fungorum number: IF556664; Facesoffungi number: FoF 06154

Disease associated with leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after 6 weeks of incubation. *Hyphae* 3–5.5 µm wide ($\bar{x}$ = 4 µm, n = 20), hyaline to pale brown, septate, branched, smooth-walled. *Conidiophores* 95–467 × 5–10 µm ($\bar{x}$ = 175 × 8 µm, n = 30), macronematous, mononematous, solitary or gregarious, straight to flexuous, branched,

mostly pale brown, rarely olivaceous green, septate, guttulate, constricted at upper portion, smooth-walled. *Conidiogenous cells* 6–12 × 4–8 μm ($\overline{x}$ = 9 × 6 μm, n = 30), polytretic, integrated, terminal or lateral, subcylindrical, with rounded apex, pale brown, smooth-walled. *Conidia* 18–30 × 10.5–18.5 μm ($\overline{x}$ = 23 × 14 μm, n = 30), amygdaliform to obovoid, sometimes reniform straight to slightly curved, 1–3-septate, pale brown to dark brown, rarely olivaceous green, thick- and smooth-walled.

Culture characteristics – Colonies on PDA reaching 3.0–3.5 cm diameter in 1 week at 28 ± 2°C, moderately sparse, loose, raised, circular, with entire edge, filiform, velutinous, cream-white from above, pale brown to olivaceous green from reverse, without pigmentation.

Material examined –China, Guangdong Province, Guangzhou City, Zhongkai University (23.10643 N, 113.28240 E), from disease leaf of *Wurfbainia villosa*, 30 October 2023, C.F. Liao, YP03B2 (MHZU 24-0296); living culture, ZHKUCC 24-0605.

Known hosts (based on molecular data) – *Eleusine coracana*, *Oryza sativa*, *Panicum virgatum*, *Paspalum* sp. (Ferdinandez et al., 2021), *Saccharum officinarum* (Raza et al., 2019), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Sri Lanka (Ferdinandez et al., 2021), China (Raza et al., 2019, this study)

Notes – The phylogenetic analysis indicated that our strain ZHKUCC 24-0605 clusters with *Curvularia plantarum* (CGMCC 3.19342) with 100% ML/1.00 PP support (Figure 5.31). Morphologically, our isolate is most similar to *Cu. plantarum* by having polytretic, terminal or lateral, subcylindrical conidiophores (6–12 × 4–8 μm vs. 4–15 × 3.5–6 μm), with four cells, ellipsoidal to obovoid, distoseptate, straight or slightly curved conidia (18–30 × 10.5–18.5 μm vs. 13.5–26 × 5.5–12.5 μm). However, our isolate slightly differs in having longer conidiophores (95–467 × 5–10 μm), smooth-walled, mostly pale brown, rarely olivaceous green, whereas those in the holotype of *Cu. plantarum* (Raza et al., 2019) are shorter (95–135 × 2.5–4 μm), verruculose, subhyaline to brown. *Curvularia plantarum* was initially isolated from *Saccharum officinarum* in China (Raza et al., 2019) and subsequently reported from a variety of hosts (see Known hosts). In this study, our strain was isolated from *Wurfbainia villosa*, which represents a new host record.

Note a Culture characteristic on PDA for 1 week. b, c Conidia on aerial mycelia on PDA after 6 weeks. d–h Conidiogenous cells with conidia. i Conidia. Scale bars: d = 100 μm, e–h = 20 μm, i = 10 μm.

Figure 5.33 *Curvularia plantarum* (MHZU 24-0296, new host record)

Curvularia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.34

Index Fungorum number: IF904017; Facesoffungi number: FoF 17915

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0225

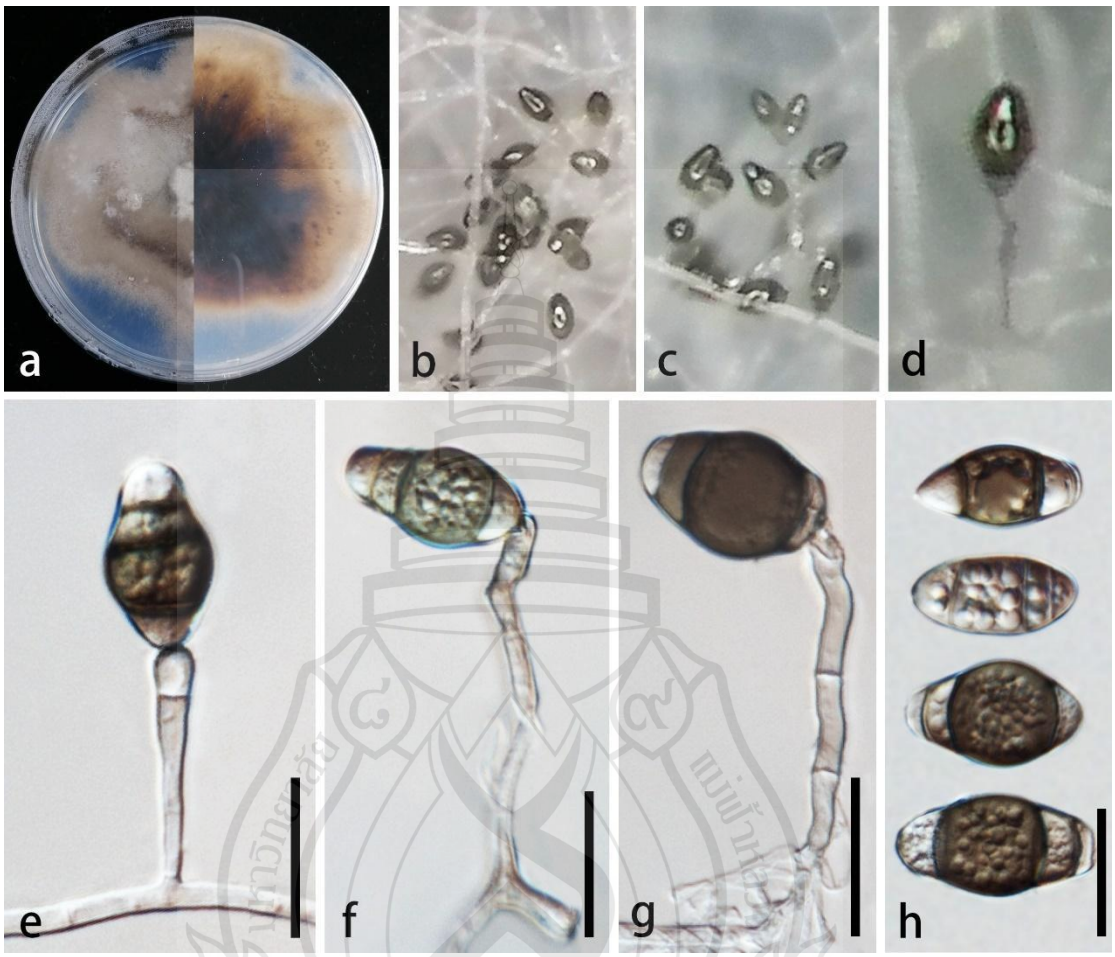
Endophytic associated with asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after 2 months of incubation. *Hyphae* 3–5 µm wide ($\overline{x}$ = 4 µm, n = 20), hyaline to pale brown, septate, branched, smooth-walled. *Conidiophores* 31–91 × 3–8.5 µm ($\overline{x}$ = 57 × 5 µm, n = 30), micronematous, mononematous, solitary or gregarious, straight to flexuous, unbranched, pale brown, septate, smooth-walled. *Conidiogenous cells* 10–33 × 3–6.5 µm ($\overline{x}$ = 19.5 × 4 µm, n = 30), monoblastic, integrated, determinate, terminal or lateral, subcylindrical, hyaline, with a rounded apex, smooth-walled. *Conidia* 20–24 × 10–15 µm ($\overline{x}$ = 22 × 12 µm, n = 30), ellipsoidal to ovoid, straight or curved, initially hyaline to pale brown, becoming hyaline to pale brown in terminal cells, brown to dark brown in median cells at maturity, 2–3-septate, middle cells enlarged, multi-guttulate, thick- and smooth-walled.

Culture characteristics – Colonies on PDA reaching 8.0–8.5 cm diameter in 4 weeks at 28 ± 2°C, moderately dense, flat, irregular, filiform, dry, pale brown to pale brown from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS12C-4 (MHZU 24-0225, holotype); ex-type culture, ZHKUCC 24-0517.

Notes – The phylogenetic study revealed that *Curvularia wurfbainiae* is closely related to *Cu. oryzae* and forms a sister branch with 100 ML/1.00 PP support (Figure 5.31). Morphologically, *Cu. wurfbainiae* differs from *Cu. oryzae* in having smaller conidiophores (31–91 × 3–8.5 µm vs. 40–400 × 3–8 µm) and smaller conidia (20–24 × 10–15 µm vs. 20–37.5 × 11–21.5 µm) (Marin-Felix et al., 2020). In addition, the conidia of *Cu. wurfbainiae* are oblong to ovoid, smooth-walled, with multiple guttules, however, *C. oryzae* has ellipsoidal to broadly ellipsoidal or obovoid, smooth-walled to

finely verruculose conidia, lacking guttules, Hence, we introduce *Cu. wurfbainiae* as a novel species.



Note a Culture characteristic on PDA after 4 weeks. b–d Conidia on aerial mycelia on PDA after 2 months. e–g Conidiogenous cells with conidia. h Conidia. Scale bars: e–h = 20.

Figure 5.34 *Curvularia wurfbainiae* (MHZU 24-0225, holotype)

Roussoellaceae J.K. Liu, Phook., D.Q. Dai & K.D. Hyde, in Liu et al., Phytotaxa 181(1): 7

Notes – Roussoellaceae was introduced by Liu et al. (2014) to accommodate the genera *Neoroussoella*, *Roussoella*, and *Roussoellopsis*. Members of this family are mainly saprobic, but they can also be pathogenic or endophytic. They are commonly associated with woody plants, monocots, and bamboo (Yang et al., 2024). Currently, 12 genera are recognized in the family, with *Roussoella* as the type genes (Hyde et al.

2024). Morphological descriptions follow Hyde et al. (2013), Liu et al. (2014), Hongsanan et al. (2020), and Pem et al. (2024).

Neoroussoella J.K. Liu, Phook. & K.D. Hyde, in Liu et al., Phytotaxa 181(1): 21 (2014)

Notes – *Neoroussoella* was established by Liu et al. (2014), with *N. bambusae* designated as the type species. Most species in this genus are saprobes with various host ranges. The genus has been reported to include both sexual and asexual morphs. The phylogenetic analyses are based on the combined ITS, LSU, SSU, *tef1-α,* and *rpb2* sequences (Htet et al., 2024). At present, 16 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we report *Neoroussoella leucaenae* as a new host record from *Wurfbainia villosa* in China.

Neoroussoella leucaenae Jayasiri, E.B.G. Jones & K.D. Hyde, in Jayasiri et al., Mycosphere 10(1): 106 (2019) Figure 5.36

Index Fungorum number: IF555570; Facesoffungi number: FoF 05277

Endophytic in asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: Sporulating on PDA with sterilized leaf tissues of *Wurfbainia villosa* after 3 months of incubation, *Conidiomata* 75–200 × 150–320 μm ($\bar{x}$ = 143 × 230 μm, n = 10), solitary, erumpent to superficial, subglobose, appearing as black spots on culture, with ostiole. *Conidiomata walls* 5.5–22 μm wide ($\bar{x}$ = 10.5 μm, n = 30), composed of 2-6 layers of inner hyaline to outer brown cells of textura prismatica or textura angularis, thick-walled. *Conidiophores* 2.5–4.5 μm wide ($\bar{x}$ = 3.5 μm, n = 30), aseptate, branched, hyaline to pale brown. *Conidiogenous cells* globose, polyoblastic, gregarious, lateral, aseptate, hyaline. *Conidia* 4–5.5 × 2–3 μm ($\bar{x}$ = 5 × 2.5 μm, n = 30), oblong, rounded at both ends, hyaline, aseptate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 5.0–5.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, raised, circular, with entire edge, velutinous, cream-white from above; brown circle in center towards to cream-white from the reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML12C-2 (MHZU 24-0195); living culture, ZHKUCC 24-0475.

Known hosts (based on molecular data) – *Leucaena* sp., *Pterocarpus* sp. (Jayasiri et al., 2019), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Thailand (Jayasiri et al., 2019), China (Raza et al., 2019, this study)

Notes – The strain ZHKUCC 24-0475 clustered with *Neoroussoella leucaenae* with 99 ML/0.99 PP (Figure 5.35). Our phylogenetic results are consistent with Htet et al. (2024). Morphologically, our isolate closely resembles *N. leucaenae* in having pale brown, subcylindrical, oblong to ovoid, aseptate conidia with rounded ends. Moreover, our isolate differs from *N. leucaenae* in having larger conidiomata (150–320 × 75–200 µm vs.135–175 × 120–180 µm vs. 150 µm diam.) (Jayasiri et al., 2019). Based on phylogenetic analyses and morphological similarity, we identify our isolate as *N. leucaenae*, representing a new host record.

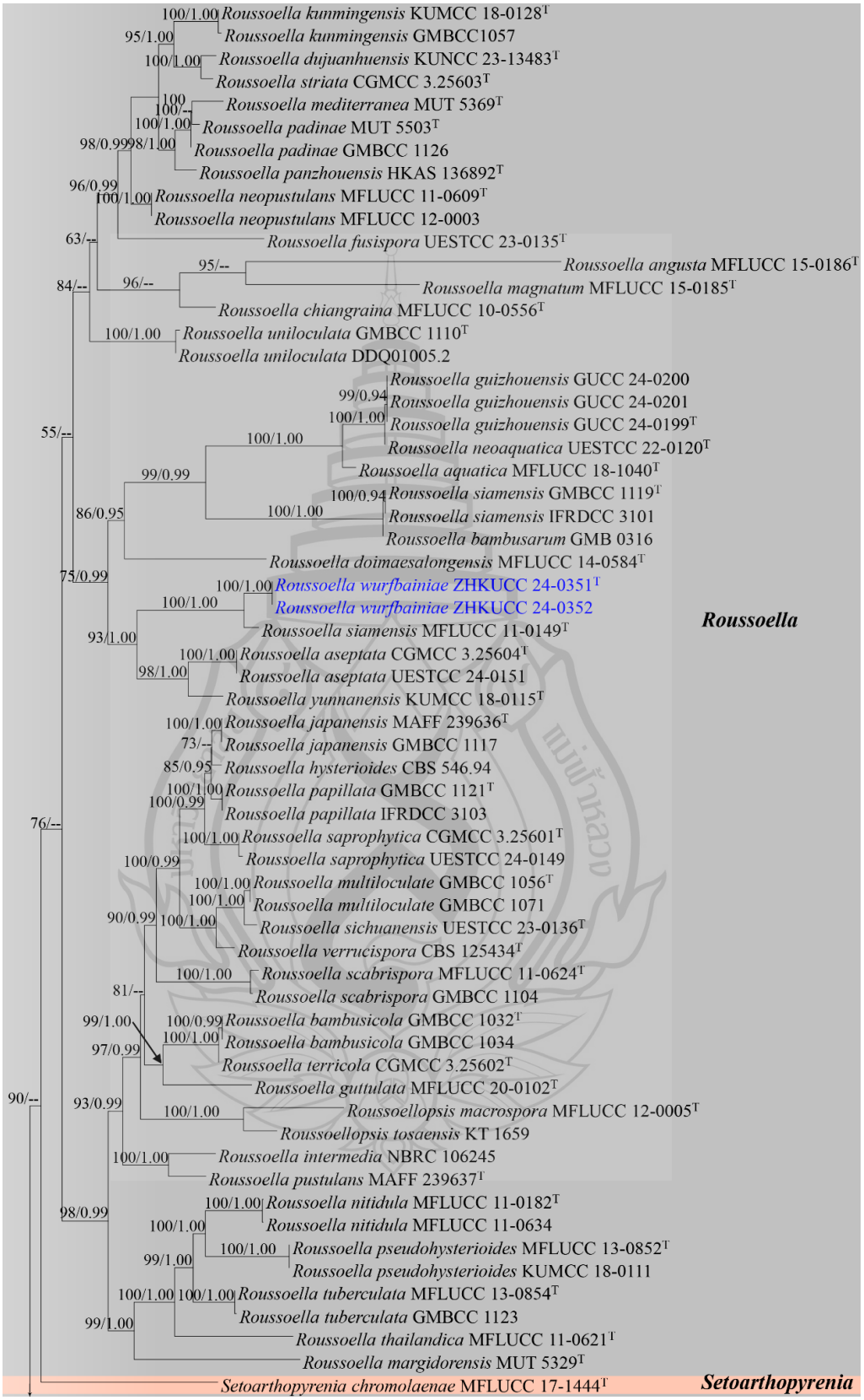
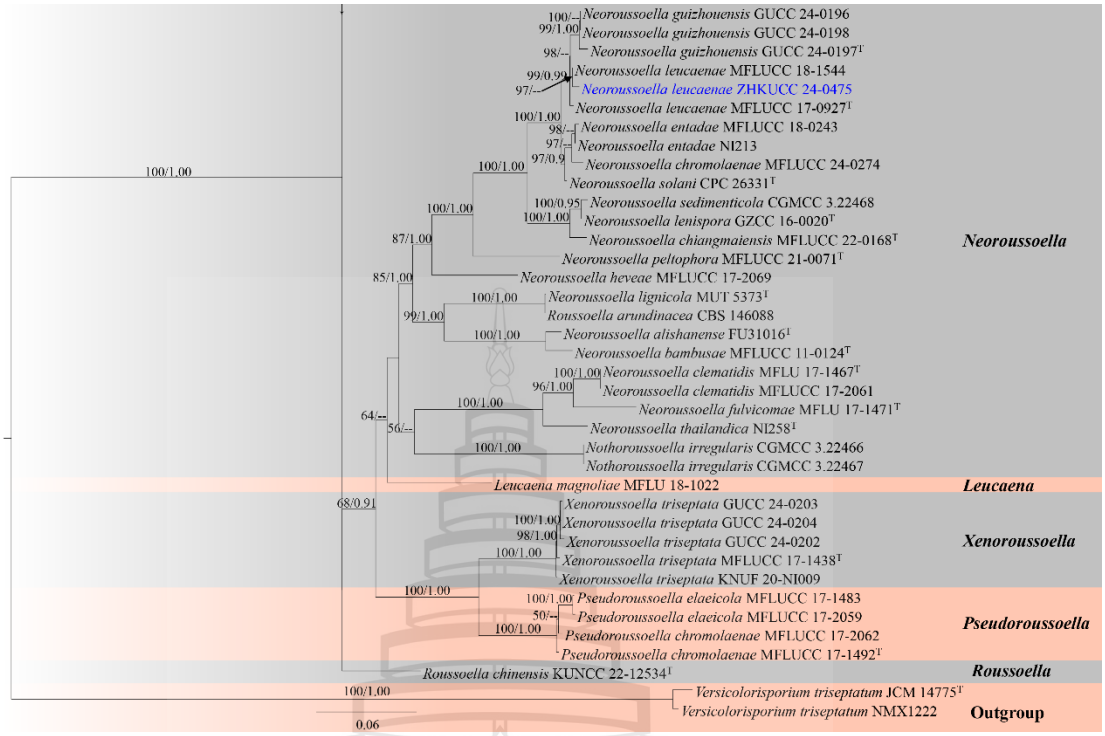
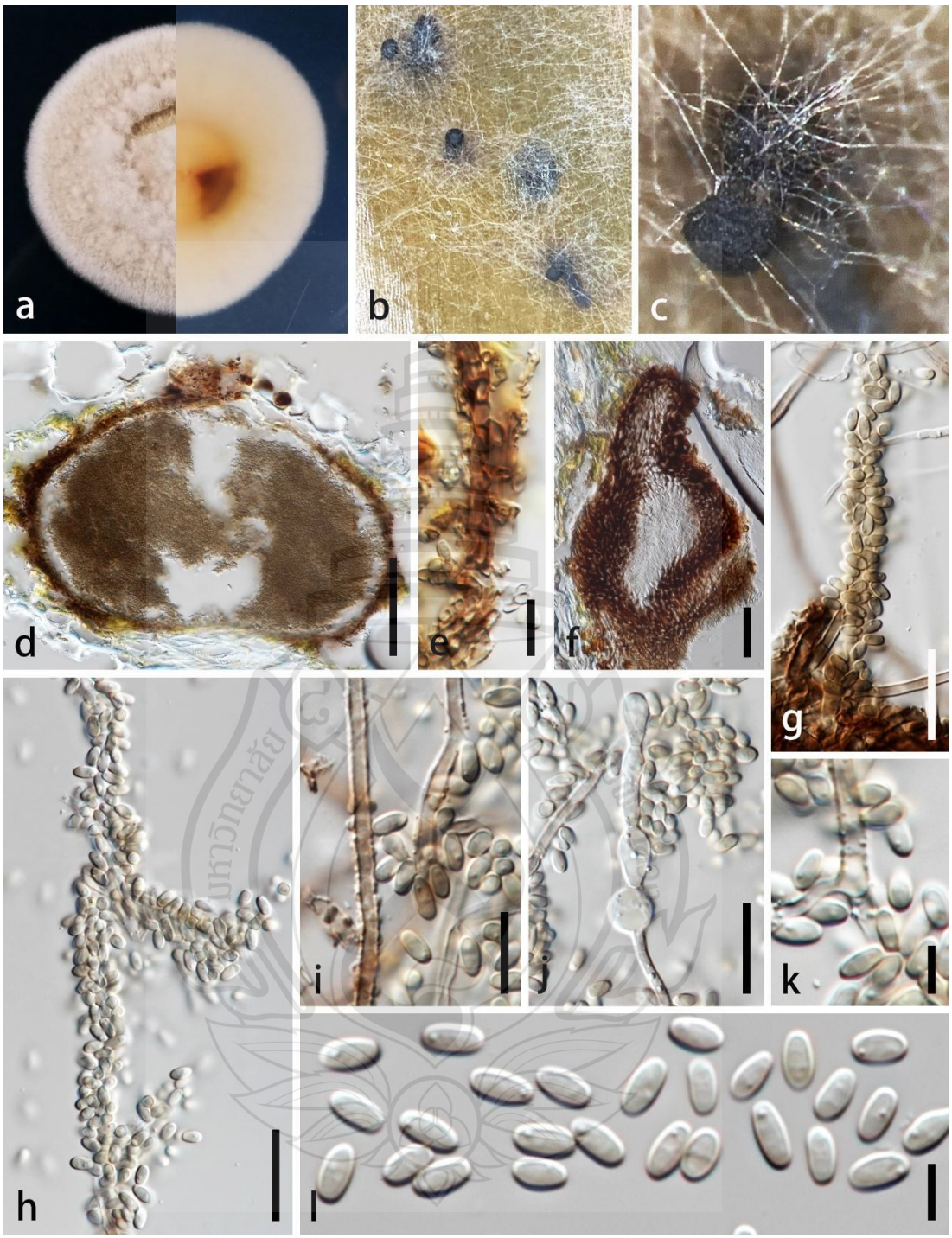


Figure 5.35 Maximum likelihood phylogeny based on the combined LSU, ITS, SSU, *tef1-α*, and *rpb2* sequences data of *Neoroussoella*



Note Tree rooted as *Torula herbarum* (CBS 111855) and *T. hollandica* (CBS 220.69). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.35 (continued)



Note a Culture characteristic on PDA for 2 weeks. b, c Appearance of conidiomata on sterilized leaf tissue of *Wurfbainia villosa* on PDA after 3 months. d Section through conidioma. e Peridium. f Ostiole. g–i, k Conidiogenous cells with conidia. j Chlamydospore. l Conidia. Scale bars: d = 50 μm, e = 10 μm, f = 20 μm, g, h, j = 20, i = 10 μm, k, l = 5 μm.

Figure 5.36 *Neoroussoella leucaenae* (MHZU 24-0195)

Roussoella Sacc., Atti dell´Istituto Veneto Scienze, 6: 410. 1888.

Notes – *Roussoella* was introduced by Saccardo and Paoletti (1888) and typified by *R. nitidula*. It is mostly reported as saprobic fungus and predominantly isolated from monocotyledonous plants, such as grasses, bamboo and palms (Liu et al., 2014). *Roussoella* is characterized by immersed, loculate ascostromata, bitunicate, cylindrical asci, two-celled, fusiform to ellipsoidal ascospores, with longitudinal striation, sometimes surrounded by a sheath (Dai et al., 2022). *Cytoplea* is the asexual morph, characterized by enteroblastic, ampulliform conidiogenous cells, and oblong to ellipsoidal conidia (Jiang et al., 2019). Up to now, 67 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we introduce a novel species *Roussoella wurfbainiae* isolated from dead stem of *Wurfbainia villosa* in China.

Roussoella wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.37

Index Fungorum number: IF904018; Facesoffungi number: FoF 17916

Etymology – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*, from which the holotype was isolated

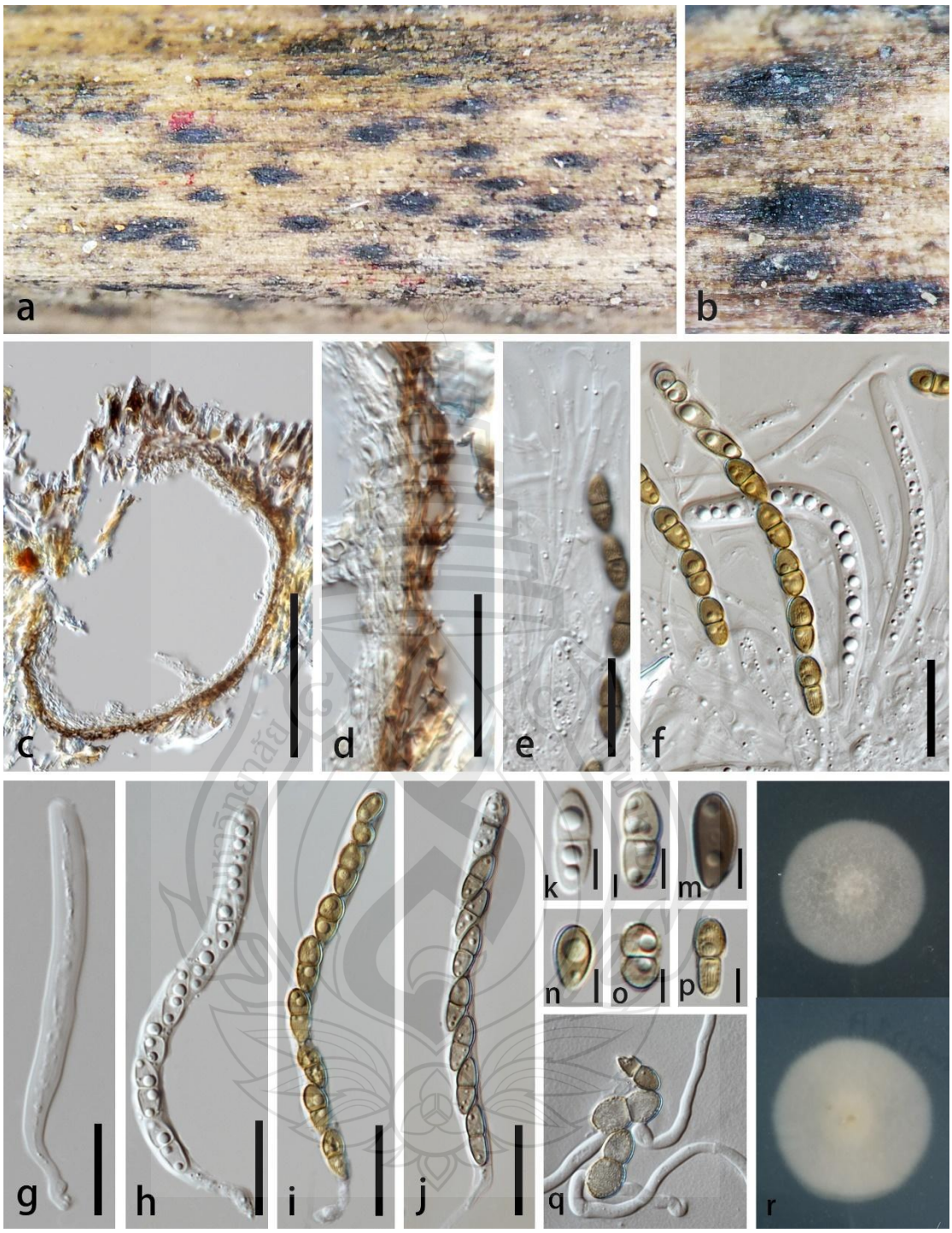
Holotype – MHZU 24-0110

Saprobic on dead stem of *Wurfbainia villosa*. Sexual morph: *Ascomata* 170–230 × 125–160 μm ($\bar{x}$ = 199 × 144 μm, n = 10), solitary, unilocular, coriaceous, immersed to erumpent, subglobose, brown to black, with a longitudinal ostiolar slit. *Peridium* 13–44 μm wide ($\bar{x}$ = 29 μm, n = 30), composed of 2–5 layers of hyaline to brown cells of *textura prismatica* or *textura angularis*, thin-walled. *Hamathecium* 1.5–4 μm wide ($\bar{x}$ = 2.5 μm, n = 30), paraphyses, numerous, hyaline, branched, septate, smooth-walled, longer than asci. *Asci* 62–90 × 5–7.5 μm ($\bar{x}$ = 79 × 6.5 μm, n = 30), 8-spored, bitunicate, cylindrical, slightly curved, apically rounded, short pedicellate, with an ocular chamber. *Ascospores* 10–16 × 4–6 μm ($\bar{x}$ = 12.5 × 5.5 μm, n = 30), uniseriate, oblong to ovoid, ellipsoidal to broadly fusiform, 1-2-celled, upper cells equal or larger, occasionally curved, constricted at the septum, hyaline to golden brown to dark brown, with longitudinal striations. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 5.0–5.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, umbonate, circular, with entire edge, velutinous, cream-white from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), on dead stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YAM123 (MHZU 24-0110, holotype); ex-type culture, ZHKUCC 24-0351; *ibid*., living culture ZHKUCC 24-0352.

Notes – In the phylogenetic analysis, strains (ZHKUCC 24-0351 and ZHKUCC 24-0352) formed a sister branch with *Roussoella siamensis* with 100 ML/1.00 PP support (Figure 5.35). Morphologically, *R. wurfbainiae* are similar to *R. siamensis* in having bitunicate, cylindrical asci and ellipsoidal to fusiform ascospores. However, *R. wurfbainiae* differs from *R. siamensis* in having unilocular and smaller ascomata (170–230 × 125–160 μm vs. 130–150 × 600–750 μm), with a thick peridium (13–44 μm vs. 7–13 μm), and 1–2-celled, hyaline to golden brown to dark brown ascospores. In contrast, *R. siamensis* has uni- to multilocular ascomata, asci with short to long foot-like pedicels, and 2-celled, brown to dark brown ascospores (Liu et al. 2014). Based on distinct morphological characteristics and phylogenetic evidence, we introduce *R. wurfbainiae* as a novel species.



Note a, b Appearance of ascomata on substrate. c Section through ascoma. d Peridium. e Paraphyses. f Paraphyses, asci, with ascospores. g–j Asci. k–p Ascospores. q Germinated ascospores. r Culture characteristics on PDA. Scale bars: c = 100 μm, d = 50 μm, e, f = 20. g–j = 20 μm, k–p = 5 μm.

Figure 5.37 *Roussoella wurfbainiae* (MHZU 24-0110, holotype)

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., in et al., Stud. Mycol. 64: 177 (2009)

Notes – Tetraplosphaeriaceae (Pleosporales) was established by Tanaka et al. (2009) to accommodate five genera, viz., *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura, Tetraplosphaeria* and *Triplosphaeria*. *Tetraplosphaeria* is the type genus, although Hyde et al. (2013) treated the genus as a synonym of *Tetraploa*. Currently, ten genera are accepted in this family, *Aquatisphaeria*, *Byssolophis*, *Ernakulamia*, *Polyplosphaeria*, *Pseudopolyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa* (=*Tetraplosphaeria*), and *Triplosphaeria* (Hyde et al., 2024).

Tetraploa Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 459 (1850)

Notes – *Tetraploa* was introduced by Berkeley and Broome (1850) with *T. aristata* as the type species. *Tetraploa* species can be found as endophytes and saprobes on plant leaves and stems in terrestrial and aquatic habitats (Dong et al., 2020; Hyde et al., 2020). They mostly occur on bamboo and other herbaceous plants (Phookamsak et al., 2022) and in rotten wood and soil (Dong et al., 2020). Thirty-two species have been placed in the genus (http://www.indexfungorum.org/names/Names.asp). In this study, a novel species *Tetraploa wurfbainiae* was proposed, which was isolated from decaying stems of *Wurfbainia villosa*.

Tetraploa wurfbainiae C.F. Liao & Doilom, sp. nov. Figure 5.39

Index Fungorum number: IF 901165; Facesoffungi number: FoF 14925

Etymology: – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*, from which the holotype was isolated.

Holotype: – MHZU 23-0231.

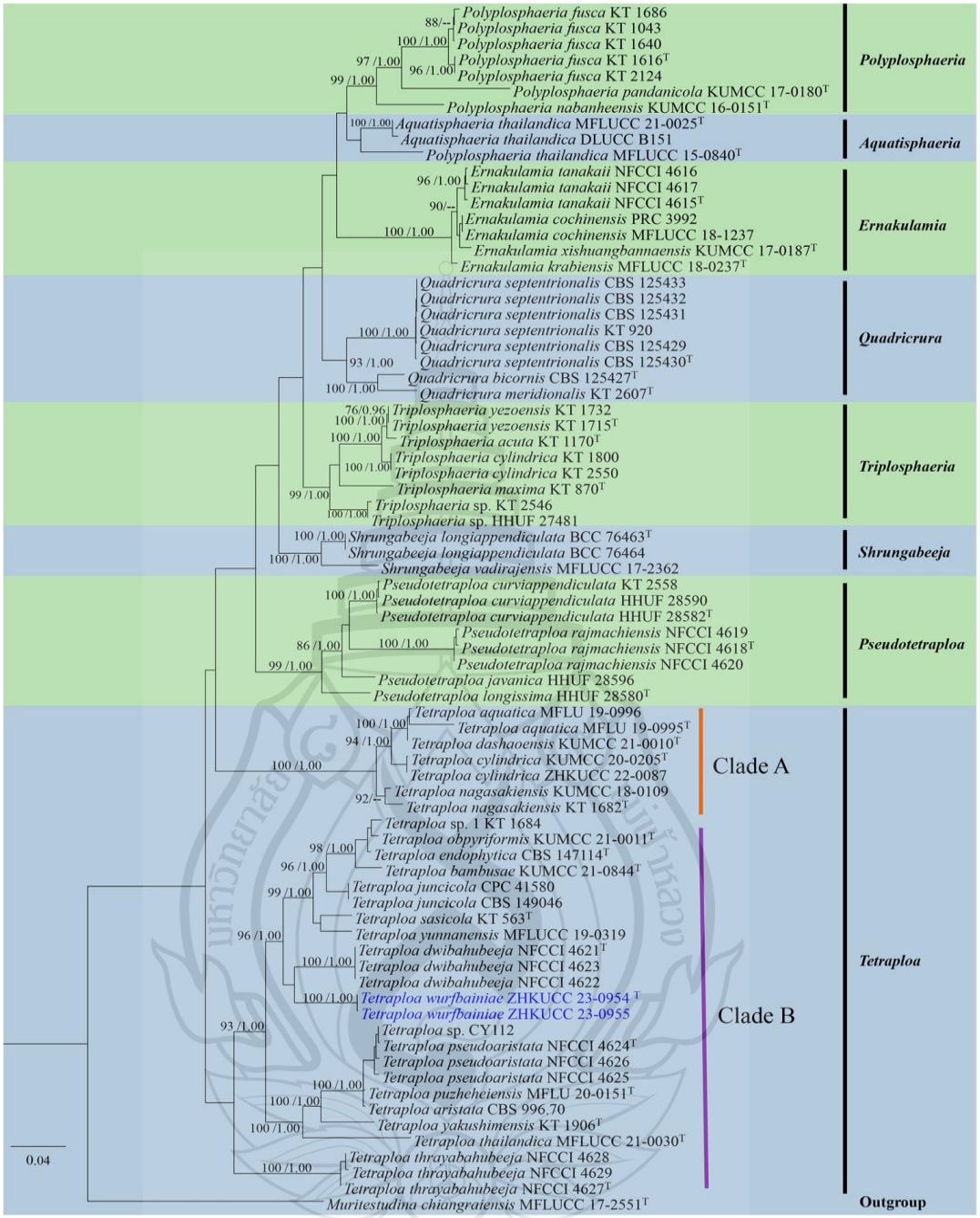
Saprobic on decaying stems of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: Hyphomycetous. Colonies effuse to powdery, gregarious or cluster in small groups, dark brown to black. *Mycelium* hyaline, branched, septate. *Conidiophores* absent. *Conidiogenous cells* monoblastic, integrated, determinate. *Conidia* 27–38 × 18–28 µm ($\overline{x}$ = 32 × 22 µm, n = 30), solitary, cylindrical to obovate, with obtuse basal end, brown to dark brown, composed of four columns of cells, 3–4-septate or sometimes 5-septate in each column, smooth, mostly with four apical appendages, occasionally one (in young conidia) or three appendages. *Appendages* 20–150 µm long

($\bar{x}$ = 81 µm, n = 30), 5–8 µm wide at the base, gradually tapering to 3–6 µm wide at the apex, brown, divergent, 1–7-septate, straight or slightly flexuous, smooth, unbranched.

Culture characteristics: – Conidia germinated on PDA at room temperature (25 ± 2°C) within 24 h, germination tubes grew from both ends. Colonies reaching 30–35 mm in diameter after two weeks at 28°C. Colonies dense, circular in shape, and raised in the middle. Top side grey, flossy, velvety; reverse center dark brown to orange-brown, turning pale gray towards the margin.

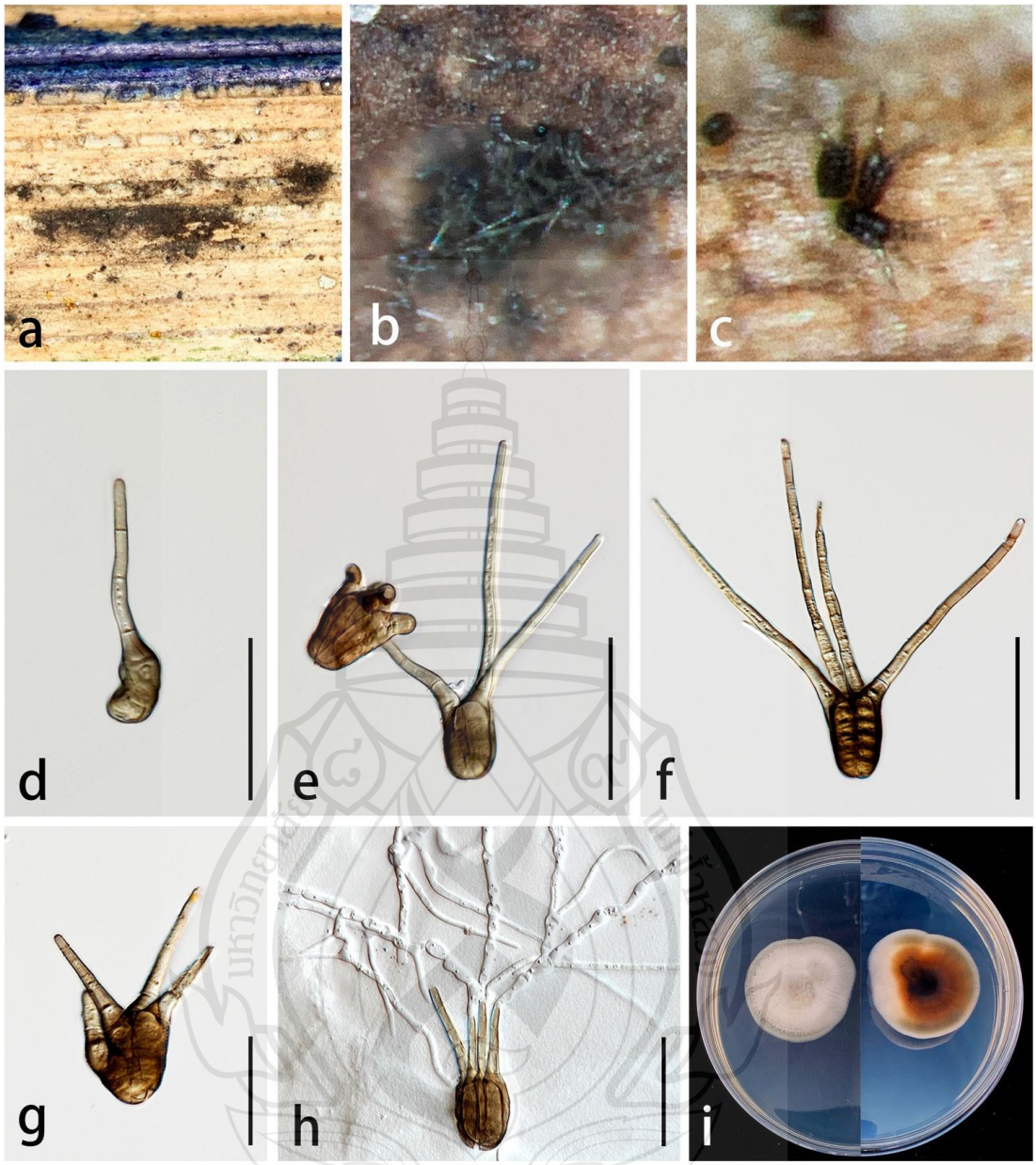
Material examined: – China, Guangdong Province, Yangchun City, from decaying stems of *Wurfbainia villosa* (Zingiberaceae), 9 April 2023, C.F. Liao, (MHZU 23-0231, holotype), ex-type living culture ZHKUCC 23-0954; *ibid*., ZHKUCC 23-0955.

Notes: – *Tetraploa wurfbainiae* forms a sister clade with *T. dwibahubeeja* in our multi-locus phylogenetic analyses (Figure 5.38). In contrast to our species, *T. dwibahubeeja* has V-shaped bifurcate conidia, with a rudimentary tertiary arm (Hyde et al., 2020). *Tetraploa wurfbainiae* resembles *T. sasicola* in having cylindrical conidia and four columns of cells with four appendages, however, the latter has larger conidia ((32–)35–50(–52.5) × 20–30 µm) and shorter appendages ((88–)113–190(–200) µm). *Tetraploa wurfbainiae* resembles *T. yunnanensis* in having brown, cylindrical conidia with several appendages but the latter has longer conidia (30–50 × 16–22 µm) and shorter appendages (25–83 µm). Thus, we establish *Tetraploa wurfbainiae* as a novel species based on morphology and multi-locus phylogeny.



Note Bootstrap support values for ML equal to or greater than 75%, and PP equal to or greater than 0.95 are given near the branches as ML /PP. The tree is rooted with *Muritestudina chiangraiensis* (MFLUCC 17- 2551). Ex-type cultures are indicated using "T" after strain codes, and the newly introduced taxa are indicated in blue.

Figure 5.38 Maximum likelihood phylogeny based on the combined LSU, SSU, ITS, *tef1-α*, and *tub2* sequences data of *Tetraploa*



Note a–c, Colonies on natural substrates. d–g, Conidia bearing 1–4 appendages. h, Germinating conidium. j, Colony on PDA (left-top, right-reverse). Scale bars: d–h= 50 μm.

Figure 5.39 *Tetraploa wurfbainiae* (MHZU 23-0231, holotype)

Torulaceae Corda, in Sturm, *Deutschl. Fl.*, 3 Abt. (Pilze Deutschl)(2-3): 71 (1829)

Notes – *Torulaceae* (Pleosporales) was introduced by Sturm (1829) and typified by the asexual genus *Torula*. *Torulaceae* are worldwide distributed and mainly found as saprobes on dead or decaying wood in freshwater and terrestrial habitats (Hyde et al.,

2020; Boonmee et al., 2021). The asexual morphs are hyphomycetous, characterized by septate, subcylindrical conidiophores with or without apical branches, doliiform to ellipsoid or clavate, smooth to verruculose, mono- to polyblastic conidiogenous cells, and subcylindrical or fusiform, smooth to verrucose conidia which form branched chains (Crous et al., 2015; Hyde et al., 2016; Wang et al., 2023b). Currently, *Torulaceae* accepted six genera, viz., *Cylindrotorula*, *Dendryphion*, *Neopodoconis*, *Neotorula*, *Rutola* and *Torula* (Hyde et al., 2024).

Torula Pers., Ann. Bot. (Usteri) 15: 25 (1795)

Notes: *Torula* was described by Persoon (1795) with *T. monilis* as the type, but it was invalidly published (for detailed history, see Crous et al., 2015; Li et al., 2023). The genus is characterized by dark brown to black, effuse, superficial colonies; semi-macronematous to macronematous, mononematous, septate conidiophores, or conidiophores reduce to conidiogenous cells; dark brown, monoblastic to polyblastic, smooth-walled to verruculose conidiogenous cells, and terminal or lateral, acrogenous, monilioid, verrucose conidia (Crous et al., 2015). *Torula* species are commonly reported as saprobes from submerged wood, dead branches, and herbaceous litter of vascular plants, though some are plant pathogens and endophytes (Li et al., 2023; Luan et al., 2023; Dong et al., 2023; Liao et al., 2024). Many *Torula* species are described solely based on morphology, and there are 559 epithets listed under *Torula* (Index Fungorum, 2025). However, sequence data are available for only 29 species. In this study, we provide additional sequence data for *Torula* species and describe *Torula wurfbainiae* sp. nov., isolated from decaying stems of *Wurfbainia villosa*, with morphological illustrations.

Torula wurfbainiae C.F. Liao, Doilom & K.D. Hyde, *sp. nov.* Figure 5.41

Index Fungorum number: ***; Facesoffungi number: FoF ***

Etymology – in reference to the host "*wurfbainiae*" from which it was isolated.

Holotype – MHZU 24-0050

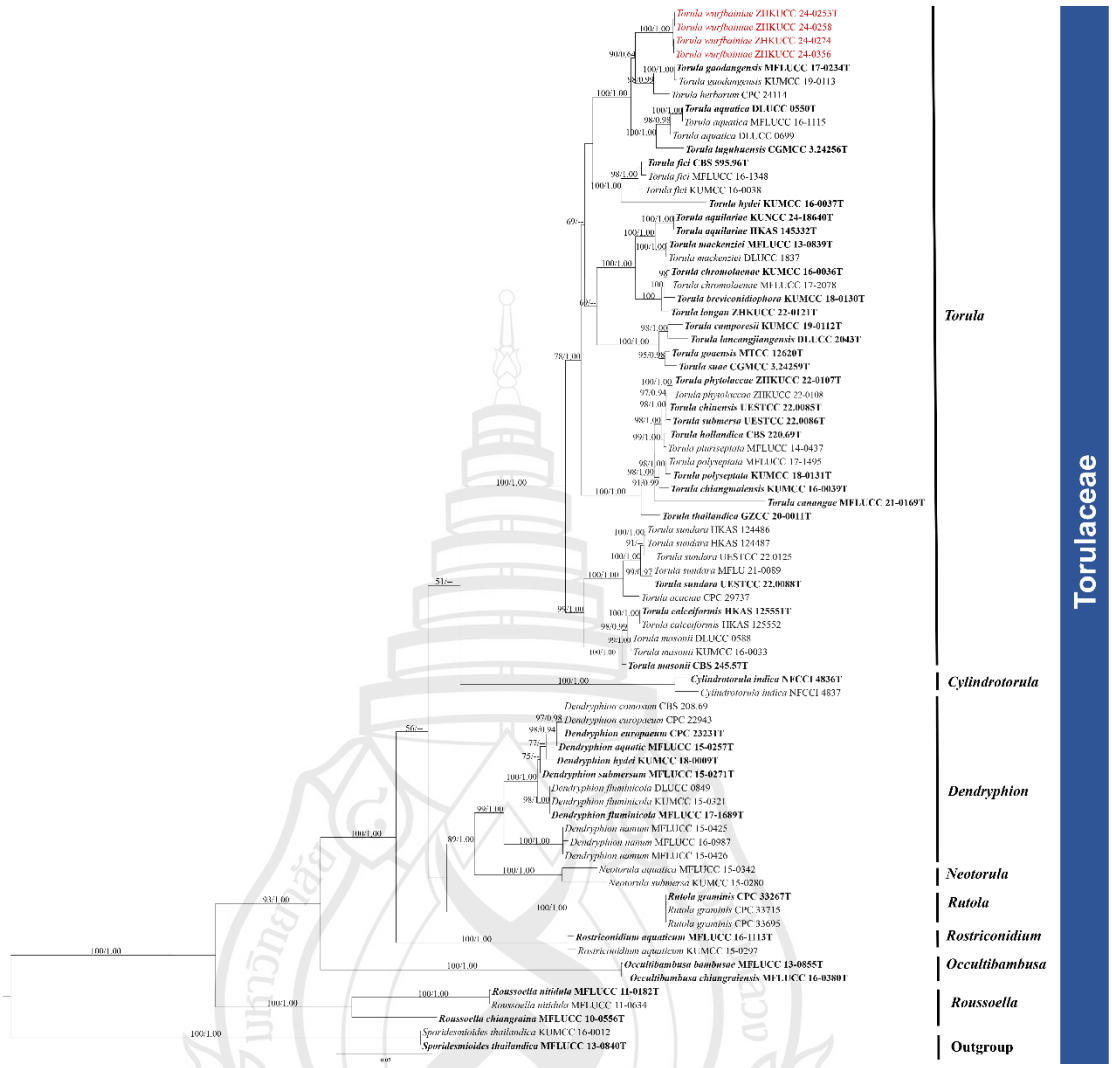
Saprobic on decaying stems of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: *Colonies* superficial, gregarious, dense, powdery, black on host. *Conidiophores* 14–46 × 5–8 μm ($\bar{x}$ = 26 × 6.5 μm, n = 30), semi-macronematous to macronematous, mononematous, solitary, doliiform, straight to flexuous, pale brown, composed of 1–2 cells, verrucose. *Conidiogenous cells* 7–9 × 5–8.5 μm ($\bar{x}$ = 8 × 7 μm,

n = 30), monoblastic to polyblastic, intercalary or terminal, subglobose to cupulate, dark brown, verrucose. *Conidia* 15–51 × 6–9 μm ($\bar{x}$ = 34 × 7 μm, n = 30), catenate, acrogenous, monilioid, hyaline to yellow-brown when young, pale brown to dark brown when mature, straight or curved, 3–9-septate, constricted at septa, verrucose.

Culture characteristics – Colonies on PDA reaching 5.0–5.5 cm diameter after 14 days at 25°C, irregular, dense, cottony, flattened, with undulate margin, filiform, pale brown at center, cream-white at margin from above, cream-white at margin to dark brown at center from reverse, no pigmentation.

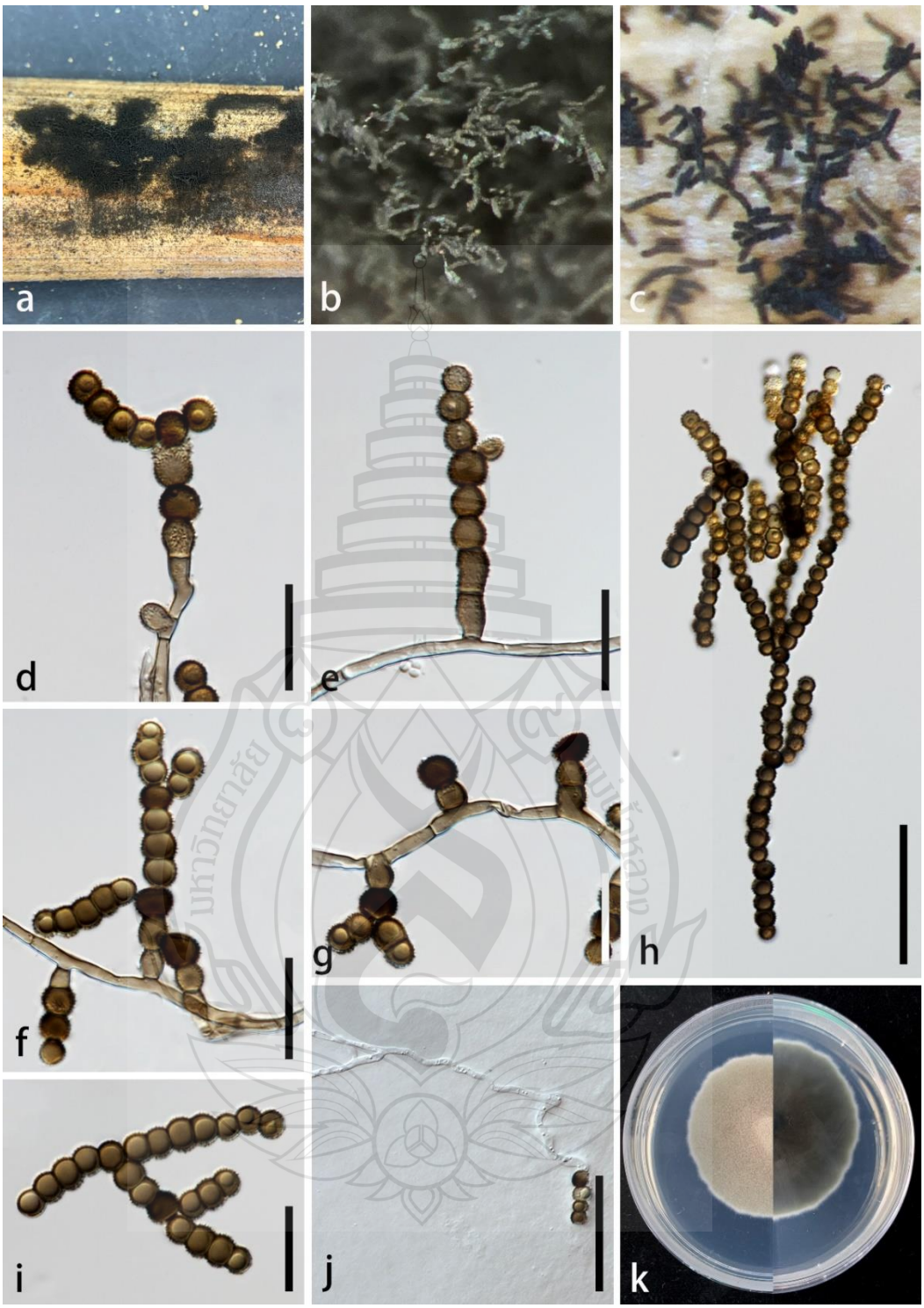
Material examined – China, Guangdong Province, Yangchun City, Heshui Town, on decaying stem of *Wurfbainia villosa*, 9 April 2023, C.F. Liao, YAM53 (MHZU 24-0050, holotype); ex-type culture ZHKUCC 24-0253; *ibid*., living culture ZHKUCC 24-0258, ZHKUCC 24-0274; *ibid*., Xinyi City, Qianpai Town, on decaying stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YAM125A (MHZU 24-0112), living culture ZHKUCC 24-0356.

Notes – In the phylogenetic analysis, our strains (ZHKUCC 24-0253, ZHKUCC 24-0258, ZHKUCC 24-0274, ZHKUCC 24-0356) formed a distinct branch sister to *Torula gaodangensis* (MFLUCC 17-0234, KUMCC 19-0113) with 90% ML and 0.64 BYPP (Figure 5.40). Morphologically, our collection differs from *T. gaodangensis* in having doliiform, verrucose conidiophores, whereas *T. gaodangensis* has ellipsoidal to ampulliform, or oblong, and smooth conidiophores (Hyde et al., 2020). Additionally, it is clearly distinguished from *T. gaodangensis* by its larger conidiophores (14–46 ×5–8 μm vs. 1–4 × 1–2.5 μm), larger conidiogenous cells (7–9 ×5–8.5 μm vs. 1–3 × 2–3 μm), and longer conidia (15 – 51 × 6 – 9 μm vs. (4.5–)6–11(–12) × 2.5–3 μm). Based on these morphological differences and phylogenetic evidence, we identify *T. wurfbainiae* as a novel species.



Note The tree is rooted to *Sporidesmioides thailandica* (KUMCC 16-0012, MFLUCC 13-0840). Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. Ex-type strains are indicated with "T". The newly generated sequences are indicated in red.

Figure 5.40 Maximum likelihood phylogeny based on the combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequences data of *Torula*



Note a–c Appearance of conidiophores and conidia on woody substrate. d–g Conidiophores, conidiogenous cells with conidia. h, i Conidiogenous cells and conidia. j Germinated conidium. k Colony on PDA (front and below). Scale bars: d–g, i = 20 µm, h, j = 50 µm.

Figure 5.41 *Torula wurfbainiae* (MHZU 24-0112, holotype)

Dothideomycetes orders incertae sedis

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2007)

Notes – Botryosphaeriales, introduced by Schoch et al. (2006), has a worldwide distribution and is commonly found as pathogens or saprobes on woody plant trunks and branches (Phillips et al., 2019; Zhang et al., 2021). Up to now, six families, Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae, and Saccharataceae are accepted in Botryosphaeriales (Wijayawardene et al., 2022; Hyde et al., 2024).

Botryosphaeriaceae Theiss. & Syd [as 'Botryosphaeriacae'], Annls mycol. 16(1/2): 16 (1918)

Notes – Botryosphaeriaceae, introduced by Theissen and Sydow (1918) with *Botryosphaeria* as the type genus, has a global distribution across diverse hosts and exhibits a variety of lifestyles (Wang et al., 2023). Members of Botryosphaeriaceae are dominant as pathogenic and saprobic fungi, and also occur as endophytes (Doilom et al., 2015, 2017; Jash et al., 2025). To date, Botryosphaeriaceae comprises more than 24 genera and 280 species (Manawasinghe et al., 2022, 2025; Wijayawardene et al., 2022). Its host range includes 1692 plant species distributed across approximately 149 countries (Batista et al., 2021).

Lasiodiplodia Ellis & Everh., in Clendenin, Bot. Gaz. 21: 92 (1896)

Notes – *Lasiodiplodia* is known as an important plant pathogenic genus, mostly distributed in tropical and subtropical regions, causing diseases in various economic crops, such as mango dieback, pear root rot, leaf spot, branch blight, and stem end rot papaya (Ocampo-Padilla et al., 2024). *Lasiodiplodia* is characterized by immersed to erumpent, oblong to subglobose conidiomata, hyaline and smooth conidiogenous cells, and oblong, 1-septate, hyaline to brown conidia, with longitudinal striations (Dou et al., 2017). Up to now, 92 epithets are listed in the Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we introduce a novel species, *Lasiodiplodia wurfbainiae*, based on phylogenetic analyses and morphological characteristics.

Lasiodiplodia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 4.43

Index Fungorum number: IF904004; Facesoffungi number: FoF 17899

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0048

Saprobic on dead stems and endophytic in asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 192–255 × 178–258 μm ($\overline{x}$ = 227 × 223 μm, n = 20), pycnidial, solitary, unilocular, coriaceous, immersed to erumpent, oblong to subglobose, black. *Peridium* 26–75 μm wide ($\overline{x}$ = 48 μm, n = 30), composed of 6–10 layers of thin, hyaline inner cells to thick, brown to dark outside cells of *textura angularis*. *Paraphyses* 40–68 × 3–5 μm ($\overline{x}$ = 55 × 4 μm, n = 30), hyaline, filiform, aseptate, branched, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 11–21 × 4–7 μm ($\overline{x}$ = 15 × 6 μm, n = 30), cylindrical to oblong, hyaline, smooth-walled, straight to slightly curved. *Conidia* 20–29 × 13–16 μm ($\overline{x}$ = 26 × 15 μm, n = 30), oblong to oval, hyaline, aseptate, with minute guttules when young, becoming ellipsoidal to oval, olivaceous green to brown or dark brown, 1-septate, with a dark septum, rounded at the ends, multi-guttulate, smooth- and thick-walled, with longitudinal striations.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse at center, dense at the edge, appressed, velutinous, with abundant aerial hyphae, cream-white from the above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.19027 N, 111.91027 E), on dead stem of *Wurfbainia villosa*, 9 April 2023, C.F. Liao, YAM50 (MHZU 24-0048, holotype); ex-type culture, ZHKUCC 24-0250; China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *W. villosa*, 1 October 2022, C.F. Liao, AMR14C-2, living culture ZHKUCC 24-0554.

Notes – The phylogenetic analyses revealed that our strains (ZHKUCC 24-0250 and ZHKUCC 24-0554) separated from *Lasiodiplodia iraniensis* (CBS 124710 and CBS 124711) with 85 ML/0.84 PP support (Figure 4.42). Morphologically, *L. wurfbainiae* and *L. iraniensis* share similarities, including solitary, globose to subglobose, dark conidiomata, hyaline, branched paraphyses, hyaline, cylindrical conidiogenous cells, and one-septate

conidia with longitudinal striations. However, the conidiomata of *L. wurfbainiae* are immersed to erumpent, oblong to subglobose, while *L. iraniensis* are superficial, globose. The paraphyses of *L. wurfbainiae* are aseptate and branched, while those of *L. iraniensis* are 1–6 septate and rarely branched. The conidia of *L. wurfbainiae* are oblong when young, becoming clavate to oval, reniform to lunate, olivaceous green to dark brown when mature. In contrast, the conidia of *L. iraniensis* are subglobose to subcylindrical when young, ellipsoid to ovoid, and pale brown when mature. Furthermore, *L. wurfbainiae* can be distinguished from *L. iraniensis* by its smaller conidiomata (192–255 × 178–258 μm vs. up to 980 μm), shorter paraphyses (40–68 × 3–5 μm vs. up to 127 μm long, 2–4 μm wide), and slightly longer conidiogenous cells (11–21 × 4–7 μm vs. 9–16 × 3–5 μm). Hence, we identify *L. wurfbainiae* as a novel species.

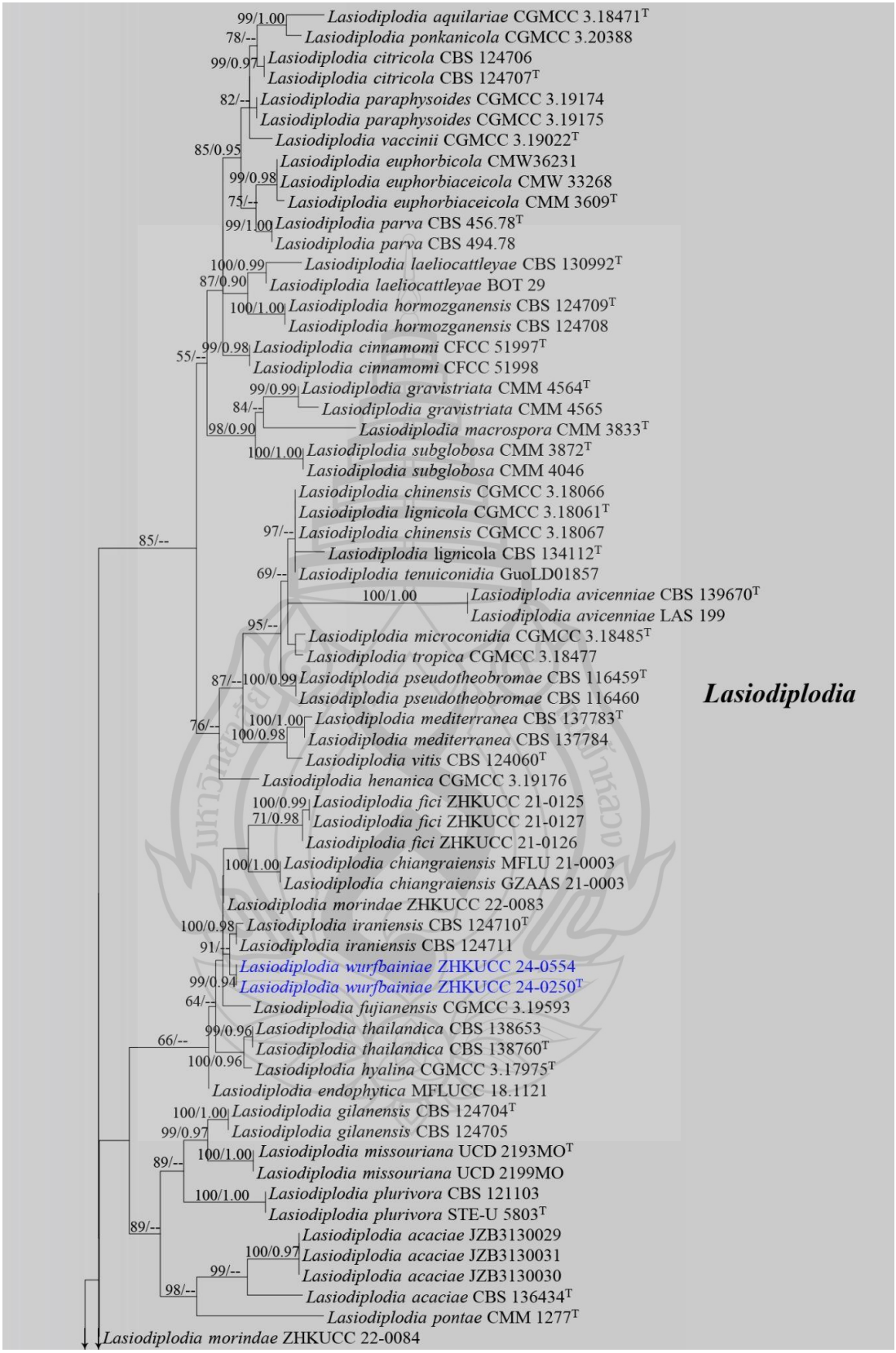
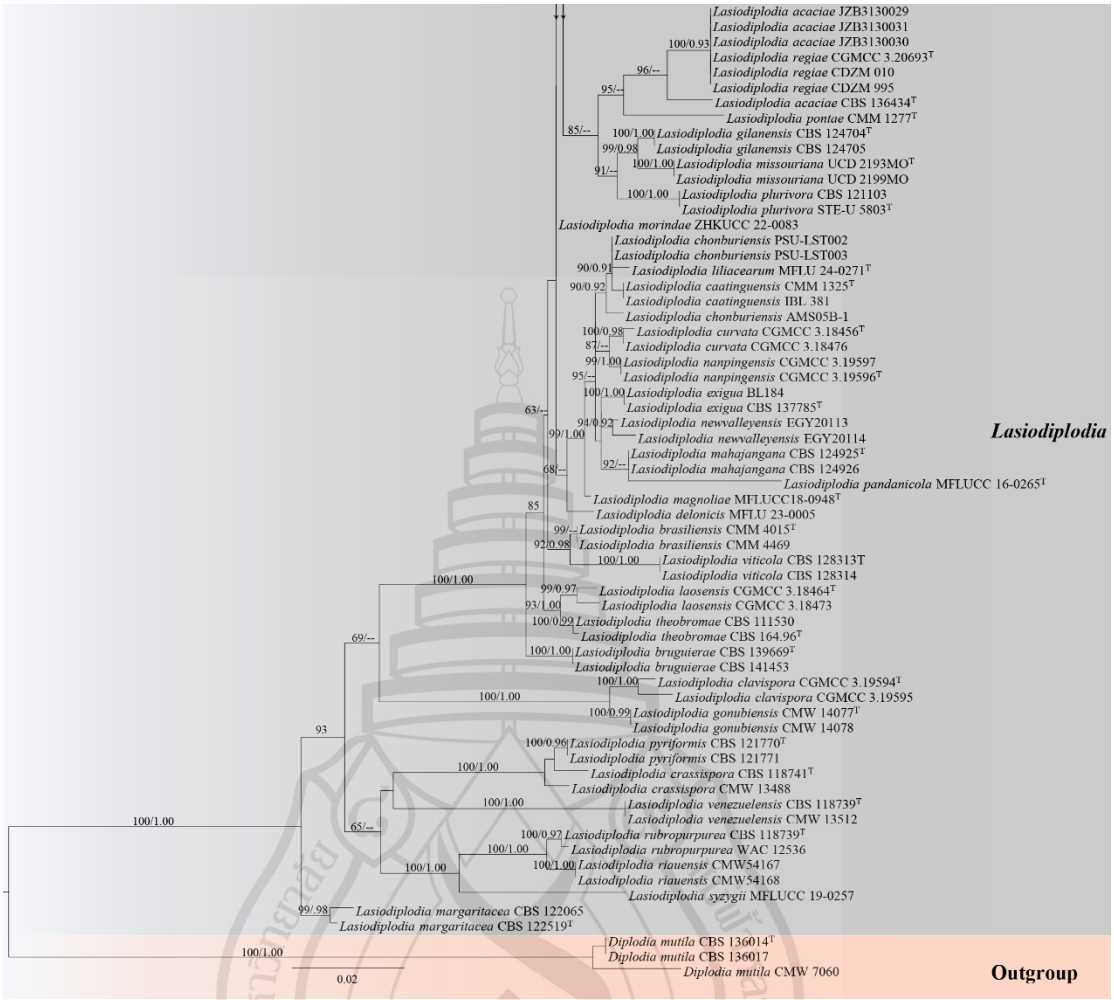
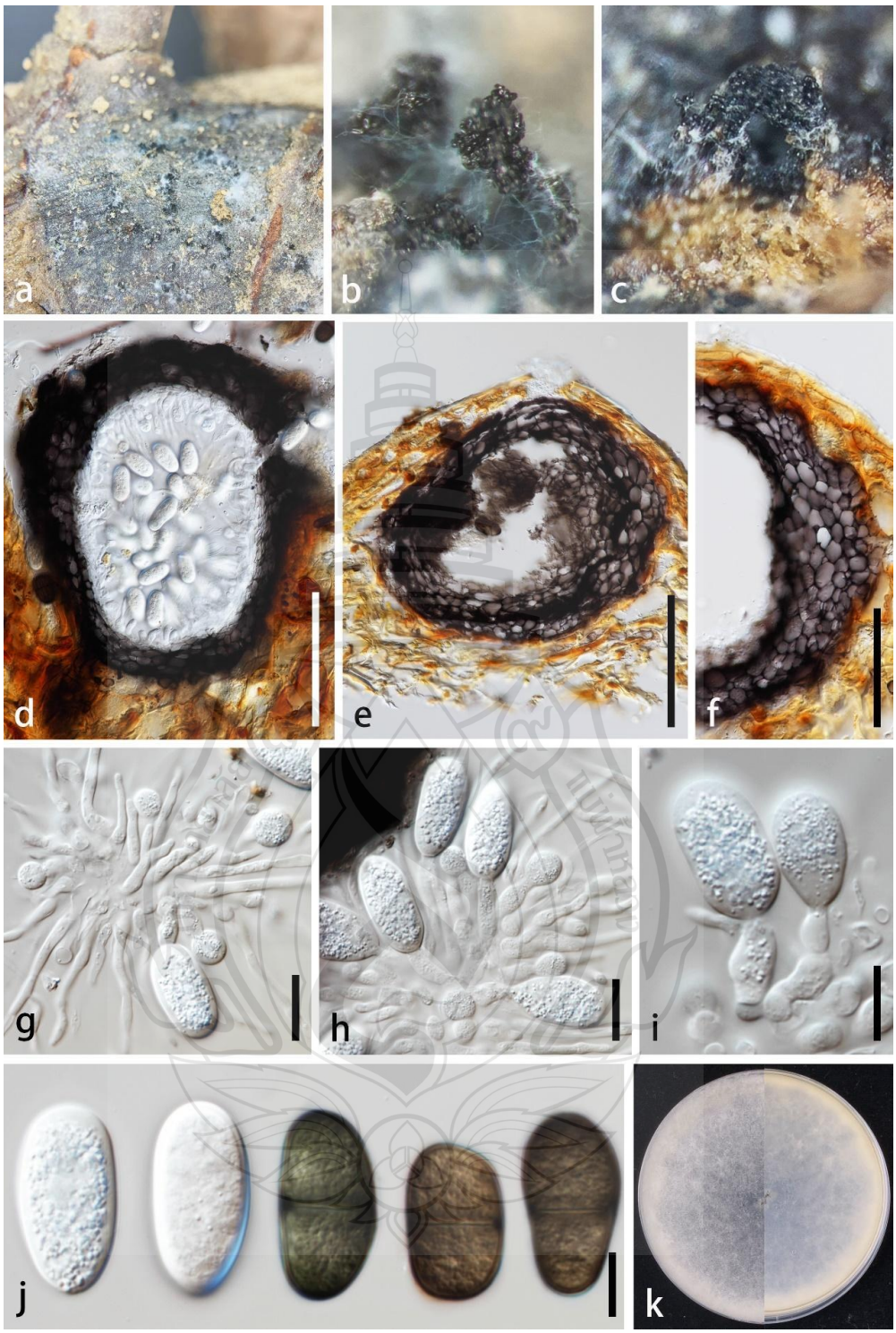


Figure 5.42 Maximum likelihood phylogeny based on combined ITS, *tef1-α*, and *tub2* sequences data of *Lasiodiplodia*



Note Tree rooted as *Diplodia mutila* (CBS 136014, CBS 136017, CMW 7060). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.42 (continued)



Note a–c Appearance of conidiomata on host substrate. d, e Section through conidiomata. f Peridium. g–i Conidiogenous cells with conidia. j Conidia. k Culture characteristics on PDA. Scale bars: d, e = 100 μm, f = 50 μm, g, h = 20 μm, i, j = 10 μm.

Figure 5.43 *Lasiodiplodia wurfbainiae* (MHZU 24-0048, holotype)

Neodeightonia C. Booth, in Punithalingam, Mycol. Pap. 119: 17 (1969)

Notes – *Neodeightonia* was established by Booth (1969), with *Neodeightonia subglobosa* as the type species. *Neodeightonia* species are mainly reported from bamboo and palms (Phukhamsakda et al., 2022). The asexual morph of *Neodeightonia* is characterized by dark brown to black, immersed ascomata, clavate to cylindric-clavate asci, hyaline, aseptate ascospores, with polar apiculi and surrounded by a mucilaginous sheath. The asexual morph is characterized by initially hyaline, aseptate, becoming brown, 1-septate conidia when maturity, with smooth to finely roughened walls or fine striations (Xiong et al., 2022; Wu et al., 2022; https://dothideomycetes.org/botryosphaeriales/botryosphaeriaceae/neodeightonia-/). Currently, 16 epithets are listed in the Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we introduce a novel species, *Neodeightonia wurfbainiae*, based on the phylogenetic analysis and morphological characteristics.

Neodeightonia wurfbainiae C.F. Liao & Doilom sp. nov. Figure 5.45

Index Fungorum number: IF904005; Facesoffungi number: FoF 17900

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

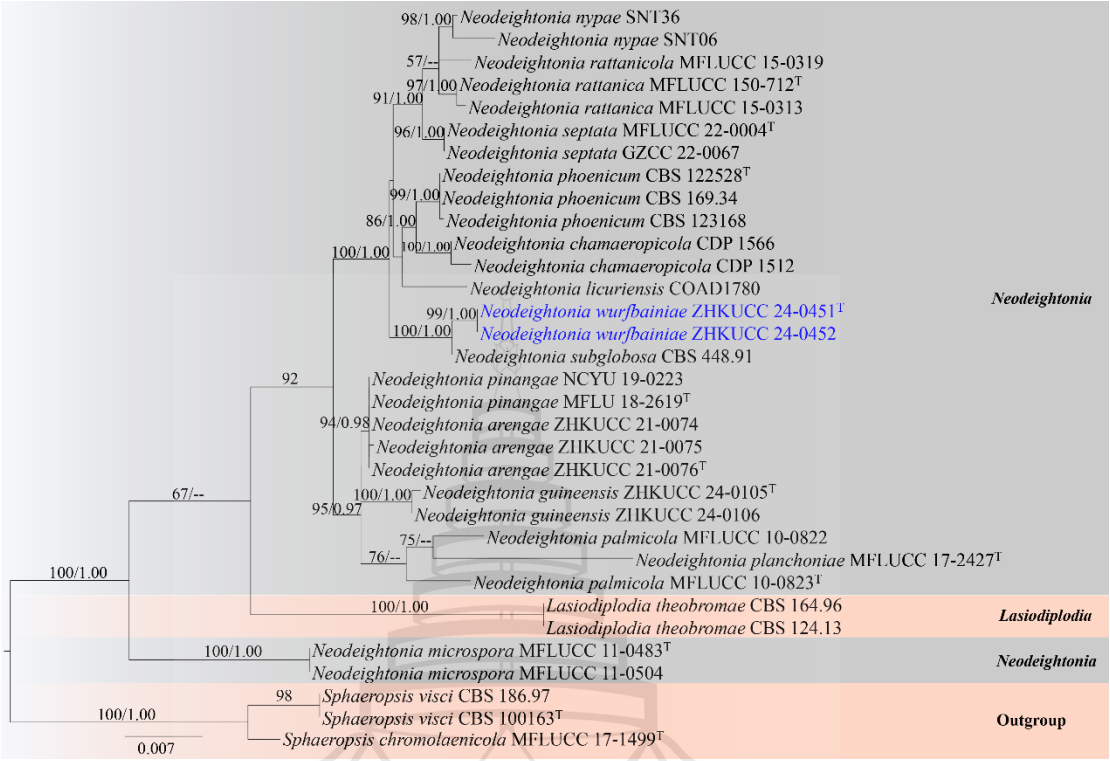
Holotype – MHZU 24-0179

Endophytic in the asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: on a sterilized pine needle or leaf of *Wurfbainia villosa* on PDA. *Conidiomata* 131–203 × 305–544 μm ($\bar{x}$ = 165 × 401 μm, n = 20), pycnidial, solitary, unilocular, coriaceous, superficial, short oblong, flat, dark black, with long ostiole neck. *Peridium* 43–68 μm wide ($\bar{x}$ = 54 μm, n = 20), composed of 7–10 layers of thin hyaline inner cells to thick brown to dark outside cells of *textura angularis* or *textura globulosa*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9–18 × 3–5 μm ($\bar{x}$ = 14 × 4 μm, n = 30), holoblastic, simple, cylindrical, hyaline, straight to slightly curved, smooth-walled. *Conidia* 11–15 × 7–10 μm ($\bar{x}$ = 13 × 9 μm, n = 30), subglobose, ellipsoidal to obovoid, aseptate, obtuse end, hyaline, multi-guttulate, smooth- and thick-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, mycelia radiating outwards, flat, filiform, pale brown from above, black mixture with pale brown from reverse, no pigmentation.

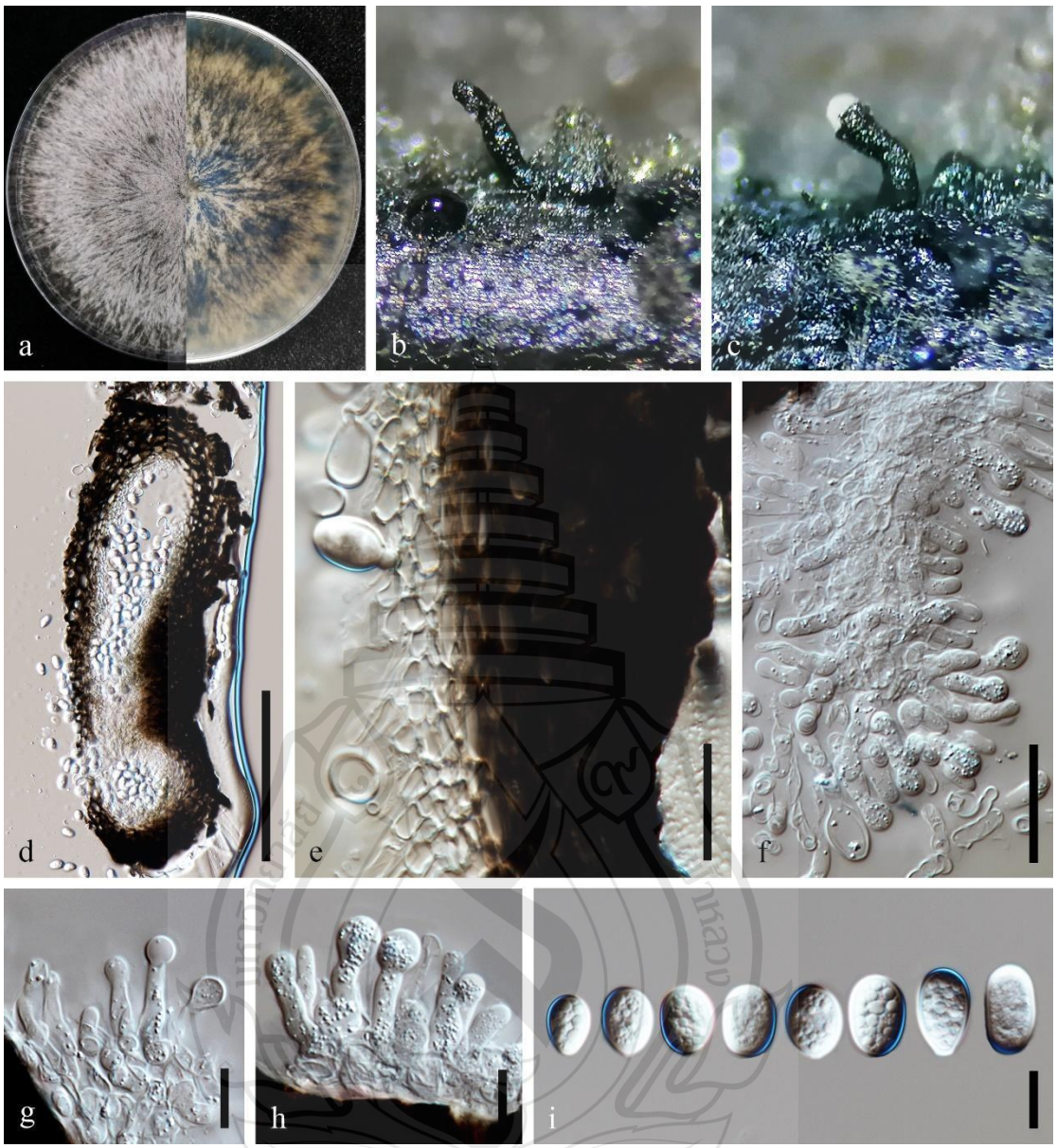
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML16B-6 (MHZU 24-0179, holotype); ex-type culture, ZHKUCC 24-0451; *ibid*., living culture, ZHKUCC 24-0452.

Notes – Phylogenetic analyses placed our strains (ZHKUCC 24-0451 and ZHKUCC 24-0452) in a distinct branch sister to *Neodeightonia subglobosa* (CBS 448.91) with 100% ML/1.00 PP support (Figure 5.3). Morphologically, the solitary, unilocular, superficial conidiomata, holoblastic, simple conidiogenous cells, and spherical to globose conidia of *Neodeightonia wurfbainiae* align with the generic characteristics (Phillips et al., 2013). However, the conidiomata of *N. wurfbainiae* are short and oblong, with a long ostiolar neck. This contrasts with *N. subglobose*, which has globose conidiomata that lacks an ostiolar neck. Moreover, the conidia of *N. wurfbainiae* are globose to subglobose, ellipsoidal to elongate, obovoid, smooth-walled, and hyaline. In contrast, *N. subglobose* have spherical to globose, pale to dark brown when mature, smooth to finely rough-walled conidia. Additionally, *N. wurfbainiae* has larger conidiomata (131–203 × 305–544 μm vs. up to 200 μm broad) and larger conidia (11–15 × 7–10 μm vs. 9–12 × 6–9 μm) than those of *N. subglobose*. Therefore, we identify *N. wurfbainiae* as a new species based on morphological differences and molecular phylogeny.



Note Tree rooted as *Sphaeropsis chromolaenicola* (MFLUCC 17-1499) and *Sphaeropsis visci*. Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.44 Maximum likelihood phylogeny based on combined ITS, LSU, SSU, and tef1-α sequences data of *Neodeightonia*



Note a Culture characteristic on PDA for two weeks. b, c Appearance of conidiomata on sterilized pine needle or leaf of *Wurfbainia villosa*. d Section through conidioma. e Peridium. f–h Conidiogenous cells with conidia. i Conidia. Scale bars: d = 200 μm, e, f = 20 μm, g–i = 10 μm.

Figure 5.45 *Neodeightonia wurfbainiae* (MHZU 24-0179, holotype)

Neofusicoccum Crous, Slippers & A.J.L. Phillips, Stud. Mycol. 55: 247 (2006)

Notes – *Neofusicoccum* was introduced by Crous et al. (2006), with *N. parvum* as the type species. The asexual morph is known as fusicoccum-like and dichomera-like, and characterized by fusiform to ellipsoidal, aseptate conidia when young, becoming septate

and brown when mature (Crous et al., 2006). The phylogenetic analyses were based on the combined ITS, *tef1-α*, *tub2*, and *rpb2* sequences (Si et al., 2023). Currently, 71 epithets are listed in the Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we introduce a novel species, *Neofusicoccum wurfbainiae*, based on the phylogenetic analyses and morphological characteristics as detailed below.

Neofusicoccum wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.47

Index Fungorum number: IF904006; Facesoffungi number: FoF 17901

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0259

Endophytic in the asymptomatic roots of *Wurfbainia villosa*. Sexual morph: on PDA and sporulate with sterilized pine needle after 2 months. *Ascomata* 160–228 × 201–276 μm ($\overline{x}$ = 205 × 233 μm, n = 20), unilocular, gregarious, coriaceous, immersed to erumpent, subglobose, black, non-papillate or with short conical papilla. *Peridium* 39–107 μm wide ($\overline{x}$ = 71 μm, n = 20), composed of 8–13 layers, inner layers hyaline to pale brown, thin-walled cells of *textura angularis*, outer layers dark brown to black, thick-walled cells of *textura globulosa* or *textura angularis*. *Hamathecium* 2.5–5.5 μm wide ($\overline{x}$ = 4.0 μm, n = 30), comprising pseudoparaphyses, that are sparse, hyaline, unbranched, septate, constricted at the septa, smooth-walled. *Asci* 62–118 × 19–27 μm ($\overline{x}$ = 94 × 22.5 μm, n = 30), 8-spored, bitunicate, cylindrical to clavate, slightly curved, evanescent when mature, apically rounded, short pedicellate, with an ocular chamber. *Ascospores* 18–25 × 9–13 μm ($\overline{x}$ = 22 × 11 μm, n = 30), 1–2-seriate, ellipsoidal to ovoid, aseptate, slightly swollen at the middle, hyaline, multi-guttulate, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C. Hyphae initially radiate from the center to the edge, then cover the entire petri-dish, producing abundant aerial hyphae. Colonies raised, fluffy, dense, cream-white to grey at the center, pale brown to grey at the edge from the above; dull white to grey at the center, intermixed with scattered black dots from the reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), asymptomatic roots of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR26D-1 (MHZU 24-0259, holotype); ex-type culture, ZHKUCC 24-0565; *ibid*., living culture ZHKUCC 24-0566.

Notes – In the phylogenetic analyses, ZHKUCC 24-0565 and ZHKUCC 24-0566 formed a branch separated from *Neofusicoccum parvum* (Figure 5.5). The morphology of *N. wurfbainiae* MHZU 24-0259 is similar to *N. parvum* in having erumpent, globose ascomata clavate asci, and hyaline, ellipsoidal ascospores (Slippers et al., 2005). However, the asci of *N. wurfbainiae* are pyriform, cylindrical to clavate, slightly curved, with hyaline, unbranched pseudoparaphyses, but *N. parvum* are clavate, without paraphyses. Furthermore, it can be distinguished from *N. parvum* by having larger ascomata (160–228 × 201–276 μm vs. 5–50(–100) μm high) and smaller asci (62–118 × 19–27 μm vs. 75–143(–210) μm). Therefore, we introduce *N. wurfbainiae* as a novel species.

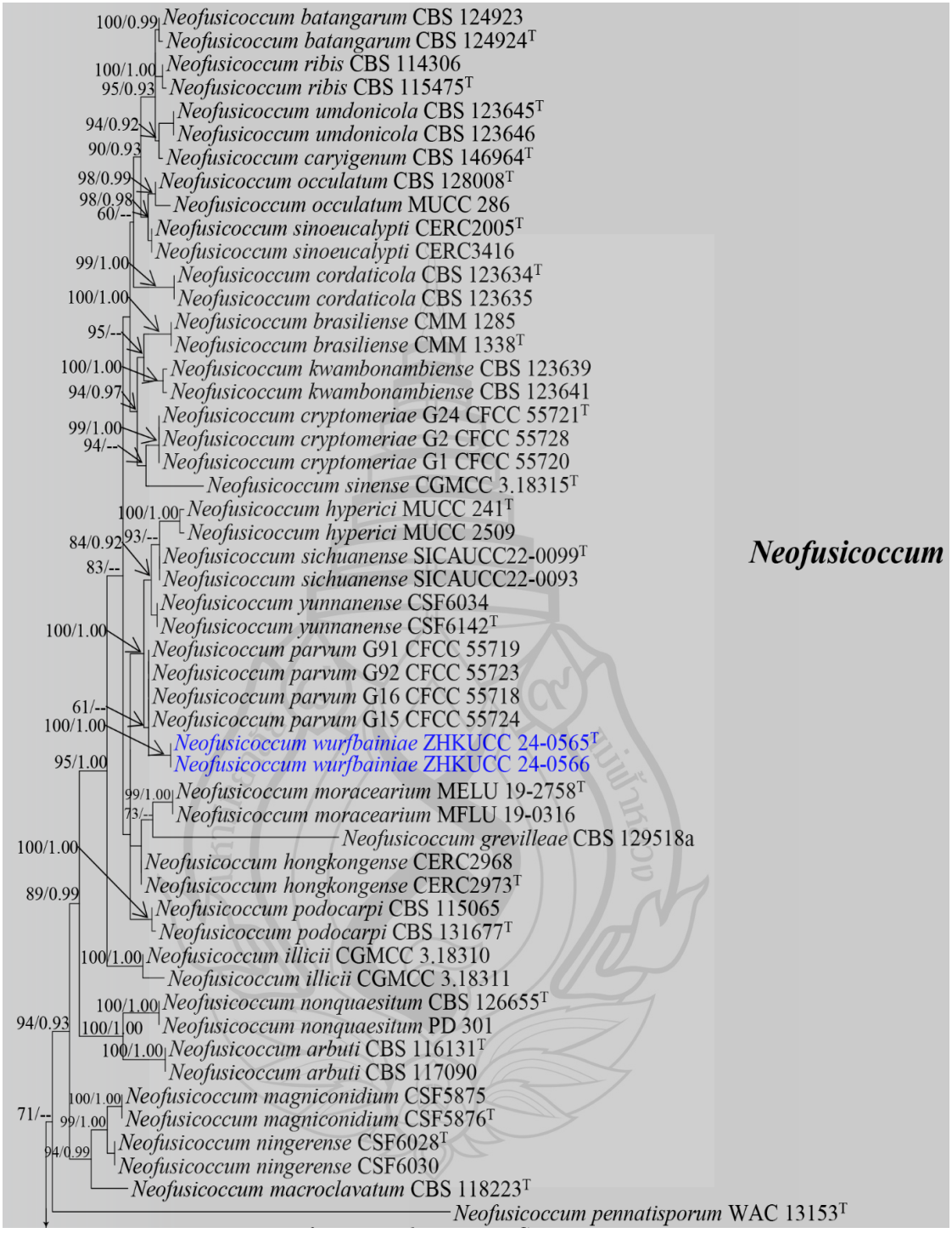
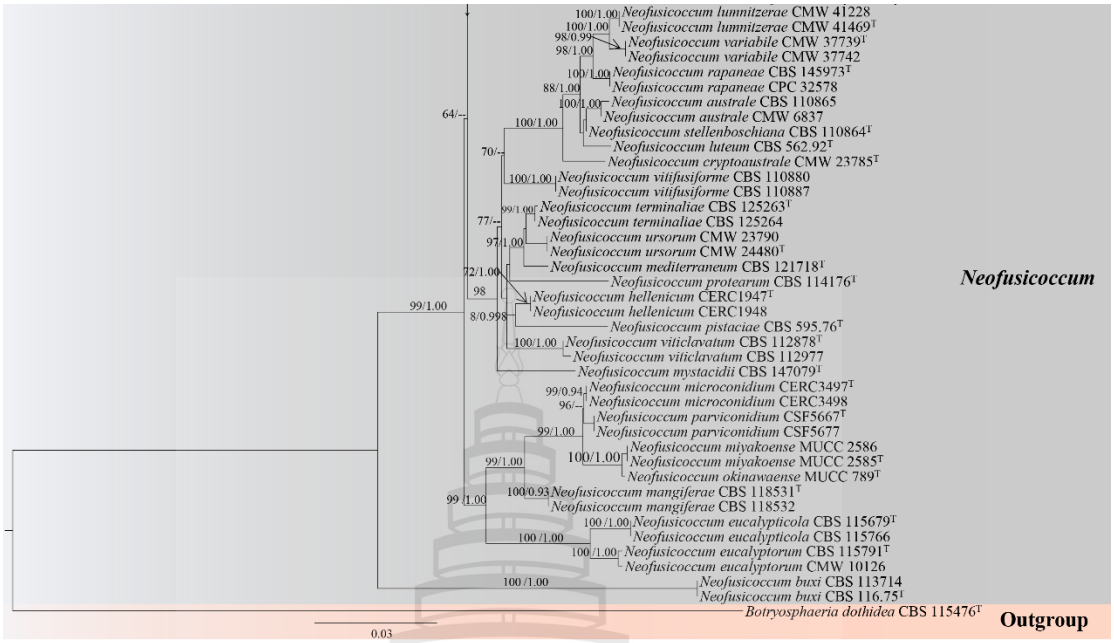
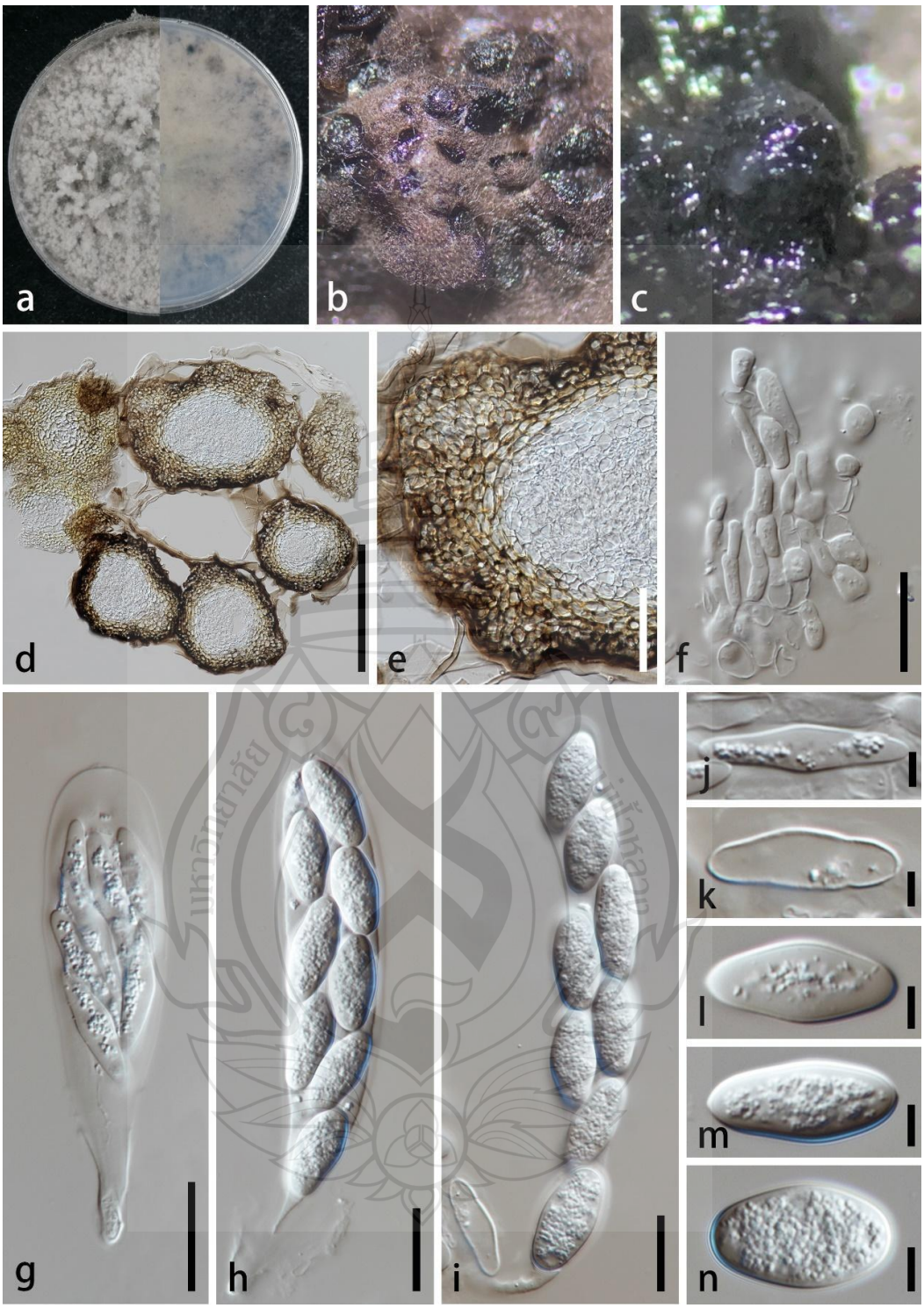


Figure 5.46 Maximum likelihood phylogeny based on combined ITS, *tef1-α*, *tub2*, and *rpb2* sequence data of *Neofusicoccum*



Note Tree rooted as *Botryosphaeria dothidea* (CBS 115476a). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.46 (continued)



Note a Culture characteristic on PDA. b, c Appearance of ascomata on PDA with sterilized pine needle after 2 months. d Section through ascomata. e Peridium. f Pseudoparaphyses. g–i Asci. j–n Ascospores. Scale bars: d = 200 μm, e, f, g–i = 20 μm, j–n = 5 μm.

Figure 5.47 *Neofusicoccum wurfbainiae* (MHZU 24-0259, holotype)

Phyllostictaceae Fr. [as 'Phyllostictei'], Summa veg. Scand., Sectio Post. (Stockholm): 420 (1849)

Notes – Species in Phyllostictaceae are globally distributed and can colonize a wide range of hosts (Liu et al., 2012). They exhibit diverse lifestyles as plant pathogens, endophytes and saprobes (Wikee et al., 2013; Wang et al., 2023). The family currently includes two genera: *Phyllosticta* and *Pseudofusicoccum*, with *Phyllosticta* as the type genus (Phillips et al., 2019; Hyde et al., 2024).

Phyllosticta Pers., Traité champ. Comest. (Paris): 55, 147 (1818)

Notes – *Phyllosticta*, an important plant pathogen genus, causes various leaf spots and fruit brown/black spot diseases worldwide (Wikee et al., 2011; Chaiwong et al., 2024). The genus was first established by Persoon (1818), with *P. convallariae* designated as the type species. Traditionally, *Phyllosticta* was classified based on its asexual morph, while its sexual morph was placed under *Guignardia*. However, molecular phylogenetic studies have confirmed that *Guignardia* is congeneric with *Phyllosticta*, leading to its synonymization (Wikee et al., 2013; Norphanphoun et al., 2020). *Phyllosticta* species have a broad host range, recorded in over 800 plant species, including economically important crops, forest trees, and ornamental plants (Liu et al., 2012). Presently, 3227 epithets are listed under the *Phyllosticta* (https://www.indexfungorum.org/names/names.asp). In this study, we report *Phyllosticta capitalensis* as a new host record on *Wurfbainia villosa*.

Phyllosticta capitalensis Henn., Hedwigia 48: 13 (1908) [1909] Figure 5.49

Index Fungorum number: IF168326; Facesoffungi number: FoF 06888

Endophytic associate on the asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: on PDA after 2 months, *Ascomata* 83–163 × 71–152 μm ($\bar{x}$ = 125 × 109 μm, n = 10), solitary to gregarious, unilocular, coriaceous, immersed or superficial, globose to subglobose, brown to dark brown, ostiolate. *Peridium* 18–37.5 μm wide ($\bar{x}$ = 27.5 μm, n = 30), composed of 3–6 layers of hyaline to brown, thick-walled cells of *textura angularis*. *Hamathecium* 6–10 μm wide ($\bar{x}$ = 8 μm, n = 30), paraphyses, hyaline, septate, strictly constricted at septate, smooth-walled, shorter than asci. *Asci* 52–96 × 16–21 μm ($\bar{x}$ = 71 × 18 μm, n = 30), 8-spored, overlapping bitunicate, cylindrical, slightly curved, apically rounded, short pedicellate. *Ascospores* 15–18 × 7–8 μm ($\bar{x}$ = 16 × 7.7 μm, n = 30), biseriate, fusiform to ellipsoid, straight or curved, aseptate, hyaline, multi-guttulate, swollen at the mid-region, both ends rounded with obtuse

gelatinous caps, smooth-walled. Asexual morph: *Conidiomata* 110–460 × 90–360 μm ($\bar{x}$ = 289 × 203 μm, n = 20), pycnidial, gregarious, multilocular, coriaceous, superficial, subglobose or irregularly shaped, brown to black. *Peridium* 15–3 μm wide ($\bar{x}$ = 23 μm, n = 20), composed of 5–8 layers of hyaline inner cells to brown to black outer cells of *textura angularis* or *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 10–33 × 3.5–7 μm ($\bar{x}$ = 16 × 5 μm, n = 30), phialidic, cylindrical to subulate, hyaline, smooth-walled, straight to slightly curved. *Conidia* 9–12.5 × 6–8 μm ($\bar{x}$ = 11 × 7 μm, n = 30), subglobose, ellipsoid to elongate, limoniform to obpyriform, variable in shape, multi-guttulate when young, single-guttulate when mature, aseptate, hyaline, with rounded to obtuse ends, smooth-walled, enclosed in a thin mucilaginous sheath, 1.5–3 μm wider, bearing a single, short, hyaline, unbranched, straight to curved apical appendage, 3–8 × 1–2 μm ($\bar{x}$ = 5 × 1.5 μm, n = 30). *Spermatia* 7–12.5 × 1.5–3.5 μm ($\bar{x}$ = 9.5 × 2.5 μm, n = 30) hyaline, bacilliform with swollen ends.

Culture characteristics – Colonies on PDA reaching 4.0–4.5 cm in diameter after 1 month at 28 ± 2°C, moderately dense, flat, irregular, undulate, composed of abundant stromata produced on the surface, pale brown to black from above and in reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), asymptomatic leaf of *Wurfbainia villosa*, 1 October 2021, C.F. Liao, AML22C-3 (MHZU 24-0181); living culture, ZHKUCC 24-0456; *ibid*., ZHKUCC 24-0457.

Known hosts (based on molecular data) – from leaf spots of Arecaceae, *Ficus benjamina*, *Ophiopogon japonica*, *Punica granatum*, Orchidaceae, unidentified wild plant; from healthy leaf of *Alocasia* sp., *Anthurium* sp., *Calophyllum* sp., *Codiaeum variegatum*, *Dieffenbachia* sp., *Euphorbia milli*, *Hibiscus syriacus*, Magnoliaceae, *Philodendron* sp., *Poloalthia longifolia*, *Polyscias* sp., *Saccharum officinarum*, *Sansevieria hyacinthodes*, *Tectona grandis*, *Tinospora craspa* (Wikee et al., 2013), *Camellia sinensis* (Cheng et al., 2019), *Citrus* sp. (Guarnaccia et al., 2019; Tran et al., 2019), Curry leaf (Oraon et al., 2025), *Hymenocallis littoralis* (Wu et al., 2024), oil palm (*Elaeis guineensis*) (Nasehi et al., 2020), olive (*Canarium album*) (Zhuang et al., 2025), *Psidium guajava* (Liao et al., 2020), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Australia (Tran et al., 2019), Thailand (Wikee et al., 2013), China (Cheng et al., 2019; Liao et al., 2020; Wu et al., 2024; Zhuang et al., 2025; this study), India (Oraon et al., 2025), Malaysia (Nasehi et al., 2020), worldwide (Guarnaccia et al., 2019).

Notes – In phylogenetic analyses, our strains (ZHKUCC 24-0456 and ZHKUCC 24-0457) clustered with *Phyllosticta capitalensis* with 100% ML/1.00 PP support (Figure 5.48). Morphologically, MHZU 24-0181 resembles *P. capitalensis* in having gregarious, subglobose, brown to black conidiomata and subglobose to ellipsoid, hyaline conidia (Wikee et al., 2013). We observed its sexual morph on PDA after two months, which is characterized by globose to subglobose, brown, ostiolate ascomata, cylindrical asci, fusiform to ellipsoid, hyaline ascospores, swollen at the mid-region, with rounded to obtuse ends bearing gelatinous caps and smooth-walled. Based on molecular and morphological evidence, we identify our isolates as a new host record of *P. capitalensis* from *Wurfbainia villosa.*

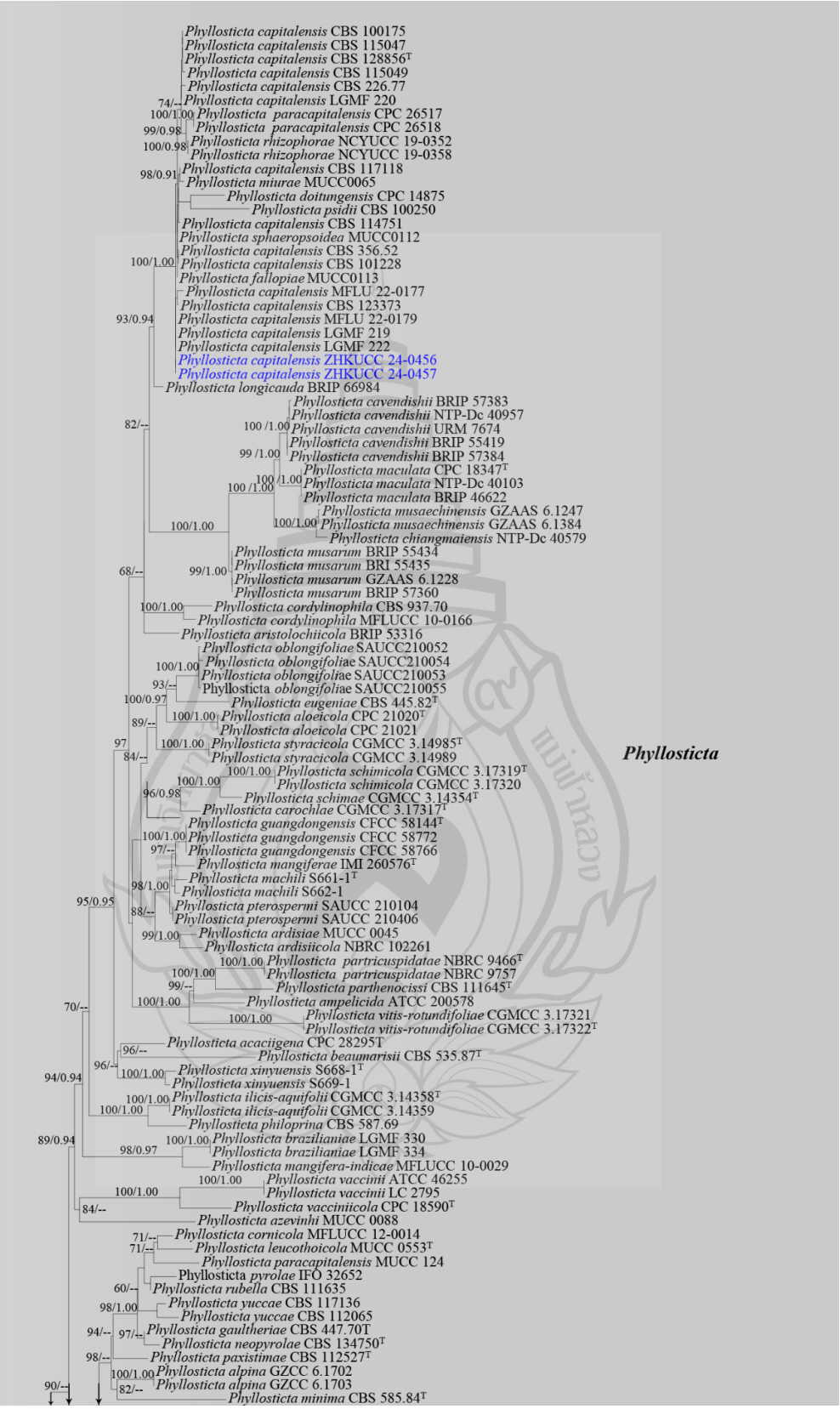
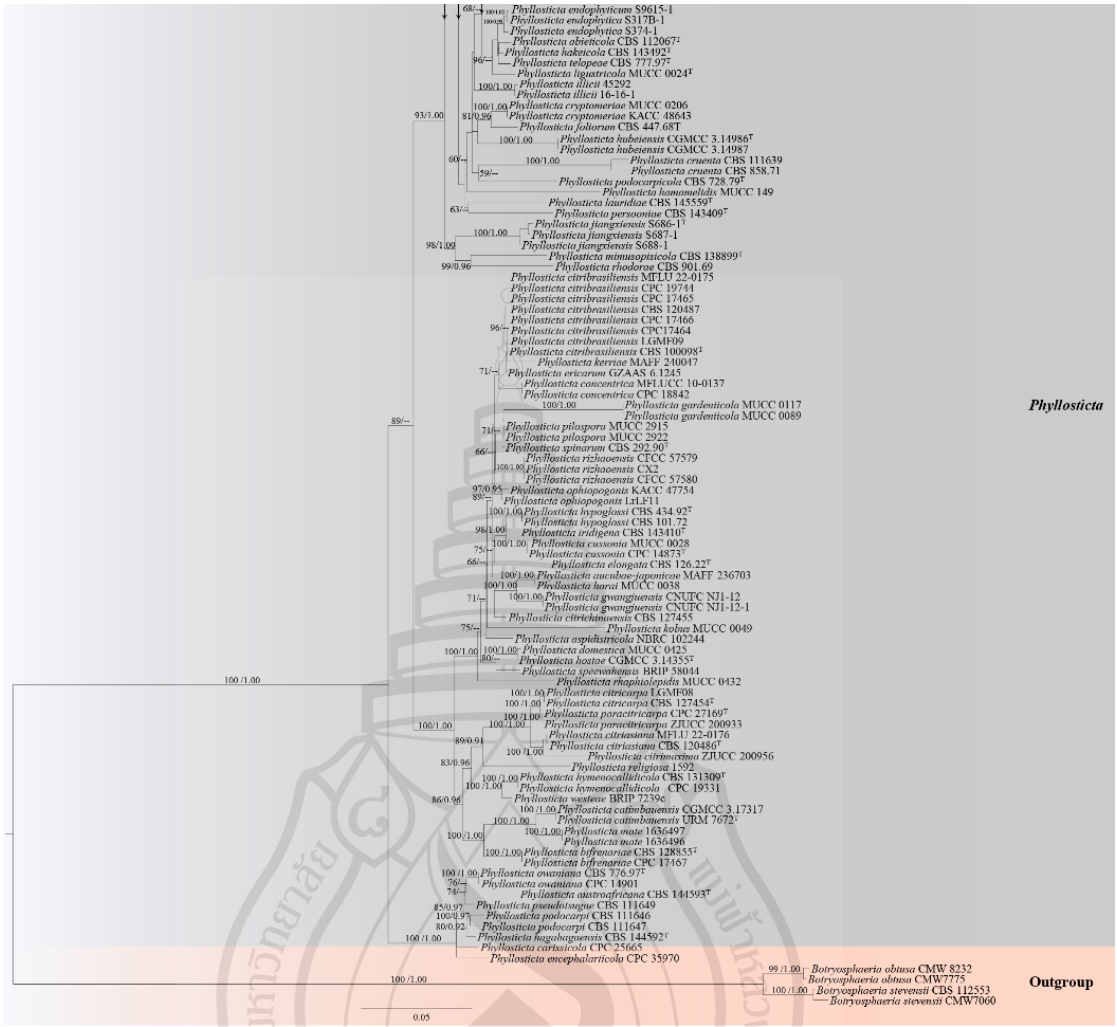
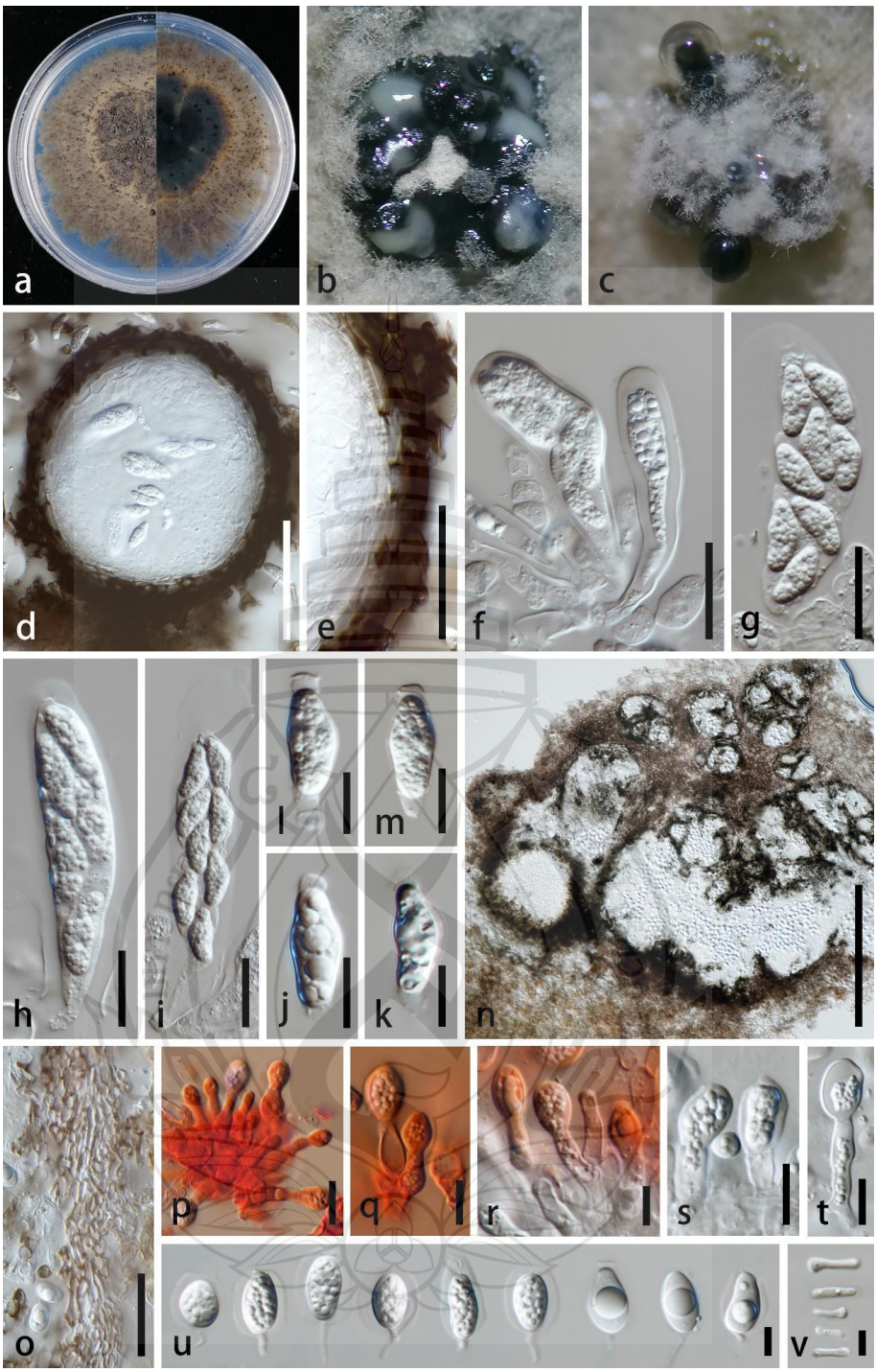


Figure 5.48 Maximum likelihood phylogeny based on combined ITS, LSU, *tef1-α*, *act*, and *gapdh* sequences data of *Phyllosticta*



Note Tree rooted as *Botryosphaeria obtuse* (CMW 8232, CMW7775), *B. stevensii* (CBS 112553, CMW7060). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.48 (continued)



Note a Culture characteristic on PDA after 1 month. b, c Appearance of ascomata on PDA after 2 months. d Section through ascoma. e Peridium. f Paraphyses with asci. g–i Asci. l–k Ascospores. n Section through conidiomata. o Peridium. p–t Conidiogenous cells with conidia. u Conidia. v Spermatial state. Scale bars: d, e = 50 μm, f–i, o = 20 μm, j–l, p–t, v = 10 μm, n = 300 μm, u = 5 μm.

Figure 5.49 *Phyllosticta capitalensis* (MHZU 24-0181, new host record)

Eurotiomycetes O.E. Erikss. & Winka, Myconet 1(1): 6 (1997)

Eurotiales G.W. Martin ex Benny & Kimbr., Mycotaxon 12(1): 23 (1980)

Notes – Five families Aspergillaceae, Elaphomycetaceae, Penicillaginaceae, Thermoascaceae, and Trichocomaceae are accepted in this order. This order includes several ecologically, medically, and industrially important genera, including *Aspergillus*, *Elaphomyces*, *Penicillium*, and *Talaromyces* (Tsang et al., 2018; Hyde et al., 2019; Doilom et al., 2020; Visagie et al., 2024).

Aspergillaceae Link, Abh. K. Akad. Wiss. Berlin: 165 (1826) [1824]

Notes – Members of Aspergillaceae are predominantly saprobic filamentous fungi. They are commonly isolated from diverse environments, including air, foods, fruits, indoor habitats, soil, vegetation, and water (Visagie et al., 2024). Several species in Aspergillaceae have significant industrial applications, such as food fermentation (*Aspergillus oryzae*), and pharmaceutical production (*Penicillium camemberti* and *P. nalgiovense*). However, some species can be pathogens to humans and plants, such as *A. fumigatus* and *P. digitatum* (Nguyen et al., 2020). Currently, over 1000 species have been described in this family, with most taxa belonging to *Aspergillus* and *Penicillium* (Steenwyk et al., 2019; Visagie et al., 2024).

Penicillium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 16 (1809)

Notes – *Penicillium* was described by Link (1809), with *P. expansum* designated as the type species. *Penicillium* species are ubiquitous fungi commonly found in soil, decaying organic matter, indoor environments, and spoiled food (Srinivasan et al., 2020). Some species can be human and plant pathogens; others have significant applications in food industries and enzyme production. The current taxonomic framework recognizes 535 accepted species, classified into two subgenera, 32 sections, and 89 series (Houbraken et al., 2020; Visagie et al., 2024). In this study, we introduced two new species, *Penicillium guangdongensis*, *Pe. wurfbainiae*, and three new records, *Pe. allaniae*, *Pe. meleagrinum*, and *Pe. polonicum*, based on the multi-gene phylogenetic analyses and morphological studies.

Penicillium allaniae Y.P. Tan, Bishop-Hurley, Marney, R.G. Shivas, in Tan & Shivas, Index of Australian Fungi 3: 6 (2022) Figure 5.51

Index Fungorum number: IF900139; Facesoffungi number: FoF 17917

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 1 month, *Conidiophores* mostly monoverticillate, short, smooth-walled. *Stipes* 5–22 × 2–3.3 μm ($\overline{x}$ = 10.5 × 2.5 μm, n = 30), septate, branched, straight, smooth-walled. *Phialides* 3–5.5 × 2–3.5 μm ($\overline{x}$ = 4.5 × 2.5 μm, n = 30), ampulliform to lageniform, hyaline, green at the tips, longitudinally striation, smooth-walled. *Conidia* 3 –4 × 2.7–3.8 μm ($\overline{x}$ = 3.5 × 3.2 μm, n = 30), globose, hyaline to pale green or pale brown, longitudinally striation, rough-walled, tuberculate.

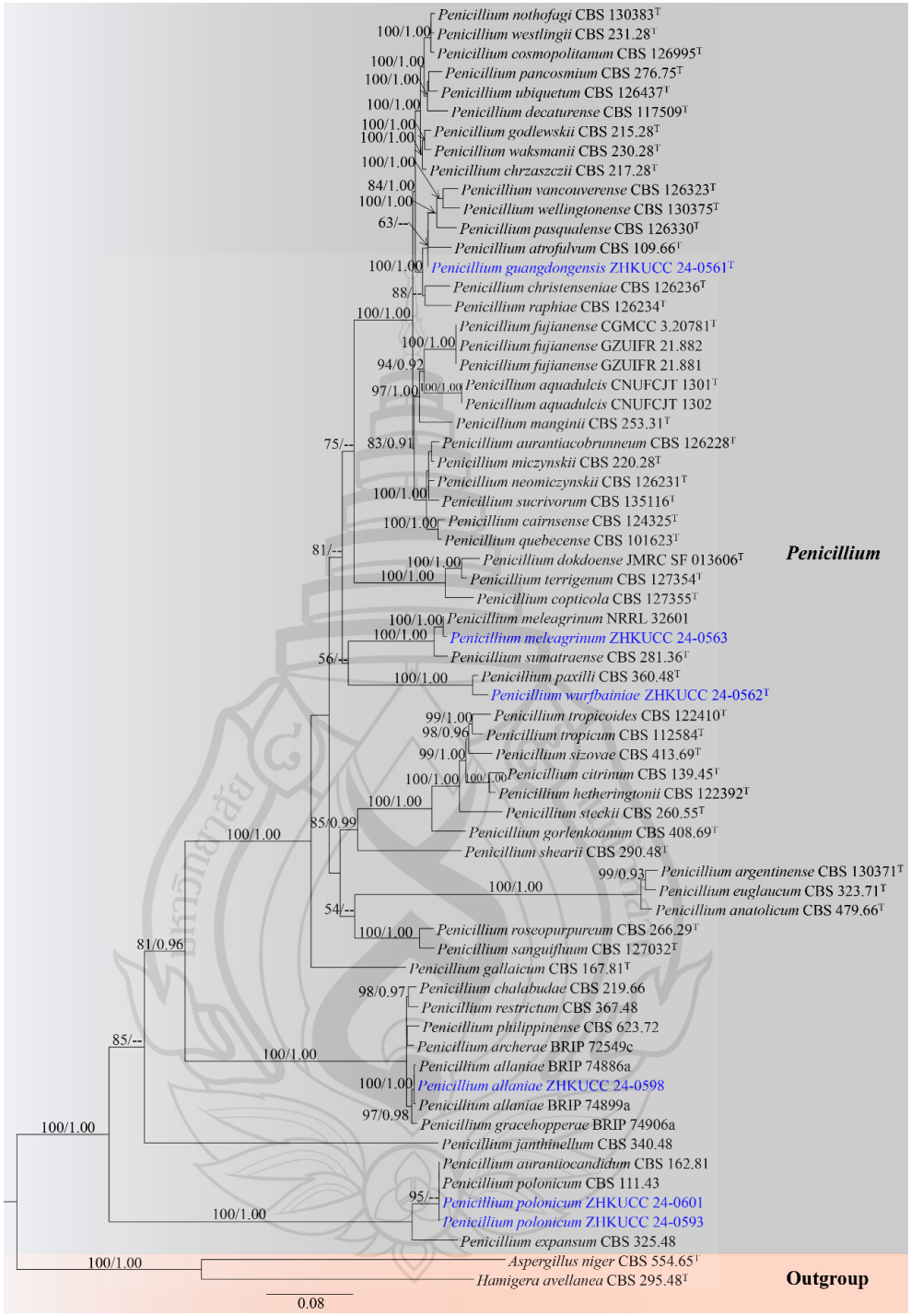
Culture characteristics – Colonies on PDA reaching 3.5–4.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, protuberant at center, with entire edge, velutinous, forming three radially and concentrically circles from above, center circle pale green and exuding abundant droplet-like exudates, middle circle pale yellow, edge circle cream-white, buff from reverse.

Material examined – China, Guangdong Province, Yangchun City, Jinghuaken (22.19027 N, 111.91027 E), from asymptomatic root of *Wurfbainia villosa*, 10 April 2023, C.F. Liao, R5A1 (MHZU 24-0290); living culture, ZHKUCC 24-0598.

Known hosts (based on molecular data) – Soil (Tan & Shivas, 2022), *Wurfbainia villosa* (this study).

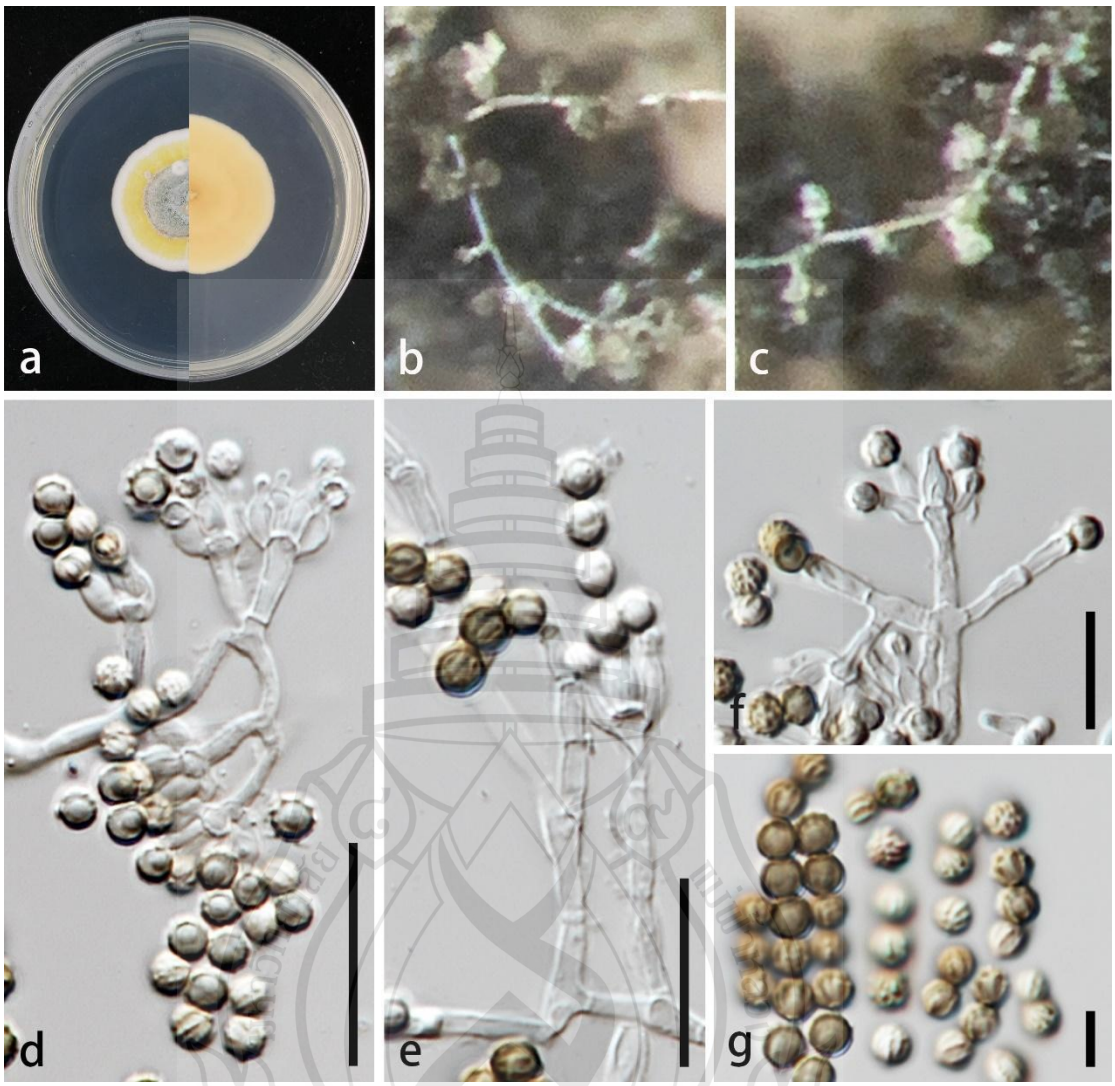
Known distribution (based on molecular data) – *Australia* (Tan & Shivas, 2022), China (this study).

Notes – In the phylogenetic analysis, strain ZHKUCC 24-0598 formed a cluster with *Penicillium allaniae* (BRIP 74886A and BRIP 74899A) with 100 ML/1.00 PP support (Figure 5.50). Tan and Shivas (2022) introduced *Pe. allaniae* isolated from soil in Australia based solely on molecular analysis without providing a detailed morphological description. However, ITS comparison of our strain showed no nucleotides differences (0/459 bp) compared to *Pe. allaniae*. Hence, we identify our isolate as *Pe. allaniae*, which represents a new host and geographical record.



Note Tree rooted with *Aspergillus niger* (CBS 554.65) and *Hamigera avellanea* (CBS 295.48). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.50 Maximum likelihood phylogeny based on the combined ITS, *rpb2*, *tub2*, and CaM sequences data of *Penicillium*



Note a Culture characteristic on PDA after 2 weeks. b, c Conidia on aerial mycelia on PDA after 1 month. d–f Conidiophores with conidia. g Conidia. Scale bars: d = 20 μm, e, f = 100 μm, g = 5 μm.

Figure 5.51 *Penicillium allaniae* (MHZU 24-0290, new host record)

Penicillium guangdongensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.52

Index Fungorum number: IF904019; Facesoffungi number: FoF 17918

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China, where the holotype was collected

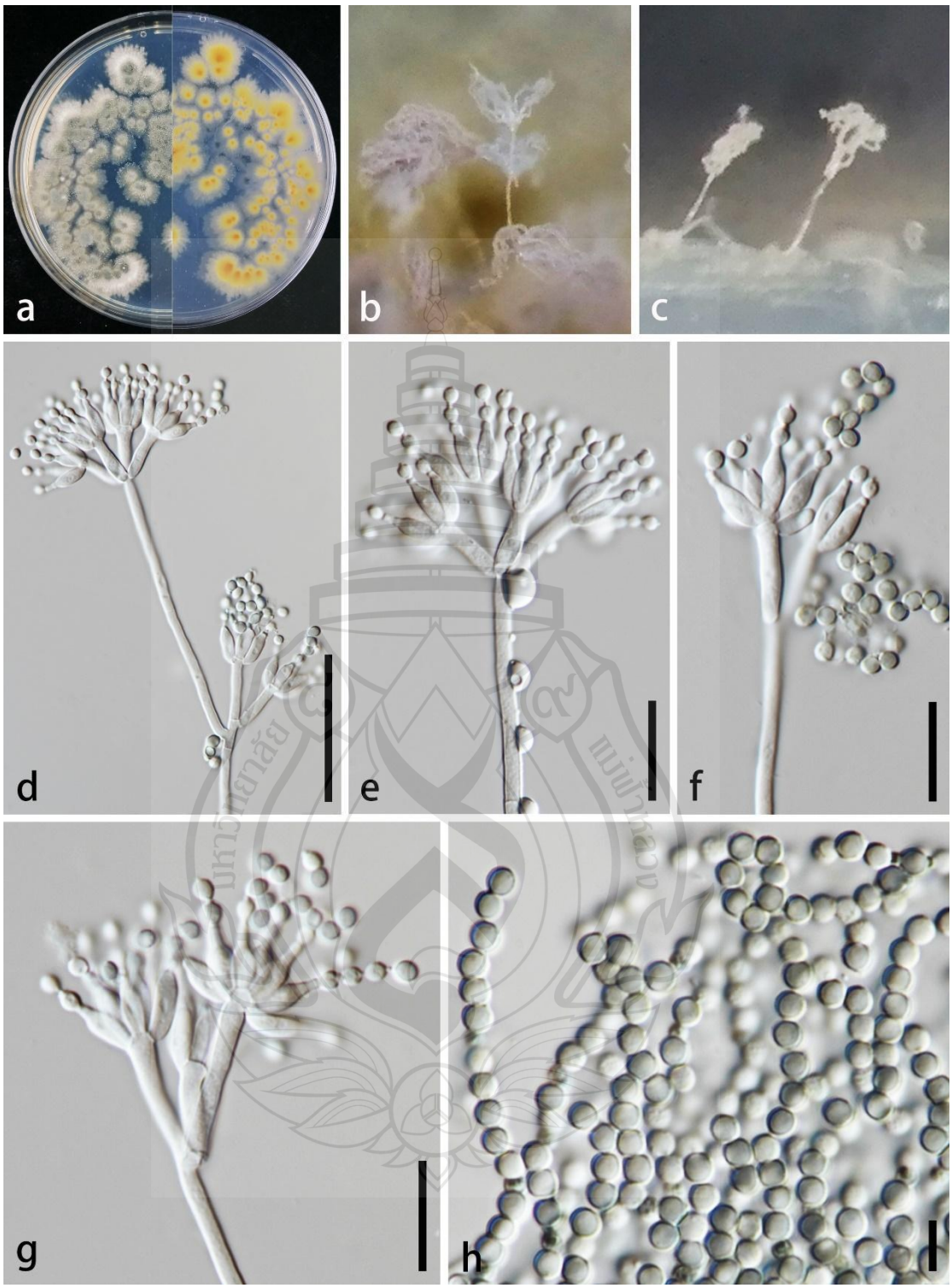
Holotype – MHZU 24-0255

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 1 month, *Conidiophores* biverticillate, sometimes monoverticillate, smooth-walled. *Stipes* 25–123 × 3–4 μm ($\overline{x}$ = 65 × 3.5 μm, n = 30), septate, branched, straight or flexuous, smooth-walled. *Metulae* 9–27 × 2–5 μm ($\overline{x}$ = 14 × 3.5 μm, n = 30), mostly 2–4 per stipe. *Phialides* 8–11 × 2.5–4 μm ($\overline{x}$ = 9.5 × 3 μm, n = 20), flask-shaped, mostly 4–8 per metula, hyaline, aseptate, smooth-walled. *Conidia* 2.5–3.5 × 2–2.8 μm ($\overline{x}$ = 3 × 2.5μm, n = 30), globose to subglobose, hyaline to pale green, smoothed-walled.

Culture characteristics – Colonies on PDA reaching 0.5–1.5 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, protuberant in center, circular, with entire edge, pale green at the center, white at the edge from above, orange to buff at center and cream-white at edge from reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR22C-1 (MHZU 24-0255, holotype); ex-type culture, ZHKUCC 24-0561.

Notes – Phylogenetic analyses placed our strain (ZHKUCC 24-0561) in a sister branch with *Penicillium atrofulvum* (Figure 5.50). *Penicillium guangdongensis* shares morphological similarities with *Pe. atrofulvum* by having biverticillate conidiophores and subglobose conidia (Houbraken et al., 2011). However, *P. guangdongensis* differs from *Pe. atrofulvum* in having shorter stipes (25–123 × 3–4 μm vs. 300–500 × 2.5–3.5 μm) and longer metulae (9–27 × 2–5 μm vs. 10–14 × 2.5–3.5 μm). Based on these morphological and phylogenetic differences, we introduced *Pe. guangdongensis* as a novel species.



Note a Culture characteristic on PDA for 2 weeks. b, c Conidia on aerial mycelia on PDA after 1 month. d–g Conidiophores with conidia. h Conidia. Scale bars: d = 50 µm, e–g = 20 µm, h = 5 µm.

Figure 5.52 *Penicillium guangdongensis* (MHZU 24-0255, holotype)

Penicillium meleagrinum Biourge, La Cellule 33(1): 147 (1923). Figure 5.53

Index Fungorum number: IF904019; Facesoffungi number: FoF 17919

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Conidiophores* mostly monoverticillate, sometimes biverticillate, rarely terverticillate, smooth-walled. *Stipes* 55–133 × 3–5 μm ($\overline{x}$ = 89 × 3.5 μm, n = 30), septate, straight to flexuous, smooth-walled. *Metulae* 9–56 × 2.5–5 μm ($\overline{x}$ = 19.5 × 3.5 μm, n = 20), mostly 1–2 per stipe. *Phialides* 7–10 × 2–4 μm ($\overline{x}$ = 8 × 3 μm, n = 30), ampulliform, 5–10 per metula, hyaline, aseptate, smooth-walled. *Conidia* 2.2–3 × 1.8–2.7 μm ($\overline{x}$ = 2.7 × 2.2 μm, n = 30), globose to subglobose, pale green, smooth-walled.

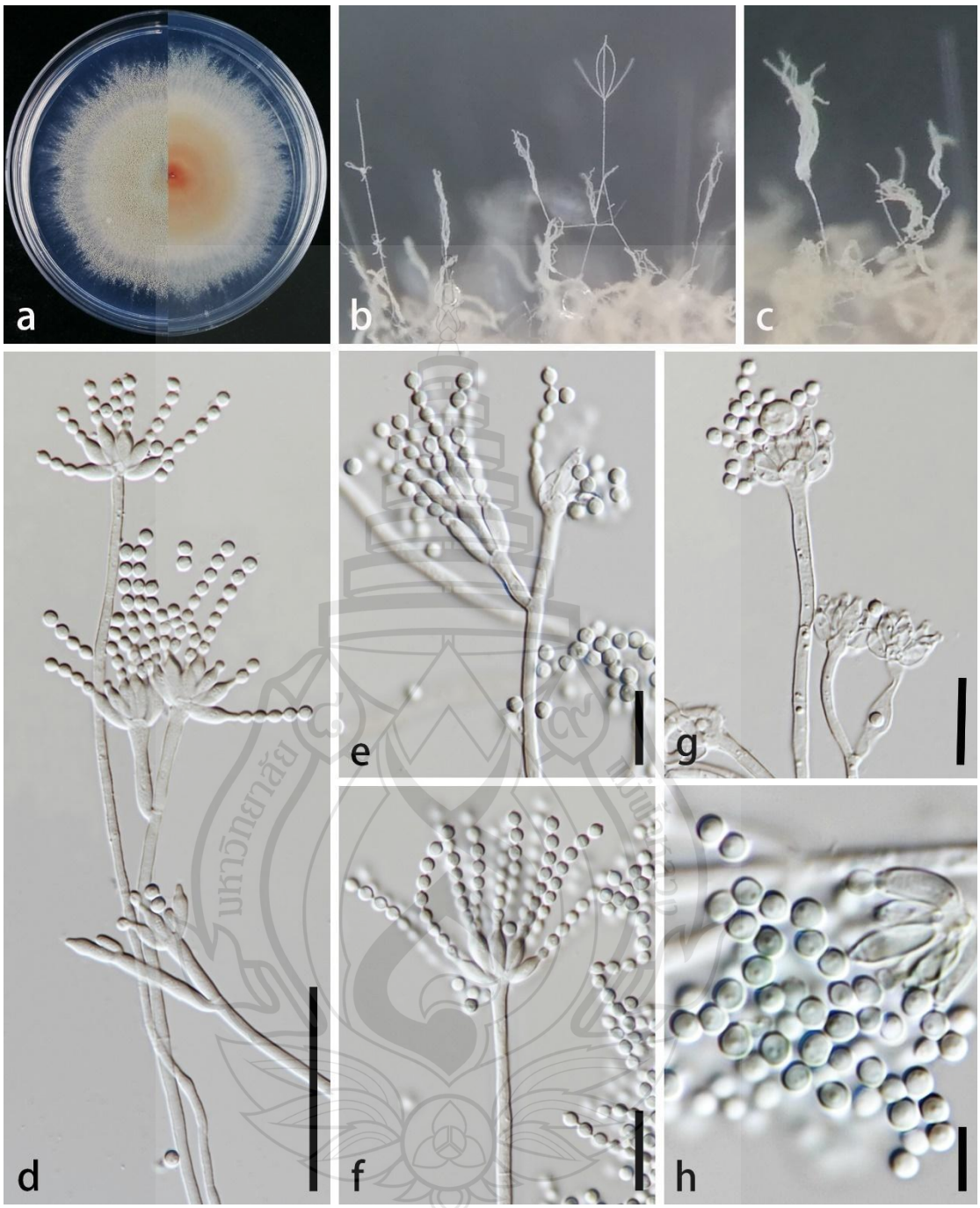
Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 1 month at 28 ± 2°C, moderately dense, protuberant in center, filamentous, with entire edge, velutinous, forming three radially and concentrically circles, pale green to pale brown from above, orange to buff at center and cream-white from reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR26A-1 (MHZU 24-0257); living culture, ZHKUCC 24-0563.

Known hosts – *Lycopersicon esculentum* (Pantidou, 1973), *Wurfbainia villosa* (this study).

Known distribution – Greece (Pantidou, 1973), China (this study).

Notes – In the phylogenetic analyses, strain ZHKUCC 24-0563 clustered with *Penicillium meleagrinum* (NRRL 32601) with 100% ML/1.00 PP support (Figure 5.50). Sequence comparison of the ITS region revealed a single-nucleotide gap difference between our strain and *Pe. meleagrinum*, which suggests that they are the same species. However, we cannot compare the morphology with *Pe. meleagrinum*, which lacks available morphological data. *Penicillium meleagrinum* was originally described from *Lycopersicon esculentum* in Greece (Pantidou, 1973). Here, we report our collection as an endophyte from *Wurfbainia villosa* in China, which represents a new host and geographical record for this species.



Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on PDA. d–g Conidiophores with conidia. h Conidia. Scale bars: d = 50 μm, e–g = 20 μm, h = 5 μm.

Figure 5.53 *Penicillium meleagrinum* (MHZU 24-0257, new host and geographical record)

Penicillium polonicum K.W. Zaleski, Bull. Acad. Polon. Sci., Math. et Nat., Sér. B: 445 (1927) Figure 5.54

Index Fungorum number: IF274889; Facesoffungi number: FoF 16048

Endophytic in asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Conidiophores* terverticillate to eight-whorled, verruculose. *Stipes* 36–71 × 6–14 μm ($\overline{x}$ = 54 × 11 μm, n = 30), septate, branched, straight, verruculose. *Metulae* mostly 2–5 per stipe. *Phialides* 4–62 × 2–10 μm ($\overline{x}$ = 25 × 7 μm, n = 30), ampulliform, cylindrical to lageniform, mostly 2–5 per metula, hyaline, smooth-walled. *Conidia* 3.8–5.6 × 2.8–5.0 μm ($\overline{x}$ = 4.6 × 4.0 μm, n = 30), limoniform to subglobose, hyaline, smooth-walled.

Culture characteristics – Colonies on PDA reaching 0.5–1.5 cm diameter in 5 days at 28 ± 2°C, moderately dense, flat, circular or irregular, entire, pale green from above, reddish orange from reverse, without pigmentation.

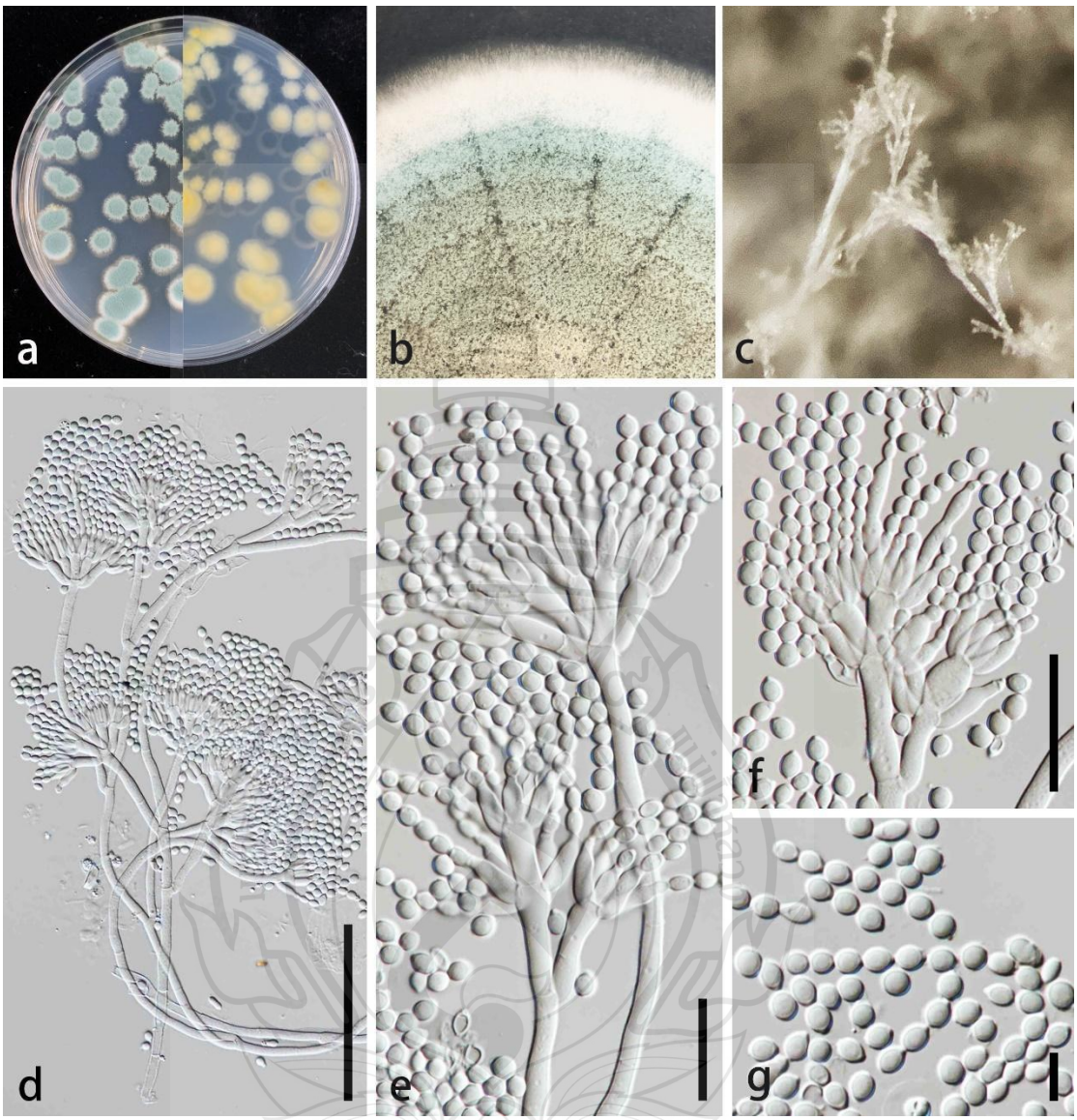
Material examined – China, Guangdong Province, Yangchun City, Jinghuaken (22.19027 N, 111.91027 E), on asymptomatic stem of *Wurfbainia villosa*, 10 April 2023, C.F. Liao, T9C1 (MHZU 24-0293); living culture, ZHKUCC 24-0601, ZHKUCC 24-0593.

Known hosts (based on molecular data) – *Allium cepa* (Duduk et al., 2014, Cakir & Maden, 2015), *Allium sativum* (Bashir et al., 2017), apple (Bradshaw et al., 2022), *Beta vulgaris* (Strausbaugh, 2018), *Dioscorea batatas* (Kim et al., 2008), *Ginko biloba* (Abdel-Fatah et al., 2021), *Malus domestica* (Basson et al., 2019), *Polygonatum cyrtonema* (Chen et al., 2017), *Pyrus bretschneideri* (Khokhar et al., 2019), *Solanum lycopersicum* (Chatterton et al., 2012), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Canada (Chatterton et al., 2012), China (Chen et al., 2017; Khokhar et al., 2019; this study), Egypt (Abdel-Fatah et al., 2021), Pakistan (Bashir et al., 2017), South Africa (Basson et al., 2019), South Korea (Kim et al., 2008), Serbia and Montenegro (Duduk et al., 2017), Turkey (Cakir & Maden, 2015), United States (Strausbaugh, 2018; Bradshaw et al., 2022).

Notes – In the phylogenetical analyses, strains ZHKUCC 24-0593 and ZHKUCC 24-0601 clustered with *Penicillium polonicum* (CBS 111.43) with 100 ML/0.99 PP support (Figure 5.50). Additionally, our strains match *Pe. polonicum* in having terverticillate conidiophores, ampulliform phialides, and globose to subglobose conidia. Based on these

molecular and morphological data, we identify our isolates as *Pe. polonicum*, representing a new host record.



Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on PDA. d–f Conidiophores with conidia. g Conidia. Scale bars: d = 200 μm, e, f = 50 μm, g = 20 μm.

Figure 5.54 *Penicillium polonicum* (MHZU 24-0293, new host record)

Penicillium wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.55

Index Fungorum number: IF904020; Facesoffungi number: FoF 17920

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

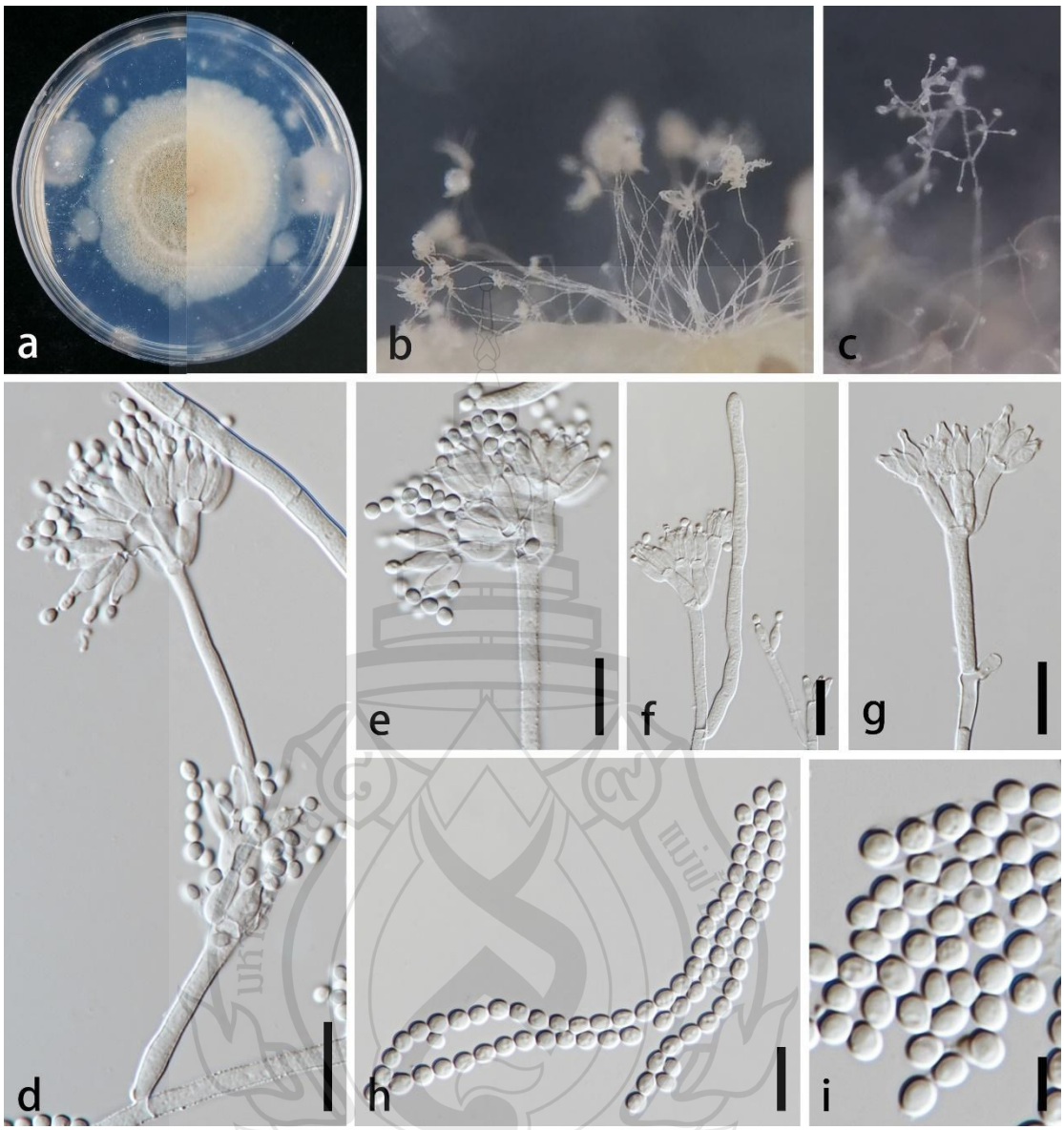
Holotype – MHZU 24-0256

Endophytic in asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 1 month: *Conidiophores* monoverticillate, sometimes biverticillate, rarely terverticillate, smooth or occasionally verruculose. *Stipes* 20–117 × 4–6.5 μm ($\overline{x}$ = 60 × 5 μm, n = 20), septate, branched, straight or flexuous, smooth. *Metulae* 9–21 × 2–6 μm ($\overline{x}$ = 13 × 4 μm, n = 20), mostly 2–4 per stipe. *Phialides* 7–11 × 3–4.5 μm ($\overline{x}$ = 9 × 3.5 μm, n = 20), ampulliform, mostly 4–6 per metula, up to 9 per metula, hyaline, aseptate, smooth-walled. *Conidia* 2.7–3.8 × 2.1–2.8 μm ($\overline{x}$ = 3.3 × 2.5 μm, n = 20), globose to subglobose, hyaline, smoothed-walled.

Culture characteristics – Colonies on PDA reaching 5.5–6.0 cm diameter in 1 month at 28 ± 2°C, moderately dense, protuberant in center, circular, with entire edge, velutinous, pale green to pale brown at the center and cream-white at the edge from above, pale brown to cream-white from reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR25E-5 (MHZU 24-0256, holotype); ex-type culture, ZHKUCC 24-0562.

Notes – The phylogenetic analyses placed our strain (ZHKUCC 24-0562) in a well-supported sister branch with *Penicillium paxilli* with 100% ML/1.00 PP support (Figure 5.50). Morphologically, *Pe. wurfbainiae* differs from *P. paxillin* in having 4–6 verticil, mostly 4–6 per metula, up to 9 per metula, in contrast to 4–8 verticil, 3–6 per metula in *P. paxillin* (Houbraken & Samson, 2011). Based on phylogenetic and molecular differences, we introduce *P. wurfbainiae* as a novel species.



Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on PDA. d–g Conidiophores with conidia. h, i Conidia. Scale bars: d–g = 20 μm, h = 10 μm, i = 5 μm.

Figure 5.55 *Penicillium wurfbainiae* (MHZU 24-0256, holotype)

Talaromyces C.R. Benj., Mycologia 47(5): 681 (1955)

Notes – *Talaromyces* was described by Benjamin (1955) and typified by *T. vermiculatus*. Members of *Talaromyces* are widely distributed across various substrates, including soil, living or decaying plants, sponges, and spoiled foods. They occur as endophytes, saprobes, and pathogens (Lei et al., 2022). For example, *Talaromyces*

marneffei (known as *Penicillium marneffei*) is a significant opportunistic pathogen that primarily infects individuals with weakened immune systems, particularly HIV patients (Mahajan, 2021). There are 297 epithets listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp), of which 203 species are accepted and classified into seven sections (Visagie et al., 2024). In this study, we report a new host record *T. dimorphus* and a new species *Talaromyces wurfbainiae* from *Wurfbainia villosa* in China, as detailed below.

Talaromyces dimorphus X.Z. Jiang & L. Wang, in Jiang, Yu, Ruan & Wang, Scientific Reports 8(no. 4932): 2 (2018) Figure 5.57

Index Fungorum number: IF570521; Facesoffungi number: FoF 17921

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Conidiophores* 34–156 × 2.5–4 μm ($\overline{x}$ = 91 × 3 μm, n = 20), biverticillate, sometimes monoverticillate, smooth-walled. *Stipes* 24–114 × 2.5–4 μm ($\overline{x}$ = 66 × 3 μm, n = 20), straight, smooth-walled. *Metulae* 10–24 × 2.5–4.5 μm ($\overline{x}$ = 15.5 × 3.5 μm, n = 30), mostly 2–4 per vertical, divergent. *Phialides* 11–16 × 2.5 –4 μm ($\overline{x}$ = 13.5 × 3.5 μm, n = 30), ampulliform to lageniform, 4–6 per metula, hyaline, aseptate, smooth-walled. *Conidia* 3.5–4.5 × 2–3.5 μm ($\overline{x}$ = 4 × 2.5 μm, n = 30), ellipsoidal to limoniform, hyaline to pale green, smoothed-walled.

Colonies on PDA reaching 2.5–3.0 cm diameter in 1 week at 28 ± 2°C, moderately dense, raised, circular, with entire edge, velutinous, initially hyaline hyphae, becoming greenish to dull green upon sporulation, greenish to dull green from the above, pale brown to brown from the reverse.

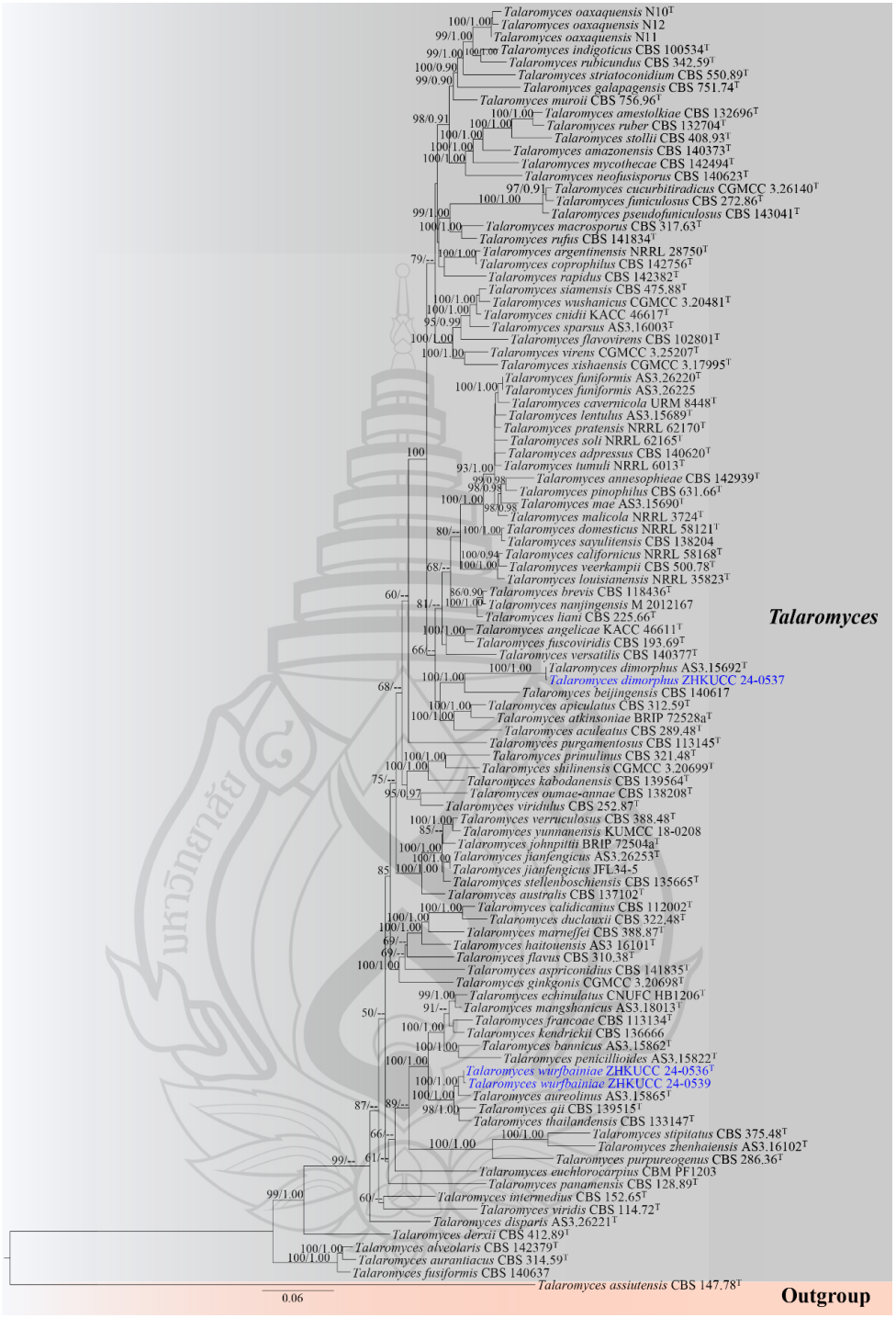
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR26E-3 (MHZU 24-0238); living culture, ZHKUCC 24-0537.

Known hosts (based on molecular data) – Soil (Jiang et al., 2018), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – China (Jiang et al., 2018; this study).

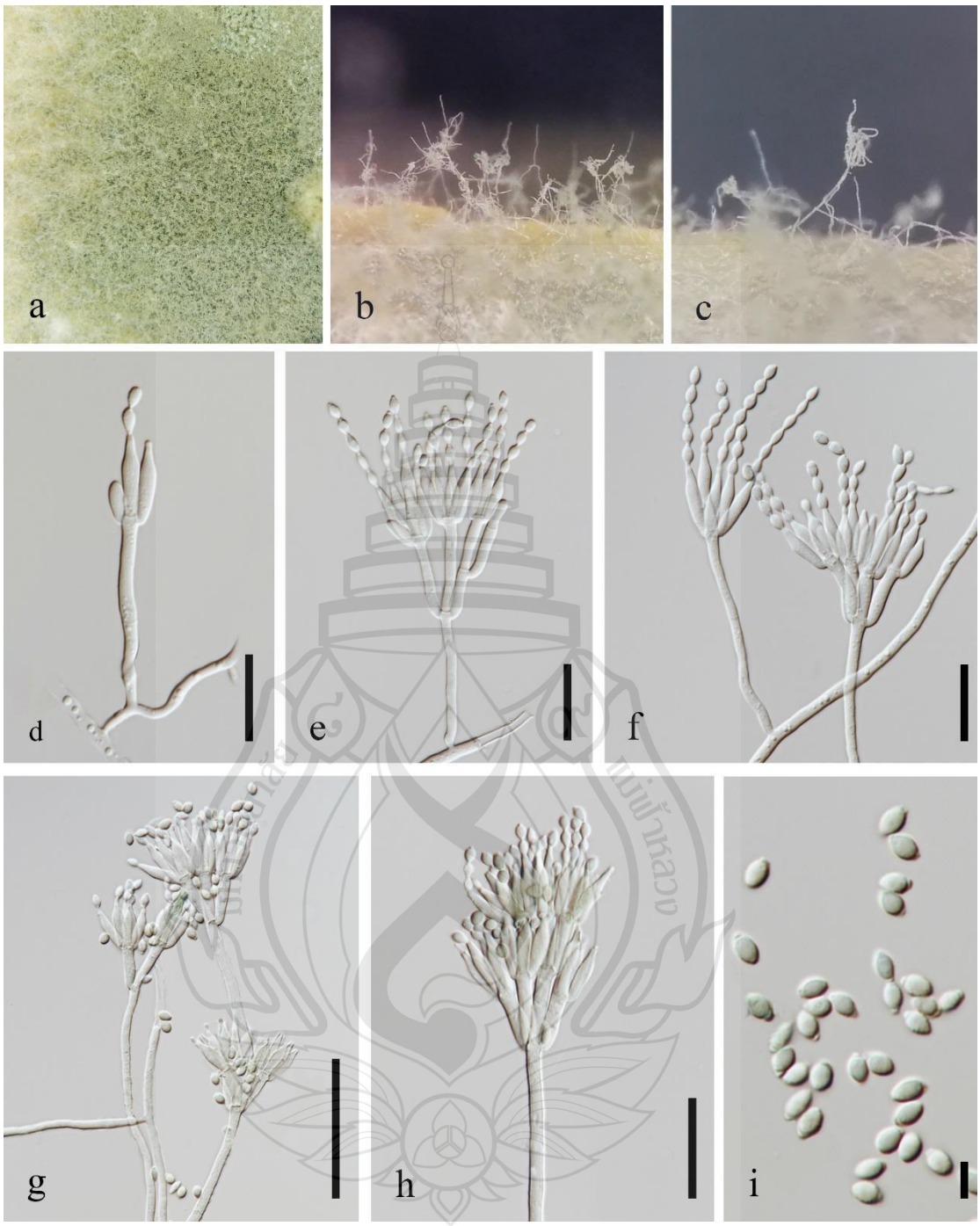
Notes – In the phylogenetic analyses, strain ZHKUCC 24-0537 clustered with *Talaromyces dimorphus* (AS3.15692) with 100 ML/0.99 PP support (Figure 5.56). Our

isolate is similar to *T. dimorphus* in having mostly biverticillate, sometimes monoverticillate conidiophores, mostly bearing two to four per vertical, ampulliform paialides, and ellipsoidal conidia (Jiang et al., 2018). However, our isolate compared with *T. dimorphus* also shows some differences in having longer stipes (24–114 × 2.5–4 μm vs. (15–) 25–50 (−70) × 2.5–3.5 μm) and larger metulae (10–24 × 2.5–4.5 μm vs. 9–13 × 2.5–3.5 μm). Our collection is the new host record from *Wurfbainia villosa*.



Note Tree rooted with *Trichocoma paradoxa* (CBS 788.83). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.56 Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tub2* sequences data of *Talaromyces*



Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d–h Conidiophores with conidia. i Conidia. Scale bars: d–h = 20 µm, i = 5 µm.

Figure 5.57 *Talaromyces dimorphus* (MHZU 24-0238, new host record)

Talaromyces wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.58

Index Fungorum number: IF904021; Facesoffungi number: FoF 17922

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0237

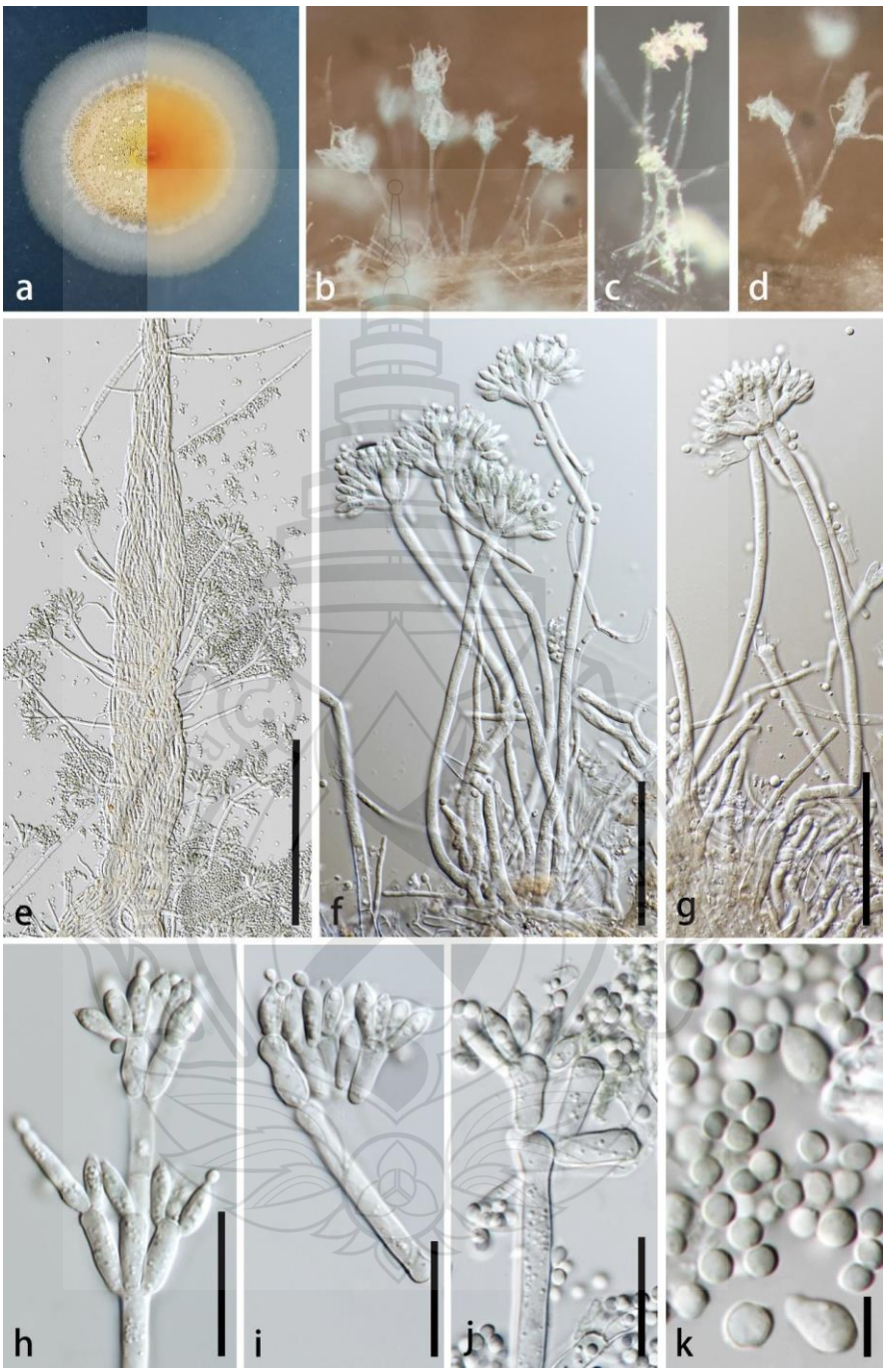
Endophytic in asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On sterilized leaf and stem tissues of *W. villosa* tissues with pine needles on PDA after 2 weeks, *Conidiophores* 137–285 × 4–9 μm ($\overline{x}$ = 194 ×6 μm, n = 20), mostly single verticillate, rarely biverticillate, septate, unbranched, multi-guttulate, smooth- and thick-walled. *Stipes* 75–160 × 4–7 μm ($\overline{x}$ = 112 × 5 μm, n = 20) straight, septate, smooth-walled. *Metulae* 7–15 × 2–7 μm ($\overline{x}$ = 11 × 4.5 μm, n = 30), mostly 6–8 per verticil, oblong, cylindrical to clavate, apically rounded or obtuse, divergent. *Phialides* 8–16 × 3–6 μm ($\overline{x}$ = 10.5 × 4 μm, n = 30), ampulliform, clavate, cylindrical, apically acute or rounded, 3–7 per metula, hyaline, aseptate, smooth-walled. *Conidia* 2.5 –5 μm ($\overline{x}$ = 3 μm, n = 30), globose to subglobose, oval, hyaline to slightly pale green, smoothed-walled.

Colonies on PDA reaching 3.5–4.0 cm diameter in 3 weeks at 28 ± 2°C, moderately dense, raised, circular, with entire edge, pale green to pale brown in center and cream-white at edge from the above, pale orange to cream-white from the reverse

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic roots of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR09A-2 (MHZU 24-0237, holotype); ex-type culture, ZHKUCC 24-0536; *ibid*., living culture, ZHKUCC 24-0539.

Notes – In the phylogenetic analyses, *Talaromyces wurfbainiae* ZHKUCC 24-0536 and ZHKUCC 24-0539 formed a sister branch with *T. aureolinus* (AS3.15864) with 100 ML/1.00 PP support (Figure 5.56). Morphologically, our isolate differs from *T. aureolinus* by having shorter stipe (75–160 × 4–7 μm vs. 300–450 × 3–3.5 μm), larger metula (7–15 × 2–7 μm vs. 9–10 × 4–4.5 μm), larger phialides (8–16 × 3–6 μm vs. 9–10 × 2.5–3 μm), more metula per verticil (6–8 vs. 4–6), slightly larger conidia (2.5 –5 μm vs. 2.5–3 μm) (Wei et al., 2021). Moreover, the conidiophores of our isolate are mostly single verticillate, rarely biverticillate, but *T. aureolinus* are penicilli biverticillate. Additionally, the phialides of our isolate are ampulliform, clavate, cylindrical, but *T. aureolinus* are only ampulliform. However, morphological comparisons may vary due to differences in media used.

Nevertheless, phylogenetic analyses support *T. wurfbainiae* as a distinct species within *Talaromyces*.



Note a Culture characteristic on PDA for 2 weeks. b–d Conidia on aerial mycelia sterilized leaf and stem tissues of *W. villosa* with pine needles on PDA after 2 weeks. e–j Conidiophores with conidia. k Conidia. Scale bars: e = 200 μm, f, g = 50 μm, h–j = 20μm, k = 5 μm.

Figure 5.58 *Talaromyces wurfbainiae* (MHZU 24-0237, holotype)

Sordariomycetes O.E. Erikss. & Winka

Notes – The taxonomic detail please Hyde et al. (2020).

Amphisphaeriales Hawksw. & O.E. Erikss., Syst. Ascom. 5: 177 (1986)

Notes – Amphisphaeriales belongs to the subclass Xylariomycetidae and comprises 16 families Amphisphaeriaceae, Appendicosporaceae, Apiosporaceae, Beltraniaceae, Castanediellaceae, Clypeophysalosporaceae, Hyponectriaceae, Iodosphaeriaceae, Melogrammataceae, Oxydothidaceae, Phlogicylindriaceae, Pseudomassariaceae, Pseudosporidesmiaceae, Pseudotruncatellaceae, Sporocadaceae, and Vialaeaceae (Hyde et al., 2024).

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, Sydowia 50(1): 23 (1998)

Notes – Apiosporaceae was introduced by Hyde (1998), with *Apiospora* designated as the type genus. This family previously comprises five genera: *Appendicospora*, *Arthrinium*, *Dictyoarthrinium*, *Endocalyx*, and *Nigrospora* (Hyde et al., 2020). Later, *Dictyoarthrinium* was transferred to Didymosphaeriaceae by Samarakoon et al. (2020). *Endocalyx* was reclassified in Cainiaceae by Konta et al. (2021). *Appendicospora* was placed in the newly established *Appendicosporaceae* based on morphological and multi-gene phylogenetic evidence by Samarakoon et al. (2022). While *Apiospora*, *Arthrinium*, and *Nigrospora* represent distinct genera through phylogenetic analyses in Apiosporaceae (Pintos & Alvarado, 2021; Liao et al., 2023). Currently, Apiosporaceae includes three accepted genera *Apiospora*, *Arthrinium*, and *Nigrospora* (Han et al., 2024; Hyde et al., 2024).

Apiospora Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 85 (1875)

Notes – *Apiospora* was introduced by Saccardo (Saccardo, 1875) and *Apiospora montagnei* Sacc. as the type species. Crous and Groenewald (Crous & Groenewald, 2013), treated the sexual genus *Apiospora* as a synonym of *Arthinium* on the basis that *Arthinium* is earlier proposal and in more frequent usage (Hawksworth et al., 2011; Réblová et al., 2016). Subsequently, Pintos and Alvarado (2021) re-evaluated the phylogenetic placements of *Apiospora* and *Arthrinium* and distinct them as two separate genera based on multi-locus phylogeny and morphological characters. *Apiospora* is accepted with conidia that are globose to subglobose in the face view and lenticular in the side view with a pale equatorial slit, whereas *Arthrinium* possesses conidia of

various shapes (angular, curved, fusiform, globose, polygonal, and navicular) (Pintos & Alvarado, 2021). Up to now, 211 epithets are listed under *Apiospora* in the Index Fungorum (https://www.indexfungorum.org/names/names.asp).

Apiospora endophytica C.F. Liao & Doilom, sp. nov. Figure 5.60

Index Fungorum number: IF900356; Facesoffungi number: FoF14658.

Etymology – The epithet "*endophytica*" refers to the endophytic lifestyle of the species.

Holotype – ZHKU 23-0002

Endophytic in leaves of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: sporulating on PDA after one month, spore mass visible as black, scattered on white colonies. *Hyphae* 2–5 µm wide ($\bar{x}$ = 2.5 µm, n = 30), branched, hyaline to golden brown, septate, smooth-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–14 × 2–7 µm ($\bar{x}$ = 7.5 × 5 µm, n = 35), aggregated in clusters or solitary, hyaline to golden brown, erect, unbranched, cylindrical or clavate, ampulliform or obtriangular, and smooth-walled. *Conidia* 14–19 × 12–18 µm ($\bar{x}$ = 17 × 15 µm, n = 30) in the face view, 11–19 × 9–16 µm ($\bar{x}$ = 15 × 12 µm, n = 20) in the side view, initially hyaline, becoming pale brown to dark brown, globose to subglobose, obovoid to ellipsoidal in the face view, lenticular with a thick equatorial slit in the side view, and smooth-walled. Sterile cells not observed.

Culture characteristics – colonies on PDA reached 2.6 cm in one week at 28 ± 2°C, fluffy, spreading, with dense, aerial mycelium, composed of small bumps, forming a circle around the center, surface and reverse both golden yellow in the center, and turning white at the edge.

Material examined – China, Guangdong Province, Yangjiang City, Yongning town, 24◦40′53″ N 118◦41′31″ E, asymptomatic leaves of *Wurfbainia villosa*, 1 October 2021, Chunfang Liao, (ZHKU 23-0002, holotype, dried culture); ex-type living culture ZHKUCC 23-0006, *ibid*., and living culture ZHKUCC 23-0007.

Notes – In the phylogenetic analyses (Figure 5.59), *Ap. endophytica* (ZHKUCC 23-0006, ZHKUCC 23-0007) clustered sister to *Ap. hydei* (CBS 114990 and KUMCC 16-0204) with 96% ML bootstrap support and 1.00 BYPP and formed a distinct lineage separated from *Ap. cordylines* (GUCC 10026) with 100% ML bootstrap support and 1.00 BYPP) and *Ap. aurea* (CBS 244.83) by 100% ML bootstrap support and 1.00 BYPP.

Morphologically, conidiogenous cells of *Ap. endophytica* are cylindrical or clavate, ampulliform or obtriangular, while they are subcylindrical to doliiform to lageniform in *Ap. hydei*. The conidia of *Ap. endophytica* are dark brown and smooth, while they are brown and roughened in *Ap. hydei*. In addition, *Ap. endophytica* has larger conidiogenous cells compared to those of *Ap. hydei* (4–14 × 2–7 µm vs. 5–8 × 4–5 µm). *Apiospora endophytica* differs from *Ap. cordylines* and *Ap. aurea* based on the size and shape of conidiogenous cells and conidia. Both morphological and molecular evidence supported *Ap. endophytica* as a new species.

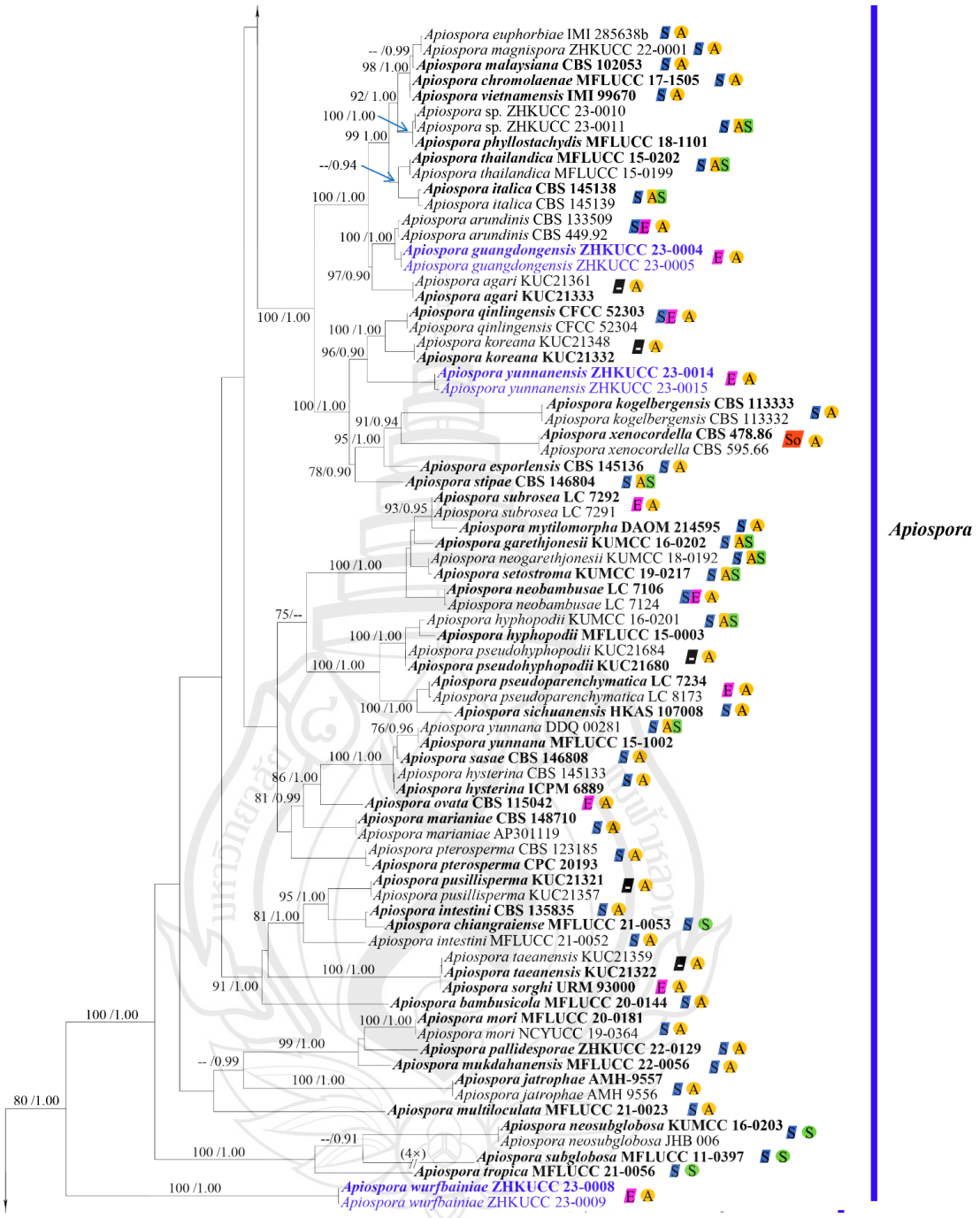
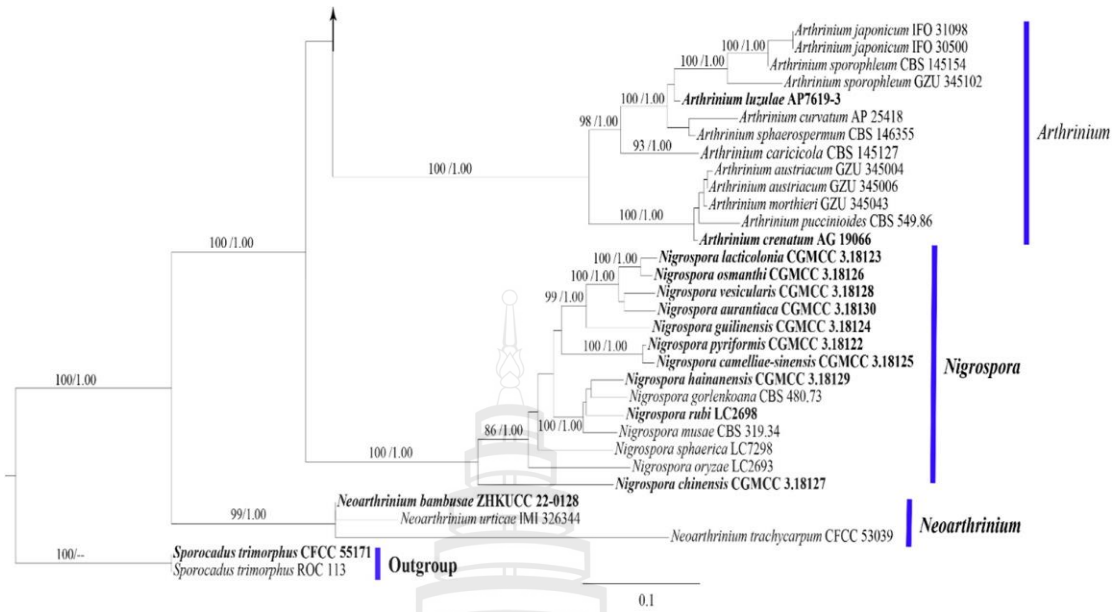
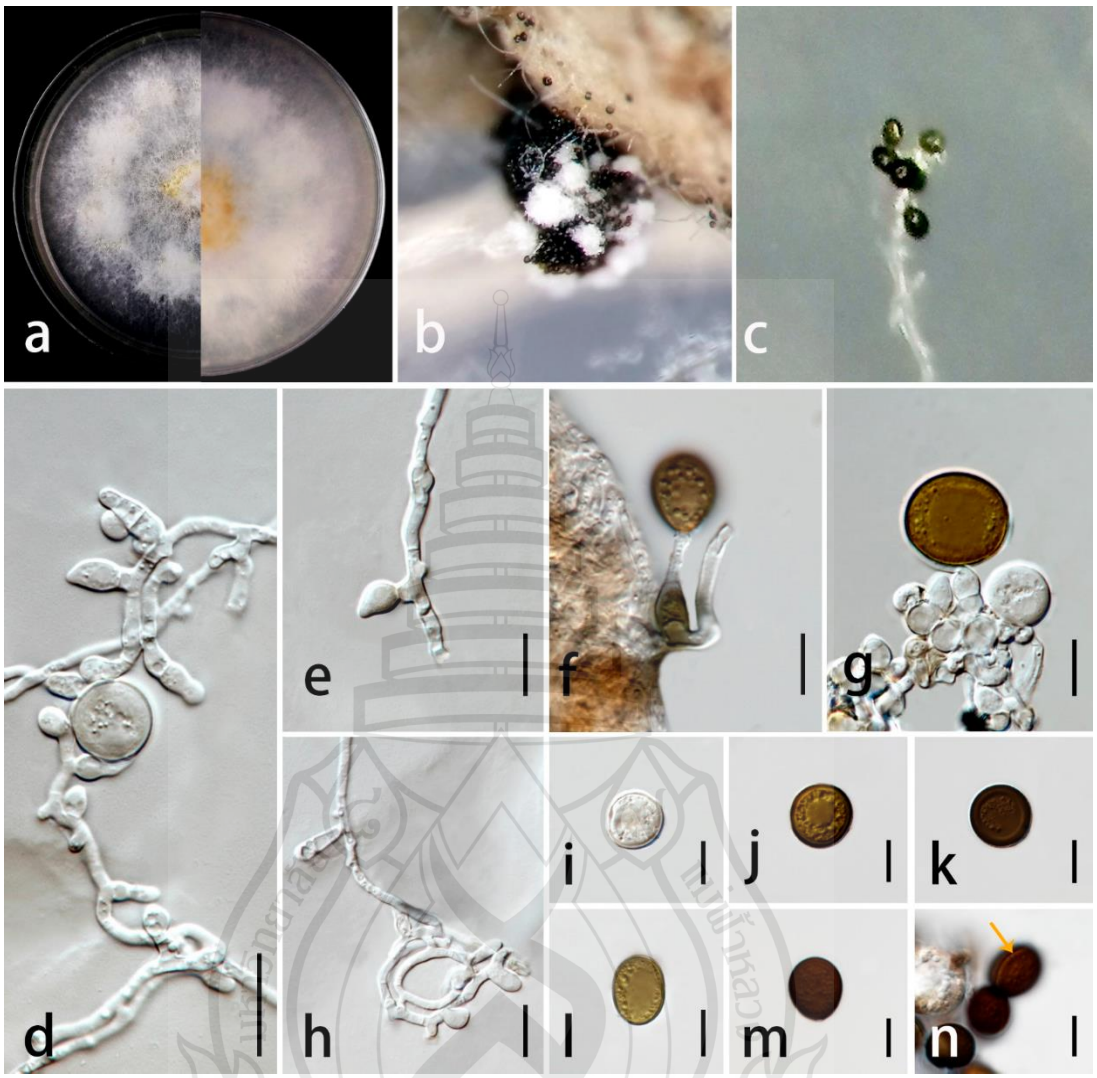


Figure 5.59 Maximum likelihood phylogeny based on the combined ITS, LSU, *tef1-α*, and *tub2* sequences data of *Talaromyces*



Note Maximum likelihood bootstrap values equal or above 75%, and Bayesian posterior probabilities equal or above 0.90 (ML/BYPP) are given at the nodes. A strain number is noted after the species name. The tree is rooted with *Sporocadus trimorphus* (CFCC 55171) and (ROC 113). Hyphen (-) represents support values below 75% ML and 0.90 BYPP. The ex-type strains are bolded black, and the new isolates are in blue.

Figure 5.59 (continued)



Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d–h Conidiophores with conidiogenous cells. i–m Conidia in the face view. n Conidia with germ-slit. Scale bars: d–n = 10 µm.

Figure 5.60 *Apiospora endophytica* (ZHKU 23-0002, holotype)

Apiospora guangdongensis C.F. Liao & Doilom, sp. nov. Figure 5.61

Index Fungorum number: IF900357; Facesoffungi number: FoF14659.

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China where the holotype was collected.

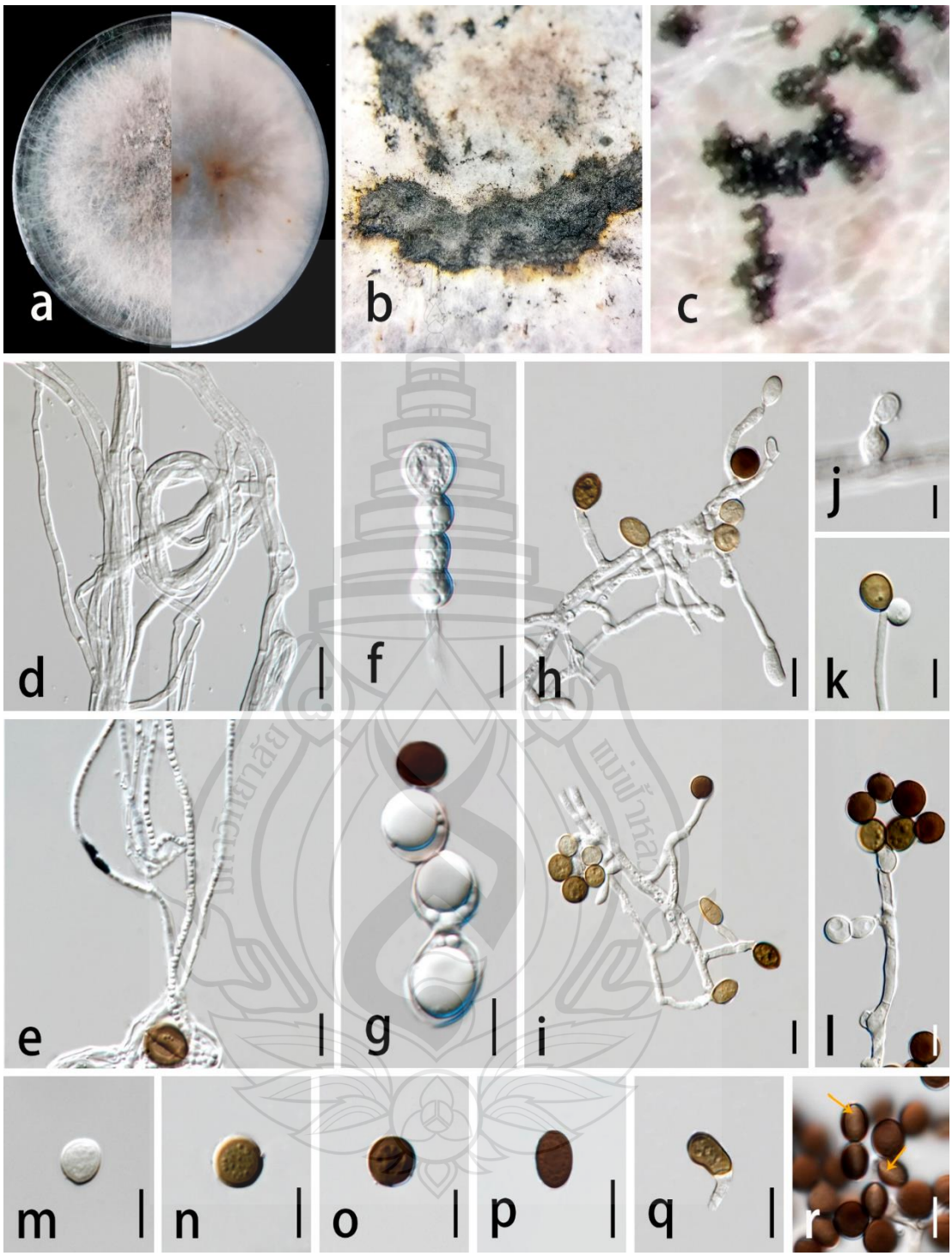
Endophytic in asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: sporulated on PDA after one month, spore mass visible as black, scattered to aggregated on white colonies. *Hyphae* 2–3 µm diam. ($\overline{x}$ = 2.5 µm,

n = 30), branched, hyaline, septate, smooth, thin-walled, forming hyphal coils. *Conidiophores* 45–53 × 2–4 µm ($\bar{x}$ = 49 × 2.5 µm, n = 30), micronematous, mononematous, erect, solitary, subcylindrical, unbranched, straight or flexuous, hyaline, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 4–9 × 2–5 µm ($\bar{x}$ = 6 × 3.5 µm, n = 30), arising from hyphae, aggregated in clusters or solitary, terminal or lateral, smooth, straight or slightly curved, cylindrical or ampulliform, and sometimes ovate or obpyriform. *Conidia* 6–9 × 5–9 µm ($\bar{x}$ = 8 × 7 µm, n = 30) in the face view, 5–8 × 4–6 µm ($\bar{x}$ = 6.5 × 5 µm, n = 30) in the side view, initially hyaline, becoming pale brown to dark brown, globose to ellipsoidal in face view, lenticular with broad equatorial slit in the side view, aseptate, smooth-walled. Sterile cells 9–16 × 3–8 µm ($\bar{x}$ = 12 × 5 µm, n = 30), light brown, elongate. *Chlamydospores* produced in chain, terminal, globose to subglobose, hyaline, smooth-walled.

Culture characteristics – colonies on PDA reaching 6.6 cm in one week at 28 ± 2°C, floccose, sparse, concentrically spreading, forming aerial mycelia, edge irregular, surface pale brown in center, white at the edge, with punctate or flaky black spores, reverse white to pale brown with some pale brown spot, no pigment.

Material examined – China, Guangdong Province, Yangjiang City, Yongning town, 24◦40′53″ N 118◦41′31″ E, asymptomatic leaves of *Wurfbainia villosa*, 1 October 2021, Chunfang Liao, (ZHKU 23-0001, holotype, dried culture); ex-type cultures ZHKUCC 23-0004, *ibid*., living culture ZHKUCC 23-0005.

Notes – The phylogenetic analyses showed that *Ap. guangdongensis* (ZHKUCC 23-0004 and ZHKUCC 23-0005) formed a sister branch to *Ap*. *arundinis* with 100% ML bootstrap support and 1.00 BYPP (Figure 5.59). The morphology of *Ap. guangdongensis* differs from *Ap*. *arundinis* by having shorter conidiogenous cells (4–9 × 2–5 µm vs. 6–12 × 3–4 µm) and larger conidia (6–9 × 5–9 µm vs. (5–)6–7 µm in the face view, 5–8 × 4–6 µm vs. 3–4 µm) (Crous & Groenewald, 2013). The conidiogenous cells of *Ap*. *guangdongensis* are cylindrical or ampulliform, sometimes ovate or obpyriform, while they are ampulliform in *Ap*. *arundinis*. Based on distinct morphological and molecular evidence, we propose *Ap*. *guangdongensis* as a new species.



Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d, e Mycelium. f, g Chlamydospores. h–l Conidiophores with conidiogenous cells. m–p Conidia in the face view. q Elongated conidia (sterile cells). r Conidia with germ-slit (arrows). Scale bars: d–r = 10 µm.

Figure 5.61 *Apiospora guangdongensis* (ZHKU 23-0001, holotype)

Apiospora phyllostachydis (C.L. Yang, X.L. Xu & K.D. Hyde) Pintos & P. Alvarado. Fungal Systematics and Evolution. 7: 206 (2021) Figure 5.62

Index Fungorum number: IF55739; Facesoffungi number: FoF 05498

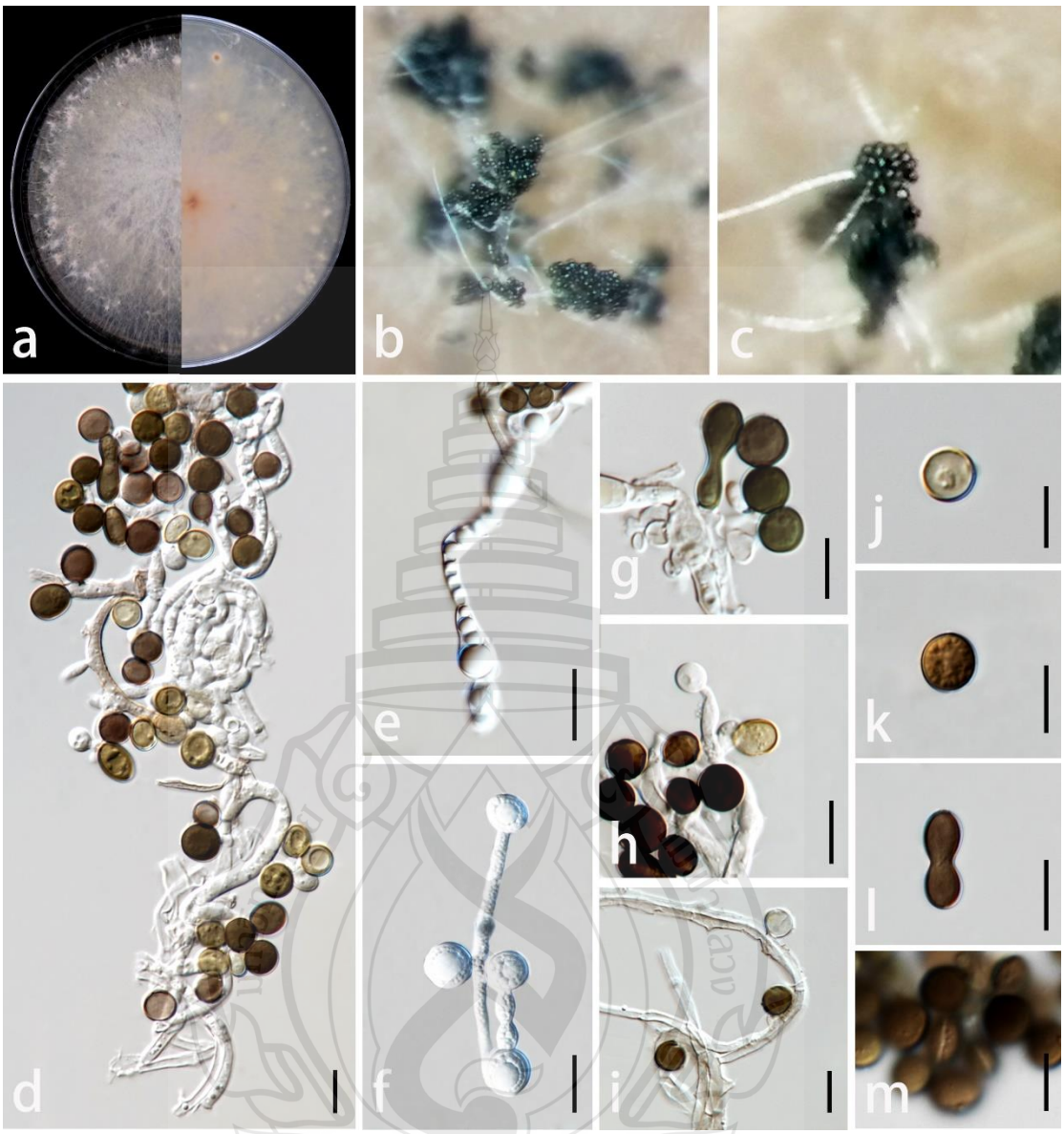
Endophytic from asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: sporulated on PDA after two months, spore massed visible as black, scattered on colonies. *Hyphae* 2–4 μm diam. ($\bar{x}$ = 3 μm, n = 30), branched, hyaline to pale brown, septate, smooth-walled. *Conidiophores* mostly reduce to conidiogenous cells. *Conidiogenous cells* 3–21 × 3–5 μm ($\bar{x}$ = 11 × 4 μm, n = 10), hyaline, oblong to obpyriform, aggregated in clusters. *Conidia* in the face view 5–9 × 4–8 μm ($\bar{x}$ = 7 × 6 μm, n = 30), in the side view 5–7 × 4–5 μm ($\bar{x}$ = 6 × 4.5 μm, n = 30), initially hyaline, becoming pale brown to dark brown, guttulate, globose to subglobose in the face view, lenticular with pale equatorial slit in the side view, aseptate, smooth-walled. *Sterile cells* 8–20 × 2–6 μm ($\bar{x}$ = 12 × 5 μm, n = 15), brown to dark brown, pyriform to cylindrical, vase-shaped.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District, on living leaf of *Wurfbainia villosa*, 1 October 2021, Chunfang Liao, AML12A-2 (MHZU 23-0010, dried culture), living culture ZHKUCC 23-0010; *ibid.*, living culture ZHKUCC 23-0011.

Known distribution (based on molecular data) — China (Yang et al., 2019, this study),

Known hosts (based on molecular data) — *Phyllostachys heteroclada* (Yang et al., 2019), *Wurfbainia villosa* (this study).

Notes – In the phylogenetic analyses (Figure 5.59), *Apiospora* isolates (ZHKUCC 23-0010, ZHKUCC 23-0011) clustered with *A. phyllostachydis* with 100 % ML and 1.00 BYPP. The comparison of ITS, LSU, *tef1-α*, and *tub2* sequence data of our collection are identical to those of *A. phyllostachydis* (MFLUCC 18-1101; ex-type). Morphologically, our collection is different from *A. phyllostachydis* (MFLUCC 18-1101) in having shorter and wider conidiogenous cells (3–21 × 3–5 μm *vs.* 20–55 × 1.5–2.5 μm) (Yang et al., 2019). We conclude that our collection is *A. phyllostachydis* based on molecular evidence, despite the minor differences in conidia and conidiogenous cells size being negligible. This is the first report of *A. phyllostachydis* from *W. villosa*.



Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d, g–i Conidiophores with conidiogenous cells. e, f Chlamydospores. j, k Conidia. l Elongated conidium (sterile cell). m Conidia with germ-slit. Scale bars: d–m = 10 μm.

Figure 5.62 *Apiospora phyllostachydis* (MHZU 23-0010, a new host record)

Apiospora wurfbainiae C.F. Liao & Doilom, sp. nov. Figure 5.63

Index Fungorum number: IF900355; Facesoffungi number: FoF 14660.

Etymology: The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*, from which the holotype was collected.

Endophytic in asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: sporulated on PDA after three months, spore mass visible as black, scattered on colonies. *Hyphae* 1–3 µm diam. ($\overline{x}$ = 2 µm, n = 30), branched, hyaline, septate, smooth, forming hyphal coils. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, branched. *Conidiogenous cells* 7–50 × 2–8 µm ($\overline{x}$ = 22 × 5 µm, n = 60), holoblastic, monoblastic, discrete, hyaline, straight or curved, cylindrical to lageniform, smooth-walled. *Conidia* 7–9 × 5–9 µm ($\overline{x}$ = 8 × 7 µm, n = 30) in the face view, 6–9 × 3–6 µm ($\overline{x}$ = 7 × 4.5 µm, n = 20) in the side view, obovoid, globose to subglobose in face view, lenticular with pale equatorial slit in the side view, initially hyaline, becoming pale brown to dark brown, multi-guttulate, smooth-walled. *Sterile cells* 8–31 × 2–12 µm ($\overline{x}$ = 14 × 5 µm, n = 30), light brown, elongated, cylindrical, ovate, triangular-shaped.

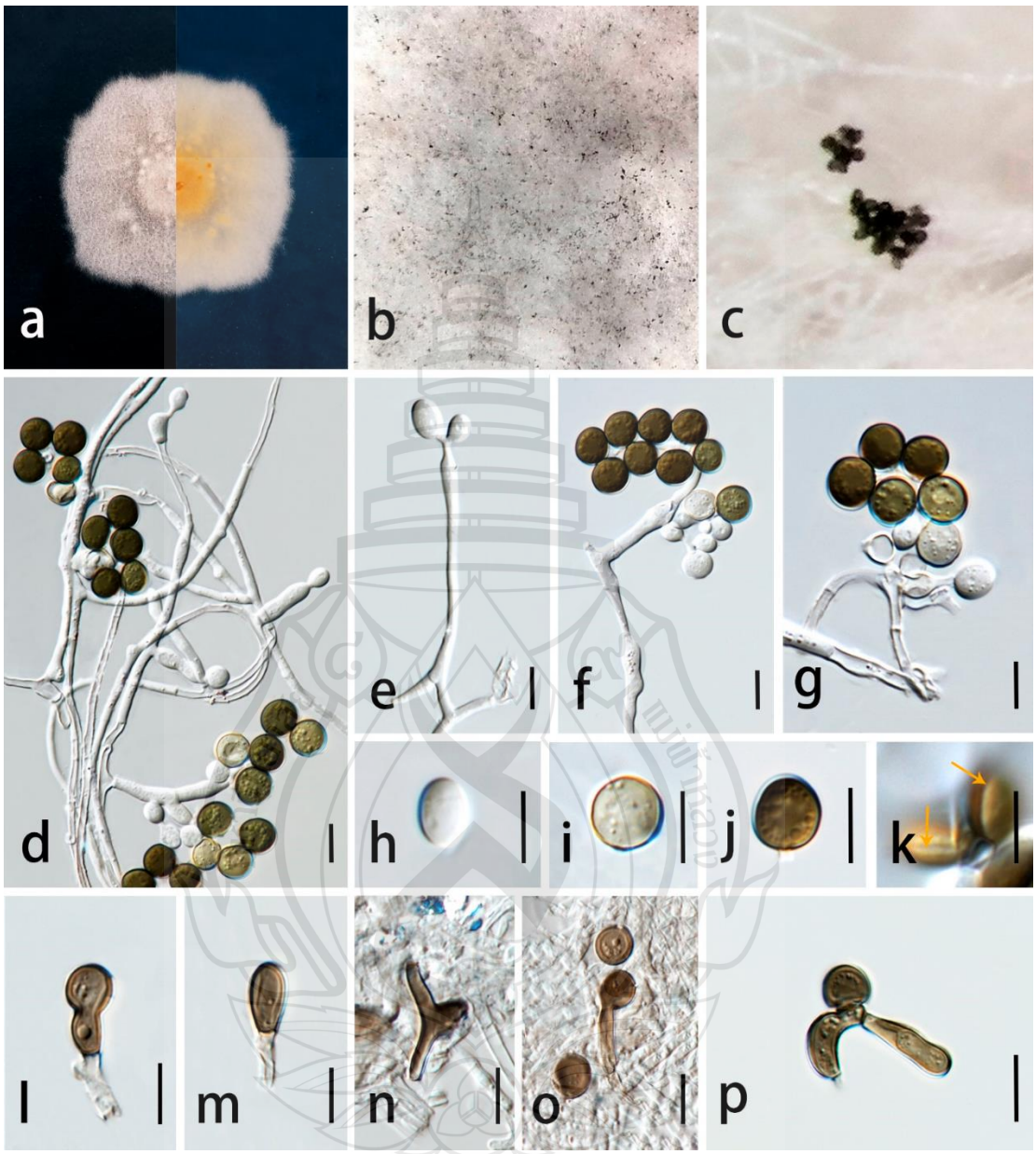
Culture characteristics: colonies on PDA reaching 6.8 cm in one week at 28 ± 2°C, flatted, dense mycelium, edge regular, gray in the center, with some white globular spots from above; pale yellow to gray with some orange spots from below.

Material examined: China, Guangdong Province, Yangjiang City, Yongning town, 24◦40′53″ N 118◦41′31″ E, asymptomatic leaves of *Wurfbainia villosa*, 1 October 2021, Chunfang Liao, (ZHKU 23-0003, holotype, dried culture); ex-type living culture ZHKUCC 23-0008, *ibid*., living culture ZHKUCC 23-0009.

Notes: *Apiospora wurfbainiae* shares morphological similarities to *Ap. guangdongensis* in having globose conidia as well as overlapping conidial size (7–9 × 5–9 µm vs. 6–9 × 5–9 µm in the face view). However, *Ap. wurfbainiae* has larger conidiogenous cells (7–50 × 2–8 µm vs. 4–9 × 2–5 µm) than *Ap. guangdongensis*. The sterile cells of *Ap. wurfbainiae* are elongated, cylindrical, ovate, triangular shaped, while only elongated cells were observed in *Ap. guangdongensis*.

In the phylogenetic analysis (Figure 5.59), *Ap. wurfbainiae* (ZHKUCC 23-0008, ZHKUCC 23-0009) form a distinct subclade which is basal to *Apiospora* clade with 80% ML and 1.00% BYPP. Further, this subclade is closely related to another subclade consisting of *Ap. tropica*, *Ap. subglobosa*, and *Ap. neosubglobosa*. Morphologically, *Ap. tropica*, *Ap. subglobosa*, and *Ap. neosubglobosa* were described based on their sexual morph but *Ap. wurfbainiae* was identified solely by its asexual morph. Thus, their morphological characteristics could not be compared. However,

molecular evidence clearly separates *Ap*. *wurfbainiae* from other known *Apiospora* species. Hence, we introduce *Ap*. *wurfbainiae* as a novel species.



Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. d–j Conidia. k Conidia in the side view with germ-slit (arrows). l–n Sterile cells. o, p Sterile cell with conidia. Scale bars: d–p = 10 µm.

Figure 5.63 *Apiospora wurfbainiae* (ZHKU 23-0003, holotype)

Nigrospora Zimm., Centbl. Bakt. ParasitKde, Abt. I 8: 220 (1902)

Notes – *Nigrospora* was introduced by Zimmerman (1902) with the type species *N. panici*. Members of *Nigrospora* are widely distributed in various habitats, including living and decaying plants, detritus, dead larvae, soil, air, marine environments, and indoor environment (Lee et al., 2023). They are known as saprobes and endophytes, as well as opportunistic pathogens causing onychomycosis in humans (Wang et al., 2017; Hao et al., 2020; Lee et al., 2023). *Nigrospora* represents a significant source of bioactive compounds, with over 200 compounds (Xu et al., 2022). The phylogenetic analyses have been carried out based on ITS, *tef1-α*, and *tub2* sequences (Zhang et al., 2024). Currently, 53 epithets are recorded in Index Fungorum (https://www.indexfungorum.org/names/names.asp).

Nigrospora camelliae-sinensis Mei Wang & L. Cai, in Wang et al., Persoonia 39: 127 (2017)Figure 5.65

Index Fungorum number: IF820731; Facesoffungi number: FoF 09396

Endophytic in asymptomatic leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on the sterile pine needles on PDA after one month of incubation. *Mycelia* 2.0–5.0 μm wide ($\overline{x}$ = 3.5 μm, n = 30), superficial, forming aerial hyphae, septate, branched, pale brown, smooth- and thick-walled, the terminal cell swollen and catenate 3–8 cells as a chin; immersed mycelium hyaline, thin-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9.0–17.0 × 5.0–14.0 μm ($\overline{x}$ = 12.5 × 8.5 μm, n = 30), cuneiform, ellipsoidal to subglobose, clavate (club-shaped), smooth, hyaline to pale brown, thick-walled. *Conidia* 13–17 μm ($\overline{x}$ = 15 μm, n = 30), solitary, subglobose to globose, aseptate, brown-black to black, smooth- and thick-walled.

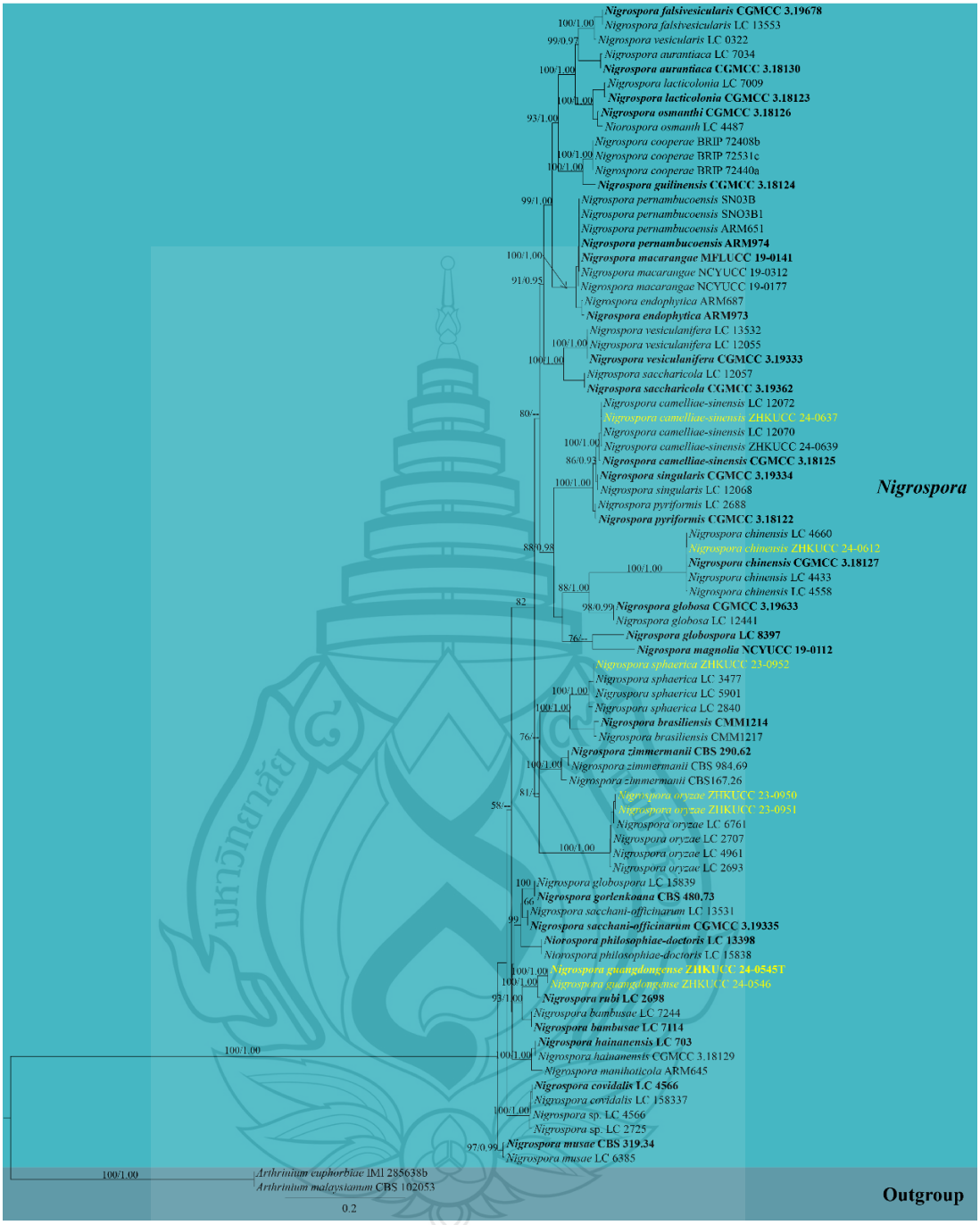
Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 1 week at 28 ± 2°C, moderately sparse, raised, irregular, filiform, dry, cream white to pale brown from above, pale brown to black from reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.29861 N, 111.98444 E), from disease leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP20A1, YP22B1 (MHZU 24-0323); living culture, ZHKUCC 24-0637, ZHKUCC 24-0639.

Known hosts (based on molecular data) – *Camellia sinensis, Musa paradisiaca, Castanopsis* sp. (Wang et al., 2017), dead leaves of *Ananas comosus* (Wang et al., 2017), *Rhododendron simsii* (Wang et al., 2025), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – China (Wang et al., 2017; Wang et al., 2025; this study).

Notes – In the phylogenetic analyses, our strains ZHKUCC 24-0637 and ZHKUCC 24-0639 grouped with *Nigrospora camelliae-sinensis* (LC12070, LC12072, and CGMCC 3.18125 (ex-type) with 100 ML/1.00 PP support (Figure 5.64). Morphologically, our isolate resembles *N. camelliae-sinensis* in having clavate (ear-shaped), hyaline to pale brown conidiogenous cells and subglobose to globose, aseptate, smooth-walled conidia. Conidial dimensions of our isolate are similar (13–17 μm vs. 12–18 × 9–14.5 μm) to those of *N. camelliae-sinensis* (Wang et al., 2017). We report our isolate as a new host record of *N. camelliae-sinensis* from *Wurfbainia villosa*.



Note Tree rooted with *Arthrinium euphorbiae* (IMl 285638b) and *A. malaysianum* (CBS 102053). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with yellow bold, strains from this study are shown in yellow.

Figure 5.64 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *tub2* sequences data of *Nigrospora*

Note a Upper view and reverse view of culture on PDA. b–d Conidia on aerial mycelia on PDA. e–i Conidia with conidiogenous cells. j Conidia. Scale bars: e–g, i, j = 20 μm, h = 10 μm.

Figure 5.65 *Nigrospora camelliae-sinensis* (MHZU 24-0323, new host record)

Nigrospora chinensis Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 129 (2017) Figure 5.66

Index Fungorum number: IF820732; Facesoffungi number: FoF 09446

Endophytic associated with asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: on PDA after 2 months, *Mycelia* superficial and immersed, composed of septate or aseptate, branched, 2.0–4.0 μm wide ($\overline{x}$ = 3.0 μm, n = 30), hyaline to brown, smooth- and thin-walled hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.0–15 × 3.0–7.5 μm ($\overline{x}$ = 9.0 × 5.5 μm, n = 30), ampulliform, cylindrical to obpyriform, ellipsoidal to subglobose, guttulate, smooth, hyaline to pale brown. *Conidia* 9–13 × 7–12 μm ($\overline{x}$ = 11 × 10 μm, n = 30), solitary, globose to subglobose, aseptate, olivaceous green to brown or black.

Culture characteristics – Colonies on PDA reaching 8.5–9.0 cm diameter in 1 week at 28 ± 2°C, moderately sparse, flat, irregular, filiform, dry, cream-yellow from above and reverse, without pigmentation.

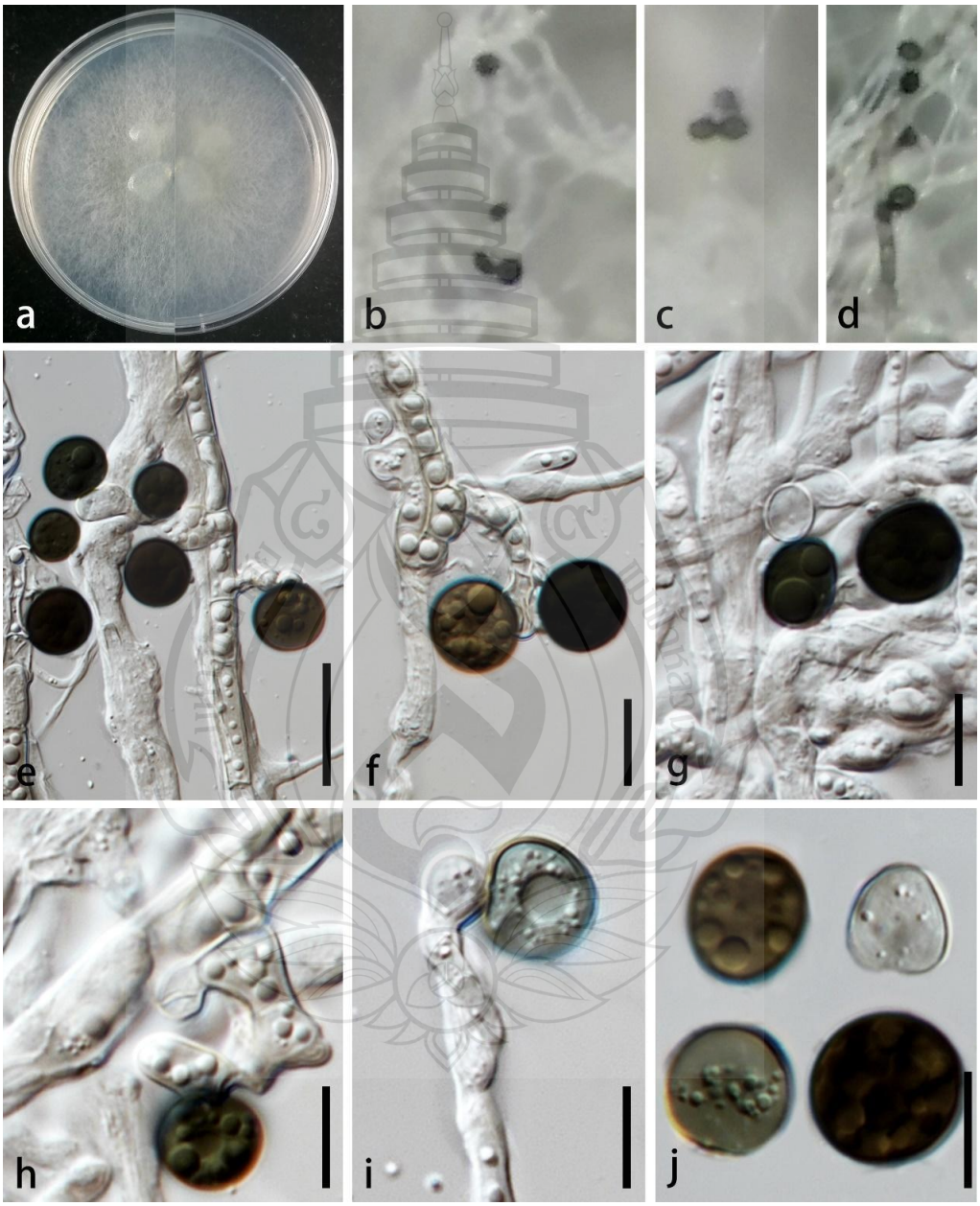
Material examined – China, Guangdong Province, Guangzhou City, Zhongkai University (23.10643 N, 113.28240 E), from symptomatic leaf of *Wurfbainia villosa*, 30 October 2023, C.F. Liao, YP04C3 (MHZU 24-0300); living culture, ZHKUCC 24-0612.

Known hosts (based on molecular data) – *Aucuba japonica*, *Camellia sinensis*, *Castanopsis* sp., *Lindera aggregate*, *Machilus breviflora*, *Machilus duthiei*, *Musa paradisiaca*, *Osmanthus* sp., *Quercus* sp., *Smilax ocreat* (Wang et al., 2017), causing stem spot of dragon fruit (*Selenicereus monacanthus*) (Guo et al., 2024), *Corylus heterophylla* (Wang et al., 2024a), *Cyclocarya paliurus* (Zheng et al., 2021), Gannan navel orange pulp (Wang et al., 2024b), rice and wild rice (Liu et al., 2024), tobacco (Zhong et al., 2022), *Zanthoxylum bungeanum* (Cheng et al., 2025), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – China (Wang et al., 2017; Zheng et al., 2021; Zhong et al., 2022; Guo et al., 2024; Liu et al., 2024; Wang et al., 2024a; Wang et al., 2024b; Cheng et al., 2025; this study).

Notes – The phylogenetic analyses showed that our strain ZHKUCC 24-0612 clusters with *Nigrospora chinensis* (LC4660, LC4558, CGMCC3.18127 (ex-type), and LC4433) (Figure 5.64). Morphologically, our isolate resembles the holotype of

N. chinensis in having ampulliform, hyaline conidiogenous cells, and globose, black, aseptate conidia. Conidial dimensions of our isolate are similar (9–13 × 7–12 μm vs. 10–14.5 × 7.5–11 μm) to *N. chinensis* (Wang et al., 2017). However, our isolate differs in having longer conidiogenous cells (5.0–15 × 3.0–7.5 μm vs. 5–9.5 × 4–7 μm). We report our isolate as a new host record of *N. chinensis*.



Note a Upper view and reverse view of culture on PDA 1 week. b–d Conidia on aerial mycelia on PDA after 2 months. e–i Conidia with conidiogenous cells. j Conidia. Scale bars: e = 20 μm, f–j = 10 μm.

Figure 5.66 *Nigrospora chinensis* (MHZU 24-0300, new host record)

Nigrospora guangdongense C.F. Liao, Y.X. Li & Doilom. Figure 5.67

Index Fungorum Number: #####; Facesoffungi Number: ####

Etymology – Referring to the collecting location, Guangdong province in China.

Holotype. MHZU 24-0242

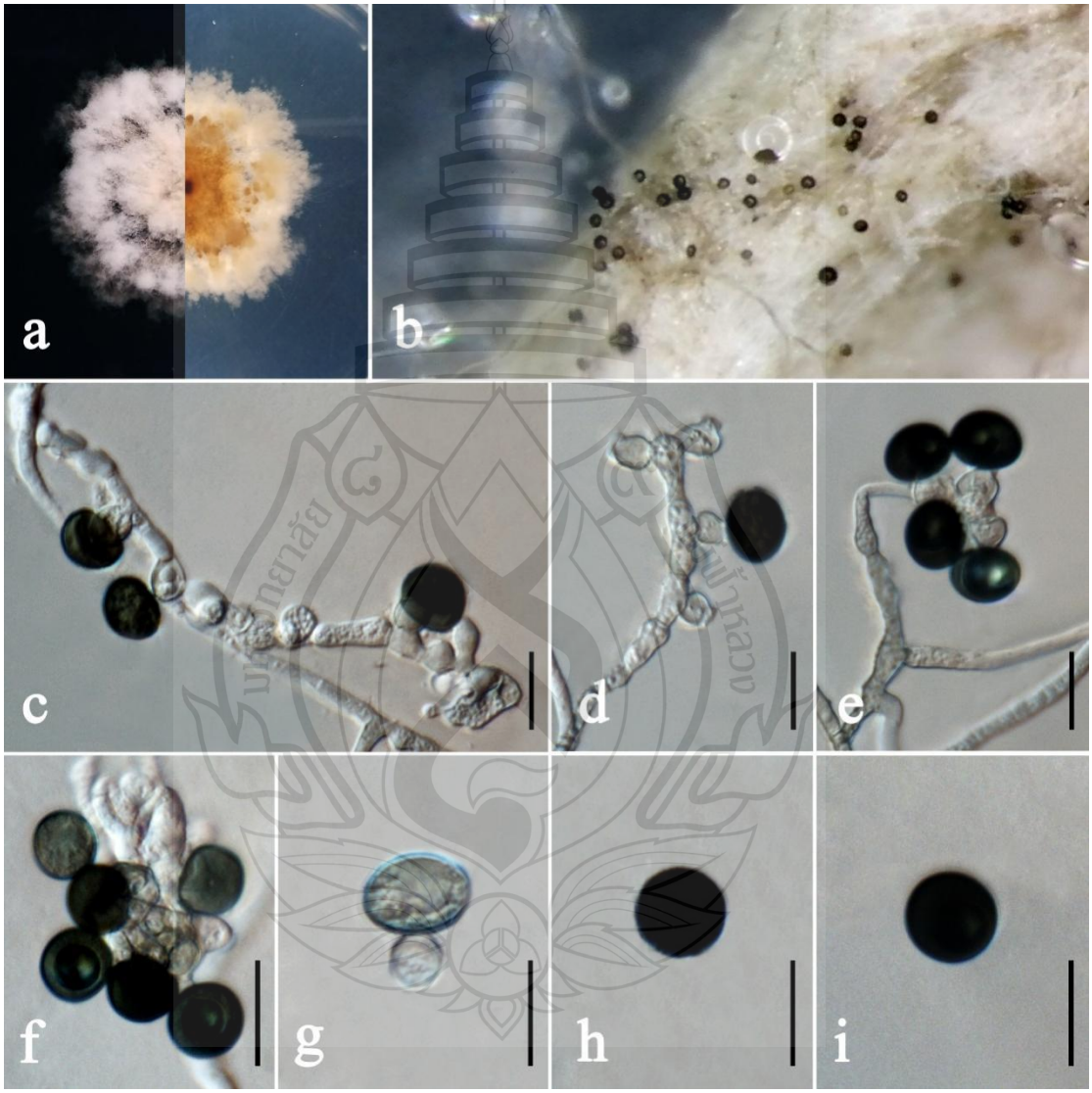
Description – *Endophytes* from asymptomatic leaves of *Wurfbainia villosa* (Zingiberaceae). Sexual morph: Undetermined. Asexual morph: *Mycelia* 3.0–5.5 μm wide ($\overline{x}$ = 4.0 μm, n = 30), superficial, immersed aseptate, rarely septate, branched, hyaline, smooth-walled with thick-walled hyphae. *Conidiophores* nodule proliferate, cylindrical, subglobose to filiform, septate, multi-guttulated, swollen, constricted at septate, hyaline to pale brown, sometimes reduce as conidiogenous cell. *Conidiogenous cells* 3–11 × 4–10 μm ($\overline{x}$ = 7 × 6.5 μm, n = 30), arising from aerial hyphae or conidiophores, solitary to aggregated, aseptate, unbranched, smooth-walled, subglobose to ellipsoidal, ampulliform to mucronate, reniform to cylindrical, hyaline to pale brown. *Conidia* 10–15 × 4–15 μm ($\overline{x}$ = 12 × 12.5 μm, n = 30), solitary, smooth, subglobose to globose in front view, umbrella ellipsoidal in side view, shiny, aseptate, blue brown to blackwish.

Culture characteristics – On PDA, colonies floccose, velvety, edge irregular, reached 2.5–3 cm in two weeks at room temperature (25 ± 2°C). Surface duty white to cream white, reverse orange yellow to duty white.

Material examined – China, Guangdong Province, Yangjiang City, 23°11'39"N; 113°21'22"E, in leaving plants of *Wurfbainia villosa* (Zingiberaceae), 1 October 2021, Chun-Fang Liao, (MHZU 24-0242, holotype); ex-type living culture (ZHKUCC 24-0545), *ibid.*, living culture ZHKUCC 24-0546.

Notes – The phylogenetic analyses revealed that our strain (ZHKUCC 24-0545) formed a sister branch with *Nigrospora rubi* (LC2698) with 100 % ML and 1.00 PP. Morphologically, our isolate has superficial and immersed, aseptate, rarely septate hyphae, nodule proliferate, cylindrical, subglobose to filiform, swollen, constricted at septate, hyaline to pale brown conidiophores, while *N. rubi* has septate hyphae and conidiophores reduced to conidiogenous cells (Wang et al., 2017). Moreover, our isolate produced subglobose to ellipsoidal, ampulliform to mucronate, reniform to cylindrical, hyaline to pale brown, larger (3–11 × 4–10 μm vs. 6.5–14 × 5–9 μm) conidiogenous cells and blue brown to blackwish, subglobose to globose conidia in

front view, umbrella ellipsoidal in side view, however, *N. rubi* has subglobose to ampulliform to lageniform, pale brown conidiogenous cells and spherical or subglobose, black conidia. Additionally, the culture characters of *N. guangdongense* reached 2.5–3 cm in two weeks at room temperature (25 ± 2°C) on PDA, slower than *N. rubi* which reached 9 cm diam. in 6 days at 25°C. Therefore, we identified our isolate as a novel species.



Note a Upper view and reverse view of culture on PDA. b Conidia on aerial mycelia on PDA. c–g Conidia, conidiogenous cells with conidiophores. h, i conidia. Scale bars: c–i = 10 μm.

Figure 5.67 *Nigrospora guangdongense* (MHZU 24-0242, holotype)

Nigrospora sphaerica (Sacc.) E.W. Mason, Trans. Br. mycol. Soc. 12(2-3): 158 (1927) Figure 5.68

Index Fungorum number: IF254776; Facesoffungi number: FoF 06599

Endophytic from fresh leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* 2–6 μm wide ($\overline{x}$ = 4 μm, n = 30), smooth, hyaline to pale brown, septate, branched. *Conidiophores* mostly reduced to conidiogenous cells. *Conidiogenous cells* 9–20 × 8–15 μm ($\overline{x}$ = 13.5 × 11 μm, n = 30), aggregated in clusters on hyphae, monoblastic, ampulliform, subspherical, unbranched, smooth, hyaline to pale brown. *Conidia* 16–22 μm diam. ($\overline{x}$ = 18.5 μm, n = 30), solitary, globose, aseptate, black.

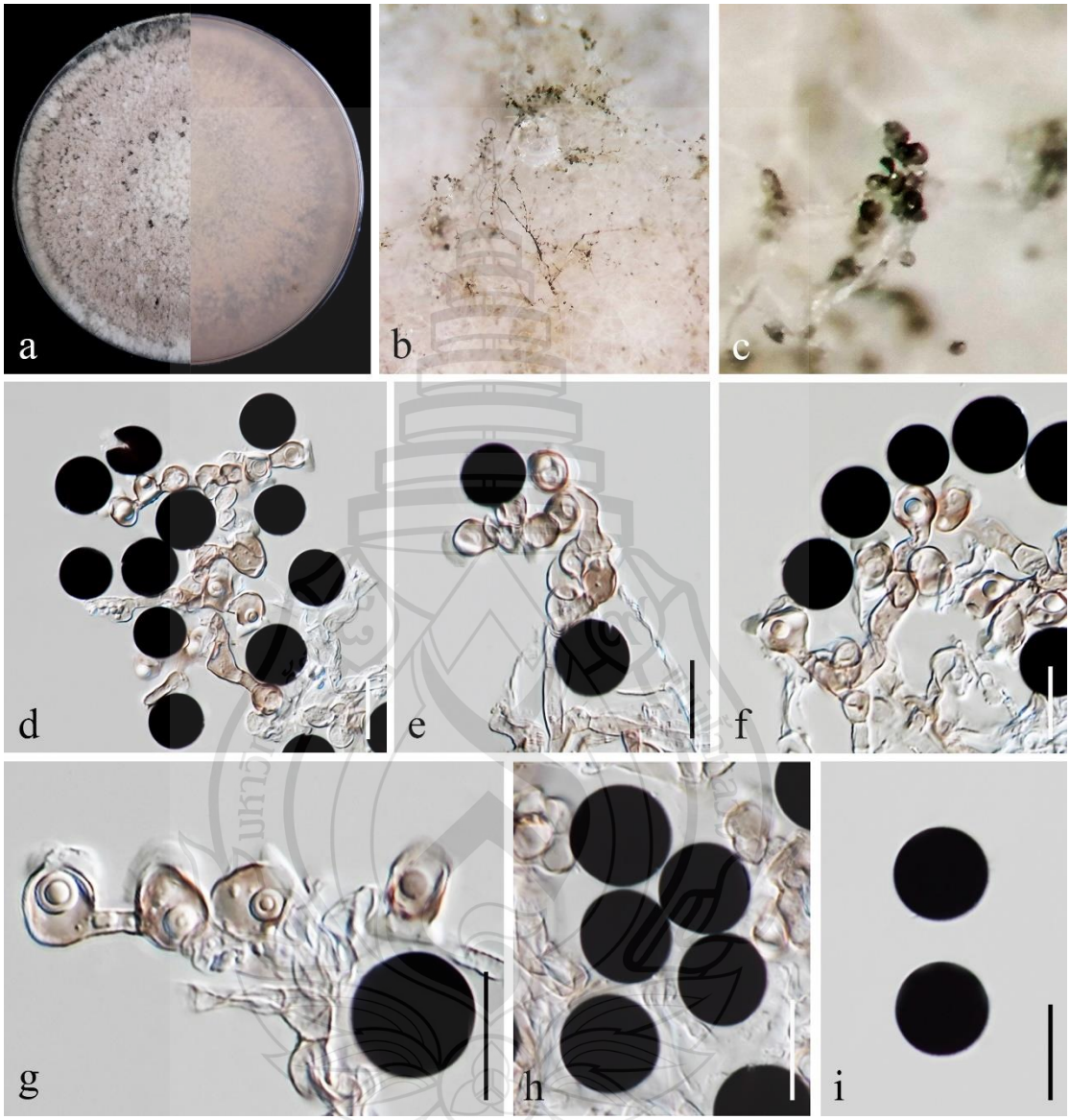
Material examined – China, Guangdong Province, Yangjiang City, Yongning District, on living leaf of *Wurfbainia villosa* (Zingiberaceae), 1 October 2021, Chunfang Liao, AMR13A-1 (MHZU 23-0230), living culture ZHKUCC 23-0952; i*bid.*, living culture ZHKUCC 23-0953.

Known distribution (based on molecular data) – Argentina (Wright et al., 2008), China (Liu et al., 2016a; Wang et al., 2017; Chen et al., 2018; Hong et al., 2021; this study), India (Dutta et al., 2015; Arunakumar et al., 2019; Deepika et al., 2021), Malaysia (Kee et al., 2019), Pakistan (Rehman et al., 2022).

Known hosts (based on molecular data) – *Akebia trifoliata* (Hong et al., 2021), Blueberry (Wright et al., 2008), *Camellia sinensis* (Liu et al., 2016c), *Castanopsis* sp., *Cephalotaxus sinensis*, *Citrus reticulate*, *Cleyera japonica* (Wang et al., 2017), Cowpea (Deepika et al., 2021), *Daphniphyllum macropodum*, *D. oldhamii*, dragon fruit (Kee et al., 2019), *Hamamelis mollis*, Mulberry (Chen et al., 2018; Arunakumar et al., 2019), *Musa paradisiacal*, *Nelumbo* sp., *Osmanthus* sp., *Pentactina rupicola*, Pitaya (Liu et al., 2016a), *Pittosporum illicioides*, *Rhododendron* sp., *Rhododendron* sp., *Rubus reflexus*, Sesame (Rehman et al., 2022), *Symplocos zizyphoides*, Tea (Dutta et al., 2015), *Ternstroemia* sp., *Tutcheria macrocarpa*, *Wurfbainia villosa* (this study).

Notes – According to the phylogenetic analysis, our strains (ZHKUCC 23-0952 and ZHKUCC 23-0953) clustered with *N. sphaerica* strains (LC 7312, LC 5901, and LC 3477) with 100% ML and 1.00 BYPP bootstrap support (Figure 5.65). The morphology of asexual morphs of our collection shares similar characteristics to the holotype of *N. sphaerica*. However, our collection has larger conidiogenous cells (3.5–

9–20 × 8–15 µm *vs.* 6–12 µm diam.) compared to those of *N. sphaerica*. Based on morphology and multi-gene phylogeny we identified our collection is *N. sphaerica*. This study presents a new host record of *N. sphaerica* on *Wurfbainia villosa* in China.



Note a Colony on PDA; (a) upper and (b) reverse views. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h, i Conidia. Scale bars: d–k = 10 µm

Figure 5.68 *Nigrospora sphaerica* (MHZU 23-0230, new host record)

Sporocadaceae Corda [as 'Sporocadeae'], Icon. fung. (Prague) 5: 34 (1842)

Notes – Sporocadaceae was introduced by Corda (1842), with *Sporocadus* designated as the type genus. Phylogenetic resolution of Sporocadaceae has been

carried out through multi-gene phylogenetic analysis using LSU, ITS, *tef1-α*, *tub2* and *rpb2* regions (Liu et al., 2019). According to the current taxonomic framework (Hyde et al., 2024), 35 genera are accepted in Sporocadaceae.

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 180 (2014)

Notes – *Pseudopestalotiopsis* was introduced by Maharachchikumbura et al. (2014), with *P. theae* designated as the type species. *Pseudopestalotiopsis* species are reported as saprobes and plant pathogens, causing gray blight disease on leaves, stem rot, and fruit rot (Darapanit et al., 2021; Weerasekara et al., 2024). *Pseudopestalotiopsis* shares morphological similarities with *Pestalotiopsis* but they can be distinguished by color of the concolorous median cells. Multi-phylogenetic analyses of ITS, *tef1-α*, and *tub2* database support them as distinct genera (Maharachchikumbura et al., 2016; Zhang et al., 2024). Currently, 31 epithets are recorded in Index Fungorum (https://www.indexfungorum.org/names/names.asp). In this study, we report *Pseudopestalotiopsis avicenniae* as a new host and geographical record isolated from root of *Wurfbainia villosa.*

Pseudopestalotiopsis avicenniae Shuns. Nozawa & K. Watan., Mycoscience 58(5): 332 (2017) Figure 5.70

Index Fungorum number: IF556442; Facesoffungi number: FoF 05776

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Colonies on the PDA after 1 month, *Conidiomata* superficial, immersed or erumpent, scattered or gregarious, black to yellowish. *Conidiophores* hyaline to pale brown, branched, cylindrical, filiform, septate, sometimes reduced to conidiogenous cells, smooth- and thick-walled. *Conidiogenous cells* 6–23 × 2.5–5.5 μm ($\bar{x}$ = 11 × 3.5 μm, n = 30), phialidic, cylindrical, clavate, oval, obpyriform, hyaline, branched, aseptate, thick-walled, smooth-walled. *Conidia* 22–31 × 7–9 μm ($\bar{x}$ = 25 × 8 μm, n = 30), fusoid, oval to lunate, straight to curved, 4-septate, with darker septal bands, slightly constricted at septa, thick-walled; basal cell obconic, hyaline, thin-walled; three median cells 14–19 μm long ($\bar{x}$ = 17 μm, n = 30), pale brown to dark brown, doliiform to elongate, concolourous, with darker septa, smooth-walled (second cell from the base: 5–7 μm long, $\bar{x}$ = 6 μm; third cell: 4–6.5 μm long, $\bar{x}$ = 5.5 μm; fourth cell: 4.5–7.5 μm long, $\bar{x}$ = 6 μm); apical cell hyaline, cylindrical or conical with

truncate base, thin-walled; apical appendages 15–30 μm ($\overline{x}$ = 20 μm) long, 1–3 tubular (mostly 3), hyaline, filiform, tubular, unbranched; basal appendages 5–9 μm long ($\overline{x}$ = 7 μm, n = 30), single, hyaline, tubular, centric, unbranched, straight to curved.

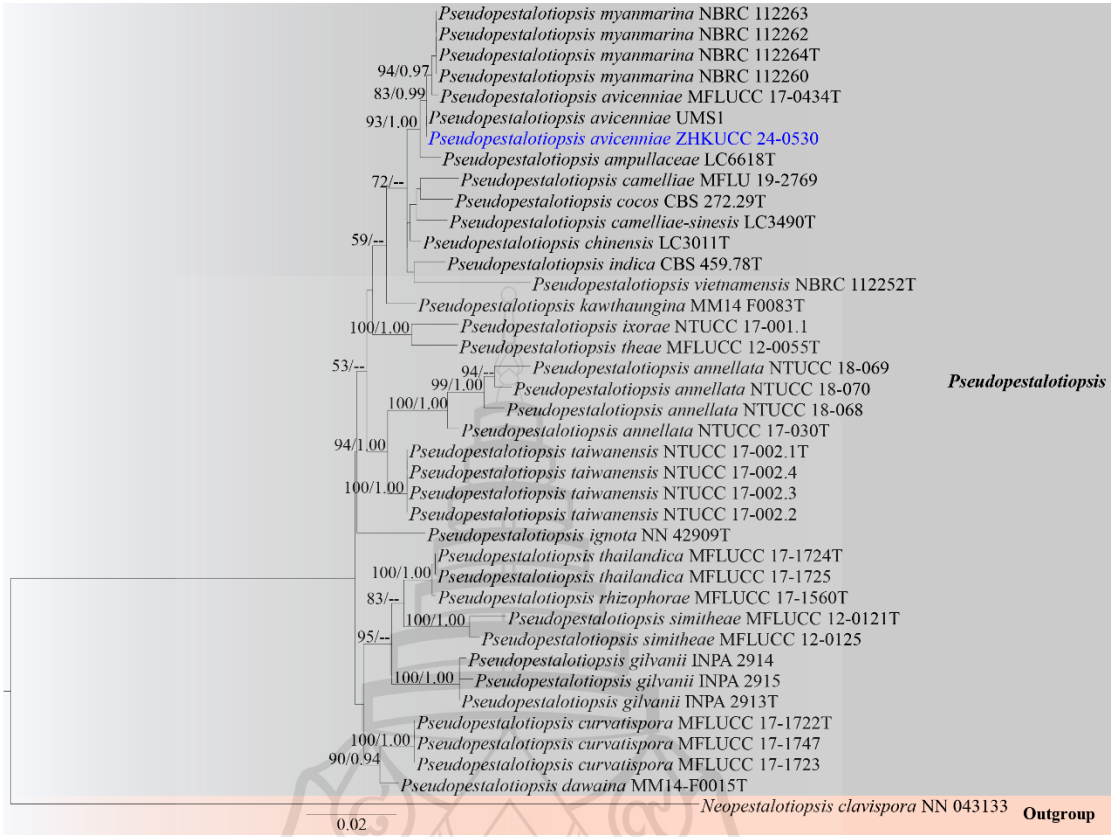
Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 1 week at 28 ± 2°C, moderately sparse, flat, undulate, producing abundant black conidial masses on the surface, cream-white from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR06A-1 (MHZU 24-0233); living culture ZHKUCC 24-0530.

Known hosts (based on molecular data) – leaf spots of *Avicennia marina* (Nozawa et al., 2017), *Wurfbainia villosa* (this study).

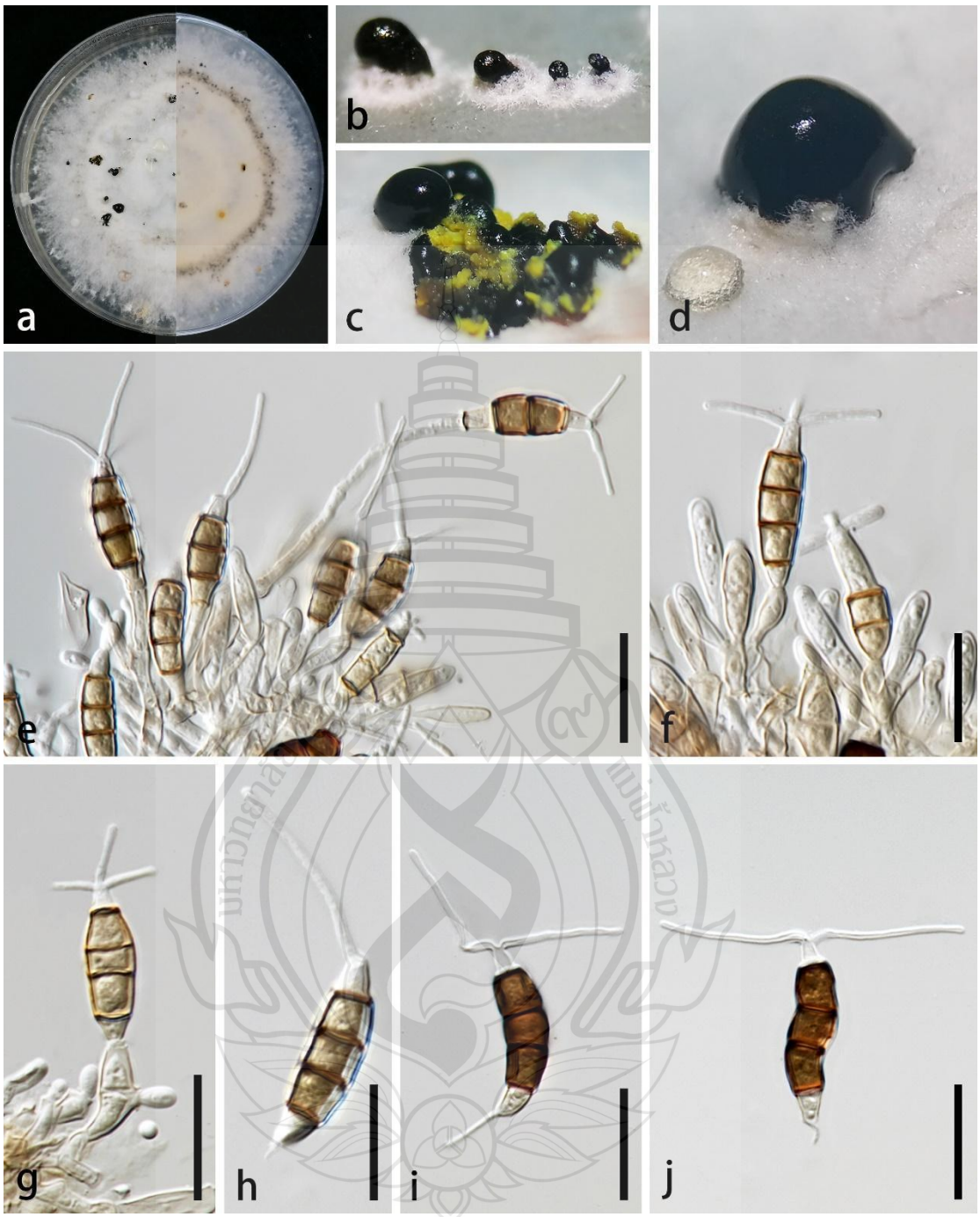
Known distribution (based on molecular data) – Thailand (Norphanphoun et al., 2019), China (this study).

Notes – In the phylogenetic analyses, ZHKUCC 24-0530 clustered with *Pseudopestalotiopsis avicenniae* USM1 with 93 ML/1.00 PP support (Figure 5.69). Morphologically, our isolate resembles *P. avicenniae* (Norphanphoun et al., 2019) in having cylindrical conidiogenous cells, with a single basal appendage, and three apical appendages. However, differences were observed in conidiogenous cells which are cylindrical, variable in shape (clavate, oval, obpyriform) in our isolate ZHKUCC 24-0530, but they are lageniform in *P. avicenniae*. Ecologically, our strain was isolated from asymptomatic root of *Wurfbainia villosa* in China, while *P. avicenniae* was isolated from leaf spots of *Avicennia marina* in Thailand (Norphanphoun et al., 2019). We report *P. avicenniae* as a new host and geographical record.



Note Tree rooted with *Neopestalotiopsis clavispora* (NN 043133). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strain from this study is shown in blue.

Figure 5.69 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, and *tub2* sequences data of *Pseudopestalotiopsis*



Note a Culture characteristic on PDA after 1 month. b–d Colonies on PDA. e–g Conidiophores, conidiogenous cells with conidia. h–j Conidia. Scale bars: e–j = 20 µm.

Figure 5.70 *Pseudopestalotiopsis avicenniae* (MHZU 24-0233, new host and geographical record)

Diaporthales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 53 (1932)

Notes – *Diaporthales* has a broad host range, occurring as saprobes, endophytes, or pathogens on terrestrial or aquatic plants, as well as animals, and in soil. Morphological characteristics of this order follow the descriptions by Hyde et al. (2020). The taxonomic framework follows the updated classification by Hyde et al. (2024).

Diaporthaceae Höhn., Am. J. Bot. 13: 638 (1926)

Notes – Diaporthaceae species are widely reported in terrestrial environments as endophytic, pathogenic or saprobic fungi. They produce both sexual and coelomycetous asexual morphs (Hyde et al., 2020). This family was first classified in Diaporthales by Höhnel (1917). Initial molecular phylogenetic study using LSU rDNA supported its position within Diaporthales (Castlebury et al., 2002). Multi locus phylogeny of the combined LSU, ITS, *rpb2*, and *tef1-α* further refined the circumscription of the family, excluding *Diaporthella* Senanayake et al. (2017). Based on phylogenetic analyses of the combined ITS, *tef1-α*, *tub2*, *cal*, and *his3* sequences, 15 genera are recognized in *Diaporthaceae* (Wijayawardene et al., 2022). To date, eighteen genera are listed in this family (Hyde et al., 2024).

Diaporthe Nitschke, Pyrenomyc. Germ. 2: 240 (1870)

Notes – *Diaporthe* was introduced by Nitschke (1867), with *D. alnea* designated as the type species. Several *Diaporthe* species are significant pathogens that cause various diseases, including dark streaks, black fruit rot, branch dieback, and seed decay in economically important plants such as soybean, citrus, and grapevines (Doilom et al., 2017; Zhou et al., 2024). Some species also produce mycotoxins that can poison livestock (Buccioni et al., 2024). The morphological details are described by Udayanga et al. (2012) and Senanayake et al. (2017). Current classification recognizes seven sections and 15 species complexes within *Diaporthe* (Dissanayake et al., 2024).

Diaporthe neoceratozamiae C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.72

Index Fungorum number: IF ###; Facesoffungi number: FoF ###

Etymology – The epithet "*neoceratozamiae*" refers to its morphological similarity to *Diaporthe ceratozamiae*.

Associated with leaf spots of *Wurfbainia villosa*. *Mycelium* diffuse, radial, velutinous, hyaline to pale brown, branched, normally aseptate, rarely septate, smooth-walled. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 30–70 µm diam ($\bar{x}$ = 55 µm, n = 10), pycnidial on PDA sporulating poorly, scattered, erumpent, brown to black. *Conidiophores* 16–40 × 2–4 µm ($\overline{x}$ = 29 × 3 µm, n = 15), hyaline, unbranched, septate, rarely, cylindrical, straight, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 2–18 × 1.5–3.0 µm ($\overline{x}$ = 10.5 × 2.5 µm, n = 10), hyaline, phialidic, subcylindrical to cylindrical, terminal or lateral, straight or slightly curved, aseptate. *Alpha conidia* 7–12.5 × 2.5–4.0 µm ($\overline{x}$ = 9 × 3 µm, n = 30), hyaline, multi-guttulate, ellipsoid to elongate, fusiform, smooth-walled, aseptate. *Beta conidia* 18–24 × 1.5–2.2 µm ($\overline{x}$ = 21 × 2 µm, n = 10), hyaline, filiform to board filiform, straight to curved aseptate. *Gamma conidia* 12–19 × 1.5–2.5 µm ($\overline{x}$ = 16 × 2.1 µm, n = 10), hyaline, aseptate, fusiform, both ends rounded, smooth-walled.

Material examined – China, Guangdong province, Guangzhou City, Zhongkai University, 30 October 2023, C.F. Liao, (MHZU 24-0299, holotype); ex-type living culture, ZHKUCC 24-0610, *ibid*; living culture, ZHKUCC 24-0611.

Notes – The morphology of this species resembles *Diaporthe ceratozamiae* in having erumpent pycnidia, phialidic, cylindrical conidiogenous cells, and fusiform alpha conidia (Crous et al., 2011). However, our species differ with *D. ceratozamiae* in having small pycnidia (30–70 µm diam vs. up to 300 µm diam), longer conidiophores (16–40 × 2–4 µm vs. 15–30 × 3–4 µm). Our specie also produces sparse conidiogenous cells and ellipsoid to elongate alpha conidia, but *D. ceratozamiae* produces rich conidiogenous cells and fusiform alpha conidia. Our species resembles *D. hunanensis* in having solitary pycnidia, cylindrical conidiogenous cells, and ellipsoidal alpha conidia (Yang et al., 2021). However, our species can be distinguished from *D. hunanensis* by having smaller, erumpent pycnidia (30–70 µm diam vs. 180–300 µm in diam), elongate, fusiform, and bigger alpha conidia (7–12.5 × 2.5–4.0 µm vs. 6.5–7.5(–8.5) × 2.4–2.9 µm). Our ITS, *tef1-α*, *tub2*, *cal*, and *his3* combined phylogenetic analyses (Figure 5.71) reveal that our strain form a distinct clade with *D. ceratozamiae* (CBS 131306) with 29% maximum likelihood and 0.53 posterior probability support. Thus, we introduce *Diaporthe neoceratozamiae* ass a novel species in Chia.

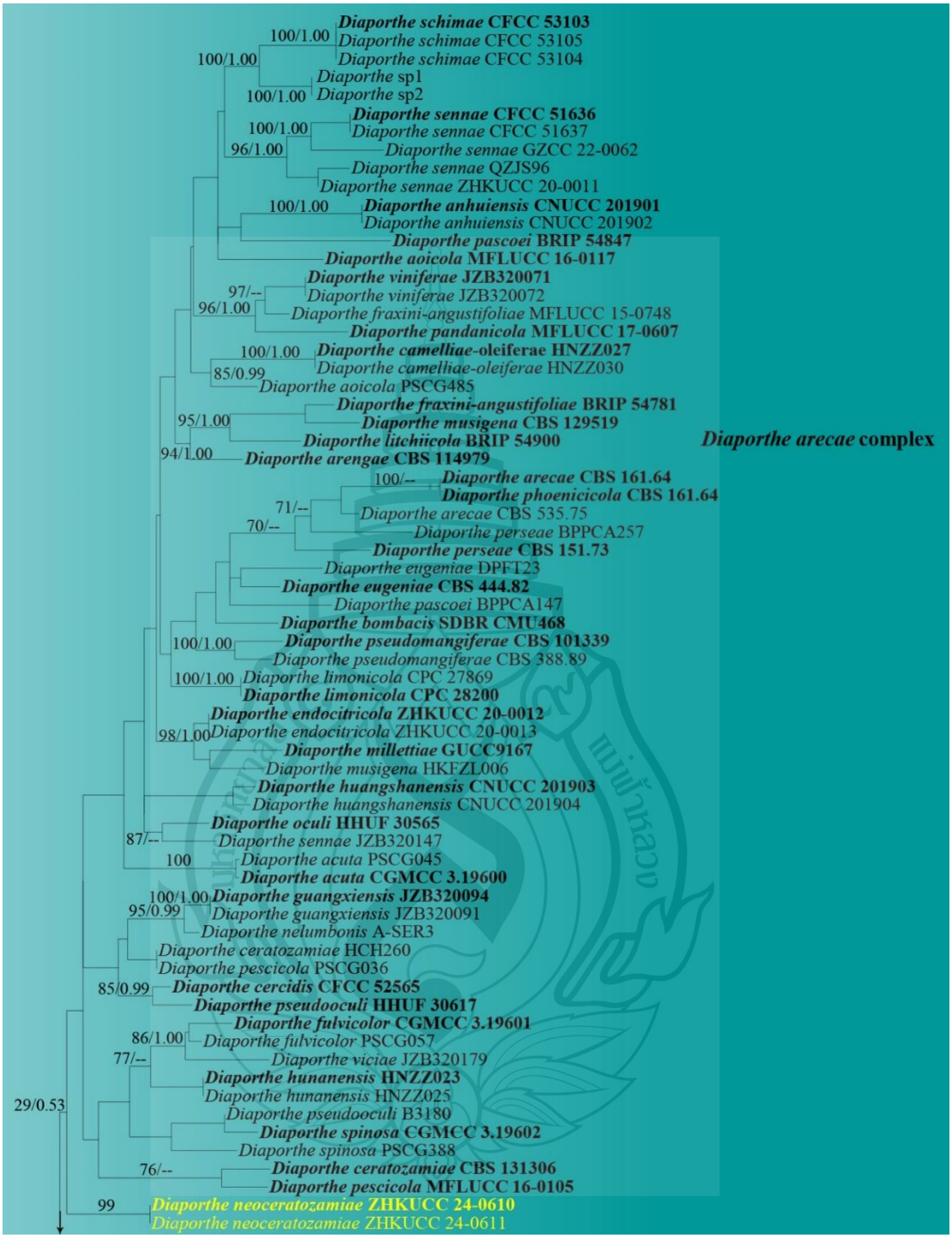
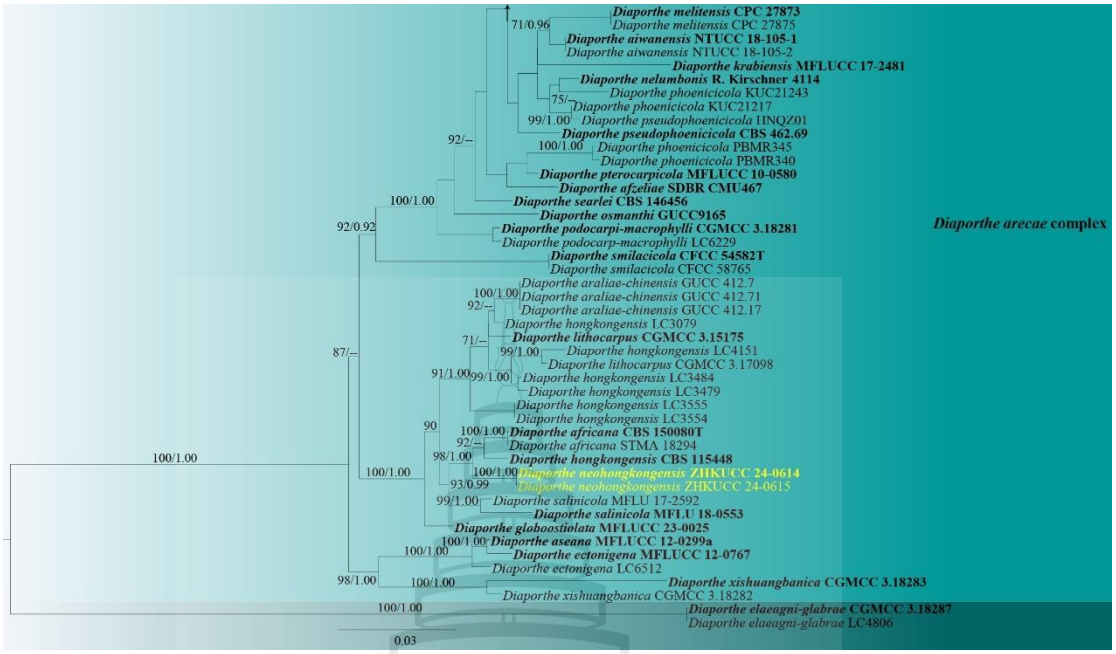
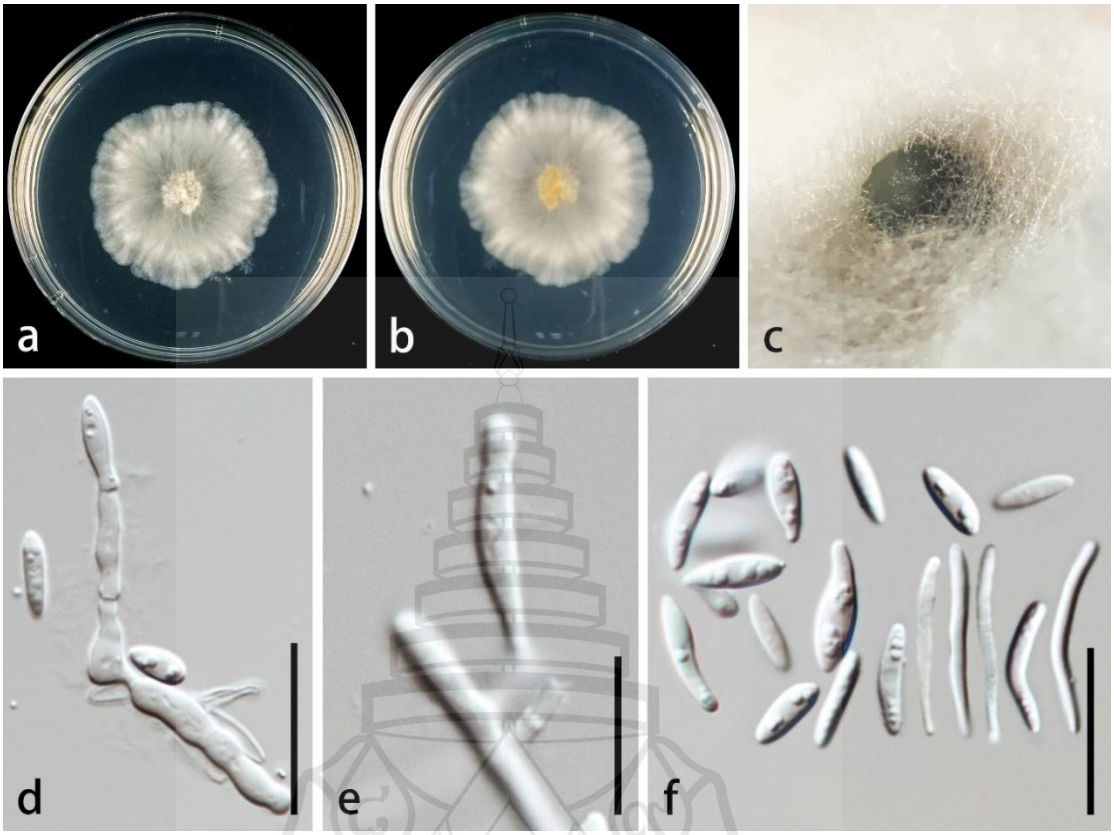


Figure 5.71 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, *tub2*, *cal*, and *his3* sequences data of *Diaporthe arecae* species complex



Note *Diaporthe elaeagni-glabrae* (CGMCC 3.18287, LC4806) is used as the outgroup taxon. Bootstrap values for maximum likelihood equal to or greater than 70 and Bayesian posterior probabilities equal to or greater than 0.90 are placed above or below the branches, respectively. Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Figure 5.71 (continued)



Note a Upper view of culture on PDA. b Reverse view of culture on PDA. c Conidiomata with conidia mass sporulating on PDA. d, e Conidiogenous cells with conidia. f Alpha, beta, and gamma conidia. Scale bars: d–f = 20 μm.

Figure 5.72 *Diaporthe neoceratozamiae* (MHZU 24-0299, Holotype)

Diaporthe neohongkongensis C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.73

Index Fungorum number: IF ###; Facesoffungi number: FoF ###

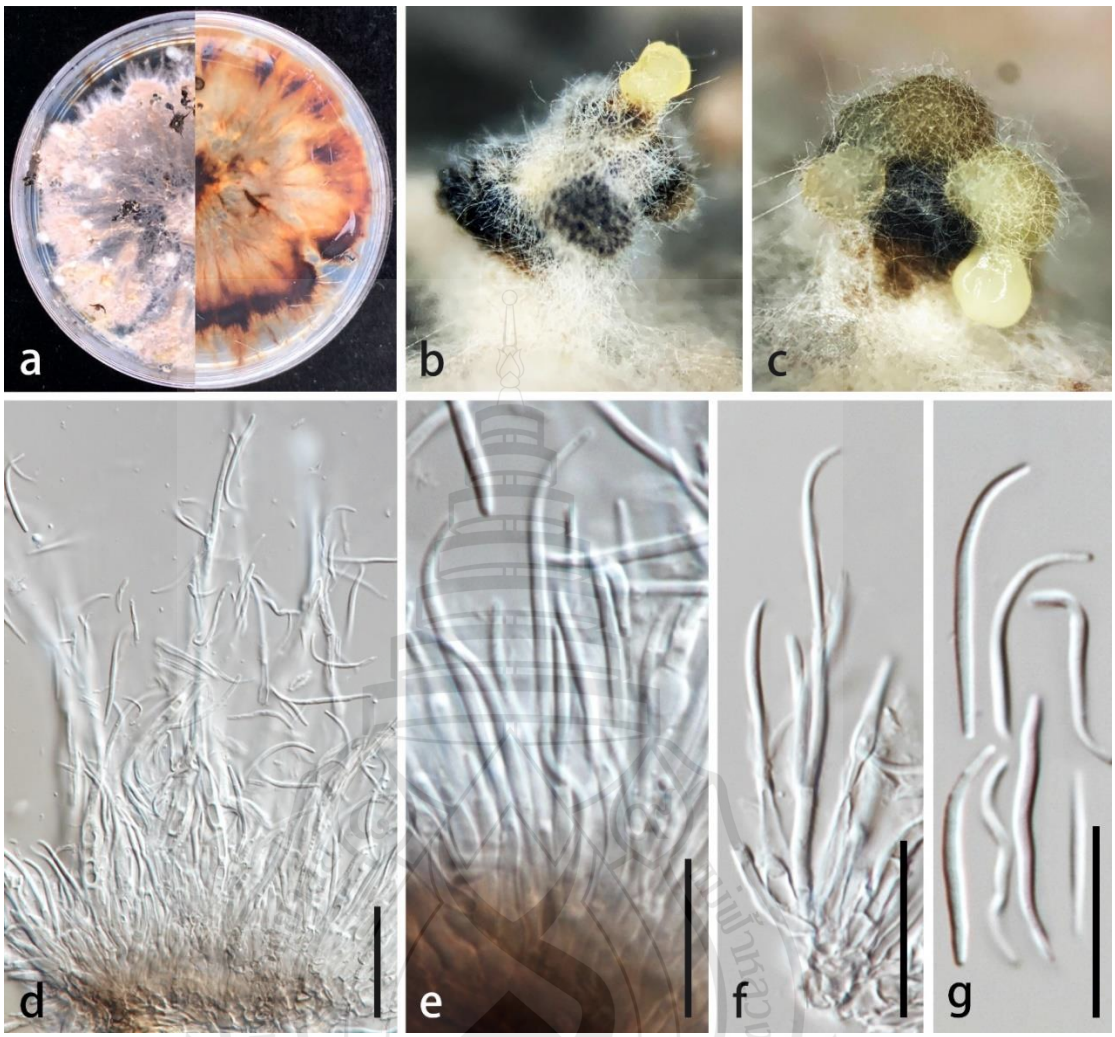
Etymology – The epithet "*neohongkongensis*" refers to its morphological similarity to *Diaporthe hongkongensis*.

Associated with leaf spots of *Wurfbainia villosa*. *Mycelium* diffuse, radial, hyaline, branched, septate, smooth-walled. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 230–615 × 115–310 μm ($\bar{x}$ = 460 × 218 μm, n = 15), pycnidial on PDA sporulating poorly, scattered or aggregated, superifical, irregular, brown to black. *Conidiophores* 23–79 × 2–6 μm ($\bar{x}$ = 44 × 3 μm, n = 30), dense, hyaline, septate, branched, short-cylindrical to cylindrical, straight or slightly curved, smooth-walled,

sometimes reduced to conidiogenous cells. *Conidiogenous cells* 8–33 × 2–3 µm ($\overline{x}$ = 17 × 2.5 µm, n = 30), hyaline, phialidic, subcylindrical to filiform, terminal, straight or slightly curved, aseptate, branched, smooth-walled. *Alpha conidia* not observed. *Beta conidia* 19–31 × 1.4–2 µm ($\overline{x}$ = 26 × 1.8 µm, n = 30), hyaline, filiform, straight to curved, aseptate, smooth-walled.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town, 9 November 2023, C.F. Liao, (MHZU 24-0302, holotype); ex-type living culture, ZHKUCC 24-0614, *ibid*; living culture, ZHKUCC 24-0615.

Notes – The morphology of this species resembles *Diaporthe hongkongensis* in having phialidic, subcylindrical conidiogenous cells and straight to curved beta conidia (Li et al., 2020). However, our species differs from *D. hongkongensis* in having larger *conidiomata* (230–615 × 115–310 µm vs. up to 200 µm diam), larger conidiogenous cells (23–79 × 2–6 µm vs. 5–12 × 2–4 µm), and larger beta conidia (19–31 × 1.4–2 µm vs. 18–22 × 1.5–2 µm). Our ITS, *tef1-α*, *tub2*, *cal*, and *his3* combined phylogenetic analyses (Figure 7.71) reveal that our strain form a sister clade with *D. hongkongensis* (IFRDCC 3000) with 98% maximum likelihood and 1.00 posterior probability support. Thus, we introduce *D. neohongkongensis* as a novel species in China.



Note a Upper view and reverse view of culture on PDA. b, c Conidiomata with conidial mass sporulating on PDA. d–f Conidiophores, conidiogenous cells with conidia. f Beta conidia. Scale bars: d, f, g = 20 μm, e = 10 μm.

Figure 5.73 *Diaporthe neohongkongensis* (MHZU 24-0302, Holotype)

Diaporthe kochmanii R.G. Shivas, S.M. Thompson & A.J. Young, Persoonia 27, 86 (2011) Figure 5.75

Index Fungorum number: IF 561571; Facesoffungi number: FoF ###

Etymology – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*.

Endophytic on asymptomatic fruit of *Wurfbainia villosa*. Sexual morph: *Perithecia* superficial, coriaceous, gregarious, pale brow to black-brown. *Asci* 34–40 × 7.5–10 μm ($\overline{x}$ = 36.5 × 8.5 μm, n = 30), 8-spored, overlapped-bitunicate, cylindric-clavate, straight to slight curved, apically rounded, with J- apical ring. *Ascospores* 8–13 × 2.5–4.5 μm

($\bar{x}$ = 10 × 4 µm, n = 30), hyaline, often 4-guttulate, elongated to ellipsoidal, 1-septate, constricted at the septum, with round ends, smooth-walled. Asexual morph: *Conidiophores* 7–35 × 2–6 µm ($\bar{x}$ = 17 × 4 µm, n = 30), hyaline, smooth, unbranched, dense, short-cylindrical, straight, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 7–18 × 2–9 µm ($\bar{x}$ = 13 × 4 µm, n = 30), hyaline, phialidic, terminal or lateral, ampulliform to subulate, ventricose, straight to curved, tapering towards the apex, aseptate. *Alpha conidia* 4.5–8.5 × 2–4 µm ($\bar{x}$ = 6.5 × 3 µm, n = 30), hyaline, two guttulate, ellipsoid to elongate, obtuse at apex, smooth-welled, aseptate. *Beta conidia* 16–24 × 1.5–2.5 µm ($\bar{x}$ = 20.5 × 2 µm, n = 30), hyaline, filiform, curved, aseptate. *Gamma conidia* 10–16 × 1.5–3.0 µm ($\bar{x}$ = 13 × 2 µm, n = 30), hyaline, aseptate, filiform to fusiform, both ends rounded, smooth-walled.

Material examined – China, Guangdong province, Yangjiang City, Chunwan Town, on asymptomatic fruit of *Wurfbainia villosa* (Zingiberaceae), 29 Oct 2022, C.F. Liao, (MHZU 24-0148, holotype); ex-type living culture, ZHKUCC 24-0401.

Known distribution (based on molecular data) – Australia (Thompson et al., 2011), China (this study).

Known hosts (based on molecular data) – *Helianthus annuus* Experimental Line and *Helianthus annuus* hybrid PDAS (Thompson et al., 2011), *Wurfbainia villosa* (this study).

Notes – The morphology of this species resembles *Diaporthe kochmanii* in having aggregated in clusters on the stems, surrounded by a black ectostroma, cylindrical asci, ellipsoidal ascospores, and oval alpha conidia, with flexuous beta conidia (Thompson et al., 2011). However, our species have larger conidiogenous cells (7–18 × 2–9 µm vs. 5–10 × 1.5–3 µm) compared to the *D. kochmanii*. The comparisons of the ITS sequences show no base pair differences across 406 bp. Our ITS, *tef1-α*, *tub2*, *cal*, and *his3* combined phylogenetic analyses (Figure 5.74) reveal that our strain clusters with *D. kochmanii* (BRIP 54033, BRIP 54034, and MAFF 239531) with 100% maximum likelihood and 1.00 posterior probability support. Thus, we report the first host record of *D. kochmanii* in China.

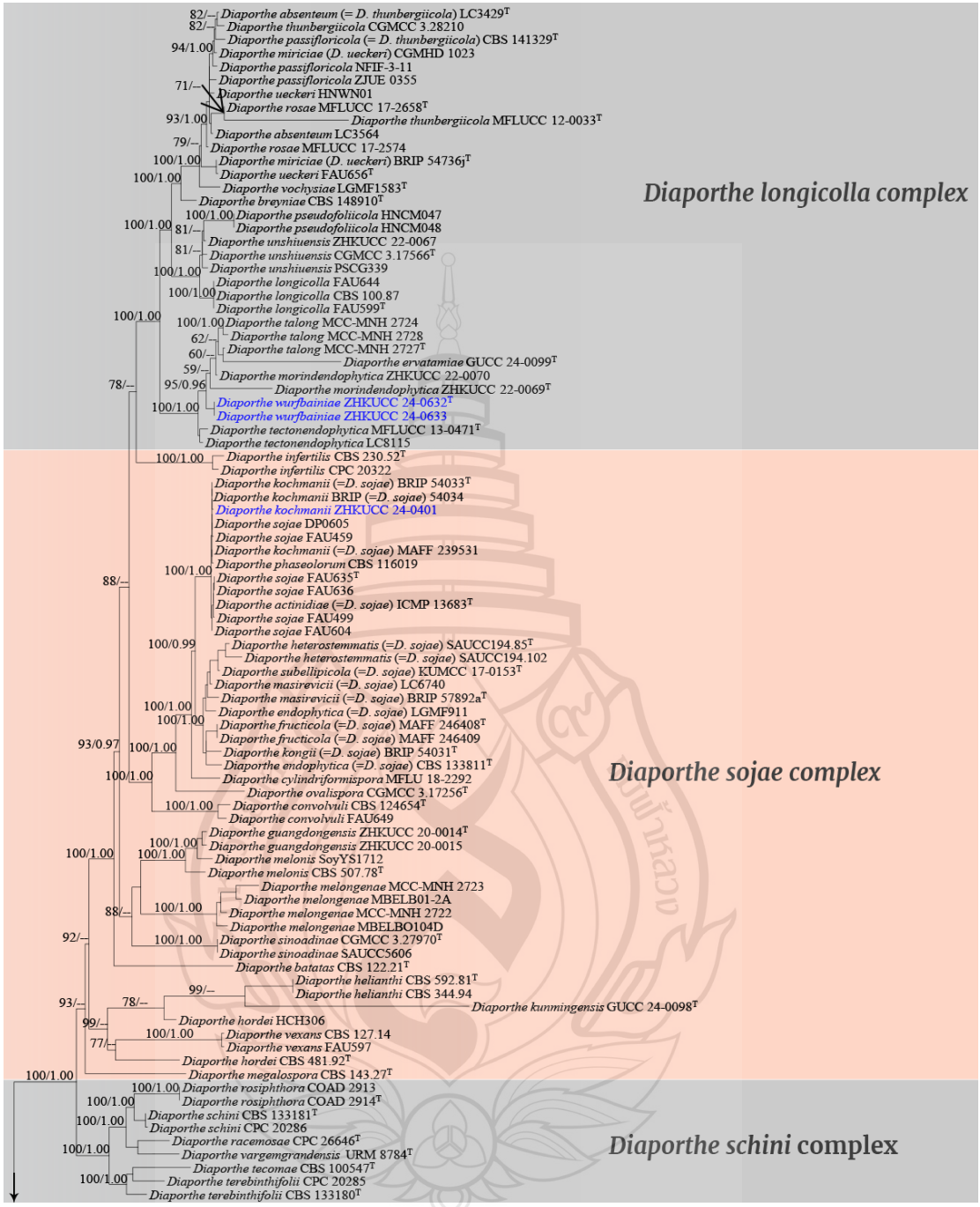


Figure 5.74 Maximum likelihood phylogeny based on the combined ITS, *tef1-α*, *tub2*, *cal*, and *his3* sequences data of *Diaporthe sojae* section

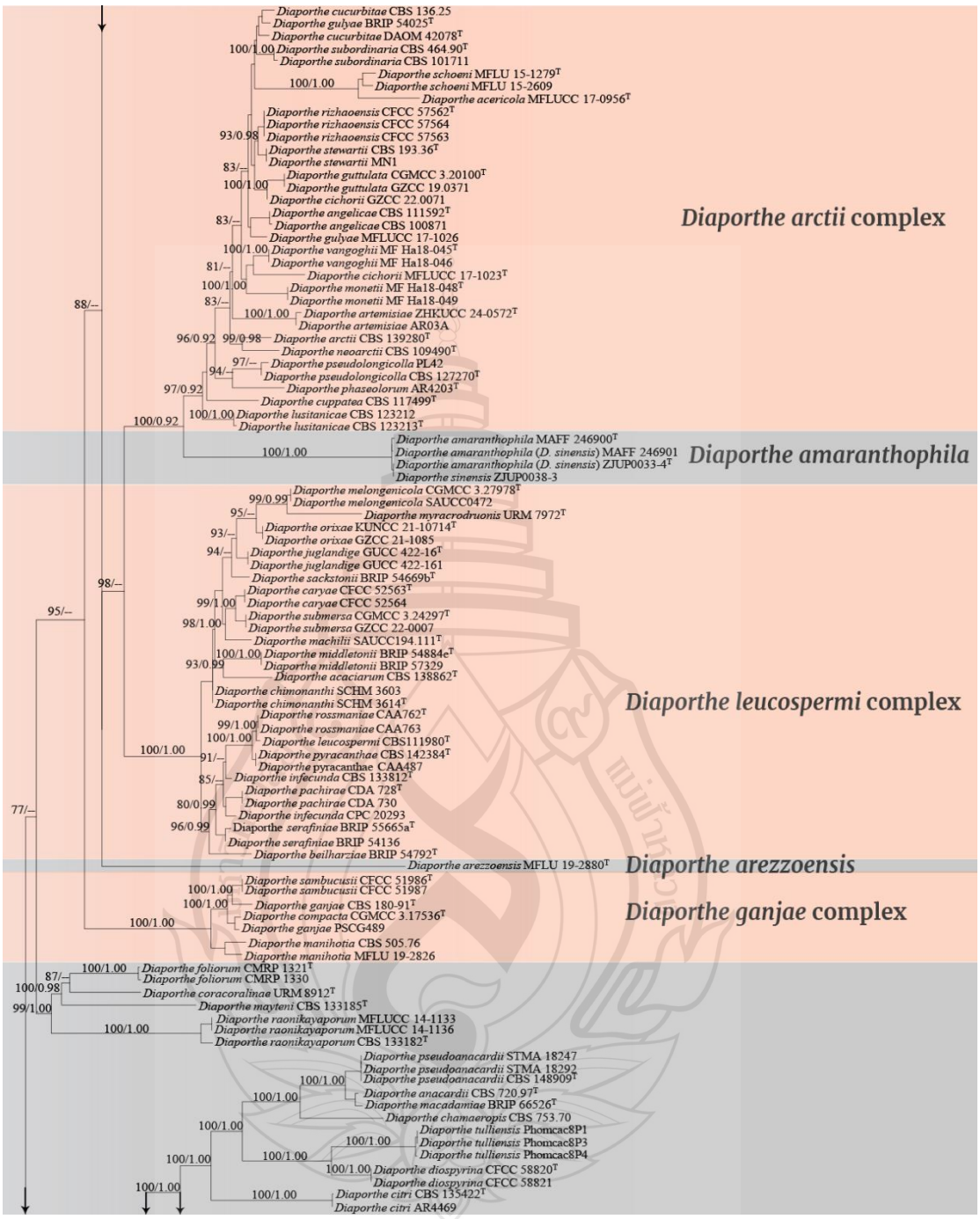
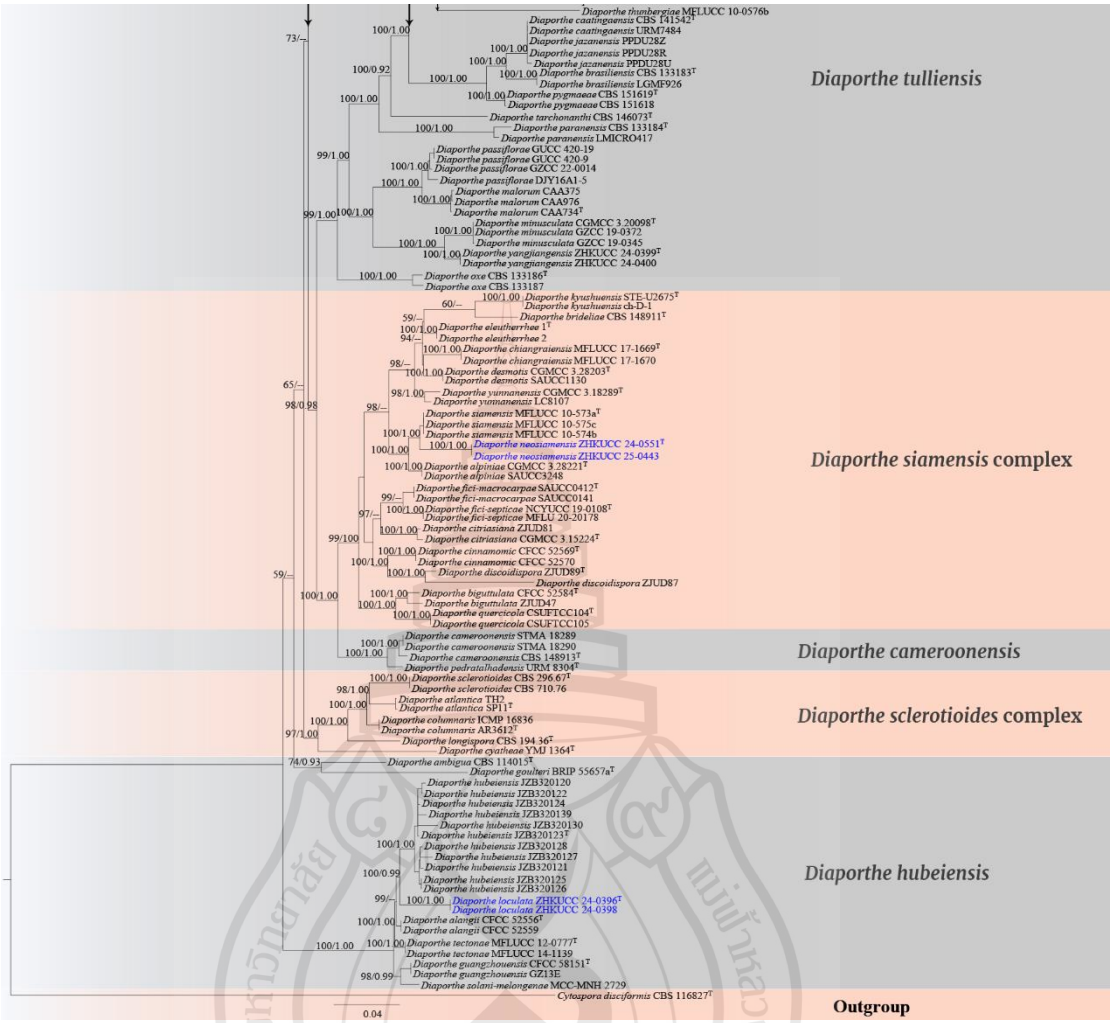
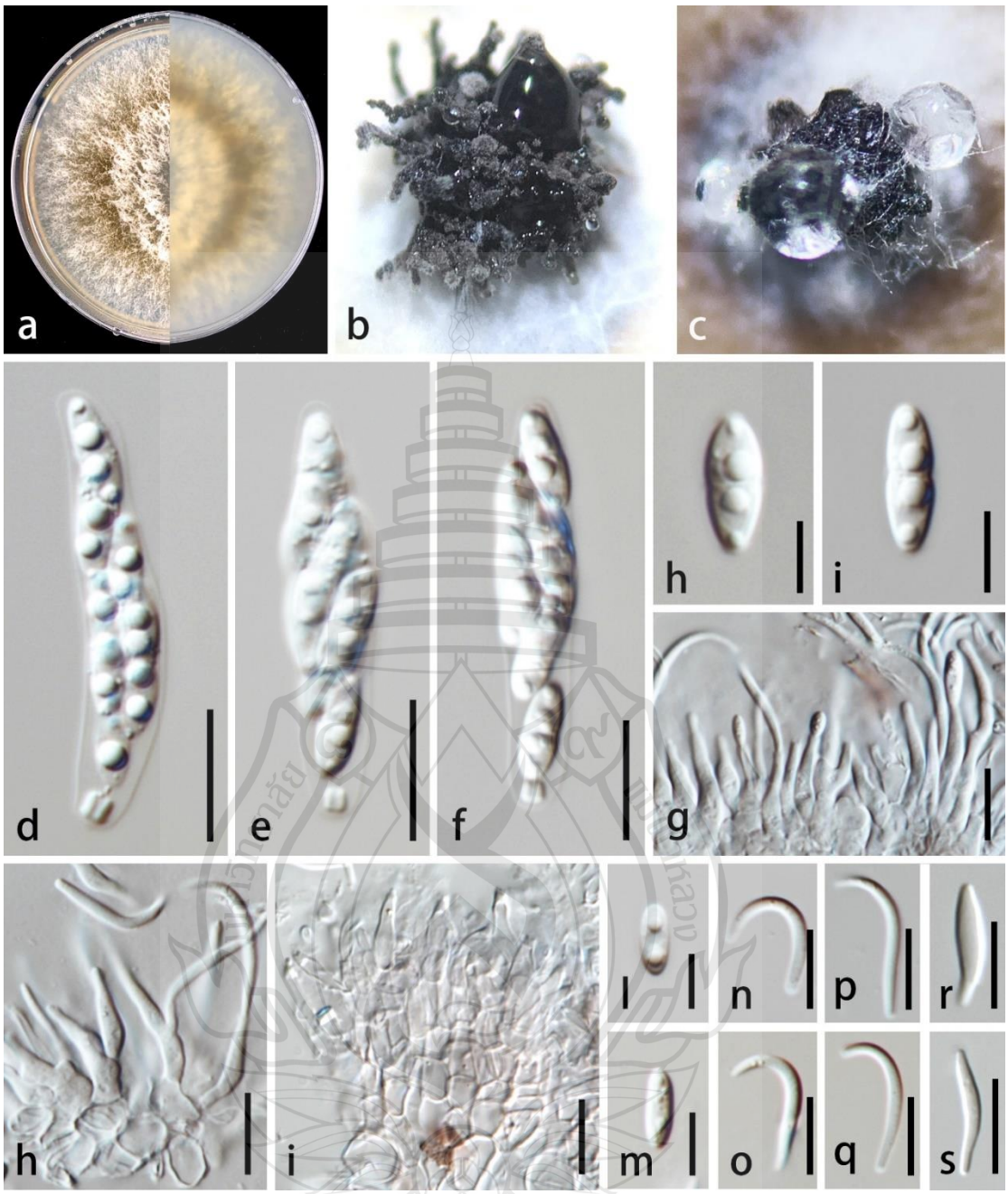


Figure 5.74 (continued)



Note Tree rooted with *Cytospora disciformis* (CBS 116827). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strain from this study is shown in blue.

Figure 5.74 (continued)



Note a Upper view and reverse view of culture on PDA. b, c Ascomata, conidiomata with conidial mass sporulating on PDA. d–f Asci. h, i Ascospore. G, j, k Conidiophores, conidiogenous cells with conidia. l Alpha conidia. n–q Beta conidia. r, s gamma conidia. Scale bars: d–f, g–I, n–s = 10 μm, h, i, l, m = 10 μm.

Figure 5.75 *Diaporthe kochmanii* (MHZU 24-0148, new host record)

Diaporthe loculata C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.76

Index Fungorum number: ####; Facesoffungi number: FoF###

Etymology – epithet "*loculata*" reference to the loculate ascostromata.

Holotype. MHZU 24-0146

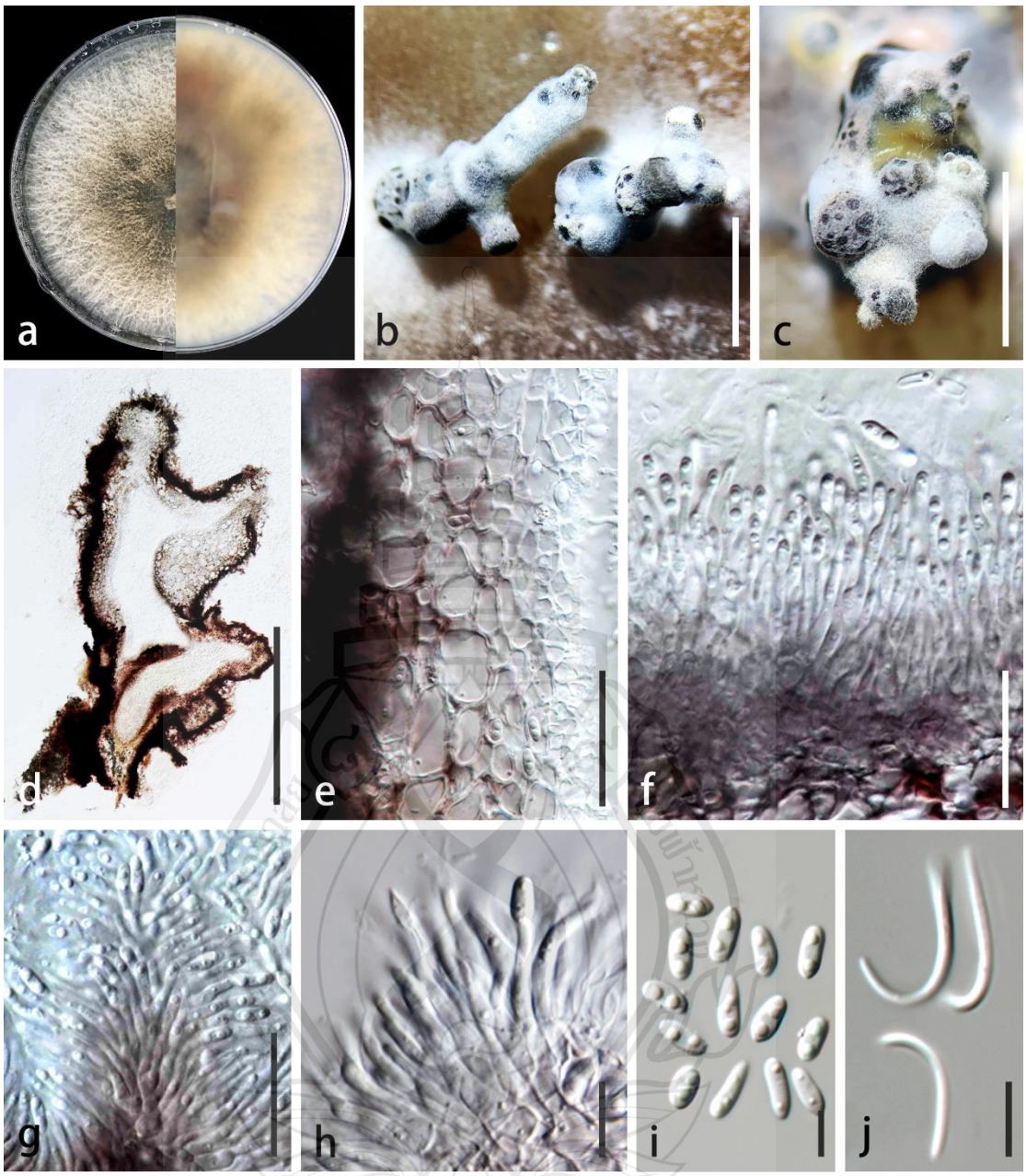
Endophytic on asymptomatic fruits of *Wurfbainia villosa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 510–970 × 265–460 µm ($\overline{x}$ = 692 × 355 µm, n = 15), pycnidial on PDA, solitary, immerse to erumpent, multi-loculate, various shaped, cream white to black, with or without necks, white to cream conidial mass exuded from ostioles when mature. *Peridium* 47–160 µm, consisting of 5–11 layers and composed of *textura angularis*, inner hyaline layers, outer layers brown to black. *Conidiophores* 5–16.5 × 2–3.5 µm ($\overline{x}$ = 10.5 × 2.5 µm, n = 30), hyaline, smooth, branched or unbranched, septate, densely aggregated, short-cylindrical, straight, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 11–33.5 × 2–7 µm ($\overline{x}$ = 19 × 4 µm, n = 30), hyaline, phialidic, subcylindrical to ampulliform, terminal, straight or slightly curved, tapering towards the apex, aseptate. *Alpha conidia* 5–8 × 2–3.5 µm ($\overline{x}$ = 6.5 × 3 µm, n = 30), hyaline, with two big guttules, subglobose, ellipsoid to elongate, fusiform, obtuse at apex, smooth-walled, aseptate. *Beta conidia* 17–23.5 × 1–2.5 µm ($\overline{x}$ = 21.5 × 2 µm, n = 30), hyaline, filiform, curved to hamate, aseptate.

Culture characteristics – Colonies on PDA reaching 9.0 cm in two weeks at 28 ± 2°C, medium dense, raised, sparse, effuse, fluffy, brown to black patches, yellowish center towards to pale brown from above and reverse.

Material examined – China, Guangdong province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), on asymptomatic fruit of *Wurfbainia villosa* (Zingiberaceae), 29 Oct 2022, C.F. Liao, AMF75A (MHZU 24-0146, holotype); ex-type living culture, ZHKUCC 24-0396, *ibid*., living culture ZHKUCC 24-0398.

Notes – In the phylogenetic tree, *Diaporthe loculata* (ZHKUCC 24-0396, ZHKUCC 24-0397, and ZHKUCC 24-0398) formed a distinct clade with *D. hubeiensis* (JZB320123 type strain) and *D. alangii* (CFCC 52556 type strain) with 100% ML/0.99 PP support (Figure 5.74). Morphologically, *Diaporthe loculata* differ from *D. hubeiensis* by having larger conidiomata (510–970 × 265–460 µm vs up to 510 µm in diam.) with shorter beta conidia (17–23.5 × 1–2.5 µm vs. 17–27 × 1–1.5µm). *Diaporthe loculata* can be distinguished from *D. alangii* by its larger conidiomata (510–

970 × 290–445 µm vs. 135–330 µm diam.) with larger conidiophores (5–16.5 × 2–3.5 µm vs 6–12 × 1.4–2 µm). Furthermore, conidiomata of *Diaporthe loculata* has various shapes, and multi-loculate with densely aggregated, short-cylindrical, straight conidiophores, but *D. hubeiensis* has subglobose, solitary conidiomata and conidiophores that are reduced to conidiogenous cells (Manawasinghe et al., 2019). In addition, *D. hubeiensis* was collected from diseased trunk of *Vitis vinifera* in Wuhan province, China and *D. alangii* was collected from symptomatic branches of *Alangium kurzii*, whereas our taxa collected from asymptomatic fruit of *Wurfbainia villosa* in Guangdong province, China. Hence, we introduce *Diaporthe loculata* as a novel species.



Note (a) Upper view and reverse view of culture on PDA. (b, c) Pycnidia with conidial mass sporulating on PDA after three months. (d) A section through a conidioma. (e) Pycnidial walls. (f–h) Conidiophores, conidiogenous cells with conidia. (i) Alpha conidia. (j) Beta conidia. Scale bars: b, c = 500 µm, d = 300 µm, e = 50 µm, f, g = 20 µm, h, j = 10 µm, i = 5 µm.

Figure 5.76 *Diaporthe loculata* (MHZU 24-0146, holotype)

Diaporthe neosiamensis C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.77

Index Fungorum number: IF904022; Facesoffungi number: FoF 17923

Etymology – epithet "*neosiamensis*" refers to the fungi most resembling *Diaporthe siamensis*

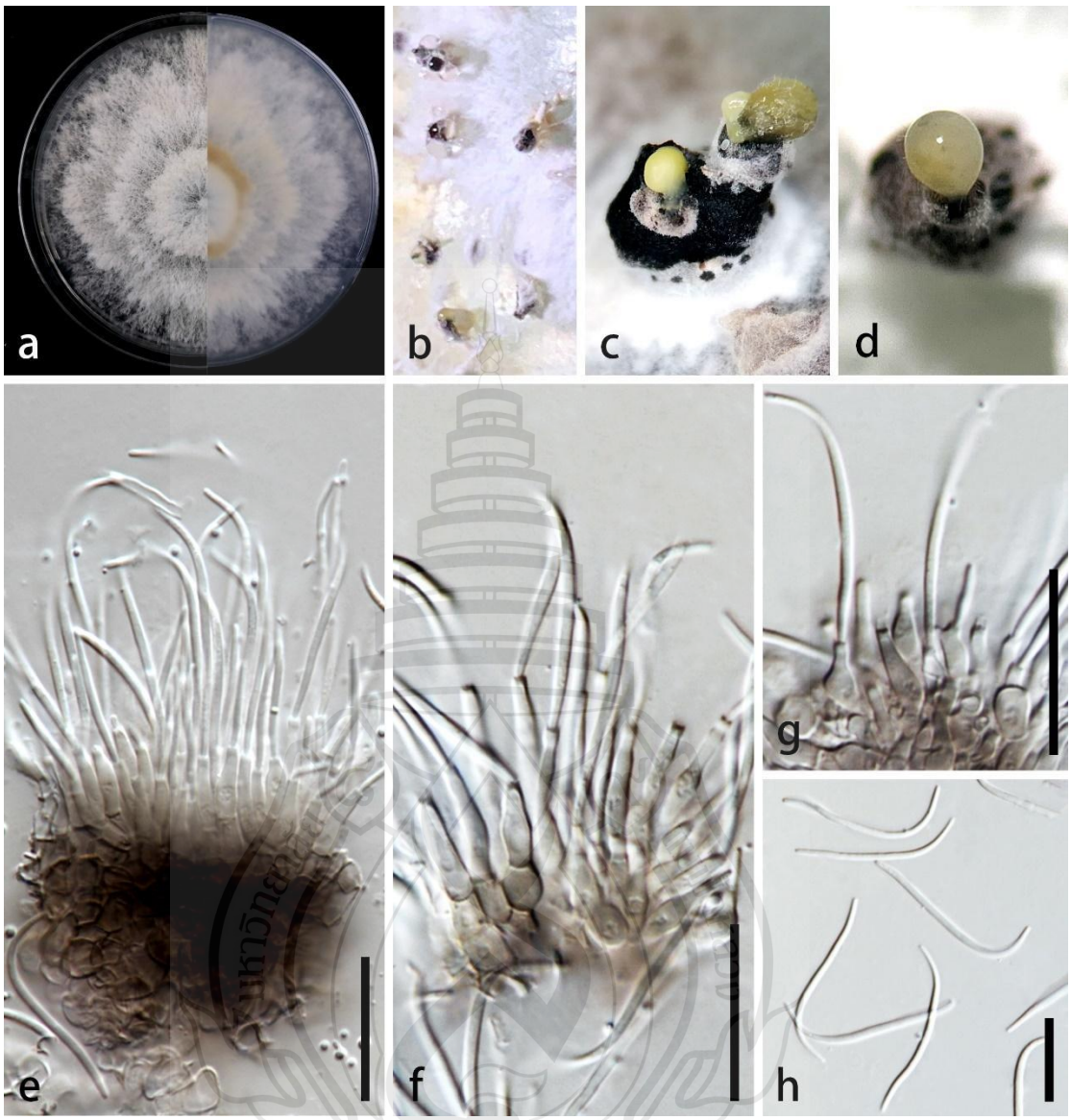
Holotype. MHZU 24-0247

Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 2 months: *Conidiomata* pycnidial, solitary to gregarious, superficial, pale brown to black, with short necks, with white to cream conidial mass exuding from ostioles when mature. *Beta conidiophores* 14–26 × 2.5–4.5 µm ($\bar{x}$ = 19 × 3.8 µm, n = 30), pale brown, cylindrical, septate, smooth-walled. *Beta conidiogenous cells* 6–17 × 2–7 µm ($\bar{x}$ = 10.5 × 3 µm, n = 30), phialidic, ovoid to obpyriform, flask-shaped, hyaline to pale brown, terminal, straight or slightly curved, aseptate. *Beta conidia* 29–37 × 1.5–2.5 µm ($\bar{x}$ = 32.5 × 1.8 µm, n = 30), hyaline, filiform, curved, aseptate.

Culture characteristics: Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, radially spreading with concentric zonation, undulate, flat, curled, pale brown from above, pale brown to cream-white from reverse.

Material examined – China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), from asymptomatic root of *Wurfbainia villosa* (Zingiberaceae), 29 October 2022, C.F. Liao, AMR16A-1 AMR16A-1A (MHZU 24-0247, holotype); ex-type culture, ZHKUCC 24-0551, ZHKUCC 25-0443.

Notes – In the phylogenetic analyses, our strain (ZHKUCC 24-0551) formed a well-supported sister branch with *Diaporthe siamensis* (MFLUCC 10-0573a, MFLUCC 10-0573b, and MFLUCC 10-0573c) with 100% ML/0.99 PP support (Figure 5.74). Morphologically, *D. neosiamensis* differs from *D. siamensis* in having superficial (vs. erumpent) conidiomata, ovoid to obpyriform, flask-shaped, terminal conidiogenous cells (vs. cylindrical, terminal and lateral in *D. siamensis*) (Udayanga et al., 2012). Moreover, *D. neosiamensis* has larger conidiophores (14–26 × 2.5–4.5 µm vs. 7–18 × 1–1.5 µm) and wider conidia (29–37 × 1.5–2.5 µm vs. (14–)15–18(–19) × (1.5–)2 µm). Based on these distinct phylogenetic and morphological differences, we propose *D. neosiamensis* as a novel species.



Note a Upper view and reverse view of culture on PDA for 2 weeks. b–d Conidiomata with conidial mass sporulating on PDA after 2 months. e–g Conidiophores, conidiogenous cells with beta conidia. h Beta conidia. Scale bars: e–h = 20 µm.

Figure 5.77 *Diaporthe neosiamensis* (MHZU 24-0247, holotype)

Diaporthe wurfbainiae C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.78

Index Fungorum number: ####; Facesoffungi number: FoF ####

Etymology – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*.

Holotype. MHZU 24-0317

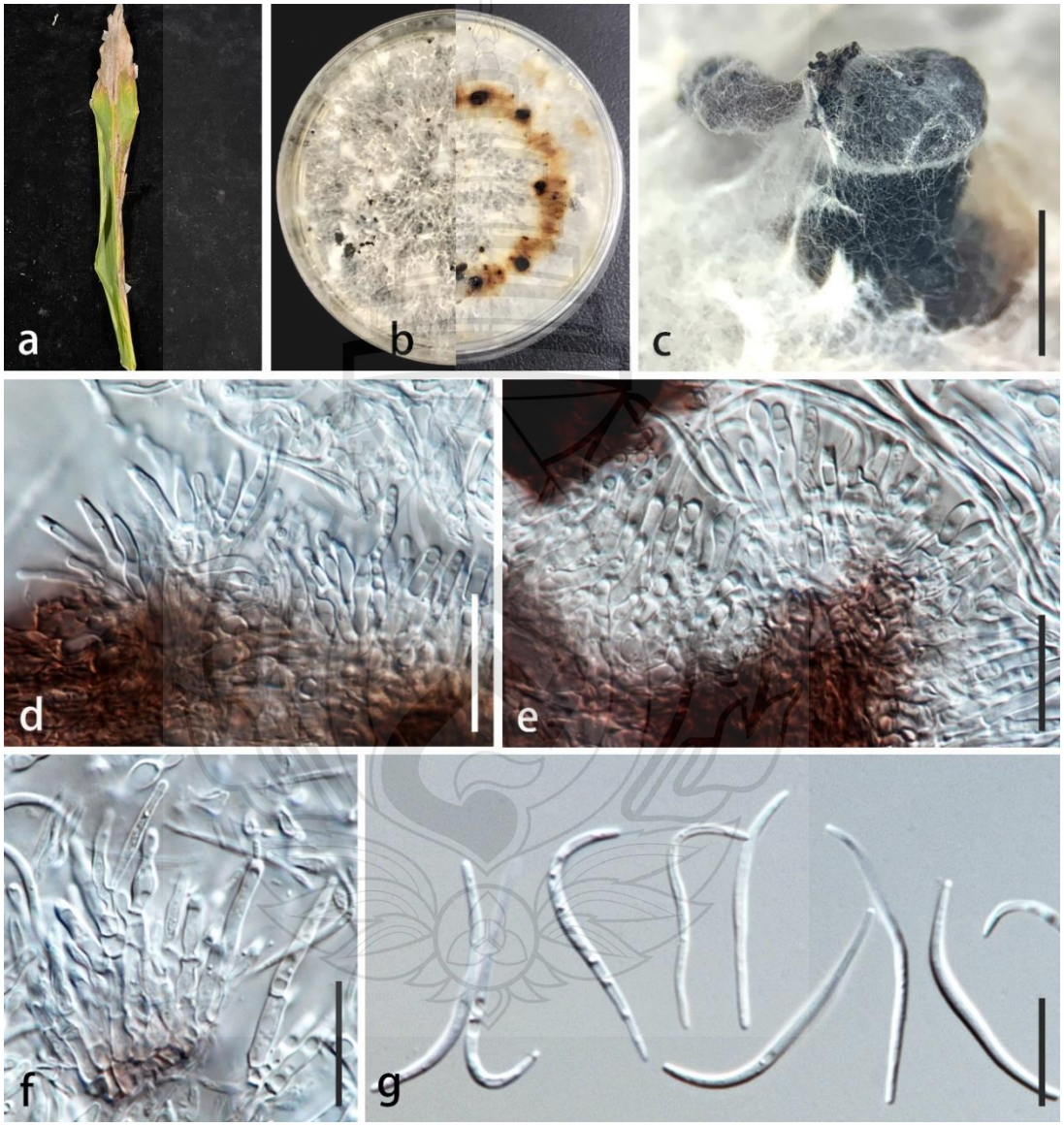
Associated with leaf spots of *Wurfbainia villosa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 296–1334 × 250–667 μm ($\bar{x}$ = 701 × 460 μm, n = 15), pycnidial on PDA sporulating poorly, scattered or aggregated, immerse to erumpent, subglobose or irregulate, brown to black, covering the surface. *Peridium* walls consisting of 4–8 layers of *textura angularis*, inner hyaline layers and outer brown layers. *Conidiophores* 10–34 × 2–6.5 μm ($\bar{x}$ = 5 × 3.6 μm, n = 30), hyaline, smooth, branched or unbranched, septate, dense, short-cylindrical to cylindrical or clavate, straight or slightly curved, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 7–21 × 1.8–3.5 μm ($\bar{x}$ = 12 × 2.7 μm, n = 30), hyaline, phialidic, subcylindrical to cylindrical, ampulliform, terminal or lateral, straight or slightly curved, aseptate. *Alpha conidia* not observed. *Beta conidia* 20–31 × 1.3–2.1 μm ($\bar{x}$ = 26 × 1.6 μm, n = 30), hyaline, filiform, curved to hamate, tapering towards end, aseptate.

Culture characteristics – Colonies on PDA reaching 9.0 cm in two weeks at 28 ± 2°C, medium dense, raised, sparse, effuse, fluffy, undulate, with concentric rings of brown to black patches, irregular margin, yellowish to pale brown from above and reverse.

Material examined – China, Guangdong Province, Yangjiang City, Heshui Town (22.298611 N, 111.98444 E), on leaf spots of *Wurfbainia villosa* (Lour.) Škorničk. & A.D. Poulsen. (Zingiberaceae), 9 Nov 2023, C.F. Liao, YP16B2 (MHZU 24-0317, holotype); ex-type living culture, ZHKUCC 24-0632, *ibid*., living culture ZHKUCC 24-0633.

Notes – In the phylogenetic tree, *Diaporthe wurfbainiae* (ZHKUCC 24-0632, ZHKUCC 24-0633) formed a sister clade with *D. tectonendophytica* (MFLUCC 13-0471 type strain and LC8115) with 96% ML and 1.00 BYPP bootstrap support (Figure 5.74). Morphologically, *Diaporthe wurfbainiae* are similar to *D. tectonendophytica* in having scattered or aggregated, immerse to erumpent conidiomata, hyaline, septate conidiophores, hyaline, cylindrical conidiogenous cells with filiform, curved to hamate conidia. *Diaporthe wurfbainiae* lacks a neck in the conidiomata and possesses cylindrical, ampulliform, terminal or lateral conidiogenous cells. However, the endophytic *D. tectonendophytica* is characterized by an elongated black neck in the conidiomata (Doilom et al., 2017) and cylindrical, terminal conidiogenous cell. Moreover, *Diaporthe wurfbainiae* differs from *D. tectonendophytica* in having larger

conidiomata (296–1334 × 250–667 µm vs. (250–)550–675(−1048) µm × (300–)770–1000(−1490) µm), longer conidiogenous cell (7–21 × 1.8–3.5 µm vs. 4–8 × 1.5–2 µm), and larger conidia (7–21 × 1.8–3.5 µm vs. 4–8 × 1.5–2 µm). Additionally, *D. tectonendophytica* has been reported in Thailand, while *D. wurfbainiae* is reported in China, allowing for easy distinction between the two species. Hence, we are introducing *Diaporthe wurfbainiae* as a novel species.



Note a Disease symptom on leaf substructure. b Upper and reverse views of the culture on PDA. c Conidiomata with conidial mass exudating on PDA after 4 months. d–f Conidiophores, conidiogenous cells with conidia. g Beta conidia. Scale bars: b, c = 500 µm, e, f = 10 µm, g = 5 µm.

Figure 5.78 *Diaporthe wurfbainiae* (MHZU 24-0317, holotype)

Diaporthe yangjiangensis C.F. Liao, K.D. Hyde & Doilom sp. nov., Figure 5.79

Index Fungorum number: ####; Facesoffungi number: ####

Etymology – epithet "*yangjiangensis*" refers to the city where the sample was collected, Yangjiang City.

Holotype. MHZU 24-0147

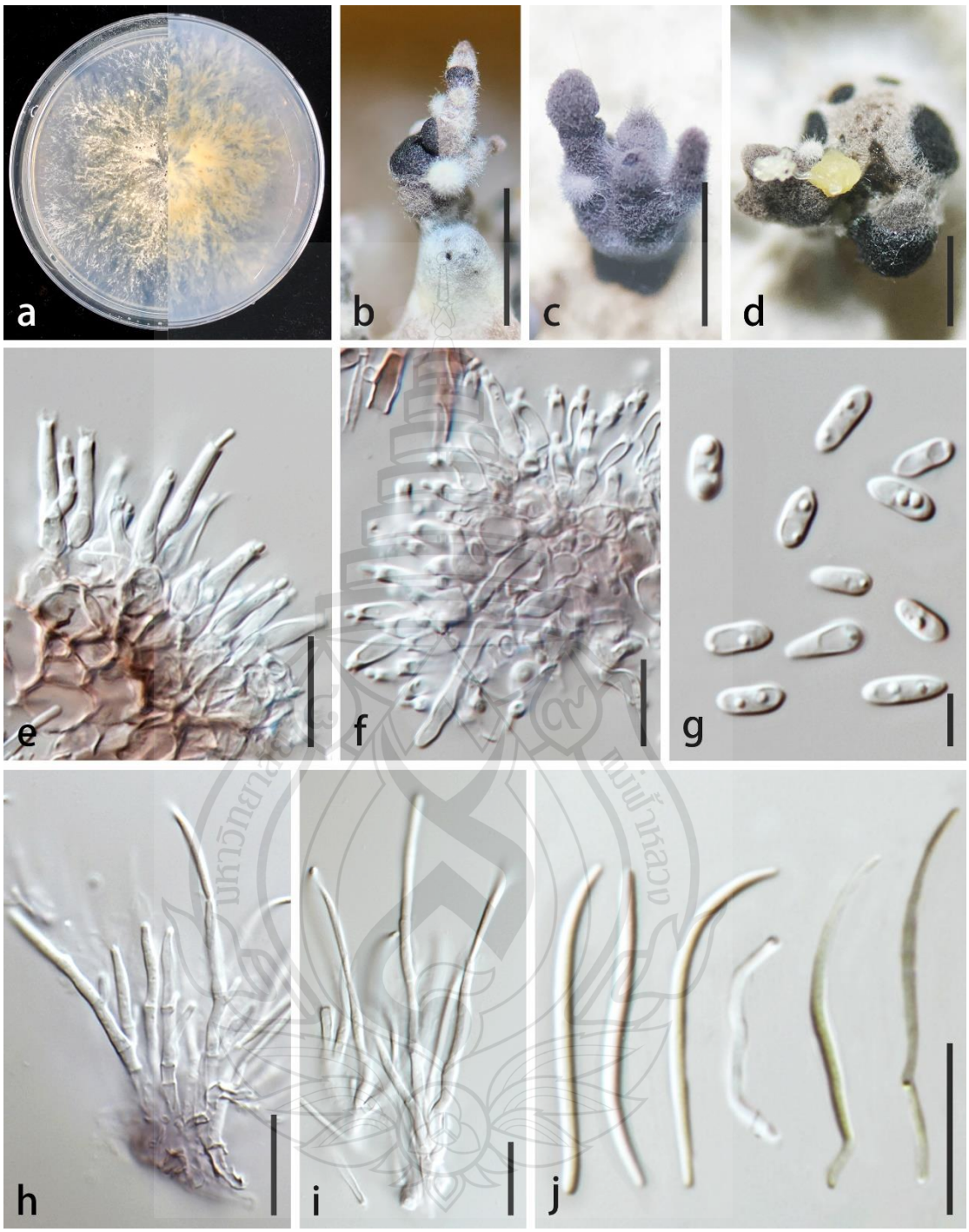
Endophytic on asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 300–1090 × 150–360 µm ($\overline{x}$ = 627 × 250 µm, n = 15), pycnidial on PDA, solitary, immerse to erumpent, multi-loculate, variously shaped, cream white to black, without necks, white to cream conidial mass exuded from ostioles when mature. *Peridium* comprising of 5–8 layers of *textura angularis*, inner hyaline layers, outer layers brown to black. *Alpha conidiophores* 11–23 × 3–7 µm ($\overline{x}$ = 17 × 4.5 µm, n = 30), hyaline, densely aggregated, short-cylindrical, smooth-walled, unbranched, aseptate, straight, sometimes reduced to conidiogenous cells. *Alpha conidiogenous cells* 4.5–13 × 2–5 µm ($\overline{x}$ = 8 × 3 µm, n = 30), phialidic, hyaline, terminal, subcylindrical to ampulliform, straight or slightly curved, tapering towards the apex, aseptate. *Alpha conidia* 5.5–8 × 2–3.5 µm ($\overline{x}$ = 6.5 × 2.8 µm, n = 30), hyaline, ellipsoid to elongate, fusiform, obtuse at apex, smooth-walled, aseptate, with one or two guttules. *Beta conidiophores* 7–50 × 1–2.5 µm ($\overline{x}$ = 23 × 2 µm, n = 30), hyaline, cylindrical, smooth-walled, branched, 1–4-septate, straight to slightly-curved. *Beta conidiogenous* cells 3–15 × 1–2 µm ($\overline{x}$ = 9 × 1.5 µm, n = 30), phialidic, hyaline, terminal or lateral, cylindrical, straight or slightly curved, aseptate. *Beta conidia* 15–22 × 1–1.5 µm ($\overline{x}$ = 18.5 × 1.2 µm, n = 30), hyaline, filiform, curved, aseptate.

Culture characteristics – Colonies on PDA reaching 9.0 cm in two weeks at 28 ± 2°C, medium sparse, flat, thinly hairy, rhizoid, mycelia radiating outwards, brown to yellowish brown from above and reverse.

Material examined – China, Guangdong province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), on asymptomatic fruit of *Wurfbainia villosa* (Zingiberaceae), 29 Oct 2022, C.F. Liao, AMF58C (MHZU 24-0147, holotype); ex-type living culture, ZHKUCC 24-0399.

Notes – In the phylogenetic tree, *Diaporthe yangjiangensis* (ZHKUCC 24-0399) formed a sister clade with *D. minusculata* (CGMCC 3.20098 type strain) with 100% ML

and 1.00 BYPP bootstrap support (Figure 5.74). Morphologically, *Diaporthe yangjiangensis* differ from *D. minusculata* in having larger conidiomata (300–1090 × 150–360 µm vs. up to 430 µm in diam) and larger alpha conidiophores (11–23 × 3–7 µm vs. 11–18 × 1.5–2.5 µm). *Diaporthe yangjiangensis* have solitary, immerse to erumpent, variously shaped, cream white to black conidiomata without necks, while *D. minusculata* are solitary or clustered in groups of 3–5 pycnidia, superficial to erumpent, globose, dark brown to black, with prominent necks that are 130–320 µm long. Furthermore, *D. minusculata* was collected from a decaying branch in Guizhou province, China, whereas our taxon was collected from the asymptomatic fruits of *Wurfbainia villosa* in Guangdong province, China. Hence, we introduce *Diaporthe yangjiangensis* as a novel taxon.



Note a Upper and reverse views of culture on PDA. b–d Conidiomata with conidial mass exudating on PDA after 3 months. e–f Conidiophores, conidiogenous cells with alpha conidia. g Alpha conidia. h, i Conidiophores, conidiogenous cells with beta conidia. j Beta conidia. Scale bars: b, c = 500 µm, d = 200 µm, e, f, h–j = 10 µm, g = 5 µm.

Figure 5.79 *Diaporthe yangjiangensis* (MHZU 24-0147, holotype)

Glomerellales Chadef. ex Réblová, W. Gams & Seifert, Stud. Mycol. 68: 170 (2011)

Notes – Glomerellales was first established by Chadefaud (1960) but was invalidly published. Réblová et al. (2011) formally proposed Glomerellales based on the phylogenetic analyses of the combined ITS, LSU, SSU and *rpb2* sequences. The current classification of Glomerellales was provided by Hyde et al. (2024).

Glomerellaceae Locq., Mycologia 98(6): 1083 (2007)

Notes – Glomerellaceae was first introduced by Locquin (1984), with *Glomerella* designated as the type genus. Réblová et al. (2011) clarified the taxonomic position of this family based on phylogenetic analyses of ITS, SSU, LSU, and *rpb2* sequences. Glomerellaceae is represented solely by the genus *Colletotrichum*.

Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.)(12): 41 (1831)

Notes – *Colletotrichum* was introduced by Corda (1831) with the type species *C. lineola*. This genus represents a major group of plant pathogens that cause anthracnose diseases in a wide variety of plants, while also occurring as endophytes and saprobes (Hyde et al., 2020; Jayawardena et al., 2021). Talhinhas and Baroncelli (2023) listed over 760 host plant species associated with *Colletotrichum* species, based on 3400 fungus-host association records. To date, *Colletotrichum* comprises 20 species complexes and 340 species (Zapata et al., 2024). As a highly adaptable and destructive fungal genus with significant importance in global agriculture, understanding its lifestyles, infection mechanisms, life cycle, and control measures is crucial for disease management and crop protection. In this study, we provide detailed morphological characteristics and molecular phylogenies of *Colletotrichum fructicola*, *C. siamense*, and *C. plurivorum* from *Wurfbainia villosa*.

Colletotrichum fructicola Prihast., L. Cai & K.D. Hyde, in Prihastuti et al., Fungal Diversity 39: 96 (2009) Figure 5.81

Index Fungorum number: IF515409; Facesoffungi number: FoF 06767

Endophytic in asymptomatic leaves, stems, and fruits, associated with symptomatic leaves and stems of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: on PDA after 2 months, *Mycelium* 1.5–3 μm wide ($\overline{x}$ = 2.5 μm, n = 30), hyaline, septate, branched. *Conidiomata* globose, directly on mycelium,

orange. *Conidiophores* 19–100 × 1–7 µm ($\overline{x}$ = 53 × 3.5 µm, n = 20), hyaline, branched, septate, sometimes reduced to conidiogenous cells, smooth-walled. *Conidiogenous cells* 9–21 × 2.5–6.5 µm ($\overline{x}$ = 14.5 × 4 µm, n = 30), phialidic, cylindrical to filiform, hyaline, branched, aseptate, smooth-walled. *Conidia* 12–16 × 4.5–7 µm ($\overline{x}$ = 15 × 5.5 µm, n = 30), hyaline, cylindrical to oblong, aseptate, straight, with rounded ends, smooth-walled.

Culture characteristics – Colonies on PDA reaching 8.5–9.0 cm diameter in 3 weeks at 28 ± 2°C, moderately sparse, raised, circle, pale to pale brown from above and reverse, no pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML03B-3 (MHZU 24-0161); living culture, ZHKUCC 24-0421; *ibid*., from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS12C-3, ZHKUCC 24-0425; *ibid*., from asymptomatic fruit of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMF56C, ZHKUCC 24-0391; *ibid*., Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from symptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP51B2; living culture, ZHKUCC 24-0691; China, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), from symptomatic leaf of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YP25A1; living culture, ZHKUCC 24-0643.

Known hosts (based on molecular data) – wide host range, including Andean blackberry (Afanador-Kafuri et al., 2014), apple (Velho et al., 2015), *Arachis* sp. (Fabaceae), avocado fruits (Fuentes-Aragón et al. 2018), *Camellia oleifera* (Li et al., 2016), *c*herry (Tang et al., 2022), *Citrus bergamia* (Rutaceae) (Lijuan et al., 2012), coffee berries, *Camellia sinensis* (Liu et al., 2015), *Citrus reticulata* cv. *nanfengmiju* and *Fortunella margarita* (Huang et al., 2013), *Crinum asiaticum* (Yang et al., 2009), mangrove (Norphanphoun & Hyde, 2024), eucalyptus (Negi et al., 2025), pear (Tang et al., 2024), *Ficus altissima* (Xie et al., 2025), *Pennisetum purpureum* (Manamgoda et al., 2013), strawberry (Chung et al., 2022).

Known distribution (based on molecular data) – worldwide, including Australia, Egypt, France, Germany, Indonesia, Israel, Italy, Japan, Korea, New Zealand, Nigeria,

Panama, Puerto Rico, Thailand, Uruguay (Manamgoda et al., 2013; Norphanphoun & Hyde, 2024), Brazil (Velho et al., 2015), China (Yang et al., 2009; Lijuan et al., 2012; Huang et al., 2013; Liu et al., 2015; Li et al., 2016; Chung et al., 2022; Tang et al., 2022; Tang et al., 2024; Xie et al., 2025; also in this study), Colombia (Afanador-Kafuri et al., 2014), India (Negi et al., 2025), Mexico (Fuentes-Aragón et al., 2018).

Notes – The phylogenetic analyses revealed that our strains (ZHKUCC 24-0430) clusters with *Colletotrichum fructicola* (Figure 5.80). Morphologically, our isolate produced characters similar to *C. fructicola* in having one-celled, cylindrical to oblong, smooth-walled conidia, with rounded ends (Prihast et al. 2009). However, our strains have longer conidia (12–16 × 4.5–7 μm vs. 9.7–14 × 3–4.3 μm) compared to *C. fructicola* described by Prihast. et al. (2009). *Colletotrichum fructicola* has a wide host range, which was reported across more than 80 plant genera (Norphanphoun & Hyde, 2024). The type specimen was isolated from berries of *Coffea arabica* in Thailand, while Song et al. (2021) reported it causing leaf spot on *Amomum villosum* in China. In the present study, we isolated *C. fructicola* from both symptomatic and asymptomatic leaves and stems, as well as asymptomatic fruit tissues of *Wurfbainia villosa* (= *Amomum villosum*).

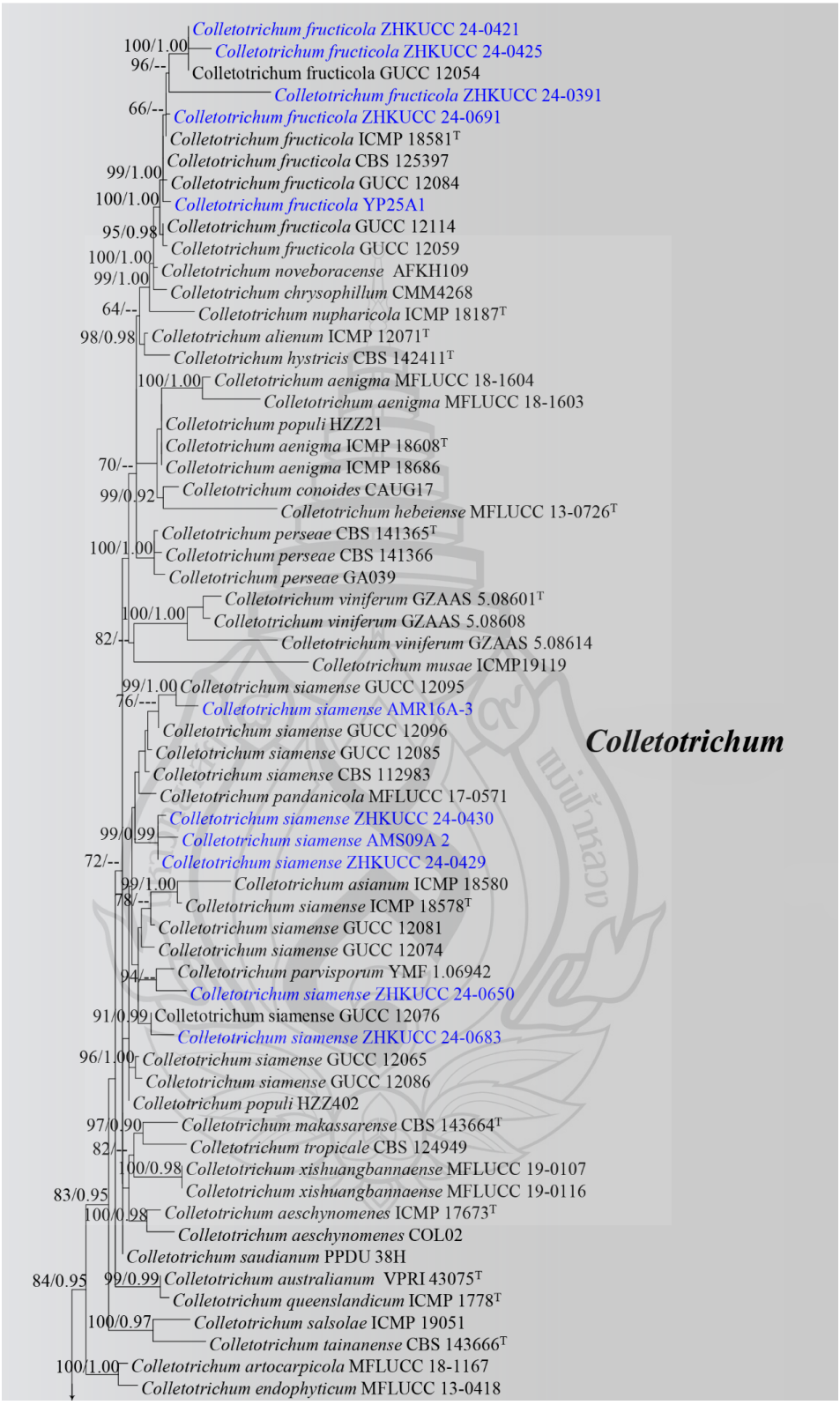
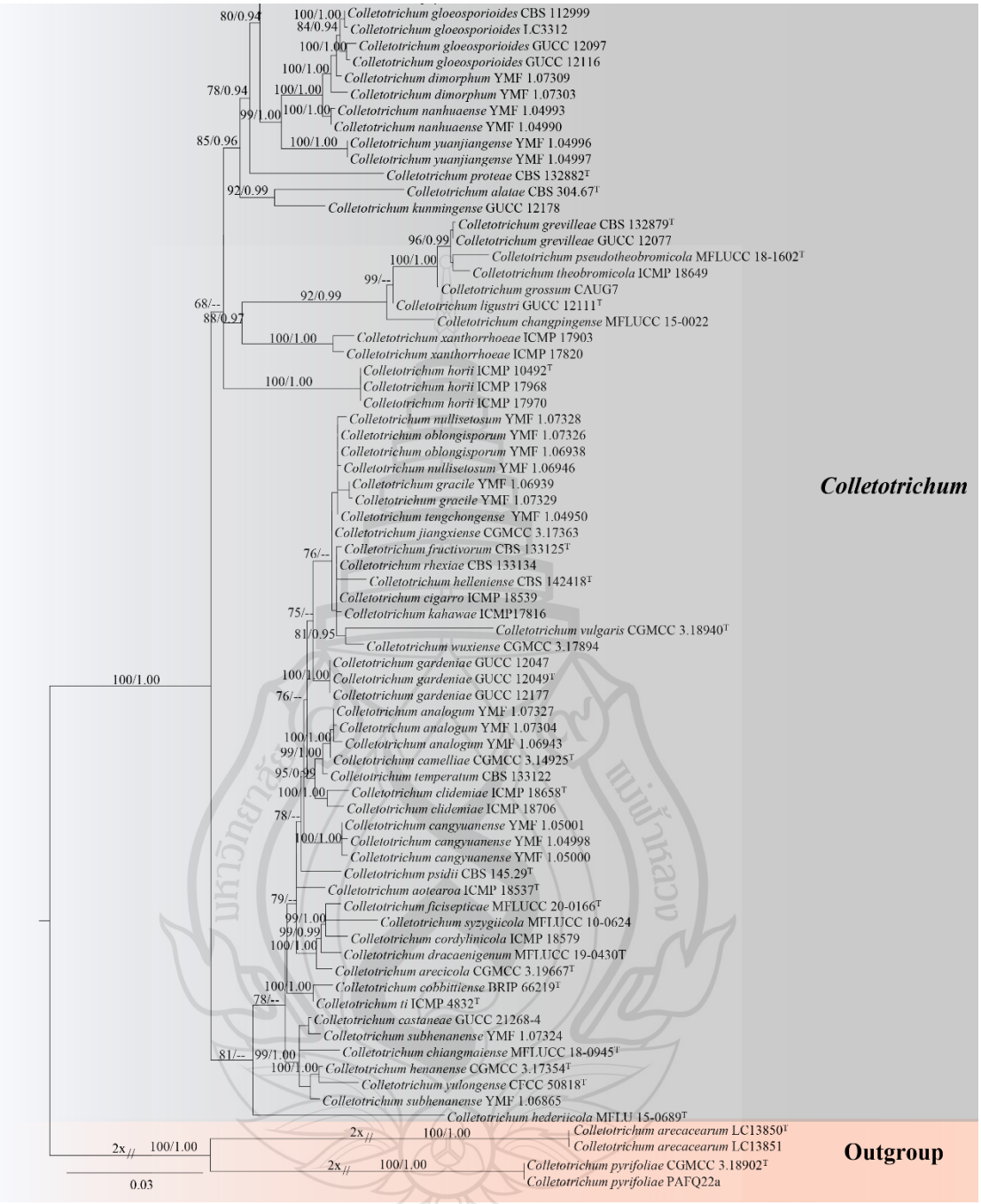
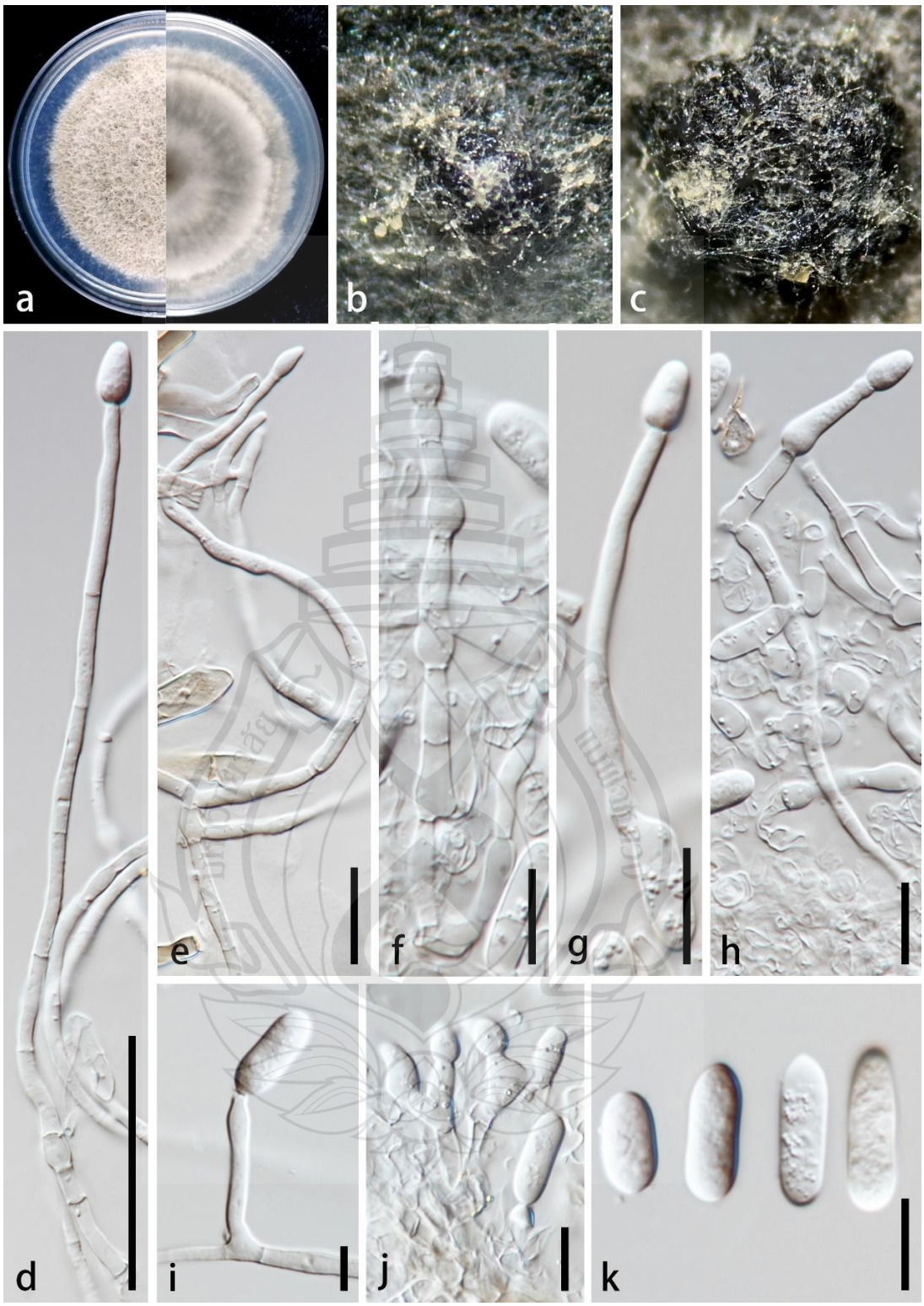


Figure 5.80 Maximum likelihood phylogeny based on the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequences data of *Colletotrichum gloeosporioides* species complex



Notes Tree rooted with *Colletotrichum arecacearum* (LC13850 and LC13851) and *C. pyrifoliae* (CGMCC 3.18902 and PAFQ22a). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.80 (continued)



Note a Culture characteristic on PDA for 3 weeks. b, c Colonies on PDA after 2 months. d–j Conidiophores, conidiogenous cells with conidia. k Conidia. Scale bars: d = 50 μm, e, g = 20 μm, f, h–k = 10 μm.

Figure 5.81 *Colletotrichum fructicola* (MHZU 24-0161, record)

Colletotrichum siamense Prihast., L. Cai & K.D. Hyde, in Prihastuti et al., Fungal Diversity 39: 98 (2009) Figure 5.82

Index Fungorum number: IF515410; Facesoffungi number: FoF 03599

Endophytic in leaf and root, symptomatic leaf and stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: on sterilized carnation leaves with pine needle on water agar after one month. *Mycelium* 2–4 μm wide ($\overline{x}$ = 3 μm, n = 30), hyaline, septate, branched. *Conidiomata* teardrop-shaped oozing on PDA surface, with pale orange conidial mass exuding on sterilized leaf tissues of *W. villosa* and pine needles. *Conidiophores* 21–66 × 4–7 μm ($\overline{x}$ = 39 × 5 μm, n = 20), hyaline, branched, septate, sometimes reduced to conidiogenous cell, smooth-walled. *Conidiogenous cells* 8–47 × 2.5–6 μm ($\overline{x}$ = 23 × 4.5 μm, n = 30), phialidic, cylindrical to obclavate, hyaline, branched, aseptate, smooth-walled. *Conidia* 11.5–16 × 4.5–6 μm ($\overline{x}$ = 14 × 5.5 μm, n = 30), cylindrical to oblong, clavate, aseptate, straight, with obtuse ends, hyaline, smooth-walled. *Appressoria* 9–16 × 7–10 μm ($\overline{x}$ = 13 × 8 μm, n = 30), solitary, dark olivaceous green, smooth-walled, elliptical to oblong in outline, with slightly crenate to undulate edge, smooth-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, flat, cream-white from above and reverse, without pigmentation.

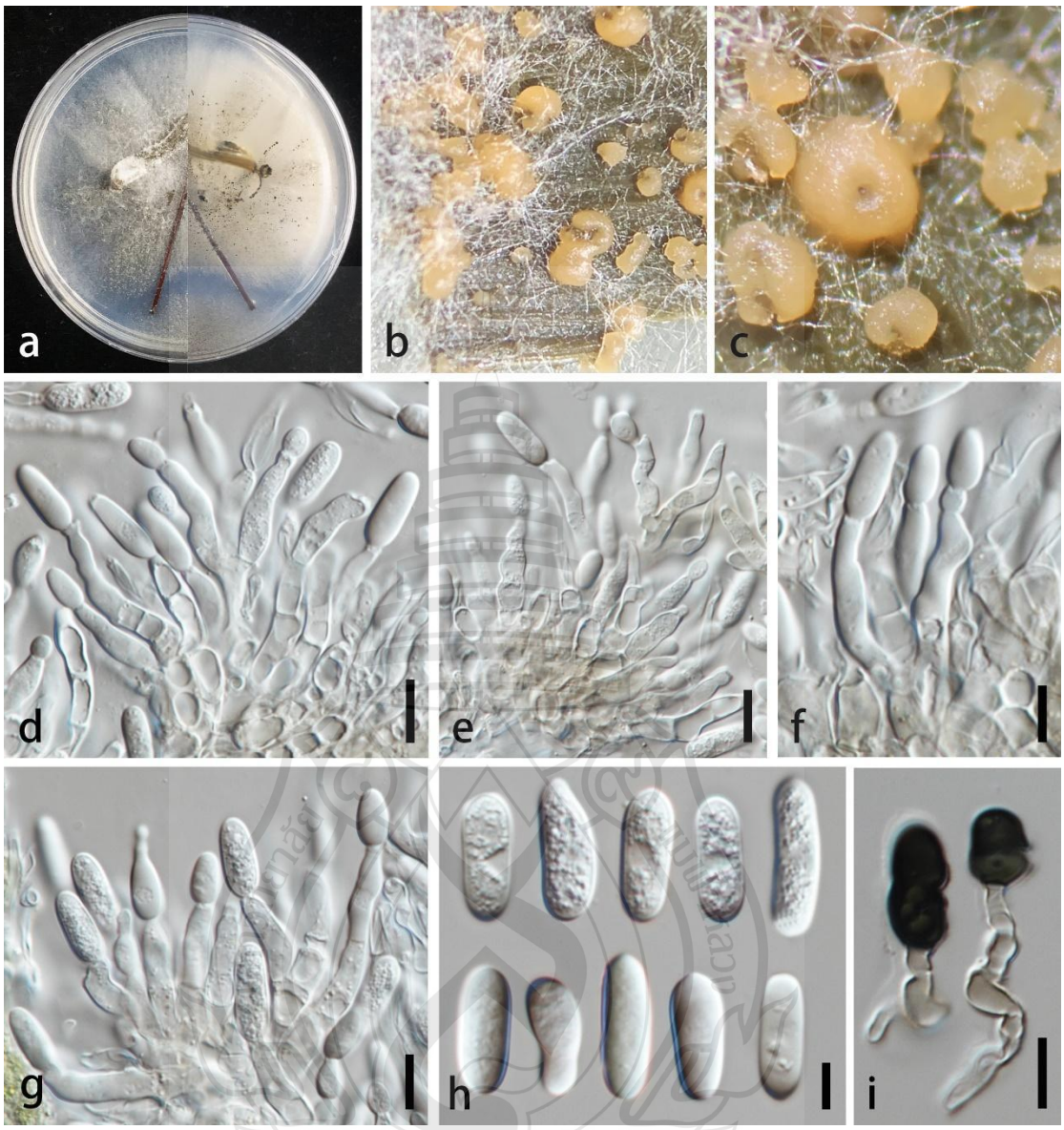
Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS09A-2, AMS12C-5, AMR16A-3 (MHZU 24-0165); living culture, ZHKUCC 25-0445, ZHKUCC 24-0429, ZHKUCC 25-0444; *ibid.*, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), from symptomatic leaf of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YP28A2; living culture, ZHKUCC 24-0650; *ibid.*, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), on symptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YP48A1; living culture, ZHKUCC 24-0683.

Known hosts (based on molecular data) – *Alocasia macrorrhiza*, *Ardisia japonica*, *Aucuba japonica*, *Bauhinia championii*, *Camellia japonica*, *Chamaedorea elegans*, *Curcuma phaeocaulis*, *Eriobotrya japonica*, *Fatsia japonica*, *Heteropanax*

fragrans, *Hymenocallis littoralis*, *Houttuynia cordata*, *Ilex chinensis*, *Osmanthus fragrans*, *Piper sarmentosum* (Zhang et al., 2023a), avocado (Thanh et al., 2025), *Bauhinia variegata*, *Cassia fistula*, *Cassia* sp., *Citrus* sp., *Ficus elastica*, *Mangifera indica*, *Psidium guajava*, *Saraca indica*, *Bauhinia variegata*, *Cocos nucifera* (Sharma et al., 2015), *Cinnamomum burmanni* (Cao et al., 2025), *Coffea arabica* (Prihastuti et al., 2009), *Capsicum annuum*, *Carica papaya*, *Commelina* sp., *Dioscorea rotundata*, *Fragaria ananassa*, *Persea americana*, *Pistacia vera*, *Hymenocallis americana*, *Malus domestica*, *Vitis vinifera* (Weir et al., 2012), jackfruit (Khuna et al., 2024), *Michelia maudiae* (Huang et al., 2025), silver date palm (Yang et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Australia, China, Nigeria, South Africa, USA (Weir et al., 2012), India (Sharma et al., 2015), Thailand (Prihastuti et al., 2009), China (Zhang et al., 2023; Fang et al., 2024; Yang et al., 2024; Cao et al., 2025; Huang et al., 2025; this study), Thailand (Kaewchai et al., 2024; Khuna et al., 2024), Vietnam (Thanh et al., 2025).

Notes – In the phylogenetic analyses, our strains clustered with *Colletotrichum siamense* (Fig 5.80). Morphologically, MHZU 24-0165 has larger appressoria (9–16 × 7–10 μm vs. 4.7–8.3 × 3.5–5 μm) compared to the type of *C. siamense* (ICMP 18578) (Prihastuti et al., 2009). *Colletotrichum siamense* has a broad host range (Zhang et al., 2023, see known hosts). To the best of our knowledge, this species has not previously been reported from *Wurfbainia villosa*. We therefore propose our *C. siamense* isolates as representing a new host record from this plant.



Note a Culture characteristic on sterilized carnation leaves with pine needles on water agar after 1 month. b, c Colonies on PDA. d–g Conidiophores, conidiogenous cells with conidia. h Conidia. i Appressoria. Scale bars: d–g, i = 10 μm, h = 5 μm.

Figure 5.82 *Colletotrichum siamense* (MHZU 24-0411, new host record)

Colletotrichum plurivorum Damm, Alizadeh & Toy. Sato, in Damm et al., Stud. Mycol. 92: 31 (2018) Figure 5.84

Index Fungorum number: IF824228; Facesoffungi number: FoF 10691

Endophytic in asymptomatic fruit and leaf, associated with symptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after

1 month: *Mycelium* hyaline to pale brown, septate, branched. *Conidiomata* rarely produced. *Conidiophores* pale brown, unbranched, septate, sometimes reduced to conidiogenous cells, smooth-walled. *Conidiogenous cells* 4–17 × 3.5–5 μm ($\bar{x}$ = 10 × 4 μm, n = 10), cylindrical to obpyriform, hyaline to pale brown, smooth-walled. *Conidia* 11–22 × 6–9 μm ($\bar{x}$ = 17 × 7.5 μm, n = 30), cylindrical to oblong, clavate to reniform, allantoid to fusiform, mostly aseptate, rarely 1-septate, straight to curved, with obtuse ends, hyaline, smooth-walled. *Appressoria* 8–18 × 6–12 μm ($\bar{x}$ = 14 × 9.5 μm, n = 30), solitary, dark olivaceous green, elliptical to subglobose in outline, with crenate to undulate edge, guttulate, smooth-walled.

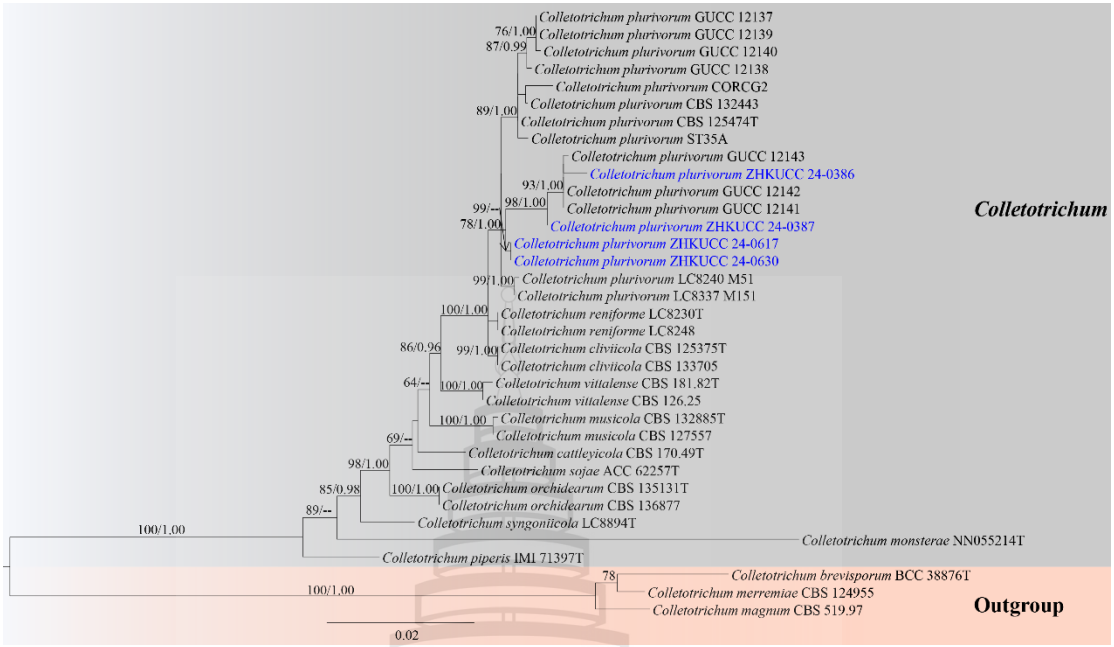
Culture characteristics – Colonies on PDA reaching 6.0 cm diameter in 1week at 28 ± 2°C, moderately dense, raised, circular, with entire edge, wooly, pale brown to cream-white from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.29861 N, 111.98444 E), from symptomatic leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP09A1, YP14A6 (MHZU 24-0304); living culture, ZHKUCC 24-0617, ZHKUCC 24-0630; *ibid.*, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic fruit of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMF37A; living culture, ZHKUCC 24-0386; *ibid.*, from asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML06C-7; living culture, ZHKUCC 24-0387.

Known hosts (based on molecular data) – *Abelmoschus esculentus*, *Amorphophallus rivieri*, *Arundina graminifolia*, *Citrus limon*, *Coffea* sp., *Cymbidium hookerianum*, *Dioscorea* sp., *Glycine max*, *Gossypium* sp., *Musa* sp., *Myrianthus arboreus*, *Oncidium* sp., *Passiflora edulis*, *Phaseolus vulgaris*, *Solanum lycopersicum*, *Spathiphyllum wallisi*, *Vitis* spp., *Zamioculcas zamiifolia* (Damm et al., 2019), banana (Kurera et al., 2023), *Carica papaya* (Sun et al., 2019), *Carya illinoinensis* (Zhang et al., 2023c), cowpea (Dai et al., 2024), *Cucumis sativus* (Silva et al., 2025), *Cyclocarya paliurus* (Zheng et al., 2024), *Dracaena fragrans*, *Hoya kerrii* (Scheck, 2019), *Manihot esculenta* (Liu et al., 2019c), melon (Assunção et al., 2024), *Piper sarmentosum*, *Syngonium podophyllum* (Zhang et al., 2023b), Passion fruit (Zhao et al., 2024), *Phaseolus lunatus* (Cavalcante et al., 2019), *Pyrus bretschneideri* (Fu et al., 2019), soybean (Mello et al., 2024), *Wurfbainia villosa* (this study).

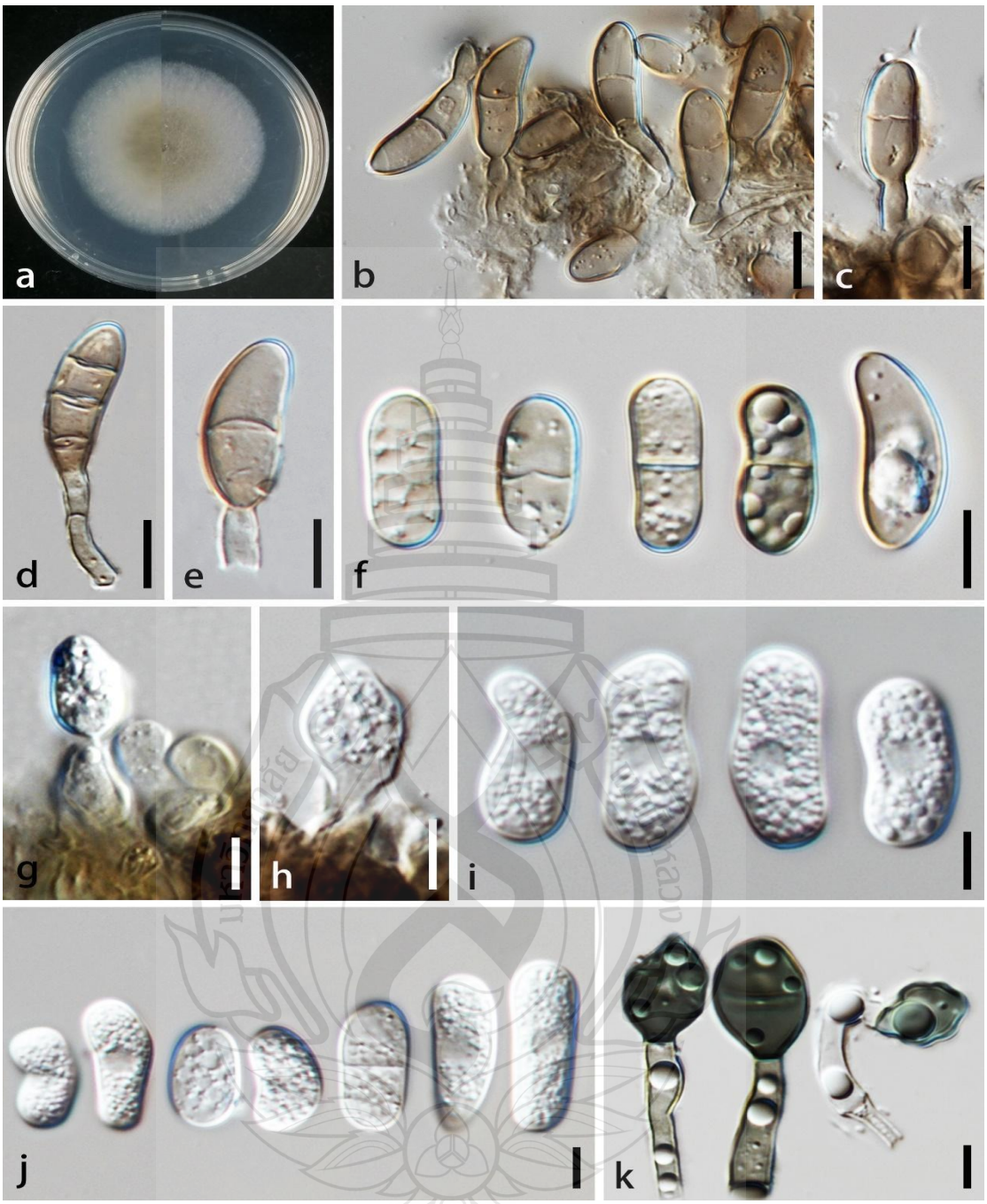
Known distribution (based on molecular data) – Benin, Brazil, Iran, Vietnam (Damm et al., 2019), Brazil (Cavalcante et al., 2019; Assunção et al., 2024; Mello et al., 2024; Silva et al., 2025), China (Fu et al., 2019; Sun et al., 2019; Zhang et al., 2023a, c; Dai et al., 2024; Zhao et al., 2024; Zheng et al., 2024; this study), India (Sharma et al., 2015), Sri Lanka (Kurera et al., 2023), USA (Scheck, 2019).

Notes – In the phylogenetic analyses, our strains clustered within *Colletotrichum plurivorum* species complex (Figure 5.84). Morphologically, our isolate produced two types of asexual conidia, one of which resembled the sexual morph of *C. plurivorum* (Figure 5.83). The conidia of our isolate showed similarity to *C. plurivorum* in having cylindrical-clavate conidiogenous cells and cylindrical, allantoid to fusiform conidia. Moreover, our isolate has similar size conidiogenous cells (4–17 × 3.5–5 μm vs. 6.5–19 × 3.5–4.5 μm), conidia (11–22 × 6–9 μm vs. (13–)14.5–18(–22) × (4–)5–6(–7) μm), and appressoria (8–18 × 6–12 μm vs. 12.5–18.5(–22.5) × (4.5–)6.5–11.5(–15.5) μm) when compared with *C. plurivorum* (Damm et al. 2019). We identify our isolate as a new host record of *C. plurivorum*.



Note Tree rooted with *Colletotrichum brevisporum* (BCC 38876), *C. magnum* (CBS 519.97), and *C. merremiae* (CBS 124955). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.83 Maximum likelihood phylogeny based on the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequences data of *Colletotrichum orchidearum* species complex



Note a Culture characteristic on PDA for 1 month. b–e Conidiogenous cells with conidia. f Conidia. g, h Conidiogenous cells with conidia. i, j Conidia. k Appressoria. Scale bars: b–f = 10 μm, g–k = 5 μm.

Figure 5.84 *Colletotrichum plurivorum* (MHZU 24-0304, new host record)

Trichosphaeriaceae G. Winter (= Plectosphaerellaceae W. Gams, Summerb. & Zare)*FWF, Crous et al. 2023; Hou et al. 2023

Notes – Plectosphaerellaceae was introduced by Zare et al. (2007) and typified by *Plectosphaerella cucumerina.* However, Crous et al. (2023) synonymized Plectosphaerellaceae to Trichosphaeriaceae, as Trichosphaeriaceae gets the priority as the older name. Members of this family are mainly saprobic fungi found in soil or on decaying plants but also include plant pathogens and endophytes (Giraldo & Crous, 2019). The identification of this family is based on morphology and phylogenetical analyses using ITS, LSU, *tef1-α*, and *rpb2* sequences (Crous et al., 2023). Currently, 31 genera are accepted in this family (Wijayawardene et al., 2022; Hyde et al., 2024).

Acrostalagmus Corda, Icon. fung. (Prague) 2: 15 (1838)

Notes – *Acrostalagmus* is a filamentous fungal genus commonly found in soil, plant-associated environments, and marine habitats, which occurs as endophytes, saprobes, or opportunistic pathogens. The genus is characterized by mononematous or synnematous conidiophores, monophialidic conidiogenous cells, and hyaline to bright orange or reddish, ellipsoidal to oblong, oval conidia (Hyde et al., 2020). Some species have been shown to have significant ability to produce numerous bioactive natural products, with 82% of marine *Acrostalagmus* isolates exhibiting this ability (Shi et al., 2023). Currently, 55 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we propose *Acrostalagmus annulatu* as a new fungal associate of *Wurfbainia villosa* and report it as a new geographical record for China, as detailed below.

Acrostalagmus annulatu (Berk. & M.A. Curtis) Seifert, in Réblová et al., Stud. Mycol. 68: 186 (2011) Figure 5.86

Index Fungorum number: IF518663; Facesoffungi number: FoF 14302

Endophytic in asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: on PDA after 2 months. Colonies superficial on PDA or immersed, gregarious, orange and globose liquid water drops at younger stage, becoming reddish patched when mature. *Conidiophore axis* 74–97 × 3–5.5 μm ($\overline{x}$ = 84 × 4 μm, n = 30), erect, solitary or repeatedly branched, hyaline to pale orange, septate, wide at the base, tapering toward apex. *Phialides* 13.5–32.5 × 1–5 μm ($\overline{x}$ = 23 × 2.5 μm, n = 30), monophialidic, integrated, determinate, terminal or intercalary, cylindrical,

flask-shaped, arising in whorls of 1–5 along the main stipe and branches, hyaline, septate, smooth-walled. *Conidia* 4–7 × 2–5 μm ($\overline{x}$ = 5.5 × 3 μm, n = 30), unicellular, obovoid, oval to cylindrical, hyaline, smooth-walled.

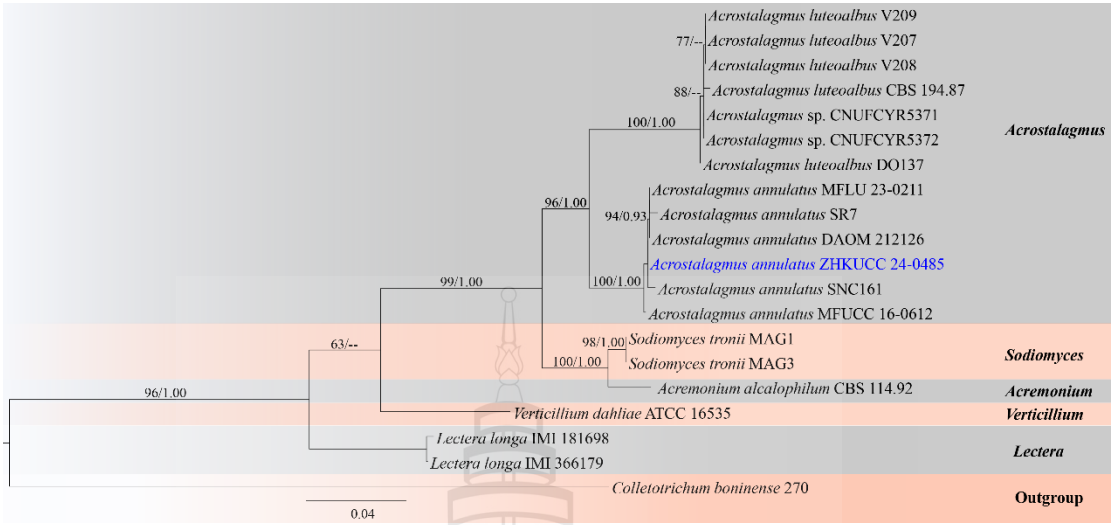
Culture characteristics – Colonies on PDA reaching 2.5–3.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, diffuse, raised, undulate, irregular, pale orange from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML20C-2 (MHZU 24-0202); living culture, ZHKUCC 24-0485.

Known hosts (based on molecular data) – Saprophytic on wood, bark, leaves, herbaceous stems, occasionally on boletes; occasionally isolated from soil. Recorded from *Ananas comosus* (Tian et al., 2024), Bromeliaceae (*Ananas camases*), Cruciferae (*Brassica* sp.), Gnetaceae (*Gnetum gnemon*), Leguminaceae (*Glycine max*). Malvaceae (*Gossypium* sp., *Manihot utilissima*), Moraceae (*Ficus elastica*), Musaceae (*Musa* sp.), Palmae (*Cocos* sp., *Elaeis guineensis*), Sterculiaceae (*Theobroma cacao*), and Umbelliferae (*Pastinaca sativa*) (Réblová et al., 2011; Giraldo & Crous, 2019), Sea sand (Lee et al., 2025), *Wurfbainia villosa* (this study).

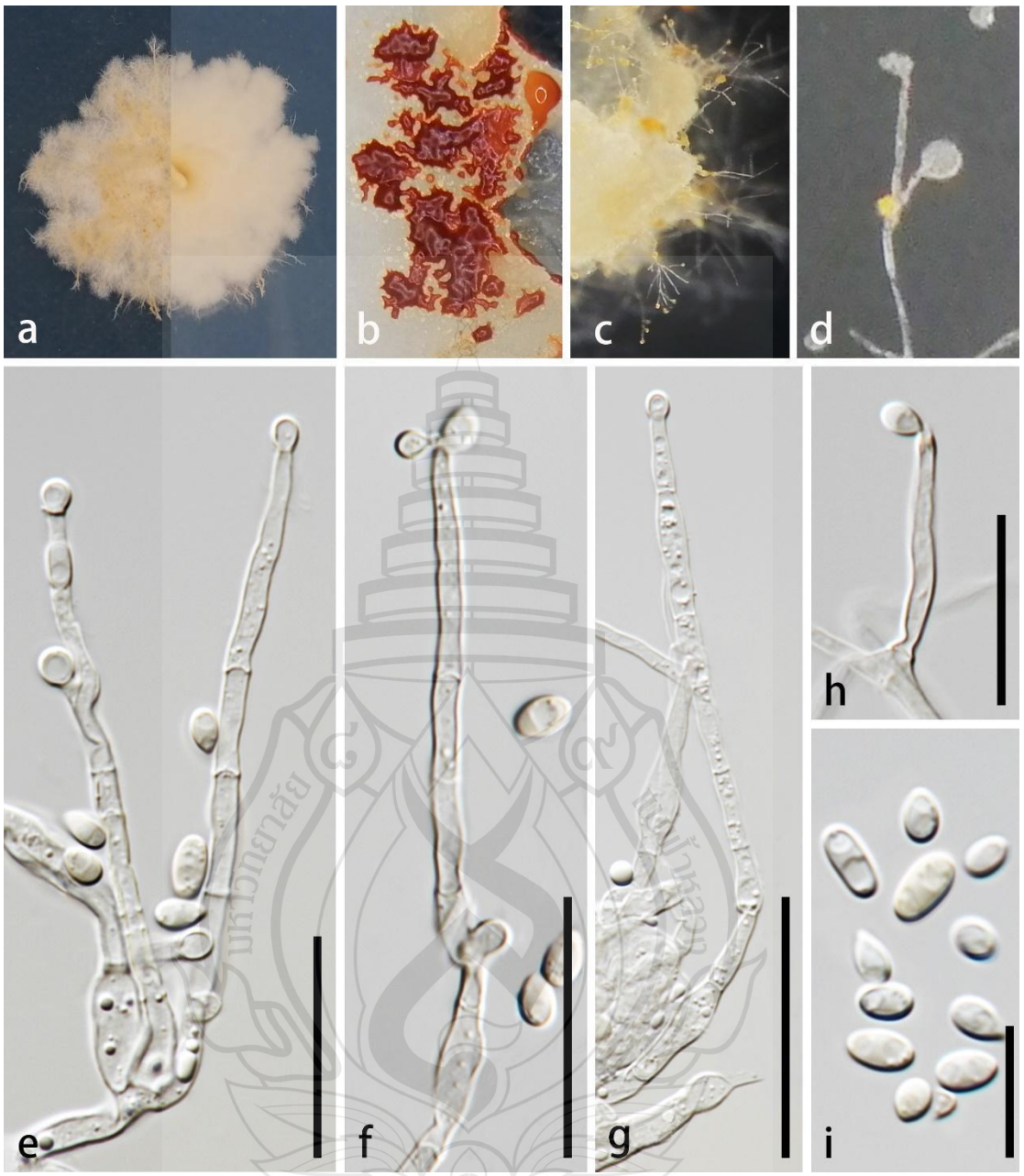
Known distribution (based on molecular data) – Africa (Sierra Leone), Central America (Costa Rica, Mexico), North America (Arizona, Louisiana, Ontario), South America (Peru, Surinam, Venezuela), Europe (Netherlands, Czechoslovakia) (Réblová et al., 2011; Giraldo & Crous, 2019). West Indies (Cuba). South Korea (Lee et al., 2025), SE Asia (Japan, Malaya, New Guinea), Thailand (Tian et al., 2024), China (this study).

Notes – In the phylogenetic analysis, ZHKUCC 24-0485 clustered with *Acrostalagmus annulatu* with 100% ML/1.00 PP support (Figure 5.85). Morphologically, our new isolate fits with *Acrostalagmus annulatu* by having branched conidiophores, cylindrical, straight or sinuous, lateral and terminal phialides, and ellipsoidal to oblong-ellipsoidal conidia (Seifert, 1985; Réblová et al., 2011). This represents a new host and geographical record of *Acrostalagmus annulatu* isolated from *Wurfbainia villosa* in China.



Note Tree rooted with *Colletotrichum boninense* (270). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strain from this study is shown in blue.

Figure 5.85 Maximum likelihood phylogeny based on the combined ITS and LSU sequence data of *Acrostalagmus*



Note a Culture characteristic on PDA for 2 weeks. b–d Conidia on aerial mycelia on PDA after 2 months. e–h Conidiogenous cells with conidia. i Conidia. Scale bars: e–h = 20 μm, i = 10 μm.

Figure 5.86 *Acrostalagmus annulatu* (MHZU 24-0202, new host and geographical record)

Musicillium Zare & W. Gams, Nova Hedwigia 85: 482. 2007.

Notes – *Musicillium* was introduced by Zare et al. (2007) and typified by *M. theobromae*. Members of this genus have been reported as saprobes isolated from *Musa* and *Pandanus* (Tibpromma et al., 2018; Samarakoon et al., 2024), while *M. theobromae* has been documented as pathogens causing cigar-end rot in bananas (Giraldo & Crous, 2019). Currently, four species are accepted in the genus, most of which are hyphomycetes, only *M. elettariae* has been reported to produce both sexual and asexual morphs (Samarakoon et al., 2014). In this study, we report *Musicillium tropicale* (asexual morph from both natural substrate and cultured on PDA medium) as a newly recorded fungal associate of *Wurfbainia villosa*, with detailed morphological descriptions and phylogenetic analyses presented below.

Musicillium tropicale Giraldo López & Crous, Stud. Mycol. 92: 268 (2018) Figure 5.88, 5.89

Index Fungorum number: IF828066; Facesoffungi number: FoF 13535

Saprobic on decaying leaf and stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Conidiophores* 251–601 × 6–18 μm ($\bar{x}$ = 422 × 11 μm, n = 30), simple or branched, erect to curved, black at the base, gradually paler towards the apex, hyaline at terminal whorls, verticillately branched towards the apex, swollen at nodes, bearing 3–6 whorls of 5–9 phialides, smooth or verrucose, cell walls thicker than the hyaline hyphae. *Phialides* 11–36 × 2–4 μm ($\bar{x}$ = 25 × 3 μm, n = 30), solitary or in divergent whorls of 1–3, lateral to terminal, hyaline to pale brown, subulate to acicular, tapering towards the apex, with a minute collarette and inconspicuous periclinal wall thickening at the conidiogenous locus, thick- and smooth-walled. *Conidia* 5–6 × 2–3 μm ($\bar{x}$ = 5.5 × 2.5 μm, n = 30), hyaline, ellipsoidal, unicellular, aseptate, 0–2 guttules, arranged in slimy glistering heads, thick-walled.

Culture characteristics – Colonies on PDA reaching 5.0–5.5 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, raised, circle, filiform, forming four concentric circles from center to the edge, pale to brown to dull white to cream-white. *Hyphae* 2.0–5.0 μm wide ($\bar{x}$ = 3.5 μm, n = 30), branched, hyaline to olivaceous green, septate, smooth-walled, multi-guttulate. *Conidiophores* 188–548 × 3–7 μm ($\bar{x}$ = 313 × 4.5 μm, n = 30), simple or branched, erect to curved, pale brown at the base, hyaline toward the terminal whorls, verticillately branched towards at the apex, bearing 3–5 whorls of

2–5 phialides, smooth or verrucose, with thicker cell walls than the hyaline hyphae some. *Phialides* 13–66 × 2–5 μm ($\bar{x}$ = 35 × 3.5 μm, n = 30), mostly directly from mycelium, some grow from conidiophores, solitary or in divergent whorls of 1–2, lateral to terminal, hyaline, subulate to acicular, tapering towards the apex, with a minute collarette and inconspicuous periclinal wall thickening at the conidiogenous locus, thin- and smooth-walled. *Conidia* 5–13 × 2–5 μm ($\bar{x}$ = 8.5 × 3.5 μm, n = 30), hyaline, ellipsoidal, unicellular, aseptate, multi-guttulate, some are middle thinner than the ends, arranged in slimy glistering heads thick-walled.

Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), on decaying leaf of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YAM84, (MHZU 24-0073); living culture, ZHKUCC 24-0290, ZHKUCC 24-0335; China, Guangdong Province, Yangchun City, Jinghuaken (22.19027 N, 111.91027 E), on decaying stem of *Wurfbainia villosa*, 10 April 2023, C.F. Liao, YAM40; living culture, ZHKUCC 24-0239.

Known hosts (based on molecular data) – Leaf of *Musa* sp., rotten banana, leaf litter, *Lactarius* sp. (Giraldo & Crous, 2019; Samarakoon et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Bangladesh, Brazil, Cuba, Czech Republic, Japan, Zambia (Giraldo & Crous, 2019), Thailand (Samarakoon et al., 2024), China (this study).

Notes – The phylogenetic analyses showed that our strains (ZHKUCC 24-0239, ZHKUCC 24-0290, and ZHKUCC 24-0335) clustered with *Musicillium tropicale* (CBS 100951, CBS 121212) with 98 % ML/0.99 PP support (Figure 5.87). Morphologically, our isolate matches *M. tropicale* in having erect conidiophores, which are brown at the base and hyaline at terminal whorls, verticillately branched near the apex. The conidiogenous cells are hyaline, subulate to acicular, occurring either singly or in divergent whorls, tapering towards the apex, with a minute collarette and inconspicuous periclinal wall thickening at the conidiogenous locus. Additionally, the conidia are hyaline, ellipsoidal, unicellular, aseptate, arranged in slimy glistering heads (Giraldo & Crous, 2019). Based on these molecular and morphological concordances, we designate our isolates as a new host record of *M. tropicale* from *Wurfbainia villosa.*

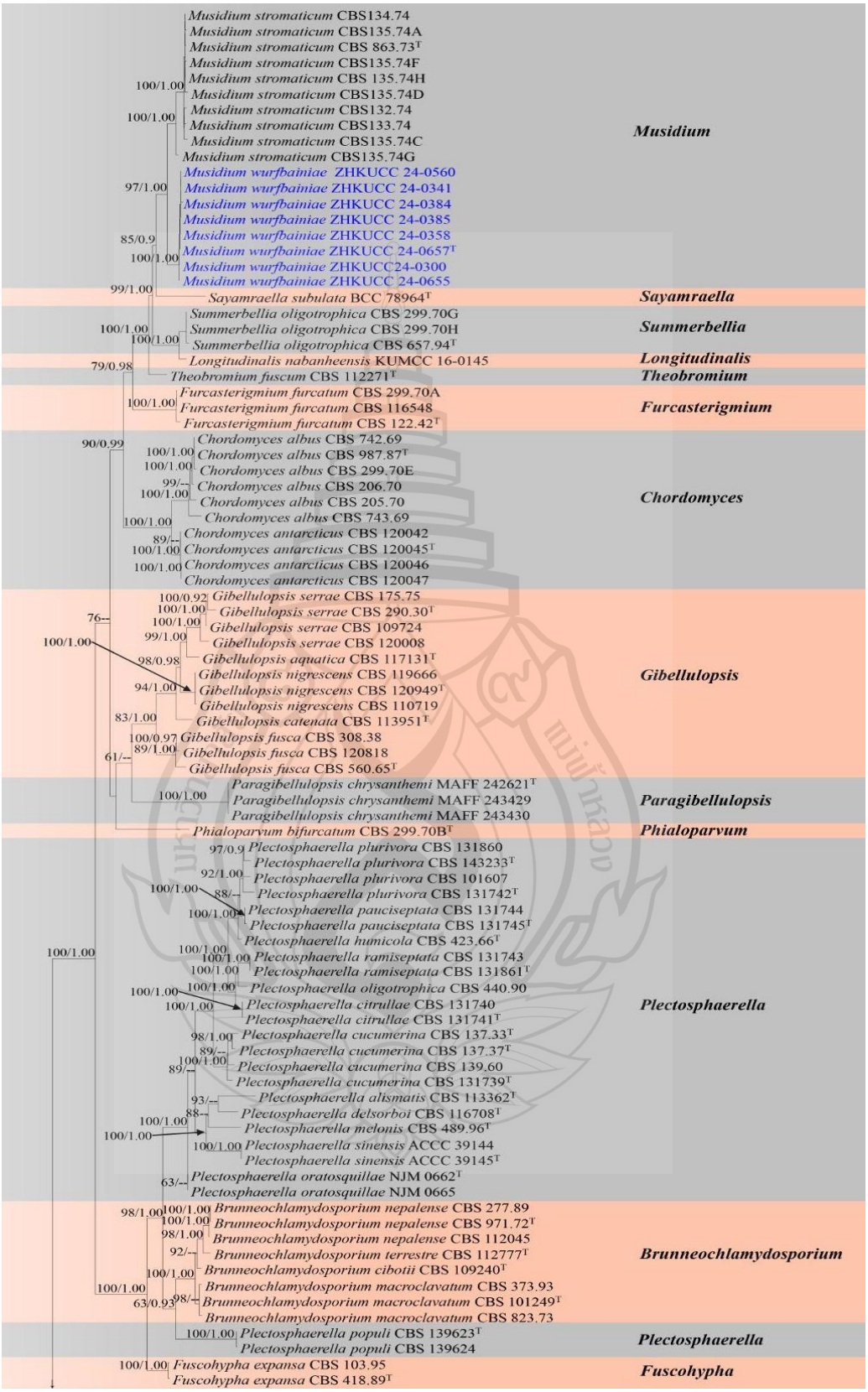
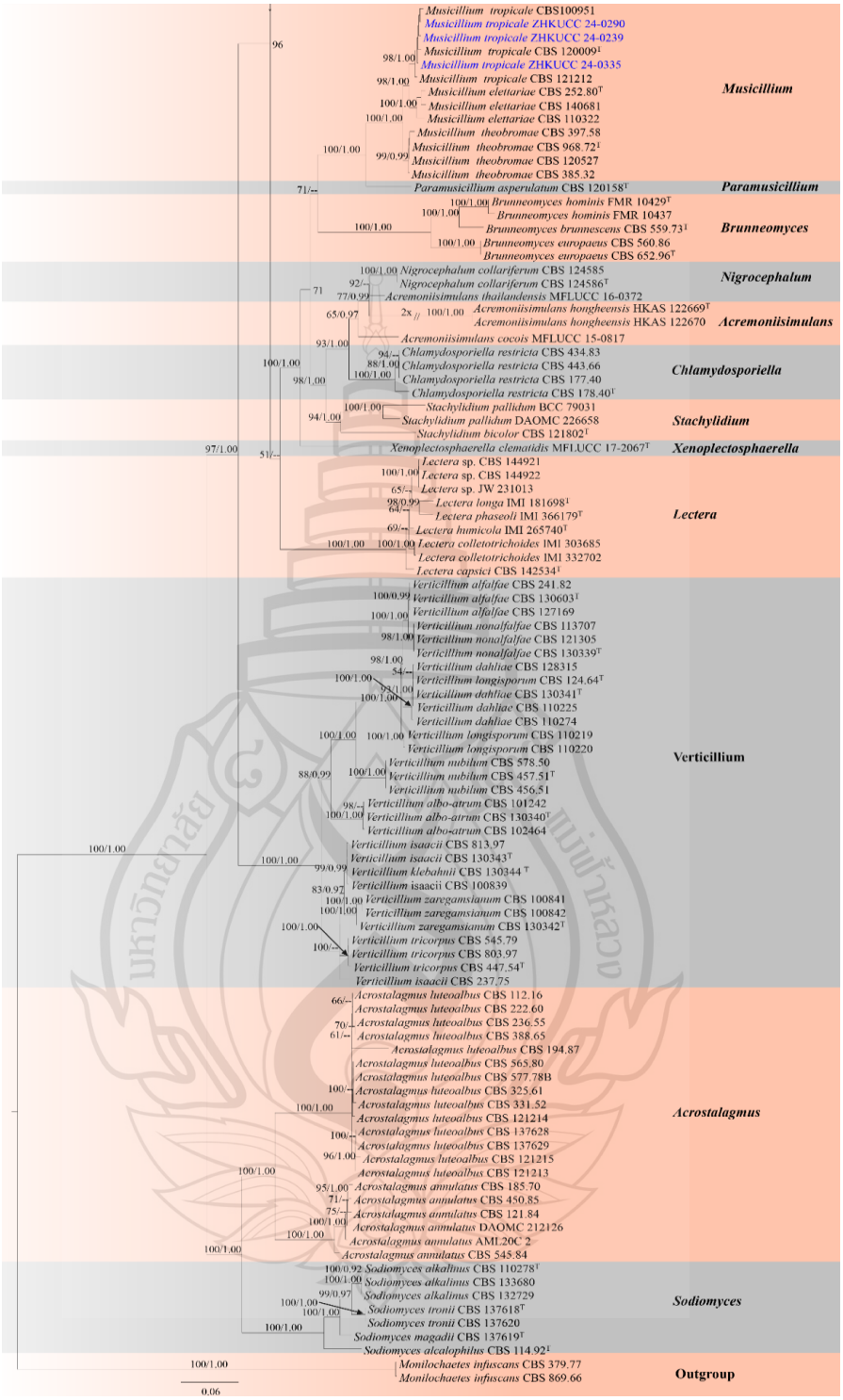


Figure 5.87 Maximum likelihood phylogeny based on the combined LSU, ITS, *tef1-α*, and *rpb2* sequences data of Plectosphaerellaceae

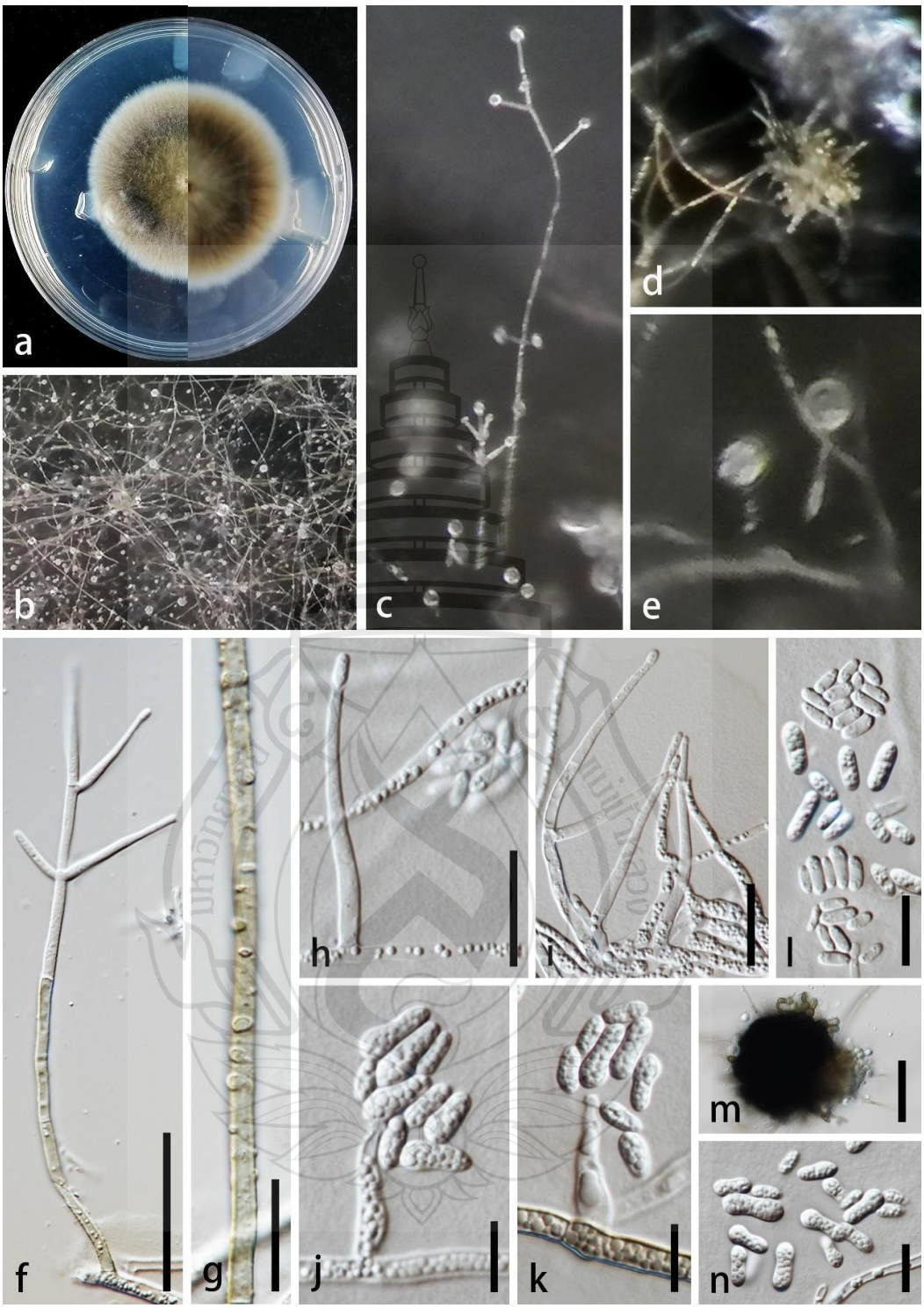


Note Tree rooted with *Monilochaetes infuscans* (CBS 379.77, CBS 869.66). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.87 (continued)

Note on decaying leaf of *Wurfbainia villosa*. a–c Colonies on the surface substrate. d–j Conidiophores, phialides, and conidia. k Conidiogenous cells and conidia. l Germination conidia. Scale bars: d = 200 μm, e, f = 100 μm, g–l = 20 μm.

Figure 5.88 *Musicillium tropicale* on the substrate (MHZU 24-0073, new host record)



Note on PDA for 2 weeks. a Culture characteristic on PDA after 2 weeks. b, c, e Conidiophores, phialides, and conidia on aerial mycelia on PDA. d Sclerotium on aerial mycelia. f, g Conidiophores. h–k Phialides with conidia. m Sclerotium. l, n Conidia. Scale bars: f, g, m = 50 μm, h, i = 20 μm, j–l, n = 10 μm.

Figure 5.89 *Musicillium tropicale* on the culture (MHZU 24-0073)

Musidium Giraldo López & Crous, Stud. Mycol. 92: 253 (2018)

Notes– *Musidium* was introduced by Giraldo López and Crous (2018) and typified by *M. stromaticum*. The *M. stromaticum* was a synonym for *Acremonium stromaticum* and isolated from *Musa* sp. in Honduras. *M. stromaticum* was also reported as pathogens caused brown rhizome rot and brown blotted root rot of ginger (*Zingiber officinale*) in Japan (Hayashi et al., 2024). Currently, a single species is accepted in the genus with a hyphomycete morph. In this study, we report a new species *M. wurfbainiae* from decaying stems, asymptomatic fruits, roots, and symptomatic leaf of *Wurfbainia villosa*.

Musidium wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.90

Index Fungorum number: IF904023; Facesoffungi number: FoF 17924

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0339

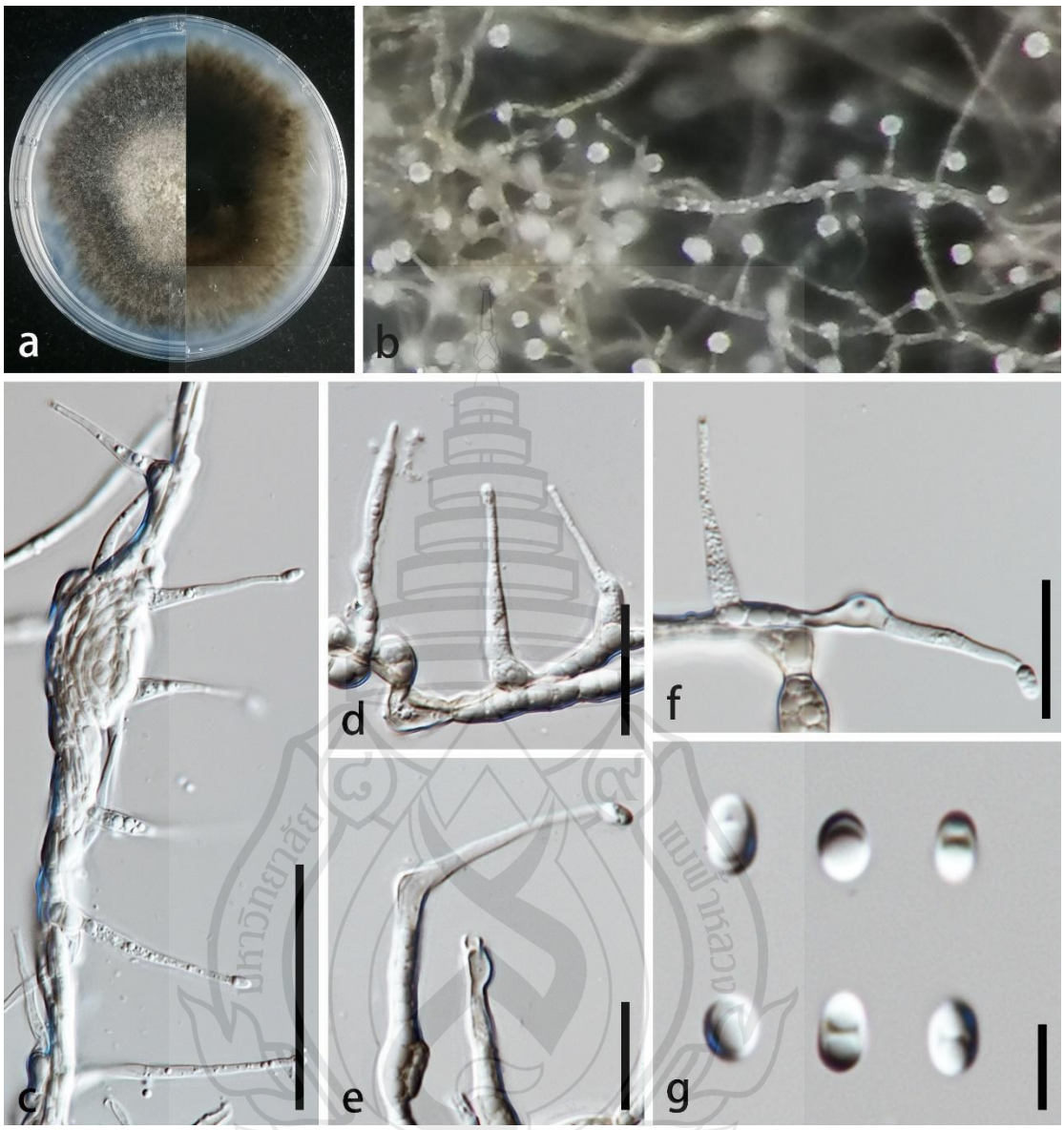
Saprobic on decaying stems, *endophytic* in asymptomatic fruits, roots, and associated with symptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* 1.5–3.5 µm wide ($\bar{x}$ = 2.5 µm, n = 30), branched, hyaline to pale brown, septate, distinctly constricted at septa, smooth-walled, some cells swollen, forming mycelial rings, occasionally, large aggregations of hyphae develop into thick mycelial bundles. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 17–36 × 3–5 µm ($\bar{x}$ = 23 × 4 µm, n = 30), terminal or lateral, cylindrical to subulate, tapering toward the apex, arising directly from hyphae, straight to slightly flexuous, hyaline, mostly aseptate, rarely 1-septate, unbranched, multi-guttulate, smooth-walled. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 30), unicellular, subglobose to ovoid, with rounded ends, hyaline, 1–2-guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 8.0–8.5 cm diameter in 4 weeks at 28 ± 2°C, moderately dense, raised, sparse, irregular, undulate, dull white at center, brown or dark brown at edge from the above and reverse, without pigmentation.

Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), from diseased leaf of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YP30B1 (MHZU 24-0339, holotype); ex-type culture, ZHKUCC 24-0657; *ibid*., living culture,

ZHKUCC 24-0655; *ibid.*, on decaying stem of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YAMZ90 living culture, ZHKUCC24-0300; China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR22B-2, ZHKUCC 24-0560; *ibid.*, from asymptomatic fruit of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMF35B, AMF55D, ZHKUCC 24-0384, ZHKUCC 24-0385; *ibid.*, Yangchun City, Heshui Town, (22.41410 N, 111.27459 E), on decaying stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YAM118, living culture, ZHKUCC 24-0341; *ibid.*, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), on decaying stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, YAM127, living culture, ZHKUCC 24-0358;

Notes – The phylogenetic analysis showed that our strains formed a distinct branch with *Musidium stromaticum* strains with 97% ML and 1.00 PP support (Figure 5.87). Morphologically, our isolate differs from *M. stromaticum* in having swollen mycelial cells, forming mycelial rings, and occasionally developing large aggregations of hyphae into thick mycelial bundles, as well as producing subglobose to ovoid conidia with 1–2-guttules. In contrast, *M. stromaticum* lacks swollen mycelial cells, does not form mycelial rings, and produces cylindrical or ellipsoidal conidia without guttules. Additionally, *M. wurfbainiae* has shorter conidiogenous cells (17–36 × 3–5 μm compared to those of *M. stromaticum* vs. (23–55 × 2–2.5 μm). Moreover, the culture characteristics of *M. wurfbainiae* are dull white at center and brown or dark brown at margin when viewed from above and reverse. In comparison, *M. stromaticum* appears dirty white on PDA with cream white reverse. Thus, we introduce *N. wurfbainiae* as a novel species.



Note a Culture characteristic on PDA. b Conidia on aerial mycelia on PDA. c–f Conidiogenous cells with conidia. g Conidia. Scale bars: c =50 µm, d–f = 20 µm, g = 10 µm.

Figure 5.90 *Musidium wurfbainiae* (MHZU 24-0339, holotype)

Hypocreales Lindau, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 343 (1897)

Notes – The most recent treatment and updated classifications of Hypocreales as outlined by Hyde et al. (2024).

Hypocreaceae De Not., G. bot. ital. 2(1): 48 (1844)

Notes – Hypocreaceae, a family in the order Hypocreales, was accepted by Lindau (1897). Previously, Hypocreaceae and Nectriaceae were considered a single family (Rossman et al., 1999; Lombard et al., 2015). Later, Rossman et al. (1999) revised Hypocreaceae and recognized it as a distinct family from Nectriaceae. Members of Hypocreaceae are widely distributed worldwide as biotrophic, hemibiotrophic, saprobic or hypersaprobic fungi on plants. Currently, 18 genera are accepted in this family (Hyde et al., 2024).

Trichoderma Pers., Neues Mag. Bot. 1: 92 (1794)

Notes – *Trichoderma*, a largest genus in the Hypocreaceae, was introduced by Persoon (1794), with *T. viride* designated as the type species. Although its sexual morph, *Hypocrea*, was described earlier, Rossman et al. (2013) proposed retaining the widely used name *Trichoderma*, following the Melbourne Code of Nomenclature (ICN) rules. *Trichoderma* species occur as saprobes and endophytes, commonly isolated from soil, plant roots and decaying woody materials (Perera et al., 2023). Many species, including *T. harzianum* and *T. viride*, are widely used for biocontrol, plant growth promotion, and enzyme production. Morphological characteristics of the genus have recently been reviewed by Perera et al. (2023). Additionally, Visagie et al. (2024) recognized 203 species within this genus. In this study, we describe two new species *Trichoderma guangdongensis* and *T. wurfbainiae*, with morphological characterization and phylogenetic analyses presented below.

Trichoderma guangdongensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.92

Index Fungorum number: IF904024; Facesoffungi number: FoF 17925

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China, where the holotype was collected

Holotype – MHZU 24-0235

Endophytic in asymptomatic roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On sterilized pine needles in PDA after 1 week: *Conidiophores* tree-like, short, simple or long with asymmetric branches, solitary or in whorls of 4–10 around a common axis, septate, smooth- and thin-walled. *Phialides* 4–10 × 3–5 μm ($\overline{x}$ = 6 × 3.5 μm, n = 30), 1.5–3 ($\overline{x}$ = 2 μm, n = 30) wide at base, flask-shaped, ampulliform to lageniform, subglobose to papillate, middle wider than the base,

hyaline, aseptate, smooth-walled. *Conidia* 2.5–4 × 2–3 μm ($\overline{x}$ = 3 × 2.8 μm, n = 30), globose to subglobose, hyaline to pale green, lacking a visible scar, smoothed-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, dense at the center, moderately sparse toward the edge, radially furrowed, velutinous, conidiation staring after 3 days, turning green after 5 days, cream-white to pink-gray from the above and reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic roots of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR06A-5 (MHZU 24-0235, holotype); ex-type culture, ZHKUCC 24-0533; *ibid*., living culture ZHKUCC 24-0534.

Notes – *Trichoderma guangdongensis* shares flask-shaped, ampulliform to lageniform phialides and globose conidia with *T. guizhouense*, *T. pholiotae*, *T. pseudoasiaticum*, and *T. wujiangense*. However, *T. guangdongensis* has subglobose to papillate phialides, solitary or in whorls of 4–10 around a common axis. In contrast, phialides of *T. guizhouense* are mostly in whorls of 2–3 (Li et al., 2013). In *Trichoderma pholiotae*, phialides are varied, borne in regular levels around the axis, some regular ampulliform or lageniform and others apex and inequilateral to curved, with one terminal whorl of generally 3–4 phialides (Zheng et al., 2021); *T. pseudoasiaticum* has ampulliform phialides, sometimes with narrow cylindrical or slightly bent neck, solitary or in whorls of 2–4 (Zheng et al., 2021; Cao et al., 2022), and *T. wujiangense* has phialides at the base is slightly narrow, the middle of the bottle is enlarged, the top is constricted, and in whorls of 2–4 phialides (Tan et al., 2025). Phylogenetic analysis revealed that *T. guangdongensis* (ZHKUCC 24-0533) is genetically distinct from other *Trichoderma* species, forming a sister lineage with *Trichoderma wujiangense* (ZHKUCC 24-0783, ZHKUCC 24-0784, ZHKUCC 24-0785, ZHKUCC 24-0786, and ZHKUCC 24-0787) (Figure 5.91). Hence, we identify *T. guangdongensis* as a novel species.

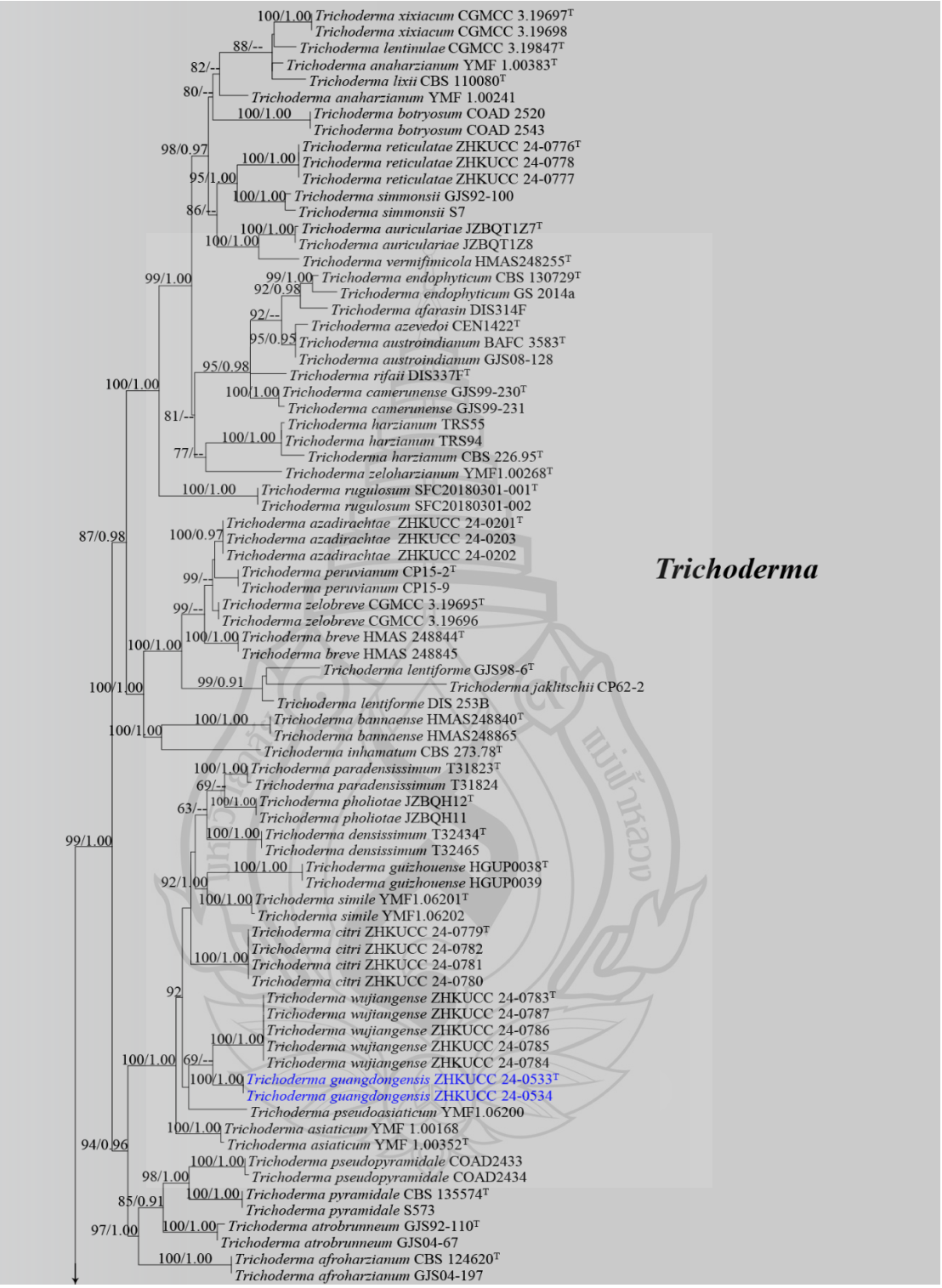
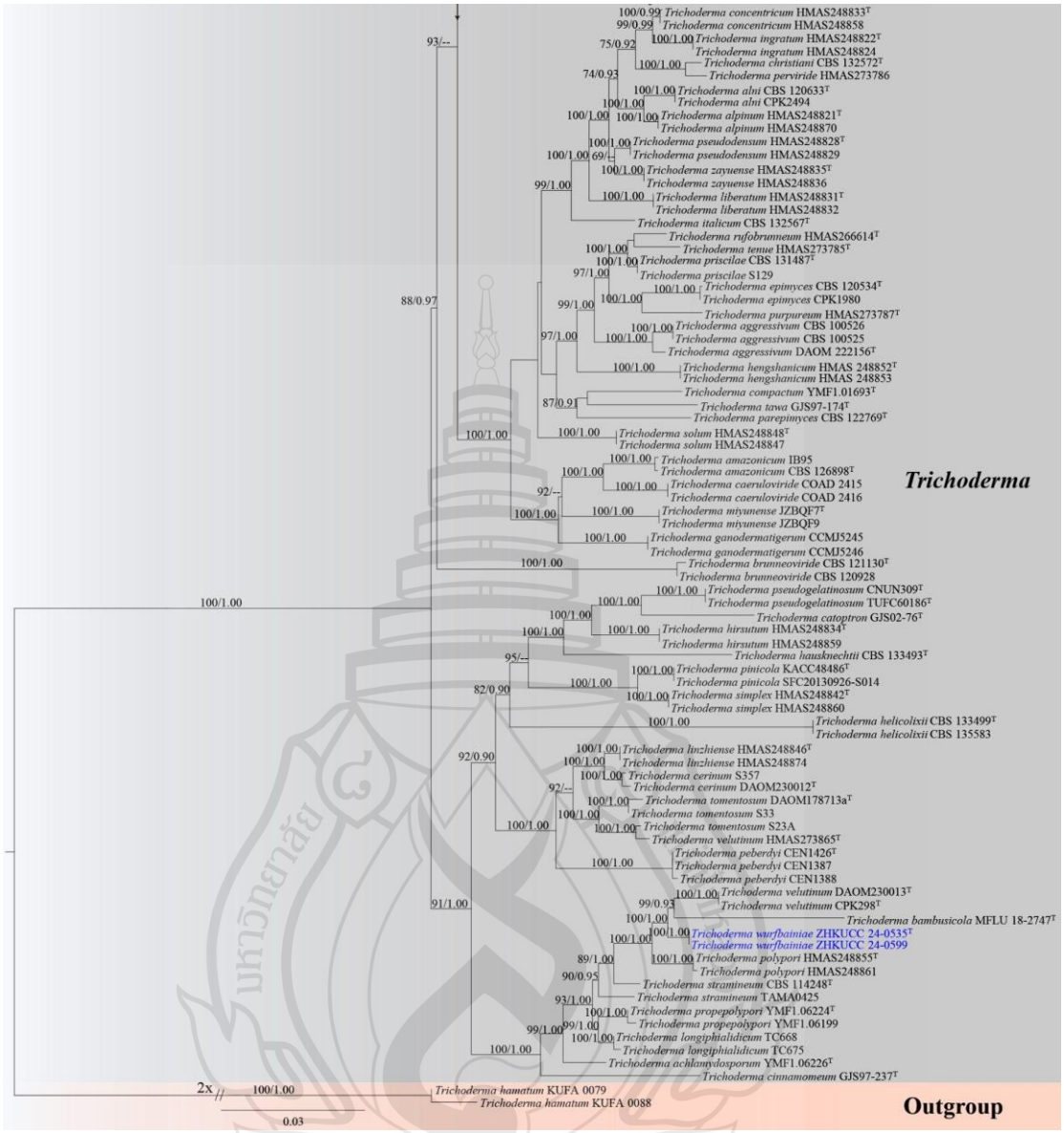
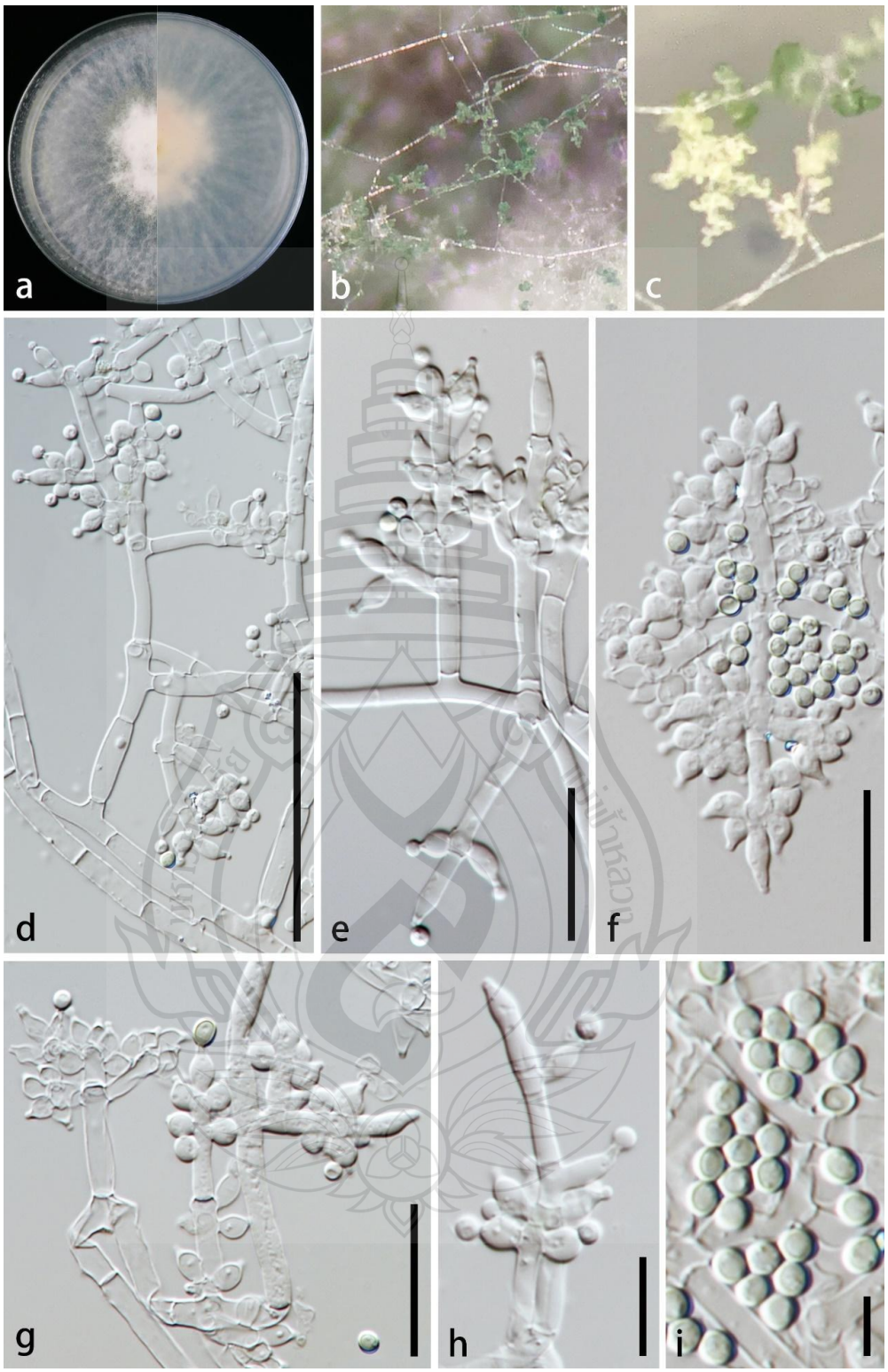


Figure 5.91 Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tef1-α* sequences data of *Trichocoma*



Note Tree rooted with *Trichocoma hamatum* (KUFA 0079, KUFA 0088). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.91 (continued)



Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on PDA. d–h Conidiophores, phialides, with conidia. i Conidia. Scale bars: d = 50 µm, e–g = 20 µm, h = 10 µm, i = 5 µm.

Figure 5.92 *Trichoderma guangdongensis* (MHZU 24-0235, holotype)

Trichoderma wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.93

Index Fungorum number: IF904025; Facesoffungi number: FoF 17926

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0236

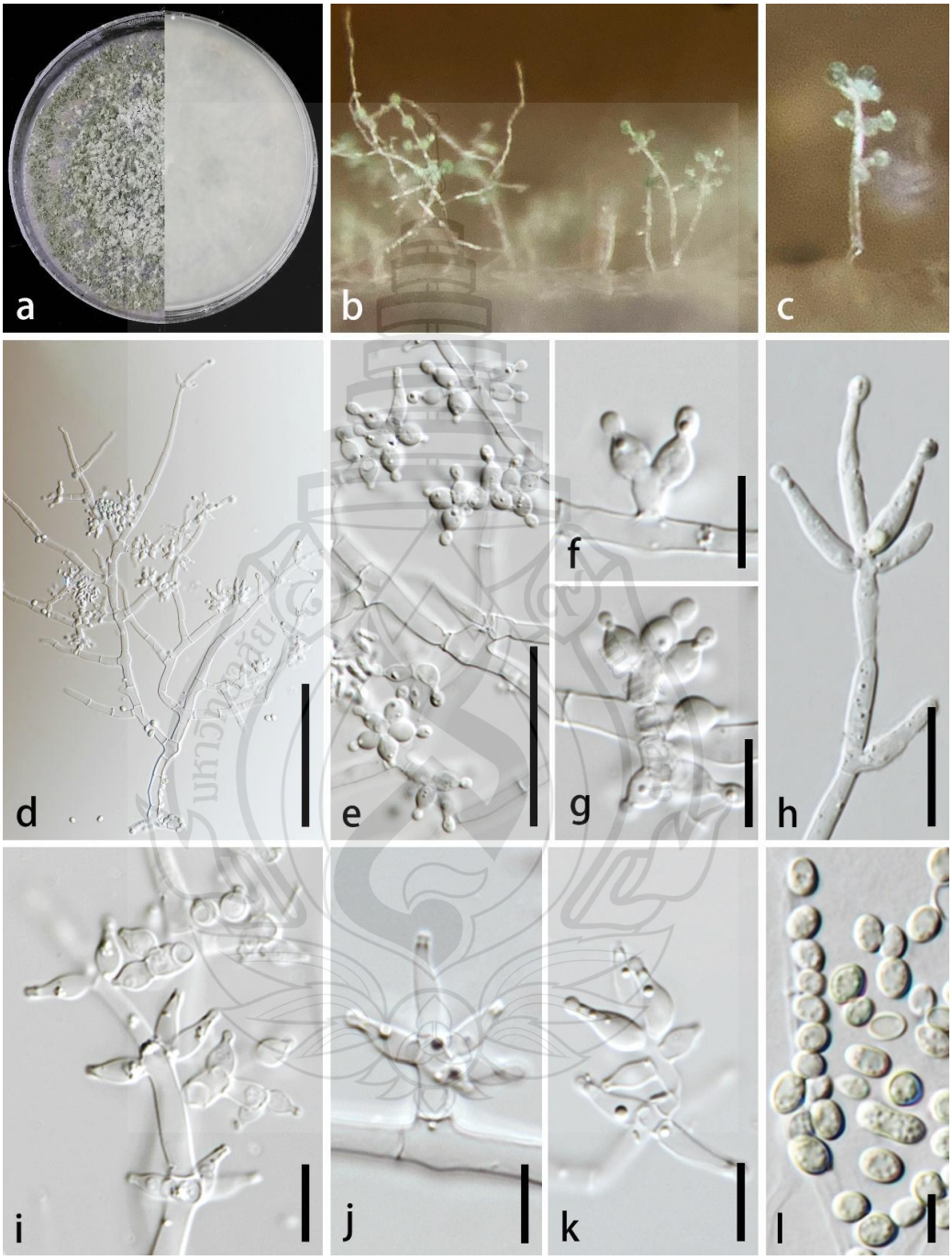
Endophytic in asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On sterilized soil media after 1 week: *Conidiophores* tree-like, short, simple or long with asymmetric branches, solitary or in whorls of 4–8 around a common axis, septate, smooth- and thick-walled. *Phialides* 7–23 × 3–7 μm ($\overline{x}$ = 11 × 5 μm, n = 30), 3 –5 ($\overline{x}$ = 4 μm, n = 30) wide at base, flask-shaped, ampulliform to lageniform, or cylindrical, subglobose to papillate, middle wider than the base, hyaline, aseptate, smooth-walled. *Conidia* 3–6 × 2.5–4 μm ($\overline{x}$ = 4 × 3 μm, n = 30), subglobose to ellipsoidal, or oblong, hyaline to pale green, with minute guttules, scar indistinct, smoothed-walled.

Culture characteristics–Colonies on PDA reaching 9.0 cm diameter in 4 weeks at 28 ± 2°C, moderately dense, radial, pulvinate, rough, pale green to dull green from the above, gray from the reverse

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, Amr23C-1 (MHZU 24-0236, holotype); ex-type culture, ZHKUCC 24-0535.

Notes – In the phylogenetic analyses, our strain ZHKUCC 24-0533 formed a sister lineage with *Trichoderma velutinum* (DAOM 230013) and *T. bambusicola* with 100 ML/1.00 PP support (Figure 5.91). However, the morphological data of *T. velutinum* are unavailable and *T. bambusicola* only reported the sexual morph, so we cannot compare. *Trichoderma wurfbainiae* is distinct from *T. polypori* by its flask-shaped, ampulliform to lageniform, subglobose to papillate, solitary or in whorls of 4–8 around a common axis phialides, subglobose, oblong to ellipsoidal, hyaline to slight pale green conidia, in contrast to the verticillium-like, in whorls of 3 phialides, ellipsoidal or globose, green conidia of the latter (Chen et al., 2017). In addition, *T. wurfbainiae* can be distinguished from *T. polypore* by its slightly longer phialides

(7–23 × 3–7 µm vs. (8.9–)11.7–16.6(−20.0) × 2.4–3.6 µm) and slightly larger conidia (3–6 × 2.5–4 µm vs. 2.8–3.6(−4.2) × 2.5–3.3 µm). Therefore, we identified *T. wurfbainiae* as a novel species.



Note a Culture characteristic on PDA for 4 weeks. b, c Conidia on aerial mycelia on soil media after 1 week. d–k Conidiophores, phialides, with conidia. l Conidia. Scale bars: d = 200 µm, e = 50 µm, f, g, i–k = 10 µm, h = 20 µm, l = 5 µm.

Figure 5.93 *Trichoderma wurfbainiae* (MHZU 24-0236, holotype)

Ophiocordycipitaceae G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Notes – Ophiocordyceps was established by Petch (1931) and typified by *Ophiocordyceps.* Species in Ophiocordyceps are known as entomopathogenic (insect-parasitizing), mycoparasitic, and endophytic fungi. They have significant medicinal and pharmacological importance, such as *Ophiocordyceps sinensis* (Al-Khayri et al., 2024). Twelve genera and over 500 species are recognized in this family (Peng et al., 2024).

Purpureocillium (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson, FEMS Microbiol. Lett. 321(2): 144 (2011)

Notes – *Purpureocillium* was delineated from the medicinal species of *Paecilomyces lilacilus* (Luangsa-Ard et al., 2011). *Purpureocillium* species have been isolated from wide habitats, such as soils, nematodes and plant roots, and are considered as effective biocontrol agents against root-knot nematodes (Hyde et al., 2020; Chen et al., 2024). *Purpureocillium* has no reported sexual morph so far. Currently, seven species are accepted in this genus (Chen et al., 2024). In this study, we report *Purpureocillium lilacinum* as a new host record from asymptomatic stem of *Wurfbainia villosa* in China.

Purpureocillium lilacinum (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson, in Luangsa-ard, Houbraken, Doorn, Hong, Borman, Hywel-Jones & Samson, FEMS Microbiol. Lett. 321(2): 144 (2011) Figure 5.95

Index Fungorum number: IF519530; Facesoffungi number: FoF 14520

Endophytic in asymptomatic stem of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 1 month: *Hyphae* 1.5–3.0 µm wide ($\overline{x}$ = 2 µm, n = 30), hyaline, aseptate, branched or unbranched, smooth-walled, forming mycelial rings. *Conidiophores* 102–345 × 3–6 µm ($\overline{x}$ = 205 × 4 µm, n = 20), mostly biverticillate, sometimes monoverticillate, smooth-walled. *Stipes* aseptate, straight, guttulate, smooth-walled. *Metulae* 7–10 × 2.6 –4 µm ($\overline{x}$ = 8.5 × 3.5 µm, n = 30), cylindrical, hyaline, guttulate, bearing whorls of 2–4 phialides each. *Phialides* 6–13 × 2–5 µm ($\overline{x}$ = 9.5 × 3 µm, n = 30), ampulliform to obclavate, straight to flattened, 4–6 per metula, hyaline, aseptate, guttulate, smooth-walled. *Conidia* 3–4 × 2–3.5 µm ($\overline{x}$ = 3.5 × 2.8 µm, n = 20), subglobose, hyaline, smooth-walled.

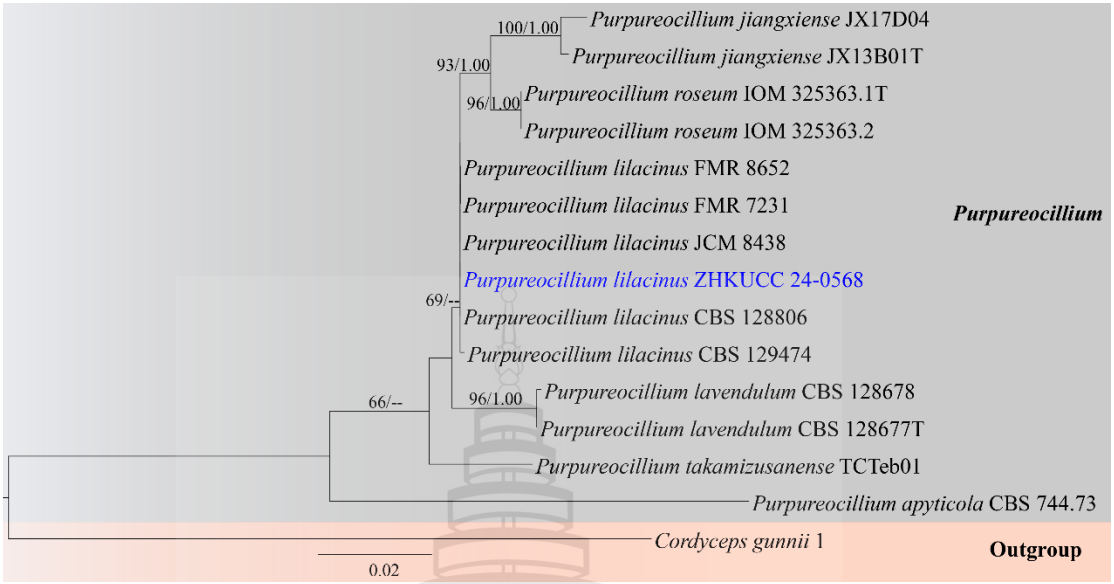
Culture characteristics – Colonies on PDA reaching 3.5–4.0 cm diameter in 1 week at 28 ± 2°C, moderately dense, raised, circular, with entire edge, filiform, pinkish to light pinkish from the above, cream-white from the reverse.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic stem of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS06C-3 (MHZU 24-0261); living culture, ZHKUCC 24-0568.

Known hosts (based on molecular data) – Soil, decaying vegetation, insects, nematodes and laboratory air (as contaminant), insect and animal pathogen (Luangsa-Ard et al., 2011), *Wurfbainia villosa* (this study).

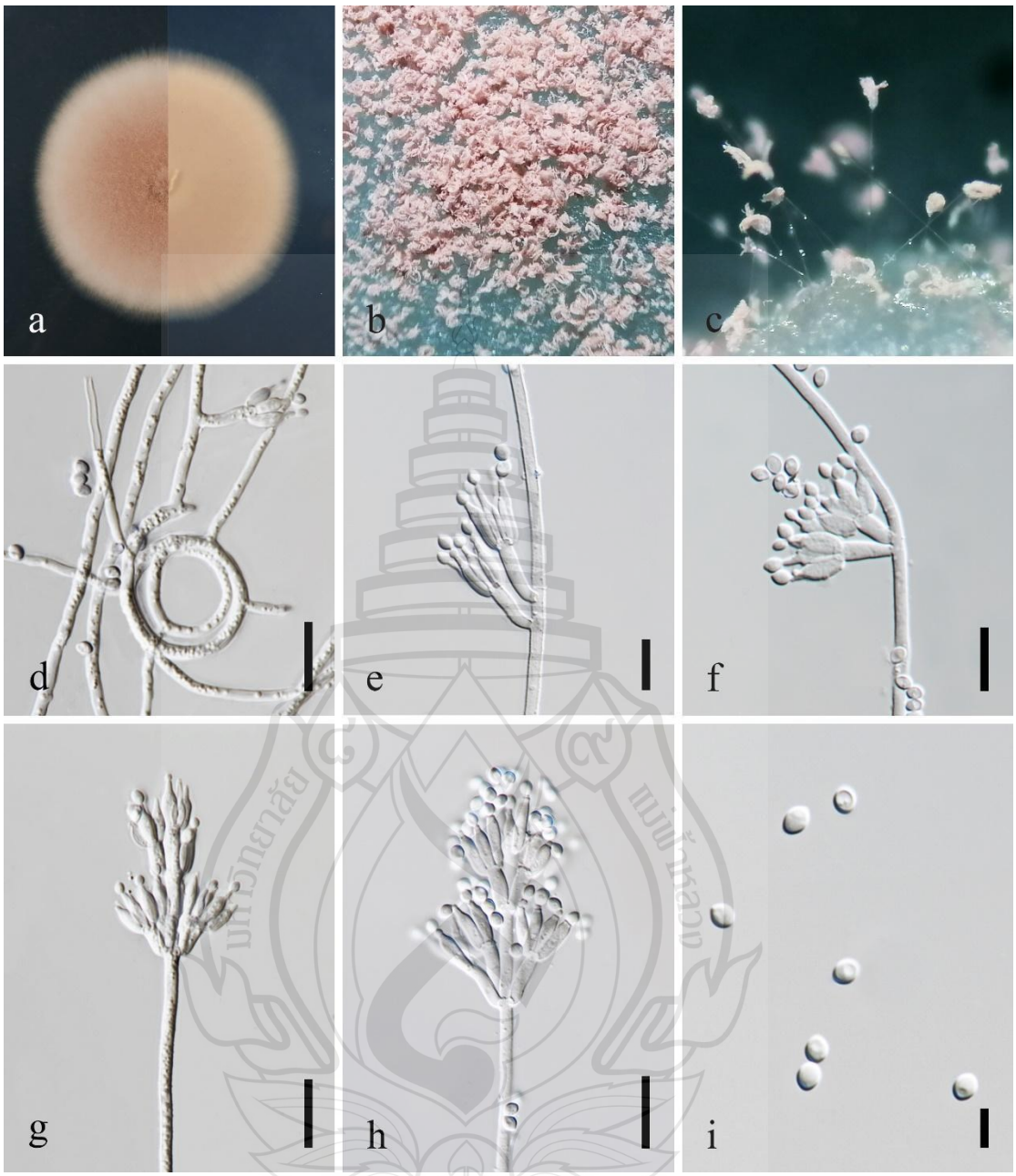
Known distribution (based on molecular data) – Australia, Canada, France, Germany, Ghana, India, Indiana, Ireland, Israel, Japan, Kent County, Italy, Ithaca, Netherlands, Peru, Philippines, UK, USA, Venezuela (Luangsa-Ard et al., 2011), China (this study).

Notes – In the phylogenetic analyses, the strain ZHKUCC 24-0568 clustered with *Purpureocillium lilacinum* (FMR 8652, JCM 8438, CBS 128806, FMR 7231, and CBS 129474) (Figure 5.94). Morphologically, our isolate shares similar characteristics with *P. lilacinum*, which has verticillate conidiophores, with each whorl consisting of 2–4 phialides, subglobose conidia. We introduce *Purpureocillium lilacinum* as a new host record in this study.



Note Tree rooted with *Cordyceps gunnii* (1). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strain from this study is shown in blue.

Figure 5.94 Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Purpureocillium*



Note a Culture characteristic on PDA for 1 week. b, c Conidia on aerial mycelia on PDA. d Mycelium ring. e–h Conidiophores with conidia. i Conidia. Scale bars: d–f = 10 μm, g, h = 20 μm, i = 5 μm.

Figure 5.95 *Purpureocillium lilacinum* (MHZU 24-0261, new host record)

Sarocladiaceae Lombard, Persoonia 41: 343 (2018)

Notes – Sarocladiaceae was introduced by Crous et al. (2018) and typified by *Sarocladium*. The family comprises two genera: *Parasarocladium* and *Sarocladium*.

Sarocladium W. Gams & D. Hawksw., Kavaka 3: 57 (1976) [1975].

Notes – *Sarocladium* was introduced by Gams and Hawksworth (1975) and typified by *S. oryzae.* (≡ *Acrocylindrium oryzae*). *Sarocladium* has cylindrical, phialidic conidiogenous cells arising singly from vegetative hyphae or conidiophores, with ellipsoidal to cylindrical conidia (Bao et al., 2023). Currently, 37 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we report *Sarocladium wurfbainiae* as a new species, isolated from both saprobic and endophytic lifestyles.

Sarocladium wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.97, 5.98

Index Fungorum number: IF904026; Facesoffungi number: FoF 17927

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0077

Saprobic on dead stem and endophytic in fruit, stem and root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Colonies* on the substratum superficial, erect to curved, effuse, scattered or gregarious, hyaline to brown. *Conidiophores* 466–650 × 9.5–13 μm ($\bar{x}$ = 557 × 11 μm, n = 20), macronematous, mononematous, straight or slightly curved, cylindrical, septate, black at the base, hyaline at apex to dark brown towards the base, smooth-walled, robust at the base, 4–5 μm wide, slender at apex 1–3 μm wide, bearing short branches in the upper part with verticils of 3 phialides. *Phialides* 15–24 × 2.5–4.5 μm ($\bar{x}$ = 17.5 × 3.5 μm, n = 30), flask-shaped, enteroblastic, monophialidic, terminal or lateral, tapering at the apex, hyaline, aseptate, verrucose. *Conidia* 5–7 × 2–3 μm ($\bar{x}$ = 6 × 2.5 μm, n = 30), unicellular, ellipsoidal to ovoid, aseptate, hyaline, smooth, thick-walled, with 1–3-guttulate, truncated at the base, rounded at the apex.

Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, raised, circular, with entire edge, cream-white from above; pale brown in center toward to cream-white from the reverse, no

pigmentation. Sporulation occurring on PDA after one month. *Mycelium* 1–2 µm wide ($\bar{x}$ = 1.5 µm, n = 30), diffuse, radially arranged, hyaline, branched or unbranched, normally aseptate, rarely septate, smooth-walled, guttulate. *Conidiophores* 45–112 × 1.5–4 µm ($\bar{x}$ = 73.5 × 2.5 µm, n = 30), micronematous, mononematous, straight or slightly curved, cylindrical, non-septate or have one septate at base, hyaline, smooth-walled, sometimes reduced to conidiogenous cells. *Phialides* 38–82 × 1.5–2.5 µm ($\bar{x}$ = 40.5 × 2 µm, n = 30), arising directly from hyphae, terminal or lateral, cylindrical, tapering toward the apex, lateral or intermediate whorls, straight or flexuous, hyaline, aseptate, branched or unbranched, smooth-walled. *Conidia* 3.5–6 × 1–2.5 µm ($\bar{x}$ = 5 × 1.9 µm, n = 30), unicellular, cylindrical to ellipsoidal, with both rounded ends, hyaline, two guttulate, smooth-walled.

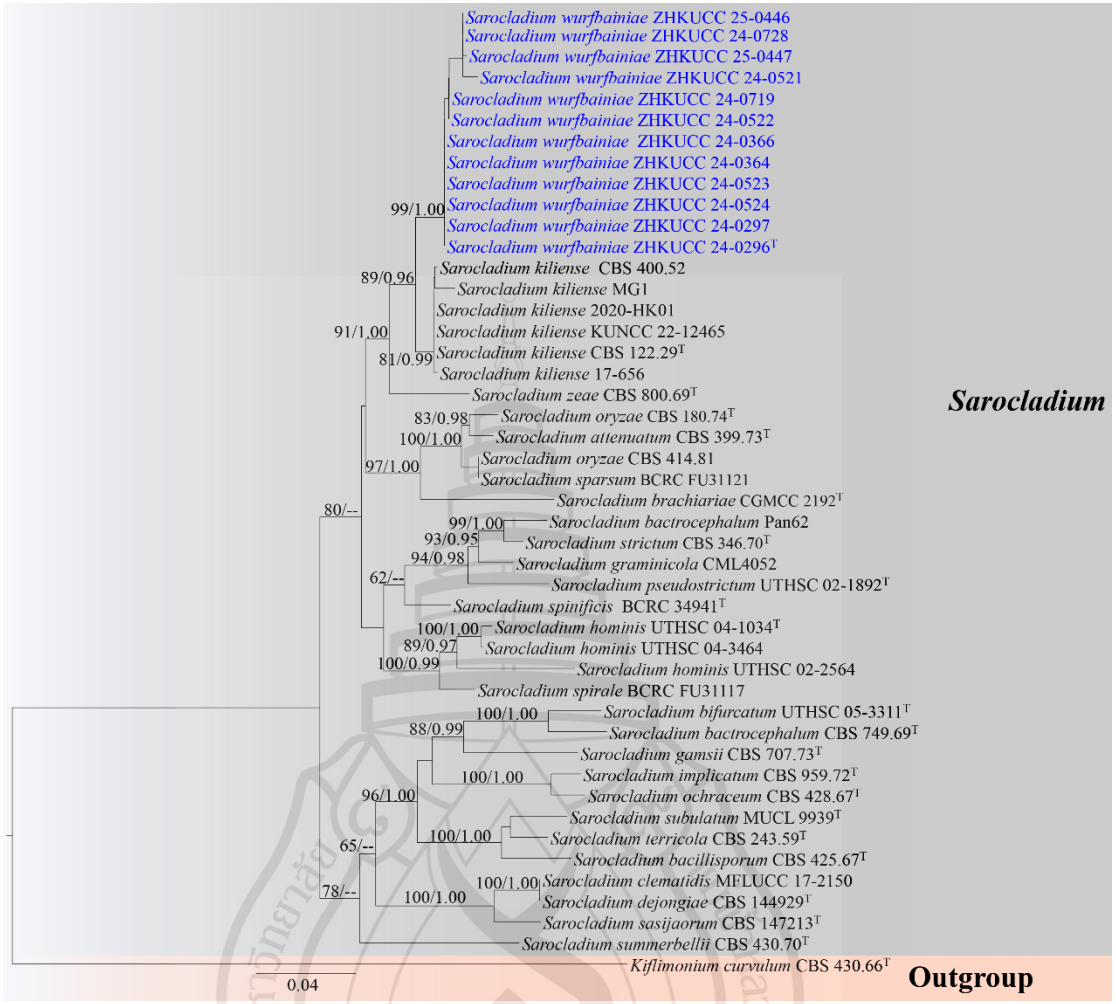
Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Tropical Botanical Garden of Chinese Academy of Sciences (21.91797 N, 101.27400 E), on dead stem of *Wurfbainia villosa*, 15 January 2024, C.F. Liao, YAM88 (MHZU 24-0077, holotype); ex-type culture, ZHKUCC 24-0296; China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic stem and root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS06B-1, AMS06B-2, AMS06C-5, AMS06C-7, AMR04B-1, AMR04B-7; living culture, ZHKUCC 24-0524, ZHKUCC 24-0523, ZHKUCC 25-0446, ZHKUCC 24-0728, ZHKUCC 24-0521, ZHKUCC 24-0522; *ibid.*, Chunwan Town (22.436461 N, 111.938281 E), asymptomatic fruit of *Wurfbainia villosa*, 29 October 2022, C.F. Liao, AMD13C, AMD14A, AMD30A, AMF25D; living culture, ZHKUCC 25-0447, ZHKUCC 24-0364, ZHKUCC 24-0366, ZHKUCC 24-0297.

Known hosts (based on molecular data) – Human non-valvular endocarditis (Kitamura et al., 2022), *Hypsizygus marmoreus* (Xu et al., 2022), leaf of *Malus domstica* (Ebrahimi & Fotouhifar, 2016), maize (Harish et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – India (Harish et al., 2024), Iran (Ebrahimi & Fotouhifar, 2016), Japan (Kitamura et al., 2022), China (Xu et al., 2022; this study).

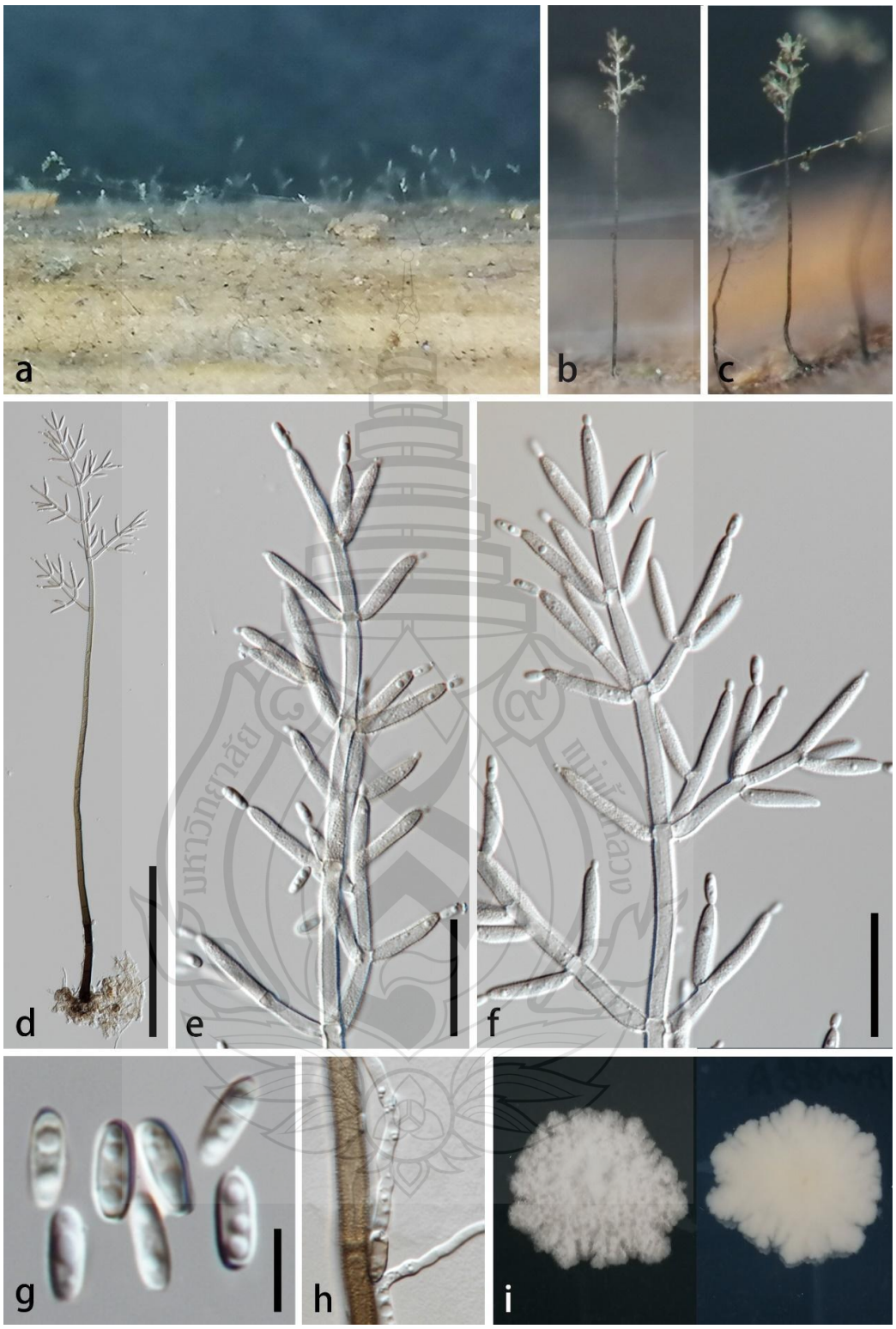
Notes – In the phylogenetic analyses, our strains formed a sister branch to *Sarocladium kiliense* with 85 ML/0.92 PP support (Figure 5.96). Sequence comparisons of these strains with *Sarocladium kiliense* (CBS 122.29) revealed 1.80%

(9/499 bp) differences in ITS and 0.58% (5/863 bp) in LSU. However, sequence data for act gene of our strains were unavailable. MHZU 24-0077 resemble *Sarocladium kiliense* by having hyaline, septate, branched mycelium, erect, branched, aseptate or have one septate at base conidiophores, and hyaline, ellipsoidal, smooth-walled conidia (Sukapure & Thirumalachar, 1965). *Sarocladium kiliense* was originally described as *Cephalosporium incoloratum* by Sukapure and Thirumalachar (1965), which was isolated from soil sample and grow in PDA. However, our isolate can be easily distinguished with *S. kiliense* by having larger conidiophores (45–112 × 1.5–4 μm vs. 25–50 × 1.5–3 μm). Bao et al. (2023) also reported the asexual morph of *S. kiliense* from decaying woods in China. Their isolate was sporodochial, superficial, solitary to gregarious, and hairy; the conidiomata appeared velvety and brown with white conidia, bearing setae and conidiophores that arose from a basal stroma. In contrast, our isolate lacks conidiomata and setae, and the conidiophores emerge directly from the natural substrate. Hence, we introduced *Sarocladium wurfbainiae* as a new species.



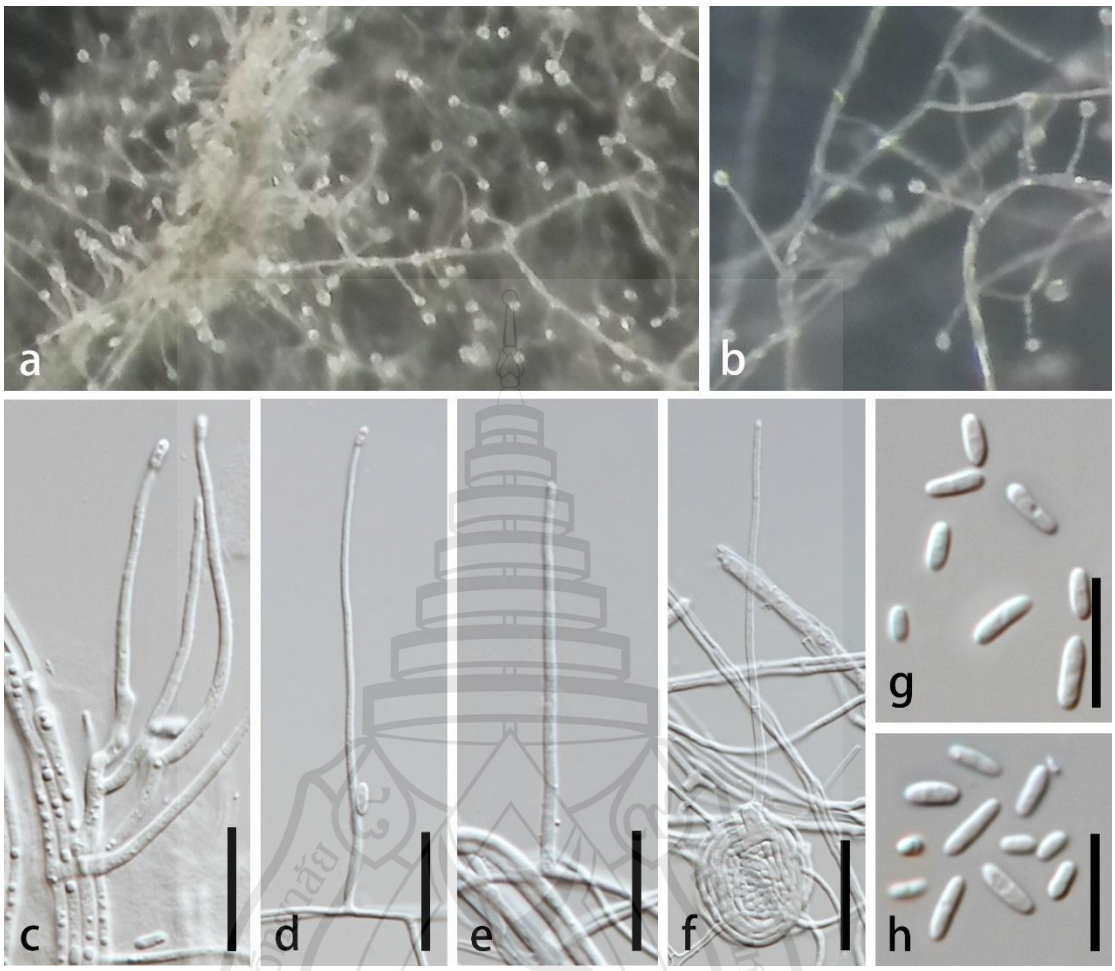
Note Tree rooted with *Kiflimonium curvulum* (CBS 430.66). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.96 Maximum likelihood phylogeny based on the combined ITS, LSU, and act sequences data of *Sarocladium*



Note a–c Colonies on the surface substrate. d–f Conidiophores, conidiogenous cells, and conidia. g Conidia. h Germinated conidia. i Colonies on PDA (front and below). Scale bars: d = 300 μm, e, f = 20 μm, g = 5 μm.

Figure 5.97 *Sarocladium wurfbainiae* on the substrate (MHZU 24-0077, holotype)



Note a, b Conidia on aerial mycelia on PDA. c–f Conidiogenous cells. g, h Conidia. Scale bars: c–h = 10 μm.

Figure 5.98 *Sarocladium wurfbainiae* on the culture (MHZU 24-0077, new host record)

Stachybotryaceae L. Lombard & Crous [as 'Stachybotriaceae'], in Crous et al., Persoonia 32: 283 (2014)

Notes – Stachybotryaceae was established to accommodate the genera *Myrothecium*, *Peethambara*, and *Stachybotrys*, with *Stachybotrys* as the type (Crous et al., 2014). The members of this family are commonly isolated from soil and dead plant materials (Lombard et al., 2016; Hyde et al., 2017). Some species have been reported as pathogenic to plants and animals, with some posing a substantial risk to human health (Ben et al., 2015). Currently, 46 genera are reported: *Achroiostachys*, *Albifimbria*, *Albosynnema*, *Alfaria*, *Alfariacladiella*, *Brevistachys*, *Capitofimbria*, *Cymostachys*, *Didymostilbe*, *Digitiseta*, *Dimorphiseta*, *Globobotrys*, *Grandibotrys*, *Gregatothecium*,

Hyalinostachys, *Inaequalispora*, *Kastanostachys*, *Koorchalomella*, *Melanopsamma*, *Memnoniella*, *Myrothecium*, *Myxospora*, *Neomyrothecium*, *Nigrosynnema*, *Paracymostachys*, *Paramyrothecium*, *Parasarcopodium*, *Parvothecium*, *Peethambara*, *Pottera*, *Pseudoornatispora*, *Septomyrothecium*, *Sirastachys*, *Smaragdiniseta*, *Stachybotrys*, *Striatibotrys*, *Striaticonidium*, *Tangerinosporium*, *Virgatospora*, *Xenomyrothecium*, *Xepicula*, and *Xepiculopsis* (Hyde et al., 2024; Liao et al., 2025b).

Brevistachys L. Lombard & Crous, in Lombard et al., Persoonia 36: 182 (2016)

Notes – *Nigrosynnema* was established by Lombard et al. (2016) and typified by *B. variabilis*. Currently, six species were accepted in the genus (Lombard et al., 2016).

Brevistachys wurfbainiae C.F. Liao, K.D. Hyde & Doilom, sp. nov. Figure 5.100

Index Fungorum number: IF902005; Facesoffungi number: FoF 15745

Etymology – In reference to the host genus "*wurfbainiae*" from which the holotype was isolated.

Holotype – MHZU 23-0254

Saprobic on dead stem of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: *Colonies* superficial on host substrate, effuse, hairy, gregarious, with numerous dark conidia on the substrate visible as black granular powder. *Conidiophores* 80–235 × 3–5.5 μm (av. 155 × 4.5 μm, n = 20), macronematous, mononematous, erect, simple, unbranched, straight or flexuous, subcylindrical, unevenly olivaceous brown, 1–3-septate, not constricted at septa, smooth-walled to finely verruculose in the above half, thick-walled, with bulbous apices, bearing 5–8 conidiogenous cells at the tip, often intermixed with setiferous, flexuous, sterile filaments. Setae 230–390 × 3–6 μm (av. 305 × 4.5 μm, n = 20), arising from the basal stroma, adjacent to cells that give rise to fertile conidiophores, unbranched, straight and subhyaline at base, mostly flexuous, olivaceous green, in above half, moderately thick-walled, smooth, septate, acute at apex. *Conidiogenous cells* 6–10 × 4–7 μm (av. 7.5 × 5.5 μm, n = 30), enteroblastic, monophialidic, discrete, determinate, terminal, elongate doliiform, pale to dark brown, smooth-walled, with a conspicuous collarette. *Conidia* 5–9 μm diam. (av. 7 μm, n = 30), acrogenous, solitary, dry, obovoid to subglobose,

aseptate, hyaline and smooth-walled when young, pale brown, mostly olivaceous to dark brown, verrucose to warty-surfaced at maturity.

Culture characteristics – Colonies on PDA reaching 2.0 cm in two weeks at 28 ± 2°C, medium dense, raised, sparse, filamentous, floccose to fluffy, velvety, filiform at margin, cream to pale brown from above; brown to pale luteous from reverse.

Material examined – China, Guangdong Province, Yangchun City, Yongning Town (22.256185 N; 111.609037 E, 270 m), on dead stems of *Wurfbainia villosa* Škorničk. & A.D. Poulsen. (Zingiberaceae), 10 April 2022, C.F. Liao & Y.H. Yang, YAM16 (MHZU 23-0254, holotype); ex-type living culture, ZHKUCC 23-1011; ibid., living culture ZHKUCC 23-1012, and ZHKUCC 23-1013.

Notes – *Brevistachys wurfbainiae* differs from other known species in the genus *Brevistachys* in having the erect to flexuous, sterile, setiferous filaments intermixed with fertile conidiophores. *Brevistachys wurfbainiae* resembles *B. subsimplex* but differs from the latter in having comparatively longer conidiophores with bulbous apices (80–235 × 3–5.5 µm vs. 80–200 (most frequently 100–140) × 3–5.5 µm), and shorter conidiogenous cells (6–10 × 4–7 µm vs. 8–13 × 4–6 µm). The conidiophores of *B. wurfbainiae* are 1–3-septate, while they are 2–6-septate in *B. subsimplex* (Deighton, 1960). The phylogenetic analyses revealed that *B. wurfbainiae* (ZHKUCC 23-1011, ZHKUCC 23-1012, and ZHKUCC 23-1013) formed a separate branch from *B. subsimplex* (ex-type CBS 100155) with 75 % ML bootstrap support and 0.93 BYPP (Figure 5.99). Based on distinct morphology and phylogenetic support, we propose *B. wurfbainiae* as a new species.

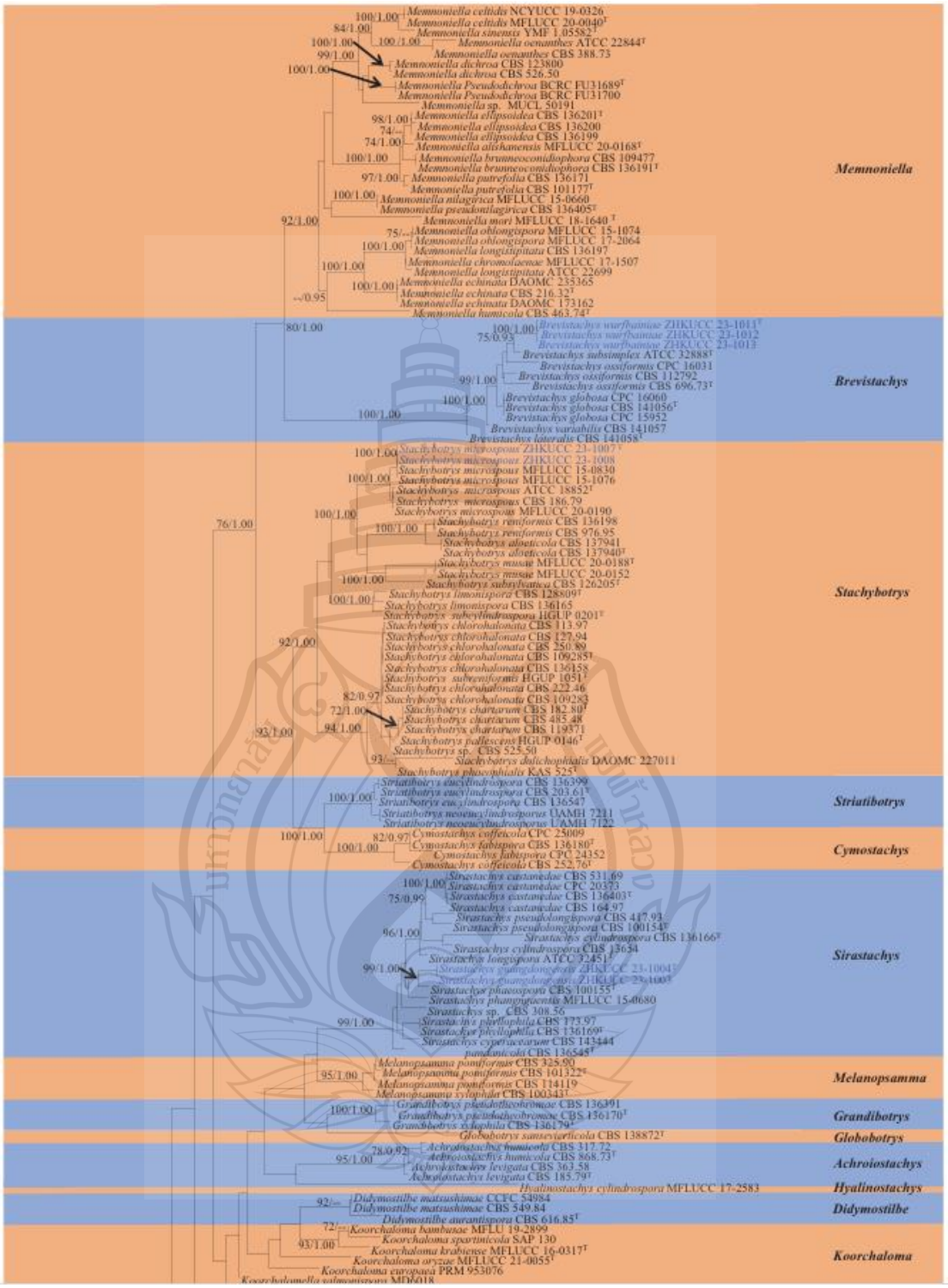
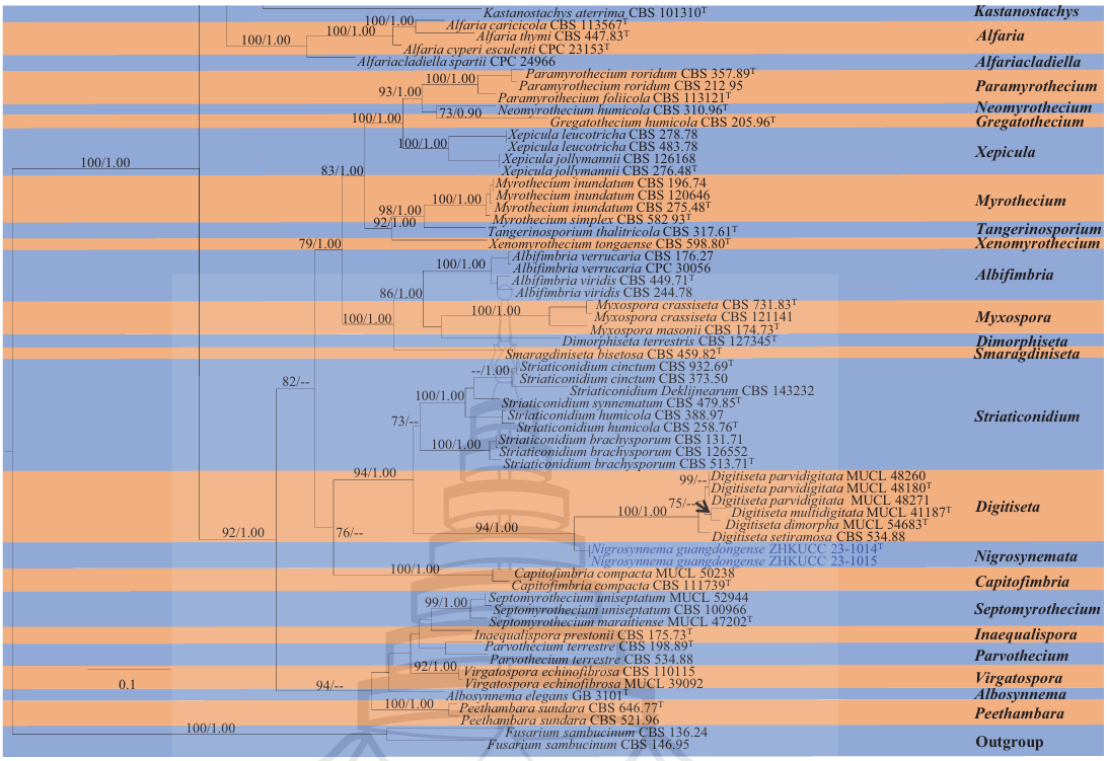


Figure 5.99 Maximum likelihood phylogeny based on the combined *cmdA*, ITS, LSU, *rpb2*, *tef1-α*, and *tub2* sequences data of Stachybotryaceae



Note Maximum likelihood bootstrap values ≥ 70% (ML) and Bayesian posterior probabilities ≥ 0.90 (ML/BYPP) are provided at the nodes. The tree is rooted with *Fusarium sambucinum* strains CBS 136.24 and CBS 146.95. The hyphen (-) represents support values < 70% ML and < 0.90 BYPP. The ex-type strains are denoted as "T", while the newly isolated strains are highlighted in blue.

Figure 5.99 (continued)

Note a, b Colonies on the surface substrate. c, d Conidiophores, setae or conidiophore-like (arrow), conidiogenous cells and conidia. e, f Conidiogenous cells with conidia. g Conidia. h Germinated conidium. i, j Colonies on PDA (front and below). Scale bars: b–d = 100 µm e, f = 10 µm, g = 5 µm, h = 20 µm.

Figure 5.100 *Brevistachys wurfbainiae* (MHZU 23-0254, holotype)

Nigrosynnema C.F. Liao, K.D. Hyde & Doilom, in Liao, Doilom, Bhat, Chethana, Tangtrakulwanich, Yang, Al-Otibi, Hyde & Dong, MycoKeys 114: 310 (2025)

Notes – *Nigrosynnema* was established by Liao et al. (2025b) and typified by *Ni. guangdongense*. Currently, *Nigrosynnema* has a single species and isolated from the dead stems of *Wurfbainia villosa* (Liao et al., 2025b).

Nigrosynnema guangdongense C.F. Liao, K.D. Hyde & Doilom, sp. nov. Figure 5.101, 5.102

Index Fungorum: IF902007; Facesoffungi Number: FoF 15746

Etymology – The epithet "*guangdongense*" refers to the locality, Guangdong Province, China, where the holotype was collected.

Holotype – MHZU 23-0255.

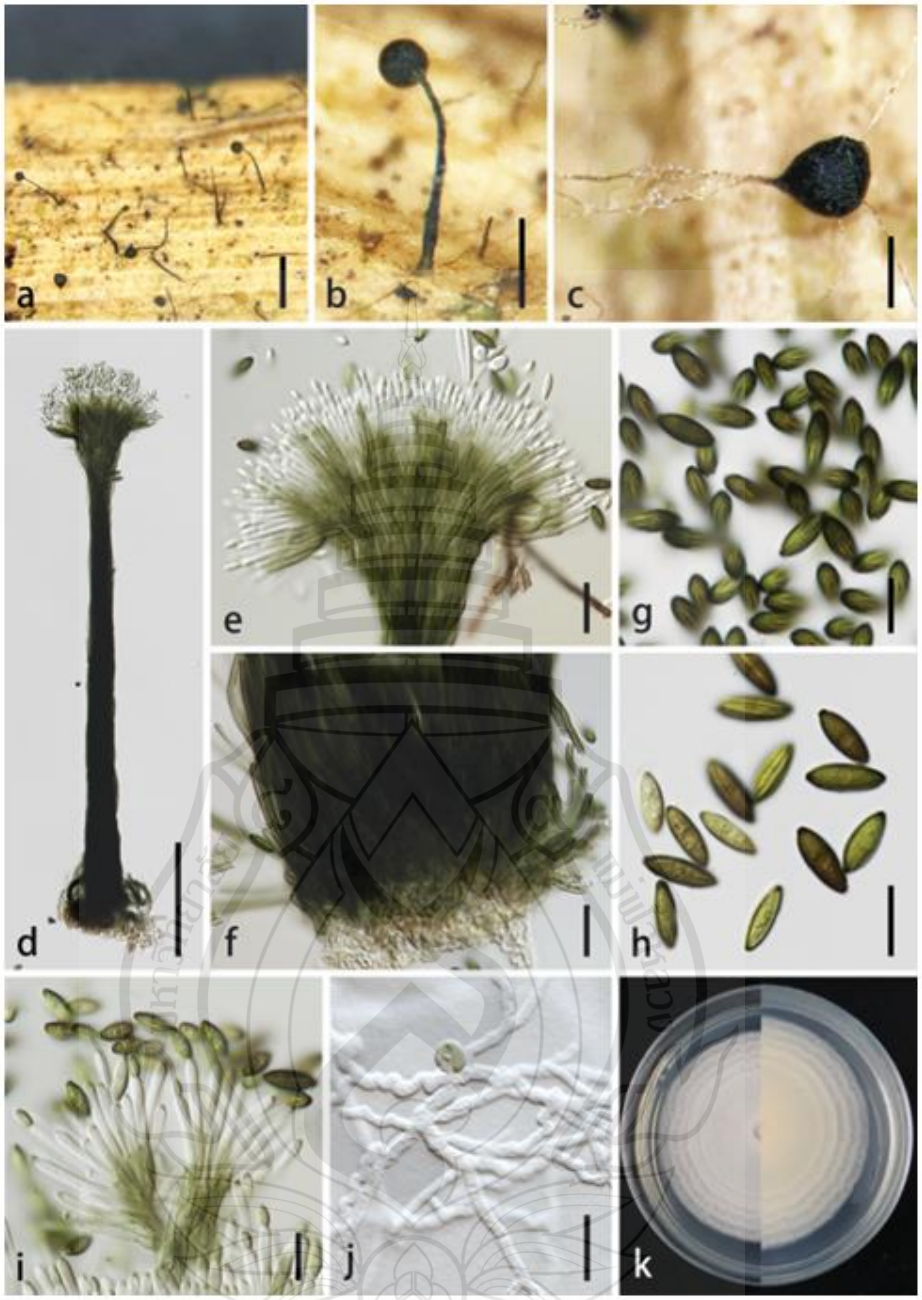
Saprobic on dead stem of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: *Synnemata* on the natural substrate, 370 570 × 20–50 µm (av. 470 × 33 µm, n = 20), erect, unbranched, subcylindrical, with a robust base, narrowed towards fertile apex, olivaceous brown to black, straight or curved in the upper portion, consisting of parallelly arranged, tightly compacted conidiophores. *Conidiophores* 2–4 µm wide, subcylindrical, branched, olivaceous brown, slightly tapering towards the apex, verrucose. *Conidiogenous cells* 10.5–32.5 × 1.5–3 µm (av. 22 × 2.5 µm, n = 30), enteroblastic, monophialidic, discrete, terminal, subcylindrical, mostly hyaline, sometimes pale olivaceous brown in the lower portion, mostly smooth-walled in above half, often verruculose at below half, with a conspicuous collarette. *Conidia* 10–12.5 × 3–4.5 µm (av. 11.5 × 4 µm, n = 30), solitary, slimy, fusiform to ellipsoidal, aseptate, longitudinally striated, olivaceous brown to dark brown, guttulate, obtuse at both ends, with a distinct dark basal hilum.

Culture characteristics – Colonies on PDA reaching 4.5–6.5 cm in two weeks at 28 ± 2°C, medium dense, flat or effuse, diffuse, rough, circular, filiform with curled, large circle in the middle becoming a wave and extends outward, cream from above; cream from the reverse. The spores produced on PDA after three weeks. *Conidiomata* 220–300 × 15–20 µm, sporodochial, superficial, scattered, irregular, with white mycelia surrounding an olivaceous green mass of conidia, with or without covering the slimy mass of conidia, without setae. *Conidiophores* arising from the basal stroma, consisting of a stipe and a penicillately branched conidiogenous apparatus; stipes unbranched or

rarely branched, hyaline, septate, smooth, 10–30 × 2.5–3.5 µm (av. 18 × 3.0 µm, n = 20), conidiogenous apparatus consisting of a whorl of 2–5 primary branches, each terminating in 2–5 conidiogenous cells; primary branches, 1, 2-septate, smooth, un branched, 8–20 × 2–6 µm, secondary branches, aseptate, smooth, unbranched, 6–20 × 2–5 µm. *Conidiogenous cells* 10–20 × 2–4 µm (av. 14 × 2.5 µm, n = 30), phialidic, terminal, with a conspicuous collarette, clavate to cylindrical, hyaline, smooth. *Conidia* 7–10 × 3–5 µm (av. 8.5 × 3.5 µm, n = 30), acrogenous, longitudinally striated, fusiform to ellipsoidal, aseptate, initially hyaline, becoming olivaceous green when mature.

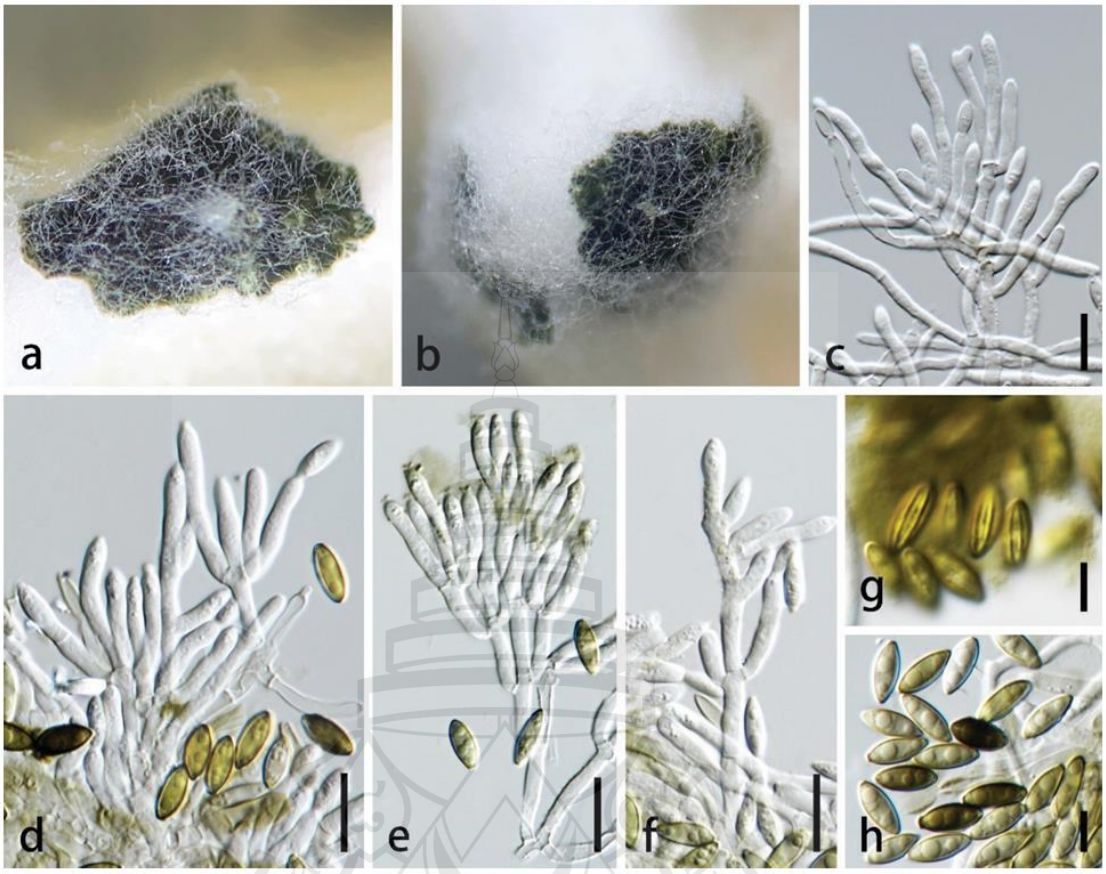
Material examined – China, Guangdong Province, Yangchun City, Yongning Town (22.256185°N, 111.609037°E, 270 m), on dead stems of *Wurfbainia villosa* (Lour.) Škorničk. & A.D. Poulsen. (Zingiberaceae), 10 April 2022, C.F. Liao & Y.H. Yang, YAM19 (MHZU 23-0255, holotype), ex-type, ZHKUCC 23-1014, *ibid*., living culture ZHKUCC 23-1015.

Notes – *Nigrosynnema guangdongense* is established here as the type species. It is similar to *Virgatospora natarajanensis* described by D'Souza et al. (2002) in having synnematous conidiomata, with fusiform, aseptate, and striated conidia. However, *N. guangdongense* has verrucose, olivaceous, brown conidiophores, conidia with obtuse apices, and a distinct dark basal hilum, whereas *V. natarajanensis* has distinctly echinulate, subhyaline conidiophores that are narrower and smooth towards the apex, and conidia are rounded at both ends. Additionally, the conidiogenous cells of *V. natarajanensis* are occasionally found in the subterminal position, while they have not been observed in *N. guangdongense*. *Nigrosynnema guangdongense* has longer conidiogenous cells (10.5 32.5 × 1.5–3 µm) compared to *V. natarajanensis* (18–25 × 1.5–3.5 µm). *Nigrosynnema guangdongense* and *Virgatospora echinofibrosa* (the type species of *Virgatospora*) (Finley, 1967) are similar in having synnematous con idiomata and striate, phialidic conidia. However, *N. guangdongense* has short er synnemata (370–570 × 20–50 µm) than *V. echinofibrosa* (up to 1500 µm). Synnemata of *N. guangdongense* are robust at the base, narrower towards the apex of the stipe, and olivaceous brown to black, whereas they are simple or branched, sometimes proliferated, cylindrical throughout the greater part, somewhat broader at the apex and base, white or yellow at the base, yellow-black or blackish black at the apex in *V. echinofibrosa*.



Note *Nigrosynnema guangdongense* (MHZU 23-0255, holotype) on natural substrate a–c Synnemata on substrate. d Synnema. e Top of synnema. f Base of synnema. g, h Conidia. i Conidiogenous cells with conidia. j Germinated conidium. k Colonies on PDA (front and below). Scale bars: a = 500 µm, b = 200 µm, c, d =100 µm, e, f =20 µm, g–j = 10 µm.

Figure 5.101 *Nigrosynnema guangdongense* on the substrate (MHZU 23-0255, holotype)



Note a, b Conidial masses on PDA. c–f Conidiophores, conidiogenous cells with conidia. g, h Conidia. Scale bars: c–f = 10 µm, g, h = 5 µm.

Figure 5.102 *Nigrosynnema guangdongense* on the culture (MHZU 23-0255)

Magnaporthales Thongk., Vijaykr. & K.D. Hyde, Fungal Divers. 34: 168 (2009)

Notes – Magnaporthales comprises five families: Ceratosphaeriaceae, Magnaporthaceae, Ophioceraceae, Pseudohalonectriaceae, and Pyriculariaceae. This order includes several important pathogens, including *Pyricularia oryzae* (known as *Magnaporthe oryzae*), *Nakataea oryzae* (known as *Magnaporthe salvinii*), and *Magnaporthiopsis poae* (Klaubauf et al., 2014).

Magnaporthaceae P.F. Cannon, Syst. Ascom. 13(1): 26 (1994)

Notes – Magnaporthaceae was established by Cannon and Alcorn (1994). Later, Thongkantha et al. (2009) introduced the new order Magnaporthales in Sordariomycetes, which included Magnaporthaceae. Magnaporthaceae species have been reported as saprobes and plant pathogens that mainly infect monocotyledonous plants, particularly

the shoots of Poaceae, including rice, maize, and wheat (Feng et al., 2021). Twenty-seven genera are accepted in this family (Hyde et al., 2024).

Bussabanomyces Klaubauf, M.-H. Lebrun & Crous, Stud. Mycol. 79: 99 (2014)

Notes – *Bussabanomyces* was introduced as a monotypic genus by Klaubauf et al. (2014), typified by *B. longisporus* (≡ *Pyricularia longispora*). *Bussabanomyces longisporus* has been reported as an endophytic fungus from leaves of *Amomum siamense.* In this study, we describe *Bussabanomyces wurfbainiae* sp. nov., a saprobic fungus, isolated from dead stem of *Wurfbainia villosa*. Additionally, we report the first documented sexual morph of *Bussabanomyces*, characterized by globose to subglobose, brown to black, deeply immersed ascomata, with erumpent neck; fasciculate, cylindrical asci, with distinct apical ring; hyaline, filiform, aseptate ascospores. Previously, only the asexual morph was known for this genus, characterized by unbranched conidiophores, cylindrical, denticulate conidiogenous cells and hyaline to pale brown, obclavate, smooth, 4(–5)-septate conidia (Klaubauf et al., 2014).

Bussabanomyces wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.104

Index Fungorum number: IF904027; Facesoffungi number: FoF 17928

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0045

Saprobic on dead stem, endophytic in asymptomatic stem and associated with symptomatic leaf of *Wurfbainia villosa*. Sexual morph: *Ascomata* solitary, deeply immersed, with erumpent neck protruding through the host surface, globose to subglobose, brown to black. *Hamathecium* 2.5–8 μm wide ($\overline{x}$ = 5 μm, n = 30), paraphyses, hyaline, branched, septate, broad at the base, tapering toward the apex, longer than asci, smooth-walled. *Asci* 65–106 × 7–10 μm ($\overline{x}$ = 78 × 8.5 μm, n = 30), 8-spored, fasciculate, cylindrical, slightly curved, hyaline, with distinct apical ring. *Ascospores* 50–90 × 2–4 μm ($\overline{x}$ = 65 × 3 μm, n = 30), straight to slightly curved, filiform, aseptate, hyaline, containing large guttules, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 4.5–5.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, flat, circular, with entire edge, pale brown from above, black to brown from the reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.19027 N, 111.91027 E), on dead stem of *Wurfbainia villosa*, 9 April 2023, C.F. Liao, YAM45 (MHZU 24-0045, holotype); ex-type culture, ZHKUCC 24-0245; China, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from asymptomatic stem of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, ST29B; living culture, ZHKUCC 24-0734; China, Guangdong Province, Xinyi City, Qianpai Town (22.41410 N, 111.27459 E), from symptomatic leaf of *Wurfbainia villosa*, 9 April 2023, C.F. Liao, YP64A1, YP70A1; living culture, ZHKUCC 24-0702, ZHKUCC 24-0715.

Notes – Four strains of *Bussabanomyces wurfbainiae* (ZHKUCC 24-0245, ZHKUCC 24-0734, ZHKUCC 24-0702, and ZHKUCC 24-0715) showed sequence similarities to the ex-type strain *B. longisporus* (CBS 125232) in blastn analyses (99.66% LSU, 97.20% ITS, and 96.48% *rpb1*). However, *tef1-α* sequence data were unavailable for ZHKUCC 24-0442, ZHKUCC 24-0443, ZHKUCC 24-0613, and ZHKUCC 24-0616. Phylogenetic analyses placed these strains in a distinct sister branch (99 ML/1.00 PP; Figure 5.103) with *Bussabanomyces longisporus* (≡ *Pyricularia longispora*, (Bussaban, 2003). Morphologically, *B. longisporus* is characterized by straight, rarely branched, septate conidiophores; cylindrical, denticulate conidiogenous cells; solitary, obclavate, hyaline to pale brown, 4(–5)-septate conidia. While the holotype of *B. wurfbainiae* (MHZU 24-0045) produces only the sexual morph, characterized by solitary, brown to black, deeply immersed, with erumpent neck protruding through the host surface, globose to subglobose ascomata; hyaline, cylindrical, with distinct apical ring asci; and hyaline, filiform, aseptate, ascospores. Based on the blastn analyses, these four strains are classified in *Bussabanomyces* and phylogenetic analyses further support them as a distinct species.

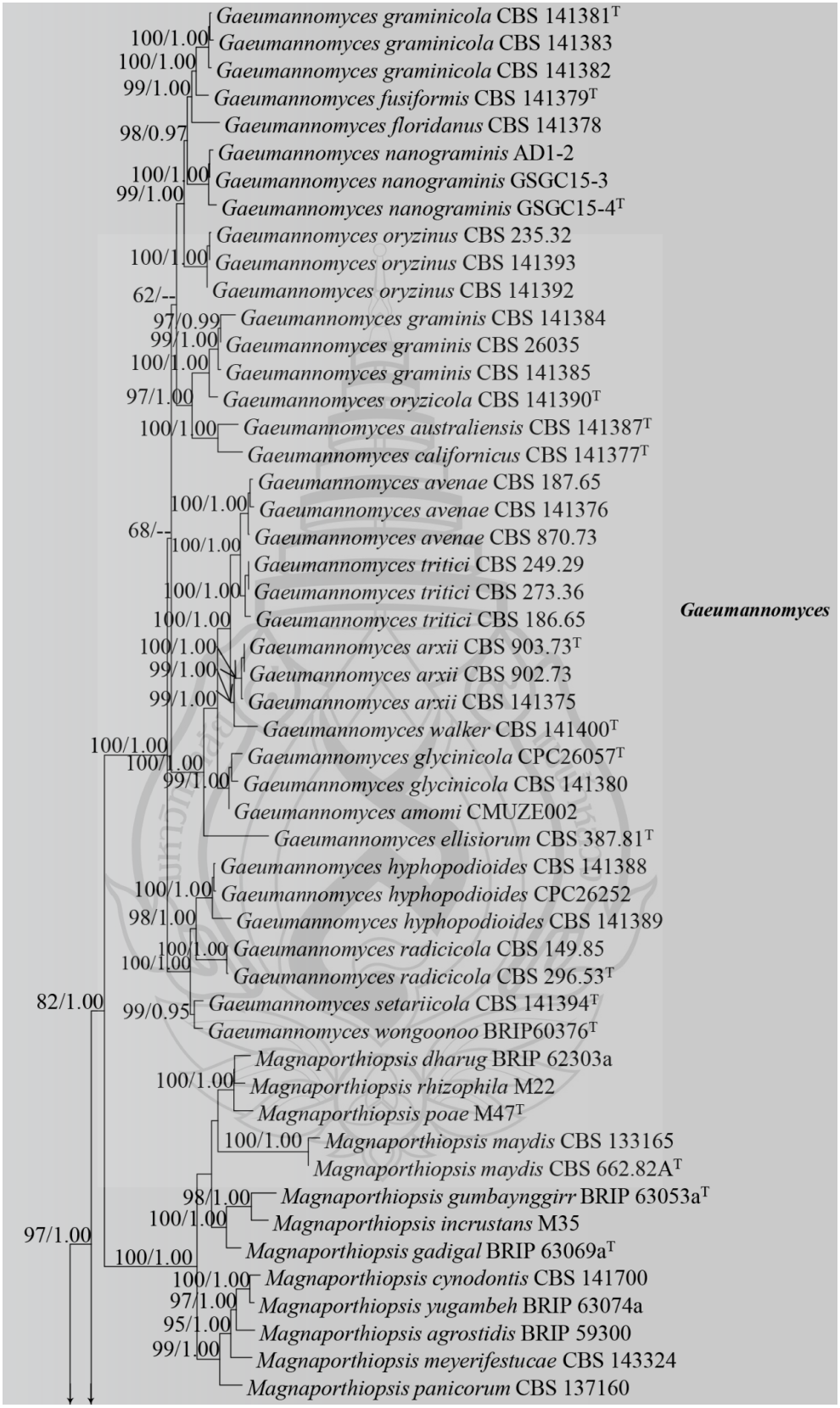
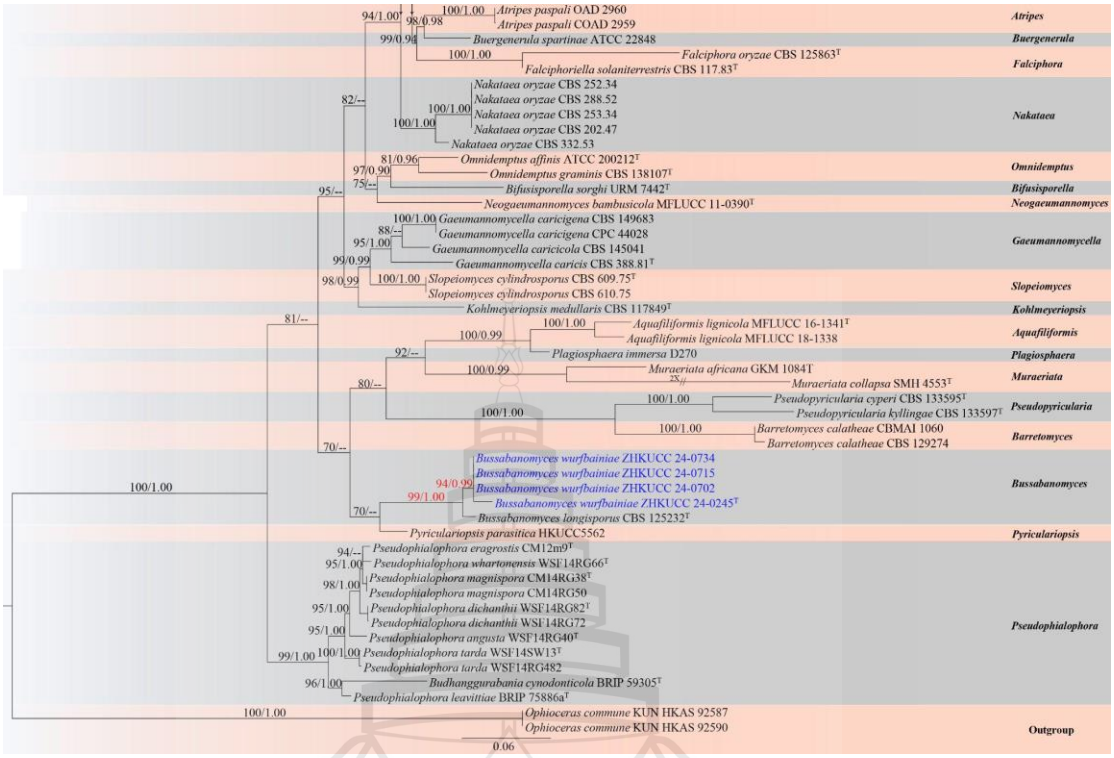
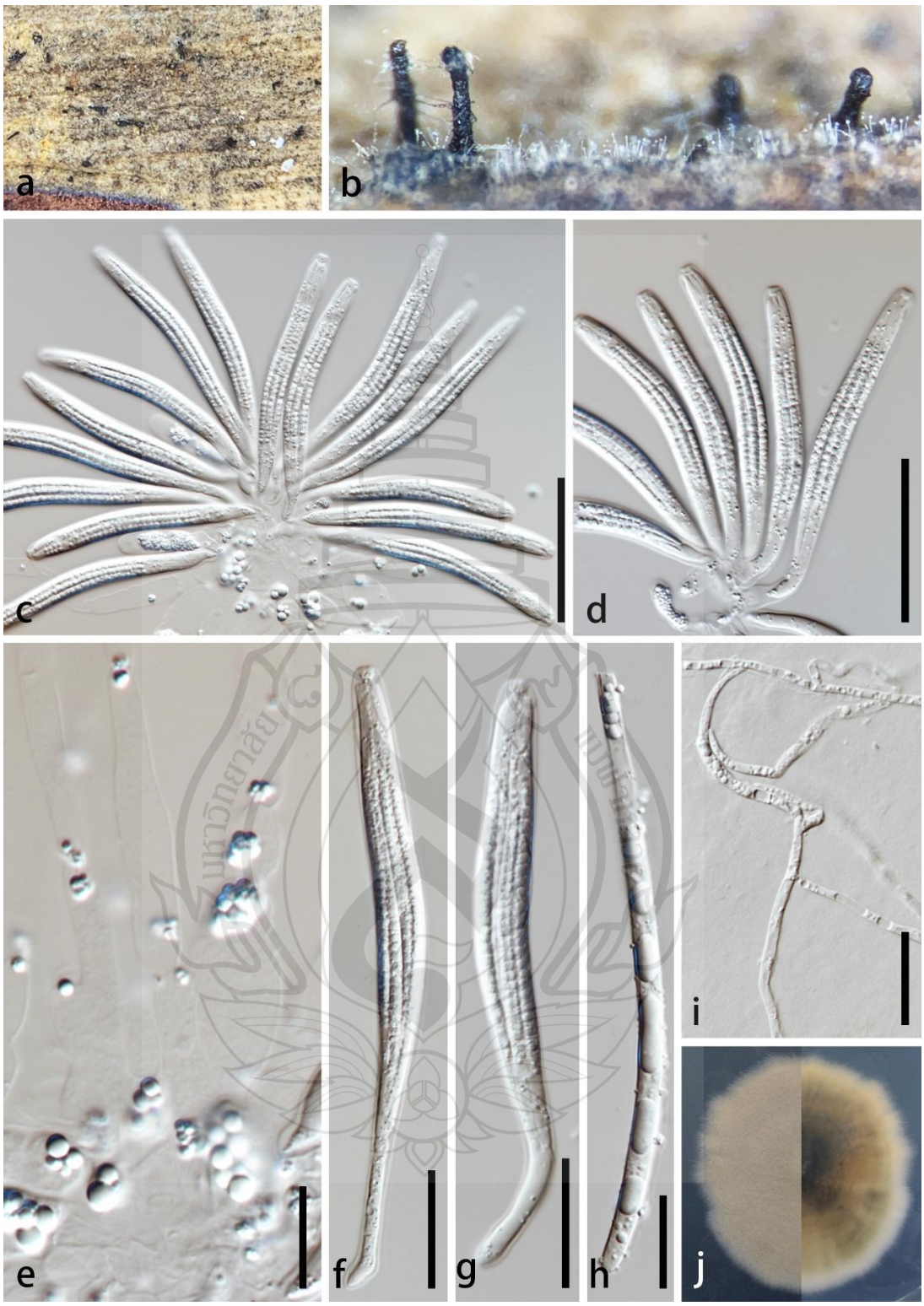


Figure 5.103 Maximum likelihood phylogeny based on the combined ITS, LSU, *rpb1*, and *tef1-α* sequences data of c



Note Tree rooted with *Ophioceras commune* (KUN-HKAS 92587, KUN-HKAS 92590). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.103 (continued)



Note a, b Appearance of ascomata on the substrate. c, d Asci and ascospores. e Paraphyses. f, g Asci. h Ascospore. i Germinated ascospore. j Culture characteristics on PDA. Scale bars: c, d = 50 µm, e, h = 10 µm, f, g, i = 10 µm.

Figure 5.104 *Bussabanomyces wurfbainiae* (MHZU 24-0045, holotype)

Pyriculariaceae Klaubauf, M.-H. Lebrun & Crous, Stud. Mycol. 79: 104 (2014)

Notes – Pyriculariaceae was introduced by Klaubauf et al. (2014) to accommodate *Deightoniella* and *Pyricularia* (the type genus). The species in this family are commonly isolated from monocotyledons as pathogens and saprobes, as well as endophyte. The morphology is detailed in Klaubauf et al. (2014) and Hyde et al. (2020). The species identification remains problematic due to the lack of sequence data for many species. Currently, 11 genera are accepted in this family (Hyde et al., 2024).

Bulbopyricularia C.F. Liao & Doilom gen. nov.

Index Fungorum number: IF904028; Facesoffungi number: FoF 17931

Etymology – The epithet "*Bulbopyricularia*" refers to the unique character of terminal conidiophores forming a bulbous shape

Endophytic in asymptomatic leaves, stems, and roots plant material. Sexual morph: Undetermined. Asexual morph: *Conidiophores* macronematous, fascicles, straight or flexuous, branched or unbranched, septate, brown to dark brown at base part, hyaline to pale brown at tip, cylindrical, 2 – 10 sympodial proliferations, forming 2 – 10 bulbous swelling, with a forming a bulbous at intercalary or terminal. *Conidiogenous cells* sympodial, cylindrical, terminal and intercalary, denticulate, smooth-walled, hyaline to pale brown, percurrent proliferation. *Conidia* solitary, ovoid, obpyriform to obclavate, narrowed toward tip, rounded at the base, hyaline, granular to guttulate, 2-spetate, U-shape septa, smooth-walled, thick-walled, no hilum.

Type species: ***Bulbopyricularia wurfbainiae*** C.F. Liao & Doilom

Notes – *Bulbopyricularia* resembles *Pyricularia* in having terminal and intercalary, denticulate conidiogenous cells and solitary, pyriform, 2-septate conidia. However, it differs from *Pyricularia* by having cylindrical conidiophores, brown to dark brown at base part, hyaline to pale brown at tip, with a forming a bulbous at terminal, bamboo-like growth, percurrently proliferating conidiogenous cells, and hyaline conidia with U-shaped septa and no hilum. Nevertheless, the conidiophores of *Pyricularia* are subcylindrical, brown, the conidiogenous cells show rhexolytic secession, and the conidia are pyriformto obclavate, with almost straight septa, with a distinct basal hilum, sometimes with marginal frill.

Bulbopyricularia also resembles *Bambusicularia*, *Barretomyces*, and *Neocordana* by having septate conidiophores, terminal and intercalary, denticulate conidiogenous

cells, and solitary, septate conidia. However, *Bulbopyricularia* can be distinguished by having fascicles, 2–10 sympodially proliferating, forming 2–10 swollen, pyriform conidiophores, with a bulbous at the terminal, and conidia with U-shaped septa and no hilum. The blastn analysis against the NCBI GenBank database demonstrated that four *Bulbopyricularia* strains (ZHKUCC 24-0442, ZHKUCC 24-0443, ZHKUCC 24-0613, and ZHKUCC 24-0616) exhibit sequence similarities of 98.09% (LSU), 90.06% (ITS), 73.96% (*cal*), and 90.12% (*act*), respectively, to the ex-type strain of *Barretomyces calatheae* (CBS 129274). However, *rpb1* sequences are unavailable for *Bulbopyricularia* strains (ZHKUCC 24-0442, ZHKUCC 24-0443, ZHKUCC 24-0613, ZHKUCC 24-0616).

The phylogenetic analysis support that our strains (ZHKUCC 24-0442, ZHKUCC 24-0443, ZHKUCC 24-0613, ZHKUCC 24-0616, ZHKUCC 24-0264, ZHKUCC 24-0265, ZHKUCC 24-0379, ZHKUCC 24-0380, ZHKUCC 24-0381, ZHKUCC 24-0415, ZHKUCC 24-0419, ZHKUCC 24-0420; ZHKUCC 24-0416, ZHKUCC 24-0613, ZHKUCC 24-0619, ZHKUCC 24-0746, ZHKUCC 24-0759, ZHKUCC 24-0757, ZHKUCC 24-0762) formed a distinct clade with other morphologically closely related taxa and is well-supported related to *Barretomyces* with 99% ML and 1.00 PP statistical support. Based on morphological and molecular evidence, we introduce a novel asexual genus *Bulbopyricularia*, characterized by fascicles, cylindrical, sympodial proliferation, swollen, with a forming a bulbous at terminal conidiophores; cylindrical, terminal and intercalary, denticulate, percurrent secession conidiogenous cells; solitary, ovoid, obpyriform to obclavate, 2-spetate, U-shape septa, no hilum conidia.

Bulbopyricularia guangdongensis C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.106

Index Fungorum number: IF904029; Facesoffungi number: FoF 17929

Etymology – The epithet "*guangdongensis*" refers to the locality, Guangdong Province, China, where the holotype was collected

Holotype – MHZU 24-0306

Endophytic in asymptomatic leaves, stems, and roots of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after two months. *Hyphae* hyaline, septate, branched, smooth-walled. *Conidiophores* 335–675 × 5.5–9 μm

($\overline{x}$ = 515 × 7 μm, n = 10), arising directly from hyphae, fascicles, hyaline to brown, smooth-walled, with 6–10 sympodial proliferations, forming 6–10 swollen, 8–11-septate, branched or unbranched, forming terminal bulbous swellings (8–11 μm). *Conidiogenous cells* terminal or lateral, cylindrical, pale brown, aseptate, smooth-walled, with several protruding denticles. *Conidia* 15–20 × 8–11 μm ($\overline{x}$ = 17.5 × 10 μm, n = 20), solitary, ovoid to obpyriform, pale brown, granular to guttulate, 2-septate, with U-shaped septa; apical cell 4.5–9 × 4–7 μm ($\overline{x}$ = 6 × 5 μm, n = 30), cuneiform; basal cell 3–7 × 6.5–10 μm ($\overline{x}$ = 5 × 8 μm, n = 30), rounded; no hilum truncate.

Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 40 days at 28 ± 2°C, moderately sparse, flat, circular, forming three radially and concentrically circular, with entire edge, granular, center brown to dark brown towards to pale at the edge from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangchun City, Heshui Town (22.29861 N, 111.98444 E), from symptomic leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP09A3 (MHZU 24-0306, holotype); ex-type culture, ZHKUCC 24-0619; *ibid.*, living culture, ZHKUCC 24-0613; living culture, ZHKUCC 24-0616; *ibid.*, YAM65A, YAM65B; living culture, ZHKUCC 24-0264, ZHKUCC 24-0265; *ibid.*, Chunwan Town (22.436461 N, 111.938281 E), asymptomatic fruits of *Wurfbainia villosa*, 29 October 2023, C.F. Liao, AMF21B, AMF49C, AMF68B; living culture, ZHKUCC 24-0379, ZHKUCC 24-0380, ZHKUCC 24-0381; *ibid.*, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaves of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML03B-2, AML05A-4, AML06A-4, AML09A-3, AML19C-1; living culture, ZHKUCC 24-0415, ZHKUCC 24-0419, ZHKUCC 24-0420; ZHKUCC 25-0448, ZHKUCC 24-0416; *ibid.*, on asymptomatic leaves of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, living culture, AMS04C-2, ZHKUCC 25-0449; *ibid.*, Xinyi City, Qianpai Town, (22.41410 N, 111.27459 E), from asymptomatic stems of *Wurfbainia villosa*, 10 December 2023, C.F. Liao, LL04B, LL16B, LL17A, LL20C, living culture, ZHKUCC 24-0746, ZHKUCC 24-0759, ZHKUCC 24-0757, ZHKUCC 24-0762.

Notes – The phylogenetic analysis of our strains (ZHKUCC 24-0264, ZHKUCC 24-0265, ZHKUCC 24-0379, ZHKUCC 24-0380, ZHKUCC 24-0381, ZHKUCC 24-0415, ZHKUCC 24-0419, ZHKUCC 24-0420; ZHKUCC 24-0416, ZHKUCC 24-0613,

ZHKUCC 24-0619, ZHKUCC 24-0746, ZHKUCC 24-0759, ZHKUCC 24-0757, ZHKUCC 24-0762) formed a sister clade with *Bulbopyricularia wurfbainiae* with 100 ML/1.00 PP support (Figure 5.105). Morphologically, *Bulbopyricularia guangdongensis* are morphologically unique with *B. wurfbainiae* by having fascicles, hyaline to brown, 6–10 sympodial proliferating, forming 6–10 swollen, 8–11-septate conidiophores, forming a bulbous of 8–11 μm at the terminal, but *B. wurfbainiae* are single to fascicles, brown to dark brown at base part, hyaline to pale brown at tip, 2–6 sympodial proliferations, forming 2–6 swollen, 2–12-septate conidiophores, with a forming a bulbous 6–23 at intercalary and terminal. The conidia of *B. guangdongensis* are ovoid to obpyriform, smaller (15–20 × 8–11 μm vs. 33–45 × 8–11 μm), with cuneiform, smaller apical cell (4.5–9 × 4–7 μm vs. 13–25 × 2.5–4 μm), however, *B. wurfbainiae* have obpyriform to obclavate conidia with corniform, filiform apical cell. Therefore, we would introduced *Bulbopyricularia wurfbainiae* as a novel species based on the phylogenetic analysis and unique morphology.

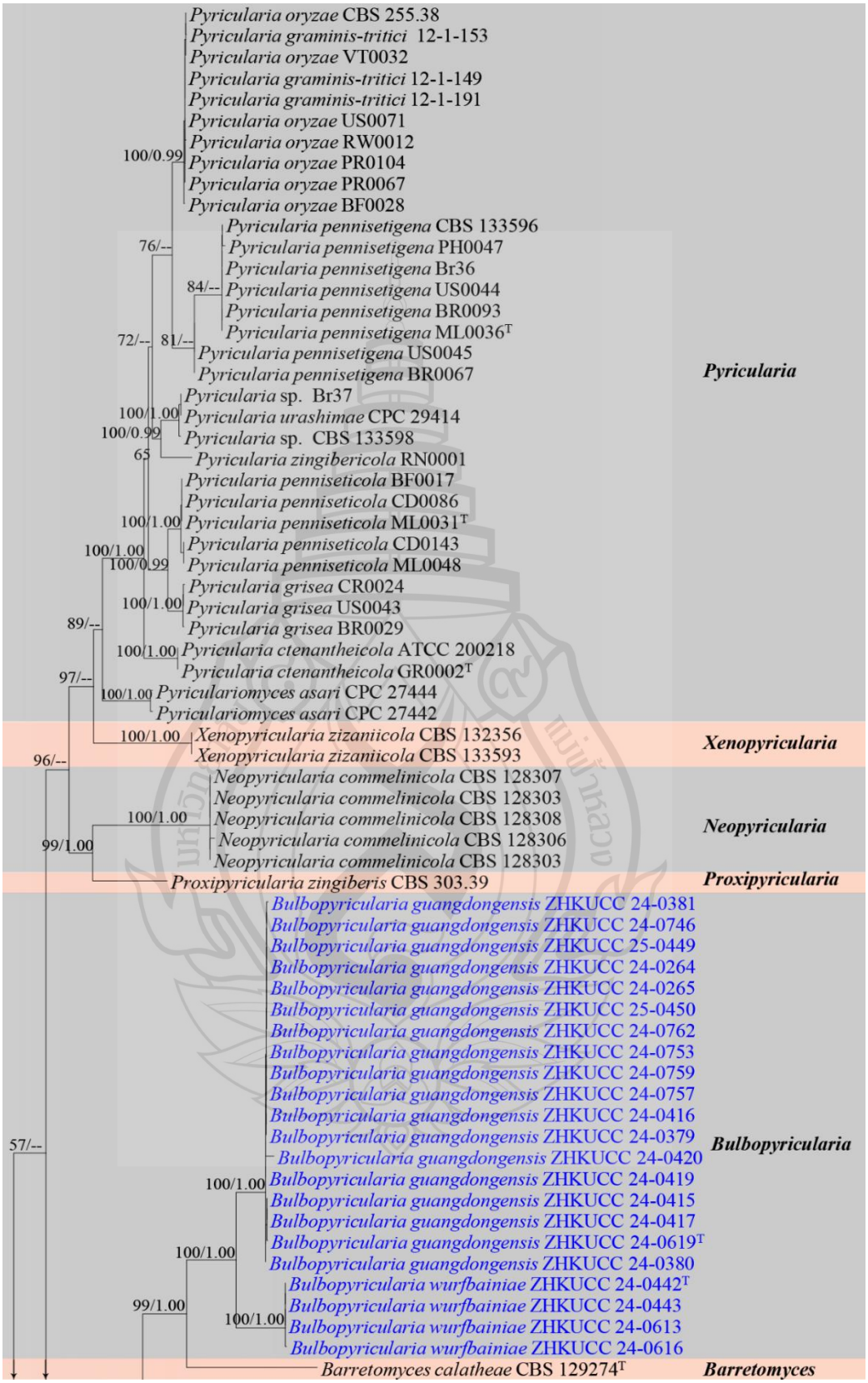
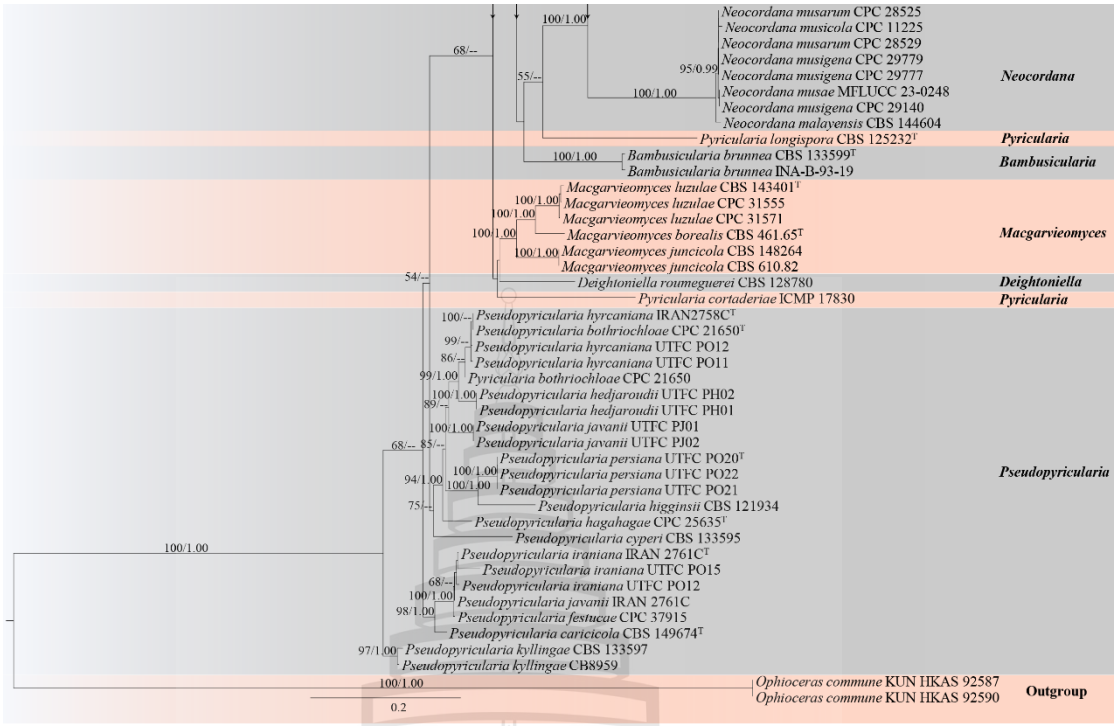
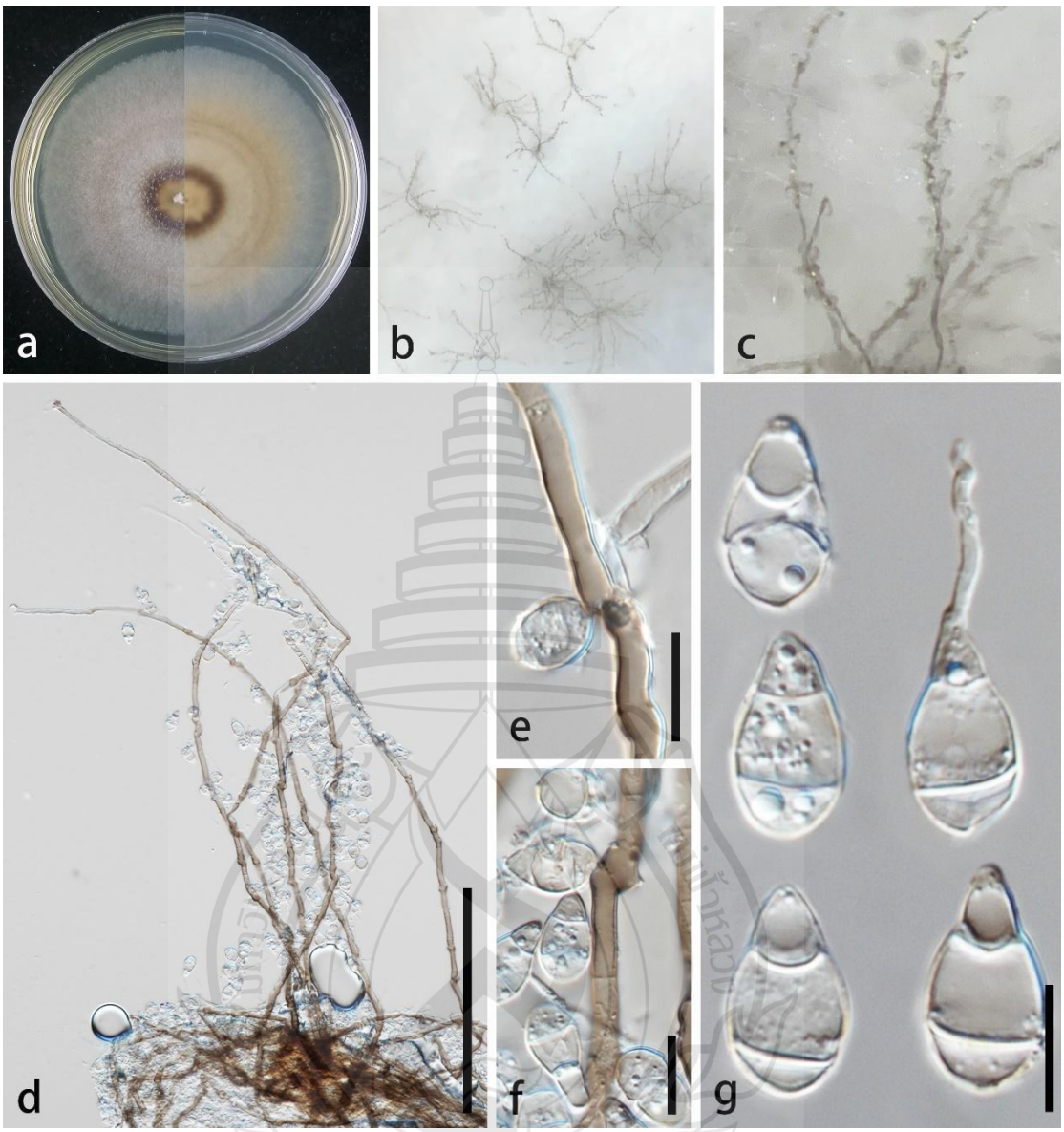


Figure 5.105 Maximum likelihood phylogeny based on the combined LSU, ITS, *rpb1*, *cal*, and *act* sequences data of *Bulbopyricularia*



Note Tree rooted with *Ophioceras commune* (KUN_HKAS_92587, KUN-HKAS 92590). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.105 (continued)



Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d–f Conidiophores, conidiogenous cells with conidia. g Conidia. Scale bars: d = 200 μm, e, f = 20 μm, g = 10 μm.

Figure 5.106 *Bulbopyricularia guangdongensis* (MHZU 24-0306, holotype)

Bulbopyricularia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.107

Index Fungorum number: IF904030; Facesoffungi number: FoF 17930

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0173

Endophytic associate with asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On SNA and OA after 1 month. *Hyphae* hyaline, septate, branched, smooth-walled. *Conidiophores* 75–240 × 6–9.5 μm ($\overline{x}$ = 156 × 7.5 μm, n = 20), arising directly from hyphae, single to fascicles, brown to dark brown at base, hyaline to pale brown at tip, 2–12-septate, 2–6 sympodial proliferations, forming 2–6 bulbous swelling, branched or unbranched, forming bulbous swellings (6–23 μm) at intercalary and terminal, smooth-walled. *Conidiogenous cells* terminal or intercalary, denticulate, cylindrical, pale brown to brown, aseptate, smooth-walled. *Conidia* 33–45 × 8–11 μm ($\overline{x}$ = 38 × 10 μm, n = 30), solitary, obpyriform, hyaline to pale brown, granular to guttulate, 2-septate, with U-shape septa; apical cell 13–25 × 2.5–4 μm ($\overline{x}$ = 18.5 × 3 μm, n = 30), filiform to corniform; basal cell 7.5–10 × 6.5–8.5 μm ($\overline{x}$ = 9 × 7.5 μm, n = 30), rounded; hilum inconspicuous. *Appressoria* 12–14 × 10–12 μm ($\overline{x}$ = 13 × 11 μm, n = 10), solitary, hyaline to olivaceous green, subglobose to elliptical, with an entire, crenate to undulate margin, smooth-walled.

Culture characteristics – Colonies on PDA reaching 7.5–8.0 cm diameter in 1 month at 28 ± 2°C, moderately sparse, flat, circular, forming three distinct concentric zones, with entire edge, granular, brown at center, towards to grey in the next concentric zone, whitish at the edge from above and reverse, no pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), on asymptomatic leaf of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AML18C-2 (MHZU 24-0173, holotype); ex-type culture, ZHKUCC 24-0442; *ibid.*, AML21A-5, living culture, ZHKUCC 24-0443; *ibid.*, Yangchun City, Heshui Town (22.29861 N, 111.98444 E), from symptomatic leaf of *Wurfbainia villosa*, 9 November 2023, C.F. Liao, YP07A3, YP07B3; living culture, ZHKUCC 24-0613, ZHKUCC 24-0616.

Notes – In the phylogenetical analyses, strains (ZHKUCC 24-0442, ZHKUCC 24-0443, ZHKUCC 24-0613, ZHKUCC 24-0616) formed a distinct subclade with *Barretomyces calatheae* with 100 ML/1.00 PP support (Figure 5.105). Moreover, *Bulbopyricularia wurfbainiae* can be easily differentiated from *Barretomyces calatheae* by having single to fascicles, 2–6 sympodially proliferating conidiophores, forming 2–6 bulbous swelling at intercalary and terminal and conidia with U-shaped

septa and a filiform, corniform, longer apical cell (13–25 vs. 9–12 μm). Additionally, *Bulbopyricularia wurfbainiae* also can be easily distinguished from *B. guangdongensis* by having shorter conidiophores (75–240 × 6–9.5 μm vs. 335–675 × 5.5–9 μm), less sympodial proliferations (2–6 vs. 6–10), larger bulbous, and longer apical cell (13–25 × 2.5–4 μm vs. 4.5–9 × 4–7 μm). Thus, we introduced *Bulbopyricularia wurfbainiae* as a novel specs based on the phylogenetic analysis and unique morphology.

Note a Culture characteristic on PDA for 1 month. b, c Conidia on aerial mycelia on SNA or OA after 1 month. d–g Conidiophores, conidiogenous cells with conidia. h Appressoria. i–l Conidia. Scale bars: d = 200 μm, e–g = 50 μm, h–l = 20 μm.

Figure 5.107 *Bulbopyricularia wurfbainiae* (MHZU 24-0173, holotype)

Pleurotheciaceae Réblová & Seifert, in Réblová, Seifert, Fournier & Štěpánek, Persoonia 37: 63 (2015)

Pleurotheciaceae was introduced by Réblová et al. (2016) to accommodate six monophyletic clades comprising eleven genera, viz., *Adelosphaeria, Brachysporiella, Helicoön, Melanotrigonum, Phaeoisaria, Phragmocephala, Pleurothecium, Pleurotheciella, Pleurothecium* s.str, *Sterigmatobotrys*, and *Taeniolella*.

Dematipyriforma L. Yan Sun, Hai Y. Li, Xiang Sun & L.D. Guo, Cryptog. Mycol. 38(3): 345 (2017)

Dematipyriforma was introduced by Sun et al. (2017) with *D. aquilaria* as the type species. This hyphomycetes fungus was characterized by micronematous, hyaline to pale brown, brown, or black-brown, smooth, septate conidiophores that may be present or absent; monoblastic, integrated, intercalary, or terminal cylindrical conidiogenous cells that are pale brown to brown, determinate; and conidial secession that is rhexolytic. The conidia are solitary, pale brown to black-brown, smooth, thick-walled, pyriform, oblong, or subglobose, often with transverse and oblique or longitudinal septations, usually having a single small basal cell (Sun et al., 2017; Boonmee et al., 2021; Bao et al., 2022; Jayawardena et al., 2022).

Dematipyriforma wurfbainiae C.F. Liao & Doilom, sp. nov. Figure 5.109

nov.

Index Fungorum number: ####; Facesofungi number: FoF####; Figure ####

Etymology – The epithet "*wurfbainiae*" refers to the host genus *Wurfbainia*, from which the holotype was collected.

Holotype – MHZU 23-0249

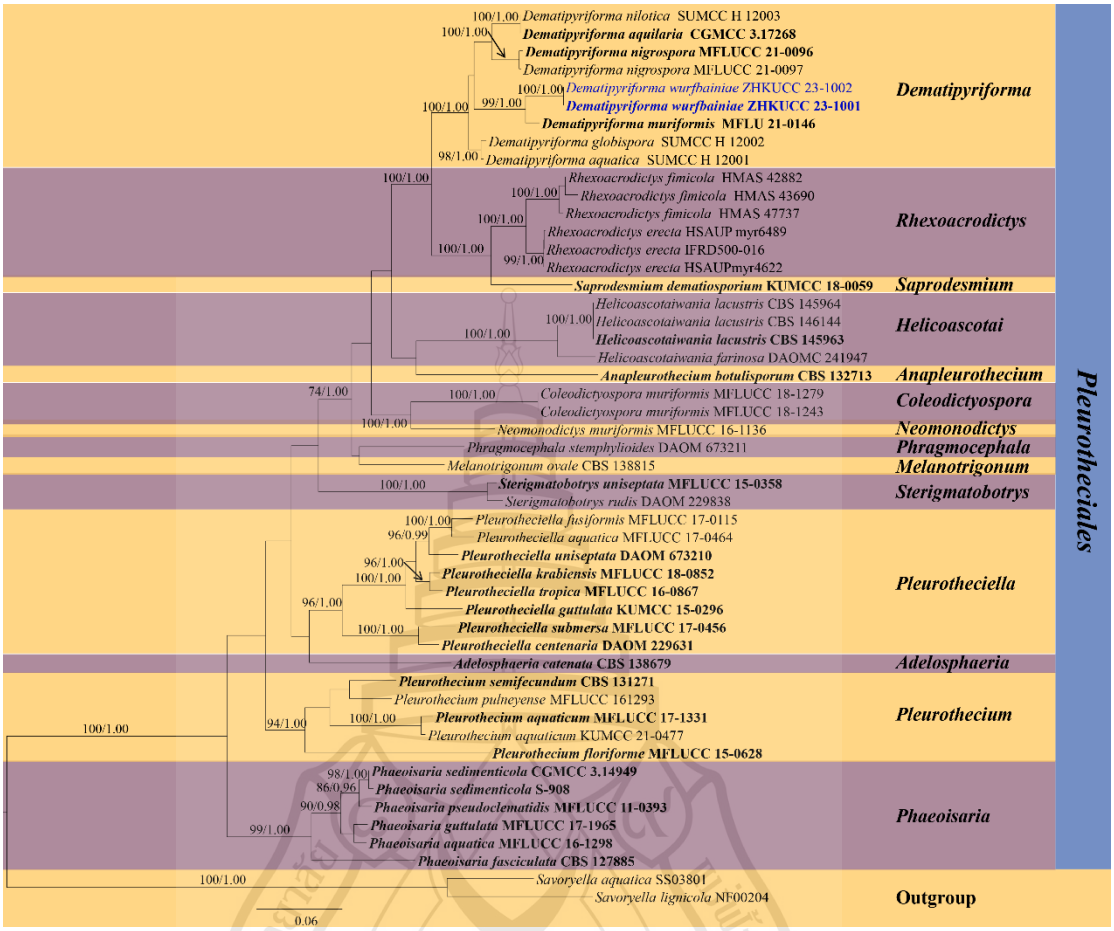
Saprobic on decaying stems of *Wurfbainia villosa*. Sexual morph: undetermined. Asexual morph: hyphomycetes. *Colonies* superficial, scattered, composed of hyaline basal and black, shiny spore. *Mycelium2*–3.5 µm wide, superficial or immerse, hyaline, septate, smooth walled. *Conidiophores* 20–80 × 3–6 µm, ($\bar{x}$ =48 × 5 µm n = 30), macronematous or semi-macronematous, mononematous, catenate, fasciculate, straight or slightly flexuous, composed of 3–10 hyaline, filamentous cells forming a long chain with a terminal swollen conidiogenous cell, hyaline, brunched, smooth-walled. *Conidiogenous cell* 8–33 × 5–14 µm, ($\bar{x}$ =17 × 7.5 µm n = 30), monoblastic, terminal, integrated, subglobose, fabiform, limoniform, cylindrical,

clavate or triangular, determine, hyaline, smooth-walled. *Conidial secession* rhexolytic. *Conidia* 22–33 × 12–21 μm, ($\bar{x}$ =27 × 15 μm n = 30), acrogenous, solitary, pale brown to black-brown, pyriform, oblong, subglobose, obovoid or clavate, smooth-, thick-walled, rounded at the apex, pointed at base, with 3–5 transverse septa, 1-longitudinal septum, slightly constricted at the septa.

Culture characteristics – Conidia germinated on PDA at room temperature (25±2°C) within 24 hours, germ tubes produced from the basal cell. Colonies reaching 12 to 15 mm in diam. after two weeks at 28°C. Colonies dense, irregular in shape, raised, tight mycelia on the surface. Front brown to cream at margin; reverse pale gray mix with brown. The conidia directly grow from mycelium, conidia 15–45 × 8–20 μm, ($\bar{x}$ =30 × 15 μm n = 30), solitary or aggregated, pale brown to black brown, pyriform, oblong, subglobose, obovoid or clavate, black brown, smooth, thick-walled, rounded at apical, pointed at base, with 4–8 transverse septa, 1-longitudinal septum, strictly constricted at the septa.

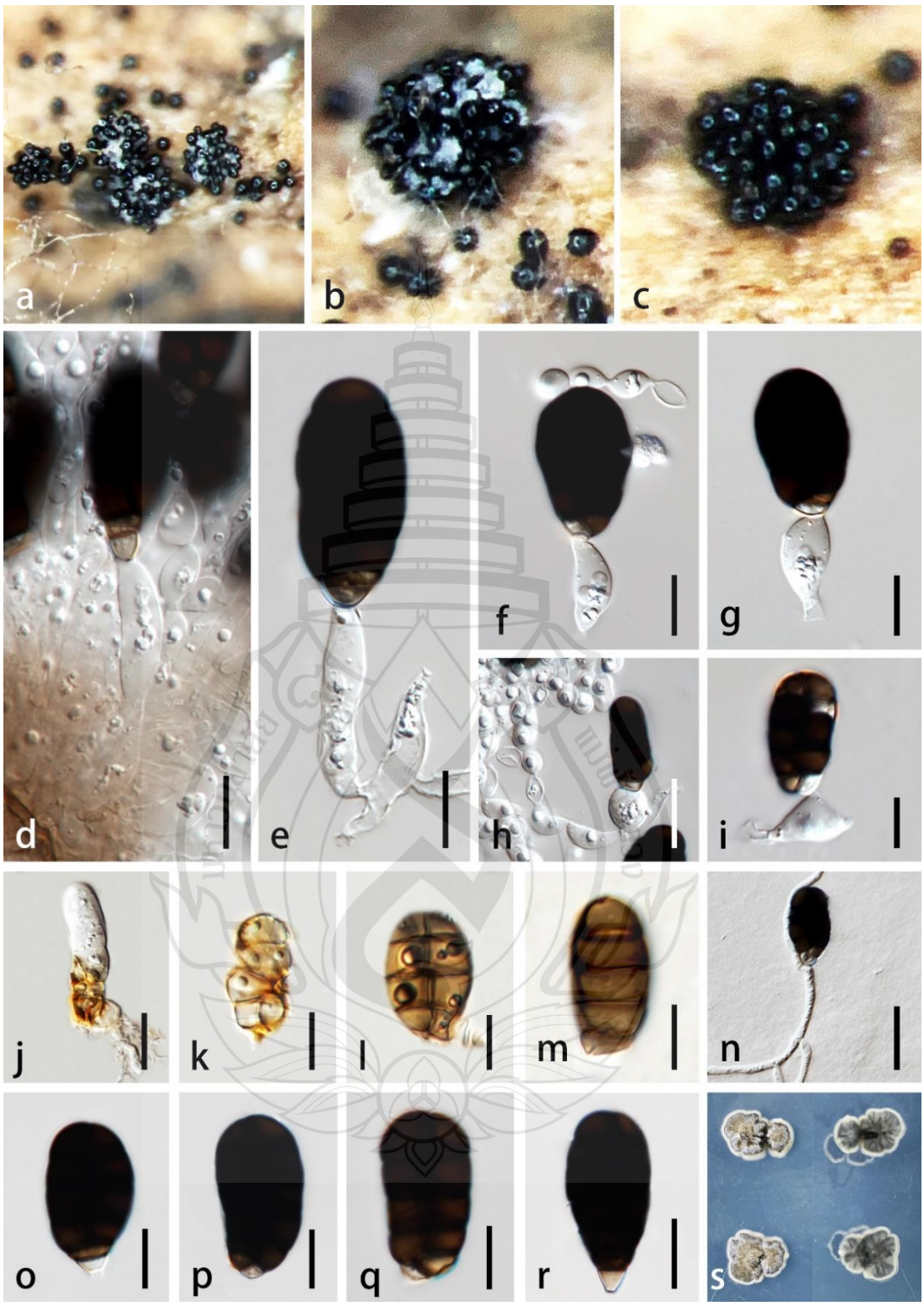
Material examined – China, Guangdong Province, Yangchun city, from decaying stems of *Wurfbainia villosa* (Zingiberaceae), 9 April 2023, C.F. Liao, (MHZU 23-0249, holotype), ex-type living culture ZHKUCC 23-1001 *ibid*., ZHKUCC 23-1002.

Notes – In phylogenetic analyses, our collection formed a sister cluster with *Dematipyriforma muriformis* (MFLU 21-0146) with 100% ML and 1.00 BYPP (Figure 5.108). In the morphology, *D. wurfbainiae* shares unique conidiophores with *D. muriformis*, *D. wurfbainiae* has catenate, fasciculate, straight or slightly flexuous conidiophores, composed of 3–10 hyaline, filamentous cells forming a long chain, with terminally formed swollen conidiogenous cell. However, *D. muriformis* has fasciculate, simple or branched, hyaline, cylindrical conidiophores. *Dematipyriforma wurfbainiae* also differs by having larger conidiophores compared to those of *D. muriformis* (20–80 × 3–6 μm vs 10–26.5 × 2–3 μm). Thus, we proposed *D. wurfbainiae* as a novel species based on unique conidiophores characters and molecular evidence support.



Note The rooted with *Savoryella aquatica* (SS03801) and *Savoryella lignicola* (NF00204). Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities (PP) greater than 0.95 are given as ML/PP above the nodes. Newly obtained sequences are indicated in blue and ex-type strains are in bold.

Figure 5.108 Maximum likelihood phylogeny based on the combined LSU, ITS, SSU, *rpb2*, and *tef1-α* sequences data of Pleurotheciales



Note a–c colonies on wood substrate. d conidia and conidiophores. e–i conidia attach on conidiogenous cell. j–m, o–r conidia. n germinated conidia. s colony on PDA (left-front, right-reverse). Scale bars: h, n = 20 µm, d–i, j–m, o–r = 10 µm.

Figure 5.109 *Dematipyriforma wurfbainiae* (MHZU 23-0249, holotype)

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 182 (1986)

Notes – Sordariales was introduced by Hawksworth & Eriksson (1986). The current taxonomic treatments are detailed in Hyde et al. (2024).

Chaetomiaceae G. Winter (as "Chaetomieae"), Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 153 (1885)

Notes – Chaetomiaceae, introduced by Winter (1885) with *Chaetomium* as the type genus, includes members that are reported as saprobic or parasitic fungi. They occur on a wide range of substrates, including decaying plant materials, seeds, dung, air, soil, mushrooms, animals, and humans (Hyde et al., 2020; Fortes et al., 2023). Phylogenetic analyses based on combined ITS, LSU, *rpb2*, and *tub2* sequences have been used to delineate the family (Condé et al., 2023). The family comprises 51 genera (Hyde et al., 2024).

Chaetomium Kunze, Mykologische Hefte (Leipzig) 1: 15 (1817)

Notes – *Chaetomium* was introduced by Kunze (1817) with *Ch. globosum* as the type species. *Chaetomium* species can colonize various substrates and can degrade cellulose, producing over 200 bioactive metabolites (Wang et al., 2016; Dwibedi et al., 2023). *Chaetomium* species have been applied as bio-fungicide and bio-stimulants in agriculture, such as for protection against rice blast caused by *Magnaporte oryzae*, durian and black pepper rot caused by *Phytophthora palmivora*, tomato wilt caused by *Fusarium oxysporum* f, sp. *lycopersici*, and anthracnose caused by *Colletotrichum* spp. (Soytong et al., 2021). Conversely, some species. *Ch. globosum* is known to produce various toxic metabolites and can grow in indoor environments, including contaminated building materials and feathers. It has been reported as a causal agent of onychomycosis (McMullin et al., 2013; Ahmed et al., 2015). Currently, 446 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). In this study, we reported *Chaetomium globosum* as a new host record, which was isolated from symptomatic leaf of *Wurfbainia villosa* in China.

Chaetomium globosum Kunze, Mykol. Hefte 1: 16. 1817 Figure 5.111

Index Fungorum number: IF172545; Facesoffungi number: FoF 02196

Associated with symptomatic leaf of *Wurfbainia villosa*. Sexual morph: *Ascomata* 250–358 × 115–287 μm ($\overline{x}$ = 303 × 195 μm, n = 20), superficial, solitary to

gregarious, unilocular, coriaceous, oval to subglobose, ovoid to obpyriform, olivaceous green to black, with the opening ostiolate. *Terminal hairs* 3 –5 μm wide ($\bar{x}$ = 4 μm, n = 30), straight when young, undulate to loosely coiled in upper part, erect in lower part when mature, brown to olivaceous green in reflected light, narrowing towards the apex, septate, unbranched, verrucose; lateral hairs erect or apical flexuous, shorter than terminal hairs. *Hamathecium* 7–10 μm wide ($\bar{x}$ = 8 μm, n = 30), paraphyses, numerous, hyaline, unbranched, septate, smooth-walled, longer than asci. *Asci* 47–73 × 17–27 μm ($\bar{x}$ = 61 × 21 μm, n = 30), 8-spored, unitunicate, crowded, clavate to spathulate, pedicellate, evanescent when mature. *Ascospores* 9–12 × 7–10 μm ($\bar{x}$ = 11 × 9 μm, n = 30), globose to subglobose, broad fusiform to limoniform, hyaline, multi-guttulate when younger, becoming olivaceous to brown when mature, unicellular, aseptate, with a germ pore. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 8.0–8.5 cm diameter in 4 weeks at 28 ± 2°C, moderately sparse, raised, irregular, undulate, pale yellow to pale brown at the center, olivaceous green and yellow dots of ascomata at the edge from above, pale yellow to pale brown from reverse, without pigmentation.

Material examined – China, Guangdong province, Guangzhou City, Zhongkai University (23.10643 N, 113.28240 E), from symptomatic leaf of *Wurfbainia villosa*, 30 October 2023, C.F. Liao, YP04B1 (MHZU 24-0298); living culture, ZHKUCC 24-0608.

Known hosts (based on molecular data) – *Averrhoa carambola* (Deepak Reddy et al., 2024), fingernail of *Homo sapiens*, from compost, dead stem of *Juncus* sp., mouldy book, clay soil at 120 cm depth (Wang et al., 2016), human toenails onychomycosis (Kim et al., 2013), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – China, Germany, Hungary, Iran (Abdollahi et al., 2016), India (Deepak Reddy et al., 2024), Korea (Kim et al., 2013), Netherlands, Poland, USA (Wang et al., 2016), cherry trees (*Prunus avium*) (Abdollahi et al., 2016), China (this study).

Notes – In the phylogenetic analyses, our strain (ZHKUCC 24-0608) nested with *Chaetomium globosum* (CBS 160.62 (ex-type), CBS105.40, and CBS147.60) with 92% ML/0.97 PP support (Figure 5.110). Morphologically, our isolate fits with *C. globosum* by having superficial, oval to subglobose, greenish olivaceous, ostiolate

ascomata; brown, undulate to loosely coiled terminal hairs at upper part, erect at lower part, usually unbranched, septate, verrucose, with erect or apical flexuous lateral hairs, 8-spored, clavate asci, and limoniform, olivaceous ascospores. Our isolate has ascomata, terminal hairs, and ascospores with dimensions nearly identical to those of *C. globosum*, the holotype described in Wang et al. (2016). However, differences were observed in certain characteristics. Our isolate differs in having crowded, spathulate, larger asci (47–73 × 17–27 μm) compared to the holotype of *C. globosum* (30–40 × 12–17 μm), which are characteristically biseriate and fusiform (Wang et al., 2016). Additionally, our isolate has hyaline, unbranched, septate hamathecium, but they have not been observed in the holotype of *C. globosum* (Wang et al., 2016). As *Chaetomium globosum* has not been recorded from *Wurfbainia villosa* (see known hosts), we designate our isolate as a new host record for this species.

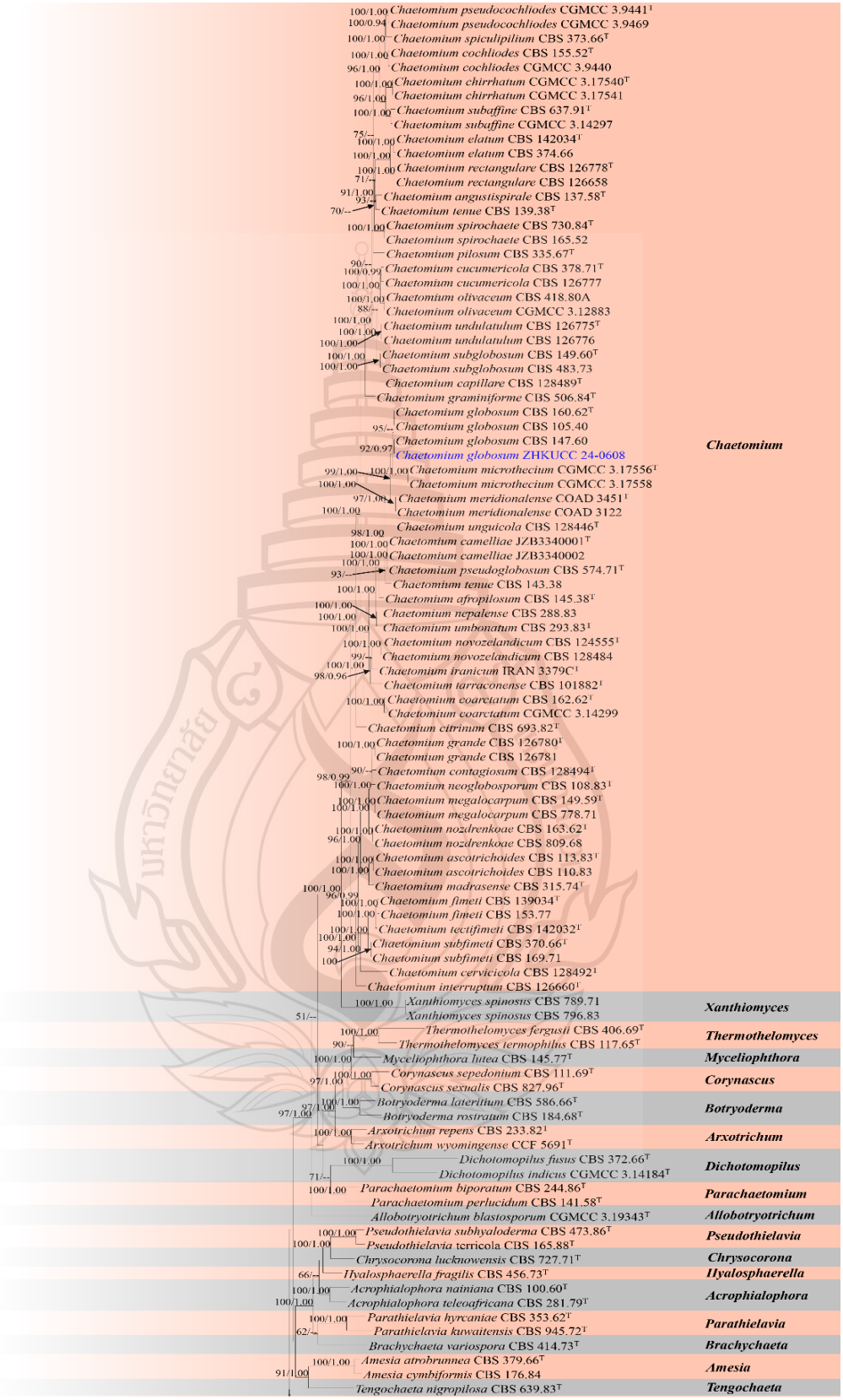
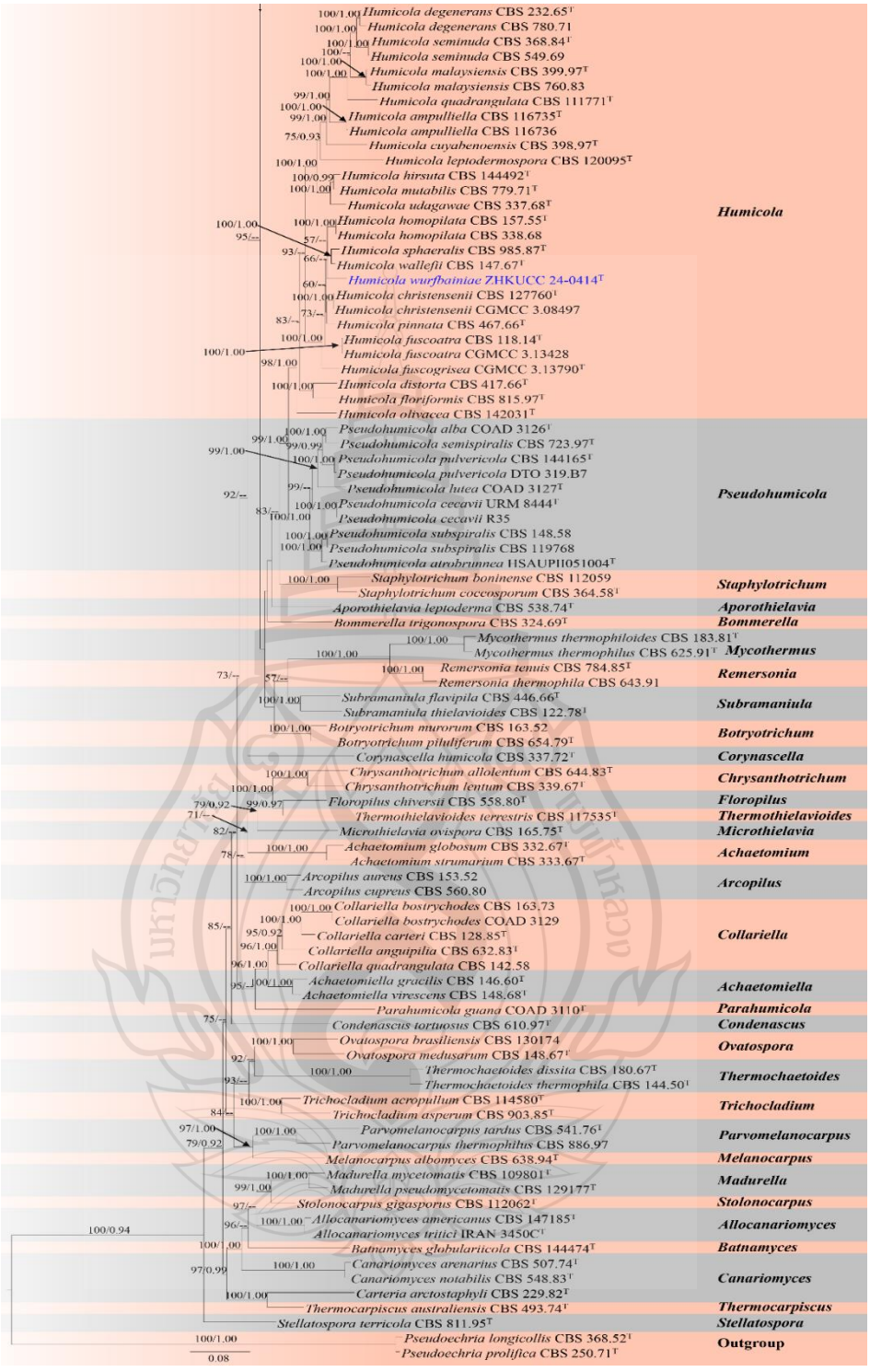
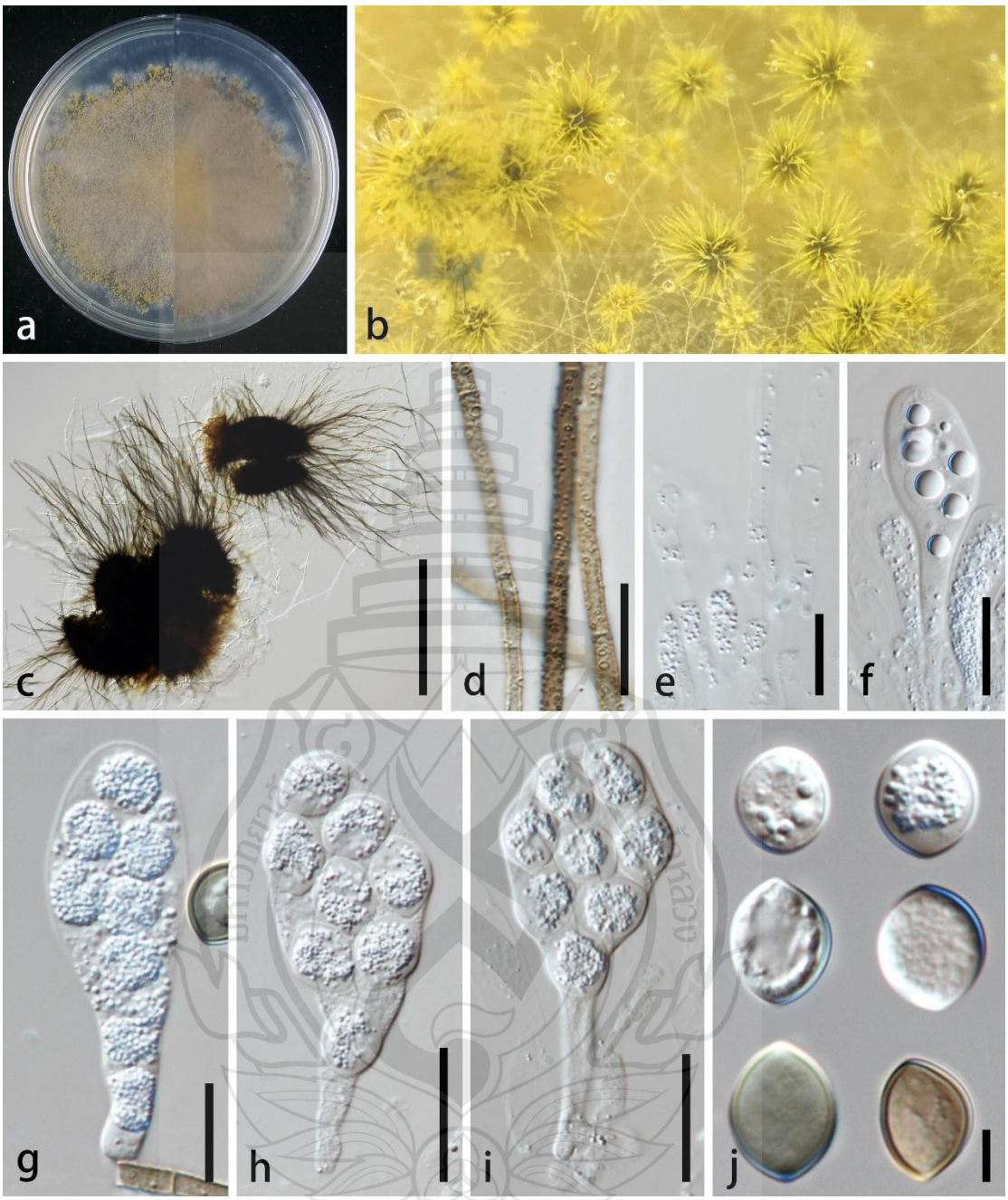


Figure 5.110 Maximum likelihood phylogeny based on the combined ITS, LSU, *rpb2*, and *tub2* sequences data of Chaetomiaceae



Note Tree rooted with *Pseudoechria longicollis* (CBS 368.52), *P. prolifica* (CBS 250.71). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strains from this study are shown in blue.

Figure 5.110 (continued)



Note a Culture characteristic on PDA. b Appearance of ascomata on substrate. c Ascomata. d Setae. e Paraphyses. f Paraphyses and asci. g–i Asci. j Ascospores. Scale bars: c = 500 µm, d–i = 20 µm, j = 5 µm.

Figure 5.111 *Chaetomium globosum* (MHZU 24-0298, new host record)

Humicola Traaen, Nytt Mag. Natur. 52: 31 (1914)

Notes – *Humicola* was introduced by Traaen (1914) with *H. fuscoatra* as the type species. Wang et al. (2019) refined *Humicola* based on morphology with molecular analyses using *rpb2*, *tub2*, ITS and LSU. *Humicola* species are usually found in soil, indoor environments, and compost habitats, where they occur as saprobes, pathogens, and endophytes (Wang et al., 2019). Currently, 104 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp), but only 21 species have available sequence data (Hyde et al., 2020; Wang et al., 2022).

Humicola wurfbainiae C.F. Liao & Doilom, sp. nov. Figure 5.112

Index Fungorum number: IF904031; Facesoffungi number: FoF 17932

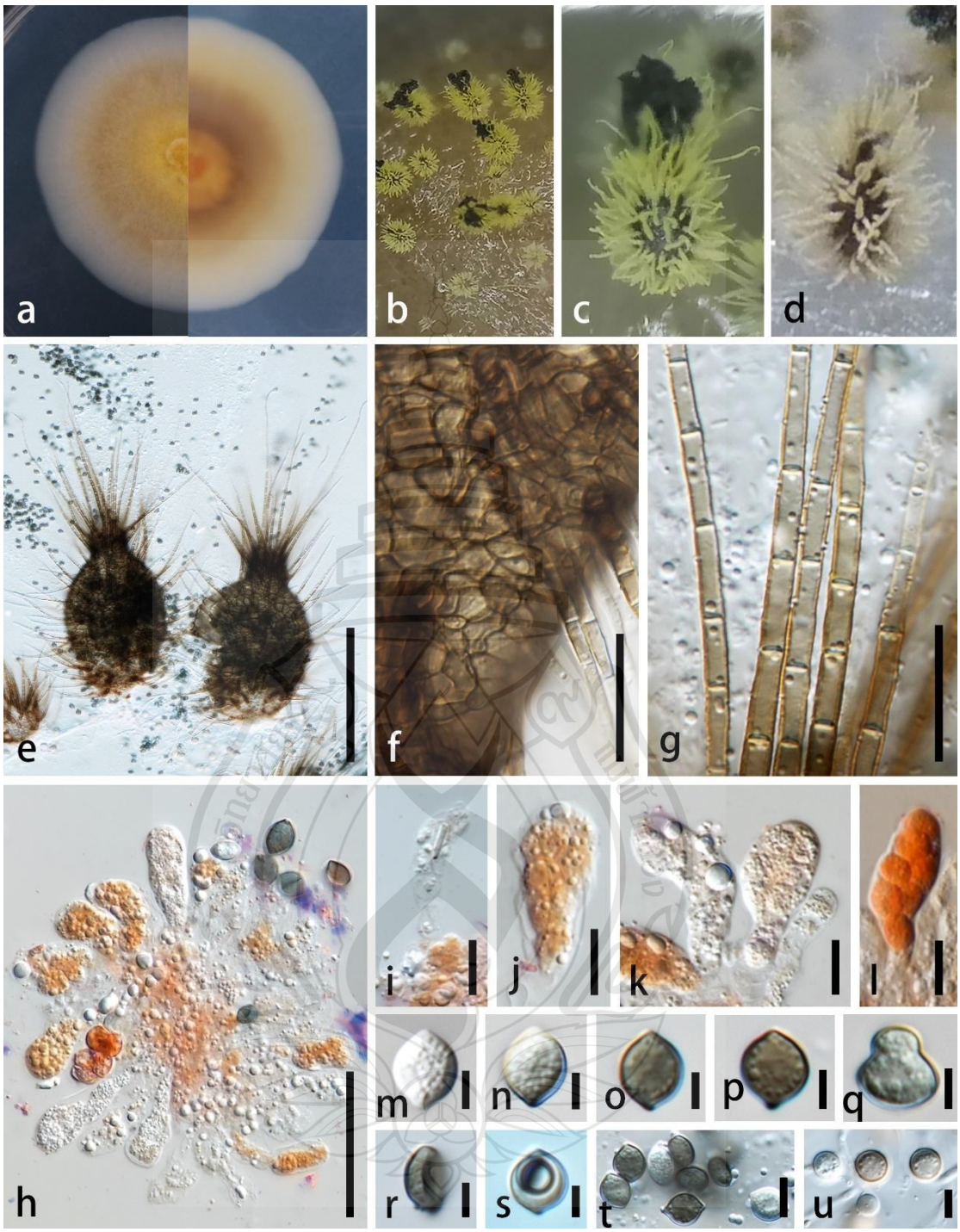
Endophytic in asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: On PDA after 1 month: *Ascomata* 127–288 × 112–221 μm ($\bar{x}$ = 219 × 155 μm, n = 20), superficial, solitary to gregarious, unilocular, coriaceous, ampulliform to ovoid, cylindrical to subglobose, yellowish to brown, ostiolate. *Peridium* membranaceous, composed of hyaline pseudoparenchymatous of inner cells, pigmented outer cells of *textura angularis* to *textura prismatica*. *Terminal hairs* 1.5–2.5 μm wide ($\bar{x}$ = 2 μm, n = 30) at apex, 5–8 μm wide ($\bar{x}$ = 6 μm, n = 30) near the base, straight to arcuate, hyaline to brown, narrowing towards the apex, septate, unbranched, smooth-walled; lateral hairs erect, septate, shorter than terminal hairs. *Asci* 30–45 × 10–15 μm ($\bar{x}$ = 37 × 12.5 μm, n = 30), 8-spored, unitunicate, crowded, clavate to pyriform, pedicellate, evanescent when mature. *Ascospores* 9–12 × 7–10 μm ($\bar{x}$ = 10.5 × 8.5 μm, n = 30), irregular with lateral bulge, broad fusiform to limoniform when mature, hyaline, becoming olivaceous to brown when mature, unicellular, aseptate, with a germ pore. *Chlamydospores* 10–12 μm wide ($\bar{x}$ = 11.5 μm, n = 20), globose, hyaline to brown. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 4.5–5.0 cm diameter in 1 week at 28 ± 2°C, moderately dense, flat, circular, with entire edge, yellowish to brown at the center, cream white at the edge from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic leaf of *Wurfbainia villosa*,

1 October 2022, C.F. Liao, AML23A-4 (MHZU 24-0155); living culture, ZHKUCC 24-0414.

Notes – Phylogenetic analyses revealed that ZHKUCC 24-0414 clusters within a subclade comprising *Humicola homopilata*, *H. sphaeralis*, and *H. wallefii* (Figure 5.110) and forms a sister lineage to *H. wallefii*. Morphologically, our isolate differs from *H. wallefii* in having obpyriform to obclavate or ampulliform ascomata, and straight to curved hairs, while *H. wallefii* has subglobose to ovoid ascomata, and flexuous to undulate hairs (Wang et al., 2019). Additionally, the ascospores of our isolate are sometimes irregular with a lateral bulge, which is not observed in *H. wallefii*, and they are larger compared to the latter (9–12 × 7–10 μm vs. 6.5–8 × 4.5–6.5 μm). Sequence comparison of ITS, LSU, *rpb2*, and *tub2* between our strain and *H. wallefii* CBS 147.67 revealed nucleotide differences of 1.86% (9/482 bp), 0.36% (2/550 bp), 5.97% (50/837 bp), 7.16% (27/377 bp), respectively. Comparison with *H. bomopilat* CBS 157.55 showed differences of 2.17% (10/460 bp) in ITS, 0.36% (2/550 bp) in LSU, 5.25% (44/837 bp) in *rpb2*, and 5.02% (21/418 bp) in *tub2*. Comparison with *H. sphaeralis* CBS 985.87 revealed differences of 1.91% (9/469 bp) in ITS, 0.36% (2/550 bp) in LSU, 6.21% (52/837 bp) in *rpb2*, 6.10% (23/377 bp) in *tub2*. Based on these morphological and molecular distinctions, we propose our isolate, *H. wurfbainiae*, as a novel species.



Note a Culture characteristic on PDA. b–d Appearance of ascomata on PDA after 1 month. e Ascomata. f Peridium. g Setae. h Asci and ascospores i–l Asci. m–t Ascospores. u Chlamydospores. Scale bars: e = 200 μm, f, g, i–l = 10 μm, h = 50 μm, m–s = 5 μm, t, u = 20 μm.

Figure 5.112 *Humicola wurfbainiae* (MHZU 24-0155, new host and geographical record)

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Notes – Xylariales was introduced by Eriksson & Winka (1997) as a single order placed in Xylariomycetidae. To date, three orders, Amphisphaeriales, Delonicicolales, and Xylariales are accepted in Xylariomycetidae with an estimated divergence time of approximately 152–187 million years ago (MYA) (Samarakoon et al., 2022). The Xylariales includes 22 accepted families: Anungitiomycetaceae, Barrmaeliaceae, Cainiaceae, Clypeosphaeriaceae, Coniocessiaceae, Diatrypaceae, Fasciatisporaceae, Graphostromataceae, Gyrotrichaceae, Hansfordiaceae, Hypoxylaceae, Lopadostomataceae, Microdochiaceae, Nothodactylariaceae, Pallidoperidiaceae, Polystigmataceae, Requienellaceae, Spirodecosporaceae, Vamsapriyaceae, Xyladictyochaetaceae, Xylariaceae, and Zygosporiaceae (Hyde et al., 2024).

Diatrypaceae Nitschke [as 'Diatrypeae'], Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869)

Notes – Diatrypaceae was introduced by Nitschke (1869) with the type genus *Diatrype*. Diatrypaceae species are distributed in aquatic, terrestrial, and marine habitats as saprobes, endophytes, and plant pathogens (Long et al., 2021; Samarakoon et al., 2022). Some species are known to cause perennial cankers, dieback, and discoloration in poplar trees, and grapevine trunk disease (Li et al., 2023; Kang et al., 2024). For example, *Cryptosphaeria pullmanensis* causes canker disease of willow and poplar in China (Ma et al., 2016). Twenty-six genera are accepted in Diatrypaceae (Li et al., 2023).

Peroneutypa Berl., Icon. fung. (Abellini) 3(3-4): 80 (1902)

Notes – *Peroneutypa* was introduced by Berlese (1902) and the type species, *P. bellula*, was designated by Rappaz (1987). *Peroneutypa* are commonly reported as saprobic on dead wood, while also acting as the endophytes and pathogens (Hyde et al., 2020). Some species are reported from marine environments and can produce polyketide- and terpenoid-derived metabolites (de Amorim et al., 2023). Currently, 67 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp), but only 16 species have been sequenced (Du et al., 2022). In this study, we provide the first description of an asexual morph for the genus *Peroneutypa*, represented by *Peroneutypa wurfbainiae* sp. nov., isolated from asymptomatic root of *Wurfbainia villosa*, as detailed below.

Peroneutypa wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.114

Index Fungorum number: IF904032; Facesoffungi number: FoF 17933

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

Holotype – MHZU 24-0226

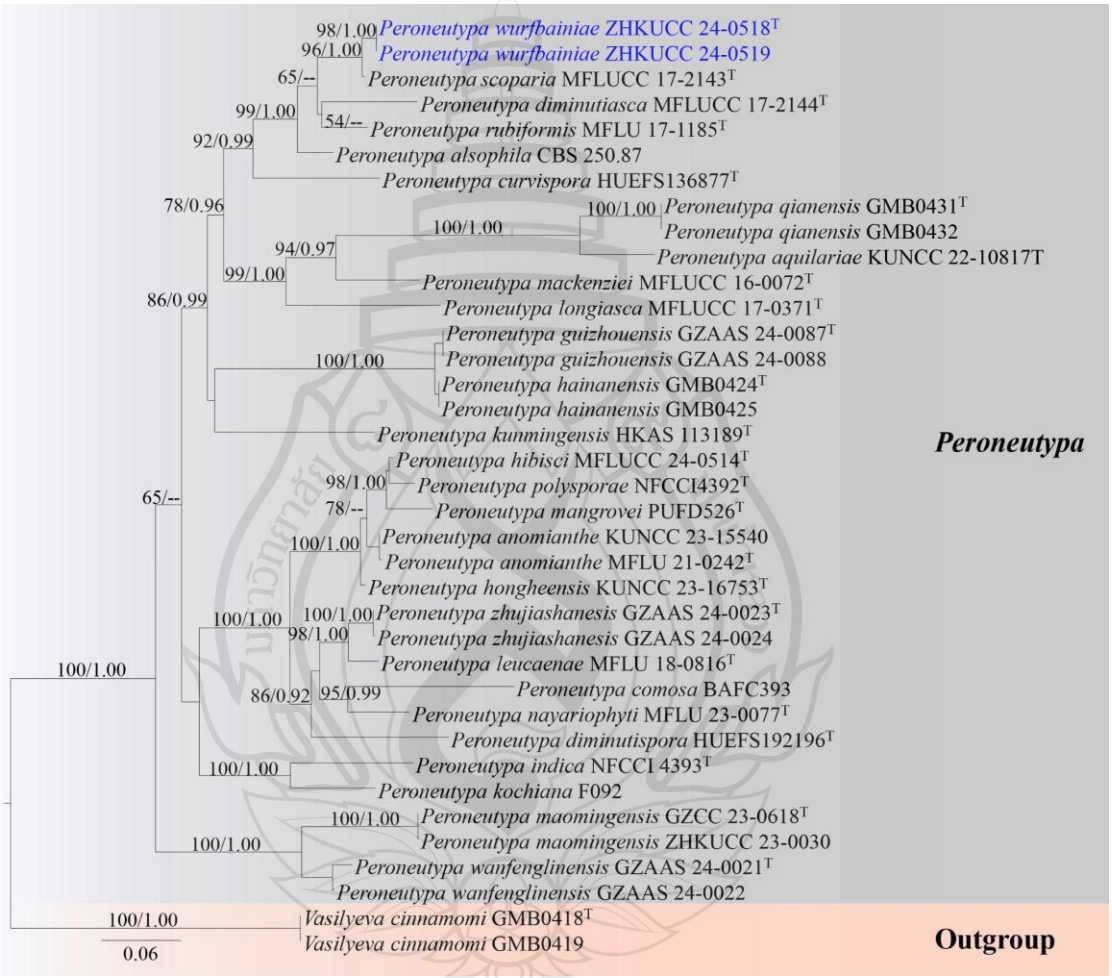
Endophytic associate on asymptomatic root of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: On PDA after 2 months: *Hyphae* hyaline, septate, branched, smooth-walled. *Conidiophores axis* 12 – 133 × 2 – 4 μm ($\overline{x}$ = 35 × 3 μm, n = 30), macronematous, mononematous, solitary or gregarious, straight to flexuous, rarely branched, hyaline, septate scattered, smooth-walled. *Conidiogenous cells* 17 – 61 × 1 – 3 μm ($\overline{x}$ = 37 × 2 μm, n = 30), polyblastic, integrated, terminal or intercalary, subcylindrical, subulate to corniform, hyaline, extending wavily toward apex or appearing jagged, tapering toward the apex, smooth-walled; conidiogenous loci occurring after the distal 1/2 to 2/3 portion. *Conidia* 3.5 – 5 × 2 – 4 μm ($\overline{x}$ = 4 × 2.5 μm, n = 30), ellipsoidal to oval, straight, aseptate, hyaline, thick-walled, smooth-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately dense, raised, fluffy, with fimbriate edge; mycelium initially white, developing pale brown to dark brown patches centrally from above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), asymptomatic root of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR03C-2 (MHZU 24-0226, holotype); ex-type culture, ZHKUCC 24-0518.

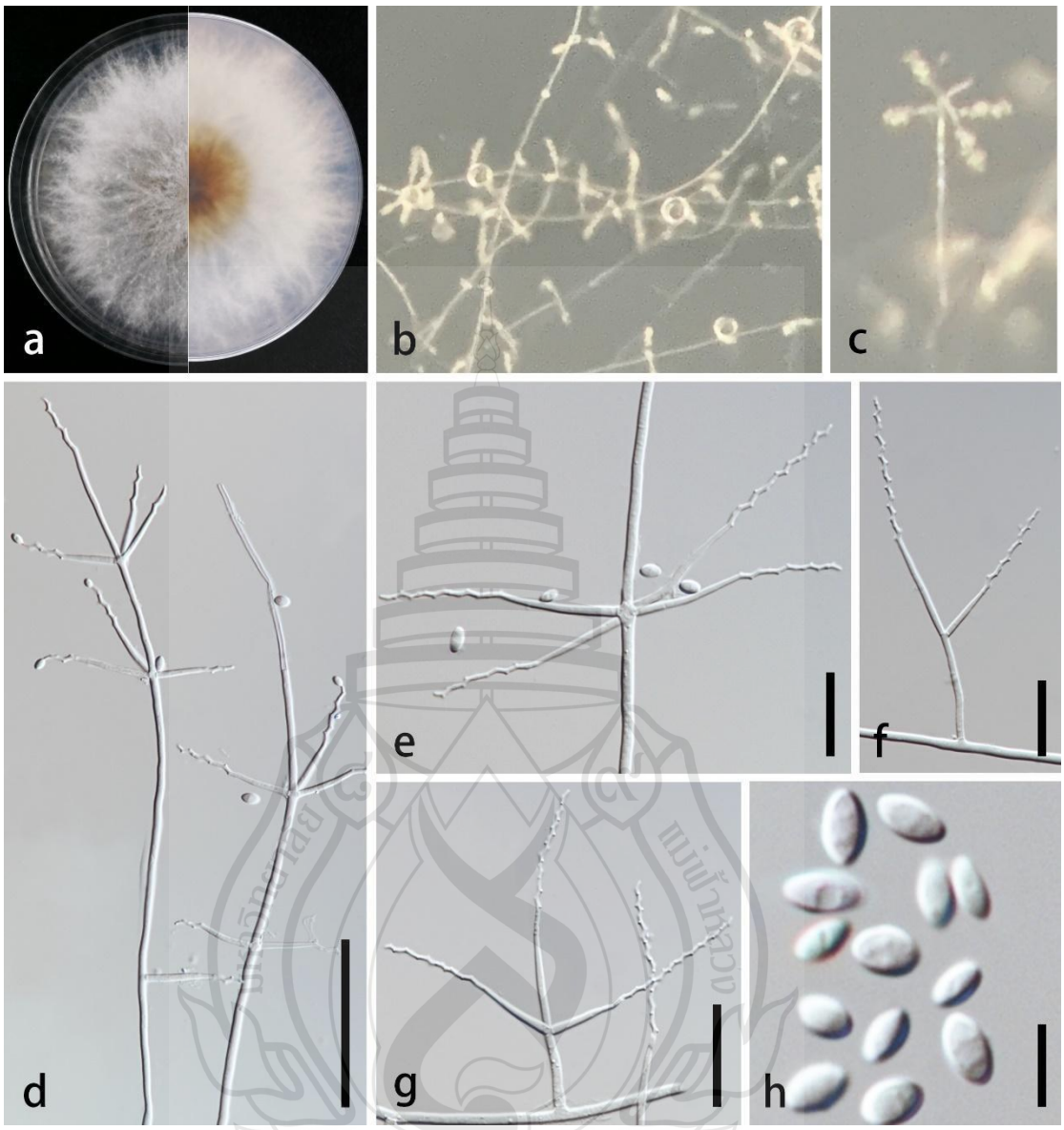
Notes – In the phylogenetic analyses, strain ZHKUCC 24-0518 formed a sister clade with *Peroneutypa scoparia* (MFLUCC 17-2143) with 96 ML/1.00 PP support (Figure 5.113). *scoparia* is known to exhibit both sexual and coelomycetous asexual morphs resembling Cytospora-like structures (Shang et al., 2018). In this study, *P. wurfbainiae* was found to produce a hyphomycetous asexual morph when cultured on PDA. The colony characteristics of our strain are consistent with those of *Peroneutypa*, showing dense, flat to effuse growth with fimbriate margins, and initially white mycelium (Shang et al., 2018). Furthermore, the ITS sequence of our strain

differs from that of *P. scoparia* by 2.96% (16/540 bp). However, the *tub2* sequence for *P. scoparia* is currently unavailable for comparison. Notably, this is the first report of a hyphomycetous asexual morph in this genus, characterized by solitary or gregarious, rarely branched, hyaline, septate conidiophores; hyaline, subcylindrical to subulate or corniform conidiogenous cells; and hyaline, ellipsoidal to oval conidia. Based on the morphological characteristics and molecular evidence, we propose *P. wurfbainiae* as a new species.



Note Tree rooted with *Vasilyeva cinnamomi* (GMB0418, GMB0419). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strain from this study is shown in blue.

Figure 5.113 Maximum likelihood phylogeny based on the combined ITS and *tub2* sequences data of *Peroneutypa*



Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d–g Conidiogenous cells with conidia. h Conidia. Scale bars: d = 50 μm, e–g = 20 μm, h = 10 μm.

Figure 5.114 *Peroneutypa wurfbainiae* (MHZU 24-0226, holotype)

Astrocystis Berk. & Broome, J. Linn. Soc., Bot. 14(no. 74): 123 (1873)

Notes – *Astrocystis* was introduced by Berkeley and Broome (1873) and typified by *A. mirabilis*. Species of this genus are mostly associated with monocotyledonous plants, particularly bamboo, and are distributed in tropical and subtropical regions (Hyde et al., 2020). The genus is known only for its sexual morph, characterized by

uni- or rarely multi-peritheciate superficial stromata, short stipe asci, with a relatively small apical apparatus, amyloid and stopper-shaped ascospores (Li et al., 2022). Currently, 45 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp), but only ten species have sequence data available (Li et al., 2022). In this study, we identified an endophytic isolate of *A. heterocyclae* from leaf of *Wurfbainia villosa*.

Astrocystis heterocyclae S.H. Long & Q.R. Li, in Li et al., Mycosphere 15(1): 307 (2024) Figure 5.116

Index Fungorum number: IF850409; Facesoffungi number: FoF 17934

Endophytic associated with asymptomatic leaf of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: Sporulating on the PDA after 2 of incubation. *Colonies* 1.5–3.5 µm wide ($\bar{x}$ = 2.5 µm, n = 30), superficial, pale brown spot, composed of numerous conidiophores and conidia. *Conidiophores* 38 – 152 × 3 – 6.5 µm ($\bar{x}$ = 75 × 4.5 µm, n = 30), micronematous, mononematous, gregarious, straight to flexuous, branched, hyaline to pale brown, septate, smooth-walled. *Conidiogenous cells* 17 – 67 × 3 – 5 µm ($\bar{x}$ = 34 × 3.5 µm, n = 30), monoblastic, integrated, terminal, clavate, hyaline, smooth-walled. *Conidia* 7 – 9 × 4 – 7 µm ($\bar{x}$ = 8 × 6 µm, n = 30), cuneiform, aseptate, pale brown, smooth-walled.

Culture characteristics – Colonies on PDA reaching 7.0 cm diameter in 4 weeks at 28 ± 2°C, moderately sparse, with radiating mycelia, irregular, filiform, cream-white from above and reverse, without pigmentation.

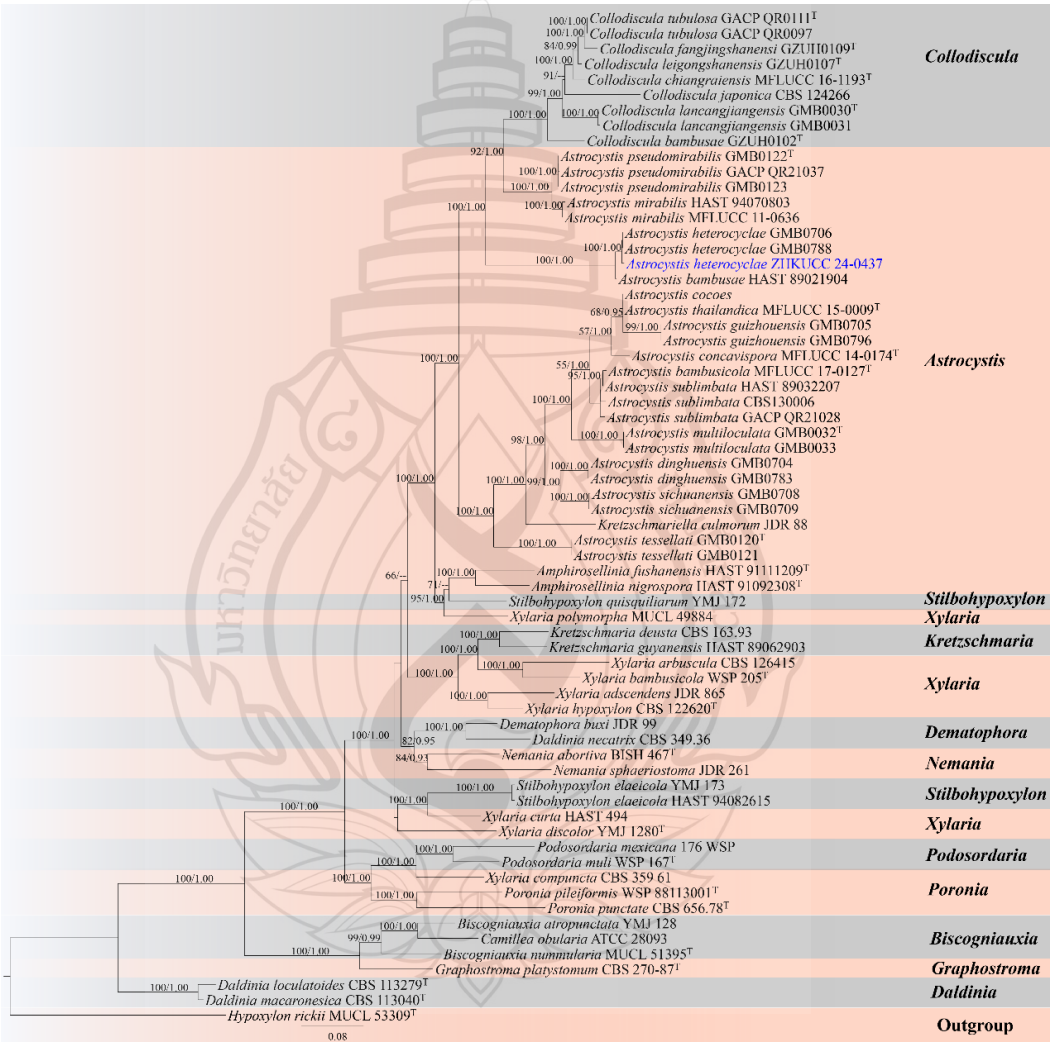
Material examined – China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), from asymptomatic leaf of *Wurfbainia villosa*, 29 October 2023, C.F. Liao, AML04C-3 (MHZU 24-0169); living culture, ZHKUCC 24-0437.

Known hosts (based on molecular data) – dead culms of *Phyllostachys heterocycla* (Li et al., 2024), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – China (Li et al., 2024; this study).

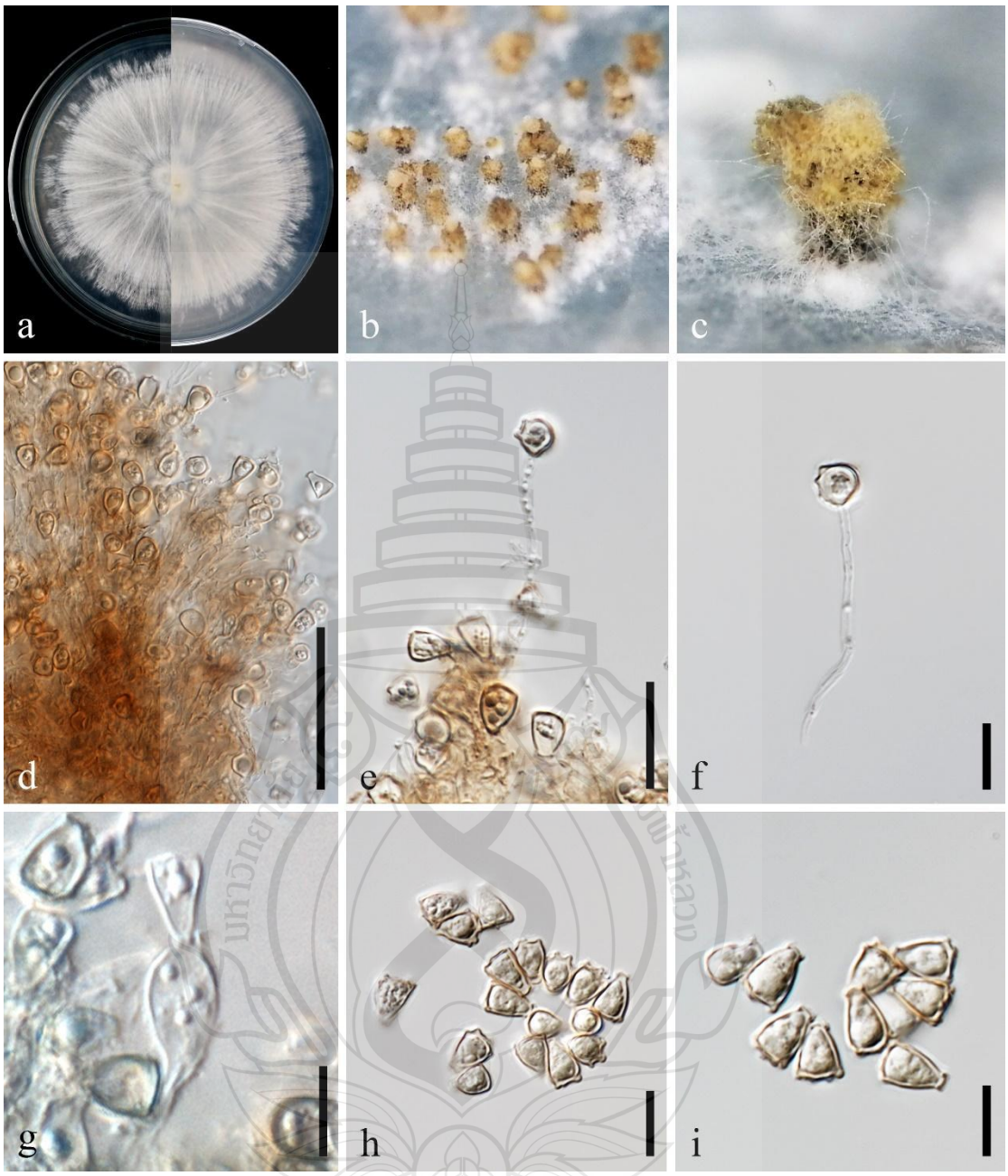
Notes – In the phylogenetic analyses, two strains (ZHKUCC 24-0437 and) formed a clade with *Astrocystis heterocyclae* (GMB0706, GMB0788) with 100% ML/0.99 PP support (Figure 5.115). The culture characteristics of our isolate produced

mycelia radiating outwards, irregular edge, cream-white coloration conform to those typical for the genus *Astrocystis* (Li et al., 2022). *Astrocystis heterocyclae* was originally isolated from the dead culms of *Phyllostachys heterocycle* (Li et al., 2024), but our strain was isolated from asymptomatic leaf of *Wurfbainia villosa*. We identify our isolate as *A. heterocyclae* based on the culture characteristics and phylogenetic analyses, and this is the first time that a hyphomycete asexual morph has been reported for this genus.



Note Tree rooted with *Hypoxylon rickii* (MUCL 53309). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "^{T}", strain from this study is shown in blue.

Figure 5.115 Maximum likelihood phylogeny based on the combined ITS, *rpb2*, and *tub2* sequences data of *Astrocystis*



Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d–f Conidiogenous cells with conidia. g Conidiogenous cell. h, i Conidia. Scale bars: d, e = 20 µm, f–i = 10 µm.

Figure 5.116 *Astrocystis heterocyclae* (MHZU 24-0169, new host record)

Basidiomycota R.T. Moore, Bot. Mar. 23(6): 371 (1980)

Agaricomycetes Doweld, Prosyllabus Tracheophytorum, Tentamen Systematis Plantarum Vascularium (Tracheophyta) (Moscow): LXXVIII (2001)

Notes – Agaricomycetes is a major class of Basidiomycota which comprises over 21,000 described species. Agaricales, as the largest order, includes more than 13,000 species (Kües & Navarro-González., 2015).

Polyporales Gäum., Vergl. Morph. Pilze (Jena): 503 (1926)

Notes – Many species are reported as the saprotrophs and grow on dead wood, logs, and some woody debris. They are important wood decomposers, and over 1800 species are recorded in the order (Money, 2016).

Phanerochaetaceae Jülich, Bibliotheca Mycologica 85:384. 1982.

Notes – Phanerochaetaceae was introduced by Jülich (1982) with the type genus Phanerochaete. Chen et al. (2021) accepted 23 genera in the Phanerochaetaceae, including *Alboefibula*, *Bjerkandera*, *Cremeoderma*, *Crepatura*, *Donkia*, *Efibulella*, *Gelatinofungus*, *Geliporus*, *Hapalopilus*, *Hyphodermella*, *Odontoefibula*, *Oxychaete*, *Phanerina*, *Phanerochaete*, *Phaeophlebiopsis*, *Phlebiopsis*, *Pirex*, *Porostereum*, *Quasiphlebia*, *Rhizochaete*, *Riopa*, *Roseograndinia*, *Terana*. Additional four genera (*Callosus*, *Cremeoefibula*, *Donkiella*, and *Pseudohyphodermella*) have since been included in this family (Xu et al., 2025), increasing the total number of accepted genera to 27 (Hyde et al., 2024).

Phanerochaete P. Karst., Bidrag till Kännedom av Finlands Natur och Folk 48:426. 1889.

Notes – *Phanerochaete* was introduced by Karst (1889) with *P. velutina* as the type species, representing the largest corticioid genus in Phanerochaetaceae (Zhang et al., 2023). *Phanerochaete* species are distributed worldwide, and over 100 species have been reported (Chen et al., 2021). *Phanerochaete chrysosporium* has been considered the model fungus for white rot fungi, especially because of its ability to produce high levels of ligninase enzyme, which promotes the rapid decomposition of lignin (Konan et al., 2024). In this study, we report *Phanerochaete chrysosporium* as a new host record isolated from stems and leaves of *Wurfbainia villosa.*

Phanerochaete chrysosporium Burds., in Burdsall & Eslyn, Mycotaxon 1(2): 124 (1974) Figure 5.118

Index Fungorum number: IF319705; Facesoffungi number: FoF 17935

Endophytic associated with asymptomatic stems and leaves of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* 1.0–3.0 µm wide ($\overline{x}$ = 2.3 µm, n = 30), hyaline, septate, branched, smooth-walled. *Conidiophores* and conidiogenous cells not observed. *Conidia* 10–13 × 7–12 µm ($\overline{x}$ = 11 × 9 µm, n = 30), unicellular, terminal, globose to subglobose, oval to ellipsoidal, pyriform to quadrangular, hyaline, aseptate, multi-guttulate, smooth- and thick-walled. *Arthrocondia* fusiform to cylindrical, intercalary, truncate at one or both ends. *Chlamydospores* 21–43 µm ($\overline{x}$ = 27 µm, n = 30), subhyaline, globose to subglobose, intercalary or terminal, thick-walled.

Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in 2 weeks at 28 ± 2°C, moderately sparse, flat, cream-white with many white granular zones from the above and reverse, without pigmentation.

Material examined – China, Guangdong Province, Yangjiang City, Yongning District (22.256185 N, 111609037 E), from asymptomatic stems of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMS06A-1 (MHZU 24-0231); living culture, ZHKUCC 24-0527; *ibid.*, from asymptomatic leaves of *Wurfbainia villosa*, 1 October 2022, C.F. Liao, AMR05A-1, living culture, ZHKUCC 24-0526.

Known hosts (based on molecular data) – *Populus fremontii* (Floudas & Hibbett, 2015), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – USA (Arizona, Illinois, Florida) (Floudas & Hibbett, 2015), China (Li et al., 2024; this study).

Notes – In the phylogenetic analyses, our strain (ZHKUCC 24-0527) clustered with *Phanerochaete chrysosporium* (He 5778 and HHB 6251) with strong statistical support (100% ML/0.99 PP) (Figure 5.117). Morphologically, our isolate resembles *P. chrysosporium* in having subhyaline, terminal, smooth, fusiform to cylindrical, and subhyaline, globose, intercalary or terminal, thick-walled chlamydospores (Hjortstam & Ryvarden, 2010). *Phanerochaete chrysosporium* was isolated from rice grains in Taiwan Province, China, and our strains were obtained from asymptomatic stems and leaves of *Wurfbainia villosa* in Guangdong Province, China. We identify our isolates as a new host record of *P. chrysosporium*.

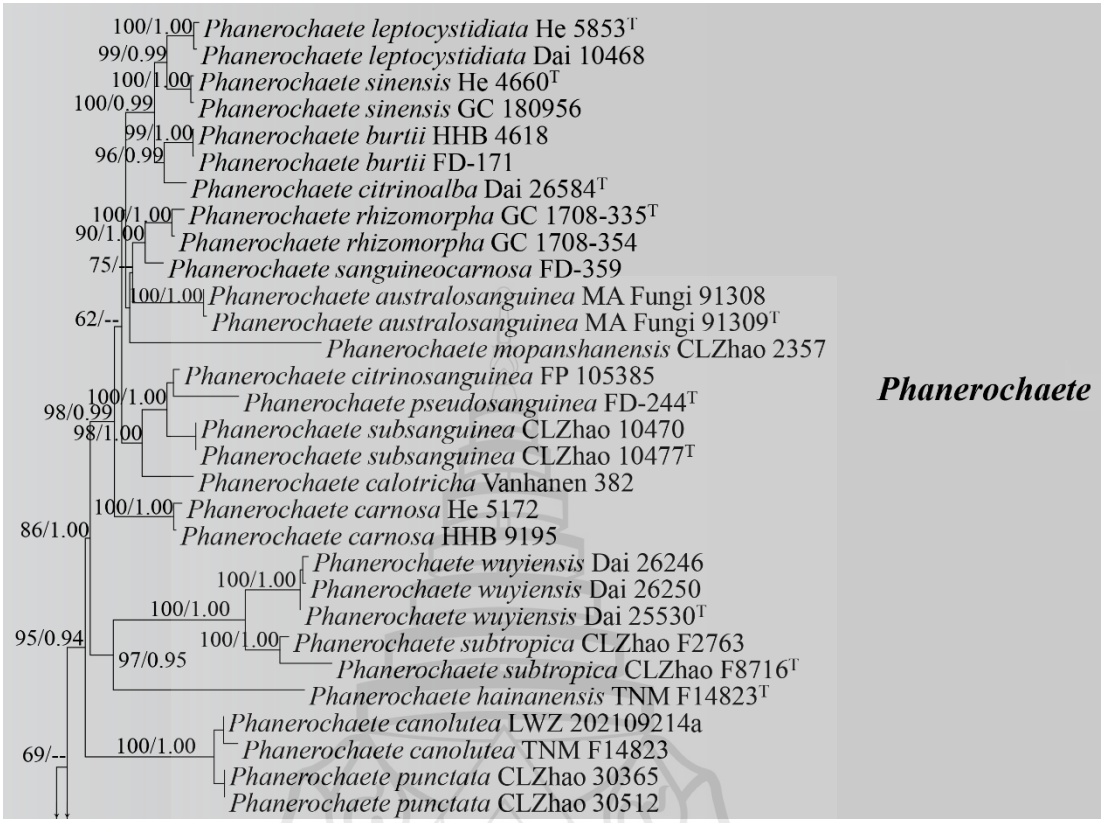
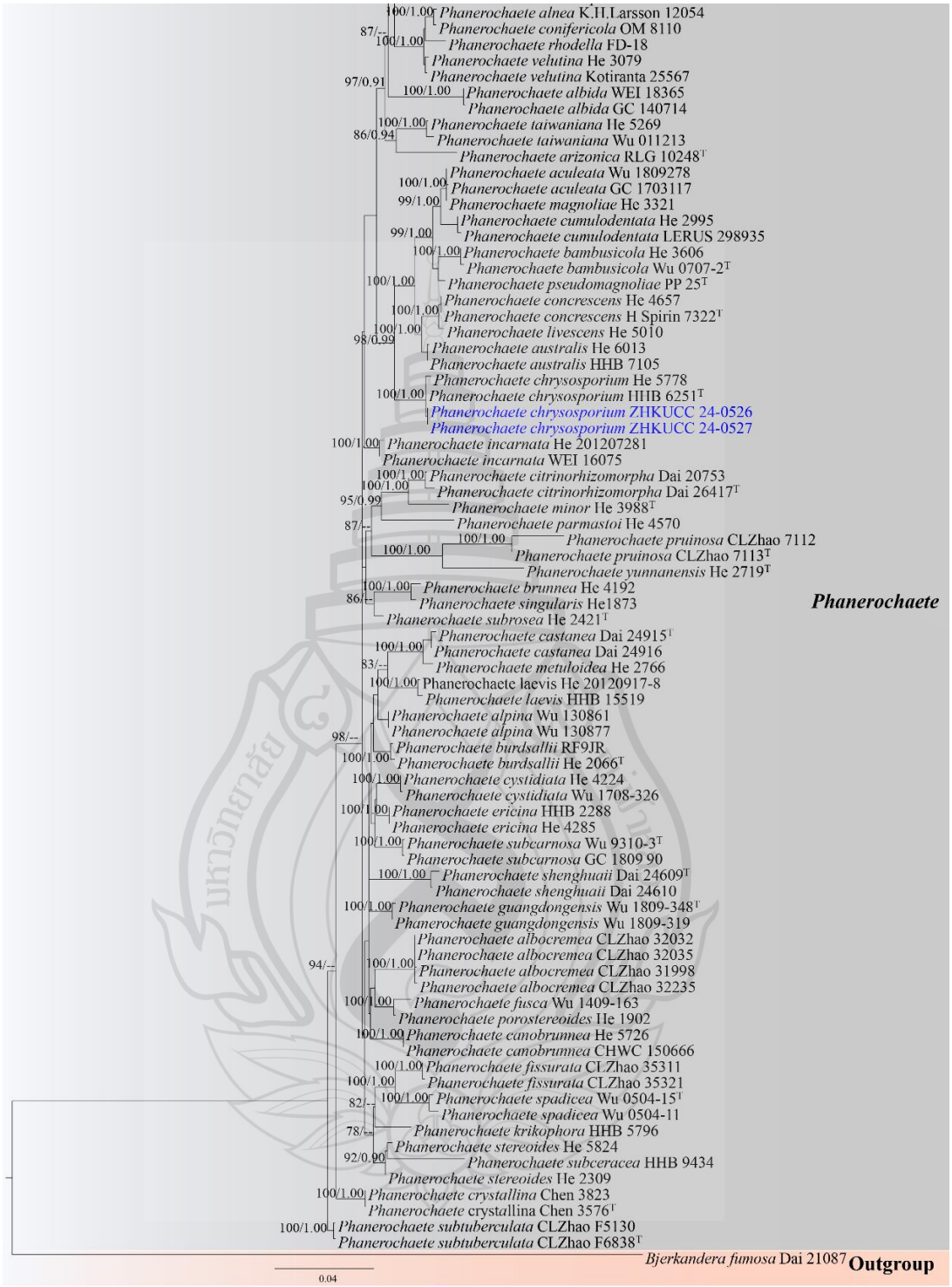
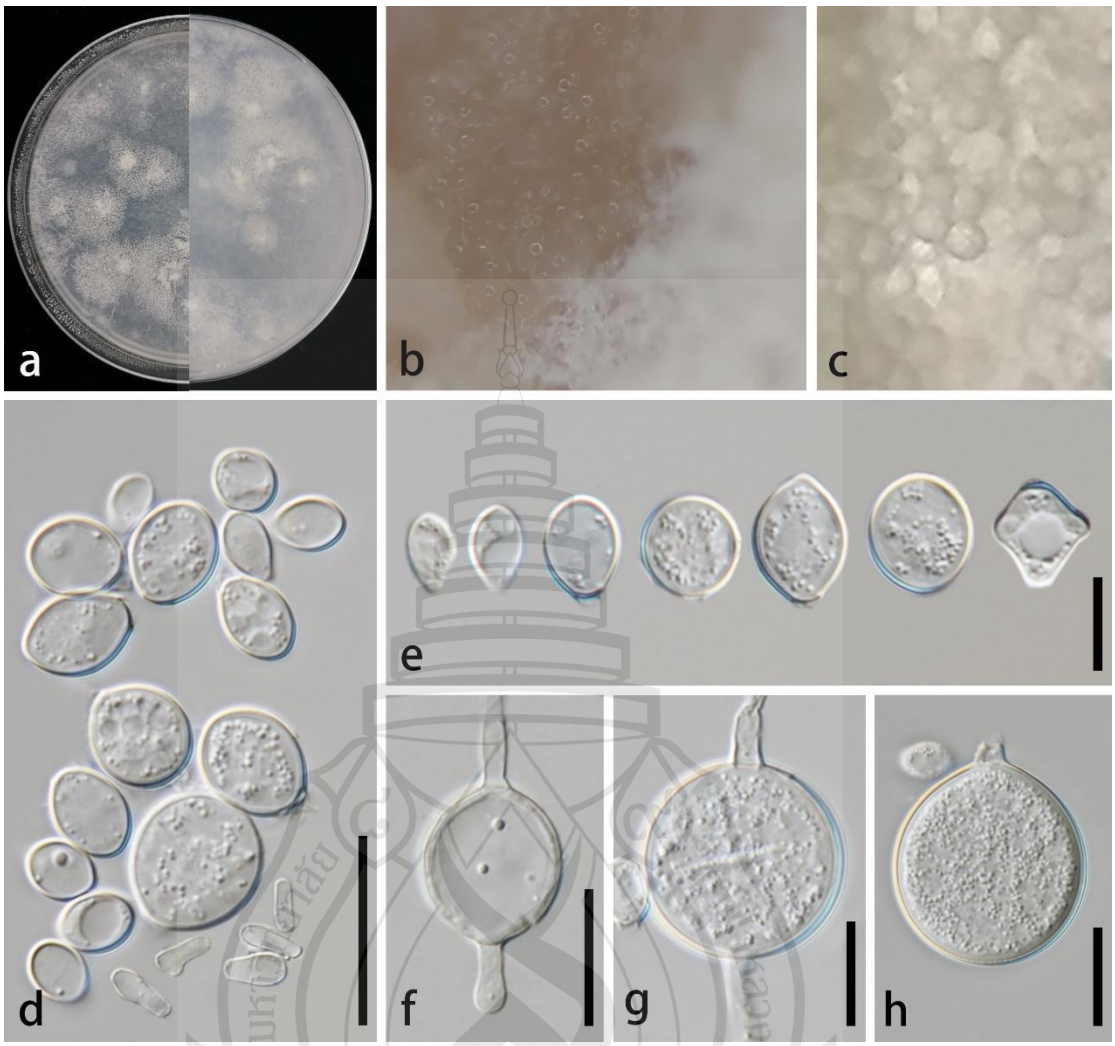


Figure 5.117 Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Phanerochaete*



Note Tree rooted with *Bjerkandera fumosa* (Dai 21087). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.117 (continued)



Note a Culture characteristic on PDA. b, c Conidia on aerial mycelia on PDA. d, e Conidia. f–h Chlamydospores. Scale bars: d, f–h = 20 μm, e = 10 μm.

Figure 5.118 *Phanerochaete chrysosporium* (MHZU 24-0231, new host record)

Mucoromycota Doweld, Prosyllabus Tracheophytorum, Tentamen Systematis Plantarum Vascularium (Tracheophyta) (Moscow): LXXVII (2001)

Mucoromycetes Doweld, Prosyllabus Tracheophytorum, Tentamen Systematis Plantarum Vascularium (Tracheophyta) (Moscow): LXXVII (2001)

Notes – Mucoromycetes includes one order (Mucorales), 17 families and 61 genera (Hyde et al., 2024). Zhao et al. (2023) estimated the divergence time of Mucoromycetes or Mucorales at 547 Mya.

Mucorales Dumort. [as 'Mucorarieae'], Analyse des familles des plantes: avec l'indication des principaux genres qui s'y rattachent: 73 (1829)

Notes – Members of Mucorales are ubiquitous environmental fungi that include human pathogens. Mucorales has been designated as high-priority pathogens by the WHO because they can infect various body organs in immunocompromised individuals, causing various clinical presentations, such as rhino-orbital-cerebral mucormycosis, gastrointestinal (Pham et al., 2023). Current, 17 families accepted in this order and estimated the divergence time of each family: Backusellaceae, Circinellaceae, Cunninghamellaceae, Lentamycetaceae, Lichtheimiaceae, Mucoraceae, Phycomycetaceae, Pilobolaceae, Protomycocladceae, Radiomycetaceae, Rhizomucoraceae, Rhizopodaceae, Saksenaeaceae, Syncephalastraceae, Syzygitaceae, Thermomucoraceae, and Mycocladaceae (sequence unavailable) (Zhao et al., 2023; Hyde et al., 2024).

Mucoraceae Fr. [as 'Mucoroidei'], Syst. mycol. (Lundae) 1: xlix (1821)

Notes – Members of Mucoraceae are commonly isolated as saprobic fungi with a worldwide distribution, typically found in soil, woody substrates, feces, hay, and air (Hurdeal et al., 2021). Species in this family can also be endophytes or human pathogens. *Mucor indicus* has been used in applications for food fermentation, organic acids as flavoring agents, traditional Chinese medicine to treat various diseases, such as leprosy, eczema, and abscesses (Deng et al., 2024). Currently, 20 genera are accepted in this family (Hyde et al., 2024).

Mucor P. Micheli, Nov. pl. gen. (Florentiae): 215 (1729)

Notes – *Mucor* represents the largest and most prominent genus in Mucorales. Species of *Mucor* have been isolated from various environments, including soil, indoor environment, clinical environment (Karimi & Zamani, 2013; Wagner et al., 2019). The role of *Mucor* in human life is extremely contradictory. Not only can it act as an opportunistic human pathogen, but it is also used in the fermentation of food in Asia and cheese ripening in French (Lebreton et al., 2020). *Mucor* is divided into six groups: *M. amphibiorum*, *M. flavus*, *M. hiemalis*, *M. mucedo*, *M. racemosus*, and *M. recurvus* (Walther et al., 2013), with 771 epithets are listed in Index Fungorum (https://www.indexfungorum.org/names/Names.asp). We report one new record of *M. nidicola* and a newly identified species, *M. wurfbainiae*, as endophytes isolated from fruits of the traditional Chinese medicinal plant *Wurfbainia villosa*.

Mucor nidicola A.A. Madden, Stchigel, Guarro, Deanna A. Sutton & Starks, Int. J. Syst. Evol. Microbiol. 62(7): 1712 (2012) Figure 5.120

Index Fungorum number: IF561980; Facesoffungi number: FoF 12291

Endophytic in asymptomatic fruit of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* branched, hyaline, septate, smooth-walled. *Sporangiophores* 2–17 μm wide ($\bar{x}$ = 9 μm, n = 30), erect, hyaline, branched, verrucose, with golden multi guttules, arising abundantly from aerial hyphae. *Sporangia* 9–51 × 8 – 47 μm ($\bar{x}$ = 25 × 23 μm, n = 30), globose, hyaline to yellow-brown, rapidly deliquescent. *Sporangiospores* 4–9 × 2–5 μm ($\bar{x}$ = 6 × 3 μm, n = 30), oval to ellipsoidal, hyaline, aseptate, smooth-walled.

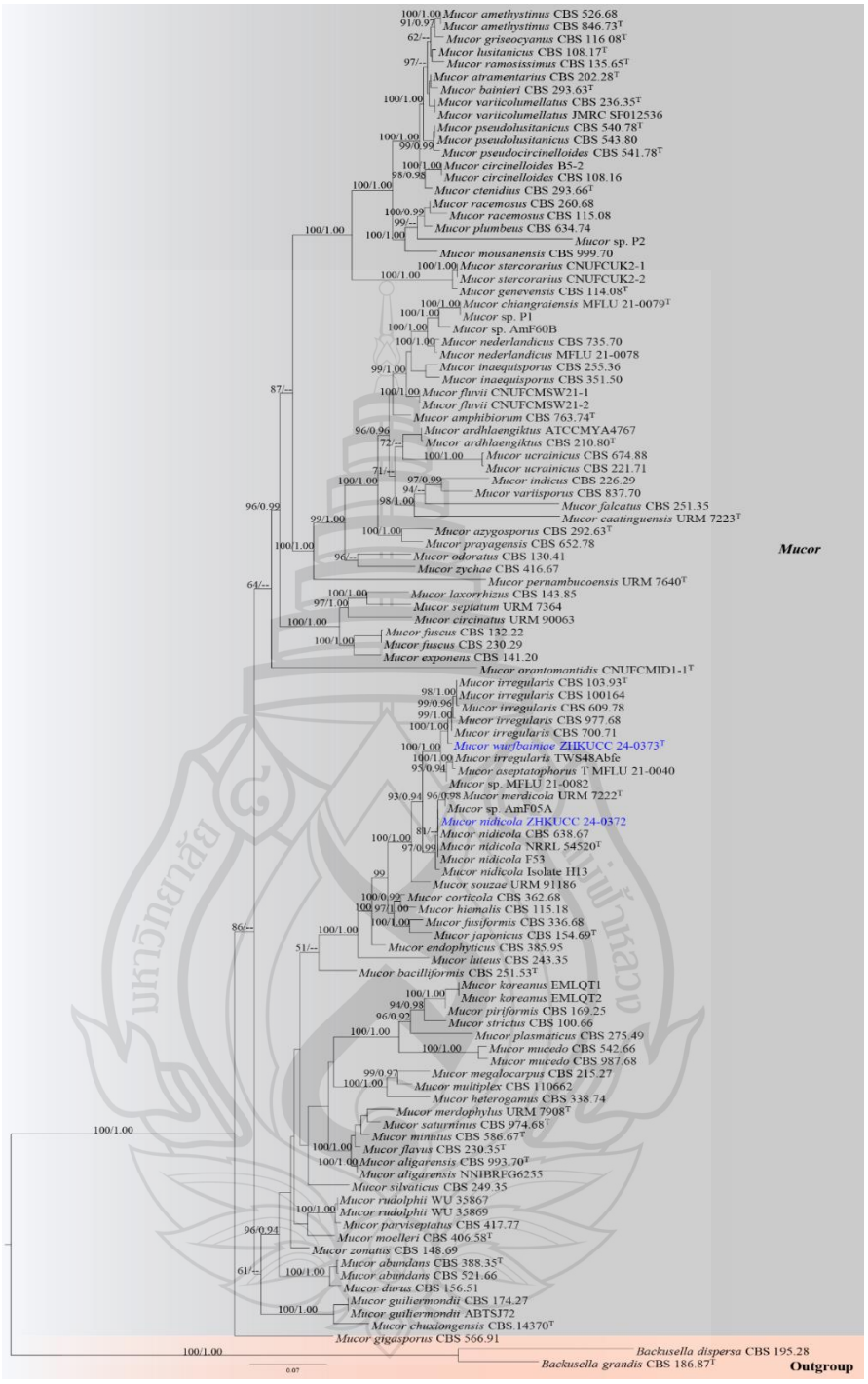
Culture characteristics – Colonies on PDA reaching 9.0 cm diameter in two weeks at 28 ± 2°C, moderately dense, raised, aerial hyphae sparse, filiform, initially white, becoming pale yellowish from above; pale yellowish from the reverse, no pigmentation.

Material examined –China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461°N, 111.938281°E), from asymptomatic fruit of *Wurfbainia villosa*, 30 October 2023, C.F. Liao, AMF19A (MHZU 24-0125); living culture, ZHKUCC 24-0372.

Known hosts (based on molecular data) – from a nest of the invasive paper wasp, *Polistes dominulus* (Madden et al., 2012), *Wurfbainia villosa* (this study).

Known distribution (based on molecular data) – Massachusetts (Madden et al., 2012), China (this study).

Notes – The phylogenetic analyses showed that our strain (ZHKUCC 24-0372) clustered closely with *Mucor nidicola* (H13) with 83% ML/0.96 PP support (Figure 5.119). Morphologically, our isolate produced characters resembling those of *M. nidicola*, including erect, brunched sporangiophores, globose, hyaline to yellow-brown sporangia, and ellipsoidal sporangiospores (Madden et al., 2012). *Mucor nidicola* was reported to grow on MEA media (Madden et al., 2012). Our isolate, cultured on PDA media, produced overlapping sized sporangiophores (2 – 17 μm wide vs. 10–15 μm) and similar sized sporangiospores (4 – 9 × 2 – 5 μm vs. 3–10×2–6 μm). The ITS, and LSU sequence of our strain (ZHKUCC 24-0372) comparison with *Mucor nidicola* (H13) revealed differences of 1.87% (10/533 bp), and 0.31% (3/955 bp), respectively. Hence, we identified our isolate as a new host record of *M. nidicola.*



Note Tree rooted with *Backusella dispersa* (CBS 195.28) and *B. grandis* (CBS 186.87). Support values shown at nodes (ML bootstrap ≥50% /BI posterior probability ≥0.95); hyphens indicate values below these thresholds. Type strains are marked with "T", strains from this study are shown in blue.

Figure 5.119 Maximum likelihood phylogeny based on the combined ITS and LSU sequences data of *Mucor*

Note a Culture characteristic on PDA for 1 month. b, c Focus on sporangia and sporangiospores. d Columella. e Sporangia and sporangiospores. f Sporangiophores. g Sporangiospores. Scale bars: d, e = 50 μm, f, g = 20 μm.

Figure 5.120 *Mucor nidicola* (MHZU 24-0125, new host record)

Mucor wurfbainiae C.F. Liao, Doilom & K.D. Hyde, sp. nov. Figure 5.121

Index Fungorum number: IF904033; Facesoffungi number: FoF 17936

Etymology – The epithet "*wurfbainiae*" is derived from the host genus, from which the holotype was isolated

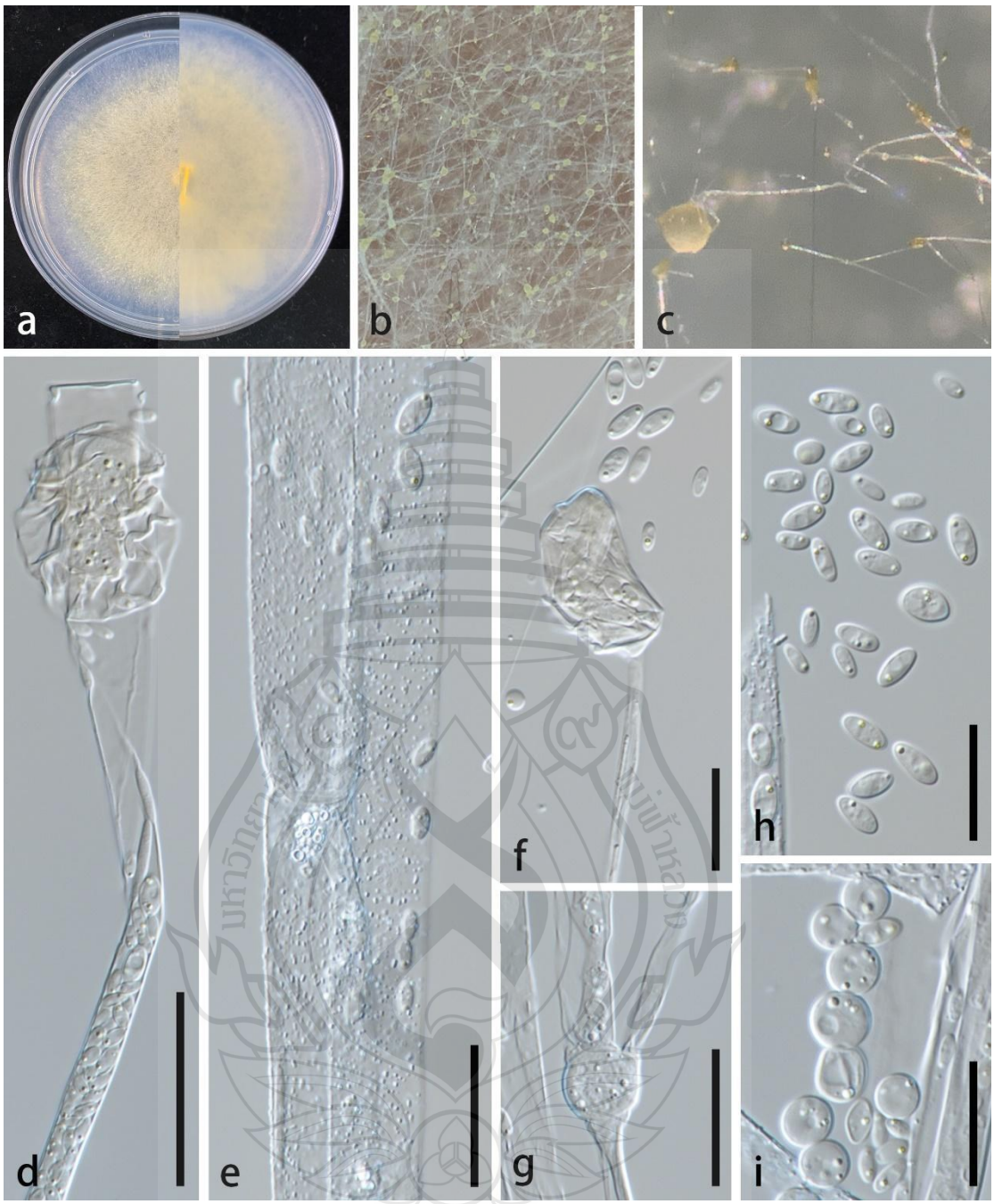
Holotype – MHZU 24-0126

Endophytic associated with asymptomatic fruit of *Wurfbainia villosa*. Sexual morph: Undetermined. Asexual morph: *Hyphae* wide, branched, hyaline, septate, smooth-walled. *Sporangiophores* 8 – 16 µm wide ($\overline{x}$ = 13 µm, n = 30) erect, hyaline, unbranched, smooth-walled in upper portion, verrucose in lower portion. *Sporangia* 18 – 33 × 14 – 25 µm ($\overline{x}$ = 27 × 20 µm, n = 30), globose, hyaline to yellow-brown, rapidly deliquescent, not observed columellae. *Sporangiospores* 3 – 11 × 2 – 10 µm ($\overline{x}$ = 6.5 × 4 µm, n = 30), oval to ellipsoidal, hyaline, aseptate, with 1–2-golden guttulate, smooth-walled. *Chlamydospores* 8 – 16 × 7 – 16 µm ($\overline{x}$ = 13 × 12 µm, n = 30), globose, hyaline, multi-guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 8.5–9.0 cm diameter in 14 days at 28 ± 2°C, moderately dense, raised, aerial hyphae sparse, circular, filiform, yellowish at the center, cream-white at the edge from above and reverse, without pigmentation.

Material examined –China, Guangdong Province, Yangjiang City, Chunwan Town (22.436461 N, 111.938281 E), from asymptomatic fruit of *Wurfbainia villosa*, 29 October 2023, C.F. Liao, AMF36B (MHZU 24-0126, holotype); ex-type culture, ZHKUCC 24-0373.

Notes – The phylogenetic analyses showed that our strain (ZHKUCC 24-0373) clusters with *Mucor irregularis* (CBS 103.93, CBS 977.68, CBS 700.71, CBS 100164, CBS 609.78) with 98% ML/1.00 PP support (Figure 5.119). Morphologically, our isolate resembles *M. irregularis* in having globose sporangia and ellipsoidal sporangiospores, with overlapping sporangiospores size (3 – 11 × 2 – 10 µm vs. 7.5–10 × 12–15 µm) (Sarbhoy, 1965). However, our isolate can be easy distinguished from *M. irregularis* by having smaller sporangia (18 – 33 × 14 – 25 µm ($\overline{x}$ = 27 × 20 µm vs. 73–160.6 µm). In addition, we did not observe columellae, and found the hyaline, globose chlamydospores. In contrast, *M. irregularis* has variable, oval, globose, or pyriform columellae, but did not observe the chlamydospores. The ITS, and LSU sequence of our strain (ZHKUCC 24-0372) comparison with *Mucor irregularis* (CBS 103.93) revealed differences of 4.30% (23/534 bp) and 0.43% (4/923 bp), respectively. We designate our isolate as a new species.



Note a Culture characteristic on PDA for 1 month. b, c Focus on sporangia and sporangiospores. d, f Columella with sporangiospores. e Sporangiophores. g, i Chlamydospores. h Sporangiospores. Scale bars: d = 50 µm, e–i = 50 µm.

Figure 5.121 *Mucor wurfbainiae* (MHZU 24-0126, holotype)

5.3 Global Checklist

A compilation of fungal taxa associated with *Wurfbainia villosa* is provided in Table 5.1. This checklist integrates records from the present study and published literature, covering diverse geographic regions, plant tissues, and ecological roles. For each taxon, the table lists its distribution (country and province), host tissue from which it was recorded, lifestyle (e.g., endophyte, pathogen, or saprotroph), and the corresponding climate zone. This dataset offers a comprehensive overview of the known fungal diversity on *W. villosa* and serves as a reference point for further studies on host–fungus associations, biogeography, and ecological adaptation**.**

In this study, we also summarize the global distribution of fungal lifestyles (a) and the frequency of fungal isolation from different host tissues (b) associated with *Wurfbainia villosa* (Figure 5.122). Endophytes accounted for the largest proportion of records (46%), followed by potential pathogens (23%), fungi with various lifestyles (15%), saprobes (13%), and epiphyllous fungi (3%). In terms of host tissue association, the majority of isolates were obtained from leaves (39%), with roots and stems each contributing 19%, various tissues 14%, and fruits 9%. These patterns highlight the predominance of endophytic fungi and the importance of leaf-associated communities in the fungal diversity of *W. villosa*.

Table 5.1 Global checklist of fungal taxa associated with *Wurfbainia villosa* (species name, country, life mode, climate) do analysis, like fungi from different country, life model, climate, order

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Acrocalymma guangdongensis	China, Guangdong	Root	EN	Subtropical	This study
Acrocalymma sp.	China, Guangdong	Root/stem	EN	Subtropical	This study
Acrocalymma wurfbainiae	China, Guangdong	Fruit	EN	Subtropical	This study
Acrostalagmus annulatu	China, Guangdong	Leaf	EN	Subtropical	This study

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Apiospora endophytica	China, Guangdong	Leaf	EN	Subtropical	Liao et al. (2023)
Apiospora guangdongensis	China, Guangdong	Leaf	EN	Subtropical	Liao et al. (2023)
Apiospora phyllostachydis	China, Guangdong	Leaf	EN	Subtropical	This study
Apiospora wurfbainiae	China, Guangdong	Leaf	EN	Subtropical	Liao et al. (2023)
Bipolaris bicolor	China, Guangdong	Leaf	EN	Subtropical	This study
Bipolaris wurfbainiae	China, Guangdong	Leaf/root	EN	Subtropical	This study
Brevistachys wurfbainiae	China, Guangdong	Stem	S	Subtropical	Liao et al. (2025)
Bulbopyricularia guangdongensis	China, Guangdong	Leaf/Stem/ fruit/root	EN/S/P	Subtropical	This study
Bulbopyricularia wurfbainiae	China, Guangdong	Leaf	EN/P	Subtropical	This study
Bussabanomyces wurfbainiae	China, Guangdong	Stem	EN/S/P	Subtropical	This study
Chaetomium globosum	China, Guangdong	Leaf	P	Subtropical	This study
Cladosporium oxysporum	China		P		Zhang (2003)
Colletotrichum plurivorum	China, Guangdong	Leaf/Fruit	EN/P	Subtropical	This study
Colletotrichum siamense	China, Guangdong, Xishuangbanna	Stem/Leaf/ Root	EN/P	Subtropical / Tropical	This study
Cladosporium variabile	China			Tropical	Zhuang (2001)
Colletotrichum capsici	China		P	Tropical	Zhuang (2001)

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Colletotrichum fructicola	China, Guangxi, Guangdong, Xishuangbanna	Leaf, stem, fruit	EN/P	Subtropical / Tropical	Song et al. (2021), this study
Colletotrichum gloeosporioides	China		P	Tropical	Zhuang (2001)
Colletotrichum zingiberis	China	leaf	P	Tropical	Zhuang (2001)
Corynespora cassiicola	China, Guangdong	Root/Leaf	EN/P	Subtropical	This study
Corynespora wurfbainiae	China, Guangdong	Root/Leaf/ Root	EN/P	Subtropical	This study
Curvularia geniculata	China, Guangdong	Root	EN	Subtropical	This study
Curvularia plantarum	China, Guangdong	Leaf	P	Subtropical	This study
Curvularia wurfbainiae	China, Guangdong	Stem	EN	Subtropical	This study
Dematipyriforma wurfbainiae	China, Guangdong	Stem	EN	Subtropical	This study
Diaporthe neoceratozamiae	China, Guangdong	Leaf	P	Subtropical	This study
Diaporthe neohongkongensis	China, Guangdong	Leaf	P	Subtropical	This study
Diaporthe neosiamensis	China, Guangdong	Root	EN/P	Subtropical	This study
Diaporthe kochmanii	China, Guangdong	Fruit		Subtropical	This study
Diaporthe loculata	China, Guangdong	Fruit		Subtropical	This study
Diaporthe yangjiangensis	China, Guangdong	Fruit		Subtropical	This study
Diaporthe wurfbainiae	China, Guangdong	Leaf		Subtropical	This study

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Dictyoarthrinium wurfbainiae	China, Yunnan	Stem	S	Tropical	This study
Epicoccum thailandicum	China, Guangdong	Leaf	P	Tropical	Wang et al. (2023)
Fusarium solani	China		P	Tropical	Zhuang (2001)
Gonatopyricularia amomi	China	Leaf	P	Tropical	Zhuang (2001), Bussaban et al. (2002)
Humicola wurfbainiae	China, Guangdong	Leaf	EN	Subtropical	This study
Immersiella wurfbainiae	China, Guangdong	Stem	S	Subtropical	This study
Lasiodiplodia wurfbainiae	China, Guangdong	Root	EN/S	Subtropical	This study
Micropeltis amomi	Thailannd	Leaf	EP	Tropical	Zeng et al. (2019)
Mucor wurfbainiae	China, Guangdong	Fruit	EN	Subtropical	This study
Mucor nidicola	China, Guangdong	Fruit	EN	Subtropical	This study
Musicillium tropicale	China, Guangdong, Xishuangbanna	Stem	S	Subtropical / Tropical	This study
Muyocopron laterale	China, Guangdong	Leaf	P	Subtropical	This study
Musidium wurfbainiae	China, Guangdong, Xishuangbanna	Leaf/Stem/ Fruit/Root	EN/S/P	Subtropical / Tropical	This study
Neoroussoella leucaenae	China, Guangdong	Leaf	EN	Subtropical	This study
Nigrospora camelliae-sinensis	China, Guangdong	Leaf	P	Subtropical	This study
Nigrospora chinensis	China, Guangdong	Leaf	P	Subtropical	This study

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Nigrospora guangdongense	China, Guangdong	Root	EN	Subtropical	This study
Nigrospora oryzae	China, Guangdong	Stem	EN	Subtropical	This study
Nigrospora sphaerica	China, Guangdong	Leaf	EN	Subtropical	This study
Nigrosynnema guangdongense	China, Guangdong	Stem	S	Subtropical	Liao et al. (2025)
Penicillium allaniae	China, Guangdong	Root	EN	Subtropical	This study
Penicillium guangdongensis	China, Guangdong	Root	EN	Subtropical	This study
Penicillium meleagrinum	China, Guangdong	Root	EN	Subtropical	This study
Penicillium polonicum	China, Guangdong	Stem	EN	Subtropical	This study
Penicillium wurfbainiae	China, Guangdong	Root	EN	Subtropical	This study
Periconia endophytica	China, Guangdong	Leaf	EN	Subtropical	Liao et al. (2024)
Periconia epilithographicola	China, Guangdong	Stem	EN	Subtropical	This study
Periconia neoyangjiangensis	China, Xishuangbanna	Leaf	S	Tropical	This study
Periconia wurfbainiae	China, Guangdong	Stem	S	Subtropical	Liao et al. (2024)
Periconia yangjiangensis	China, Guangdong	Stem	S	Subtropical	Liao et al. (2024)
Peroneutypa wurfbainiae	China, Guangdong	Root	EN	Subtropical	This study
Phanerochaete chrysosporium	China, Guangdong	Stem	EN	Subtropical	This study
Phyllosticta capitalensis	China, Guangdong	Leaf	EN	Subtropical	This study

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Pseudocercospora amomi	India	Leaf	P	Tropical	Liu and Guo (1998)
Pseudopestalotiopsis avicenniae	China, Guangdong	Root	EN	Subtropical	This study
Purpureocillium lilacinum	China, Guangdong	Stem	EN	Subtropical	This study
Pyrenochaetopsis endophytica	China, Guangdong	Stem	EN/P	Subtropical	This study
Pyrenochaetopsis guangdongensis	China, Guangdong	Leaf/Stem	EN/P	Subtropical	This study
Pyrenochaetopsis wurfbainiae	China, Guangdong	Leaf/Stem	P	Subtropical	This study
Pyricularia costina	China, Guizhou	Leaf	P	Subtropical	Li et al. (2010)
Rhizoctonia solani	China		P	Tropical	Zhuang (2001)
Roussoella wurfbainiae	China, Guangdong	Stem	S	Subtropical	This study
Sarocladium wurfbainiae	China, Xishuangbanna	Stem/fruit/ root	EN/S	Tropical	This study
Scolecopeltidium menglaense	China, Xishuangbanna	Leaf	EP	Tropical	Zeng et al. (2019)
Scolecopeltidium wangtianshuiense	China, Xishuangbanna	Leaf	EP	Tropical	Zeng et al. (2019)
Septoria amomi	China	Leaf	P	Tropical	Zhuang (2001)
Setophoma wurfbainiae	China, Guangdong	Root	EN	Subtropical	Liao et al. (2024)
Talaromyces dimorphus	China, Guangdong	Root	EN	Subtropical	This study
Talaromyces wurfbainiae	China, Guangdong	Root	EN	Subtropical	This study
Tetraploa wurfbainiae	China, Guangdong	Stem/Root	S	Subtropical	Liao et al. (2024)
Torula wurfbainiae	China, Guangdong	Stem	S	Subtropical	This study

Table 5.1 (continued)

Taxa	Country, province	Plant tissue	Lifestyle	Climate zone	Reference
Trichoderma guangdongensis	China, Guangdong	Root	EN	Subtropical	This study
Trichoderma wurfbainiae	China, Guangdong	Root	EN	Subtropical	This study

Notes EN=endophytes, EP= epiphytes, P= associated with lesion, S=saprobes

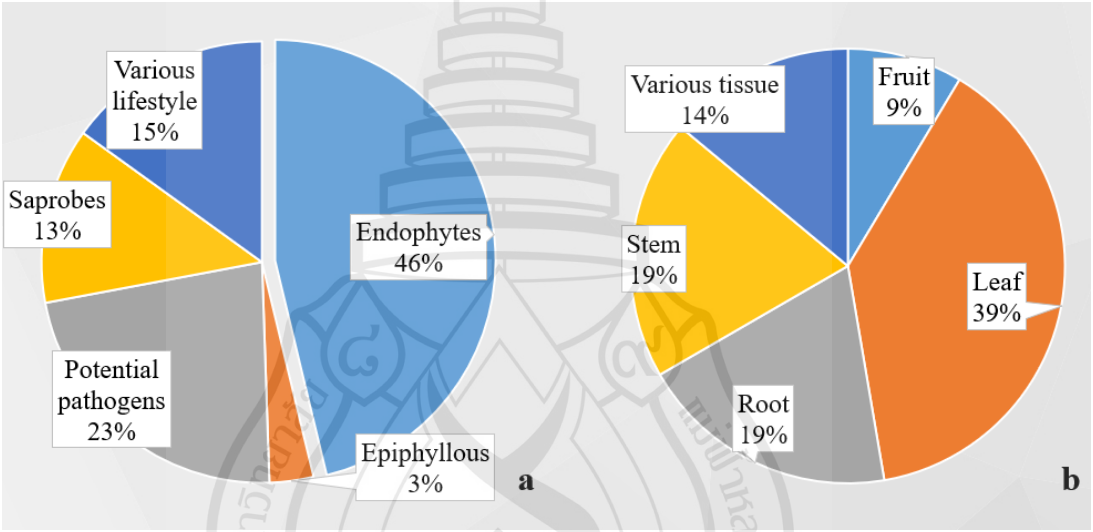


Figure 5.122 a Fungal lifestyle in global distribution; b Fungal isolation frequence in global distribution

5.4 Discussion

In this study, we investigated fungal species with diverse ecological lifestyles associated with different tissues of *Wurfbainia villosa* in Guangdong and Yunnan provinces. Our collection yielded 503 fungal strains, representing 77 species from 41 genera in 32 families. Most species belonged to Sordariomycetes (38 species), followed by Dothideomycetes (29 species), Eurotiomycetes (7 species), Agaricomycetes (1 species) and Mucoromycetes (2 species). The present study revealed significant novel diversity, including two new genera, 47 new species, 31 new host/geographical records, and one new combination. Among the isolates, 30% endophytic species isolated from asymptomatic

tissues failed to sporulate despite employing multiple sporulating methods and conditions (data not shown), and the genera that are most difficult to sporulate include *Xylaria*, *Cercospora*, *Pseudocercospora*, and *Ceratobasidium*. *Wurfbainia villosa* is a famous Chinese traditional plant. However, most studies have focused on its cultivation, phytochemistry, and secondary metabolites (Zeng et al., 2022; Wu et al., 2023). Zhang et al. (2010) isolated endophytic fungi from *Wurfbainia villosa*, but their taxonomic study relied solely on morphological identification, without systematic fungal identification. Importantly, Zhang's study revealed that the leaves harbor the richest diversity of endophytic fungi, followed by the roots and stems. Among these, *Colletotrichum* and *Phyllosticta* were identified as dominant genera.

Our study reveals *Colletotrichum*, *Bulbopyricularia*, *Fusarium*, and *Diaporthe* were identified as the dominant genera. We documented ten fungal species (e.g., *Bulbopyricularia guangdongensis*, *Bussabanomyces wurfbainiae*, *Corynespora cassiicola*, *Curvularia geniculata*, *Muyocopron laterale*, *Neomusidium wurfbainiae*, *Nigrospora camelliae-sinensis*, *Nigrospora oryzae*, *Nigrospora sphaerica*, *Bulbopyricularia guangdongensis*) (Table 4.1) capable of transitioning between endophytic, saprobic, and potentially pathogenic roles on *Wurfbainia villosa*, reflecting their ecological plasticity. Furthermore, 29 endophytic fungi transition to others two lifestyles (saprobic or potentially pathogenic). Such adaptability may be driven by environmental factors, host physiology, or fungal genomic flexibility, enabling survival under varying nutrient conditions. For example, endophytic-pathogenic shifts, such as *Chaetomium globosum* and *Curvularia plantarum* exhibited dual endophytic and pathogenic behaviors, suggesting that host immune status or environmental stress may trigger virulence. This aligns with evidence that some endophytes can become opportunistic pathogens under specific conditions (Liao et al., 2025). Additionally, several *Colletotrichum* species in this study, including *Colletotrichum siamense*, *C. plurivorum*, *C. fructicola*, were isolated from both asymptomatic and symptomatic tissues of *Wurfbainia villosa* and were found to produced infection structures such as appressoria. This evidence suggests that *Colletotrichum* may act as a latent pathogen, usually existing in a symbiotic, latent, or neutral state before transitioning to a pathogenic role under favorable conditions. Furthermore, pathogenicity test, metabolite

profiling, and genomic analyses are needed to better understand the ecological and health implications of some species such as *S. kiliense* in medicinal plants.

The fungal species were isolated across leaves, stems, roots, and fruits of *Wurfbainia villosa*, with most species isolated only from specific plant organs, while certain species were found in overlapping plant tissues. For example, *Astrocystis heterocyclae*, *Bipolaris bicolor*, and *Phyllosticta capitalensis* were isolated only from leaves; *Talaromyces* spp., and *Trichoderma* spp. were unique to roots; *Immersiella wurfbainiae* occurred solely in stems and *Acrocalymma wurfbainiae* was found only in fruits. Conversely, some species, such as *Bulbopyricularia guangdongensis*, *Corynespora wurfbainiae*, and *Musidium wurfbainiae*, were isolated from all tissues (roots, stems, leaves, and fruits). Notably, 12 strains of *Sarocladium wurfbainiae* were obtained from stems, fruits and roots, demonstrating its ability for systemic colonization across multiple plant tissues. This broad distribution may result from: (1) seed transmission, where the fungus is vertically transmitted via seeds and subsequently colonizes roots and stems during plant growth, or (2) vascular system transmission, where the fungus might spread through the xylem or phloem, enabling systemic infection of the plant. While this study provides insights into the tissue-specific distribution of fungal species in *W. villosa*, several limitations should be considered. First, the isolation method (e.g., culture-dependent techniques) may have overlooked unculturable or fastidious fungi, leading to an incomplete representation of the mycobiome. Second, the sampling strategy (e.g., number of plants, developmental stages, or environmental conditions) could influence fungal detectability, as some species may be transient or seasonally dependent. Third, the proposed transmission pathways, such as for *Sarocladium wurfbainiae* (seed or vascular spread), remain speculative without experimental validation (e.g., microscopic tracking or molecular assays). Additionally, the absence of fungal quantification (e.g., relative abundance) limits conclusions about their ecological roles whether they are dominant colonizers or minor symbionts. Finally, environmental factors (soil microbiota, host health, or agricultural practices) were not controlled, which may confound observed tissue specificity. Addressing these limitations in future work would strengthen inferences about fungal ecology and transmission mechanisms.

Regarding cross-host transitions, the presence of fungi (e.g., *Sarocladium wurfbainiae*) on *W. villosa* and unrelated hosts highlights their broad ecological range, possibly facilitated by spore dispersal or shared plant metabolites. *Sarocladium wurfbainiae* has been reported as a phytopathogen causing maize stalk rot in India (Harish et al., 2024), and is known as an opportunistic pathogen in humans and animals. Etienne et al. (2016) reported 25 isolates associated with outbreaks of *S. kiliense* bloodstream infections in Colombia and Chile. Fernández-Silva et al. (2014) noted that *S. kiliense* is often involved in human mycetoma, keratitis, and onychomycosis, and can be refractory to antifungal therapy. Furthermore, several studies have reported that *S. kiliense* produces many chemical compounds and secondary metabolites (Guo et al., 2018; Li et al., 2018; Eskander et al., 2020). Given that *W. villosa* is consumed daily as food and medicine, the presence of this opportunistic human pathogen raises concerns about the safety of consuming raw fruits and roots of *W. villosa*. This finding highlights the need for further investigation into the symbiotic relationships between *S. kiliense* and its hosts, as well as the potential implications for human health and secondary metabolite production.

Numerous microfungi (e.g., *Acrocalymma wurfbainiae*, *Bipolaris wurfbainiae*, *Colletotrichum wurfbainiae*) are specifically associated with *Wurfbainia villosa*, as indicated by their species epithets (*Wurfbainiae*), suggesting host-specific interactions. The majority of these fungi are reported from Guangdong Province, China, with secondary occurrences in Xishuangbanna (Yunnan Province). Climate zones are predominantly subtropical, with some overlapping tropical regions. Fungi colonize diverse tissues of *W. villosa*, including roots (most frequent), stems, leaves, and fruits. Some species exhibit multi-tissue colonization (e.g., *Bulbopyricularia guangdongensis*: leaf/stem/fruit/root). Fungi display varied lifestyles: (1) Endophytic (EN): Most common (e.g., *Acrocalymma* spp., *Penicillium* spp.). (2) Associated with lesion (P): Notable in *Colletotrichum* and *Cladosporium* species. (3) Saprophytic (S) or mixed lifestyles (e.g., EN/S/P in *Musidium wurfbainiae*). While most records are from China, a few species (e.g., *Micropeltis amomi* from Thailand, *Pseudocercospora amomi* from India) suggest broader geographic associations, though data outside China remain sparse. *Wurfbainia villosa* is also found in some Southeast Asian countries, including Cambodia, India, Indonesia, Laos, Myanmar, Thailand, and Vietnam, but the fungal

data are largely missing, which tells us that there is still much to be studied in Southeast Asian countries. *Wurfbainia villosa* hosts a rich, specialized microfungal community in subtropical China, with ecological roles ranging from mutualism to parasitism. Further studies are needed to explore global distributions and host-fungus dynamics. (Table 5.3)

In this study, a comparison of isolation methods indicated that plant tissue culture was the most effective technique for isolating endophytic fungi from *Wurfbainia villosa* across all tissue types. In contrast, the effectiveness of other methods remains uncertain. Tissue maceration may be useful for isolating slow-growing fungi, while intercellular fluid culture could be suitable for isolating root-associated endophytes in *W. villosa*. Among the sporulation-inducing methods tested for endophytic fungi, the combination of host tissue with ¼ strength malt extract agar (MEA) supplemented with pine needles, as well as the fruit juice medium (prepared with 200 g fruit and 20 g agar), proved to be the most effective. Both can be categorized as host tissue-associated media. For further methodological details, refer to Section 3. Interestingly, synthetic nutrient-poor agar (SNA) and oat agar (OA) also showed promising results in stimulating sporulation. However, there remains considerable room for improvement in this area, as approximately 30% of the endophytic isolates in this study failed to sporulate. Notably, this includes several important genera such as *Xylaria*, *Cercospora*, and *Lasiodiplodia*. Therefore, further research is needed to identify effective sporulation strategies for these recalcitrant fungi and to better understand their ecological and functional roles.

From a historical perspective, the exploration of endophytic fungi spans over two centuries. The journey began with their discovery, followed by defining what constitutes an endophyte, isolating them, and investigating their roles in forming micro-ecosystems with host plants. This has been a challenging yet fascinating process. While we continue to uncover and address various questions, our exploring of endophytic fungi remains insufficient. For instance, isolating true endophytes presents significant challenges. How can we ensure that the fungi isolated are genuine endophytes and not surface fungi or pathogens? This requires rigorous surface sterilization prior to the isolation process. Pre-experiments must be conducted to establish stringent sterilization

protocols with precise time control. Moreover, the isolated fungi may need to be reinoculated into the host to confirm their status as true endophytes.

Another unresolved question is the mechanism that how endophytic fungi can enter plant tissues without triggering the plant's immune response. Why endophytic fungi also can produce the infection structures such as appressoria? This aspect likely demands advanced genetic and molecular research for a comprehensive understanding. Furthermore, many endophytes cannot survive on artificial culture media, making traditional isolation methods ineffective. Beyond next-generation sequencing (NGS), are there better techniques to detect such endophytes? is still a question. Even for fungi that can grow on culture media, 30–50% of fungi also fail to produce spores. Certain strategies have been developed to promote sporulation, such as (1) trying to use different culture media like MEA, CLA, OA, or SNA, (2) adding pine needles, toothpicks, or host plant tissues to the media, (3) damaging fungal hyphae using toothpicks or blades when the colony approaches full coverage of the Petri dish, (4) exposing cultures to varied conditions such as low temperatures or UV radiation; and using host tissues from the specific isolation site to prepare specialized agar media, and these methods also not universally effective. More research is needed to uncover reliable approaches to induce sporulation in non-sporulating fungi. In addition, it has been observed that many endophytes exhibit changes in their lifestyles depending on their location within the same plant or after transitioning to different host plants. What drives these changes? Could they be linked to a weakened plant immune system, external environmental pressures, or chemical signals that activate specific fungal genes? Understanding these mechanisms will require substantial advancements in technology and extensive research efforts in the future. The study of endophytic fungi is still in its infancy and much remains to be discovered. Addressing these challenges will not only advance our understanding of fungal ecology but also potentially unlock their vast potential for applications in agriculture, medicine, and beyond.

CHAPTER 6

OVERALL CONCLUSIONS

6.1 Conclusions

This study focused on investigating microfungi inhabiting *Wurfbainia villosa* (Zingiberaceae) from 2020 to 2025, with an emphasis on taxonomy, phylogeny, and lifestyle relationships of fungi associated with this medicinal plant in southern China. A total of 503 fungal isolates were obtained (Figure 6.1). Among them, endophytic fungi accounted for the majority with 301 isolates (60%), followed by saprobic and potential pathogenic fungi with 101 isolates (40%). These isolates belonged to four fungal phyla, with Ascomycota being the most dominant group, comprising 96% of the total isolates. The remaining isolates were classified into Basidiomycota (2%), Mucoromycota (1%), and Oomycota (1%). Within Ascomycota, approximately 90% of the isolates were distributed across two major classes: Sordariomycetes (62%) and Dothideomycetes (28%). The dominant fungal orders identified within these classes were Pleosporales, Hypocreales, Glomerellales, and Magnaporthales (Figure 5.1).

As a result, 77 fungi species were identified, including two new genera and 47 new species were described, along with 31 new records of host, geographic, or habitat associations based on detailed morphological and phylogenetic analyses. Some of these findings have already been published, while others are pending further validation. The identified fungi belong to the following taxonomic groups: Ascomycota, Class Dothidiomycetes: Botryosphaeriales (Botryosphaeriaceae: *Lasiodiplodia wurfbainiae*, *Neodeightonia wurfbainiae*, *Neofusicoccum wurfbainiae*, Phyllostictaceae: *Phyllosticta capitalensis*); Muyocopronales (Muyocopronaceae: *Muyocopron laterale*); Pleosporales (Acrocalymmaceae: *Acrocalymma guangdongensis*, *Acrocalymma* sp., *A. wurfbainiae*, Corynesporascaceae: *Corynespora cassiicola*, *C. wurfbainiae*, Cucurbitariaceae: *Pyrenochaetopsis endophytica*, *Py. guangdongensis*, *Py. wurfbainiae*, Didymosphaeriaceae: *Dictyoarthrinium wurfbainiae*, Periconiaceae: *Periconia endophytica*, *P. epilithographicola*, *P. neoyangjiangensis*, *P. wurfbainiae*,

P. yangjiangensis, Phaeosphaeriaceae: *Setophoma wurfbainiae*, Pleosporaceae: *Alternaria pogostemonis, Bipolaris bicolor, B. wurfbainiae, Curvularia geniculata, C. plantarum, C. wurfbainiae,* Roussoellaceae: *Neoroussoella leucaenae, Roussoella wurfbainiae,* Tetraplosphaeriaceae: *Tetraploa wurfbainiae*, Torulaceae: *Torula wurfbainiae*); Class Eurotiomycetes: Eurotiales (Aspergillaceae: *Periconia epilithographicola, Penicillium allaniae, Pen. guangdongensis, Pen. meleagrinum, Pen. polonicum, Pen. wurfbainiae, Talaromyces dimorphus, T. wurfbainiae*); Class Mucoromycetes: Mucorales (Mucoraceae: *Mucor*); Class Sordariomycetes: Amphisphaeriales (Apiosporaceae: *Apiospora endophytica, A. guangdongensis, A. phyllostachydis, A. wurfbainiae, Nigrospora camelliae-sinensis, N. chinensis, N. guangdongense, N. oryzae, N. sphaerica*); Diaporthales (Diaporthaceae: *Diaporthe kochmanii, D. loculata, D. neoceratozamiae, D. neohongkongensis, D. neosiamensis, D. wurfbainiae, D. yangjiangensis*); Glomerellales (Glomerellaceae: *Colletotrichum fructicola, C. plurivorum, C. siamense,* Plectosphaerellaceae: *Acrostalagmus annulatu, Musicillium tropicale, Musidium wurfbainiae*); Hypocreales (Stachybotryaceae: *Brevistachys wurfbainiae, Nigrosynnema guangdongense,* Hypocreaceae: *Trichoderma guangdongensis, T. wurfbainiae,* Sarocladiaceae: *Sarocladium wurfbainiae,* Ophiocordycipitaceae: *Purpureocillium lilacinum*); Magnaporthales (Magnaporthaceae: *Bussabanomyces wurfbainiae, Pyriculariaceae*: *Bulbopyricularia guangdongensis, B. wurfbainiae*); Pleurotheciales (Pleurotheciaceae: *Dematipyriforma wurfbainiae*); Sordariales (Chaetomiaceae: *Chaetomium globosum, Humicola wallefii, Neoschizotheciaceae*: *Immersiella wurfbainiae*); Xylariales (Xylariaceae: *Astrocystis heterocyclae, Peroneutypa wurfbainiae*); Basidiomycota, Class Agaricomycetes: Polyporales (Phanerochaetaceae: *Phanerochaete chrysosporium*); Mucoromycota, Class Mucoromycetes: Mucorales (Mucoraceae: *Mucor nidicola, Mucor wurfbainiae*).

A total of 77 fungal species were identified, 39 (50%) with dual lifestyle transitions, 10 with all three lifestyles (endophyte, saprobe, potential pathogen), include *Bulbopyricularia guangdongensis, Bussabanomyces wurfbainiae, Corynespora cassiicola, Curvularia geniculata, Musicillium tropicale, Muyocopron laterale, Numusidium wurfbainiae, Purpureocillium lilacinum,* and *Sarocladium wurfbainiae*. Twenty-nine endophytic fungi transition to others two lifestyles, including *Colletotrichum plurivorum, Diaporthe kochmanii, Lasiodiplodia wurfbainiae, Nigrospora chinensis, Phyllosticta*

capitalensis, and *Pyrenochaetopsis guangdongensis*. This highlights the high frequency of lifestyle transitions among endophytic fungi. Interestingly, we found that three fungal species, *Colletotrichum siamense*, *C. plurivorum*, and *Bulbopyricularia wurfbainiae*, were capable of producing the pathogenic infection structures, appressoria. These species were isolated from both asymptomatic and symptomatic tissues of *Wurfbainia villosa*. This observation suggests that appressoria may play a key role in enabling lifestyle transitions in fungi with multiple ecological roles.

Furthermore, the study compared various methods for isolating endophytic fungi and found that plant tissue culture yielded the most diverse range of isolates. To induce sporulation in cultures, multiple methods were tested. The most effective sporulation methods were proven to be a combination of host tissue with ¼ strength malt extract agar (MEA) supplemented with pine needles, as well as the fruit juice medium (prepared with 200 g fruit and 20 g agar). Synthetic Nutrient-poor Agar (SNA) was effective in promoting sporulation in *Apiospora* and *Nigrospora*, while Carnation Leaf Agar (CLA) proved suitable for *Colletotrichum* and *Fusarium*.

A global checklist of 93 fungal species revealed distinct ecological and geographical patterns. Geographically, species richness was highest in Guangdong, China, followed by Yunnan, China, Thailand, and India. Regarding tissue specificity, leaves (39%) and roots (39%) were the predominantly colonized tissues, substantially exceeding occurrences in stems (19%), fruits (9%), and other tissues (14%). Ecologically, endophytes dominated (46%) all the tissues, outnumbering potential pathogens (23%), saprobes (13%), and minor groups like epiphyllous fungi (3%) or other varied lifestyles (15%). The hierarchy of fungal prevalence was exhibited as endophytes > potential pathogens > saprobes, and leaf > stem/root > fruit associations (Figure 5.123; Table 5.1).

In this study, *Colletotrichum*, *Diaporthe*, and *Bulbopyricularia* were identified as the dominant genera associated with *Wurfbainia villosa* in southern China. Moreover, the research contributes to a deeper understanding of microfungal lifestyle transitions and diversity in the region by providing comprehensive morphological and phylogenetic evidence to support their taxonomic placement. The use of different isolation techniques and spore induction methods revealed the need to develop more specialized media and sporulation strategies for certain genera. For example,

Poaceascoma, *Zasmidium*, *Podospora*, *Cercospora*, and *Ceratobasidium* failed to sporulate on any tested media, highlighting ongoing challenges in cultivating some taxa. All fungal specimens obtained have been deposited in recognized herbaria and culture collections, providing valuable resources for future studies in fungal taxonomy and the exploration of their potential biomaterial applications.

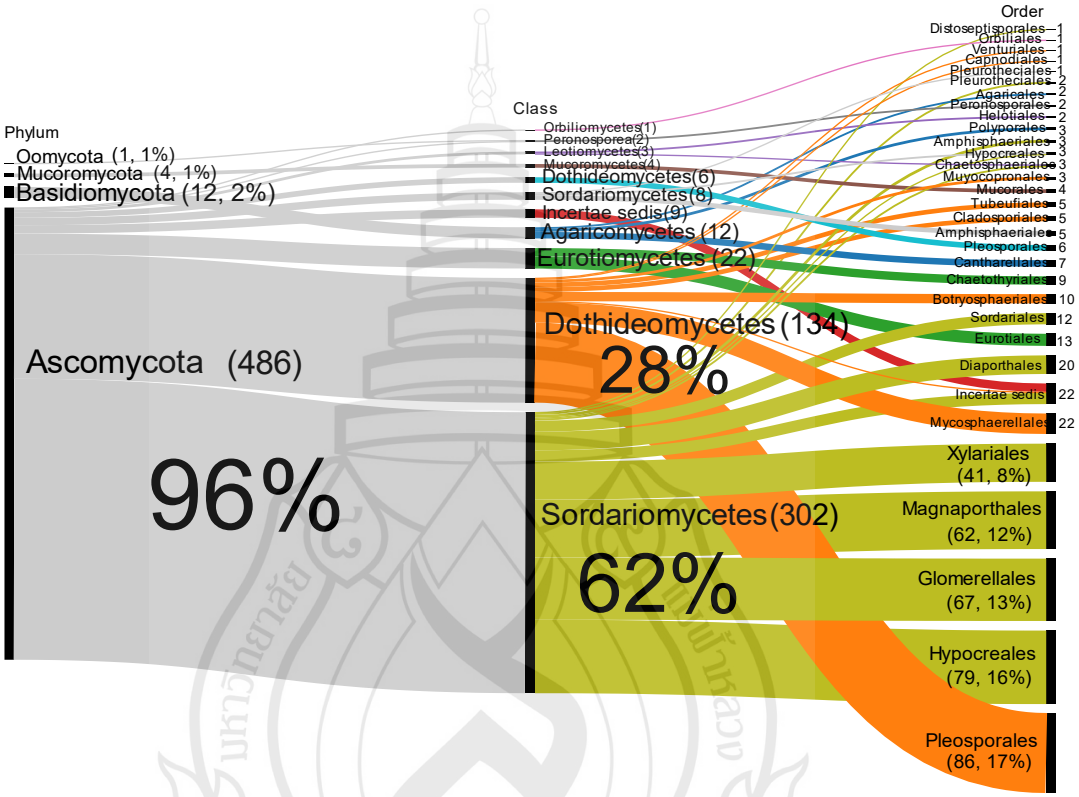


Figure 6.1 Total 503 microfungi strains isolated from *Wurfbainia villosa*

6.2 Research Advances

6.2.1 A Comprehensive and Systematic Investigation of Microfungi Associated with *Wurfbainia villosa*

This study represents the first extensive and systematic investigation of microfungi associated with *Wurfbainia villosa*, a medicinally important plant in the family Zingiberaceae. By integrating detailed morphological observations with multi-locus phylogenetic analyses, we introduced two new genera, 47 novel species, one new taxonomic combination, and documented 31 new host records. These taxonomic

advancements significantly enrich the known fungal diversity associated with this host and provide essential baseline data for future studies in fungal systematics, ecology, and natural product discovery. Additionally, we compiled and established the first global checklist of fungal taxa associated with *W. villosa*, offering a comprehensive reference for researchers working in fungal taxonomy and plant–microbe interactions.

6.2.2 Fungal Isolation Comparison and Endophytic Fungi Sporulation Test

Our research not only focused on diversity documentation but also evaluated different endophytic fungi isolation techniques associated with *Wurfbainia villosa*. Among the tested methods, the plant tissue culture isolation method proved to be the most effective for isolation endophytic fungi from all tissue types. We also explored various sporulation-inducing strategies, identifying media combinations such as host plant tissue with pine needle-enriched ¼ MEA and fruit juice medium as the most effective. These optimized protocols address common challenges in endophyte cultivation, particularly for species with poor sporulation in culture, and will serve as practical tools for researchers working with unculturable or slow-growing fungal taxa.

6.2.3 Novel Insights into Fungal Lifestyle Transitions and Ecological Versatility

One of the major contributions of this study lies in its exploration of fungal ecological strategies and lifestyle transitions. Among the 77 well-characterized fungal species, 39 were found to exhibit dual lifestyles (e.g., endophytic to saprobic or potentially pathogenic), while 10 displayed all three lifestyles: endophytic, saprobic, and potentially pathogenic. This high frequency of lifestyle transitions underscores the ecological plasticity of endophytic fungi. Notably, we observed the formation of appressoria, a key infection structure in species isolated from both symptomatic and asymptomatic tissues, further supporting their adaptive potential. Based on these findings, we propose a revised and comprehensive definition of endophytic fungi that incorporates their colonization strategies, latent pathogenicity, host benefits, and lifestyle flexibility. We also provide a comprehensive endophytic fungi review of current knowledge on endophytic fungal diversity and ecological function, contributing new perspectives to the understanding of plant-fungus symbioses.

6.3 Future Work

6.3.1 Conduct More Sampling and Taxonomic Exploration

Future studies should include broader geographic sampling across different regions of China and globally. Fungal specimens from *Wurfbainia villosa* should be collected across more diverse geographic locations and seasons, including endophytes, pathogens, and saprobes, to investigate how environmental factors like temperature and humidity shape fungal diversity, community structure, and ecological roles. We aim to gather further evidence for lifestyle changes in endophytic fungi by exploring additional, more intuitive methods.

6.3.2 Further Investigation into Fungal Lifestyle Transitions

To better understand the ecological plasticity of endophytic fungi, additional evidence is needed to support lifestyle transitions between endophytic, saprobic, and pathogenic stages. Developing more intuitive and experimentally controlled systems, such as in planta interaction models or microscopic monitoring of infection structures, could provide critical insights into these dynamic lifestyle shifts.

6.3.3 Optimization of Cultivation and Sporulation Techniques

Many isolates did not sporulate under standard conditions. Testing more alternative media and conditions is needed to induce sporulation and improve identification.

6.3.4 Pathogenicity Assessment and Functional Screening

Pathogenicity tests should be conducted on both existing and newly isolated fungal strains to clarify their ecological roles and potential risks to host plants. At the same time, the biotechnological potential of these fungi should be explored by screening for bioactive metabolites with antimicrobial, anticancer, and anti-inflammatory properties. Such efforts may lead to the discovery and development of novel therapeutic agents.

6.3.5 Integration of Multi-Omics Approaches to Uncover Ecological Functions

A more systematic study integrating genomics, transcriptomics, and metabolomics will enable researchers to comprehensively investigate the functional traits of endophytic fungi. These multi-omics strategies can provide deeper insights into

fungal metabolic capabilities, interaction mechanisms with host plants, and their roles in plant health, stress adaptation, and ecosystem dynamics.

6.4 Publications

6.4.1 First Author Paper

Liao, C. F., Doilom, M., Bhat, D. J., Chethana, K. W., Tangtrakulwanich, K., Yang, Y. H., . . . Dong, W. (2025). Unveiling four new taxa and *Nigrosynnema natarajanensis* comb. nov. in Stachybotryaceae (Hypocreales) from monocotyledon plants in Guangdong Province, China. *MycoKeys, 114*, 299–327. http://doi.org/10.3897/mycokeys.114.139325

Liao, C. F., Doilom, M., Jeewon, R., Hyde, K. D., Manawasinghe, I. S., Chethana, K. W., . . . Htet, Z. H. (2025). Challenges and update on fungal endophytes: Classification, definition, diversity, ecology, evolution and functions. *Fungal Diversity, 5*, 1–67. http://doi.org/10.1007/s13225-025-00550-5

Liao, C. F., Dong, W., Chethana, K. T., Pem, D., Phookamsak, R., Suwannarach, N., . . . Doilom, M. (2022). Morphological and phylogenetic evidence reveal *Tetraploa cylindrica* sp. nov. (Tetraplosphaeriaceae, Pleosporales) from *Saccharum arundinaceum* (Poaceae) in Yunnan Province, China. *Phytotaxa, 554*(2), 189–200. http://doi.org/10.11646/phytotaxa.554.2.7

Liao, C. F., Hyde, K. D., Chethana, K. W. T., Dong, W., Yang, Y., & Doilom, M. (2024). Three new *Periconia* species isolated from *Wurfbainia villosa* in Guangdong, China: A discussion on the doubtful taxa clustering in this genus. *Diversity, 16*(3), 141. http://doi.org/10.3390/d16030141

Liao, C. F., Karunarathne, A., Tennakoon, D. S., Doilom, M., Xu, J., Chethana, K. T., . . . Tibpromma, S. (2021). Addition to *Phaeosphaeria*: *Eriobotrya japonica*, a new host of *Phaeosphaeria acaciae*. *Chiang Mai Journal of Science, 48*(3), 922–930.

Liao, C. F., Senanayake, I. C., Dong, W., Chethana, K. W. T., Tangtrakulwanich, K., Zhang, Y. X., . . . Doilom, M. (2023). Taxonomic and phylogenetic updates on *Apiospora*: Introducing four new species from *Wurfbainia villosa* and grasses in China. *Journal of Fungi*, *9*(11), 1087. http://doi.org/10.3390/jof9111087

Liao, C. F., Yang, Y. H., Dong, W., Tangtrakulwanich, K., Zhang, Y. X., Khan, S., . . . Doilom, M. (2024). *Tetraploa wurfbainiae* sp. nov. (Tetraplosphaeriaceae, Pleosporales) isolated from *Wurfbainia villosa* in Guangdong, China. *New Zealand Journal of Botany, 62*(2-3), 303–316. http://doi.org/10.1080/0028825X.2024.2311964

6.4.2 Co-author Paper

Calabon, M. S., Hyde, K. D., Jones, E. G., Doilom, M., Liao, C. F., & Boonmee, S. (2020). *Mycoenterolobium aquadictyosporium* sp. nov. (Pleosporomycetidae, Dothideomycetes) from a freshwater habitat in Thailand. *Mycological Progress, 19*(10), 1031–1042. http://doi.org/10.1007/s11557-020-01609-0

Dai, D. Q., Wijayawardene, N. N., Tang, L. Z., Liu, C., Han, L. H., Chu, H. L., . . . Li, Y. M. (2019). *Rubroshiraia* gen. nov., a second hypocrellin-producing genus in Shiraiaceae (Pleosporales). *MycoKeys, 58*, 1–26. https://doi.org/10.3897/mycokeys.58.36723

Doilom, M., Guo, J. W., Phookamsak, R., Mortimer, P. E., Karunarathna, S. C., Dong, W., . . . Promputtha, I. (2020). Screening of phosphate-solubilizing fungi from air and soil in Yunnan, China: Four novel species in *Aspergillus*, *Gongronella*, *Penicillium*, and *Talaromyces*. *Frontiers in Microbiology, 11*, 585215. http://doi.org/10.3389/fmicb.2020.585215

Doilom, M., Hyde, K. D., Dong, W., Liao, C. F., Suwannarach, N., & Lumyong, S. (2021). The plant family Asteraceae is a cache for novel fungal diversity: Novel species and genera with remarkable ascospores in Leptosphaeriaceae. *Frontiers in Microbiology, 12*, 660261. http://doi.org/10.3389/fmicb.2021.660261

Dong, W., Hyde, K. D., Jeewon, R., Liao, C. F., Zhao, H. J., Kularathnage, N. D., . . . Doilom, M. (2023). Mycosphere notes 449–468: Saprobic and endophytic fungi in China, Thailand, and Uzbekistan. *Mycosphere, 14*(1), 2208–2262. http://doi.org/10.5943/mycosphere/14/1/26

Hongsanan, S., Khuna, S., Manawasinghe, I. S., Tibpromma, S., Chethana, K. W. T., Liao, C. F., . . . Karunarathna, S. C. (2025). Mycosphere notes 521–571: A special edition of fungal biodiversity to celebrate Kevin D. Hyde's 70th birthday and his exceptional contributions to mycology. *Mycosphere, 16*(2), 2002–2180. https://doi.org/10.5943/mycosphere/16/2/1

Hyde, K. D., Suwannarach, N., Jayawardena, R. S., Manawasinghe, I. S., Liao, C. F., . . . Bao, D. F. (2021). Mycosphere notes 325–344: Novel species and records of fungal taxa from around the world. *Mycosphere, 12*(1), 1101–1156. https://doi.org/10.5943/mycosphere/12/1/14

Hyde, K. D., Noorabadi, M. T., Thiyagaraja, V., He, M. Q., Johnston, P. R., Wijesinghe, S. N., . . . Zvyagina, E. (2024). The 2024 outline of fungi and fungus-like taxa. *Mycosphere, 15*(1), 5146–6239. http://doi.org/10.5943/mycosphere/15/1/25

Hyde, K. D., Wijesinghe, S. N., Afshari, N., Aumentado, H. D., Liao, C. F., . . . Zhang, J. Y. (2024). Mycosphere notes 469–520. *Mycosphere, 15*(1), 1294–1454. http://doi.org/10.5943/mycosphere/15/1/11

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y. R., Suwannarach, N., Sysouphanthong, P., . . . Wang, Y. (2022). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 117*, 1–272. http://doi.org/10.1007/s13225-022-00513-0

Li, Y. X., Doilom, M., Dong, W., Liao, C. F., Manawasinghe, I. S., & Xu, B. (2023). A taxonomic and phylogenetic contribution to *Torula*: *T. phytolaccae* sp. nov. on *Phytolacca acinosa* from China. *Phytotaxa, 584*(1), 1–7. http://doi.org/10.11646/phytotaxa.584.1.1

Manawasinghe, I. S., Calabon, M. S., Jones, E. B. G., Zhang, Y. X., Liao, C. F., Xiong, Y. R., . . . Hyde, K. D. (2022). Mycosphere notes 345–386. *Mycosphere, 13*(1), 454–557. http://doi.org/10.5943/mycosphere/13/1/3

Phookamsak, R., Jiang, H., Suwannarach, N., Lumyong, S., Xu, J., Xu, S., . . . Chomnunti, P. (2022). Bambusicolous fungi in Pleosporales: Introducing four novel taxa and a new habitat record for *Anastomitrabeculia didymospora*. *Journal of Fungi, 8*(6), 630. http://doi.org/10.3390/jof8060630

Senanayake, I. C., Rossi, W., Leonardi, M., Weir, A., McHugh, M., Rajeshkumar, K. C., . . . Song, J. (2023). Fungal diversity notes 1611–1716: Taxonomic and phylogenetic contributions on fungal genera and species with emphasis in South China. *Fungal Diversity, 122*, 161–403. https://doi.org/10.1007/s13225-023-00523-6

Xiong, Y., Manawasinghe, I. S., Liao, C., Hyde, K. D., & Dong, Z. Y. (2022). *Neodeightonia arengae* sp. nov., botryosphaeriaceous taxa on *Arenga tremula* (Arecaceae) from Guangdong, China. *Phytotaxa, 530*(2), 130–140. http://doi.org/10.11646/phytotaxa.530.2.1

Yang, Y. H., Manawasinghe, I. S., Wanasinghe, D. N., De Farias, A. R., Liao, C. F., & Dong, Z. Y. (2024). A novel genus and new records of Dothideomycetes associated with *Litchi chinensis* litter from Guangdong Province, China. *New Zealand Journal of Botany, 62*(2-3), 216–238. http://doi.org/10.1080/0028825X.2023.2274628

Yang, Y. H., Liao, C. F., Manawasinghe, I. S., De Farias, A. R., & Dong, Z. Y. (2023). *Neomassaria khayae* sp. nov., a novel pleosporalean species on *Khaya senegalensis* from Guangdong Province, China. *Phytotaxa*, *599*(1), 65–77. http://doi.org/10.11646/phytotaxa.599.1.4

Yang, Y. H., Liao, C. F., Manawasinghe, I. S., Hyde, K. D., Dong, Z. Y., & Xu, B. (2024). Phylogenetic and morphological characterization of Beltraniaceae species from Litchi and Longan litter in southern China. *Chiang Mai Journal of Science*, *52*(4), 1–23. http://doi.org/10.12982/CMJS.2025.045

REFERENCES

Abbo, A. S. H., Hammad, A. M., & Laing, M. D. (2015). The effect of melanin on the tolerance of fungal conidia to ultraviolet and visible light exposure. *Int. J. Sci., Environ*, *4*, 1059-1065.

Abdel-Fatah, S. S., El-Batal, A. I., El-Sherbiny, G. M., Khalaf, M. A., & El-Sayed, A. S. (2021). Production, bioprocess optimization and γ-irradiation of *Penicillium polonicum*, as a new Taxol producing endophyte from *Ginkgo biloba*. *Biotechnology Reports*, *30*, e00623. https://doi.org/10.1016/j.btre.2021.e00623

Absalan, S., Armand, A., Jayawardena, R. S., McKenzie, E. H. C., Hyde, K. D., & Lumyong, S. (2024). Diversity of pleosporalean fungi isolated from rice (*Oryza sativa* L.) in northern Thailand and descriptions of five new species. *Journal of Fungi*, *10*(11), 763. https://doi.org/10.3390/jof10110763

Afanador-Kafuri, L., González, A., Gañán, L., Mejía, J. F., Cardona, N., & Alvarez, E. (2014). Characterization of the *Colletotrichum* species causing anthracnose in Andean blackberry in Colombia. *Plant Disease*, *98*(11), 1503–1513. https://doi.org/10.1094/PDIS-07-13-0752-RE

Ahmed, S. A., Khan, Z., Wang, X. W., Moussa, T. A., Al-Zahrani, H. S., Almaghrabi, O. A., . . . van Diepeningen, A. (2016). *Chaetomium*-like fungi causing opportunistic infections in humans: A possible role for extremotolerance. *Fungal Diversity*, *76*(1), 11–26. https://doi.org/10.1007/s13225-015-0338-5

Alcorn, J. L. (1994). Appressoria in *Mycoleptodiscus* species. *Australian Systematic Botany*, *7*, 591–603.

Alvarez-Loayza, P., White, J. F. Jr., Torres, M. S., Balslev, H., Kristiansen, T., Svenning, J. C., . . . Gil, N. (2011). Light converts endosymbiotic fungus to pathogen, influencing seedling survival and niche-space filling of a common tropical tree, *Iriartea deltoidea*. *PloS One*, *6*(1), e16386. https://doi.org/10.1371/journal.pone.0016386

Alves, A., Crous, P., Correia, A., & Phillips, A. (2008). Morphological and molecular data reveal cryptic species in *Lasiodiplodia theobromae*. *Fungal Diversity*, *28*, 1–13.

Aly, A. H., Debbab, A., & Proksch, P. (2011). Fungal endophytes: Unique plant inhabitants with great promises. *Applied Microbiology and Biotechnology*, *90*(6), 1829–1845. https://doi.org/10.1007/s00253-011-3270-y

An, C., Ma, S., Shi, X., Xue, W., Liu, C., & Ding, H. (2020). Isolation, diversity, and antimicrobial activity of fungal endophytes from *Rohdea chinensis* (Baker) N. Tanaka (synonym *Tupistra chinensis* Baker) of Qinling Mountains, China. *PeerJ*, *8*, e9342. https://doi.org/10.7717/peerj.9342

Andrioli, W. J., Silva, T. M., Silva, V. B., Cavalheiro, A. J., Terenzi, H. F., Jorge, J. A., . . . Polizeli, M. L. T. M. (2012). The fungal metabolite eugenitin as additive for *Aspergillus niveus* glucoamylase activation. *Journal of Molecular Catalysis B: Enzymatic*, *74*, 156–161. https://doi.org/10.1016/j.molcatb.2011.12.016

Ao, H., Wang, J., Chen, L., Li, S., & Dai, C. (2019). Comparison of volatile oil between the fruits of *Amomum villosum* Lour. and *Amomum villosum* Lour. var. *xanthioides* TL Wu et Senjen based on GC-MS and chemometric techniques. *Molecules*, *24*(9), 1663. https://doi.org/10.3390/molecules24091663

Aragona, M., Minio, A., Ferrarini, A., Valente, M. T., Bagnaresi, P., Orrù, L., . . . Delledonne, M. (2014). De novo genome assembly of the soil-borne fungus and tomato pathogen Pyrenochaeta lycopersici. *BMC Genomics*, *15*(1), 313. https://doi.org/10.1186/1471-2164-15-313

Ariyawansa, H. A., Camporesi, E., Thambugala, K. M., Mapook, A., Kang, J. C., Alias, S. A., . . . Hyde, K. D. (2014a). Confusion surrounding *Didymosphaeria*—Phylogenetic and morphological evidence suggest Didymosphaeriaceae is not a distinct family. *Phytotaxa*, *176*(1), 102–119. https://doi.org/10.11646/phytotaxa.176.1.12

Arnold, A. E., & Engelbrecht, B. M. (2007). Fungal endophytes nearly double minimum leaf conductance in seedlings of a neotropical tree species. *Journal of Tropical Ecology*, *23*(3), 369–372. https://doi.org/10.1016/j.fbr.2007.05.003

Arunakumar, G. S., Gnanesh, B. N., Supriya, M., & Sivaprasad, V. (2019). First report of *Nigrospora sphaerica* causing shot hole disease on mulberry in India. *Plant Disease, 103*(1), 1783. https://doi.org/10.1094/PDIS-01-19-0089-PDN

Assunção, D. A., Evangelista, L. F., Costa, T. E., Silva, J. L., Bento, E. A., Neto, J. A., . . . Holanda, I. S. (2024). First report of *Colletotrichum plurivorum* and *Colletotrichum truncatum* causing anthracnose on melon plants in Brazil. *Plant Disease, 108*(9), 2927. https://doi.org/10.1094/PDIS-02-24-0379-PDN

Atsatt, P. R., & Whiteside, M. D. (2014). Novel symbiotic protoplasts formed by endophytic fungi explain their hidden existence, lifestyle switching, and diversity within the plant kingdom. *PLoS One, 9*(4), e95266. https://doi.org/10.1371/journal.pone.0095266

Aylward, J., Steenkamp, E. T., Dreyer, L. L., Roets, F., Wingfield, B. D., & Wingfield, M. J. (2017). A plant pathology perspective of fungal genome sequencing. *IMA Fungus, 8*(1), 19–15. https://doi.org/10.5598/imafungus.2017.08.01.01

Bacon, C. W., & White, J. F. Jr. (2000). Physiological adaptations in the evolution of endophytism in the Clavicipitaceae. In A. Kumar & V. K. Singh (Eds.), *Microbial endophytes* (pp. 251-276). CRC Press.

Baldrian, P., Větrovský, T., Lepinay, C., & Kohout, P. (2022). High-throughput sequencing view on the magnitude of global fungal diversity. *Fungal Diversity, 114*(1), 539–547. https://doi.org/10.1007/s13225-021-00472-y

Bao, D. F., Hyde, K. D., Maharachchikumbura, S. S., Perera, R. H., Thiyagaraja, V., Hongsanan, S., . . . Nalumpang, S. (2023). Taxonomy, phylogeny and evolution of freshwater Hypocreomycetidae (Sordariomycetes). *Fungal Diversity, 121*(1), 1–94. https://doi.org/10.1007/s13225-023-00521-8

Barr, M. E. (1979). A classification of Loculoascomycetes. *Mycologia, 71*, 935–957. https://doi.org/10.1080/00275514.1979.12021099

Barrow, J. R. (2003). Atypical morphology of dark septate fungal root endophytes of *Bouteloua* in arid southwestern USA rangelands. *Mycorrhiza, 13*(5), 239–247. https://doi.org/10.1007/s00572-003-0222-0

Bashir, U., Javed, S., Anwar, W., Nawaz, K., & Hafeez, R. (2017). First report of *Penicillium polonicum* causing blue mold on stored garlic (*Allium sativum*) in Pakistan. *Plant Disease, 101*(10), 1037–1038. https://doi.org/10.1094/PDIS-07-16-1069-PDN

Basson, E., Meitz-Hopkins, J. C., & Lennox, C. L. (2019). Morphological and molecular identification of fungi associated with South African apple core rot. *European Journal of Plant Pathology, 153*(3), 849–868. https://doi.org/10.1007/s10658-018-1601-x

Batista, E., Lopes, A., & Alves, A. (2021). What do we know about Botryosphaeriaceae? An overview of a worldwide curated dataset. *Forests, 12*(3), 313. https://doi.org/10.3390/f12030313

Berkeley, M. J., & Broome, C. E. (1850). Notices of British fungi (438–501). *Annals and Magazine of Natural History, 5*, 455–466. https://doi.org/10.1080/03745486009494947

Bezerra, J. D. P., Santos, M. G. S., Svedese, V. M., Lima, D. M. M., Fernandes, M. J. S., Paiva, L. M., . . . Souza-Motta, C. M. (2012). Richness of endophytic fungi isolated from *Opuntia ficus-indica* Mill. (Cactaceae) and preliminary screening for enzyme production. *World Journal of Microbiology and Biotechnology*, *28*(3), 1989–1995. https://doi.org/10.1007/s11274-011-1001-2

Bhunjun, C. S., Niskanen, T., Suwannarach, N., Wannathes, N., Chen, Y. J., McKenzie, E. H., . . . Lumyong, S. (2022). The numbers of fungi: Are the most speciose genera truly diverse?. *Fungal Diversity*, *114*(1), 387–462. https://doi.org/10.1007/s13225-022-00501-4

Bhunjun, C. S., Phukhamsakda, C., Hyde, K. D., McKenzie, E. H., Saxena, R. K., & Li, Q. (2023). Do all fungi have ancestors with endophytic lifestyles?. *Fungal Diversity*, *16*(1), 1–26. https://doi.org/10.1007/s13225-023-00516-5

Bills, G. F. (1996). Isolation and analysis of endophytic fungal communi ties from wood plants. In S. C. Redlin & L. M. Carris (Eds.), *Endo phytic fungi in grasses and woody plants: Systematics, ecology, and evolution* (pp 31–65). APS Press.

Boerema, G. H. (2004). *Phoma identification manual: Differentiation of specific and infra-specific taxa in culture*. CABI Publishing.

Bologna, N. G., & Voinnet, O. (2014). The diversity, biogenesis, and activities of endogenous silencing small RNAs in Arabidopsis. *Annual Review of Plant Biology*, *65*(1), 473–503. https://doi.org/10.1146/annurev-arplant-050213-035728

Boonmee, S., Wanasinghe, D. N., Calabon, M. S., Huanraluek, N., Chandrasiri, S. K., Jones, G. E., . . . Singh, P. N. (2021). Fungal diversity notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 111*(1), 1–335. https://doi.org/10.1007/s13225-022-00495-6

Bradshaw, M. J., Bartholomew, H. P., Lichtner, F., Gaskins, V. L., & Jurick, W. M. (2022). First report of blue mold caused by *Penicillium polonicum* on apple in the United States. *Plant Disease, 106*(2), 762. https://doi.org/10.1094/PDIS-06-21-1136-PDN

Brahmanage, R. S., Dayarathne, M. C., Wanasinghe, D. N., Thambugala, K. M., Jeewon, R., Chethana, K. W. T., . . . Hyde, K. D. (2020). Taxonomic novelties of saprobic Pleosporales from selected dicotyledons and grasses. *Mycosphere, 11*(1), 2481–2541. https://doi.org/10.5943/mycosphere/11/1/15

Brundrett, M. C. (2002). Coevolution of roots and mycorrhizas of land plants. *New Phytologist, 154*(2), 275–304. https://doi.org/10.1046/j.1469-8137.2002.00397.x

Brundrett, M. C. (2006). Understanding the roles of multifunctional mycorrhizal and endophytic fungi. In B. J. E. Schulz, C. J. C. Boyle & T. N. Sieber (Eds.), *Microbial root endophytes* (pp. 281-298). Springer Berlin Heidelberg.

Calabon, M. S., Jones, E. G., Boonmee, S., Li, W. J., Xiao, Y. P., & Hyde, K. D. (2023). Acrocalymmaceae (Pleosporales) from freshwater habitats in Thailand with the introduction of *Acrocalymma bilobatum* sp. nov. *Studies in Fungi, 8*. https://doi.org/10.48130/SIF-2023-0011

Cannon, P. F., & Alcorn, J. L. (1994). *Omnidemptus affinis* gen. et sp. nov., teleomorph of *Mycoleptodiscus affinis* sp. nov. *Mycotaxon, 51*, 483–487.

Cantrell, S. A., Hanlin, R. T., & Emiliano, A. (2007). *Periconia variicolor* sp. nov., a new species from Puerto Rico. *Mycologia, 99*(3), 482–487. https://doi.org/10.1080/15572536.2007.11832573

Cao, Z. J., Qin, W. T., Zhao, J., Liu, Y., Wang, S. X., & Zheng, S. Y. (2022). Three new *Trichoderma* species in *Harzianum* clade associated with the contaminated substrates of edible fungi. *Journal of Fungi, 8*(11), 1154. https://doi.org/10.3390/jof8111154

Carbone, I., & Kohn, L. M. (1999). A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia, 91*(1), 553–556.

Carneiro, G. A., & Baric, S. (2023). *Colletotrichum fioriniae* and *Colletotrichum godetiae* causing postharvest bitter rot of apple in South Tyrol (Northern Italy). *Plant Disease, 105*(10), 3118–3126. https://doi.org/10.1094/PDIS-11-20-2482-RE

Carroll, G. C. (1986). The biology of endophytism in plants with particular reference to woody perennials. In N. J. Fokkema & J. van den Heuvel (Eds.), *Microbiology of the Phyllosphere* (pp. 205–222). Cambridge University Press.

Carroll, G. C. (1992). Fungal mutualism. In G. C. Carroll & D. T. Wicklow (Eds.), *The fungal community: Its organization and role in the ecosystem* (2nd ed., pp. 327–354). Marcel Dekker.

Castlebury, L. A., Rossman, A. Y., Jaklitsch, W. J., & Vasilyeva, L. N. (2002). A phylogeny overview of the Diaporthales based on large subunit nuclear ribosomal DNA sequences. *Mycologia, 94*(6), 1017–1031. https://doi.org/10.1080/15572536.2003.11833157

Cavalcante, G. R. S., Barguil, B. M., Vieira, A. S., Lima, W. G., Michereff, S. J., Doyle, V. P., . . . Câmara, M. P. S. (2019). Diversity, prevalence and virulence of *Colletotrichum* species associated with lima bean in Brazil. *Plant Disease, 103*(8), 1961–1966. https://doi.org/10.1094/PDIS-11-18-2002-RE

Chaiwan, N., Gomdola, D., Wang, S., Monkai, J., Tibpromma, S., Doilom, M., . . . Hyde, K. D. (2021). https://gmsmicrofungi.org: An online database providing updated information of microfungi in the Greater Mekong Subregion. *Mycosphere, 12*(1), 1513–1526. https://doi.org/10.5943/mycosphere/12/1/19

Chaiwong, K., Khuna, S., Senwanna, C., Kumla, J., & Suwannarach, N. (2024). First report of *Phyllosticta capitalensis* causing postharvest brown spot disease on guava fruits in Thailand. *Plant Disease, 108*(9), 2930. https://doi.org/10.1094/PDIS-06-24-1314-PDN

Chang, J., Boer, R., Crous, P. W., & Taylor, P. W. (2014). Biology of foliar and root infection of potato plants by *Colletotrichum coccodes* in Australia. *Phytopathology, 104*(11), 22–24.

Chatterton, S., Wylie, A. C., & Punja, Z. K. (2012). Fruit infection and postharvest decay of greenhouse tomatoes caused by *Penicillium* species in British Columbia. *Canadian Journal of Plant Pathology, 34*(4), 524–535. https://doi.org/10.1080/07060661.2012.710069

Chen, J., Xiang, T. T., Liu, X. Y., Wang, W. H., Zhang, J., Liu, W., . . . Zhu, H. S. (2018). First report of *Nigrospora sphaerica* causing shot hole disease on mulberry in China. *Plant Disease, 102*(1), 245. https://doi.org/10.1094/PDIS-06-17-0914-PDN

Chen, K., & Zhuang, W. Y. (2017). Discovery from a large-scaled survey of *Trichoderma* in soil of China. *Scientific Reports, 7*(1), 9090. https://doi.org/10.1038/s41598-017-07807-3

Chen, L. S., Liu, Y. J., Xu, S. W., Chen, Y. L., Chen, M. J., & Zhou, L. J. (2017). First report of *Penicillium polonicum* causing blue mold on stored *Polygonatum cyrtonema* in China. *Plant Disease, 101*(12), 2149–2150. https://doi.org/10.1094/PDIS-05-17-0756-PDN

Chen, W. H., Li, D., Liang, J. D., Ren, X. X., Zhao, J. H., & Han, Y. F. (2024). Two new Cordyceps-like species, *Perennicordyceps zongqii* sp. nov. (Polycephalomycetaceae) and *Purpureocillium zongqii* sp. nov. (Ophiocordycipitaceae), in Hypocreales from karst region of China. *MycoKeys, 110*, 141. https://doi.org/10.3390/microorganisms12061041

Chen, W., & Hu, Q. (n.d.). Secondary metabolites of *Purpureocillium lilacinum*. *Molecules*.

Cheng, K. X., Zeng, Y., Yu, K. M., & Jiang, Y. L. (2025). First report of leaf spot on *Zanthoxylum bungeanum* caused by *Nigrospora chinensis* in China. *Plant Disease, 109*(3), 722. https://doi.org/10.1094/PDIS-11-24-2380-PDN

Cheng, L. L., Thangaraj, K., Deng, C., Deng, W. W., & Zhang, Z. Z. (2019). *Phyllosticta capitalensis* causes leaf spot on tea plant (*Camellia sinensis*) in China. *Plant Disease, 103*(11), 2964. https://doi.org/10.1094/PDIS-04-19-0768-PDN

Chethana, K. W. T., Jayawardena, R. S., Chen, Y. J., Konta, S., Tibpromma, S., Abeywickrama, P. D., . . . Hyde, K. D. (2021). Diversity and function of appressoria. *Pathogens, 10*, 746. https://doi.org/10.3390/pathogens10060746

Chung, P. C., Wu, H. Y., Chen, Y. C., Hung, T. H., & Chung, C. L. (2022). Development of a nested PCR assay for detecting *Colletotrichum siamense* and *Colletotrichum fructicola* on symptomless strawberry plants. *PLoS One, 17*, e0270687. https://doi.org/10.1371/journal.pone.0270687

Condé, T. O., Leão, A. F., Dutra, Y. L., Rosado, A. W., Neves, S. D., Fraga, L. M., . . . Pereira, O. L. (2023). Shedding light on the darkness: A new genus and four new species in the family Chaetomiaceae from Brazilian neotropical caves revealed by multi-gene phylogenetic analyses. *Mycological Progress, 22*(7), 49. https://doi.org/10.1007/s11557-023-01899-0

Coronado-Ruiz, C., Avendaño, R., Escudero-Leyva, E., Conejo-Barboza, G., Chaverri, P., & Chavarría, M. (2018). Two new cellulolytic fungal species isolated from a 19th-century art collection. *Scientific Reports, 8*(1), 7492. https://doi.org/10.1038/s41598-018-24934-7

Correia, J., Borges, A., Simões, M., & Simões, L. C. (2023). Beyond penicillin: The potential of filamentous fungi for drug discovery in the age of antibiotic resistance. *Antibiotics, 12*(8), 1250.

Croll, D., & McDonald, B. A. (2012). The accessory genome as a cradle for adaptive evolution in pathogens. *PLoS Pathogens, 8*(4), e1002608. https://doi.org/10.1371/journal.ppat.1002608

Crous, P. W., & Groenewald, J. Z. (2013). A phylogenetic reevaluation of *Arthrinium*. *IMA Fungus, 4*(1), 133–154. https://doi.org/10.5598/imafungus.2013.04.01.13

Crous, P. W., Akulov, A., Balashov, S., Boers, J., Braun, U., Castillo, J., . . . Jurjević, Ž. (2023). New and interesting fungi. 6. *Fungal Systematics and Evolution, 11*(1), 109–156. https://doi.org/10.3114/fuse.2023.11.09

Crous, P. W., Carris, L. M., Giraldo, A., Groenewald, J. Z., Hawksworth, D. L., Hernández-Restrepo, M., . . . van der Linde, E. J. (2015). The genera of fungi—Fixing the application of the type species of generic names—G 2: *Allantophomopsis, Latorua, Macrodiplodiopsis, Macrohilum, Milospium, Protostegia, Pyricularia, Robillarda, Rotula, Septoriella, Torula,* and *Wojnowicia. IMA Fungus, 6*(1), 163–198. https://doi.org/10.5598/imafungus.2015.06.01.11

Crous, P. W., Groenewald, J. Z., Risède, J. M., Simoneau, P., & Hywel-Jones, N. L. (2004). *Calonectria* species and their *Cylindrocladium* anamorphs: Species with sphaeropedunculate vesicles. *Studies in Mycology, 50*(2), 415–430.

Crous, P. W., Luangsa-Ard, J. J., Wingfield, M. J., Carnegie, A. J., Hernández-Restrepo, M., Lombard, L., . . . Martín, M. P. (2018). Fungal planet description sheets: 785–867. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 41,* 238–417. https://doi.org/10.3767/persoonia.2018.41.12

Crous, P. W., Shivas, R. G., Quaedvlieg, W. V., van der Bank, M., Zhang, Y., Summerell, B. A., . . . Braun, U. (2014). Fungal planet description sheets: 214–280. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 32,* 184–306. https://doi.org/10.3767/003158514X682395

Crous, P. W., Slippers, B., Wingfield, M. J., Rheeder, J., Marasas, W. F., Philips, A. J., . . . Groenewald, J. Z. (2006). Phylogenetic lineages in the Botryosphaeriaceae. *Studies in Mycology, 55*(1), 235–253. https://doi.org/10.3114/sim.55.1.235

Dai, D. Q., Wijayawardene, N. N., Dayarathne, M. C., Kumla, J., Han, L. S., Zhang, G. Q., . . . Chen, H. H. (2022). Taxonomic and phylogenetic characterizations reveal four new species, two new asexual morph reports, and six new country records of bambusicolous *Roussoella* from China. *Journal of Fungi, 8*(5), 532. https://doi.org/10.3390/jof8050532

Dai, Y., Gan, L., Liu, X., Lan, C., Li, Z., & Yang, X. (2024). Occurrence of leaf spot caused by *Colletotrichum plurivorum* on cowpea in Fujian Province, China. *Crop Protection, 176,* 106496. https://doi.org/10.1016/j.cropro.2023.106496

Damm, U., Sato, T., Alizadeh, A., Groenewald, J. Z., & Crous, P. W. (2019). The *Colletotrichum dracaenophilum, C. magnum* and *C. orchidearum* species complexes. *Studies in Mycology, 92*(1), 1–46. https://doi.org/10.1016/j.simyco.2018.04.001

Darapanit, A., Boonyuen, N., Leesutthiphonchai, W., Nuankaew, S., & Piasai, O. (2021). Identification, pathogenicity and effects of plant extracts on *Neopestalotiopsis* and *Pseudopestalotiopsis* causing fruit diseases. *Scientific Reports, 11*(1), 22606. https://doi.org/10.1038/s41598-021-02113-5

de Amorim, M. R., Barbosa, C. D., Paz, T. A., Ióca, L. P., Nicácio, K. J., de Oliveira, L. F., . . . Furlan, M. (2023). Polyketide- and terpenoid-derived metabolites produced by a marine-derived fungus, *Peroneutypa* sp. *Journal of Natural Products, 86*(6), 1476–1486. https://doi.org/10.1021/acs.jnatprod.3c00175

de Bary, A. (1866). *Morphologie und physiologie der pilze, flechten und myxomyceten* (Vol. 1). Engelmann.

de Gruyter, J., Woudenberg, J. H., Aveskamp, M. M., Verkley, G. J., Groenewald, J. Z., & Crous, P. W. (2010). Systematic reappraisal of species in *Phoma* section *Paraphoma, Pyrenochaeta* and *Pleurophoma*. *Mycologia, 102*(5), 1066–1081.

Deepak Reddy, B., Hemantha Kumar J., Srilatha, P., Pavani, T., Murthy, K. G. K., Neelima P., . . . Ramakrishna, A. (2024). First report of *Chaetomium globosum* causing leaf spot on *Averrhoa carambola* in India. *Plant Disease, 108*(7), 2222. https://doi.org/10.1094/PDIS-02-24-0353-PDN

Deepika, Y. S., Mahadevakumar, S., Amruthesh, K. N., & Lakshmidevi, N. (2021). First report of *Nigrospora sphaerica* associated with leaf spot disease of cowpea (*Vigna unguiculata*) from India. *Plant Disease, 105*(2), 506. https://doi.org/10.1094/PDIS-10-20-2240-PDN

Delaye, L., García-Guzmán, G., & Heil, M. (2013). Endophytes versus biotrophic and necrotrophic pathogens—are fungal lifestyles evolutionarily stable traits?. *Fungal Diversity*, *60*(1), 125–135. https://doi.org/10.1007/s13225-013-0240-y

DeMers, M. (2022). *Alternaria alternata* as endophyte and pathogen. *Microbiology, 168*(3), 1–15. https://doi.org/10.1099/mic.0.001153

Deng, Y., Chen, G., Bao, X., He, J., & Li, Q. (2024). Characterization of the complete mitochondrial genome of *Mucor indicus* Lendn. 1930 (Mucorales: Mucoraceae), isolated from the wine fermentation system. *Mitochondrial DNA Part B, 9*, 845–849. https://doi.org/10.1080/23802359.2024.2371376

Devers, E. A., Branscheid, A., May, P., & Krajinski, F. (2011). Stars and symbiosis: microRNA-and microRNA*-mediated transcript cleavage involved in arbuscular mycorrhizal symbiosis. *Plant Physiology*, *156*(4), 1990–2010. https://doi.org/10.1104/pp.111.172627

Dickinson, C. H. (1976). Fungi on the aerial surface of higher plants. In T. F. Preece & C. H. Dickinson (Eds.), *Microbiology of aerial plant surfaces* (pp. 293–324). Academic Press.

Dinakarkumar, Y., Gnanasekaran, R., Reddy, G. K., Vasu, V., Balamurugan, P., & Murali, G. (2024). Fungal bioremediation: An overview of the mechanisms, applications and future perspectives. *Environmental Chemistry and Ecotoxicology*, *6*, 293–302.

Dissanayake, A. J., Purahong, W., Wubet, T., Hyde, K. D., Zhang, W., Xu, H., . . . Yan, J. (2018). Direct comparison of culture-dependent and culture-independent molecular approaches reveal the diversity of fungal endophytic communities in stems of grapevine (Vitis vinifera). *Fungal Diversity*, *90*(1), 85–107. https://doi.org/10.1007/s13225-018-0399-3

Dissanayake, A. J., Zhu, J. T., Chen, Y. Y., Maharachchikumbura, S. S., Hyde, K. D., & Liu, J. K. (2024). A re-evaluation of *Diaporthe*: Refining the boundaries of species and species complexes. *Fungal Diversity*, *126*(1), 1–125. https://doi.org/10.1007/s13225-024-00538-7

Dixon, L. J., Schlub, R. L., Pernezny, K., & Datnoff, L. E. (2009). Host specialization and phylogenetic diversity of *Corynespora cassiicola*. *Phytopathology*, *99*(9), 1015–1027. https://doi.org/10.1094/PHYTO-99-9-1015

Doilom, M., Dissanayake, A. J., Wanasinghe, D. N., Boonmee, S., Liu, J. K., Bhat, D. J., . . . Hyde, K. D. (2017). Microfungi on *Tectona grandis* (teak) in Northern Thailand. *Fungal Diversity*, *82*(1), 107–182. https://doi.org/10.1007/s13225-016-0368-7

Doilom, M., Shuttleworth, L. A., Roux, J., Chukeatirote, E., & Hyde, K. D. (2015). Botryosphaeriaceae associated with *Tectona grandis* (teak) in Northern Thailand. *Phytotaxa*, *233*(1), 1–26. https://doi.org/10.11646/phytotaxa.233.1.1

Dong, W., Wang, B., Hyde, K. D., McKenzie, E. H., Raja, H. A., Tanaka, K., . . . Hongsanan, S. (2020). Freshwater Dothideomycetes. *Fungal Diversity, 105*(1), 319–575. https://doi.org/10.1007/s13225-020-00463-5

Dou, Z. P., He, W., & Zhang, Y. (2017). Does morphology matter in taxonomy of *Lasiodiplodia*? An answer from *Lasiodiplodia hyalina* sp. nov. *Mycosphere, 8*(2), 1014–1027. https://doi.org/10.5943/mycosphere/8/2/5

Du, T. Y., Karunarathna, S. C., Zhang, X., Dai, D. Q., Gao, Y., Mapook, A., . . . Tibpromma, S. (2022). Morphology and multigene phylogeny revealed *Peroneutypa aquilariae* sp. nov. (Diatrypaceae, Xylariales) from *Aquilaria sinensis* in Yunnan Province, China. *Studies in Fungi, 7*(1), 1. https://doi.org/10.48130/SIF-2022-0018

Duduk, N., Vasić, M., & Vico, I. (2014). First report of *Penicillium polonicum* causing blue mold on stored onion (*Allium cepa*) in Serbia. *Plant Disease, 98*(10), 1440. https://doi.org/10.1094/PDIS-05-14-0550-PDN

Dutta, J., Gupta, S., Thakur, D., & Handique, P. J. (2015). First report of Nigrospora leaf blight on tea caused by *Nigrospora sphaerica* in India. *Plant Disease, 99*(3), 417. https://doi.org/10.1094/PDIS-09-14-0924-PDN

Dwibedi, V., Rath, S. K., Jain, S., Martínez-Argueta, N., Prakash, R., Saxena, S., . . . Rios-Solis, L. (2023). Key insights into secondary metabolites from various *Chaetomium* species. *Applied Microbiology and Biotechnology, 107*(4), 1077–1093. https://doi.org/10.1007/s00253-023-12365-y

Ebrahimi, L., & Fotouhifar, K. (2016). Identification of some fungi accompanying the scab symptoms in Iran. *Mycologia Iranica, 3*(1), 25–37. https://doi.org/10.22043/mi.2017.48716.1077

Edwards Molina, J. P., Navarro, B. L., Allen, T. W., & Godoy, C. V. (2022). Soybean target spot caused by *Corynespora cassiicola*: A resurgent disease in the Americas. *Tropical Plant Pathology, 47*(3), 315–331. https://doi.org/10.1007/s40858-022-00495-z

Eevers, N., Gielen, M., Sánchez-López, A., Jaspers, S., White, J. C., Vangronsveld, J., . . . Weyens, N. (2015). Optimization of isolation and cultivation of bacterial endophytes through addition of plant extract to nutrient media. *Microbial Biotechnology, 8*(4), 707-715. https://doi.org/10.1111/1751-7915.12291

Eo, J. K., Choi, J. W., & Eom, A. H. (2022). Diversity, distribution, and host plant of endophytic fungi: A focus on Korea. *Mycobiology, 50*(6), 399–407. https://doi.org/10.1080/12298093.2022.2154044

Eskander, D. M., Atalla, S. M., Hamed, A. A., & El-Khrisy, E. D. (2020). Investigation of secondary metabolites and its bioactivity from *Sarocladium kiliense* SDA20 using shrimp shell wastes. *Pharmacognosy Journal, 12*(3), 95. http://doi.org/10.5530/pj.2020.12.95

Eydoux, L., & Farrer, E. C. (2020). Does salinity affect lifestyle switching in the plant pathogen Fusarium solani?. *Access Microbiology, 2*(6), e000114. https://doi.org/10.1099/acmi.0.000114

Fan, B., Dewapriya, P., Li, F., Grauso, L., Blümel, M., Mangoni, A., . . . Tasdemir, D. (2020). Pyrenosetin D, a new pentacyclic decalinoyltetramic acid derivative from the algicolous fungus *Pyrenochaetopsis* sp. FVE-087. *Marine Drugs, 18*(6), 281. https://doi.org/10.3390/md18060281

Feng, J. W., Liu, W. T., Chen, J. J., & Zhang, C. L. (2021). Biogeography and ecology of Magnaporthales: A case study. *Frontiers in Microbiology, 12*, 654380. https://doi.org/10.3389/fmicb.2021.654380

Feng, R., Wang, H., Zhang, X., Li, T., Huang, C., Zhang, S., . . . Gou, J. (2024). Characteristics of *Corynespora cassiicola*, the causal agent of tobacco Corynespora leaf spot, revealed by genomic and metabolic phenomic analysis. *Scientific Reports, 14*(1), 18326. https://doi.org/10.1038/s41598-024-67510-y

Fernández-Silva, F., Capilla, J., Mayayo, E., Sutton, D., & Guarro, J. (2014). Combination therapy in the treatment of experimental invasive fungal infection by *Sarocladium* (*Acremonium*) *kiliense*. *International Journal of Antimicrobial Agents, 44*(2), 136–139.

Fisher, P. J., & Petrini, O. (1992). Fungal saprobes and pathogens as endophytes of rice (*Oryza sativa* L.). *New Phytologist, 120*(1), 137–143. https://doi.org/10.1111/j.1469-8137.1992.tb01066.x

Floudas, D., & Hibbett, D. S. (2015). Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. *Fungal Biology, 119*(8), 679–719. http://doi.org/10.1016/j.funbio.2015.04.003

Fortes, N. G., & Vitoria, N. S. (2023). New records of *Chaetomium* and *Chaetomium*-like species (Ascomycota, Chaetomiaceae) on *Syagrus coronata* from the Raso da Catarina Ecological Station (ESEC), Caatinga, Bahia, Brazil. *Mycotaxon, 137*(1), 1.

Fu, M., Crous, P. W., Bai, Q., Zhang, P. F., Xiang, J., Guo, Y. S., . . . Wang, G. P. (2019). *Colletotrichum* species associated with anthracnose of *Pyrus* spp. in China. *Persoonia, 42*(1), 1–35. https://doi.org/10.3767/persoonia.2019.42.01

Fuentes-Aragón, D., Juárez-Vázquez, S. B., Vargas-Hernández, M., & Silva-Rojas, H. V. (2018). *Colletotrichum fructicola,* a member of *Colletotrichum gloeosporioides* sensu lato, is the causal agent of anthracnose and soft rot in avocado fruits cv. "Hass." *Mycobiology, 46*(2), 92–100. https://doi.org/10.1080/12298093.2018.1454010

Gamboa, M. A., & Bayman, P. (2001). Communities of endophytic fungi in leaves of a tropical timber tree (Guarea guidonia: Meliaceae) 1. *Biotropica, 33*(2), 352–360. https://doi.org/10.1111/j.1744-7429.2001.tb00187.x

Gams, W., & Hawksworth, D. L. (1975). Identity of *Acrocylindrium oryzae* Sawada and a similar fungus causing sheath-rot of rice. *Kavaka, 3,* 57–61.

Genre, A., Chabaud, M., Balzergue, C., Puech-Pagès, V., Novero, M., Rey, T., . . . Barker, D. G. (2013). Short-chain chitin oligomers from arbuscular mycorrhizal fungi trigger nuclear C a2+ spiking in *Medicago truncatula* roots and their production is enhanced by strigolactone. *New Phytologist, 198*(1), 190-202. https://doi.org/10.1111/nph.12146

Giraldo, A., & Crous, P. W. (2019). Inside Plectosphaerellaceae. *Studies in Mycology, 92*(1), 227–286. https://doi.org/10.1016/j.simyco.2018.10.005

Glass, N. L., & Donaldson, G. C. (1995). Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and Environmental Microbiology, 61*(4), 1323–1330.

Gough, C., & Cullimore, J. (2011). Lipo-chitooligosaccharide signaling in endosymbiotic plant-microbe interactions. *Molecular Plant-Microbe Interactions, 24*(8), 867–878. https://doi.org/10.1094/MPMI-01-11-0019

Gu, Y., Lv, B., Nian, X., Xie, X., & Yang, X. (2025). Optimized extraction, comprehensive chemical profiling, and antioxidant evaluation of volatile oils from *Wurfbainia villosa* (Lour.) Škorničk. & AD Poulsen Leaves. *Plants, 14*(13), 2041. https://doi.org/10.3390/plants14132041

Guarnaccia, V., Gehrmann, T., Silva-Junior, G. J., Fourie, P. H., Haridas, S., Vu, D., . . . Groenewald, J. Z. (2019). *Phyllosticta citricarpa* and sister species of global importance to Citrus. *Molecular Plant Pathology, 20*(12), 1619–1635. https://doi.org/10.1111/mpp.12861

Gunatilaka, A. L. (2006). Natural products from plant-associated microorganisms: Distribution, structural diversity, bioactivity, and implications of their occurrence. *Journal of Natural Products, 69*(3), 509–526. https://doi.org/10.1021/np058128n

Guo, B., Wang, Y., Sun, X., & Tang, K. (2008). Bioactive natural products from endophytes: A review. *Applied Biochemistry and Microbiology, 44*(2), 136–142. https://doi.org/10.1134/S0003683808020026

Guo, L. D., Hyde, K. D., & Liew, E. C. Y. (1998). A method to promote sporulation in palm endophytic fungi. *Fungal Diversity*, 1, 109–113

Guo, Q., Zeng, Y., & Jiang, Y. L. (2024). First report of *Nigrospora chinensis* causing dragon fruit (*Selenicereus monacanthus*) stem spot in China. *Plant Disease, 108*(7), 2229. https://doi.org/10.1094/PDIS-02-24-0485-PDN

Guo, W., Wang, S., Li, N., Li, F., Zhu, T., Gu, Q., . . . Li, D. (2018). Saroclides A and B, cyclic depsipeptides from the mangrove-derived fungus *Sarocladium kiliense* HDN11-112. *Journal of Natural Products, 81*(4), 1050–1054. https://doi.org/10.1021/acs.jnatprod.7b00644

Güssow, H. T. (1905). Notes on a disease of cucumbers. II. *Journal of the Royal Agricultural Society of England, 65*, 271–272.

Hallmann, J., Quadt-Hallmann, A., Mahaffee, W. F., & Kloepper, J. W. (1997). Bacterial endophytes in agricultural crops. *Canadian Journal of Microbiology, 43*(10), 895–914. https://doi.org/10.1139/m97-131

Han, L. S., Liu, C., Dai, D. Q., Promputtha, I., Elgorban, A. M., Al-Rejaie, S., . . . & Wijayawardene, N. N. (2024). Five new species, two new sexual morph reports, and one new geographical record of *Apiospora* (Amphisphaeriales, Sordariomycetes) isolated from bamboo in Yunnan, China. *Frontiers in Cellular and Infection Microbiology, 14,* 1476066. https://doi.org/10.3389/fcimb.2024.1476066

Hao, Y., Aluthmuhandiram, J. V., Chethana, K. T., Manawasinghe, I. S., Li, X., Liu, M., . . . Zhang, W. (2020). *Nigrospora* species associated with various hosts from Shandong Peninsula, China. *Mycobiology*, *48*(3), 169–183. https://doi.org/10.1080/12298093.2020.1761747

Harish, J., Venkateshbabu, G., Prasannakumar, M. K., Karan, R., Devanna, P., & Manjunatha, C. (2024). *Sarocladium kiliense*: A first report of phytopathogenic fungus causing maize stalk rot in India. *Physiological and Molecular Plant Pathology, 134,* 102449. https://doi.org/10.1016/j.pmpp.2024.102449

Hawksworth, D. L. (2001). The magnitude of fungal diversity: The 1· 5 million species estimate revisited. *Mycological Research*, *105*(12), 1422–1432. https://doi.org/10.1017/S0953756201004725

Hawksworth, D. L., & Lücking, R. (2017). Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum*, *5*(4), 10–1128. https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

Hawksworth, D. L., Crous, P. W., Redhead, S. A., Reynolds, D. R., Samson, R. A., Seifert, K. A., . . . Zhang, N. (2011). The Amsterdam declaration on fungal nomenclature. *IMA Fungus*, *2*(1), 105–112. https://doi.org/10.5598/imafungus.2011.02.01.14

Hayashi, K., Hirooka, Y., Oki, T., Shimomoto, Y., & Yano, K. (2024). First report of brown rhizome rot of ginger (*Zingiber officinale*) caused by *Musidium stromaticum*. *Journal of General Plant Pathology*, *90*(4), 223–228. https://doi.org/10.1007/s10327-024-01180-6

Hernandez-Ramirez, G., Barber, D., Tome-Amat, J., Garrido-Arandia, M., & Diaz-Perales, A. (2021). *Alternaria* as an inducer of allergic sensitization. *Journal of Fungi, 7*(10), 838. https://doi.org/10.3390/jof7100838

Hernãndez-Restrepo, M., Bezerra, J. D., Tan, Y. P., Wiederhold, N., Crous, P. W., Guarro, J., . . . Gené, J. (2019). Re-evaluation of *Mycoleptodiscus* species and morphologically similar fungi. *Persoonia, 42*(1), 205–227. https://doi.org/10.3767/persoonia.2019.42.08

Hilário, S., & Gonçalves, M. F. (2023). Mechanisms underlying the pathogenic and endophytic lifestyles in Diaporthe: An omics-based approach. *Horticulturae*, *9*(4), 423. https://doi.org/10.3390/horticulturae9040423

Hill, R., Buggs, R. J., Vu, D. T., & Gaya, E. (2022). Lifestyle transitions in fusarioid fungi are frequent and lack clear genomic signatures. *Molecular Biology and Evolution*, *39*(4), msac085. https://doi.org/10.1093/molbev/msac085

Hong, X., Chen, S., Wang, L., Liu, B., Yang, Y., Tang, X., . . . Huang, S. X. (2021). First report of *Nigrospora sphaerica* causing fruit dried-shrink disease in *Akebia trifoliata* from China. *Plant Disease, 105*(8), 2244. https://doi.org/10.1094/PDIS-11-20-2471-PDN

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., . . . Xie, N. (2020). Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere, 11,* 1553–2107. https://doi.org/10.5943/mycosphere/11/1/13

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., . . . Xie, N. (2020). Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. *Fungal Diversity, 105,* 17-318. https://doi.org/10.1007/s13225-020-00462-6

Houbraken, J., & Samson, R. A. (2011). Phylogeny of *Penicillium* and the segregation of Trichocomaceae into three families. *Studies in Mycology*, *70*(1), 1–51. https://doi.org/10.3114/sim.2011.70.01

Houbraken, J., Kocsubé, S., Visagie, C. M., Yilmaz, N., Wang, X. C., Meijer, M., . . . Frisvad, J. C. (2020). Classification of *Aspergillus*, *Penicillium*, *Talaromyces* and related genera (Eurotiales): An overview of families, genera, subgenera, sections, series and species. *Studies in Mycology*, *95,* 5–169. https://doi.org/10.1016/j.simyco.2020.05.002

Hu, Y., Wei, G. Y., Wen, J. T., Chang, L. F., Chen, Y. S., Wang, Y., . . . Nizamani, M. M. (2024). Endophytic fungi: Tracing the evolutionary roots and exploring the diversity of plant-fungal symbioses. *Current Research in Environmental & Applied Mycology (Journal of Fungal Biology)*, *14*(1), 1–48. https://doi.org/10.5943/cream/14/1/1

Huang, F., Chen, G. Q., Hou, X., Fu, Y. S., Cai, L., Hyde, K. D., . . . Li, H. Y. (2013). *Colletotrichum* species associated with cultivated citrus in China. *Fungal Diversity*, *61*(1), 61–74. https://doi.org/10.1007/s13225-013-0232-y

Huang, S., Cao, J., Huang, Y., Luo, Q., Luo, J., Li, Q., . . . Zhang, L. (2025). First report of *Michelia maudiae* leaf blight caused by *Colletotrichum siamense* in China. *Crop Protection*, *195*, 107263. https://doi.org/10.1016/j.cropro.2025.107263

Hughes, S. J. (1952). Fungi from the Gold Coast. I. *Mycological Papers*, *48*, 1–91.

Hurdeal, V. G., Gentekaki, E., Hyde, K. D., Nguyen, T. T., & Lee, H. B. (2021). Novel *Mucor* species (Mucoromycetes, Mucoraceae) from northern Thailand. *MycoKeys*, *84*, 57. https://doi.org/10.3897/mycokeys.84.71530

Hyde, K. D., & Soytong, K. (2008). The fungal endophyte dilemma. *Fungal Diversity*, *33*(163), e173.

Hyde, K. D., Baldrian, P., Chen, Y., Thilini Chethana, K. W., De Hoog, S., Doilom, M., . . . Hilário, S. (2024). Current trends, limitations and future research in the fungi. *Fungal Diversity*, *125*(1), 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde, K. D., Dong, Y., Phookamsak, R., Jeewon, R., Bhat, D. J., Jones, E. B. G., . . . Perera, R. H. (2020). Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *100*(1), 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde, K. D., Fröhlich, J., & Taylor, J. E. (1998). Fungi from palms. XXXVI. Reflections on unitunicate ascomycetes with apiospores. *Sydowia*, *50*, 21–80.

Hyde, K. D., Hongsanan, S., Jeewon, R., Bhat, D. J., McKenzie, E. H. C., Jones, E. B. J., . . . Tanaka, K. (2016). Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *80*, 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde, K. D., Jones, E. B. G., Liu, J. K., Ariyawansa, H. A., Boehm, E., Boonmee, S., . . . Zhang, M. (2013). Families of Dothideomycetes. *Fungal Diversity*, *63*, 1–313. https://doi.org/10.1007/s13225-013-0263-4

Hyde, K. D., Noorabadi, M. T., Thiyagaraja, V., He, M. Q., Johnston, P. R., Wijesinghe, S. N., . . . Zvyagina, E. (2024). The 2024 outline of fungi and fungus-like taxa. *Mycosphere*, *15*, 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

Hyde, K. D., Tennakoon, D. S., Jeewon, R., Bhat, D. J., Maharachchikumbura, S. S., Rossi, W., . . . Nguyen, T. T. (2019). Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *96*(1), 1–242. https://doi.org/10.1007/s13225-019-00429-2

Hyun Khang, C., & Valent, B. (2010). *Magnaporthe oryzae* and rice blast disease. In K. A. Borkovich & D. J. Ebbole (Eds.), *Cellular and molecular biology of filamentous fungi* (pp. 591–606). Wiley.

Jash, S., Sarkar, A., Moinuddin, G., & Kundu, R. (2025). *Botryosphaeria*. In N. Amaresan & K. Kumar (Eds.), *Compendium of phytopathogenic microbes in agro-ecology: Vol. 1 fungi* (pp. 43–74). Springer Nature Switzerland. https://doi.org/10.1007/978-3-031-81770-0_3

Jayasiri, S. C., Hyde, K. D., Jones, E. B., McKenzie, E. H., Jeewon, R., Phillips, A. J., . . . Kang, J. C. (2019). Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. *Mycosphere*, *10*, 1–186. https://doi.org/10.5943/mycosphere/10/1/1

Jayawardena, R. S., Bhunjun, C. S., Hyde, K. D., Gentekaki, E., & Itthayakorn, P. (2021). *Colletotrichum*: Lifestyles, biology, morpho-species, species complexes and accepted species. *Mycosphere*, *12*(1), 519–669. https://doi.org/10.5943/mycosphere/12/1/7

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y. R., Suwannarach, N., Sysouphanthong, P., . . . Armand, A. (2023). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *117*(1), 1–272. https://doi.org/10.1007/s13225-023-00512-z

Jayawardena, R. S., Purahong, W., Zhang, W., Wubet, T., Li, X. H., Liu, M., . . . Yan, J. (2018). Biodiversity of fungi on *Vitis vinifera* L. revealed by traditional and high-resolution culture-independent approaches. *Fungal Diversity, 90*(1), 1–84. https://doi.org/10.1007/s13225-018-0398-4

Jeewon, R., Yeung, Q. S., Wannasinghe, D. N., Rampadarath, S., Puchooa, D., Wang, H. K., . . . Hyde, K. D. (2018). Hidden mycota of pine needles: Molecular signatures from PCR-DGGE and Ribosomal DNA phylogenetic characterization of novel phylotypes. *Scientific Reports*, *8*(1), 18053. https://doi.org/10.1038/s41598-018-36573-z

Jiang, H. B., Hyde, K. D., Jayawardena, R. S., Doilom, M., Xu, J., & Phookamsak, R. (2019). Taxonomic and phylogenetic characterizations reveal two new species and two new records of *Roussoella* (Roussoellaceae, Pleosporales) from Yunnan, China. *Mycological Progress, 18*(4), 577–591. https://doi.org/10.1007/s11557-019-01471-9

Jiang, X. Z., Yu, Z. D., Ruan, Y. M., & Wang, L. (2018). Three new species of *Talaromyces* sect. *Talaromyces* discovered from soil in China. *Scientific Reports, 8*(1), 4932. https://doi.org/10.1038/s41598-018-23370-x

Jumpponen, A. (2001). Dark septate endophytes–are they mycorrhizal?. *Mycorrhiza*, *11*(4), 207–211. https://doi.org/10.1007/s005720100112

Kang, S. J., Zhao, L., Wang, H., Gao, J. M., & Qi, J. (2024). Chemical structures, biological activities, and biosynthetic analysis of secondary metabolites of the Diatrypaceae family: A comprehensive review. *Mycology, 15*(3), 322–344. https://doi.org/10.1080/21501203.2024.2341648

Karimi, K., & Zamani, A. (2013). *Mucor indicus*: Biology and industrial application perspectives: A review. *Biotechnology Advances, 31*(4), 466–481. https://doi.org/10.1016/j.biotechadv.2013.01.009

Kee, Y. J., Hafifi, A. B., Huda-Shakirah, A. R., Wong, K. L., Jin, X. L., Siti Nordahliawate, M. S., . . . Mohd, M. H. (2019). First report of reddish-brown spot disease of red-fleshed dragon fruit (*Hylocereus polyrhizus*) caused by *Nigrospora lacticolonia* and *Nigrospora sphaerica* in Malaysia. *Crop Protection, 122,* 165–170. https://doi.org/10.1016/j.cropro.2019.05.006

Khokhar, I., Jia, Y., Mukhtar, I., Wang, J., & Yan, Y. C. (2019). First report of *Penicillium polonicum* causing blue mold on stored pear (*Pyrus bretschneideri*) fruits in China. *Plant Disease, 103,* 3279. https://doi.org/10.1094/PDIS-05-19-1041-PDN

Khuna, S., Kumla, J., Thitla, T., Senwanna, C., & Suwannarach, N. (2024). First report of *Colletotrichum siamense* causing leaf anthracnose on jackfruit in Thailand. *Plant Disease, 108*(12), 3. https://doi.org/10.1094/PDIS-06-24-1273-PDN

Kim, D. M., Lee, M. H., Suh, M. K., Ha, G. Y., Kim, H., & Choi, J. S. (2013). Onychomycosis caused by *Chaetomium globosum*. *Annals of Dermatology, 25*(2), 232–236. https://doi.org/10.5021/ad.2013.25.2.232

Kim, M. S., Heinzelmann, R., Labbé, F., Ota, Y., Elías-Román, R. D., Pildain, M. B., . . . Klopfenstein, N. B. (2022). *Armillaria* root diseases of diverse trees in widespread global regions. In F. O. Asiegbu & A. Kovalchuk (Eds.), *Forest microbiology* (pp. 361–378). Academic Press.

Kim, W. K., Hwang, Y. S., & Yu, S. H. (2008). Two species of *Penicillium* associated with blue mold of yam in Korea. *Mycobiology*, *36*(4), 217–221.

Kirk, P. M., Cannon, P. F., Minter, D. W., & Stalpers, J. A. (2008). *Dictionary of the fungi*. CABI databases.

Kitamura, H., Kubota, Y., Tomimasu, R., Akashi, M., Mori, T., Mine, Y., . . . Miyahara, M. (2022). Non-valvular infective endocarditis caused by *Sarocladium kiliense* in an immunocompromised patient with aplastic anemia. *Internal Medicine, 61*(8), 1279–1283. https://doi.org/10.2169/internalmedicine.7536-21

Klaubauf, S., Tharreau, D., Fournier, E., Groenewald, J. Z., Crous, P. W., de Vries, R. P., . . . Lebrun, M. H. (2014). Resolving the polyphyletic nature of *Pyricularia* (Pyriculariaceae). *Studies in Mycology, 79*(1), 85–120. https://doi.org/10.1016/j.simyco.2014.09.004

Knapp, D. G., Kovács, G. M., Zajta, E., Groenewald, J. Z., & Crous, P. W. (2015). Dark septate endophytic pleosporalean genera from semiarid areas. *Persoonia, 35*(1), 87–100.

Konta, S., Hyde, K. D., Eungwanichayapant, P. D., Karunarathna, S. C., Samarakoon, M. C., Xu, J., . . . Tibpromma, S. (2021). Multigene phylogeny reveals *Haploanthostomella elaeidis* gen. et sp. nov. and familial replacement of *Endocalyx* (Xylariales, Sordariomycetes, Ascomycota). *Life, 11*(6), 486. https://doi.org/10.3390/life11060486

Kulik, M. M. (1984). Symptomless infection, persistence, and production of pycnidia in host and non-host plants by Phomopsis batatae, Phomopsis phaseoli, and Phomopsis sojae, and the taxonomic implications. *Mycologia, 76*(2), 274–291. https://doi.org/10.1080/00275514.1984.12023837

Kurera, W. M., Adikaram, N. K., Yakandawala, D. M., Maharachchikumbura, S. S., Jayasinghe, L., & Samarakoon, K. (2023). Molecular and phenotypic characterization of *Colletotrichum plurivorum* and *Colletotrichum musae* causing banana anthracnose disease in the Central Province of Sri Lanka. *Journal of the National Science Foundation of Sri Lanka, 51*(2), 2. https://doi.org/10.4038/jnsfsr.v51i2.11217

Lau, C. S. B., & Long, C. L. (Eds.). (n.d.). *Medicinal plants and mushrooms of Yunnan Province of China*. CRC Press.

Lebreton, A., Corre, E., Jany, J. L., Brillet-Guéguen, L., Pèrez-Arques, C., Garre, V., . . . Barbier, G. (2020). Comparative genomics applied to *Mucor* species with different lifestyles. *BMC Genomics, 21*(1), 1–21. https://doi.org/10.1186/s12864-019-6256-2

Lee, K., Missaoui, A., Mahmud, K., Presley, H., & Lonnee, M. (2021). Interaction between grasses and Epichloë endophytes and its significance to biotic and abiotic stress tolerance and the rhizosphere. *Microorganisms, 9*(11), 2186. https://doi.org/10.3390/microorganisms9112186

Lee, W., Kim, D. G., Perera, R. H., Kim, J. S., Cho, Y., Lee, J. W., . . . Lim, Y. W. (2023). Diversity of *Nigrospora* (Xylariales, Apiosporaceae) species identified in Korean macroalgae including five unrecorded species. *Mycobiology, 51*(6), 401–409. https://doi.org/10.1080/12298093.2023.2283272

Lee, W., Kim, J. S., Jo, S., Seo, C. W., & Lim, Y. W. (2025). Taxonomic study of sixteen unrecorded and five new species of Hypocreales from the Korean marine environment. *Mycobiology, 53*(2), 144–167.

Lei, L. R., Gong, L. Q., Jin, M. Y., Wang, R., Liu, R., Gao, J., . . . Deng, Y. (2022). Research advances in the structures and biological activities of secondary metabolites from *Talaromyces*. *Frontiers in Microbiology, 13*, 984801. https://doi.org/10.3389/fmicb.2022.984801

Li, F., Guo, W., Wu, L., Zhu, T., Gu, Q., Li, D., . . . Che, Q. (2018). Saroclazines A–C, thio-diketopiperazines from mangrove-derived fungi *Sarocladium kiliense* HDN11-84. *Archives of Pharmacal Research, 41*(1), 30–34. https://doi.org/10.1007/s12272-017-0961-7

Li, H. Y., Liu, C. Y., & Liu, Y. L. (2023). First report of *Mucor irregularis* causing flower rot on *Selenicereus undatus* in China. *Plant Disease, 107*(8), 2520. https://doi.org/10.1094/PDIS-01-23-0117-PDN

Li, H., Zhou, G. Y., Liu, J. A., & Xu, J. (2016). Population genetic analyses of the fungal pathogen *Colletotrichum fructicola* on tea-oil trees in China. *PLoS One, 11*(6), e0156841. https://doi.org/10.1371/journal.pone.0156841

Li, L., Pan, H., Chen, M. Y., Zhang, S. J., & Zhong, C. H. (2018). First report of *Nigrospora oryzae* causing brown/black spot disease of kiwifruit in China. *Plant Disease, 102*(1), 243. https://doi.org/10.1094/PDIS-05-17-0668-PDN

Li, Q. R., Habib, K., Long, S. H., Wu, Y. P., Zhang, X., Hu, H. M., . . . Kang, J. C. (2024). Unveiling fungal diversity in China: New species and records within the Xylariaceae. *Mycosphere, 15*(1), 275–364. https://doi.org/10.5943/mycosphere/15/1/2

Li, Q. R., Tan, P., Jiang, Y. L., Hyde, K. D., McKenzie, E. H., Bahkali, A. H., . . . Wang, Y. (2013). A novel *Trichoderma* species isolated from soil in Guizhou, *T. guizhouense*. *Mycological Progress, 12*(2), 167–172. https://doi.org/10.1007/s11557-012-0821-2

Li, Q. R., Wu, Y. P., Pi, Y. H., Long, S. H., & Wijayawardene, N. N. (2022). Two new species and a new record of *Astrocystis* from Southwestern China. *MycoAsia, 1*. https://doi.org/10.59265/mycoasia.2022-08

Liang, X., Peng, Y., Liu, Y., Wang, M., Yang, Y., & Zhang, Y. (2019). First report of *Bipolaris bicolor* causing a leaf spot disease on rubber tree. *Journal of Phytopathology, 167*(10), 553–557. https://doi.org/10.1111/jph.12839

Liao, C. F., Doilom, M., Bhat, D. J., Chethana, K. W., Tangtrakulwanich, K., Yang, Y. H., . . . Dong, W. (2025b). Unveiling four new taxa and *Nigrosynnema natarajanensis* comb. nov. in Stachybotryaceae (Hypocreales) from monocotyledon plants in Guangdong Province, China. *MycoKeys, 114*, 299. https://doi.org/10.3897/mycokeys.114.139325

Liao, C. F., Doilom, M., Jeewon, R., Hyde, K. D., Manawasinghe, I. S., Chethana, K. W., . . . Htet, Z. H. (2025a). Challenges and update on fungal endophytes: Classification, definition, diversity, ecology, evolution and functions. *Fungal Diversity, 131*(1), 301–367. https://doi.org/10.1007/s13225-025-00550-5

Liao, C. F., Hyde, K. D., Thilini Chethana, K. W., Dong, W., Yang, Y. H., & Doilom, M. (2024b). Three new *Periconia* species isolated from *Wurfbainia villosa* in Guangdong, China: A discussion on the doubtful taxa clustering in this genus. *Diversity*, *16*(3), 141. https://doi.org/10.3390/d16030141

Liao, C. F., Senanayake, I. C., Dong, W., Thilini Chethana, K. W., Tangtrakulwanich, K., Zhang, Y. X., . . . Doilom, M. (2023). Taxonomic and phylogenetic updates on *Apiospora*: Introducing four new species from *Wurfbainia villosa* and grasses in China. *Journal of Fungi*, *9*(11), 1087. https://doi.org/10.3390/jof9111087

Liao, C. F., Yang, Y. H., Dong, W., Tangtrakulwanich, K., Zhang, Y. X., Khan, S., . . . Doilom, M. (2024). *Tetraploa wurfbainiae* sp. nov. (Tetraplosphaeriaceae, Pleosporales) isolated from *Wurfbainia villosa* in Guangdong, China. *New Zealand Journal of Botany, 62*(2-3), 303-316.

Liao, R., Chen, Y., Li, L., Zhan, R., & Chen, Y. (2025c). First report of leaf spot caused by *Corynespora cassiicola* on *Pogostemon cablin* in Guangdong, China. *Plant Disease, 109*(1), 233. https://doi.org/10.1094/PDIS-09-24-1817-PDN

Liao, Y. M., Wang, Z. X., Wei, M. C., & Wang, C. (2020). First report of *Phyllosticta capitalensis* causing black spot disease on *Psidium guajava* in mainland China. *Plant Disease*, *104*(14), 3252. https://doi.org/10.1094/PDIS-02-20-0338-PDN

Lijuan, P., Youlian, Y., Kevin, D. H., Bahkali, A, H., & Zuoyi, Liu. (2012). *Colletotrichum* species on Citrus leaves in Guizhou and Yunnan provinces, China. *Cryptogamie Mycologie, 33*(3), 267–283. https://doi.org/10.7872/crym.v33.iss3.2012.267

Lim, M., & Shu, Y. (2022). *The future is fungi: How fungi can feed us, heal us, free us and save our world.* Thames & Hudson Australia.

Lin, X., Huang, L., Liang, H., Hou, C., Ling, X., Chen, Y., . . . Yang, J. (2023). Genome-wide identification and functional characterization of borneol dehydrogenases in *Wurfbainia villosa*. *Planta, 258*(4), 69. https://doi.org/10.1007/s00425-023-04221-0

Link, H. F. (1809). Observationes in ordines plantarum naturales. *Dissertatio, 1*, 1-33.

Liu, F., Wang, J., Li, H., Wang, W., & Cai, L. (2019b). *Setophoma* spp. on *Camellia sinensis*. *Fungal Systematics and Evolution, 4*, 43–57. https://doi.org/10.3114/fuse.2019.04.05

Liu, F., Weir, B. S., Damm, U., Crous, P. W., Wang, Y., Liu, B., . . . Cai, L. (2015). Unravelling *Colletotrichum* species associated with *Camellia*: Employing ApMat and GS loci to resolve species in the *C. gloeosporioides* complex. *Persoonia, 35*(1), 63–86. https://doi.org/10.3767/003158515X687597

Liu, F., Wu, J. B., Zhan, R. L., & Ou, X. C. (2016a). First report of reddish-brown spot disease on pitaya caused by *Nigrospora sphaerica* in China. *Plant Disease, 100*(8), 1792. https://doi.org/10.1094/PDIS-03-16-0313-PDN

Liu, J. K., Phookamsak, R., Dai, D. Q., Tanaka, K., Jones, E. G., Xu, J. C., . . . Hyde, K. D. (2014). Roussoellaceae, a new pleosporalean family to accommodate the genera *Neoroussoella* gen. nov., *Roussoella* and *Roussoellopsis*. *Phytotaxa, 181*(1), 1–33. https://doi.org/10.11646/phytotaxa.181.1.1

Liu, J. K., Phookamsak, R., Doilom, M., Wikee, S., Li, Y. M., Ariyawansha, H., . . . Romero, A. I. (2012). Towards a natural classification of Botryosphaeriales. *Fungal Diversity, 57*(1), 149–210. https://doi.org/10.1007/s13225-012-0207-4

Liu, J., Hu, Y., Luo, X., Castañeda-Ruíz, R. F., Xia, J., Xu, Z., . . . Ma, J. (2023). Molecular phylogeny and morphology reveal four novel species of *Corynespora* and *Kirschsteiniothelia* (Dothideomycetes, Ascomycota) from China: A checklist for *Corynespora* reported worldwide. *Journal of Fungi, 9*(1), 107. https://doi.org/10.3390/jof9010107

Liu, L. M., Zhao, K. H., Zhao, Y., Zhang, Y. L., Fu, Q., & Huang, S. W. (2021). *Nigrospora oryzae* causing panicle branch rot disease on *Oryza sativa* (rice). *Plant Disease, 105*(9), 2724. https://doi.org/10.1094/PDIS-01-21-0065-PDN

Liu, X., Shi, T., Li, B., Li, C., & Huang, G. (2019c). *Colletotrichum* species associated with cassava anthracnose in China. *Journal of Phytopathology, 167*(1), 1–9. https://doi.org/10.1111/jph.12765

Liu, Y. J., Whelen, S., & Hall, B. D. (1999). Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution, 16*(12), 1799–1808.

Liu, Y. W., & Zeng, X. Y. (2022). *Acrocalymmachuxiongense* sp. nov., a new species of Acrocalymmaceae (Pleosporales) on leaves of *Quercus*. *Biodiversity Data Journal, 10.* https://doi.org/10.3897/BDJ.10.e89635

Liu, Y., An, J., Safdar, A., Shen, Y., Sun, Y., Shu, W., . . . He, F. (2024). Identification and characterization of *Nigrospora* species and a novel species, *Nigrospora anhuiensis*, causing black leaf spot on rice and wild rice in the Anhui Province of China. *Journal of Fungi, 10*(2), 156. https://doi.org/10.3390/jof10020156

Lombard, L., Houbraken, J., Decock, C., Samson, R. A., Meijer, M., Réblová, M., . . . Crous, P. W. (2016). Generic hyper-diversity in Stachybotriaceae. *Persoonia, 36*(1), 156–246. https://doi.org/10.3767/003158516X691582

Lombard, L., van der Merwe, N. A., Groenewald, J. Z., & Crous, P. W. (2015). Generic concepts in Nectriaceae. *Studies in Mycology, 80*(1), 189–245.

Long, S., Liu, L., Pi, Y., Wu, Y., Lin, Y., Zhang, X., . . . Wang, F. (2021). New contributions to Diatrypaceae from karst areas in China. *MycoKeys, 83,* 1. https://doi.org/10.3897/mycokeys.83.68926

Lu, H., Wei, T., Lou, H., Shu, X., & Chen, Q. (2021). A critical review on communication mechanism within plant-endophytic fungi interactions to cope with biotic and abiotic stresses. *Journal of Fungi*, *7*(9), 719. https://doi.org/10.3389/fmicb.2024.1345210

Luangsa-Ard, J., Houbraken, J., van Doorn, T., Hong, S. B., Borman, A. M., Hywel-Jones, N. L., . . . Samson, R. A. (2011). *Purpureocillium*, a new genus for the medically important *Paecilomyces lilacinus*. *FEMS Microbiology Letters*, *321*(2), 141–149. https://doi.org/10.1111/j.1574-6968.2011.02322.x

Luo, M., Zhao, M., Huang, Y., Liu, J., Huang, Q., Shu, Y., . . . Dong, Z. (2022). First record of *Alternaria pogostemonis*: A novel species causing leaf spots in *Pogostemon cablin*. *Pathogens*, *11*(10), 1105. https://doi.org/10.3390/pathogens11101105

Madden, A. A., Stchigel, A. M., Guarro, J., Sutton, D., & Starks, P. T. (2012). *Mucor nidicola* sp. nov., a fungal species isolated from an invasive paper wasp nest. *International Journal of Systematic and Evolutionary Microbiology*, *62*(Pt_7), 1710–1714. https://doi.org/10.1099/ijs.0.033050-0

Mahajan, M. (2021). *Talaromyces marneffei*. *Emerging Infectious Diseases*, *27*, 2278. https://doi.org/10.3201/eid2709.210318

Maharachchikumbura, S. S. N., Guo, L. D., Liu, Z. Y., & Hyde, K. D. (2016). *Pseudopestalotiopsis ignota* and *Ps. camelliae* spp. nov. associated with grey blight disease of tea in China. *Mycological Progress*, *15*(3), 1–7. https://doi.org/10.1007/s11557-016-1162-3

Maharachchikumbura, S. S., Hyde, K. D., Groenewald, J. Z., Xu, J., & Crous, P. W. (2014). *Pestalotiopsis* revisited. *Studies in Mycology*, *79*(1), 121–186. https://doi.org/10.1016/j.simyco.2014.09.005

Maharachchikumbura, S. S., Wanasinghe, D. N., Cheewangkoon, R., & Al-Sadi, A. M. (2021). Uncovering the hidden taxonomic diversity of fungi in Oman. *Fungal Diversity*, *106*(1), 229–268. https://doi.org/10.1007/s13225-020-00467-1

Manamgoda, D. S., Cai, L., Bahkali, A. H., Chukeatirote, E., & Hyde, K. D. (2011). *Cochliobolus*: An overview and current status of species. *Fungal Diversity*, *51*(1), 3–42. https://doi.org/10.1007/s13225-011-0139-4

Manamgoda, D. S., Rossman, A. Y., Castlebury, L. A., Crous, P. W., Madrid, H., Chukeatirote, E., . . . Hyde, K. D. (2014). The genus *Bipolaris*. *Studies in Mycology, 79*(1), 221–288. https://doi.org/10.1016/j.simyco.2014.10.002

Manamgoda, D. S., Udayanga, D., Cai, L., Chukeatirote, E., & Hyde, K. D. (2013). Endophytic *Colletotrichum* from tropical grasses with a new species *C. endophytica*. *Fungal Diversity, 61*(1), 107–115. https://doi.org/10.1007/s13225-013-0256-3

Manawasinghe, I. S., Hyde, K. D., Wanasinghe, D. N., Karunarathna, S. C., Maharachchikumbura, S. S. N., Samarakoon, M. C., . . . Xu, B. (2024). Fungal diversity notes 1818–1918: Taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity, 130*(1), 1–261. https://doi.org/10.1007/s13225-024-00541-y

Manawasinghe, I. S., Zhang, Y. X., Liao, C. F., Xiong, Y. R., Kularathnage, N. D., Luo, M., . . . Doilom, M. (2022). Mycosphere notes 345–386. *Mycosphere, 13*(1), 454–557. https://doi.org/10.5943/mycosphere/13/1/3

Manzar, N., Kashyap, A. S., Sharma, P. K., & Saxena, A. K. (2021). First report of leaf spot of maize caused by *Curvularia geniculata* in India. *Plant Disease, 105*(12), 4155. https://doi.org/10.1094/PDIS-03-21-0637-PDN

Mapook, A., & Hyde, K. D. (2023). Neotypification of *Muyocopron dipterocarpi*, a new host record on *Zanthoxylum fagara* (Rutaceae) and the potential for secondary metabolite production in Muyocopronaceae. *Studies in Fungi, 8*(1), 9. https://doi.org/10.48130/SIF-2023-0009

Mapook, A., Hyde, K. D., Dai, D. Q., Li, J., Jones, E. G., Bahkali, A. H., . . . Boonmee, S. (2016). *Muyocopronales*, ord. nov., (Dothideomycetes, Ascomycota) and a reappraisal of *Muyocopron* species from northern Thailand. *Phytotaxa, 265*(3), 225–237. https://doi.org/10.11646/phytotaxa.265.3.3

Marasinghe, D. S., Hongsanan, S., Zeng, X. Y., Jones, E. B., Chomnunti, P., Boonmee, S., . . . Hyde, K. D. (2023). Taxonomic monograph of epifoliar fungi. *Fungal Diversity, 121*(1), 139–334. https://doi.org/10.1007/s13225-023-00522-7

Marin-Felix, Y., Senwanna, C., Cheewangkoon, R., & Crous, P. W. (2017). New species and records of *Bipolaris* and *Curvularia* from Thailand. *Mycosphere, 8*(9), 1556–1574. https://doi.org/10.5943/mycosphere/8/9/11

Markovskaja, S., & Kačergius, A. (2014). Morphological and molecular characterisation of *Periconia pseudobyssoides* sp. nov. and closely related *P. byssoides*. *Mycological Progress, 13*(2), 291–302. https://doi.org/10.1007/s11557-013-0914-6

Martin-Pozas, T., Nováková, A., Jurado, V., Fernandez-Cortes, A., Cuezva, S., Saiz-Jimenez, C., . . . Sanchez-Moral, S. (2022). Diversity of microfungi in a high radon cave ecosystem. *Frontiers in Microbiology, 13*, 869661.

Masi, M., Zorrilla, J. G., & Meyer, S. (2022). Bioactive metabolite production in the genus *Pyrenophora* (Pleosporaceae, Pleosporales). *Toxins, 14*(9), 588. https://doi.org/10.3390/toxins14090588

McMullin, D. R., Sumarah, M. W., & Miller, J. D. (2013). Chaetoglobosins and azaphilones produced by Canadian strains of *Chaetomium globosum* isolated from the indoor environment. *Mycotoxin Research, 29*(1), 47–54. https://doi.org/10.1007/s12550-012-0144-9

Meena, M., Gupta, S. K., Swapnil, P., Zehra, A., Dubey, M. K., & Upadhyay, R. S. (2017). *Alternaria* toxins: potential virulence factors and genes related to pathogenesis. *Frontiers in Microbiology, 8*, 1451. https://doi.org/10.3389/fmicb.2017.01451

Meenatchi, A., Ramesh, V, Bagyalakshmi, K. R., Shanmugaiah, V., Rajen dran, A. (2016). Diversity of endophytic fungi from the ornamental plant–Adenium obesum. *Studies in Fungi, 1*(1), 34–42. https://doi.org/10.5943/sif/1/1/3

Mello, F. E., Mathioni, S. M., Matos, V. O., da Silva, M. A., Marques, D. B., Rambach, O., . . . Antunes, R. F. (2024). Sensitivity of *Colletotrichum plurivorum* and *C. truncatum* isolated from soybean in Brazil to SDHIs and DMIs fungicides. *Tropical Plant Pathology, 49*(1), 83–92. https://doi.org/10.1007/s40858-023-00617-1

Mortimer, P. E., Jeewon, R., Xu, J. C., Lumyong, S., & Wanasinghe, D. N. (2021). Morpho-phylo taxonomy of novel dothideomycetous fungi associated with dead woody twigs in Yunnan Province, China. *Frontiers in Microbiology, 12,* 654683. https://doi.org/10.3389/fmicb.2021.654683

Nam, H. S., Park, H. S., & Kim, Y. C. (2024). First report of coffee leaf spot caused by *Curvularia geniculata*. *Journal of Phytopathology, 172*(1), e13245. https://doi.org/10.1111/jph.13245

Nasehi, A., Sathyapriya, H., & Wong, M. Y. (2020). First report of leaf spot on oil palm caused by *Phyllosticta capitalensis* in Malaysia. *Plant Disease, 104*(1), 288. https://doi.org/10.1094/PDIS-06-19-1232-PDN

Negi, N., Ramkrishna, Banerjee, S., Meena, R. K., Bhandari, M. S., & Pandey, S. (2025). Morphology and phylogeny revealed *Colletotrichum fructicola* causing new disease symptoms on *Eucalyptus* in India. *Journal of Plant Pathology*, 1–5. https://doi.org/10.1007/s42161-025-01865-7

Nguyen, T. T., Pangging, M., Bangash, N. K., & Lee, H. B. (2020). Five new records of the family Aspergillaceae in Korea, *Aspergillus europaeus*, *A. pragensis*, *A. tennesseensis*, *Penicillium fluviserpens*, and *P. scabrosum*. *Mycobiology*, *48*(2), 81–94. https://doi.org/10.1080/12298093.2020.1726563

Norphanphoun, C., & Hyde, K. D. (2024). First report of *Colletotrichum fructicola*, *C. rhizophorae* sp. nov. and *C. thailandica* sp. nov. on mangrove in Thailand. *Pathogens, 12*(12), 1436. https://doi.org/10.3390/pathogens12121436

Norphanphoun, C., Gentekaki, E., Hongsanan, S., Jayawardena, R., Senanayake, I. C., Manawasinghe, I. S., . . . Hyde, K. D. (2022). *Diaporthe*: Formalizing the species-group concept. *Mycosphere*, *13*(1), 752–819. https://doi.org/10.5943/mycosphere/13/1/9

Norphanphoun, C., Hongsanan, S., Gentekaki, E., Chen, Y. J., Kuo, C. H., & Hyde, K. D. (2020). Differentiation of species complexes in *Phyllosticta* enables better species resolution. *Mycosphere, 11*(1), 2542–2628. https://doi.org/10.5943/mycosphere/11/1/16

Norphanphoun, C., Jayawardena, R. S., Chen, Y., Wen, T. C., Meepol, W., & Hyde, K. D. (2019). Morphological and phylogenetic characterization of novel pestalotioid species associated with mangroves in Thailand. *Mycosphere, 10*(1), 531–578. https://doi.org/10.5943/mycosphere/10/1/9

Nozawa, S., Yamaguchi, K., Le, T. H., Van Hop, D., Phay, N., Ando, K., . . . Watanabe, K. (2017). Identification of two new species and a sexual morph from the genus *Pseudopestalotiopsis*. *Mycoscience, 58*(1), 328–337. https://doi.org/10.1016/j.myc.2017.02.008

Ocampo-Padilla, C., Malonzo, M. A., Grospe, R. A., Bagsic, J. T., Nozawa, S., Tsurumi, Y., . . . Watanabe, K. (2024). *Lasiodiplodia* species isolated from *Theobroma cacao* in the Philippines and their pathogenicity. *Journal of General Plant Pathology, 90*(5), 254–266. https://doi.org/10.1007/s10327-024-01187-z

O'Donnell, K., Kistler, H. C., Cigelnik, E., & Ploetz, R. C. (1998). Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. *Proceedings of the National Academy of Sciences of the United States of America, 95*(5), 2044–2049. https://doi.org/10.1073/pnas.95.5.2044

Oraon, S., Singh, S., Mukherjee, S., & Mondal, G. (2025). Morpho-molecular characterization of *Phyllosticta capitalensis*, causing leaf spot of curry leaf from West Bengal, India. *Journal of Crop Health, 77*(3), 1–10. https://doi.org/10.1007/s10343-025-01151-7

Orr, R., & Nelson, P. N. (2018). Impacts of soil abiotic attributes on Fusarium wilt, focusing on bananas. *Applied Soil Ecology, 132,* 20–33. https://doi.org/10.1016/j.apsoil.2018.06.019

Pak, D., You, M. P., Lanoiselet, V., & Barbetti, M. J. (2017). Reservoir of cultivated rice pathogens in wild rice in Australia. *European Journal of Plant Pathology, 147*(2), 295–311. https://doi.org/10.1007/s10658-016-1002-y

Pan, J., Geng, X., Jiang, Y., Su, P., Yu, Y., Liu, Y., . . . Liu, Q. (2024). First report of *Corynespora cassiicola* causing leaf spot on *Nanhaia speciosa* in China. *Plant Disease, 108* (8), 2577. https://doi.org/10.1094/PDIS-03-24-0562-PDN

Patel, S., Bowen, K., & Koebernick, J. (2025). First report of target spot caused by *Corynespora cassiicola* on *Senna obtusifolia* (sicklepod) in the United States. *Plant Disease, 109*(5), 1176. https://doi.org/10.1094/PDIS-12-24-2541-PDN

Pem, D., Hyde, K. D., McKenzie, E. H. C., Hongsanan, S., Wanasinghe, D. N., Boonmee, S., . . . Dong, W. (2024). A comprehensive overview of genera in Dothideomycetes. *Mycosphere, 15*(1), 2175–4568. https://doi.org/10.5943/mycosphere/15/1/18

Perera, R. H., Hyde, K. D., Jones, E. B., Maharachchikumbura, S. S., Bundhun, D., Camporesi, E., . . . Liu, Z. Y. (2023). Profile of Bionectriaceae, Calcarisporiaceae, Hypocreaceae, Nectriaceae, Tilachlidiaceae, Ijuhyaceae fam. nov., Stromatonectriaceae fam. nov., and Xanthonectriaceae fam. nov. *Fungal Diversity, 118*(1), 95–271. https://doi.org/10.1007/s13225-022-00512-1

Persoon, C. H. (1818). *Traité sur les champignons comestibles, contenant l'indication des espèces nuisibles; à l'histoire des champignons*. Belin-Leprieur. https://doi.org/10.5962/bhl.title.110115

Petrini, O. (1991). Fungal endophytes of tree leaves. In J. H. Andrews & S. S. Hirano (Eds.), *Microbial ecology of leaves* (pp. 179–197). Springer New York.

Petrini, O., Sieber, T. N., Toti, L., & Viret, O. (1993). Ecology, metabolite production, and substrate utilization in endophytic fungi. *Natural Toxins, 1*(3), 185–196. https://doi.org/10.1002/nt.2620010306

Pham, D., Howard-Jones, A. R., Sparks, R., Stefani, M., Sivalingam, V., Halliday, C. L., . . . Chen, S. C. (2023). Epidemiology, modern diagnostics, and the management of mucorales infections. *Journal of Fungi, 9*(6), 659. https://doi.org/10.3390/jof9060659

Phillips, A. J., Alves, A., Abdollahzadeh, J., Slippers, B., Wingfield, M. J., Groenewald, J. Z., . . . Crous, P. W. (2013). The Botryosphaeriaceae: Genera and species known from culture. *Studies in Mycology, 76*(1), 51–167. https://doi.org/10.3114/sim0021

Phillips, A. J., Hyde, K. D., Alves, A., & Liu, J. K. (2019). Families in Botryosphaeriales: A phylogenetic, morphological and evolutionary perspective. *Fungal Diversity, 94*, 1–22. https://doi.org/10.1007/s13225-018-0416-6

Phookamsak, R., Hongsanan, S., Bhat, D. J., Wanasinghe, D. N., Promputtha, I., Suwannarach, N., . . . Xu, J. C. (2024). Exploring ascomycete diversity in Yunnan II: Introducing three novel species in the suborder Massarineae (Dothideomycetes, Pleosporales) from fern and grasses. *MycoKeys, 104,* 9. https://doi.org/10.3897/mycokeys.104.112149

Phookamsak, R., Jiang, H. B., Suwannarach, N., Lumyong, S., Xu, J. C., Xu, S., . . . Chomnunti, P. (2022). Bambusicolous fungi in Pleosporales: Introducing four novel taxa and a new habitat record for *Anastomitrabeculia didymospora*. *Journal of Fungi, 8*(6), 630. https://doi.org/10.3390/jof8060630

Phookamsak, R., Liu, J. K., Manamgoda, D. S., Chukeatirote, E., Mortimer, P. E., McKenzie, E. H., . . . Hyde, K. D. (2014). The sexual state of *Setophoma*. *Phytotaxa, 176*(1), 260–269. https://doi.org/10.11646/phytotaxa.176.1.25

Photita, W., Lumyong, S., Lumyong, P., McKenzie, E. H. C., & Hyde, K. D. (2004). Are some endophytes of Musa acuminata latent pathogens. *Fungal Diversity, 16*, 131–140.

Phukhamsakda, C., Nilsson, R. H., Bhunjun, C. S., De Farias, A. R., Sun, Y. R., Wijesinghe, S. N., . . . Dong, W. (2022). The numbers of fungi: Contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity*, *114*(1), 327–386. https://doi.org/10.1007/s13225-022-00502-3

Pintos, Á., & Alvarado, P. (2021). Phylogenetic delimitation of *Apiospora* and *Arthrinium*. *Fungal Systematics and Evolution, 7*(1), 197–221. https://doi.org/10.3114/fuse.2021.07.10

Prihastuti, H., Cai, L., Chen, H., McKenzie, E. H., & Hyde, K. D. (2009). Characterization of *Colletotrichum* species associated with coffee berries in northern Thailand. *Fungal Diversity, 39*(1), 89–109.

Promputtha, I., Hyde, K. D., McKenzie, E. H., Peberdy, J. F., & Lumyong, S. (2010). Can leaf degrading enzymes provide evidence that endophytic fungi becoming saprobes?. *Fungal Diversity*, *41*(1), 89–99. https://doi.org/10.1007/s13225-010-0024-6

Promputtha, I., Jeewon, R., Lumyong, S., McKenzie, E. H. C., & Hyde, K. D. (2005). Ribosomal DNA fingerprinting in the identification of non sporulating endophytes from Magnolia liliifera (Magnoliaceae). *Fungal Diversity*, 20, 167–186.

Promputtha, I., Lumyong, S., Dhanasekaran, V., McKenzie, E. H. C., Hyde, K. D., & Jeewon, R. (2007). A phylogenetic evaluation of whether endophytes become saprotrophs at host senescence. *Microbial Ecology*, *53*(4), 579–590. https://doi.org/10.1007/s00248-006-9117-x

Purahong, W., & Hyde, K. D. (2011). Effects of fungal endophytes on grass and non-grass litter decomposition rates. *Fungal Diversity*, *47*(1), 1–7. https://doi.org/10.1007/s13225-010-0083-8

Ramesh, C. H., & Vijaykumar, S. (2005). Studies of fresh water foam fungi of Uttara Kannada, Karnataka. *Indian Phytopathology*, *58*(1), 89–95.

Rappaz, F. (1987). Taxonomie et nomenclature des Diatrypaceae à asques octospores. *Mycologia Helvetica*, *2*, 285–648.

Rashmi, M., Kushveer, J. S., & Sarma, V. V. (2019). A worldwide list of endophytic fungi with notes on ecology and diversity. *Mycosphere*, *10*(1), 798–1079. https://doi.org/10.5943/mycosphere/10/1/19

Raza, M., Zhang, Z. F., Hyde, K. D., Diao, Y. Z., & Cai, L. (2019). Culturable plant pathogenic fungi associated with sugarcane in southern China. *Fungal Diversity*, *99*, 1–104. https://doi.org/10.1007/s13225-019-00434-5

Réblová, M., Gams, W., & Seifert, K. A. (2011). Monilochaetes and allied genera of the Glomerellales, and a reconsideration of families in the Microascales. *Studies in Mycology*, *68*(1), 163–191. https://doi.org/10.3114/sim.2011.68.07

Réblová, M., Miller, A. N., Rossman, A. Y., Seifert, K. A., Crous, P. W., Hawksworth, D. L., . . . Huang, S. K. (2016). Recommendations for competing sexual-asexually typified generic names in Sordariomycetes (except Diaporthales, Hypocreales, and Magnaporthales). *IMA Fungus*, *7*(1), 131–153. https://doi.org/10.5598/imafungus.2016.07.01.08

Redman, R. S., Dunigan, D. D., & Rodriguez, R. J. (2001). Fungal symbiosis from mutualism to parasitism—Who controls the outcome, host or invader?. *New Phytologist, 151*(3), 705–716. https://doi.org/10.1046/j.0028-646x.2001.00210.x

Redman, R. S., Ranson, J. C., & Rodriguez, R. J. (1999). Conversion of the pathogenic fungus *Colletotrichum magna* to a nonpathogenic, endophytic mutualist by gene disruption. *Molecular Plant-Microbe Interactions, 12*(11), 969–975. https://doi.org/10.1094/MPMI.1999.12.11.969

Rehman, A., Alam, M. W., Saira, M., Naz, S., Mushtaq, R., Chohan, T. A., . . . Hussain, D. (2022). *Nigrospora sphaerica* causing leaf blight disease on sesame in Pakistan. *Plant Disease, 106*(1), 317. https://doi.org/10.1094/PDIS-07-21-1521-PDN

Rehner, S. A. (2001). *Primers for elongation factor 1-alpha (EF1-alpha).* http://ocid.nacse.org/research/deephyphae/EF1primer.pdf

Ren, G., Wanasinghe, D. N., de Farias, A. R., Hyde, K. D., Yasanthika, E., Xu, J., . . . Gui, H. (2022). Taxonomic novelties of woody litter fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. *Biology, 11,* 1660. https://doi.org/10.3390/biology11111660

Revankar, S. G., & Sutton, D. A. (2010). Melanized fungi in human disease. *Clinical Microbiology Reviews, 23*(4), 884–928. https://doi.org/10.1128/cmr.00019-10

Rodriguez, R. J., White, J. F. Jr., Arnold, A. E., & Redman, A. R. (2009). Fungal endophytes: diversity and functional roles. *New Phytologist, 182*(2), 314–330. https://doi.org/10.1111/j.1469-8137.2009.02773.x

Rodriguez, R., & Redman, R. (2008). More than 400 million years of evolution and some plants still can't make it on their own: plant stress tolerance via fungal symbiosis. *Journal of Experimental Botany, 59*(5), 1109–1114. https://doi.org/10.1093/jxb/erm342

Rossman, A. Y., Samuels, G. J., Rogerson, C. T., & Lowen, R. (1999). Genera of *Bionectriaceae, Hypocreaceae* and *Nectriaceae* (*Hypocreales, Ascomycetes*). *Studies in Mycology, 42,* 1–248.

Saccardo, P. (1875). Conspectus generum pyrenomycetum italicorum additis speciebus fungorum Venetorum novisvel criticis, systemate carpologico dispositorum. *Atti della Societa Veneziana-Trentina-Istriana di Scienze Naturali, 4*, 77–100.

Sahay, S. (2021). Cold-active microfungi and their industrial applications. In A. N. Yadav, A. A. Rastegari & N. Yadav (Eds.), *Microbiomes of extreme environments: Biodiversity and biotechnological applications* (pp. 153–176). CRC Press.

Saikkonen, K., Faeth, S. H., Helander, M., & Sullivan, T. J. (1998). Fungal endophytes: A continuum of interactions with host plants. *Annual review of Ecology and Systematics, 29*(1), 319–343. https://doi.org/10.1146/annurev.ecolsys.29.1.319

Saikkonen, K., Wäli, P., Helander, M., & Faeth, S. H. (2004). Evolution of endophyte–plant symbioses. *Trends in Plant Science, 9*(6), 275–280. https://doi.org/10.1016/j.tplants.2004.04.005

Sain, S. K., Gawande, S. P., Kumar, V., Chandrashekar, N., Prakash, A. H., & Prasad, Y. G. (2024). First report of target spot caused by *Corynespora cassiicola* on cotton in northwestern India. *Plant Disease, 108*(2), 530. https://doi.org/10.1094/PDIS-09-23-1868-PDN

Samarakoon, B. C., Wanasinghe, D. N., Samarakoon, M. C., Bundhun, D., Jayawardena, R., Hyde, K. D., . . . Chomnunti, P. (2024). Exploring fungi: A taxonomic and phylogenetic study of leaf-inhabiting Ascomycota in *Musa* species from northern Thailand, with a global checklist. *Mycosphere, 15*(1), 1901–2174. https://doi.org/10.5943/mycosphere/15/1/17

Samarakoon, B. C., Wanasinghe, D. N., Samarakoon, M. C., Phookamsak, R., McKenzie, E. H., Chomnunti, P., . . . & Karunarathna, S. C. (2020). Multi-gene phylogenetic evidence suggests *Dictyoarthrinium* belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) and *Dictyoarthrinium musae* sp. nov. on *Musa* from Thailand. *MycoKeys, 71,* 101. https://doi.org/10.3897/mycokeys.71.55493

Samarakoon, M. C., Hyde, K. D., Maharachchikumbura, S. S., Stadler, M., Jones, E. B. G., Promputtha, I., . . . Liu, J. K. (2022). Taxonomy, phylogeny, molecular dating and ancestral state reconstruction of Xylariomycetidae (Sordariomycetes). *Fungal Diversity, 112*, 1–88. https://doi.org/10.1007/s13225-021-00495-5

Sánchez, P., Vélez-del-Burgo, A., Suñén, E., Martínez, J., & Postigo, I. (2022). Fungal allergen and mold allergy diagnosis: Role and relevance of *Alternaria alternata* Alt a 1 protein family. *Journal of Fungi, 8*(3), 277. https://doi.org/10.3390/jof8030277

Sarsaiya, S., Shi, J., & Chen, J. (2019). A comprehensive review on fungal endophytes and its dynamics on Orchidaceae plants: current research, challenges, and future possibilities. *Bioengineered, 10*(1), 316–334. https://doi.org/10.1080/21655979.2019.1644854

Scheck, H. J. (2019). *California pest rating proposal for Colletotrichum plurivorum Damm, Alizadeh & Toy*. California Department of Food and Agriculture. https://blogs.cdfa.ca.gov/Section3162/?p=6604

Schoch, C. L., Shoemaker, R. A., Seifert, K. A., Hambleton, S., Spatafora, J. W., & Crous, P. W. (2006). A multigene phylogeny of the Dothideomycetes using four nuclear loci. *Mycologia, 98*(6), 1041–1052. https://doi.org/10.1080/15572536.2006.11832632

Schultz, B., & Boyle, C. (2005). The endophytic continuum. *Mycol. Res, 109*, 661–686.

Schulz, B., & Boyle, C. (2006). What are endophytes?. In B. J. E. Schulz, C. J. C. Boyle & T. N. Sieber (Eds.), *Microbial root endophytes* (pp. 1–13). Springer Berlin Heidelberg.

Senanayake, I. C., Crous, P., Groenewald, J., Maharachchikumbura, S. S. N., Jeewon, R., Phillips, A. J. L., . . . Hyde, K. D. (2017). Families of *Diaporthales* based on morphological and phylogenetic evidence. *Studies in Mycology, 86*, 217–296. https://doi.org/10.1016/j.simyco.2017.07.003

Senanayake, I. C., Pem, D., Rathnayaka, A. R., Wijesinghe, S. N., Tibpromma, S., Wanasinghe, D. N., . . . Xie, N. (2022). Predicting global numbers of teleomorphic ascomycetes. *Fungal Diversity, 114*(1), 237–278. https://doi.org/10.1007/s13225-022-00498-w

Senanayake, I. C., Rathnayaka, A. R., Marasinghe, D. S., Calabon, M. S., Gentekaki, E., Lee, H. B., . . . Xiang, M. M. (2020). Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. *Mycosphere*, *11*(1), 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Sharma, G., Pinnaka, A. K., & Shenoy, B. D. (2015). Resolving the *Colletotrichum siamense* species complex using ApMat marker. *Fungal Diversity, 71*, 247–264. http://doi.org/10.1007/s13225-014-0312-7

Shi, T., Wang, H., Li, Y. J., Wang, Y. F., Pan, Q., Wang, B., . . . Shang, E. L. (2023). Genus *Acrostalagmus*: A prolific producer of natural products. *Biomolecules, 13*(8), 1191. https://doi.org/10.3390/biom13081191

Shoemaker, R. A. (1959). Nomenclature of *Drechslera* and *Bipolaris*, grass parasites segregated from *Helminthosporium*. *Canadian Journal of Botany, 37*(5), 879–887. https://doi.org/10.1007/s13225-014-0312-7

Shoff, C. J., & Perfect, J. R. (2021). Uncommon yeasts and molds causing human disease. *Encyclopedia of Mycology, 1*, 813–834. https://doi.org/10.1016/B978-0-12-809633-8.21023-6

Si, Y. Z., Sun, J. W., Wan, Y., Chen, Y. N., He, J., Li, W. Z., . . . Zhu, L. H. (2023). *Neofusicoccum cryptomeriae* sp. nov. and *N. parvum* cause stem basal canker of *Cryptomeria japonica* in China. *Journal of Fungi, 9*(4), 404. https://doi.org/10.3390/jof9040404

Siddaiah, C. N., Satyanarayana, N. R., Mudili, V., Kumar Gupta, V., Gurunathan, S., Rangappa, S., . . . Srivastava, R. K. (2017). Elicitation of resistance and associated defense responses in *Trichoderma hamatum* induced protection against pearl millet downy mildew pathogen. *Scientific Reports, 7*(1), 43991. https://doi.org/10.1038/srep43991

Sierra-Orozco, E., Sandoya, G., Lee, S., Vallad, G., & Hutton, S. (2023). Need for disease resistance breeding against *Corynespora cassiicola* in crops. *Frontiers in Agronomy, 5*, 1275906. https://doi.org/10.3389/fagro.2023.1275906

Silva, R. M., Oliveira, T. G., Costa, A. F., Machado, A. R., Souza-Motta, C. M., & Silva, G. A. (2024). First report of *Colletotrichum plurivorum* causing anthracnose on *Cucumis sativus* in Brazil. *Plant Disease, 108*(2), 534. https://doi.org/10.1094/PDIS-10-23-2245-PDN

Slippers, B., Crous, P. W., Denman, S., Coutinho, T. A., Wingfield, B. D., & Wingfield, M. J. (2005). Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria dothidea*. *Mycologia, 96*(1), 83–101. http://dx.doi.org/10.1080/15572536.2005.11833000

Somasekhara, Y. M., Basha, C. J., Poonacha, T. T., Nayak, A. M., Ramesh, G. V., Poojashree, M. S., . . . Palanna, K. B. (2024). Novel characterisation of *Curvularia geniculata* associated with leaf blight on *Costus igneus* in India. *Physiological and Molecular Plant Pathology, 134*, 102443. https://doi.org/10.1016/j.pmpp.2024.102443

Soytong, K., Kahonokmedhakul, S., Song, J., & Tongon, R. (2021). *Chaetomium* application in agriculture. In F. Ahmad & M. Sultan (Eds.), *Technology in agriculture*. IntechOpen. https://doi.org/10.5772/intechopen.99402

Srinivasan, R., Prabhu, G., Prasad, M., Mishra, M., Chaudhary, M., & Srivastava, R. (2020). *Penicillium*. In N. Amaresan, K. Annapurna, M. Senthil Kumar & K. Kumar (Eds.), *Beneficial microbes in agro-ecology* (pp. 651–667). Academic Press. https://doi.org/10.1016/B978-0-12-823414-3.00032-0

Steenwyk, J. L., Shen, X. X., Lind, A. L., Goldman, G. H., & Rokas, A. (2019). A robust phylogenomic time tree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *MBio, 10*(5), e00925-19. https://doi.org/10.1128/mbio.00925-19

Strausbaugh, C. A. (2018). Incidence, distribution, and pathogenicity of fungi causing root rot in Idaho long-term sugar beet storage piles. *Plant Disease, 102*(11), 2296–2307.

Strobel, G., & Daisy, B. (2003). Bioprospecting for microbial endophytes and their natural products. *Microbiology and Molecular Biology Reviews, 67*(4), 491–502. https://doi.org/10.1128/mmbr.67.4.491-502.2003

Sturm, J. (1829). Deutschlands Flora, Abt. III. *Die Pilze Deutschlands, 2*, 1–136.

Su, P., Lu, Z., Tian, W., Chen, Y., & Maharachchikumbura, S. S. (2023). Six additions to the genus *Periconia* (Dothideomycetes: Periconiaceae) from graminaceous plants in China. *Journal of Fungi, 9*(3), 300. https://doi.org/10.3390/jof9030300

Sukapure, R. A., & Thirumalachar, M. J. (1965). Studies on *Cephalosporium* species from India—III. *Sydowia, 19*, 171–175.

Sun, L. Y., Li, H. Y., Sun, X., & Guo, L. D. (2017). *Dematipyriforma aquilaria* gen. et sp. nov., a new hyphomycetous taxon from *Aquilaria crassna*. *Cryptogamie, Mycologie, 38*(3), 341–351. https://doi.org/10.7872/crym/v38.iss3.2017.341

Sun, X., & Guo, L. D. (2012). Endophytic fungal diversity: Review of traditional and molecular techniques. *Mycology, 3*(1), 65–76. https://doi.org/10.1080/21501203.2012.656724

Sun, X., Qi, X., Wang, W., Liu, X., Zhao, H., Wu, C., . . . Gong, G. (2020). Etiology and symptoms of maize leaf spot caused by *Bipolaris* spp. in Sichuan, China. *Pathogens, 9*(3), 229. https://doi.org/10.3390/pathogens9030229

Sun, Y. C., Damm, U., & Huang, C. J. (2019). *Colletotrichum plurivorum*, the causal agent of anthracnose fruit rot of papaya in Taiwan. *Plant Disease, 103*(5), 1040. https://doi.org/10.1094/PDIS-08-18-1423-PDN

Sutton, B. C., & Alcorn, J. L. (1990). New species of *Mycoleptodiscus* (Hyphomycetes). *Mycological Research, 94*(5), 564–566.

Talhinhas, P., & Baroncelli, R. (2023). Hosts of *Colletotrichum*. *Mycosphere, 14*(si2), 158–261. https://doi.org/10.5943/mycosphere/14/si2/4

Tan, Q., Zhang, Y., Zhou, T., Xiong, Y., Huang, Q., Liu, G., . . . Manawasinghe, I. (2025). Endophytic *Trichoderma* (Sordariomycetes, Hypocreaceae) species associated with citrus in Guangdong province, China. *New Zealand Journal of Botany, 63*(3), 251–277. https://doi.org/10.1080/0028825X.2024.2445352

Tan, Y. P., & Shivas, R. G. (2022). *Index of Australian Fungi no. 3*. Zenodo. https://doi.org/10.5281/zenodo.7430436

Tanaka, K., Hirayama, K., Yonezawa, H., Hatakeyama, S., Harada, Y., Sano, T., . . . Hosoya, T. (2009). Molecular taxonomy of bambusicolous fungi: Tetraplosphaeriaceae, a new pleosporalean family with Tetraploa-like anamorphs. *Studies in Mycology, 64*(1), 175–209. https://doi.org/10.3114/sim.2009.64.10

Tanaka, K., Hirayama, K., Yonezawa, H., Sato, G., Toriyabe, A., Kudo, H., . . . Shirouzu, T. (2015). Revision of the *Massarineae* (*Pleosporales, Dothideomycetes*). *Studies in Mycology, 82*, 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Tang, X., Lu, F., Xiao, Z., Wang, Y., Hu, G., Cai, K., . . . Wang, W. (2024). Determination of anthracnose (*Colletotrichum fructicola*) resistance mechanism using transcriptome analysis of resistant and susceptible pear (*Pyrus pyrifolia*). *BMC Plant Biology, 24*(1), 619. https://doi.org/10.1186/s12870-024-05077-6

Tang, Z., Lou, J., He, L., Wang, Q., Chen, L., Zhong, X., . . . Wang, Z. Q. (2022). First report of *Colletotrichum fructicola* causing anthracnose on cherry (*Prunus avium*) in China. *Plant Disease, 106*(2), 317. https://doi.org/10.1094/PDIS-03-21-0544-PDN

Tejesvi, M. V., Mahesh, B., Nalini, M. S., Prakash, H. S., Kini, K. R., Subbiah, V., . . . Shetty, H. S. (2005). Endophytic fungal assemblages from inner bark and twig of Terminalia arjuna W. & A. (Combretaceae). *World Journal of Microbiology and Biotechnology*, *21*(8), 1535–1540. https://doi.org/10.1007/s11274-005-7579-5

Templeton, M. D., Rikkerink, E. H., Solon, S. L., & Crowhurst, R. N. (1992). Cloning and molecular characterization of the glyceraldehyde-3-phosphate dehydrogenase-encoding gene and cDNA from the plant pathogenic fungus *Glomerella cingulata*. *Gene, 122*(2), 225–230. https://doi.org/10.1016/0378-1119(92)90055-T

Thanh, L. T., Tien, N. T., Trang, N. T., Trieu, T. Q., Tien, N. Q., & Loc, N. H. (2025). First report of *Colletotrichum siamense* and *Colletotrichum endophyticum* associated with anthracnose on avocado (*Persea americana* Mill.) in Vietnam. *Journal of Plant Pathology, 107*(4), 633–647. https://doi.org/10.1007/s42161-024-01813-x

Thaung, M. M. (2008). Pathologic and taxonomic analysis of leaf spot and tar spot diseases in a tropical dry to wet monsoon ecosystem of lowland Burma. *Australasian Plant Pathology, 37*(2), 180–197. https://doi.org/10.1071/AP08007

Thongkantha, S., Jeewon, R., Vijaykrishna, D., Lumyong, S., McKenzie, E. H., & Hyde, K. D. (2009). Molecular phylogeny of Magnaporthaceae (Sordariomycetes) with a new species *Ophioceras chiangdaoense* from *Dracaena loureiroi* in Thailand. *Fungal Diversity*, *34*, 157–173.

Tian, W. H., Liu, J. W., Jin, Y., Chen, Y. P., Zhou, Y. F., Wu, K., . . . Maharachchikumbura, S. S. N. (2024). Morphological and phylogenetic studies of Ascomycota from gymnosperms in Sichuan Province, China. *Mycosphere*, *15*(1), 1794–1900. https://doi.org/10.5943/mycosphere/15/1/16

Tian, X. G., Bao, D. F., Karunarathna, S. C., Jayawardena, R. S., Hyde, K. D., Bhat, D. J., . . . Maharachchikumbura, S. S. (2024). Taxonomy and phylogeny of ascomycetes associated with selected economically important monocotyledons in China and Thailand. *Mycosphere, 15*(1), 1–274. https://doi.org/10.5943/mycosphere/15/1/1

Tian, X., Tibpromma, S., Karunarathna, S. C., Dai, D., Bao, D., Mapook, A., . . . Jayawardena, R. S. (2022). Additions to the genus *Periconia* from northern Thailand. *Phytotaxa*, *555*(1), 73–86. https://doi.org/10.11646/phytotaxa.555.1.5

Tibpromma, S., Hyde, K. D., McKenzie, E. H. C., Bhat, D. J., Phillips, A. J. L., Wanasinghe, D. N., . . . Karunarathna, S. C. (2018). Fungal diversity notes 840–928: Micro-fungi associated with Pandanaceae. *Fungal Diversity, 93*, 1–160.

Trakunyingcharoen, T., Lombard, L., Groenewald, J. Z., Cheewangkoon, R., Toanun, C., Alfenas, A. C., . . . Crous, P. W. (2014). Mycoparasitic species of *Sphaerellopsis*, and allied lichenicolous and other genera. *IMA Fungus, 5*(2), 391–414. https://doi.org/10.5598/imafungus.2014.05.02.05

Tran, N. T., Miles, A. K., Dietzgen, R. G., & Drenth, A. (2019). *Phyllosticta capitalensis* and *P. paracapitalensis* are endophytic fungi that show potential to inhibit pathogenic *P. citricarpa* on citrus. *Australasian Plant Pathology, 48*(3), 281–296. https://doi.org/10.1007/s13313-019-00628-0

Tran-Trung, H., Le, D. G., Hoang, V. T., Vu, D. C., Thang, T. D., Nguyen-Ngoc, H., . . . Nguyen, T. H. (2024). Essential oils of two species of Zingiberaceae family from Vietnam: Chemical compositions and α-glucosidase, α-amylase inhibitory effects. *Natural Product Communications, 19*(2), 1934578X241232281. https://doi.org/10.1177/1934578X241232281

Tsang, C. C., Tang, J. Y., Lau, S. K., & Woo, P. C. (2018). Taxonomy and evolution of *Aspergillus*, *Penicillium* and *Talaromyces* in the omics era – Past, present and future. *Computational and Structural Biotechnology Journal, 16*, 197–210. https://doi.org/10.1080/12298093.2023.2290759

Udayanga, D., Liu, X., McKenzie, E. H., Chukeatirote, E., & Hyde, K. D. (2012). Multi-locus phylogeny reveals three new species of *Diaporthe* from Thailand. *Cryptogamie, Mycologie, 33*(3), 295–309. https://doi.org/10.7872/crym.v33.iss3.2012.295

USDA Fungal Databases (USDA). (2025, July). *Fungus-host database*. https://fungi-stage.ars.usda.gov/

Velho, A. C., Alaniz, S., Casanova, L., Mondino, P., & Stadnik, M. J. (2015). New insights into the characterization of *Colletotrichum* species associated with apple diseases in southern Brazil and Uruguay. *Fungal Biology, 119*(3), 229–244. https://doi.org/10.1016/j.funbio.2014.12.009

Vilgalys, R., & Hester, M. (1990). Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology, 172*(8), 4238–4246.

Viret, O., & Cole, F. M. (2003). *Botrytis cinerea* infection in grape flowers: Defense reaction, latency, and disease expression. *Phytopathology, 93*(3), 316–322. https://doi.org/10.1094/PHYTO.2003.93.3.316

Viret, O., & Gindro, K. (2024). Fungi and grapevine mycobiota. In *Science of fungi in grapevine* (pp. 109–195). Springer. https://doi.org/10.1007/978-3-031-68663-4_3

Visagie, C. M., Yilmaz, N., Kocsubé, S., Frisvad, J. C., Hubka, V., Samson, R. A., . . . Houbraken, J. (2024). A review of recently introduced *Aspergillus*, *Penicillium*, *Talaromyces* and other Eurotiales species. *Studies in Mycology, 107*(1), 1–66. https://doi.org/10.3114/sim.2024.107.01

Wagner, L., Stielow, J. B., de Hoog, G. S., Bensch, K., Schwartze, V. U., Voigt, K., . . . Walther, G. (2020). A new species concept for the clinically relevant *Mucor circinelloides* complex. *Persoonia, 44*(1), 67–97. https://doi.org/10.3767/persoonia.2020.44.03

Walther, G., Pawłowska, J., Alastruey-Izquierdo, A., Wrzosek, M., Rodriguez-Tudela, J. L., Dolatabadi, S., . . . De Hoog, G. S. (2013). DNA barcoding in Mucorales: An inventory of biodiversity. *Persoonia, 30*(1), 11–47. https://doi.org/10.3767/003158513X665070

Wanasinghe, D. N., & Maharachchikumbura, S. S. (2023). Exploring the diversity and systematics of Phaeosphaeriaceae: Taxonomic novelties from ecologically diverse habitats and their phylogenetic resolution. *Journal of Fungi, 9*(8), 853. https://doi.org/10.3390/jof9080853

Wang, H., Sang, Z., Chen, Y., Wei, S., Qiu, K., Liu, Z., . . . Tan, H. (2024). The chemical constituents of endophytic fungus *Nigrospora chinensis* of Gannan navel orange. *Natural Product Research, 38*(3), 530–538. https://doi.org/10.1080/14786419.2022.2125969

Wang, K. Y., Wu, Y. M., Chen, Y., & Jiang, Y. L. (2019). A new species of *Pyrenochaetopsis* and a key to the known species of the genus. *Mycosystema, 38*(2), 171–177. https://doi.org/10.13346/j.mycosystema.180261

Wang, M., Liu, F., Crous, P. W., & Cai, L. (2017). Phylogenetic reassessment of *Nigrospora*: Ubiquitous endophytes, plant and human pathogens. *Persoonia, 39*(1), 118–142. https://doi.org/10.3767/persoonia.2017.39.06

Wang, S. Q., Li, Z. X., Feng, W. M., Chen, Y. F., & Zhang, Y. (2023). Leaf disease caused by *Epicoccum thailandicum* on *Amomum villosum* in China. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 51*(1), 13021. https://doi.org/10.15835/nbha51113021

Wang, W. P., Shen, H. W., Bao, D. F., Lu, Y. Z., Yang, Q. X., Su, X. J., . . . Luo, Z. L. (2023). Two novel species and three new records of Torulaceae from Yunnan Province, China. *MycoKeys, 99*, 1–24. https://doi.org/10.3897/mycokeys.99.106699

Wang, X. W., Lombard, L., Groenewald, J. Z., Li, J., Videira, S. I., Samson, R. A., . . . Crous, P. W. (2016). Phylogenetic reassessment of the *Chaetomium globosum* species complex. *Persoonia, 36*(1), 83–133. https://doi.org/10.3767/003158516X689657

Wang, X., Zhang, W., Peng, J., Manawasinghe, I. S., Wu, L., Li, Y., . . . Yan, J. (2024). Lifestyle changes in Botryosphaeriaceae as evidenced by ancestral genome expansion and horizontal gene transfer. *Fungal Diversity, 125*(1), 221–241. https://doi.org/10.1007/s13225-023-00530-7

Waqar, S., Bhat, A. A., & Khan, A. A. (2024). Endophytic fungi: Unravelling plant-endophyte interaction and the multifaceted role of fungal endophytes in stress amelioration. *Plant Physiology and Biochemistry, 206*, 108174. https://doi.org/10.1016/j.plaphy.2023.108174

Wawra, S., Fesel, P., Widmer, H., Neumann, U., Lahrmann, U., Becker, S., . . . Zuccaro, A. (2019). FGB1 and WSC3 are in planta-induced β-glucan-binding fungal lectins with different functions. *New Phytologist, 222*(3), 1493–1506. https://doi.org/10.1111/nph.15711

Wawra, S., Fesel, P., Widmer, H., Timm, M., Seibel, J., Leson, L., . . . Zuccaro, A. (2016). The fungal-specific β-glucan-binding lectin FGB1 alters cell-wall composition and suppresses glucan-triggered immunity in plants. *Nature Communications, 7*(1), 13188. https://doi.org/10.1038/ncomms13188

Weerasekara, I. T., Udayanga, D., Manamgoda, D. S., Mapa, M. S., Sinniah, G. D., & Castlebury, L. A. (2024). Morphological and molecular reassessment of *Pseudopestalotiopsis* in the gray blight complex of tea with four new species from Sri Lanka. *Mycological Progress, 23*(1), 72. https://doi.org/10.1007/s11557-024-02010-x

Wei, S., Xu, X., & Wang, L. (2021). Four new species of *Talaromyces* section *Talaromyces* discovered in China. *Mycologia, 113*(3), 492–508. https://doi.org/10.1080/00275514.2020.1853457

Wei, Y. K., Gao, Y. B., Xu, H., Su, D., Zhang, X., Wang, Y. H., . . . Ren, A. Z. (2006). Occurrence of endophytes in grasses native to northern China. *Grass and Forage Science, 61*(4), 422–429. https://doi.org/10.1111/j.1365-2494.2006.00551.x

Weir, B. S., Johnston, P. R., & Damm, U. (2012). The *Colletotrichum gloeosporioides* species complex. *Studies in Mycology, 73*, 115–180. https://doi.org/10.3114/sim0011

White, J. F. Jr., Morgan-Jones, G., & Morrow, A. C. (1993). Taxonomy, life cycle, reproduction and detection of Acremonium endophytes. *Agriculture, Ecosystems & Environment, 44*(1-4), 13–37. https://doi.org/10.1016/0167-8809(93)90037-P

White, T. J. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In M. A. Innis, D. H. Gelfand, J. J. Sninsky & T. J. White (Eds.), *PCR protocols: A guide to methods and applications* (vol. 18, pp. 315–322). Academic Press.

Wijayawardene, N. N., Hyde, K. D., Dai, D. Q., Sánchez-García, M., Goto, B. T., Saxena, R. K., . . . Thines, M. (2022). Outline of fungi and fungus-like taxa – 2021. *Mycosphere, 13*(1), 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wijayawardene, N. N., Hyde, K. D., Mikhailov, K. V., Péter, G., Aptroot, A., Pires-Zottarelli, C. L., . . . Karpov, S. A. (2024). Classes and phyla of the kingdom Fungi. *Fungal Diversity, 128*, 1-165. https://doi.org/10.1007/s13225-024-00540-z

Wikee, S., Lombard, L., Crous, P. W., Nakashima, C., Motohashi, K., Chukeatirote, E., . . . Hyde, K. D. (2013). *Phyllosticta capitalensis*, a widespread endophyte of plants. *Fungal Diversity, 60*(1), 91–105. https://doi.org/10.1007/s13225-013-0235-8

Wikee, S., Udayanga, D., Crous, P. W., Chukeatirote, E., McKenzie, E. H., Bahkali, A. H., . . . Hyde, K. D. (2011). *Phyllosticta*—An overview of current status of species recognition. *Fungal Diversity, 51*(1), 43–61. https://doi.org/10.1007/s13225-011-0146-5

Wille, P. A., Aeschbacher, R. A., & Boller, T. (1999). Distribution of fungal endophyte genotypes in doubly infected host grasses. *The Plant Journal, 18*(4), 349–358. https://doi.org/10.1046/j.1365-313X.1999.00462.x

Williamson, B., Tudzynski, B., Tudzynski, P., & Van Kan, J. A. (2007). *Botrytis cinerea*: The cause of grey mould disease. *Molecular Plant Pathology, 8*(5), 561–580.

Wilson, D. (2000). Ecology of woody plant endophytes. In C. W. Bacon & J. F. White (Eds.), *Microbial endophytes* (pp. 389–420). Marcel Dekker.

Wright, E. R., Folgado, M., Rivera, M. C., Crelier, A., Vasquez, P., & Lopez, S. E. (2008). *Nigrospora sphaerica* causing leaf spot and twig and shoot blight on blueberry: A new host of the pathogen. *Plant Disease, 92*(1), 171. https://doi.org/10.1094/PDIS-92-1-0171

Wu, J. B., Zhang, C. L., Mao, P. P., Qian, Y. S., & Wang, H. Z. (2014). First report of leaf spot caused by *Nigrospora oryzae* on *Dendrobium candidum* in China. *Plant Disease, 98*(8), 996. https://doi.org/10.1094/PDIS-01-14-0065-PDN

Wu, M. Q., Zheng, C., & Liu, Y. L. (2024). First report of *Phyllosticta capitalensis* causing leaf spot in *Hymenocallis littoralis* in China. *Plant Disease, 108*(8), 2228. https://doi.org/10.1094/PDIS-08-23-1669-PDN

Wu, N., Dissanayake, A. J., Chethana, K. T., & Liu, J. K. (2022). *Neodeightonia septata* sp. nov. and *N. subglobosa* (Botryosphaeriaceae) from Northern Thailand. *Phytotaxa, 575*(2), 129–139. https://doi.org/10.11646/phytotaxa.575.2.2

Xie, A., Guo, J. M., Huang, F., Zeng, X. M., Wang, H., Li, T., . . . Yi, R. H. (2025). *Ficus altissima*, a new host of *Colletotrichum fructicola* causing anthracnose in China. *Plant Disease, 109*(7), 1591. https://doi.org/10.1094/PDIS-10-24-2131-PDN

Xie, Y., Ying, J., Fang, L., Wu, J., Mao, X., Wang, L., . . . Wang, H. (2023). First report of *Curvularia geniculata* causing leaf spot disease of *Bletilla striata* in Zhejiang Province, China. *Plant Disease, 107*, 2527. https://doi.org/10.1094/PDIS-03-23-0407-PDN

Xiong, Y., Manawasinghe, I. S., Liao, C., Hyde, K. D., & Dong, Z. (2022). *Neodeightonia arengae* sp. nov., Botryosphaeriaceous taxa on *Arenga tremula* (Arecaceae) from Guangdong, China. *Phytotaxa, 530*(2), 130–140. https://doi.org/10.11646/phytotaxa.530.2.1

Xu, T., Song, Z., Hou, Y., Liu, S., Li, X., Yang, Q., . . . Wu, S. (2022). Secondary metabolites of the genus *Nigrospora* from terrestrial and marine habitats: Chemical diversity and biological activity. *Fitoterapia, 161*, 105254. https://doi.org/10.1016/j.fitote.2022.105254

Yadav, V., Kumar, M., Deep, D. K., Kumar, H., Sharma, R., Tripathi, T., . . . Johri, A. (2010). A phosphate transporter from the root endophytic fungus *Piriformospora indica* plays a role in phosphate transport to the host plant. *Journal of Biological Chemistry, 285*(35), 26532–26544. https://doi.org/10.1074/jbc.M110.111021

Yang, C. L., Xu, X. L., Zeng, Q., Liu, L. J., Liu, F., Deng, Y., . . . Xie, J. L. (2024). Bambusicolous mycopathogens in China with an update on taxonomic diversity, novel species, pathogenicity, and new insights. *Mycosphere, 15*(1), 4788–4918. https://doi.org/10.5943/mycosphere/15/1/21

Yang, E. F., Phookamsak, R., Jiang, H. B., Tibpromma, S., Bhat, D. J., Karunarathna, S. C., . . . Promputtha, I. (2022). Taxonomic reappraisal of Periconiaceae with the description of three new *Periconia* species from China. *Journal of Fungi, 8*(3), 243. https://doi.org/10.3390/jof8030243

Yang, J., Li, M., Chen, G., Sun, J., Zhang, W., Cui, J., . . . Hu, M. (2024). First report of *Colletotrichum siamense* causing leaf spot on silver date palm in China. *Crop Protection, 180*, 106646. https://doi.org/10.1016/j.cropro.2024.106646

Yang, P., Zhao, H. Y., Wei, J. S., Zhao, Y. Y., Lin, X. J., Su, J., . . . Yang, J. F. (2022). Chromosome-level genome assembly and functional characterization of terpene synthases provide insights into the volatile terpenoid biosynthesis of Wurfbainia villosa. *The Plant Journal, 112*(3), 630-645. https://doi.org/10.3390/plants14132041

Yang, R., Wang, J., Gao, W., Jiang, Y., Su, J., Sun, D., . . . He, G. (2021). Research on the reproductive biological characteristics of *Amomum villosum* Lour. and *Amomum longiligulare* T. L. Wu. *PLoS One, 16*(8), e0250335. https://doi.org/10.1371/journal.pone.0250335

Yang, Y. L., Liu, Z. Y., Cai, L., Hyde, K. D., Yu, Z. N., & McKenzie, E. H. C. (2009). *Colletotrichum* anthracnose of Amaryllidaceae. *Fungal Diversity, 39*, 123–146.

Yoshida, N. (2022). Seasonal dynamics of the pink root fungus (*Setophoma terrestris*) in rhizosphere soil: Effect of crop species and rotation. *Plant Pathology, 71*(2), 361–372. https://doi.org/10.1111/ppa.13464

Zapata, M., Rodríguez-Serrano, E., Castro, J. F., Santelices, C., Carrasco-Fernández, J., Damm, U., . . . Palfner, G. (2024). Novel species and records of *Colletotrichum* associated with native woody plants in south-central Chile. *Mycological Progress, 23*(1), 18. https://doi.org/10.1007/s11557-024-01956-2

Zare, R., & Gams, W. (2007). *Pochonia globispora* sp. nov. *Nova Hedwigia, 84*, 421–428.

Zhai, L. F., Liu, J., Zhang, M. X., & Hong, N. (2013). The first report of leaf spots in *Aloe vera* caused by *Nigrospora oryzae* in China. *Plant Disease, 97*(10), 1256. https://doi.org/10.1094/PDIS-03-13-0293-PDN

Zhang, J., Liu, H. X., Liu, Z. M., Li, S. N., Chen, Y. C., Zhang, W. M., . . . Guo, B. H. (2021). Secondary metabolites of endophytic fungus *Letendraea helminthicola* derived from *Amomum villosum*. *Natural Product Research and Development, 33*(5), 773. https://doi.org/10.16333/j.1001-6880.2021.5.008

Zhang, L. X., Li, S. S., Tan, G. J., Shen, J. T., & He, T. (2012). First report of *Nigrospora oryzae* causing leaf spot of cotton in China. *Plant Disease, 96*(9), 1379. https://doi.org/10.1094/PDIS-06-12-0551-PDN

Zhang, Q. Y., Liu, Z. B., Liu, H. G., & Si, J. (2023). Two new corticioid species of Phanerochaetaceae (Polyporales, Basidiomycota) from southwest China. *Frontiers in Cellular and Infection Microbiology, 13*, 1105918. https://doi.org/10.3389/fcimb.2023.1105918

Zhang, Q., Nizamani, M. M., Feng, Y., Yang, Y. Q., Jayawardena, R. S., Hyde, K. D., . . . Li, C. (2023b). Genome-scale and multi-gene phylogenetic analyses of *Colletotrichum* spp. host preference and association with medicinal plants. *Mycosphere, 14*(si2), 1–106. https://doi.org/10.5943/mycosphere/14/si2/1

Zhang, W., Li, Y., Lin, L., Jia, A., & Fan, X. (2024). Updating the species diversity of pestalotioid fungi: Four new species of *Neopestalotiopsis* and *Pestalotiopsis*. *Journal of Fungi, 10*(7), 475. https://doi.org/10.3390/jof10070475

Zhang, Y. Y., Zhang, T., Li, H. Y., Zheng, R., Ren, J., Yang, Q., . . . Jiang, N. (2024). *Nigrospora humicola* (Apiosporaceae, Amphisphaeriales), a new fungus from soil in China. *Diversity, 16*(2), 118. https://doi.org/10.3390/d16020118

Zhang, Y., Crous, P. W., Schoch, C. L., & Hyde, K. D. (2012). Pleosporales. *Fungal Diversity, 53*, 1–221.

Zhang, Y., Liu, Y., Deng, K., Ma, L., Lv, S., Zhang, C., . . . Xiao, L. (2023). First report of *Colletotrichum plurivorum* causing anthracnose on pecan (*Carya illinoinensis*) in China. *Plant Disease, 107*(8), 2547. https://doi.org/10.1094/PDIS-12-22-2774-PDN

Zhao, H., Nie, Y., Zong, T. K., Wang, K., Lv, M. L., Cui, Y. J., . . . Liu, X. Y. (2023). Species diversity, updated classification and divergence times of the phylum Mucoromycota. *Fungal Diversity, 123*, 49–157. https://doi.org/10.1007/s13225-023-00525-4

Zhao, S., Sun, W., Ouyang, D., Li, Q., Huang, S., Chen, X., . . . Tang, L. (2024). First report of anthracnose caused by *Colletotrichum plurivorum* on passion fruit in Guangxi, China. *Plant Disease, 108*(7), 2239. https://doi.org/10.1094/PDIS-04-24-0812-PDN

Zheng, H., Qiao, M., Lv, Y., Du, X., Zhang, K. Q., & Yu, Z. (2021). New species of *Trichoderma* isolated as endophytes and saprobes from Southwest China. *Journal of Fungi, 7*(6), 467. https://doi.org/10.3390/jof7060467

Zheng, L., Shi, F., Kelly, D., & Hsiang, T. (2012). First report of leaf spot of Kentucky bluegrass (*Poa pratensis*) caused by *Nigrospora oryzae* in Ontario. *Plant Disease, 96*(6), 909. https://doi.org/10.1094/PDIS-03-12-0251-PDN

Zheng, X. R., Zhang, M. J., & Chen, F. M. (2024). *Colletotrichum* species causing *Cyclocarya paliurus* anthracnose in southern China. *Forests, 15*(3), 490. https://doi.org/10.3390/f15030490

Zhong, J., Sui, W. W., Li, P., Tang, Q. J., Liu, T. B., & Xiao, Y. S. (2022). Characterization of a novel victorivirus from *Nigrospora chinensis*, a fungus isolated from tobacco. *Archives of Virology, 167*(12), 2851–2855. https://doi.org/10.1007/s00705-022-05619-z

Zhong, Y. X., Liu, Y. Y., Li, M., Rothenberg, D. O., Zeng, Z., Huang, Y. H., . . . Yan, C. Y. (2024). First report of tea leaf spot disease caused by *Bipolaris bicolor* on tea plants (*Camellia sinensis* cv. Fenghuang Dancong) in China. *Journal of Plant Pathology, 106*(1), 275–276. https://doi.org/10.1007/s42161-023-01513-y

Zhou, S. Y., Zhou, X., Zhang, Z. F., Liang, J. M., & Cai, L. (2020). Attempt to isolate hitherto uncultured fungi. *Mycosystema, 39*, 766–776. https://doi.org/10.13346/j.mycosystema.190202

Zhou, Y. Q., Yao, S. C., Wang, J., Xie, X. Y., Tan, X. M., Huang, R. S., . . . Fu, P. (2022). Cultivable endophytic fungal community associated with the karst endemic plant *Nervilia fordii* and their antimicrobial activity. *Frontiers in Microbiology, 13*, 1063897. https://doi.org/10.3389/fmicb.2022.1063897

Zhuang, Q., Lai, D., Shao, X., Qin, J., Lai, R., Li, X., . . . Xiao, W. (2025). First report of *Phyllosticta capitalensis* causing leaf blotch on Chinese olive (*Canarium album*) in Guangdong province of China. *Plant Disease, 109*(3), 714. https://doi.org/10.1094/PDIS-08-24-1760-PDN

Zipfel, C., & Oldroyd, G. E. (2017). Plant signalling in symbiosis and immunity. *Nature*, *543*(7645), 328–336. https://doi.org/10.1038/nature22009

Zou, J. J., Li, J., Ma, S. S., Li, P. F., & Zhou, D. H. (2022). Subcutaneous phaeohyphomycosis caused by plant pathogenic *Corynespora cassiicola*: A case report. *Chinese Journal of Traumatology*, *25*(6), 400–403. https://doi.org/10.1016/j.cjtee.2022.09.002

APPENDIX A

CHEMICAL REAGENTS AND MEDIA

1. **Carnation leaf agar (CLA)** (or carnation leaf change as host tissue, or needle can plant tissue medium) used for inducing fungal sporulation

   Aseptic carnation leaves

   Agar 15 g

   Dissolve 15 g of agar in 1 L of water in a bottle. Place aseptic carnation leaves (host tissue, or needle) into sterilization bags. Sterilize both the agar solution and the leaf samples at 121°C for 15 minutes. After sterilization, dry the aseptic carnation leaves (host tissue, or needle) in an oven. Once the agar has cooled slightly but is still liquid, pour it into petri dishes. Place two pieces of leaf (host tissue, or needle) tissue onto the surface of the solidified agar.

2. **Malt Extract Agar (MEA)** used for fungal culturing

   Malt extract 30g

   Agar 15 g

   Soy peptone 3 g

   Add the above ingredients to 1 L of distilled water and heat to dissolve, the 1/4 MEA will used malt extract （7.5 g), soy peptone (0.75 g), and agar 15 g. Adjust the pH to 5.6 ± 0.2. Sterilize at 121°C for 15 minutes.

3. **Oatmeal Agar (OA)** used for inducing fungal sporulation

   Oatmeal: 30 g

   Agar: 15 g

   Combine 30 g of oatmeal and 15 g of agar with 1 liter of distilled water. Heating: Heat the mixture while stirring until the agar is completely dissolved. Sterilization: Autoclave the medium at 121°C for 15 minutes.

4. **Plant tissue + ¼ MEA + Pine needle + Agar (Host plant tissue medium)** used for inducing endophytic fungal sporulation

   ¼ Malt extract 7.5 g

   ¼ Soy peptone 0.75 g

Agar 15 g

Host plant tissue

Pine needle

Add the above ingredients (except host plant tissue and pine needle) to 1 L of distilled water and heat to dissolve, the 1/4 MEA will used malt extract （7.5 g), soy peptone (0.75 g), and agar 15 g. Adjust the pH to 5.6 ± 0.2. Sterilize at 121°C for 15 minutes, host plant tissue and pine needle also need to sterilized, after sterilized dry in the oven. After allowing the medium to cool to 50–60°C, pour it into Petri dishes. Before the medium dries, place the dried host plant tissue and pine needles on the surface of the medium.

5. **Plant fruits + Agar (Fruit juice medium)** used for inducing fruits endophytic fungal sporulation

Fresh fruits of *Wurfbainia villosa* 200 g

Agar 15 g

Weigh 200 grams of fresh fruit and cut it into small pieces. Boil thoroughly for 10 to 30 minutes, then filter to obtain the fruit extract. Return the extract to the pot and bring it to a gentle boil over low heat. Add 15 grams of agar powder and stir rapidly until completely dissolved. Add distilled water to adjust the final volume to 1 liter. Sterilize the medium by autoclaving at 121 °C for 15 minutes.

6. **Potato Dextrose Agar (PDA)** used for fungal culturing

Potato 200 g

Dextrose 18 g

Agar 15 g

Weigh 200 grams of potatoes and cut them into small pieces. Boil thoroughly for 10 to 30 minutes, then filter to obtain the starch solution. Pour the starch solution back into the pot, bring it to a boil over low heat, then add 18 grams of glucose and 15 grams of agar powder. Stir quickly to fully dissolve the ingredients and add water to make up the volume to 1 liter. Autoclave at 121 ℃ for 15 minutes.

7. **Soil agar (Soil medium)** used for inducing root endophytic fungal sporulation

Dry soil 50 g (The soil was collected from near the roots of the sample collection site)

Agar 15 g

Grind the dry soil into a fine powder using a mortar and pestle. Add soil powder and agar ingredients to 1 L of distilled water and heat to dissolve. Adjust the pH to 5.6 ± 0.2. Sterilize at 121°C for 15 minutes.

8. **Synthetic low-nutrient agar (SNA)** used for inducing fungal sporulation

    Potassium dihydrogen phosphate 1 g

    Potassium nitrate 1 g

    Magnesium sulfate heptahydrate 0.5 g

    Potassium chloride 0.5 g

    Glucose 0.2 g

    Sucrose 0.2 g

    Agar 15 g

    Add the above ingredients to 1 L of distilled water and heat to dissolve. Adjust the pH to 5.6 ± 0.2. Sterilize at 121°C for 15 minutes.

9. **75% Ethanol (EtOH)** used for surface sterilization of endophytic fungi. Ethanol is an effective antiseptic. It disrupts microbial cell membranes and denatures proteins, leading to microbial death.
10. **Potassium hydroxide (KOH)** used in the rehydration of dried specimens. 5% aqueous solution
11. **2.5% Sodium Hypochlorite (NaOCl)** used for surface sterilization of endophytic fungi. This is a strong oxidizing agent commonly used as a disinfectant. In this procedure, it helps to kill and remove surface microorganisms, such as bacteria and fungi, that may be present on the outer surface of the leaves.
12. **2.5% $Na_2S_2O_3$** was used to neutralize residual sodium hypochlorite (NaClO) following surface sterilization. Sodium thiosulfate is a reducing agent that reacts with and inactivates chlorine-based disinfectants, preventing further oxidative damage to plant tissues or fungal cells. In this procedure, it ensures that any remaining NaOCl is effectively removed, thereby minimizing its potential inhibitory effect on endophytic fungal isolation.
13. **0.05% Tween 20** was used as a surfactant during the surface sterilization process of endophytic fungi. It is a non-ionic detergent that reduces surface tension, allowing disinfectants like sodium hypochlorite to better penetrate and spread across the plant surface. In this procedure, Tween 20 helps improve the efficiency

of sterilization by ensuring that the sterilizing agents can effectively contact and remove microorganisms on the leaf surface.

14. **Lactophenol Cotton Blue** is a widely utilized staining agent for visualizing fungal structures under a compound light microscope. It is particularly effective in highlighting pseudoparaphyses, septa, and ascus walls, offering excellent clarity and compatibility with a broad range of fungal taxa.

    Phenol (crystals) 20 g

    Lactic acid 16 ml

    Glycerol 31 ml

    Dissolve phenol in distilled water, add lactic acid, glycerol and 0.05 g of Poirrier's (cotton) blue or acid fuchsin.

15. **Lactic acid** is used to preserve fungal structures and to obtain true-color images of fungal spores and other structures without the use of stains. This is particularly beneficial for observing naturally pigmented organisms.

    85% Lactic acid 100 ml

16. **Indian ink** used for observing appendages of ascospores in fungal species.

APPENDIX B

ABSTRACT OF PUBLICATIONS

Chiang Mai J. Sci. 2021; 48(3) : 1-10
http://epg.science.cmu.ac.th/ejournal/
Contributed Paper

Addition to Phaeosphaeria: *Eriobotrya japonica* a New Host of *Phaeosphaeria acacia*

Chunfang Liao [a,b,c,e,f], Anuruddha Karunarathne [e,g], Danushka S. Tennakoon [e,f], Mingkwan Doilom [a,b,c,e], Jianchu Xu [a,b,c,d], K.W. Thilini Chethana [e,f], Lucas A.P. Dauner [h], Samantha C. Karunarathna* [a,b,c,d], Saowaluck Tibpromma* [a,b,c,d]

[a] CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, P.R. China.
[b] World Agroforestry Centre, East and Central Asia, Kunming 650201, Yunnan, P.R. China.
[c] Centre for Mountain Futures, Kunming Institute of Botany, Kunming 650201, Yunnan, P.R. China.
[d] Yunnan Key Laboratory for Fungal Diversity and Green Development, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, 65201 P.R. China.
[e] Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand.
[f] School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand.
[g] Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand.
[h] 310 Loyola Drive, Millbrae, CA, United States 94030.

*Author for correspondence; e-mail: saowaluckfai@gmail.com; samantha@mail.kib.ac.cn

Received: 30 November 2020
Revised: 2 March 2021
Accepted: 11 March 2021

ABSTRACT

In this paper, we report a coelomycetous fungus that belongs to the family Phaeosphaeriaceae (Pleosporales), associated with the leaves of *Eriobotrya japonica* in Kunming, Yunnan Province, China. Morphologically, our fungal collection shows similarities to known asexual morphs of *Phaeosphaeria,* and exhibits pycnidial, globose conidiomata, a pycnidia wall composed of cells with *textura angularis*, ampulliform to broadly conical, hyaline, phialidic conidiogenous cells and pale brown, subcylindrical conidia that are 3-septate. Phylogenetic analyses of maximum-likelihood and Bayesian posterior probabilities of a combined dataset of SSU, LSU, ITS, and *tef1-α* sequences and morphological analysis confirmed that our fungal collection is *Phaeosphaeria acaciae*. This is the first report of a *Phaeosphaeria* taxon on *Eriobotrya japonica*.

Keywords: China, multigene phylogeny, new record, Phaeosphaeriaceae, taxonomy

1. INTRODUCTION

The family Phaeosphaeriaceae is one of the largest and most important families in the order Pleosporales, which was introduced by Barr [1]. This family is characterized by erumpent, globose to subglobose immersed ascomata; bitunicate asci and hyaline, yellowish or brown, widely obovoid, aseptate or septate ascospores [2]. Taxa of this family in Pleosporales exist as endophytes, plant pathogens, symbiotic fungi, saprobic fungi, and more rarely, as human pathogens [3]. Currently, there are 83 genera and more than 1,000 species in the family [4].

Phytotaxa 000 (0): 000–000
https://www.mapress.com/pt/
Copyright © 2022 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.00.0.0

Morphological and phylogenetic evidence reveal *Tetraploa cylindrica sp. nov.* (Tetraplosphaeriaceae, Pleosporales) from *Saccharum arundinaceum* (Poaceae) in Yunnan Province, China

CHUN-FANG LIAO[1,2,3,8], WEI DONG[1,9], K. W. THILINI CHETHANA[2,3,10], DHANDEVI PEM[2,3,11], RUNGTIWA PHOOKAMSAK[4,5,12], NAKARIN SUWANNARACH[6,7,13*] & MINGKWAN DOILOM[1,14*]

[1] *Innovative Institute for Plant Health / Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, Guangdong, P.R. China*
[2] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3] *School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[4] *Honghe Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe County 654400, Yunnan, P.R. China*
[5] *World Agroforestry Centre, East and Central Asia, Kunming 650201, Yunnan, P.R. China*
[6] *Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[7] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[8] *Fang04271@hotmail.com; https://orcid.org/0000-0002-6309-1101*
[9] *Dongwei0312@hotmail.com; https://orcid.org/0000-0003-4991-1529*
[10] *tchethi@yahoo.com; https://orcid.org/0000-0002-5816-9269*
[11] *pem.dhandevi@gmail.com; https://orcid.org/0000-0003-1831-9266*
[12] *jomjam.rp2@gmail.com; https://orcid.org/0000-0002-6321-8416*
[13] *suwan_461@hotmail.com; https://orcid.org/0000-0002-2653-1913*
[14] *j_hammochi@hotmail.com; https://orcid.org/0000-0001-6167-3637*
**Corresponding authors: Mingkwan Doilom: j_hammochi@hotmail.com, Nakarin Suwannarach: suwan_461@hotmail.com*

Abstract

During an investigation of fungal saprobes of Yunnan Province, China, a species in Tetraplosphaeriaceae was collected from decaying stems of *Saccharum arundinaceum* (Poaceae). The taxon has oblong, dark brown to black, four-columned conidia with mostly three long apical appendages. Phylogenetic analyses of combined LSU, SSU, ITS, *β-tubulin* and *tef1-α* sequence data revealed that our collection is a member of *Tetraploa* and has a close affinity to *T. aquatica*, *T. dashaoensis*, and *T. nagasakiensis*. Based on the morphological comparison and multi-locus phylogeny, we introduce *T. cylindrica* as a new species. The newly discovered taxon is described, illustrated, and compared to related taxa. A taxonomic insight is presented based on our new data regarding the classification problems of asexual and sexual morphs of *Tetraploa*. In addition, this is the first report of *Tetraploa* species that occur on *Saccharum arundinaceum*. The results of the present study will expand our ecological knowledge of *Tetraploa*.

Keywords: 1 new taxon, asexual morph, Dothideomycetes, multi-locus phylogeny, saprobe, taxonomy

Introduction

Tetraplosphaeriaceae, a member of Pleosporales (Hongsanan *et al.* 2020), was established by Tanaka *et al.* (2009) to accommodate five genera, viz. *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria*, and *Triplosphaeria*. The type genus *Tetraplosphaeria* was synonymized under *Tetraploa*, which had earlier been proposed for the asexual morph (Hyde *et al.* 2013). *Tetraploa* is therefore regarded as the type genus of Tetraplosphaeriaceae and accepted in the following studies (Dong *et al.* 2020, Hongsanan *et al.* 2020, Hyde *et al.* 2020a, Li *et al.* 2020, 2021). Tetraplosphaeriaceae has massarina-like sexual morphs, which are characterized by immersed to superficial ascomata with flattened bases, sometimes with rim-like structure at the sides, cylindrical to clavate, short pedicellate asci, and narrowly fusiform to broadly cylindrical, septate, hyaline to pale brown ascospores, often with an entire sheath or appendage-like sheath

Accepted by Ausana Mapook: 13 Jun. 2022; published: xx xxx. 2022

NEW ZEALAND JOURNAL OF BOTANY
https://doi.org/10.1080/0028825X.2024.2311964

Taylor & Francis
Taylor & Francis Group

RESEARCH ARTICLE

Check for updates

Tetraploa wurfbainiae sp. nov. (Tetraplosphaeriaceae, Pleosporales) isolated from *Wurfbainia villosa* in Guangdong, China

Chun-Fang Liao [a,b,c], Yun-Hui Yang[a,b,c], Wei Dong[a], Khanobporn Tangtrakulwanich[c], Yun-Xia Zhang[a], Sehroon Khan[d], Sadia Nadir[d], Thilini Chethana Kandawatte-Wedaralalage[a,b,c] and Mingkwan Doilom[a]

[a]Innovative Institute for Plant Health / Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou, People's Republic of China; [b]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand; [c]School of Science, Mae Fah Luang University, Chiang Rai, Thailand; [d]Department of Biotechnology, Faculty of Natural Sciences, University of Science & Technology Bannu, Khyber Pakhtunkhwa, Pakistan

ABSTRACT

During a survey for microfungi associated with traditional medicinal plants in Guangdong Province, China, an interesting species in the Tetraplosphaeriaceae was isolated from the dead stem of *Wurfbainia villosa* (Zingiberaceae). The new collection is characterised by brown to dark brown, cylindrical to ovate, four-columned conidia, mostly with four straight or slightly flexuous, smooth, and long apical appendages. The phylogenetic analysis of the combined dataset of internal transcribed spacer (ITS), large subunit nuclear rDNA (LSU), the partial translation elongation factor 1-α (*tef1-α*), and β-tubulin (*tub2*) further indicated that the new collection forms a distinct branch in *Tetraploa* and clusters as a sister taxon with *T. dwibahubeeja*. Thus, we introduce a new species, *Tetraploa wurfbainiae*, based on distinct morphology and multi-locus phylogeny, accompanied by a description, illustration, and morphological comparison with related taxa. This is the first report of *Tetraploa* species on the medicinal plant *W. villosa*. This study enhances our understanding of the fungal species associated with the medicinal plant *W. villosa*.

ARTICLE HISTORY
Received 19 October 2023
Accepted 24 January 2024
First published online 8 February 2024

HANDLING EDITOR
Milan Samarakoon

KEYWORDS
1 new species; morphology; multi-gene phylogeny; taxonomy; traditional medicinal plants; Zingiberaceae

Introduction

Wurfbainia villosa belongs to the ginger family (Zingiberaceae: Alpinioideae) and is a perennial, evergreen herb known as one of the "four great southern medicines" in China (Lai et al. 2016; Boer et al. 2018; Song et al. 2021). *Wurfbainia villosa*, also known as "Amomi fructus" (Suo et al. 2018), "Fructus amomi" (Ao et al. 2019), "Villous amomum" (Lu et al. 2011), "Sharen" (Ao et al. 2019), "Bustard cardamom" (Aungtikun and Soonwera 2020), "Chinese cardamom" (Aubertin 2004), and "Indian cardamom or Java cardamom" (Chempakam and Sindhu 2008). The plant is mainly

CONTACT Mingkwan Doilom j_hammochi@hotmail.com; Thilini Chethana Kandawatte-Wedaralalage kandawatte.thi@mfu.ac.th

© 2024 The Royal Society of New Zealand

Journal of *Fungi*

MDPI

Article

Taxonomic and Phylogenetic Updates on *Apiospora*: Introducing Four New Species from *Wurfbainia villosa* and Grasses in China

Chunfang Liao [1,2,3], Indunil Chinthani Senanayake [1], Wei Dong [1], Kandawatte Wedaralalage Thilini Chethana [1,2,3], Khanobporn Tangtrakulwanich [3], Yunxia Zhang [1] and Mingkwan Doilom [1,*]

[1] Innovative Institute for Plant Health, Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China; 6371105002@lamduan.mfu.ac.th (C.L.); indunilchinthani@gmail.com (I.C.S.); dongwei0312@hotmail.com (W.D.); kandawatte.thi@mfu.ac.th (K.W.T.C.); yx_zhang08@163.com (Y.Z.)
[2] Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[3] School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand; khanobporn.tan@mfu.ac.th
* Correspondence: j_hammochi@hotmail.com; Tel.: +86-159-0201-0761

Abstract: *Apiospora*, an ascomycetous genus in Apiosporaceae, comprises saprobes, endophytes, and pathogens of humans and plants. They have a cosmopolitan distribution with a wide range of hosts reported from Asia. In the present study, we collected and isolated *Apiospora* species from *Wurfbainia villosa* and grasses in Guangdong and Yunnan provinces in China. Multi-locus phylogeny based on the internal transcribed spacer, the large subunit nuclear rDNA, the partial translation elongation factor 1-α, and β-tubulin was performed to clarify the phylogenetic affinities of the *Apiospora* species. Based on the distinctive morphological characteristics and molecular evidence, *Ap. endophytica*, *Ap. guangdongensis*, *Ap. wurfbainiae*, and *Ap. yunnanensis* are proposed. Descriptions, illustrations, and notes for the newly discovered species are provided and compared with closely related *Apiospora* species. An updated phylogeny of *Apiospora* is presented, along with a discussion on the phylogenetic affinities of ambiguous taxa.

Keywords: Asia; Amphisphaeriales; Apiosporaceae; endophytes; saprobes; taxonomy

check for updates

Citation: Liao, C.; Senanayake, I.C.; Dong, W.; Thilini Chethana, K.W.; Tangtrakulwanich, K.; Zhang, Y.; Doilom, M. Taxonomic and Phylogenetic Updates on *Apiospora*: Introducing Four New Species from *Wurfbainia villosa* and Grasses in China. *J. Fungi* **2023**, *9*, 1087. https://doi.org/10.3390/jof9111087

Academic Editor: Gary A. Strobel

Received: 19 August 2023
Revised: 17 October 2023
Accepted: 1 November 2023
Published: 6 November 2023

Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

1. Introduction

Recent advances in fungal taxonomy and phylogeny have resulted in taxonomic revisions in numerous genera [1–4], including *Apiospora*. *Apiospora* belongs to Apiosporaceae, Amphisphaeriales, Sordariomycetes, and Ascomycota [5]. It was introduced by Saccardo [6], but the typification was not indicated. Subsequently, Clements and Shear [7] designated *Apiospora montagnei* Sacc. as the type species. However, Crous and Groenewald [8] synonymized *Ap. montagnei* under *Arthrinium arundinis* based on the presence of similar characters in their sexual morphs, including multi-locular perithecial stromata and hyaline ascospores surrounded by a thick gelatinous sheath, and also considering that *Arthrinium* is an older and more commonly referred to name than *Apiospora* [8–11]. Crous and Groenewald [8], therefore, treated the sexual genus *Apiospora* as a synonym of *Arthinium* on the basis that *Arthinium* is earlier proposal and in more frequent usage [10,11]. This taxonomic treatment has been followed by several studies [12–14]. Subsequently, Pintos and Alvarado [15] re-evaluated the phylogenetic placements of *Apiospora* and *Arthrinium* based on multi-locus phylogeny using the internal transcribed spacer (ITS), large subunit nuclear rDNA (LSU), the partial translation elongation factor 1-α (*tef1*-α), and β-tubulin (*tub2*) sequence data. The result showed that several *Arthrinium* species, including the type species *Ar. caricicola*, form a well-supported but distant clade compared to other *Arthrinium*

diversity

MDPI

Article

Three New *Periconia* Species Isolated from *Wurfbainia villosa* in Guangdong, China: A Discussion on the Doubtful Taxa Clustering in this Genus

Chunfang Liao [1,2,3], Kevin D. Hyde [1,2,3], Kandawatte Wedaralalage Thilini Chethana [1,2,3], Wei Dong [1], Yunhui Yang [1,2,3] and Mingkwan Doilom [1,*]

[1] Innovative Institute for Plant Health/Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China; 6371105002@lamduan.mfu.ac.th (C.L.); kdhyde3@gmail.com (K.D.H.); kandawatte.thi@mfu.ac.th (K.W.T.C.); dongwei0312@hotmail.com (W.D.); yyunhui1226@163.com (Y.Y.)
[2] Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[3] School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand
* Correspondence: j_hammochi@hotmail.com; Tel.: +86-15902010761

Abstract: During a survey of fungi on *Wurfbainia villosa* in Guangdong Province, China, three novel species, *Periconia endophytica*, *P. yangjiangensis*, and *P. wurfbainiae*, belonging to Periconiaceae in Pleosporales, Dothideomycetes are proposed based on morphological and phylogenetic evidence. *Periconia endophytica* was isolated from the healthy leaves of *W. villosa*, while *P. yangjiangensis* and *P. wurfbainiae* were obtained from the dead stems of the same host. Notably, holomorphs were observed in *P. wurfbainiae*. The morphological characteristics of the novel taxa are compared with closely related species within *Periconia*. Illustrations, morphological descriptions, and phylogenetic analyses are provided for the novel taxa. Multilocus phylogeny of the combined internal transcribed spacer (ITS), large subunit nuclear rDNA (LSU), small subunit nuclear ribosomal rDNA (SSU), and partial translation elongation factor 1–α (*tef1-α*) regions supported the establishment of three new species. Furthermore, the taxa clustering in *Periconia*, *Flavomyces fulophazii*, and *Sporidesmium tengii*, are discussed for further investigation of their taxonomic placements.

Keywords: three new species; traditional medicinal plant; microfungi; Periconiaceae; Ascomycota; Zingiberaceae; multilocus phylogeny; taxonomy

check for updates

Citation: Liao, C.; Hyde, K.D.; Thilini Chethana, K.W.; Dong, W.; Yang, Y.; Doilom, M. Three New *Periconia* Species Isolated from *Wurfbainia villosa* in Guangdong, China: A Discussion on the Doubtful Taxa Clustering in this Genus. *Diversity* **2024**, *16*, 141. https://doi.org/10.3390/d16030141

Academic Editor: Ipek Kurtboke

Received: 2 January 2024
Revised: 9 February 2024
Accepted: 19 February 2024
Published: 23 February 2024

Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

1. Introduction

Wurfbainia villosa is a perennial, evergreen herb belonging to the ginger family (Zingiberaceae: Alpinioideae). This traditional medicinal herb is one of the four major southern Chinese medicines [1]. The fruits of *W. villosa* are commonly used in traditional Chinese medicine due to their numerous therapeutic properties, including dampness elimination, diarrhea treatment, miscarriage prevention, spleen warming, and as appetite stimulants [2]. *Wurfbainia villosa* is mainly distributed in southeast and east Asia (e.g., Cambodia, China, India, Indonesia, Laos, Myanmar, Thailand, and Vietnam) [3,4]. In China, it is distributed in Fujian, Guangdong, Guangxi, and Yunnan provinces [5]. Yangchun City in the Guangdong Province is widely recognized as a hub for sourcing this medicinal herb [6]. However, limited taxonomic and phylogenetic information is available regarding the fungi associated with *W. villosa*, particularly in Yangchun City. A total of six fungal species have been reported on this medicinal plant in this region [7,8]. During a survey conducted in Yangchun City, Guangdong Province, China, to investigate microfungi associated with the traditional medicinal plant *W. villosa*, ascomycetous fungi resembling *Periconia* were isolated from the dead stems and healthy leaves of this plant.

MycoKeys

MycoKeys 114: 299–327 (2025)
DOI: 10.3897/mycokeys.114.139325

Research Article

Unveiling four new taxa and *Nigrosynnema natarajanensis* comb. nov. in Stachybotryaceae (Hypocreales) from monocotyledon plants in Guangdong Province, China

Chunfang Liao[1,2,3], Mingkwan Doilom[1], D. Jayarama Bhat[4], Kandawatte Wedaralalage Thilini Chethana[2,3], Khanobporn Tangtrakulwanich[3], Yunhui Yang[1,2,3], Fatimah Al-Otibi[5], Kevin D. Hyde[1,2,5], Wei Dong[1]

1 *Innovative Institute for Plant Health/Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China*
2 *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
3 *School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
4 *Vishnugupta Vishwavidyapeetam, Ashoke, Gokarna 581326, India*
5 *Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 22452, Riyadh 11495, Saudi Arabia*

Corresponding author: Mingkwan Doilom (j_hammochi@hotmail.com)

OPEN ACCESS

This article is part of:
Exploring the Hidden Fungal Diversity: Biodiversity, Taxonomy, and Phylogeny of Saprobic Fungi
Edited by Samantha C. Karunarathna, Danushka Sandaruwan Tennakoon, Ajay Kumar Gautam

Academic editor:
Samantha C. Karunarathna
Received: 15 October 2024
Accepted: 8 December 2024
Published: 5 March 2025

Citation: Liao C, Doilom M, Bhat DJ, Thilini Chethana KW, Tangtrakulwanich K, Yang Y, Al-Otibi F, Hyde KD, Dong W (2025) Unveiling four new taxa and *Nigrosynnema natarajanensis* comb. nov. in Stachybotryaceae (Hypocreales) from monocotyledon plants in Guangdong Province, China. MycoKeys 114: 299–327. https://doi.org/10.3897/mycokeys.114.139325

Copyright: © Chunfang Liao et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Abstract

Members of Stachybotryaceae are distributed worldwide, with certain species playing a significant role as bio-degraders and some causing diseases in plants, humans, and animals. Other species within this family can be found in soil and have been reported as saprobes in various plants. In this study (2021–2022), fungal taxa resembling Stachybotryaceae, isolated from dead leaves of *Agave sisalana* and a dead stem of *Wurfbainia villosa* in Guangdong Province, China, are identified based on morphological characteristics and molecular data. Multi-locus phylogeny based on calmodulin (*cmdA*), internal transcribed spacer (ITS), the large subunit nuclear rDNA (LSU), RNA polymerase II second largest subunit (*rpb2*), the partial translation elongation factor 1-α (*tef1-α*), and β-tubulin (*tub2*) revealed that nine strains were grouped within Stachybotryaceae. *Nigrosynnema guangdongense* **gen. et sp. nov.**, typical of Stachybotryaceae but having unusual olivaceous brown to black synnemata that are narrower towards the apex and produce phialidic, aseptate, slimy conidia in black and glistening heads, is introduced. Additionally, *Brevistachys wurfbainiae* and *Sirastachys guangdongensis* are introduced as new species. *Stachybotrys microsporus* is a new host record for *Agave sisalana*. The present study provides comprehensive descriptions, illustrations, and molecular data analyses of the newly discovered taxa and newly recorded species as a taxonomic and phylogenetic contribution to Stachybotryaceae. Furthermore, a new combination, *Nigrosynnema natarajanensis*, is proposed for the previously described *Virgatospora natarajanensis*.

Key words: 4 new taxa, Asparagaceae, Hyphomycetes, saprobic fungi, Sordariomycetes, taxonomy, Zingiberaceae

Fungal Diversity
https://doi.org/10.1007/s13225-025-00550-5

Challenges and update on fungal endophytes: classification, definition, diversity, ecology, evolution and functions

Chunfang Liao[1,2,3] · Mingkwan Doilom[1] · Rajesh Jeewon[4,5] · Kevin D. Hyde[1,2,6] · Ishara S. Manawasinghe[1] · K. W. Thilini Chethana[2,3] · Abhaya Balasuriya[7] · Subasingha Appuhamilage Dilini Thakshila[2,3] · Mei Luo[1] · Ausana Mapook[2] · Zin Hnin Htet[2,3] · Vidyamali Koodalugodaarachchi[2,6] · Nimeshi Wijekoon[1,2,3] · Ramesh K. Saxena[8] · Indunil C. Senanayake[9] · Nuwan D. Kularathnage[2,3,10] · Abdulwahed Fahad Alrefaei[5] · Wei Dong[1]

Received: 12 August 2024 / Accepted: 31 December 2024
© The Author(s) 2025

Abstract
Fungal endophytes have generally been considered as hidden microorganisms that reside asymptomatically within plant tissues and have been exploited for their potential in medicine and plant pathology. They are ubiquitous and associated with nearly all plant species sampled. Even though the exact roles of endophytic fungi within a plant is yet to be established, many speculate that they play important roles in obtaining nutrients and thus improve plant growth, confer plant immunity and promote resistance against biotic and abiotic stresses. It has been postulated that endophytes can exhibit different lifestyles and can even switch lifestyle (i.e., from endophytic to pathogenic or saprobic depending upon plant growth stages). However, there is limited evidence as to whether this switch really happens in vivo. Along the same line, with increasing knowledge of endophytic diversity, defining endophytes has not been easy given their multifaceted functions. The present study provides an updated account with comprehensive knowledge on several aspects including problems with existing definitions, isolation and identification techniques, theoretical and experimental evidence of the role of endophytes, contribution to fungal diversity as well as agenda for future research avenues. For years there has been a number of controversies and debates surrounding as to what exactly is an endophyte. Most of the previous definitions were ephemeral in nature and rather vague and could not realistically define an endophyte. Taking into account numerous biological aspects, we propose herein that endophytes can be defined as "asymptomatic microbial partners that are intimately associated and co-inhabit within healthy internal plant tissues with the ability to confer benefits, co-evolve and alter their lifestyle depending upon plant life stages and adverse conditions". We also discuss the evolution of endophytes based on fossil data and their co-evolution with their host partners. Studies on fungal endophytes have relied mostly on culture-dependent methods to enable their characterization. However, it is generally well known that these methods suffer drawbacks and there is a need to address the challenges associated with lack of sporulation to enable morphological characterization, slow growth on artificial media, as well as contamination issues. These issues are discussed and addressed in detail here. The molecular mechanisms underlying endophytic colonization, avoidance of plant defense mechanisms, lifestyle changes, as well as their genomics and transcriptomics, are also reviewed. We analyze the possibility of endophytes being host-specific or associated with certain hosts and finally provide an account of their economic importance. This outline of fungal endophytes will provide a more comprehensive understanding of endophytes and can serve for boost research into the exploration and their potential applications in the future.

Keywords Colonization · DNA methods · Economic importance · Isolation techniques · Lifestyles

Introduction

Endophytes, pathogens, and saprobes are the three primary lifestyles that fungi adopt in most ecological strategies. Among them, the endophytic lifestyle is one of the highly debated and controversial life mode. Endophytes are well known to cohabit with their hosts over long duration.

Handling Editor: Chitrabhanu Bhunjun.

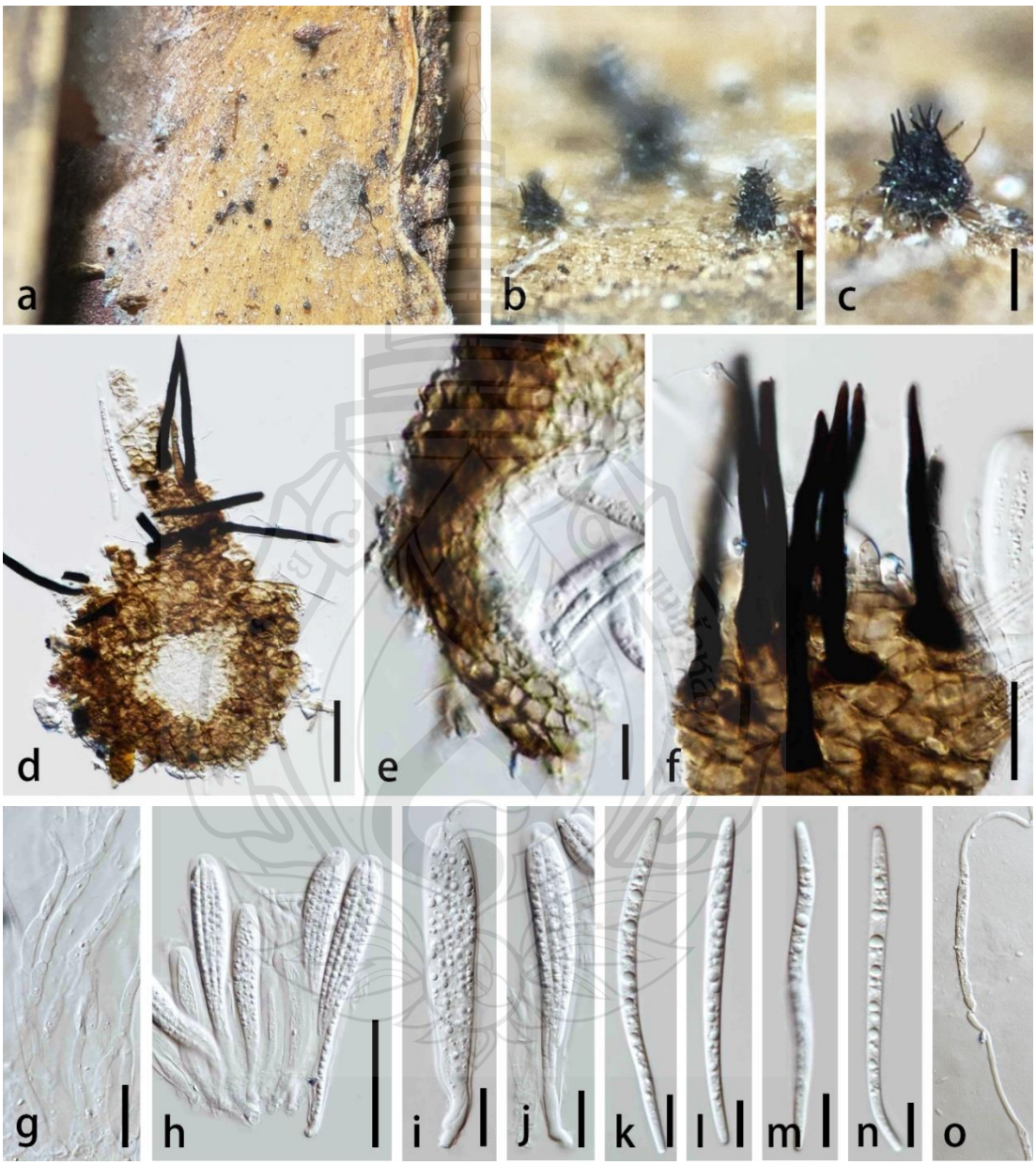
Chunfang Liao and Mingkwan Doilom made equal contributions to this study.

Extended author information available on the last page of the article

Published online: 05 March 2025

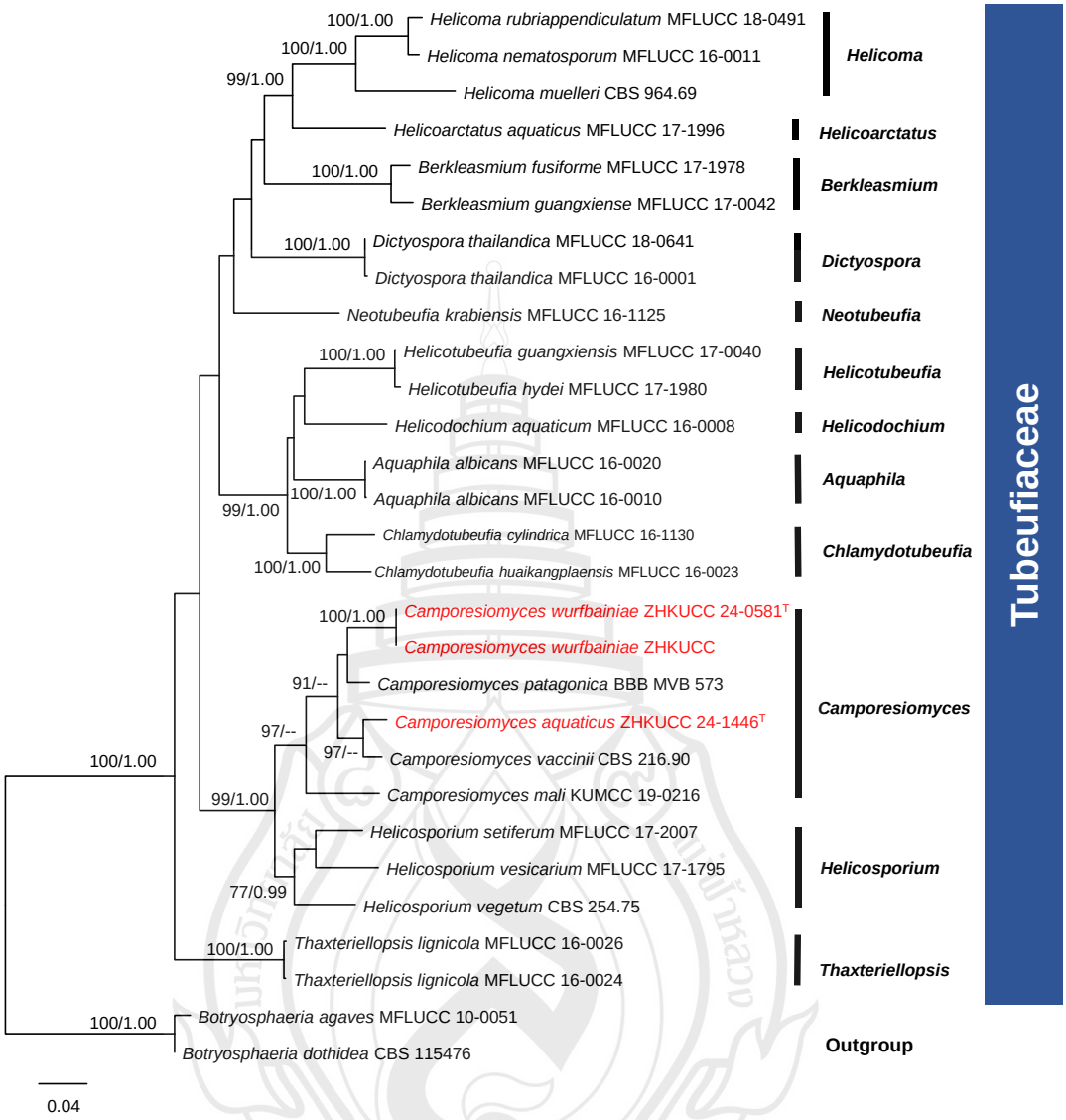
APPENDIX C

TAXA ISOLATED FROM NON *WURFBAINIA VILLOSA* HOSTS



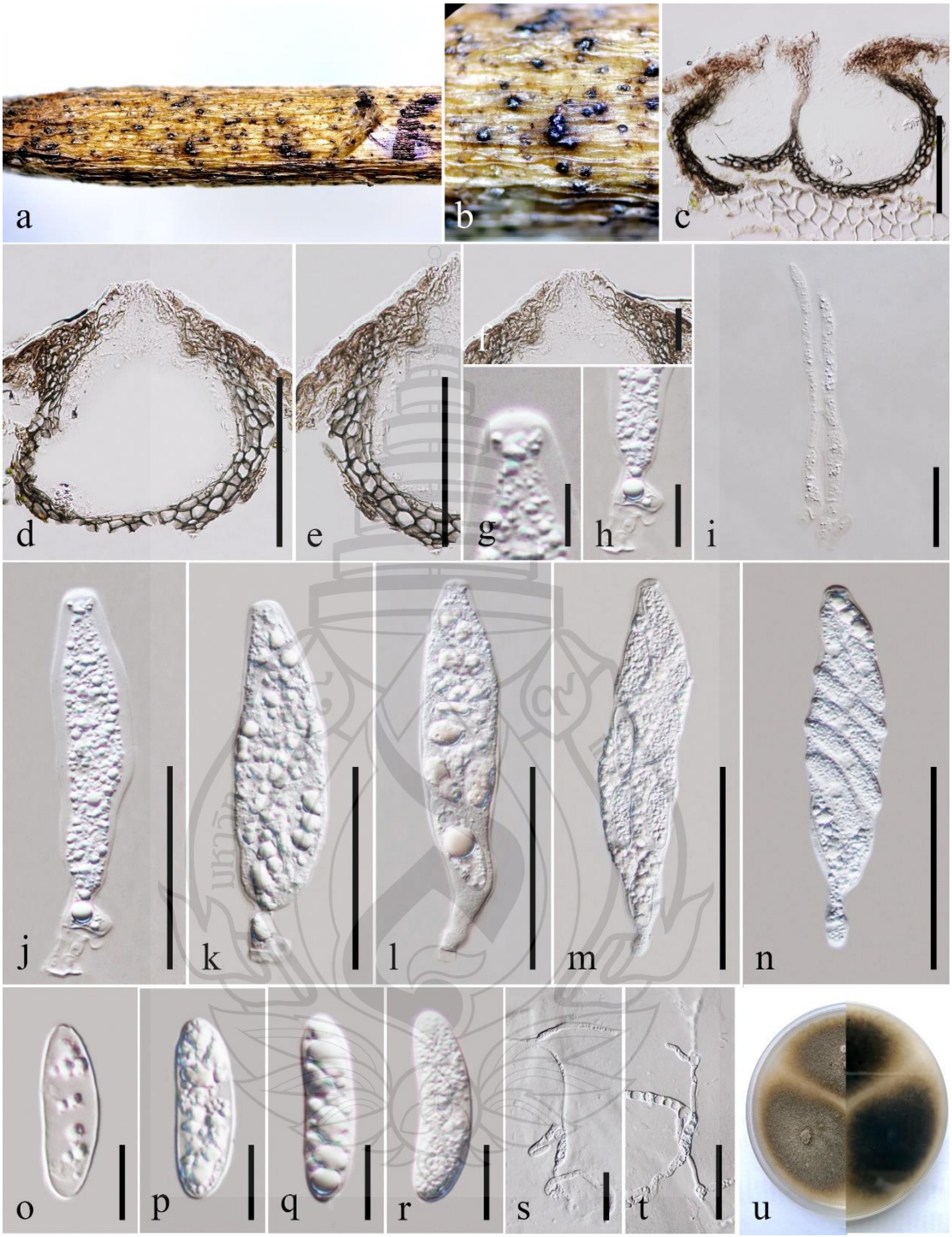
Notes a–c Appearance of ascomata on substrate. d Section through ascoma. e Peridium. f Setae. g Pseudoparaphyses. h–j Asci. k–n Ascospores. o Germinated ascospore. Scale bars: b = 200 µm, c = 100 µm, d, h = 50 µm, e–g = 20 µm, i–n = 10 µm.

Figure C1 *Camporesiomyces wurfbainiae* (MHZU 24-0273, holotype)



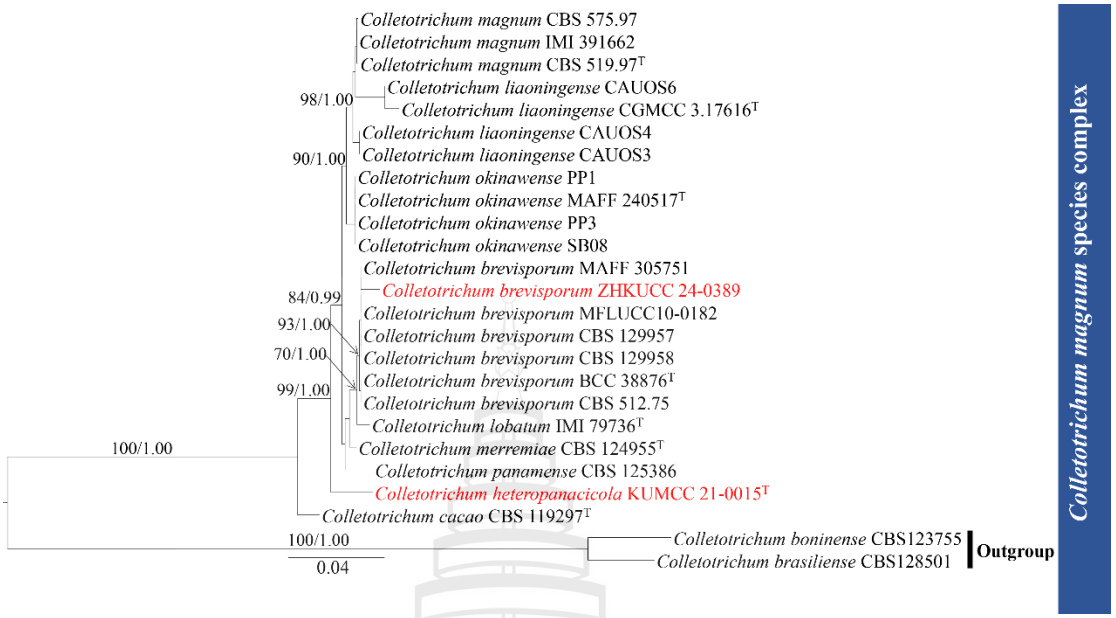
Notes Maximum likelihood consensus tree inferred from the combined ITS, LSU, and *tef-1α* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Botryosphaeria agaves* MFLUCC 10-0051 and *B. dothidea* CBS 115476. Ex-type strains are indicated with "^{T}". The newly generated sequences are indicated in red.

Figure C2 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, and *tub2* sequence data of Tubeufiaceae taxa



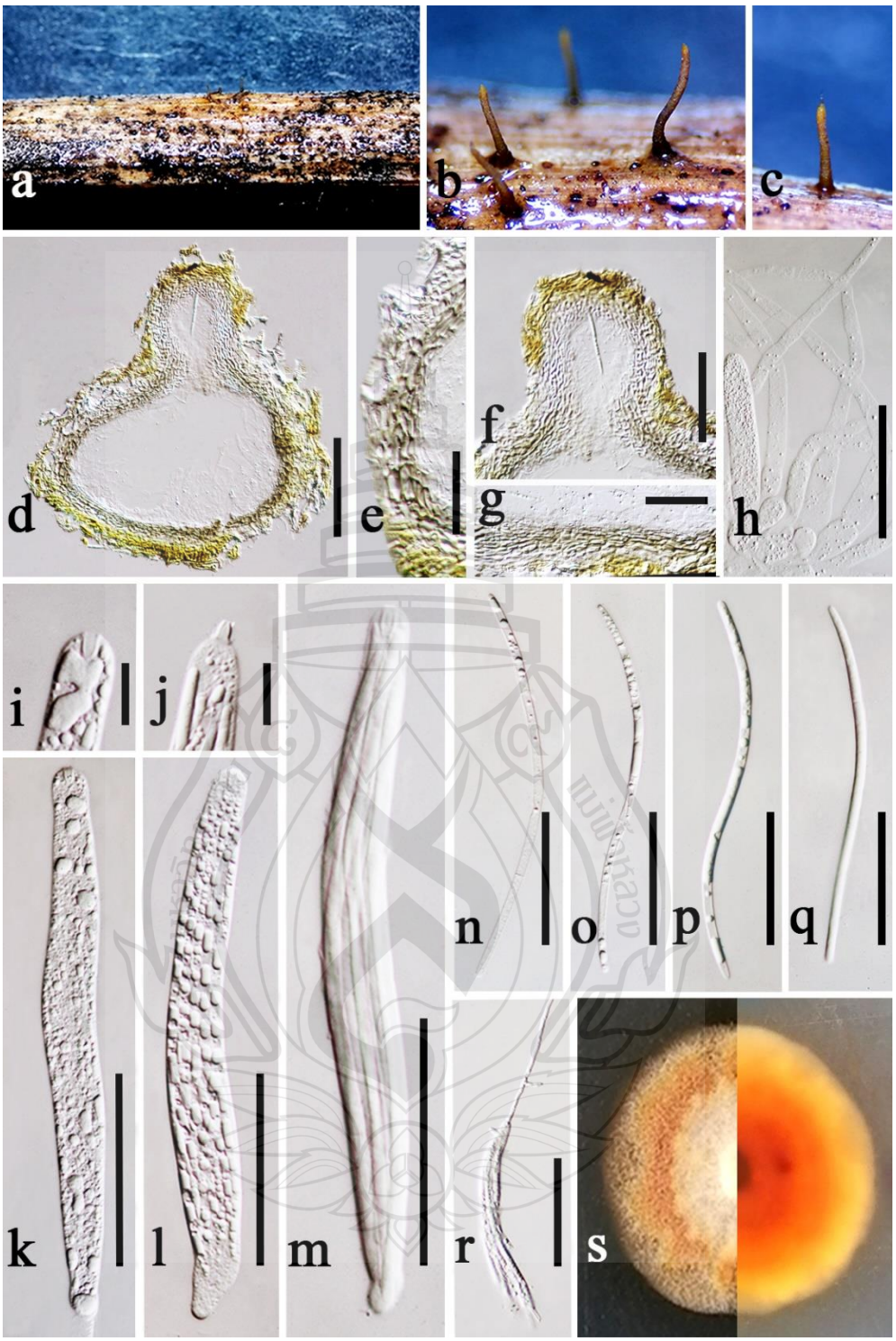
Note a, b Appearance of ascomata on substrate. c, d Section through ascomata. e Peridium. f Ostiole. g Apex of ascus. h Furcate pedicel. i Paraphyses. j–n Asci. o–r Ascospores. s, t Germinated ascospores. u Colony on PDA (front and below). Scale bars: c–e, f, i = 100 μm, g, h, o–r = 10 μm, j–n = 20 μm, s, t = 50 μm.

Figure C3 *Colletotrichum heteropanacicola* (HKAS 112880, holotype)



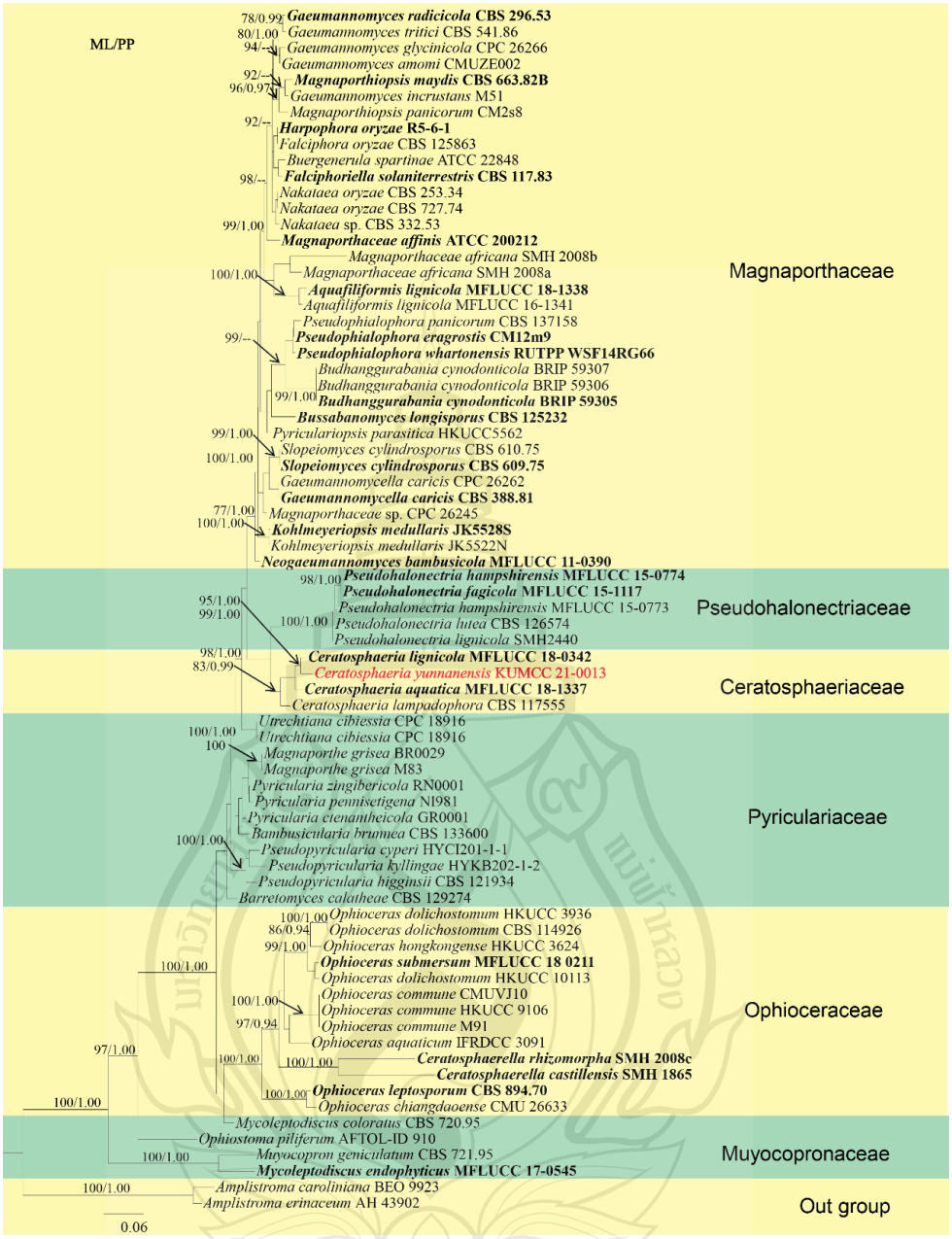
Note Maximum likelihood consensus tree inferred from the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 70% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Colletotrichum boninense* (CBS 123755) and *C. brasiliense* (CBS128501). Ex-type strains are indicated with "T". The newly generated sequences are indicated in red.

Figure C4 Phylogram generated from maximum likelihood analysis based on combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequence data of *Colletotrichum* taxa



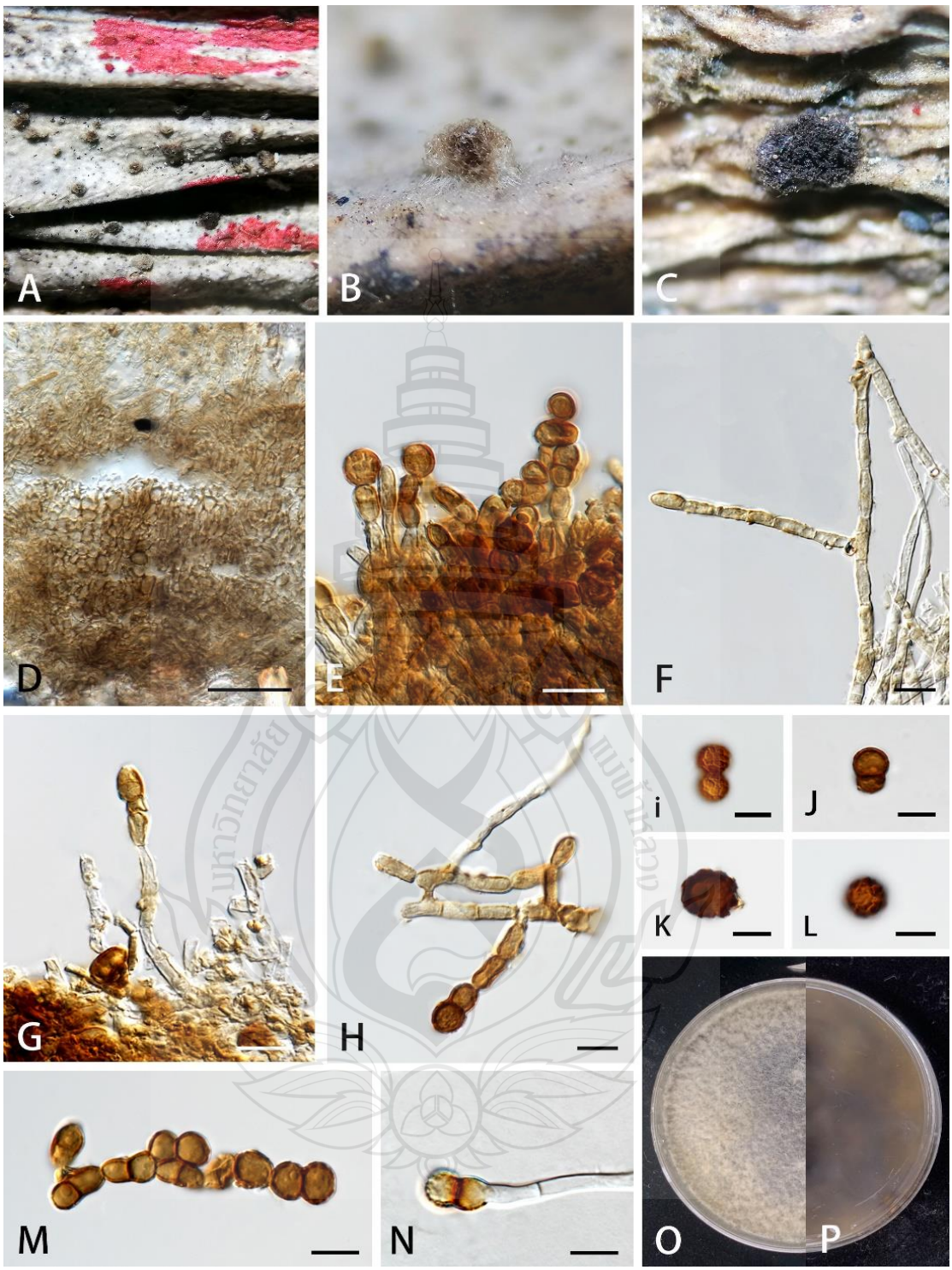
Note a, c Appearance of ascomata on substrate. d Section through ascoma. e, g Peridium. f Ostiole. h. Paraphyses. i, j Apical ring of Asci. k – m Asci. n – q Ascospores. r Germinated ascospore. s Culture characteristics on PDA. Scale bars: d =500 µm, e, f = 200 µm, h, k – q, r = 100. g, i, j =10 µm.

Figure C5 *Ceratosphaeria yunnanensis* (KUN–HKAS 107635, Holotype)



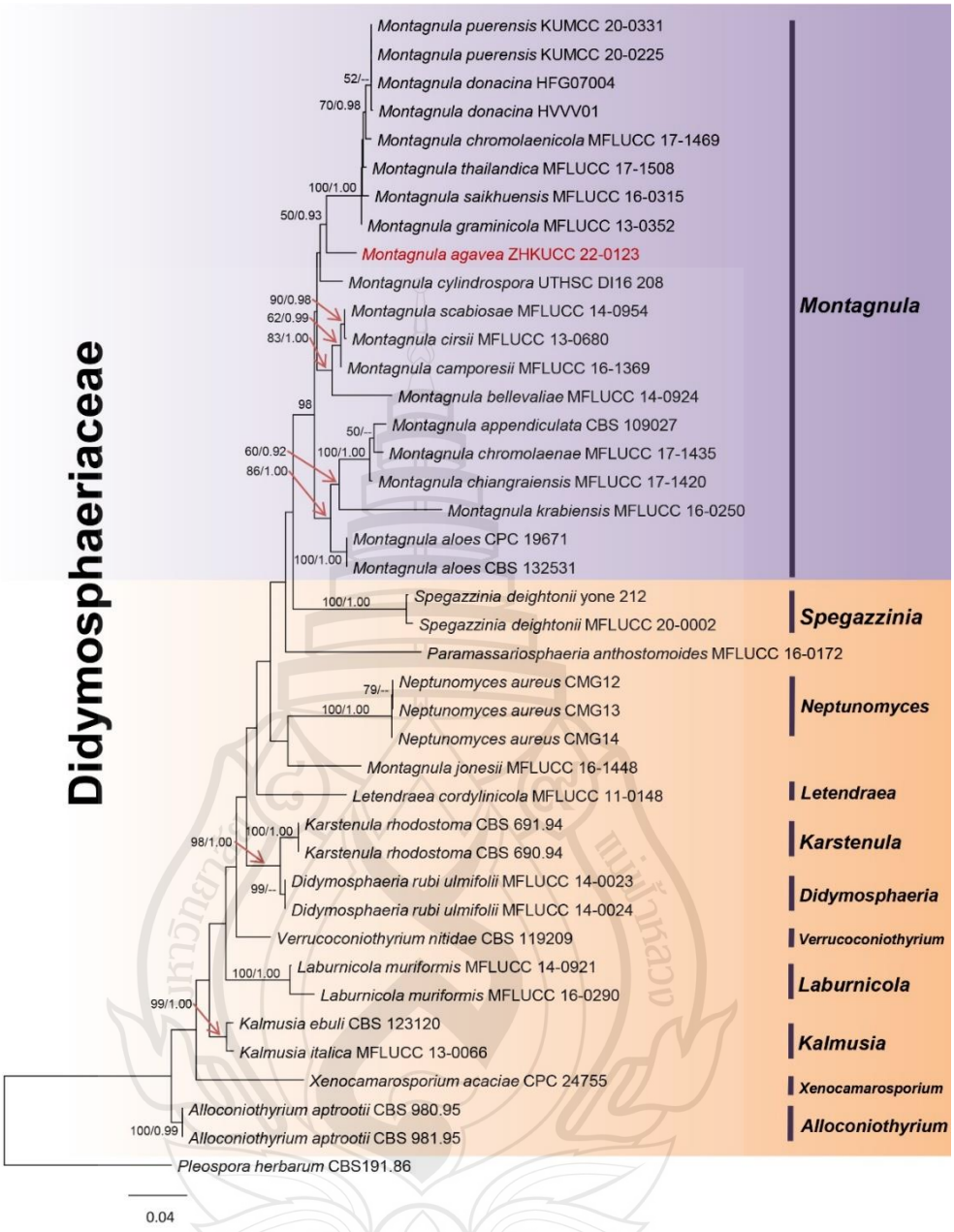
Note Phylogenetic tree derived from maximum likelihood analysis of a combined LSU, *tef-1* sequence dataset. *Amplistroma erinaceum* (AH 43902) and *Amplistroma caroliniana* (BE O9923) were used as outgroup. Branches with bootstrap values Bootstrap support values for ML and MP ≥ 75% and ≥ 0.95 are shown at each branch and the bar represents 0.06 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 75% / 0.95. Ex-type strains are in black bold, newly generated sequence is indicated in red and bold for new taxa.

Figure C6 Phylogram generated from maximum likelihood analysis based on combined LSU and *tef-1* sequence data of *Ceratosphaeria* taxa



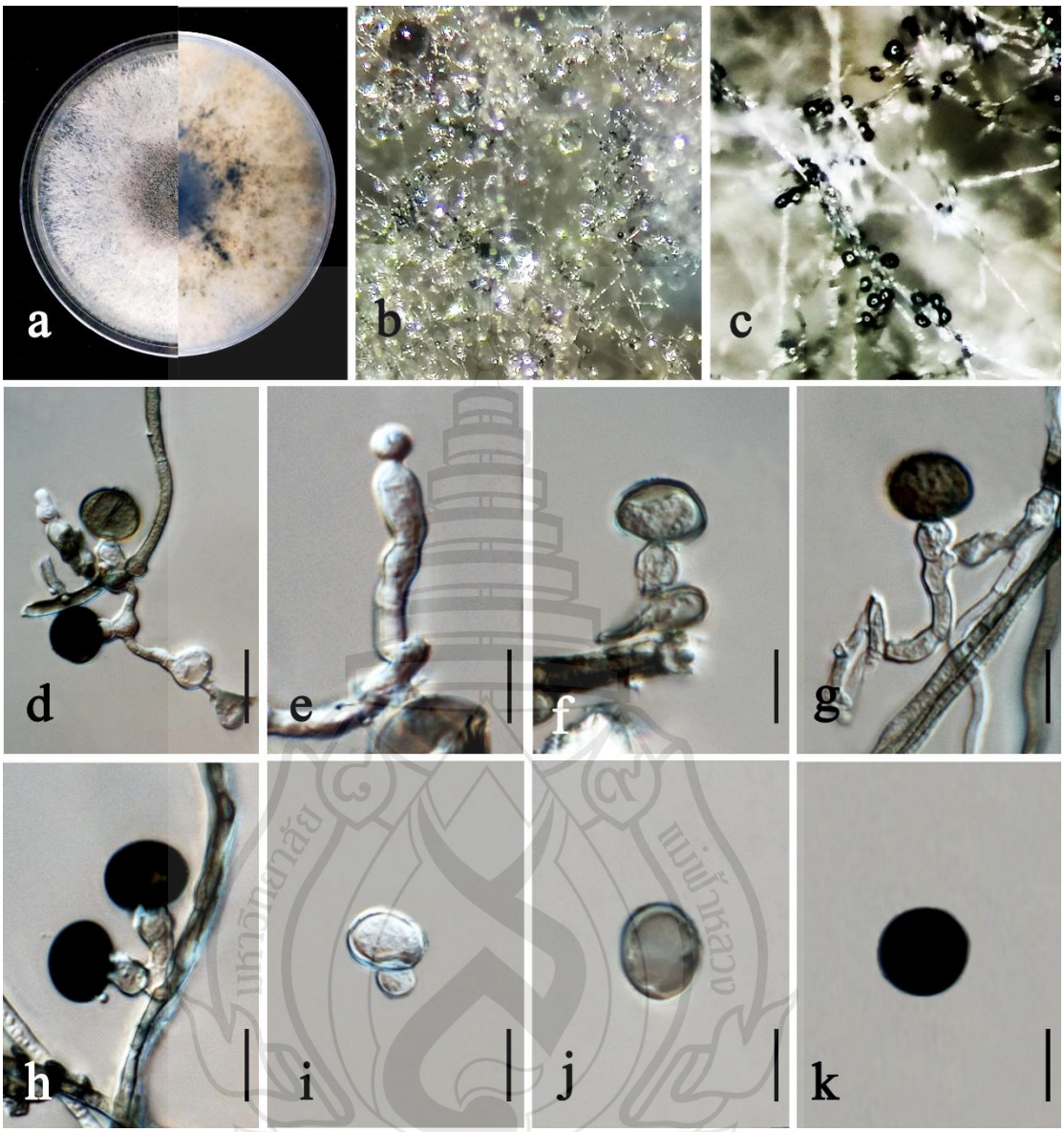
Note a–c Conidiomata on leaf substate. d Conidiomatal wall. e–h Conidiophores, conidiogenous cells and conidia. i–l Conidia (k, l Part-spores after splitting from the septum). m Catenate conidia. n Germinated conidium. o, p Colony on PDA (front and below). Scale bars: d = 50 μm, f = 10 μm, e, g–n = 5 μm.

Figure C7 *Montagnula agavea* (ZHKU 22-0067, holotype)



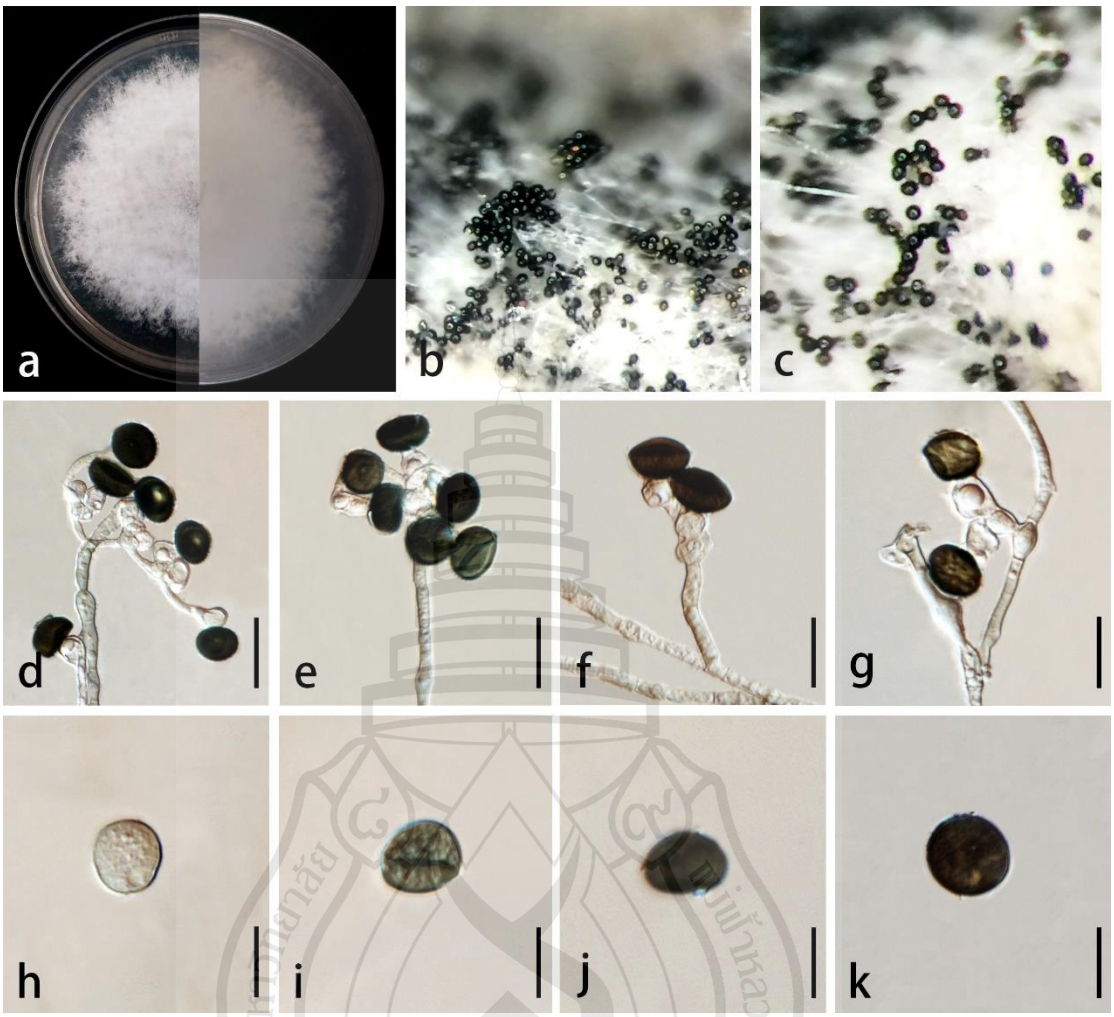
Note Maximum likelihood consensus tree inferred from the combined LSU, ITS, SSU, and *tef1-α* multiple sequence alignment. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 50% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Pleospora herbarum* CBS 191.86. Ex-type strains are indicated with "^{T}". The new species is indicated with brick-red.

Figure C8 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU, and *tef1-α* sequence data of the *Montagnula*



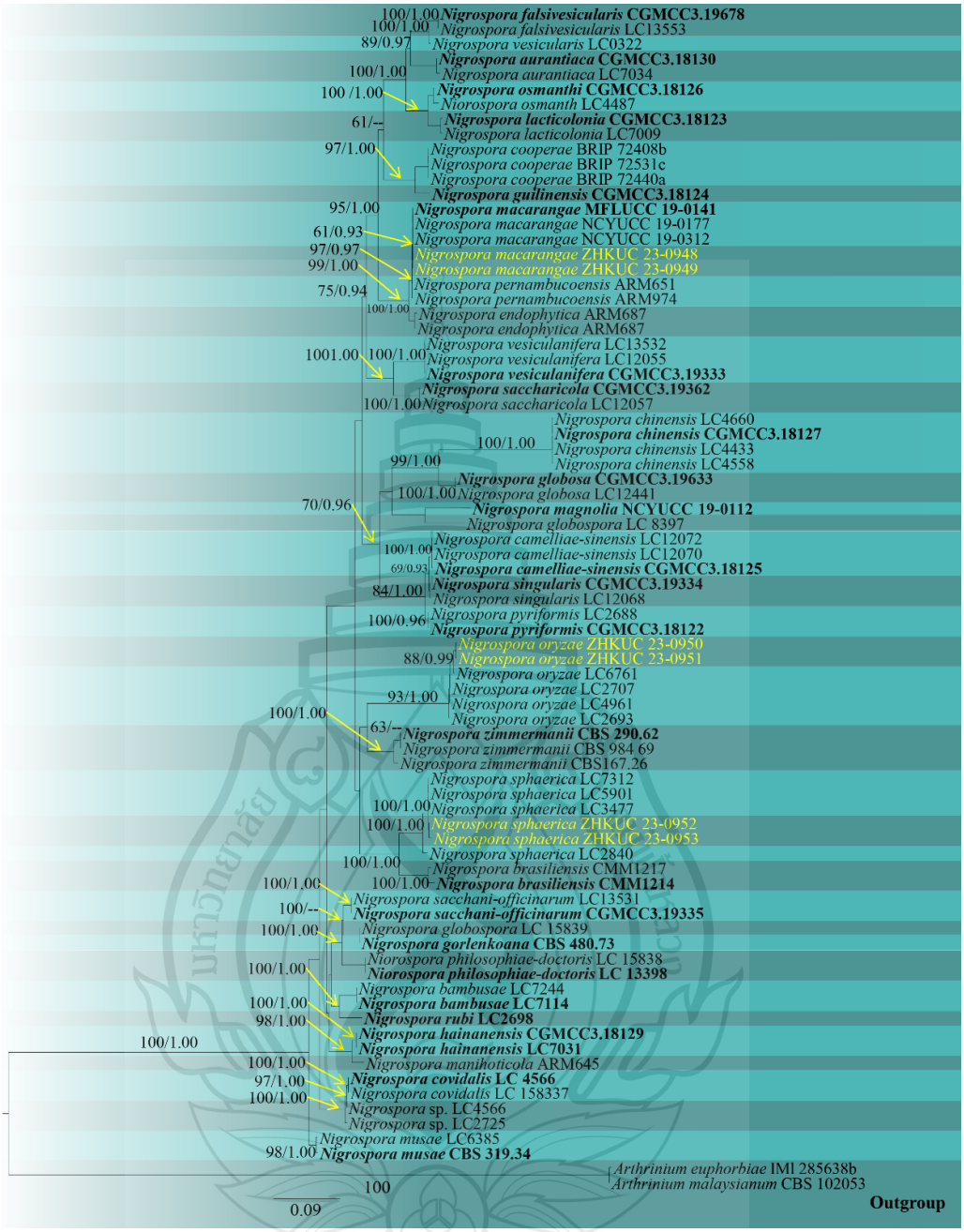
Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h–k Conidia. Scale bars: d–k = 10 μm.

Figure C9 ***Nigrospora macarangae*** (MHZU 23-0228, a new host record)



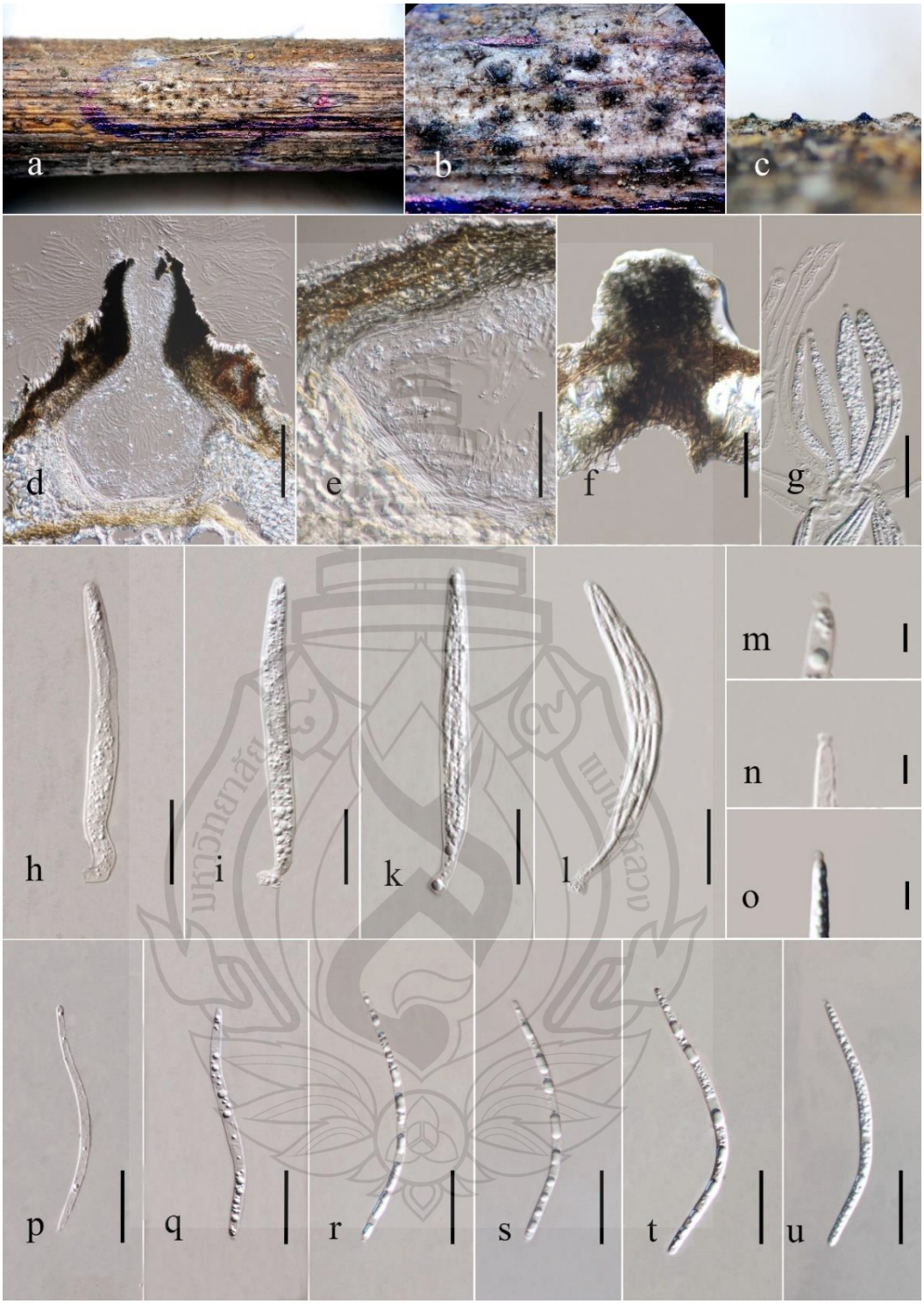
Note a Upper view and reverse view of culture on PDA. b, c Conidia on aerial mycelia on PDA. d–g Conidia with conidiogenous cells. h–k Conidia. Scale bars: d–k = 10 μm.

Figure C10 *Nigrospora oryzae* (MHZU 23-0229, a new host record)



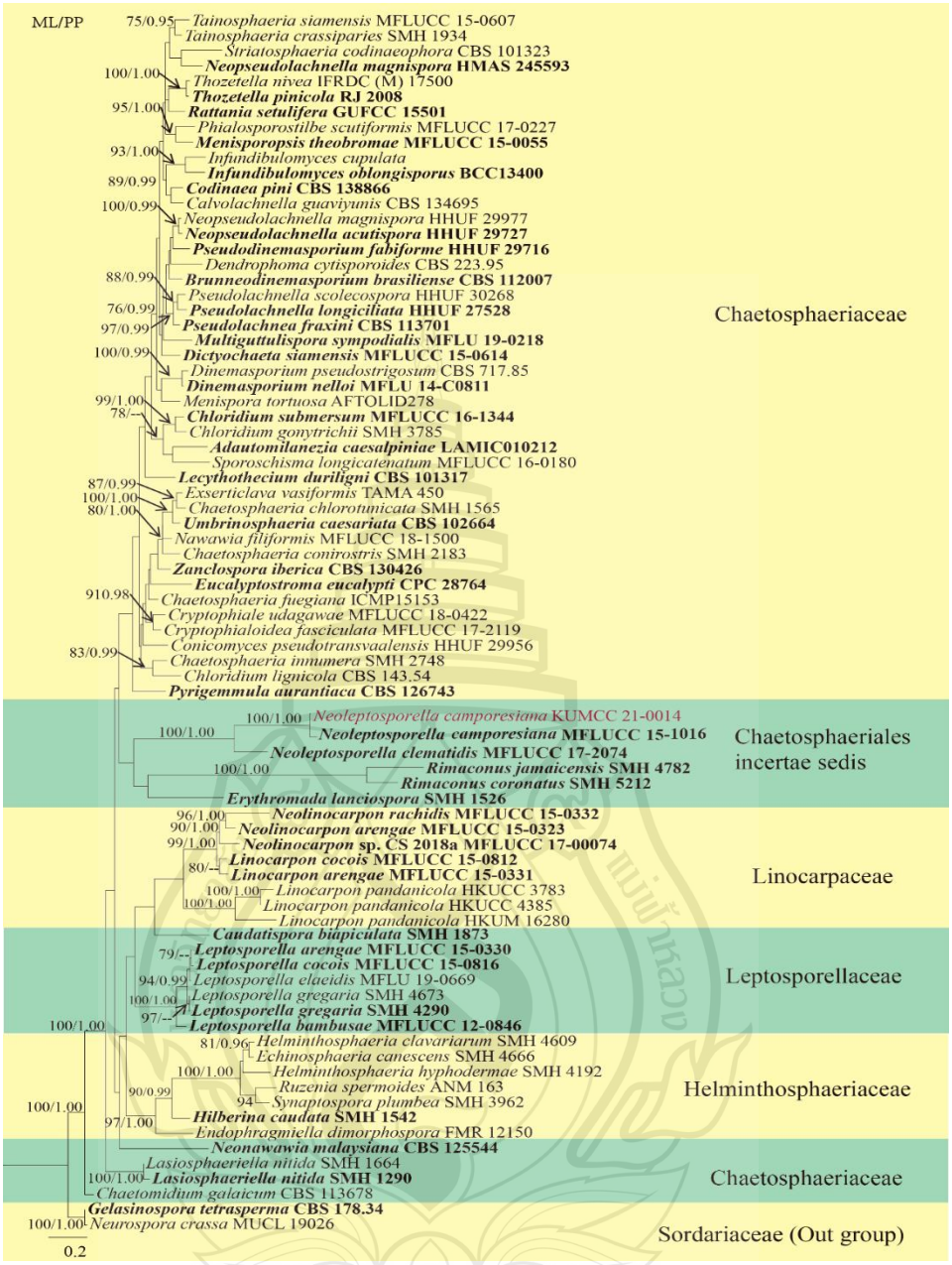
Note Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α*, and *β-tubulin* sequence data of the genus *Nigrospora*. Bootstrap support values for ML greater than 60% and 0.90 BYPP, respectively. The tree was rooted with *Arthrinium euphorbiae* (IMl 285638b) and *A. malaysianum* (CBS 102053). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Figure C11 Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1-α*, and *β-tubulin* sequence data of the *Nigrospora*



Note a, c Appearance of ascomata on substrate. d Section through ascoma. e Peridium. f Ostiole' g Paraphyses with asci. h – l Asci. m – o polar mucilaginous appendage. P – u Ascospores. Scale bars: d = 500 μm, e = 200 μm, (f, g, l, p, u) = 100 μm, (m – o) = 10 μm.

Figure C12 *Neoleptosporella yunnanensis* (KUN–HKAS 107635, new host record)



Notes Phylogenetic tree derived from maximum likelihood analysis of a combined ITS, LSU sequence dataset. *Gelasinospora tetrasperma* (CBS 178.34) and *Neurospora crassa* (MUCL 19026) were used as outgroup. Branches with bootstrap values Bootstrap support values for ML and Bayes ≥ 75% and ≥ 0.95 are shown at each branch and the bar represents 0.2 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 75% / 0.95. Ex-type strains are in black bold, the newly generated sequence is indicated in red.

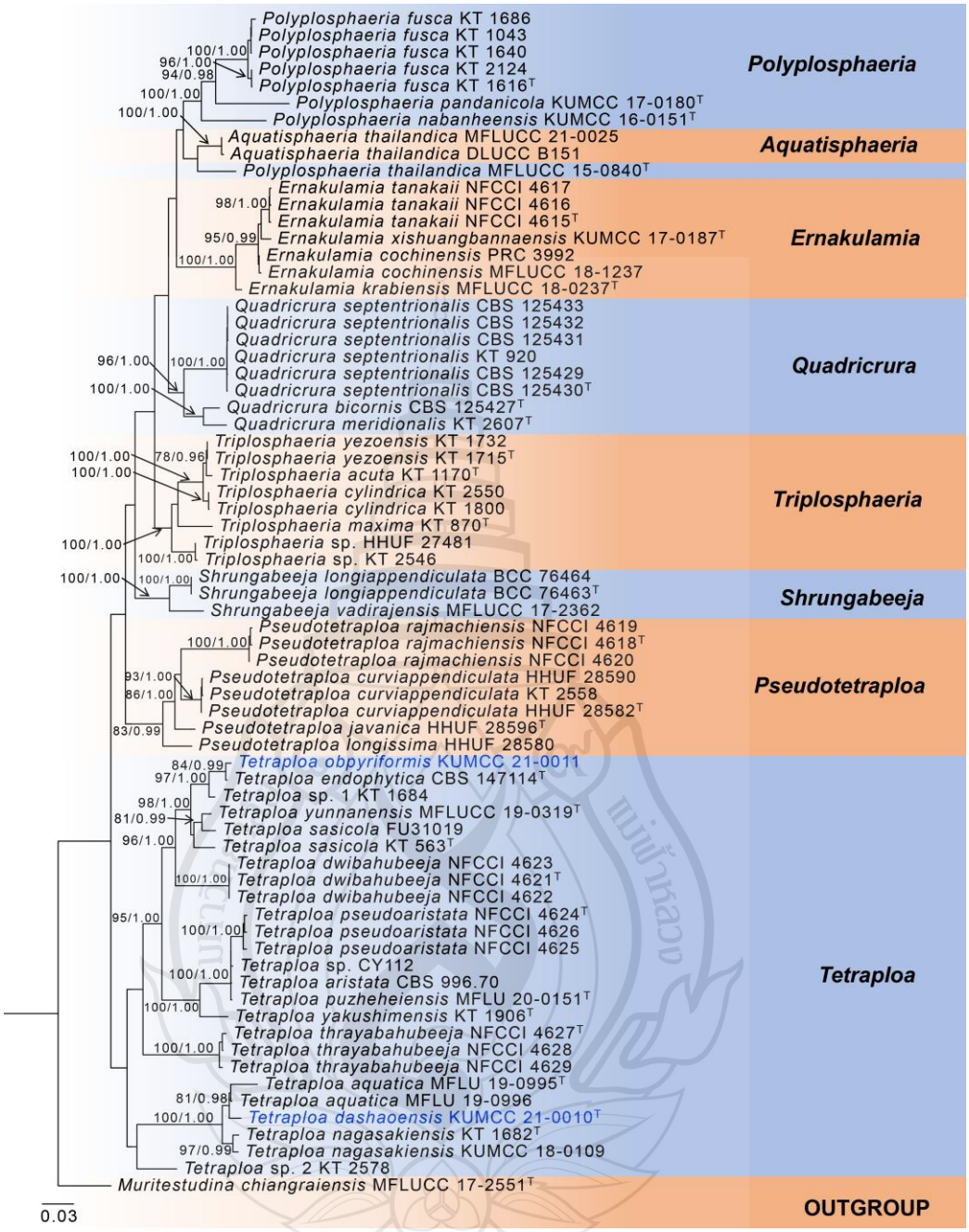
Figure C13 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of *Neoleptosporella* taxa

Note a–c. Conidia on host substrate. d–j. Conidia. k. Verrucose conidia. l. Germinating conidium. m. Colony on PDA (left-front, right-reverse). Scale bars: d–g, k = 50 μm, h-j, l = 200 μm.

Figure C14 *Tetraploa dashaoensis (KUN–HKA*S 107636, holotype)

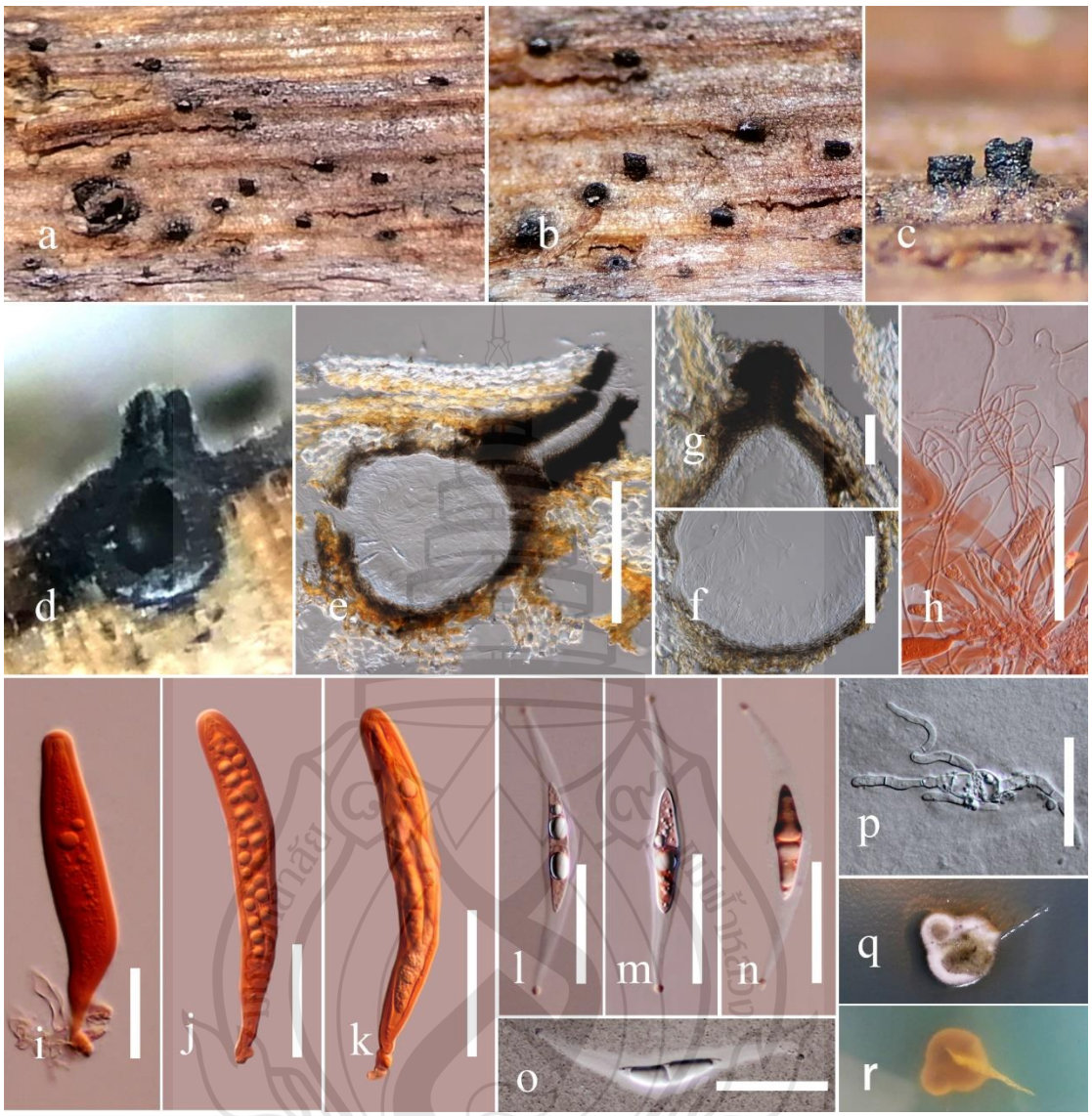
Note a–c. Conidia on host substrate; d–i. Conidia; j. Verrucose conidia; k. Germinating conidium; l, m. Colony on PDA (left-front, right-reverse); Scale bars: d, j, k = 20 μm, d = 10 μm, f–i = 50 μm.

Figure C15 *Tetraploa obpyriformis* (KUN–HKAS 107637, holotype)



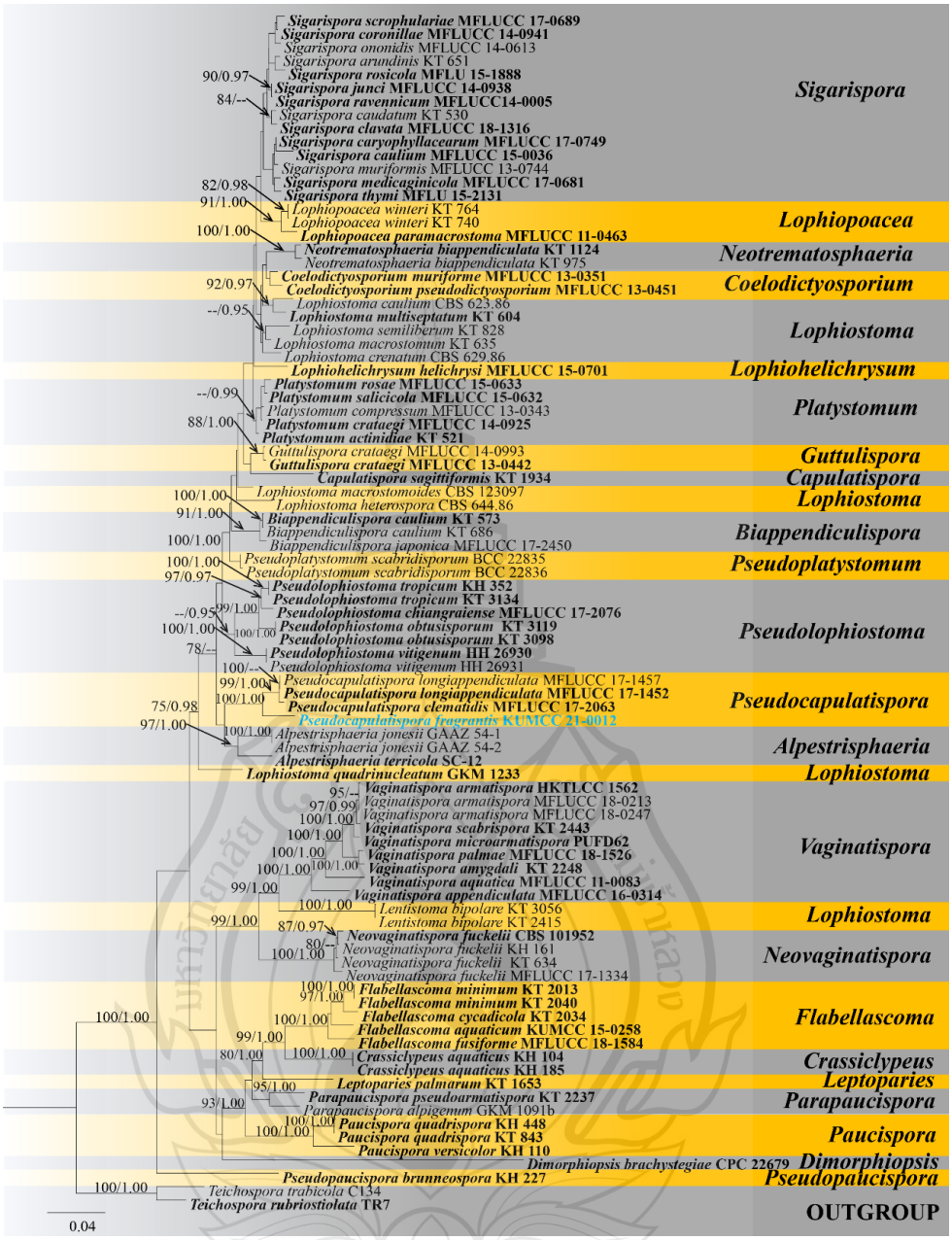
Note Phylogram generated from parsimony analysis based on combined LSU, SSU, ITS, *β-tubulin*, and *tef1-α* sequence data of *Tetraploa*. Parsimony bootstrap support values greater than 75% are indicated above or below the nodes, and branches with Bayesian posterior probabilities greater than 0.95 are given at the nodes. The ex-types (reference strains) are in *bold*; the new isolates are in *blue*. The tree is rooted with *Muritestudina chiangraiensis* (MFLUCC 17-2551).

Figure C16 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *β-tubulin*, and *tef1-α* sequence data of the *Tetraploa*



Note a–c Appearance of ascomata on substrate. d, e Section through ascoma. f Peridium. g Ostiole. h Pseudoparaphyses on Congo red. A i–k sci in Congo red. l–n Ascospores in Congo red. o Ascospore in Indian ink. p Germinated ascospore. q, r Culture characteristics on PDA. Scale bars: e = 500 μm, f, h = 200 μm, g, i–o = 50 μm, k = 20 μm.

Figure C17 *Pseudocapulatispora fragrantis* (KUN–HKAS 107635, holotype)



Note Phylogenetic tree derived from maximum likelihood analysis of a combined SSU, ITS, LSU, and *tef-1* sequence dataset. *Teichospora rubriostiolata* (TR7) and *Teichospora trabicola* (C134) were used as outgroup. Branches with bootstrap values ≥75% are shown at each branch and the bar represents 0.04 substitutions per nucleotide position. Hyphen (-) represents support values ≤ 75%/0.95. Ex-type strains are in black bold, newly generated sequence is indicated in blue and bold for new taxa.

Figure C18 Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, and *tef-1* sequence data of *Pseudocapulatispora* taxa

CURRICULUM VITAE

NAME Chunfang Liao

EDUCATIONAL BACKGROUND

2015 Bachelor of Science
Biotechnology
Qujing Normal University, Yunan, China

WORK EXPERIENCE

2019-2021 Assistant
Kunming Institute of Botany, China

SCHOLARSHIP

2020 Partial Scholarship for Doctoral Degree
from Mae Fah Luang University

PUBLICATIONS

First Author

Liao, C. F., Doilom, M., Bhat, D. J., Chethana, K. W., Tangtrakulwanich, K., Yang, Y. H., . . . Dong, W. (2025). Unveiling four new taxa and *Nigrosynnema natarajanensis* comb. nov. in Stachybotryaceae (Hypocreales) from monocotyledon plants in Guangdong Province, China. *MycoKeys, 114*, 299–327. http://doi.org/10.3897/mycokeys.114.139325

Liao, C. F., Doilom, M., Jeewon, R., Hyde, K. D., Manawasinghe, I. S., Chethana, K. W., . . . Htet, Z. H. (2025). Challenges and update on fungal endophytes: Classification, definition, diversity, ecology, evolution and functions. *Fungal Diversity, 5,* 1–67. http://doi.org/10.1007/s13225-025-00550-5

Liao, C. F., Dong, W., Chethana, K. T., Pem, D., Phookamsak, R., Suwannarach, N., . . . Doilom, M. (2022). Morphological and phylogenetic evidence reveal *Tetraploa cylindrica* sp. nov. (Tetraplosphaeriaceae, Pleosporales) from *Saccharum arundinaceum* (Poaceae) in Yunnan Province, China. *Phytotaxa, 554*(2), 189–200. http://doi.org/10.11646/phytotaxa.554.2.7

Liao, C. F., Hyde, K. D., Chethana, K. W. T., Dong, W., Yang, Y., & Doilom, M. (2024). Three new *Periconia* species isolated from *Wurfbainia villosa* in Guangdong, China: A discussion on the doubtful taxa clustering in this genus. *Diversity*, *16*(3), 141. http://doi.org/10.3390/d16030141

Liao, C. F., Karunarathne, A., Tennakoon, D. S., Doilom, M., Xu, J., Chethana, K. T., . . . Tibpromma, S. (2021). Addition to *Phaeosphaeria*: *Eriobotrya japonica*, a new host of *Phaeosphaeria acaciae*. *Chiang Mai Journal of Science, 48*(3), 922–930.

Liao, C. F., Senanayake, I. C., Dong, W., Chethana, K. W. T., Tangtrakulwanich, K., Zhang, Y. X., . . . Doilom, M. (2023). Taxonomic and phylogenetic updates on *Apiospora*: Introducing four new species from *Wurfbainia villosa* and grasses in China. *Journal of Fungi*, *9*(11), 1087. http://doi.org/10.3390/jof9111087

Liao, C. F., Yang, Y. H., Dong, W., Tangtrakulwanich, K., Zhang, Y. X., Khan, S., . . . Doilom, M. (2024). *Tetraploa wurfbainiae* sp. nov. (Tetraplosphaeriaceae, Pleosporales) isolated from *Wurfbainia villosa* in Guangdong, China. *New Zealand Journal of Botany*, *62*(2-3), 303–316. http://doi.org/10.1080/0028825X.2024.2311964

Co-author

Calabon, M. S., Hyde, K. D., Jones, E. G., Doilom, M., Liao, C. F., & Boonmee, S. (2020). *Mycoenterolobium aquadictyosporium* sp. nov. (Pleosporomycetidae, Dothideomycetes) from a freshwater habitat in Thailand. *Mycological Progress, 19*(10), 1031–1042. http://doi.org/10.1007/s11557-020-01609-0

Dai, D. Q., Wijayawardene, N. N., Tang, L. Z., Liu, C., Han, L. H., Chu, H. L., . . . Li, Y. M. (2019). *Rubroshiraia* gen. nov., a second hypocrellin-producing genus in Shiraiaceae (Pleosporales). *MycoKeys, 58*, 1–26. https://doi.org/10.3897/mycokeys.58.36723

Doilom, M., Guo, J. W., Phookamsak, R., Mortimer, P. E., Karunarathna, S. C., Dong, W., . . . Promputtha, I. (2020). Screening of phosphate-solubilizing fungi from air and soil in Yunnan, China: Four novel species in *Aspergillus*, *Gongronella*, *Penicillium*, and *Talaromyces*. *Frontiers in Microbiology, 11*, 585215. http://doi.org/10.3389/fmicb.2020.585215

Doilom, M., Hyde, K. D., Dong, W., Liao, C. F., Suwannarach, N., & Lumyong, S. (2021). The plant family Asteraceae is a cache for novel fungal diversity: Novel species and genera with remarkable ascospores in Leptosphaeriaceae. *Frontiers in Microbiology, 12*, 660261. http://doi.org/10.3389/fmicb.2021.660261

Dong, W., Hyde, K. D., Jeewon, R., Liao, C. F., Zhao, H. J., Kularathnage, N. D., . . . Doilom, M. (2023). Mycosphere notes 449–468: Saprobic and endophytic fungi in China, Thailand, and Uzbekistan. *Mycosphere, 14*(1), 2208–2262. http://doi.org/10.5943/mycosphere/14/1/26

Hongsanan, S., Khuna, S., Manawasinghe, I. S., Tibpromma, S., Chethana, K. W. T., Liao, C. F., . . . Karunarathna, S. C. (2025). Mycosphere notes 521–571: A special edition of fungal biodiversity to celebrate Kevin D. Hyde's 70th birthday and his exceptional contributions to mycology. *Mycosphere, 16*(2), 2002–2180. https://doi.org/10.5943/mycosphere/16/2/1

Hyde, K. D., Suwannarach, N., Jayawardena, R. S., Manawasinghe, I. S., Liao, C. F., . . . Bao, D. F. (2021). Mycosphere notes 325–344: Novel species and records of fungal taxa from around the world. *Mycosphere, 12*(1), 1101–1156. https://doi.org/10.5943/mycosphere/12/1/14

Hyde, K. D., Noorabadi, M. T., Thiyagaraja, V., He, M. Q., Johnston, P. R., Wijesinghe, S. N., . . . Zvyagina, E. (2024). The 2024 outline of fungi and fungus-like taxa. *Mycosphere, 15*(1), 5146–6239. http://doi.org/10.5943/mycosphere/15/1/25

Hyde, K. D., Wijesinghe, S. N., Afshari, N., Aumentado, H. D., Liao, C. F., . . . Zhang, J. Y. (2024). Mycosphere notes 469–520. *Mycosphere, 15*(1), 1294–1454. http://doi.org/10.5943/mycosphere/15/1/11

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y. R., Suwannarach, N., Sysouphanthong, P., . . . Wang, Y. (2022). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 117*, 1–272. http://doi.org/10.1007/s13225-022-00513-0

Li, Y. X., Doilom, M., Dong, W., Liao, C. F., Manawasinghe, I. S., & Xu, B. (2023). A taxonomic and phylogenetic contribution to *Torula*: *T. phytolaccae* sp. nov. on *Phytolacca acinosa* from China. *Phytotaxa, 584*(1), 1–7. http://doi.org/10.11646/phytotaxa.584.1.1

Manawasinghe, I. S., Calabon, M. S., Jones, E. B. G., Zhang, Y. X., Liao, C. F., Xiong, Y. R., . . . Hyde, K. D. (2022). Mycosphere notes 345–386. *Mycosphere, 13*(1), 454–557. http://doi.org/10.5943/mycosphere/13/1/3

Phookamsak, R., Jiang, H., Suwannarach, N., Lumyong, S., Xu, J., Xu, S., . . . Chomnunti, P. (2022). Bambusicolous fungi in Pleosporales: Introducing four novel taxa and a new habitat record for *Anastomitrabeculia didymospora*. *Journal of Fungi, 8*(6), 630. http://doi.org/10.3390/jof8060630

Senanayake, I. C., Rossi, W., Leonardi, M., Weir, A., McHugh, M., Rajeshkumar, K. C., . . . Song, J. (2023). Fungal diversity notes 1611–1716: Taxonomic and phylogenetic contributions on fungal genera and species with emphasis in South China. *Fungal Diversity, 122*, 161–403. https://doi.org/10.1007/s13225-023-00523-6

Xiong, Y., Manawasinghe, I. S., Liao, C., Hyde, K. D., & Dong, Z. Y. (2022). *Neodeightonia arengae* sp. nov., botryosphaeriaceous taxa on *Arenga tremula* (Arecaceae) from Guangdong, China. *Phytotaxa, 530*(2), 130–140. http://doi.org/10.11646/phytotaxa.530.2.1

Yang, Y. H., Manawasinghe, I. S., Wanasinghe, D. N., De Farias, A. R., Liao, C. F., & Dong, Z. Y. (2024). A novel genus and new records of Dothideomycetes associated with *Litchi chinensis* litter from Guangdong Province, China. *New Zealand Journal of Botany, 62*(2-3), 216–238. http://doi.org/10.1080/0028825X.2023.2274628

Yang, Y. H., Liao, C. F., Manawasinghe, I. S., De Farias, A. R., & Dong, Z. Y. (2023). *Neomassaria khayae* sp. nov., a novel pleosporalean species on *Khaya senegalensis* from Guangdong Province, China. *Phytotaxa, 599*(1), 65–77. http://doi.org/10.11646/phytotaxa.599.1.4

Yang, Y. H., Liao, C. F., Manawasinghe, I. S., Hyde, K. D., Dong, Z. Y., & Xu, B. (2024). Phylogenetic and morphological characterization of Beltraniaceae species from Litchi and Longan litter in southern China. *Chiang Mai Journal of Science, 52*(4), 1–23. http://doi.org/10.12982/CMJS.2025.045