

MICROFUNGI ISOLATED FROM *ROSA ROXBURGHII* AND OTHER HOSTS WITH EMPHASIS ON BIODIVERSITY, TAXONOMY AND PHYLOGENY OF BOTRYOSPHAERIALES

NA WU

DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE

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

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Dissertation Title: Microfungi Isolated from *Rosa roxburghii* and Other Hosts with Emphasis on Biodiversity, Taxonomy and Phylogeny of Botryosphaeriales

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ABSTRACT

Rosa roxburghii and *R. sterilis* are important economic fruit crops in southwestern China, widely cultivated for their nutritional and medicinal value. However, studies on saprobic fungi associated with these hosts remain scarce, and their taxonomic and phylogenetic relationships are poorly understood. In this study, extensive field surveys were conducted from 2019 to 2023 across 22 sites in Guizhou, Sichuan, and Yunnan Provinces, China, resulting in the isolation of 227 fungal specimens. Morphological examinations combined with multi-locus phylogenetic analyses (ITS, LSU, SSU, *tef1α*, *tub2*, and *rpb2*) of the isolated specimens revealed remarkable fungal diversity. My results introduce one new family (Pseudoneodictyosporiaceae), eight new genera, and 43 new species, along with seven new combinations. The newly described species are *Acrocalymma rosae*, *A. rosicola*, *Amorocoelophoma guizhouensis*, *Am. rosae*, *Am. sichuanensis*, *Anteaglonium rosae*, *Aurantiascoma rosae*, *Brunneofusispora rosae*, *Chaetosphaeria rosae*, *Chromolaenicola rosae*, *Cylindrotrichum rosae*, *Cytospora rosae*, *Floricola rosae*, *Fusivaginella rosae*, *Heleiosa rosae*, *Kalmusia rosae*, *Leucaenicola rosae*, *Lophiostoma rosae*, *Lophiotrema rosae*, *L. rosicola*, *Magnitheca rosae*, *Muyocopron rosae*, *Neohysterium rosae*, *Neoloculosulcatispora rosae*, *Nigrograna rosae*, *N. triseptata*, *Paraconiothyrium guizhouense*, *P. rosicola*, *Parasulcatispora rosae*, *Parathyridaria rosicola*, *Peroneutypa rosae*, *Phaeoacremonium rosae*, *Pseudocoleophoma rosae*, *Pseudocoleophomopsis rosae*, *Pseudolentistoma rosae*, *Pseudoneodictyosporium rosae*, *Pseudopaucispora rosae*, *Pseudorobillarda rosae*,

Virosphaerella rosae, *Xylochrysis asexualis*, *X. camelliae-sinensis*, *X. rosae* and *X. sexualis*. In addition, 47 new host records and six new geographical records from China are reported, while five known species are treated as synonyms. All new taxa are confirmed and discussed based on detailed morphological descriptions, macro- and micro-illustrations, and phylogenetic trees.

Furthermore, by integrating the USDA Systematic Mycology and Microbiology Laboratory database, relevant literature, and my own data, I compiled the first global checklist of fungi associated with *R. roxburghii* and *R. sterilis*, providing a valuable reference for understanding fungal diversity on these hosts. This study significantly expands the taxonomic framework of several lineages within Dothideomycetes and Sordariomycetes and highlights the role of *R. roxburghii* and *R. sterilis* as reservoirs of fungal diversity. The findings establish a baseline for future research on saprobic fungi and Botryosphaeriales in taxonomy, phylogeny, and ecology, and emphasize their key functions in plant litter decomposition, nutrient cycling, and plant health.

In the study of Botryosphaeriales, I also achieved important advances. Through comprehensive analyses of morphological characteristics and multi-gene datasets, the phylogenetic relationships of several lineages were clarified, and seven new species together with 25 new host records were introduced. These results not only enrich the taxonomic framework of Botryosphaeriales but also provide new evidence for understanding their pathogenic, saprobic, and endophytic lifestyles in agricultural and natural ecosystems.

In addition, I established *Botryosphaeriales.org*, a digital platform dedicated to the taxonomy, phylogeny, and information sharing of this order, offering a dynamic, comprehensive, and authoritative resource for researchers worldwide. Overall, this study fills critical gaps in the knowledge of saprobic fungi and Botryosphaeriales associated with *R. roxburghii* and *R. sterilis*, and lays a solid foundation for further investigations into the phylogenetic relationships, ecological roles, and potential applications of plant-associated fungi.

Keywords: Asexual Morph, Checklist, Dothideomycetes, Saprobic Fungi, Sexual Morph, Sordariomycetes

TABLE OF CONTENTS

CHAPTER	Page
1 INTRODUCTION	**1**
1.1 Overview of *Rosa roxburghii* and *R. sterilis*	1
1.2 Background on fungi Associated with *Rosa roxburghii* and *R. sterilis*	4
1.3 Taxonomy, Phylogeny, and Morphology of Botryosphaeriales	6
1.4 Research Gaps	8
1.5 Research Objectives	8
1.6 Thesis Outline	9
2 MATERIALS AND METHODS	**11**
2.1 Specimen Collection and Single Spore Isolation	11
2.2 Morphological Studies	13
2.3 Molecular Studies	14
2.4 Sequence Alignment and Phylogenetic Analyses	17
3 TAXONOMIC AND PHYLOGENETIC CONTRIBUTIONS TO FUNGI ASSOCIATED WITH *ROSA ROXBURGHII* AND *R. STERILIS* IN SOUTHWEST CHINA	**19**
3.1 Introduction	19
3.2 Results	21
3.3 Discussion	397
4 BIODIVERSITY, TAXONOMY AND PHYLOGENY OF BOTRYOSPHARIALES	**432**
4.1 Introduction	432
4.2 Results	434
4.3 Discussion	532

TABLE OF CONTENTS

CHAPTER	Page
5 TAXONOMY AND PHYLOGENY OF FUNGI FROM MEDICINAL PLANTS IN CHINA	**538**
5.1 Introduction	538
5.2 Results	540
5.3 Discussion	601
6 HTTPS://BOTRYOSPHAERIALES.ORG/, AN ONLINE PLATFORM FOR UP-TO-DATE CLASSIFICATION AND ACCOUNT OF TAXA OF BOTRYOSPHAERIALES	**604**
6.1 Introduction	604
6.2 Results	605
6.3 Discussion	613
7 CONCLUSIONS	**615**
7.1 Overall Conclusion	615
7.2 Research Advantages	618
7.3 Future Work	620
REFERENCES	**622**
APPENDICES	**719**
APPENDIX A MEDIA	719
APPENDIX B ABSTRACT OF PUBLICATIONS	720
CURRICULUM VITAE	**727**

LIST OF TABLES

Table		Page
2.1	Gene regions, corresponding primers, and PCR protocols used for molecular analyses in this study	16
3.1	List of fungal taxa with overlapping lifestyles	412
3.2	Checklist of fungi associated with *Rosa roxburghii* and *R. sterilis*	413
5.1	Comparison of asexual morphs in *Pseudocoleophoma*	560
5.2	Comparison of sexual morphs in *Pseudocoleophoma*	562
5.3	Comparisons of base pair differences between ex-type strain of *Torula strychnicola* (GZCC 24-0163) and members of adjoining clades	594

LIST OF FIGURES

Figure	Page
1.1 Habitats, flowers, and fruits of *Rosa sterilis* and *R. roxburghii*	3
2.1 Location of collecting sites in Southwest China	12
3.1 *Melomastia diqingensis* (UESTCC SL08, new host record)	24
3.2 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *tef1α* sequence data of *Melomastia*	25
3.3 *Melomastia puerensis* (HUEST SL38, new host record)	28
3.4 *Melomastia sichuanensis* (HUEST SL64, new host record)	31
3.5 *Heleiosa ellipsoidispora* (HUEST SL11, new host record)	35
3.6 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of *Heleiosa*	36
3.7 *Heleiosa guizhouensis* (HUEST H45, new host record)	39
3.8 *Heleiosa rosae* (HKAS ML121, holotype)	42
3.9 *Heleiosa septata* (HUEST W2; sexual morph, new host record)	45
3.10 *Heleiosa septata* (HUEST GL22; asexual morph, new host record)	46
3.11 *Muyocopron lithocarpi* (HUEST ML01, new host record)	50
3.12 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tef1α* sequence data of *Muyocopron*	51
3.13 *Muyocopron rosae* (HKAS GL48, holotype)	54
3.14 *Virosphaerella rosae* (HKAS ML96, holotype)	58
3.15 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *rpb2* sequence data of *Virosphaerella*	59
3.16 *Acrocalymma hyalinum* (HUEST H09, new geographical and host record)	62
3.17 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data of *Acrocalymma*	63
3.18 *Acrocalymma medicaginis* (HUEST W10, new host record)	66
3.19 *Acrocalymma rosae* (HKAS ML106, holotype)	69
3.20 *Acrocalymma rosicola* (HKAS ML170, holotype)	72
3.21 *Amorocoelophoma guizhouensis* (HKAS ML100, holotype)	76

LIST OF FIGURES

Figure	Page
3.22 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Amorosiaceae	77
3.23 *Amorocoelophoma rosae* (HKAS ML76, holotype)	80
3.24 *Amorocoelophoma sichuanensis* (HKAS SL47, holotype)	83
3.25 *Anteaglonium rosae* (HKAS SL35, holotype)	86
3.26 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Anteagloniaceae	87
3.27 *Corylicola italica* (HUEST SL02; sexual morph, new host record)	92
3.28 *Corylicola italica* (HUEST SL66; asexual morph, new host record)	93
3.29 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Bambusicolaceae	94
3.30 *Leucaenicola rosae* (HKAS SL68, holotype)	97
3.31 *Palmiascoma acericola* (HUEST ML145; sexual morph, new host record)	101
3.32 *Palmiascoma acericola* (HUEST GL54; asexual morph, new host record)	102
3.33 *Palmiascoma qujingense* (HUEST H30, new host record)	105
3.34 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of *Neohysterium*	109
3.35 *Neohysterium rosae* (HKAS SL15, holotype)	112
3.36 *Pseudocoleophoma rosae* (HKAS 131315, holotype; sexual morph)	115
3.37 *Pseudocoleophoma rosae* (HUEST 24.0201, asexual morph)	116
3.38 Phylogenetic tree generated from the maximum likelihood analysis based on the com-bined ITS, LSU, SSU and *tef1α* sequence data of Dictyosporiaceae	117
3.39 *Austropleospora keteleeriae* (HUEST H51, new host record)	121

LIST OF FIGURES

Figure	Page
3.40 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of Didymosphaeriaceae	122
3.41 *Austropleospora ochracea* (HUEST ML134; sexual morph, new host record)	127
3.42 *Austropleospora ochracea* (HUEST GL53; asexual morph, new host record)	128
3.43 *Chromolaenicola clematidis* (HUEST ML61, new host record)	131
3.44 *Chromolaenicola rosae* (HKAS ML131, holotype)	134
3.45 *Chromolaenicola sapindi* (HUEST SL65, new host record)	137
3.46 *Kalmusia rosae* (HKAS ML198, holotype)	140
3.47 *Montagnula verniciae* (HUEST ML44, new host record)	143
3.48 *Paraconiothyrium brasiliense* (HUEST GL94, new host record)	147
3.49 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α* and *tub2* sequence data of *Paraconiothyrium*	148
3.50 *Paraconiothyrium fuckelii* (HUEST ML15, new host record)	151
3.51 *Paraconiothyrium guizhouense* (HKAS ML188; sexual morph**,** holotype)	154
3.52 *Paraconiothyrium guizhouense* (HKAS ML64; asexual morph)	155
3.53 *Paraconiothyrium rosicola* (HKAS ML47, holotype)	158
3.54 *Paraphaeosphaeria camelliae* (HUEST ML88, new host record)	161
3.55 *Paraphaeosphaeria michotii* (HUEST ML94, new host record)	163
3.56 *Paraphaeosphaeria verruculosa* (HUEST GL104, new host record)	166
3.57 *Biappendiculispora japonica* (HUEST ML26, new host record)	170
3.58 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Lophiostomataceae	171

LIST OF FIGURES

Figure	Page
3.59 *Flabellascoma fusiforme* (HUEST SL05, new host record)	176
3.60 *Flabellascoma pistaciae* (HUEST ML60, new host record)	179
3.61 *Leptoparies magnoliae* (HUEST SL37, new host record)	182
3.62 *Neovaginatispora fuckelii* (HUEST ML12, new host record)	186
3.63 *Oleaginea sichuanensis* (HUEST GL110, new host record)	189
3.64 *Pseudolentistoma rosae* (HKAS SL36, holotype)	193
3.65 *Pseudolophiostoma rosae* (HKAS GL155, holotype)	197
3.66 *Pseudopaucispora rosae* (HKAS SL21, holotype)	201
3.67 *Lophiotrema hydei* (HUEST CL24, new host record)	205
3.68 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Lophiotremataceae	206
3.69 *Lophiotrema karsti* (HUEST GL128, new host record)	209
3.70 *Lophiotrema rosae* (HKAS ML91, holotype)	212
3.71 *Lophiotrema rosicola* (HKAS ML122, holotype)	215
3.72 *Lophiotrema rubicola* (HUEST ML90, new host record)	218
3.73 *Magnitheca rosae* (HKAS ML68, holotype)	223
3.74 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Melanommataceae	224
3.75 *Phragmocephala atra* (HUEST ML119, new host record)	227
3.76 *Neomassaria formosana* (HUEST SL33, new host record)	231
3.77 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, *tef1α* and *rpb2* sequence data of *Neomassaria*	232
3.78 *Nigrograna camelliae* (HUEST ML84, new host record)	235
3.79 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of *Nigrograna*	236
3.80 *Nigrograna oleae* (HUEST ML33, new host record)	239

LIST OF FIGURES

Figure	Page
3.81 *Nigrograna rosae* (HKAS MF08, holotype)	242
3.82 *Nigrograna thymi* (HUEST CL71, new host record)	245
3.83 *Nigrograna triseptata* (HKAS ML137, holotype)	248
3.84 *Brunneofusispora rosae* (HKAS ML123, holotype)	252
3.85 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Pleosporales	253
3.86 *Neooccultibambusa kaiyangensis* (HUEST SL40, new host record)	258
3.87 *Fusivaginella rosae* (HKAS ML114, holotype)	263
3.88 *Pseudocoleophomopsis rosae* (HKAS ML81, holotype)	267
3.89 *Loculosulcatispora hongheensis* (HUEST SL03, new host record)	271
3.90 *Loculosulcatispora paeoniae* (HUEST SL04, new host record)	274
3.91 *Neoloculosulcatispora rosae* (HKAS SL06, holotype)	278
3.92 *Parasulcatispora rosae* (HKAS SL12, holotype)	281
3.93 *Aurantiascoma minimum* (HUEST SL25, new host record)	285
3.94 *Aurantiascoma rosae* (HKAS ML38, holotype)	288
3.95 *Floricola rosae* (HKAS ML136, holotype)	292
3.96 *Magnibotryascoma mali* (HUEST ML194, new host record)	295
3.97 *Parathyridaria rosae* (HKAS ML127, holotype)	299
3.98 *Dendryphion verrucosum* (HKAS SL07, new host record)	303
3.99 *Pseudorobillarda camelliae-sinensis* (HUEST H43, new host record)	306
3.100 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU, sequence data of Pseudorobillardaceae	307
3.101 *Pseudorobillarda rosae* (HKAS ML51, holotype)	310
3.102 *Pseudoneodictyosporium rosae* (HKAS SL14, holotype)	315
3.103 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tub2* sequence data of Amphisphaeriales	316
3.104 *Discosia castaneae* (HUEST ML93, new host record)	321

LIST OF FIGURES

Figure	Page
3.105 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α*, *rpb2* and *tub2* sequence data of *Discosia*	322
3.106 *Pseudodinemasporium fabiforme* (HUEST SL58, new host record)	326
3.107 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of Chaetosphaeriaceae	327
3.108 *Stilbochaeta sinensis* (HUEST ML72, new host record)	332
3.109 *Cytospora rosae* (HKAS GL45, holotype)	336
3.110 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, *tef1α* and *tub2* sequence data of *Cytospora*	337
3.111 *Distoseptispora alangii* (HUEST SL01, new host record)	341
3.112 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tef1α* sequence data of *Distoseptispora*	342
3.113 *Distoseptispora sinensis* (HUEST SL27, new host record)	345
3.114 *Cylindrotrichum rosae* (HKAS ML147, holotype)	349
3.115 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of Reticulascaceae	350
3.116 *Xylochrysis asexualis* (HUEST ML189, holotype)	353
3.117 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Pararamichloridiales	354
3.118 *Xylochrysis lucida* (HUEST ML133, new host record)	357
3.119 *Xylochrysis rosae* (HKAS H36, holotype)	360
3.120 *Xylochrysis sexualis* (HUEST ML148, holotype)	363
3.121 *Phaeoisaria clematidis* (HUEST ML32, new host record)	367
3.122 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data of Pleurotheciaceae	368
3.123 *Phaeoacremonium argentinense* (HUEST ML83, new host record)	372

LIST OF FIGURES

Figure	Page
3.124 Phylogram generated from maximum likelihood analysis based on combined act and *tub2* sequence data of *Phaeoacremonium*	373
3.125 *Phaeoacremonium chiangmaiense* (HUEST ML62, new host record)	376
3.126 *Phaeoacremonium rosae* (HKAS GL42, holotype)	379
3.127 *Allocryptovalsa xishuangbanica* (HUEST ML63, new host record)	383
3.128 Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data of Diatrypaceae	384
3.129 *Diatrypella pseudooregonensis* (HUEST ML29, new host record)	387
3.130 Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data of Diatrypaceae	388
3.131 *Peroneutypa rosae* (HKAS ML149, holotype)	392
3.132 *Occultitheca rosae* (HUEST ML06, new host record)	396
3.133 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1α* sequence data of *Occultitheca*	397
3.134 Comparative analysis of fungal taxa shared by *Rosa roxburghii* and *R. sterilis*	401
3.135 Distribution of fungal genera isolated from *Rosa roxburghii* and *R. sterilis*	405
3.136 Circular barplot illustrating the hierarchical distribution of fungi across classes and orders in this study	409
3.137 Bar charts showing the taxonomic distribution of fungi recorded in this study across different taxonomic levels	410
3.138 Venn diagram showing the distribution of fungal taxa across four trophic modes endophytes	411
4.1 *Aplosporella javeedii* (HUEST CL43, new host record)	437
4.2 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1α* sequence data of Botryosphaeriales	438

LIST OF FIGURES

Figure	Page
4.3 *Botryosphaeria dothidea* (HUEST GL158; sexual morph, new host record)	444
4.4 *Botryosphaeria dothidea* (HUEST GL124; asexual morph, new host record)	445
4.5 Phylogram generated from maximum likelihood (ML) analysis based on combined ITS and *tef1α* sequence data of *Botryosphaeria*	446
4.6 *Botryosphaeria fujianensis* (MFLU 23-0012, new host record)	448
4.7 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined ITS, LSU, *tef1α* and *tub2* se-quence data for selected closely related genera within the family Botryosphaeriaceae	449
4.8 *Diplodia mutila* (HUEST ML98, new host record)	454
4.9 Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1α* and *tub2* sequence data of *Diplodia*	455
4.10 *Diplodia pseudoseriata* (HUEST ML111, new host record)	458
4.11 *Diplodia seriata* (GZAAS 23-0583, new host record)	460
4.12 *Dothiorella acericola* (HUEST GL160, new host record)	464
4.13 Phylogram generated from maximum likelihood analysis based on combined ITS and *tef1α* sequence data of *Dothiorella*	465
4.14 *Dothiorella camelliae* (HUEST GL151, new host record)	468
4.15 *Dothiorella citricola* (HUEST GL137, new host record)	471
4.16 *Dothiorella ovata* (MFLU 23-0009, holotype)	474
4.17 *Dothiorella rosacearum* (MFLU 23-0014, holotype)	477
4.18 *Dothiorella sarmentorum* (HUEST GL130, new host record)	480
4.19 *Dothiorella septata* (MFLU 23-0007, holotype)	483
4.20 *Dothiorella zanthoxyli* (HUEST GL152, new host record)	486
4.21 *Lasiodiplodia chiangraiensis* (MFLU 21-0003, holotype)	489
4.22 Phylogenetic tree generated from maximum parsimony (MP) analysis based on combined ITS, *tef1α* and *tub2* sequence data of *Lasiodiplodia*	490

LIST OF FIGURES

Figure	Page
4.23 *Lasiodiplodia crassispora* (MFLU 23-0011, new host record)	493
4.24 *Lasiodiplodia delonicis* (MFLU 23-0005, holotype)	495
4.25 *Lasiodiplodia mahajangana* (MFLU 23-0006, new host record)	497
4.26 *Lasiodiplodia theobromae* (HUEST CL91, new host record)	500
4.27 *Macrophomina euphorbiicola* (MFLU 23-0004, new host record)	502
4.28 *Neodeightonia septata* (MFLU 22-0003, holotype)	505
4.29 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined ITS, LSU, SSU and *tef1α* sequence data for all accepted species of *Neodeightonia* and closely related genera within the family *Botryosphaeriaceae*	506
4.30 *Neodeightonia subglobosa* (MFLU 22-0004, new host record)	509
4.31 *Neofusicoccum parvum* (HUEST GL13, new host record)	512
4.32 *Sphaeropsis eucalypticola* (MFLU 23-0008, new host record)	515
4.33 *Sphaeropsis citrigena* (HUEST H38, new host record)	518
4.34 *Sphaeropsis linhaiensis* (HUEST ML172, new host record)	521
4.35 *Phyllosticta capitalensis* (HUEST CL40, new host record)	525
4.36 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α*, *act*, and *gapdh* sequence data of *Phyllosticta*	526
4.37 *Phyllosticta rosae* (HKAS CL62, holotype; sexual morph)	530
4.38 *Phyllosticta rosae* (HKAS CL45, holotype; asexual morph)	531
4.39 Distribution of Botryosphaeriales obtained in this study	536
4.40 Distribution of Botryosphaeriales genera isolated in this study	537
5.1 *Aquadictyospora lignicola* (HUEST 23.0213, new host record)	543
5.2 Phylogenetic tree generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU and *tef1α* sequence data of Dictyosporiaceae	544
5.3 *Dendryphiella eucalyptorum* (HUEST 23.0214, new host record)	547

LIST OF FIGURES

Figure	Page
5.4 *Dendryphiella vinosa* (HUEST 23.0217, new host record)	549
5.5 *Dictyocheirospora alangii* (HKAS 131314, holotype)	552
5.6 *Dictyocheirospora rotunda* (HUEST 23.0219, new host record)	554
5.7 *Neoxylochrysis typhicola* (HKAS 131316)	558
5.8 *Neomassaria camelliae* (HKAS 131293, holotype)	566
5.9 Phylogenetic tree based on the combined LSU, SSU, *tef1α* and *rpb*2 sequences constructed by maximum likelihood (RAxML) of selected members of *Neomassaria*	567
5.10 *Neomassaria formosana* (HUEST 23.0148, new host record)	570
5.11 *Neomassaria longiasca* (HKAS 131292, holotype)	573
5.12 *Neomassaria sichuanensis* (HKAS 131294, holotype)	576
5.13 *Torula chinensis* (HUEST 24.0247, new host record)	580
5.14 Phylogenetic tree constructed from maximum likelihood (RAxML) analysis based on the combined ITS, LSU, SSU, *tef1α*, and *rpb2* sequence data for selected members of *Torula* (Torulaceae)	581
5.15 *Torula dispora* (HKAS 132495, holotype)	585
5.16 *Torula fici* (HUEST 24.0248, new host record)	588
5.17 *Torula masonii* (GZAAS 25-0020, new host record)	591
5.18 *Torula strychnicola* (HKAS 139505, holotype)	595
5.19 *Velutinus sichuanensis* (HKAS 131317, holotype)	599
5.20 Phylogenetic tree generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of Helotiales	600
6.1 The homepage of Botryosphaeriales webpage	606
6.2 Red arrow indicates search tool to enter the taxon name	607
6.3 The recent notes, genus and species to enable easy access	607
6.4 The “Taxa” view of the Botryosphaeriales webpage	608
6.5 Details of the genus *Botryobambusa*	609
6.6 Appearance of the “Archives” section in Botryosphaeriales webpage	610

LIST OF FIGURES

Figure	Page
6.7 User friendly interface of the “Archives” section in Botryosphaeriales webpage	610
6.8 An entry with description, notes and plate (15)	611
6.9 Curators of Botryosphaeriales webpage	612
7.1 Hierarchical pie chart showing the taxonomic distribution of fungi recognized in the present study	618

ABBREVIATIONS AND SYMBOLS

cm	centimeter
com.	combination
diam.	diameter
e.g.	for example
et al.,	and others
gen.	genus (singular) and genera (plural)
ibid.	ibidem
i.e.	that is
min	minute
ml	milliliter
mm	millimeter
nov.	novum (Latin for new thing)
sp.	species
spp.	species (plural)
µm	micrometer
µl	microliter
viz.	that is
vs.	versus
$\bar{x}$	average
°C	degree centigrade
%	percent

CHAPTER 1

INTRODUCTION

1.1 Overview of *Rosa roxburghii* and *R. sterilis*

Rosa roxburghii Tratt., commonly known as “Cili”, is a perennial deciduous shrub in the family Rosaceae, native to the mountainous regions of southwestern China. It is also cultivated in Japan and South Korea (Jain et al., 2024). In its native range, this plant typically grown in elevations of 500–2,500 m. *Rosa roxburghii* is characterized by thorny twigs, elliptic to oblong serrate leaves, and golden-yellow, subglobose fruits densely covered with prickles. The flowering period occurs from April to June, producing pink to red flowers with a mild fragrance (Figure 1.1). Fruits mature from August to September, with abundant seeds and a sweet-sour taste. Moreover, the fruits are rich in bioactive components, particularly vitamin C, with concentrations reported to be 10, 50, 100, and 500 times higher than those in kiwi, sweet orange, lemon, and apple, respectively (Xu et al., 2019; Huang et al., 2020). Hence, the fruit is widely acclaimed as the King of Vitamin C. In addition to ascorbic acid, the fruits contain high levels of superoxide dismutase (SOD), polyphenols, flavonoids, organic acids, and triterpenoids. These compounds are not only linked to antioxidant activity but are also considered to play potential roles in immune regulation and anticancer effects (He et al., 2016, 2025; Wang et al., 2018, 2020; Li et al., 2022a). Since the 1980s, breeding programs initiated by Guizhou Agricultural College have produced several elite cultivars, among which “Guinong No. 5” has become the most widely cultivated in commercial plantations (Xu et al., 2019). Currently, Guizhou Province represents the largest cultivation base of *R. roxburghii* in China, forming a well-developed industry chain encompassing fruit production, processing, and medicinal applications.

Rosa sterilis S.D.Shi, a species closely related to *R. roxburghii*, is commonly known as “Golden Cili”. It is distinguished by nearly seedless, ellipsoid fruits with dense prickles, which are typically yellow and occasionally turn reddish. The flowering period occurs from April to May, producing white flowers (Figure 1.1). This species was first discovered in Guizhou Province in 1981 and has since been selectively bred and cultivated on a large scale, particularly in Anshun City, China. Zhang et al. (2024) conducted chromosome-scale genome sequencing and assembly of *R. roxburghii* and *R. sterilis*, yielding high-quality assemblies of 504 Mb and 981.2 Mb, respectively. Their study also provided the first haplotype-resolved, chromosome-level genome assembly of diploid *R. sterilis*, and revealed that this species most likely originated through hybridization between *R. roxburghii* and *R. longicuspis*.



Note a, b Habitats of *Rosa sterilis*. c, d Habitats of *R. roxburghii*. e Flowers of *Rosa sterilis*. f Flowers of *R. roxburghii*. g, h Fruits of *R. sterilis*. i, j Fruits of *R. roxburghii*

Figure 1.1 Habitats, flowers, and fruits of *Rosa sterilis* and *R. roxburghii*

1.2 Background on Fungi Associated with *Rosa roxburghii* and *R. sterilis*

Fungi are eukaryotic organisms that inhabit diverse ecosystems worldwide and play an irreplaceable role in the decomposition of organic matter. Within Ascomycota, Dothideomycetes and Sordariomycetes represent the largest and most functionally diverse classes, encompassing numerous saprobic, pathogenic, and endophytic species (Schoch et al., 2009; Hyde et al., 2013). These fungi are distributed across terrestrial, freshwater, and marine environments (Suetrong et al., 2009; Hyde et al., 2013; Dayarathne et al., 2020). In recent years, several dedicated online platforms have been established to support the taxonomy and classification of these two classes, including (https://www.marinefungi.org/) (Jones et al., 2019), (https://www.dothideomycetes.org/) (Pem et al., 2019), (https://sordariomycetes.org/) (Bundhun et al., 2020), (https://www.freshwaterfungi.org/) (Calabon et al., 2020) and (https://botryosphaeriales.org/) (Wu et al., 2021b). Morphologically, Dothideomycetes are mainly characterized by their bitunicate (double-walled) asci, while most Sordariomycetes species are distinguished by their non-lichenized, perithecial (flask-shaped) ascomata and inoperculate unitunicate asci (Arx & Müller, 1975; Zhang et al., 2006; Hyde et al., 2013; Maharachchikumbura et al., 2015, 2016; Hongsanan et al., 2017).

In recent years, the widespread cultivation of *Rosa roxburghii* has attracted growing attention to its associated fungal communities. Several studies have explored the fungal diversity of *Rosa* species using high-throughput sequencing techniques. For example, Zhao et al. (2018a) identified a diverse range of fungal taxa associated with *R. multiflora* and *R. multiflora* var. carnea, indicating that *Rosa* plants serve as important hosts for a broad spectrum of fungi. As representative fruit crops in this genus, *R. roxburghii* and *R. sterilis* exhibit high nutritional and medicinal value. In Guizhou Province, the total cultivation area exceeds 170,000 hectares, thereby driving increased attention to fundamental research. Liu et al. (2021) compared phyllosphere fungal communities in healthy and diseased leaves of *R. roxburghii*, isolating 266 strains that

were identified as 61 species in 3 phyla, 6 classes, 13 orders, 30 families, and 46 genera. Their results revealed that plant health is closely related to fungal community composition, and the pathogens causing leaf spot disease mainly originate from the epiphytic microbiota. Subsequently, Zhang et al. (2021a) isolated 242 strains of endophytic Sordariomycetes from healthy *R. roxburghii* tissues and evaluated their diversity and antimicrobial activities. These isolates comprised eight orders, 19 families, 33 genera, with *Chaetomium*, *Clonostachys*, *Colletotrichum*, *Dactylonectria*, *Diaporthe*, *Fusarium* and *Graphium* being the dominant genera. In addition, α-diversity analyses indicated significant differences among fungal communities across tissue types, with the highest diversity in roots, followed by fruits, stems, flowers, leaves, and seeds. Several fungal taxa were identified as having multifunctional nutritional strategies, capable of existing as endophytes, pathogens, or saprobes. For example, *Chloridium*, *Cytospora*, *Fusarium*, *Graphium*, and *Trichoderma* were found to exhibit three or more lifestyles (Zhang et al., 2021a).

Moreover, previous studies have shown that certain endophytic fungi colonizing *Rosa roxburghii* may shift to a pathogenic lifestyle under unfavorable host conditions. Zhang et al. (2023b) isolated 60 strains from healthy roots and stems, including *Fusarium avenaceum*, *F. cugenangense*, *F. fujikuroi*, *F. lateritium*, and *Neocosmospora solani*. Notably, these taxa have been reported as pathogens of Rosaceae (McGrann et al., 2015; Zhang et al., 2023b). Fungal diseases have consequently become significant limiting factors in the *R. roxburghii* industry. Powdery mildew, caused by *Sphaerotheca* spp., severely affects young branches, tender leaves, flower buds, and immature fruits, leading to yield and quality losses and resulting in 30%–40% economic damage in Guizhou Province. Although chemical fungicides (e.g., azoxystrobin, myclobutanil, tebuconazole and triadimefon) are effective, their extensive use poses environmental risks and fosters pathogen resistance. In light of these concerns, researchers have increasingly explored alternative control measures to reduce reliance on fungicides. Shi et al. (2022) first identified *Neopestalotiopsis clavispora* as the

causal agent of postharvest fruit rot in *R. sterilis* and demonstrated that combined treatment with methyl jasmonate and calcium chloride offers a promising control strategy. Jia et al. (2024) isolated *Diaporthe eres* from diseased leaves and confirmed its pathogenicity in causing leaf spot disease. Wang et al. (2024c) identified *Fusarium annulatum* as the causal agent of fruit rot, validating its pathogenicity through reinoculation experiments. In recent years, tip rot disease (TRD), caused by *Colletotrichum fructicola*, has attracted attention due to its severe impacts, including fruit discoloration, decay, and pre-harvest fruit drop (Luo et al., 2023b). These studies have revealed the richness and complexity of fungal communities associated with *Rosa roxburghii*, encompassing primarily endophytic and pathogenic lifestyles. In addition, endophytic fungi may yield secondary metabolites with antibacterial, antioxidant, and other bioactivities, offering valuable resources for natural product discovery and medicinal development.

1.3 Taxonomy, Phylogeny, and Morphology of Botryosphaeriales

Botryosphaeriales (Dothideomycetes) was established in 2006, to accommodate a single family, Botryosphaeriaceae (Schoch et al., 2006). Nine families, Aplosporellaceae, Botryosphaeriaceae, Endomelanconiopsisaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae, Pseudofusicoccumaceae, Saccharataceae and Septorioideaceae, were accepted in Botryosphaeriales by Wijayawardene et al. (2018). However, based on morpho-molecular analyses and evolutionary divergence times, the number of families accepted in Botryosphaeriales was reduced to six, namely Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae and Saccharataceae (Phillips et al., 2019; Wijayawardene et al., 2020). Endomelanconiopsisaceae and Pseudofusicoccumaceae were synonymized under Botryosphaeriaceae and Phyllostictaceae, respectively, while Septorioideaceae was synonymized under Saccharataceae (Phillips et al., 2019). Members of

Botryosphaeriales are found worldwide, on many different host plants (Phillips et al., 2008; Wulandari et al., 2009; Liu et al., 2010, 2012; Wong et al., 2012, 2019; Alves et al., 2014; Trakunyingcharoen et al., 2014a; Dissanayake et al., 2016; Dou et al., 2017a, b; Tibpromma et al., 2018; Jayasiri et al., 2019; Berraf-Tebbal et al., 2020). They are endophytes, pathogens and saprobes and as opportunistic pathogens, they are of considerable importance to agriculture, horticulture and forestry (Chethana et al., 2016; Manawasinghe et al., 2016). They cause severe diseases of economically important crops and plants leading to huge economic losses (Slippers et al., 2007; Mehl et al., 2017). *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia*, *Neofusicoccum* and *Phyllosticta* are the major pathogenic genera in Botryosphaeriales. *Botryosphaeria dothidea*, *Diplodia seriata*, *Lasiodiplodia theobromae* and *Neofusicoccum parvum* are associated with grapevine dieback worldwide (Yan et al., 2013). *Diplodia seriata* has been reported as a pathogen on a wide range of hosts including eucalyptus, pine and stone fruits (Kaliterna et al., 2012; C´aceres et al., 2016; Zhang et al., 2017; Abbas et al., 2018; Besoain et al., 2019). *Phyllosticta citricarpa* and *P. citriasiana* cause freckle on banana and brown spots on pomelo, respectively (Wulandari et al., 2009; Wong et al., 2012). One species can occur on several hosts in the same country, and pathogenicity of a species can vary from one region to another (Manawasinghe et al., 2016). This reflects the importance of gathering data on these fungal taxa to understand disease epidemiology.

Aplosporellaceae, Melanopsaceae and Planistromellaceae have immersed or semi-immersed multiloculate ascostromata, while those of Botryosphaeriaceae, Phyllostictaceae and Saccharataceae are uniloculate (Liu et al., 2012; Monkai et al., 2013; Ekanayaka et al., 2016; Phillips et al., 2019). Asci are bitunicate, with a thick endotunica (Liu et al., 2012; Monkai et al., 2013; Ekanayaka et al., 2016; Phillips et al., 2019). Ascospores are hyaline or pigmented, septate or aseptate, ellipsoid to ovoid. Conidiomata are pycnidial, uni- to multilocular, frequently embedded in stromatic tissue. Conidiogenous cells are hyaline. Conidia are hyaline or pigmented, septate or

aseptate, thin- or thick-walled (Wikee et al., 2011; Liu et al., 2012; Monkai et al., 2013; Ekanayaka et al., 2016; Phillips et al., 2013, 2019; Hyde et al., 2020).

1.4 Research Gaps

1.4.1 Only a few studies have investigated fungi associated with *Rosa roxburghii*, which are mostly based on molecular data without detailed morphological descriptions.

1.4.2 There are no studies or records of fungi associated with *Rosa sterilis*, hampering comparisons with its sister species *R. roxburghii.*

1.4.3 No comprehensive worldwide checklist of fungi associated with *Rosa roxburghii* and *R. sterilis.*

1.4.4 Botryosphaeriales is an important order comprising pathogens, saprobes, and endophytes distributed worldwide, yet it lacks an information platform for researchers.

1.5 Research Objectives

1.5.1 To study the taxonomy and phylogeny of microfungi associated with *Rosa roxburghii* and *R. sterilis* based on morphology and multi-gene phylogenetic analyses.

1.5.2 To link sexual-asexual morphs of microfungi associated with *Rosa roxburghii* and *R. sterilis.*

1.5.3 To compile a checklist of fungi associated with *Rosa roxburghii* and *R. sterilis*.

1.5.4 To study taxonomy and phylogeny of Botryosphaeriales species based on morphology and multi-locus phylogenies.

1.5.5 To digitalize information about Botryosphaeriales taxa into one website (https://botryosphaeriales.org).

1.6 Thesis Outline

This thesis comprises seven chapters.

Chapter 1 provides a general introduction, including an overview of *Rosa roxburghii* and *R. sterilis*, the background of fungi associated with these hosts, and a detailed discussion on the taxonomy, phylogeny, and morphology of Botryosphaeriales. It also highlights the existing research gaps and outlines the objectives of the study.

Chapter 2 describes the materials and methods employed in the study. It details the procedures for specimen collection and single spore isolation, morphological investigations (stains, slide preparation, microscopic examination, and identification), molecular studies (DNA extraction, PCR amplification, and sequencing), as well as sequence alignment and phylogenetic analyses.

Chapter 3 presents a comprehensive account of the taxonomy and phylogeny of fungi collected from *R. roxburghii* and *R. sterilis*. It includes the introduction, detailed results of taxonomic treatments, and a discussion based on phylogenetic analyses and morphological evidence.

Chapter 4 focuses on the biodiversity, taxonomy, and phylogeny of the order Botryosphaeriales. It begins with an introduction that synthesizes previous research and highlights the taxonomic challenges within this group. The results section presents comprehensive analyses based on both morphological observations and multi-gene phylogeny.

Chapter 5 focuses on the taxonomy and phylogeny of fungi associated with medicinal plants in China. It includes an introduction to the subject, detailed taxonomic results, and a discussion of the findings in relation to fungal diversity, ecological functions, and host associations.

Chapter 6 introduces Botryosphaeriales.org, an online digital platform dedicated to the taxonomy, classification, and phylogeny of the order. It covers the background of the platform, presents its structure and main results, and discusses its contribution as a comprehensive and dynamic reference for fungal systematics.

Chapter 7 provides an overall conclusion of the study, summarizing the key findings. It also highlights the advantages of the research, and lists the publications that have arisen from this doctoral research.

CHAPTER 2

MATERIALS AND METHODS

2.1 Specimen Collection and Single Spore Isolation

Samples of dead or decaying woody plants were collected from China and Thailand between 2019 and 2023. *Rosa roxburghii* and *R. sterilis* were randomly collected from plantations in Guizhou (Anshun, Bijie, Guiyang, Liupanshui, Qiannan and Qianxinan Autonomous Prefecture, Tongren, and Zunyi), Sichuan (Chengdu and Leshan), and Yunnan (Qujing) Provinces, China, during 2021–2023. Most specimens were collected in Guizhou Province. A total of 227 samples were collected from 22 sampling sites across Southwestern China (Figure 2.1). Among these, *R. sterilis* were collected from Anshun City, Bijie City, and Qianxinan Buyi and Miao Autonomous Prefecture in Guizhou Province. The specimens were placed into a separate envelope and transported to the laboratory for observation and isolation of fungi, with sampling information (date, host, location, GPS, etc.) recorded. Fungi on samples showing lesions were immediately isolated, or, if they could not be processed immediately, they were refrigerated at 4°C for a few days.

Single spore isolations were carried out as described by Senanayake et al. (2020). The contents of fruiting bodies were transferred to a drop of sterile water on a sterilized spot plate. The spore suspension was spread over the Petri dishes containing potato dextrose agar (PDA) or water agar (WA) and incubated at 25°C for 12 to 24 h. Germinated spores were transferred onto fresh PDA or WA plates. These culture plates were incubated at 25°C in incubators, and colony characteristics were observed and recorded after one week following the method described in Rayner (1970).

Herbarium specimens were deposited in the herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy Sciences (KUN-HKAS), Kunming,

China and the Herbarium of University of Electronic Science and Technology (HUEST), Chengdu, China. The pure cultures were deposited in the China General Microbiological Culture Collection Centre (CGMCC), Beijing, China and the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China. New and interesting taxa were documented in the Facesoffungi database following the guidelines of Jayasiri et al. (2015), and names of the new taxa were registered in Index Fungorum.



Figure 2.1 Location of collecting sites in Southwest China

2.2 Morphological Studies

2.2.1 Stains and Slide Preparations

Several chemical preparations were occasionally used in the examination of fungal specimens by adding them to slides (Whitton et al., 2012). These included: 5 % potassium hydroxide (KOH), Indian ink, and Melzer's iodine reagent. 5 % KOH was used to rehydrate fungal structures in dried specimens. Indian ink was used to reveal the presence of gelatinous sheaths around the ascospores or conidia. Melzer's iodine reagent was applied to detect the amyloid apical apparatus in identified Sordariomycetous taxa.

2.2.2 Microscopic Examination

Morphological observations of fungal structures were made using a Nikon SMZ745 dissecting microscope (Nikon Corporation, Tokyo, Japan), following the method described in Chomnunti et al. (2014). Photomicrographs were captured using a Nikon Eclipse Ni-U compound microscope fitted with a Nikon DS-Ri2 digital camera (Nikon Corporation, Tokyo, Japan). Macro-morphological structures were photographed with a Nikon SMZ800N stereo microscope fitted with a Nikon DS-Fi3 microscope camera (Nikon Corporation, Tokyo, Japan). All measurements were made using the Tarosoft (R) Image Framework v. 0.97, the minimum, maximum dimensions, and average values were calculated based on the number of measured structures (e.g., asci, ascospores, conidia). Photographic plates were prepared using Adobe Photoshop CC extended version 21.1.2 (Adobe, USA).

2.2.3 Identification Procedures

Morphological identifications were based on general reference sources; for ascomycetes and coelomycetes, hand-sectioning of the fruiting bodies was carried out using a razor blade. Sections were removed with a sterile needle, transferred to a small drop of double distilled water on a clean slide, and covered with a cover glass for microscopic observation and photomicrography (Sutton, 1980; Sivanesan, 1984; Nag Raj, 1993; Kiffer

& Morelet, 1999; Doilom et al., 2017; Li et al., 2020; Zhang et al., 2024a). For hyphomycetes, fungal structures were picked and placed into water on the slide using a needle (Ellis, 1971, 1976; Seifert et al., 2011; Liu et al., 2024a). New taxa were established based on comparisons of morphological characteristics and molecular phylogenetic analyses with known species, following the recommendations of Jeewon and Hyde (2016). New geographical and new host records were also indicated, where applicable. The Dictionary of the Fungi (Kirk et al., 2008) was used as a definitive, mycological authority for the morphological descriptions. Colony colours were determined with the Methuen Handbook of Colour (Kornerup & Wanscher, 1967). More information such as the taxonomic rank and synonymy of fungal names was obtained from the nomenclatural database Index Fungorum (http://www.indexfungorum.org). A single name was designated for each species as practiced by Wijayawardene et al. (2014). Familial placement of taxa followed latest outline published by Hyde et al. (2024). New species are established based on the recommendations outlined by Jeewon and Hyde (2016).

2.3 Molecular Studies

2.3.1 DNA Extraction, PCR Amplification and Sequencing

In a sterile environment, fungal mycelium (about 50–100 mg) was scraped using a sterilized toothpick from colonies grown on PDA medium at 25°C for 2 weeks, transferred to sterilized 1.5 mL microcentrifuge tubes. If fungal mycelium could not be processed immediately, they were refrigerated at -20°C for long-term storage. Ezup Column Fungi Genomic DNA Purification Kit (Sangon Biotech, Shanghai, China) was used to extract DNA according to the manufacturer's instructions. The extracted DNA was divided into two tubes. One tube was stored at 4°C for subsequent polymerase chain reaction (PCR) amplification, while the other tube was kept at -20°C for long-term storage. The large subunit of the nuclear ribosomal RNA genes (LSU), the small subunit of the nuclear ribosomal RNA (SSU), the internal transcribed spacer region

(ITS), the translation elongation factor 1-alpha (*tef1α*), the beta-tubulin gene (*tub2*) and the second largest subunit of RNA polymerase II (*rpb2*) gene regions were used for identification. Details of locus, primers, and amplification conditions used in the phylogenetic study are listed in Table 2.1. DNA amplification procedure was performed by PCR in a 25 µl reaction volume, which contained 8.5 µl distilled-deionized-water, 12.5 µl of 2 × Power Taq PCR Master Mix (TIANGEN Co., China), 2 µl of DNA template and 1 µl of each forward and reverse primers. The PCR products were analyzed by electrophoresis on 1.2% agarose gels containing Safeview DNA stain, visualized under UV light using a Gel Doc™ XR imaging system. The qualified PCR products were sent to Tsingke Biotechnology Co., Ltd. (Chengdu, China) for sequencing.

Table 2.1 Gene regions, corresponding primers, and PCR protocols used for molecular analyses in this study

Locus	Primers		Optimized PCR Protocols	References
	Forward Sequence (5′–3′)	Reverse Sequence (5′–3′)		
ITS	ITS5	ITS4	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	White et al.
	GGAAGTAAAAGTCGTAACAAGG	TCCTCCGCTTATTGATATGC	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	(1990)
LSU	LR0R	LR5	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	Vilgalys and
	ACCCGCTGAACTTAAGC	TCCTGAGGGAAACTTCG	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	Hester (1990)
SSU	NS1	NS4	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	White et al.
	GTAGTCATATGCTTGTCTC	CTTCCGTCAATTCCTTTAAG	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	(1990)
tef1α	EF1-983F	EF1-2218R	94 ◦C 2 min; 35 cycles of 94 ◦C 30 s, 56 ◦C 1 min,	Rehner and
	GCYCCYGGHCAYCGTGAYTTYAT	ATGACACCRACRGCRACRGTYTG	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	Buckley (2005)
tef1α	EF-728F	EF-986R	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	Carbone and
	CATCGAGAAGTTCGAGAAGG	TACTTGAAGGAACCCTTACC	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	Kohn (1999)
tub2	Bt2a	Bt2b	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	Glass and
	GGTAACCAAATCGGTGCTGCTTTC	ACCCTCAGTGTAGTGACCCTTGGC	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	Donaldson (1995)
tub2	T1	Bt2b	94 ◦C 3 min; 35 cycles of 94 ◦C 30 s, 55 ◦C 50 s,	O'Donnell and
	AACATGCGTGAGATTGTAAGT	ACCCTCAGTGTAGTGACCCTTGGC	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	Cigelnik (1997)
rpb2	fRPB2-5F	fRPB2-7cR	94 ◦C 3 min; 40 cycles of 94 ◦C 20 s, 55 ◦C 30 s,	Liu et al. (1999)
	GAYGAYMGWGATCAYTTYGG	CCCATRGCTTGYTTRCCCAT	72 ◦C 1 min; 72 ◦C 10 min; 4 ◦C on hold	

2.4 Sequence Alignment and Phylogenetic Analyses

All sequences obtained from *Rosa roxburghii*, *R. sterilis* strains and other hosts were assembled and checked using BioEdit v. 7.0.9 (Hall, 1999) to ensure sequence quality. The closest taxa to my strains were determined with standard nucleotide BLAST searches in NCBI (http://www.ncbi.nlm.nih.gov/). Single-gene fragments were aligned using MAFFT v. 7 online (http://mafft.cbrc.jp/alignment/server/), visually inspected with AliView (Larsson, 2014), and the results were checked using BioEdit v. 7.0.9 (Hall, 1999) and manually edited where necessary. Alignments were trimmed using trimAl v.1.2 (Capella-Gutiérrez et al., 2009) with minimal coverage (-cons) = 0.8 and gap threshold (-gt) = 0.6. Single-gene alignments were combined using SequenceMatrix 1.7.8 (Vaidya et al., 2011). Nexus and Phylip files for phylogenetic analyses were generated using AliView (Larsson, 2014). The phylogenetic position of Dothideomycetes and Sordariomycetes isolates from *R. roxburghii* and *R. sterilis* were initially determined using ITS, as well as combinations of ITS, LSU, SSU, *tef1α*, *tub2* and *rpb2* sequence data. Species-level identification was subsequently accomplished using multi-gene phylogeny based on analyses of the individual and combined gene regions. Reference sequences and outgroups for each fungal group were selected based on recent relevant literature and GenBank data.

Phylogenetic analyses of the combined sequence data were performed using maximum likelihood (ML) and Bayesian inference (BI) methods, as detailed in Dissanayake et al. (2020). ML analyses were performed at the CIPRES web portal (Miller et al., 2010) with RAxML-HPC v. 8 on the XSEDE (8.2.12) tool (Stamatakis, 2014), applying a general time-reversible (GTR) model with a discrete GAMMA distribution and four rate classes. One thousand non-parametric bootstrap iterations were run with the GTR model and a discrete gamma distribution. The resulting replicates were plotted onto the best scoring tree obtained previously. BI analyses were performed in a likelihood framework implemented in MrBayes v. 3.2.6 (Ronquist et al.,

2012). MrModeltest2 v. 2.3 (Nylander, 2008) was used to select the best–fit nucleotide substitution models under the Akaike information criterion (AIC). Six simultaneous Markov chains were run for 1000000 generations, trees were sampled every 100th generation and the temperature value of the heated chain was set at 0.15. The run was terminated once the standard deviation of split frequencies was below 0.01. The first 25% of saved trees were discarded as burn-in, and the remaining trees were used to calculate posterior probabilities (PP) in the majority rule consensus tree (Cai et al., 2006; Liu et al., 2016).

Phylogenetic trees were visualized using FigTree v. 1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/), further edited on the website (https://www.chiplot.online/) following the methods described in Xie et al. (2023), and finalized in Adobe Illustrator 2020 (Adobe Systems Inc., USA). All final alignments were submitted to Figshare (https://figshare.com).

CHAPTER 3

TAXONOMIC AND PHYLOGENETIC CONTRIBUTIONS TO FUNGI ASSOCIATED WITH *ROSA ROXBURGHII* AND *R. STERILIS* IN SOUTHWEST CHINA

3.1 Introduction

Rosa roxburghii Tratt. and *R. sterilis* S.D. Shi are two widely cultivated and economically important fruit crops in China. They are valued not only for their nutritional and medicinal properties but also for their economic role in fruit production. Despite their significance, research on the fungi associated with these hosts has been uneven. Previous studies have mainly focused on endophytic fungi, while only a few saprobic species have been reported, leaving the diversity and taxonomy of saprobic fungi on these hosts largely unexplored.

During my investigations in southwestern China, a diverse range of asexual and sexual morphs of saprobic fungi were collected from *Rosa roxburghii* and *R. sterilis*. Both morphological characters and sequence data were used to confirm their natural placement. Detailed morphological descriptions, photographic illustrations, and phylogenetic analyses were provided, alongside a comparison of fungal assemblages between the two hosts. Furthermore, by integrating records from the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2020), relevant literature, and my own dataset, I compiled a worldwide checklist of fungi associated with these species.

In this study, I investigated saprobic fungi occurring on *R. roxburghii* and *R. sterilis* in southern China. Based on morphological characteristics and multi-gene phylogenetic analyses, one new family, eight new genera, and 43 new species are introduced, 47 new host records are reported from *R. roxburghii* or *R. sterilis*, six new geographical records are documented in China, and seven species are transferred to other genera. The new family, Pseudoneodictyosporiaceae, is accommodated in the order Amphisphaeriales (Sordariomycetes). New genera are *Fusivaginella* (Pseudolophiotremataceae), *Magnitheca*

(Melanommataceae), *Neohysterium* (Dictyosporiaceae), *Neoloculosulcatispora* (Sulcatisporaceae), *Pseudocoleophomopsis* (Pseudolophiotremataceae), *Pseudolentistoma* (Lophiostomataceae) and *Pseudoneodictyosporium* (Pseudoneodictyosporiaceae). The newly described species are *Acrocalymma rosae*, *A. rosicola*, *Amorocoelophoma guizhouensis*, *Am. rosae*, *Am. sichuanensis*, *Anteaglonium rosae*, *Aurantiascoma rosae*, *Brunneofusispora rosae*, *Chaetosphaeria rosae*, *Chromolaenicola rosae*, *Cylindrotrichum rosae*, *Cytospora rosae*, *Floricola rosae*, *Fusivaginella rosae*, *Heleiosa rosae*, *Kalmusia rosae*, *Leucaenicola rosae*, *Lophiotrema rosae*, *L. rosicola*, *Magnitheca rosae*, *Muyocopron rosae*, *Neohysterium rosae*, *Neoloculosulcatispora rosae*, *Nigrograna rosae*, *N. triseptata*, *Paraconiothyrium guizhouense*, *P. rosicola*, *Parasulcatispora rosae*, *Parathyridaria rosicola*, *Peroneutypa rosae*, *Phaeoacremonium rosae*, *Phyllosticta rosae*, *Pseudocoleophomopsis rosae*, *Pseudolentistoma rosae*, *Pseudolophiostoma rosae*, *Pseudoneodictyosporium rosae*, *Pseudopaucispora rosae*, *Pseudorobillarda rosae*, *Virosphaerella rosae*, *Xylochrysis asexualis*, *X. camelliae-sinensis*, *X. rosae* and *X. sexualis*. The new combinations are *Heleiosa hydeispora* (≡ *Neoheleiosa hydeispora*), *H. hydeiverrucosa* (≡ *Neoheleiosa hydeiverrucosa*), *H. septata* (≡ *Neoheleiosa septata*) and *Neohysterium puerensis* (≡ *Pseudocoleophoma puerensis*). Furthermore, I synonymize five species (*Discosia celtidis*, *Muyocopron thailandicum*, *Loculosulcatispora juglandis*, *Lophiotrema mucilaginosum*, *Paraphaeosphaeria parmeliae*). These findings not only extend the taxonomic framework of several fungal lineages within Dothideomycetes and Sordariomycetes but also highlight the role of *R. roxburghii* and *R. sterilis* as reservoirs of fungal diversity.

These findings not only extend the taxonomic framework of several fungal lineages within Dothideomycetes and Sordariomycetes but also highlight the role of *R. roxburghii* and *R. sterilis* as reservoirs of fungal diversity. Overall, this work fills a major gap in the study of saprobic fungi on *Rosa* hosts and provides valuable baseline data for future taxonomic, phylogenetic, and ecological studies. It also contributes to a broader understanding of fungal biodiversity in China and offers important insights into the ecological functions of saprobic fungi in plant litter decomposition and nutrient cycling.

3.2 Results

Ascomycota Caval.-Sm.

Dothideomycetes O.E. Erikss. & Winka

Dyfrolomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones

Pleurotremataceae Walt. Watson

Type genus – *Pleurotrema* Müll. Arg.

Notes – The family Pleurotremataceae (=Dyfrolomycetaceae) was introduced by Watson (1929) and is currently placed in Dyfrolomycetales (Dothideomycetes) based on phylogenetic analyses (Pang et al., 2013; Maharachchikumbura et al., 2016). Presently, three genera, *Dyfrolomyces*, *Melomastia* and *Pleurotrema*, are recognized within Pleurotremataceae (Pang et al., 2013; Maharachchikumbura et al., 2016; Norphanphoun et al., 2017; Li et al., 2022b; Kularathnage et al., 2023). Members of this family are known as saprobes from terrestrial, mangrove, and freshwater habitats, and characterized by semi-immersed to immersed, perithecial, ostiolate, ovoid to subglobose ascomata clavate to cylindrical, pedicellate, bitunicate or fissitunicate asci and uniseriate or overlapping uniseriate, multi-septate, hyaline, ellipsoidal to cylindrical, ascospores with or without a sheath (Watson, 1929; Barr, 1994; Zhang et al., 2017b; Li et al., 2022b; Kularathnage et al., 2023).

Melomastia Nitschke ex Fuckel, Jb. nassau. Ver. Naturk. 25–26: 306 (1871)

Type species – *Melomastia mastoidea* (Fr.) J. Schröt.

Notes – *Melomastia* was introduced as a monotypic genus and typified with *M. mastoidea* (= *M. friesii* ≡ *Sphaeria mastoidea*) by Saccardo (1875) based on the morphological examinations. Asexual morphs of *Melomastia* are unknown. Because of the lack of sequence data, the systematic placement of *Melomastia* has been subjected to continuous revisions (Maharachchikumbura et al., 2015, 2016; Wijayawardene et al., 2017). Norphanphoun et al. (2017) first employed the LSU and SSU gene sequence data and morphological characteristics to introduce *M. italica* and accommodated

Melomastia within the family Pleurotremaceae in the class Dothideomycetes. Their studies showed that *Melomastia* has a close affinity with *Dyfrolomyces*. Subsequently, Li et al. (2022b) introduced four new *Melomastia* species and synonymized *Dyfrolomyces* under *Melomastia* based on the morphology and multigene phylogeny. However, Kularathnage et al. (2023) disagreed with this conclusion and reinstated *Dyfrolomyces* as a separate genus to accommodate *M. tiomanensis* (type species) and *M. chromolaenae*, based on their ascospore morphology and septation. There are about 73 *Melomastia* epithets listed in Index Fungorum (2025, June), but only a few species have available sequence data in GenBank. *Melomastia* is characterized by semi-immersed to immersed, dark brown, papillate, coriaceous to carbonaceous, globose, subglobose or ellipsoidal ascomata, 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate asci with an ocular apical chamber and overlapping or uniseriate, smooth or rarely verruculose, 1–10-septate, not or slightly constricted at the septum, hyaline, ovoid, ellipsoid to fusiform ascospores with or without a mucilaginous sheath (Norphanphoun et al., 2017; Li et al., 2022b; Kularathnage et al., 2023; Du et al., 2024b).

Melomastia diqingensis G.C. Ren & K.D. Hyde, Mycosphere 15(1): 968 (2024) Figure 3.1

Index Fungorum number: IF901346; Facesoffungi number: FoF13890

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 420–510 μm wide, 430–560 μm high, solitary to gregarious, visible as slightly raised, black, immersed to partly erumpent, unilocular, glabrous, coriaceous to carbonaceous, globose to subglobose to pyriform, papillate, ostiolate. *Ostiole* single. *Peridium* 30–84 μm wide, narrower at base within the substrate, widest at mid-point, brittle when dry, composed of thick-walled black cells of *textura angularis* to *textura prismatica*. *Hamathecium* 1.5–3 μm wide, composed of dense, numerous, filiform, unbranched, aseptate, hyaline, pseudoparaphyses, longer than asci. *Asci* 130–150 × 5–8 μm ($\bar{x}$ = 135 × 7 μm; n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 14–20 × 4–6 μm

($\bar{x}$ = 16 × 5 μm; n = 30), uniseriate, partially overlapping, straight or slightly curved, hyaline, ellipsoidal to fusiform, slightly rounded or pointed at both ends, 2-septate, constricted at the septa, with guttulate in each cell, surrounded by a thick mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25°C in dark, flatten on the surface, the central slightly raised, with dense mycelium, milky white; in reverse, orange in the middle, white mycelium in the outer ring.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL08 (HUEST XX), living culture UESTCC XX.

Hosts – *Rhododendron rubiginosum* (Ren et al., 2024a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Ren et al. (2024a) introduced *Melomastia diqingensis*, which is phylogenetically separated from *M. italica* and has longer, oval to oblong ascospores. I recognized my collection as *M. diqingensis* since it is clustered with the ex-type strain of *M. diqingensis* (HKAS 122718) and was identical in morphology and molecular data (Figure 3.2). In the present study, I provide a new host record for *M. diqingensis*, which was isolated on *Rosa roxburghii* from China.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Peridium. h Pseudoparaphyses. i–l Asci. m–q Ascospores. r Ascospore stained with Indian ink. s Germinating ascospore. t, u Colony on PDA, above (t), below (u). Scale bars: e, f = 100 µm; g–l = 30 µm; m–s = 10 µm

Figure 3.1 *Melomastia diqingensis* (UESTCC SL08, new host record)

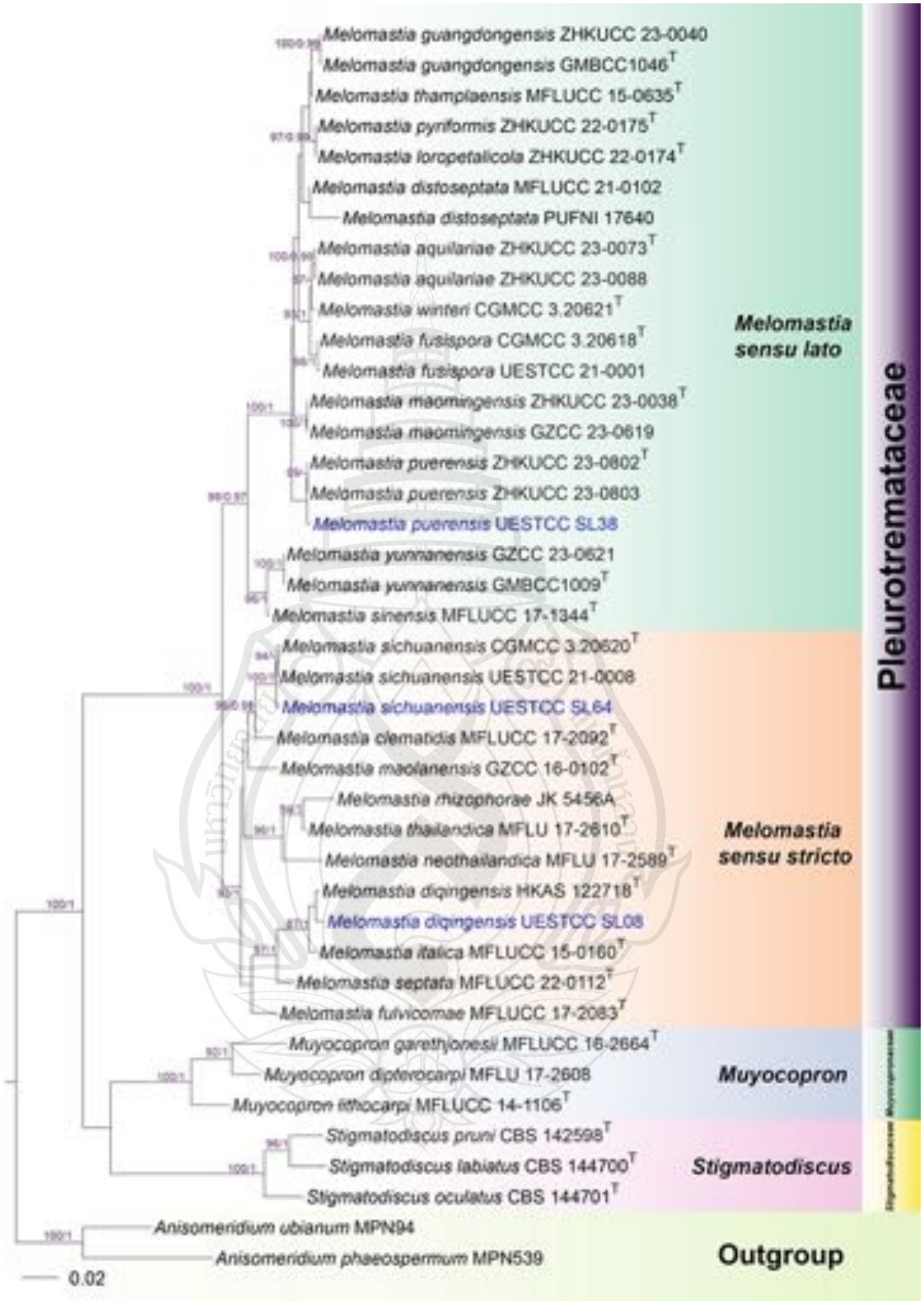


Figure 3.2 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *tef1α* sequence data of *Melomastia*

Figure 3.2 The tree is rooted with *Anisomeridium phaeospermum* (MPN539) and *A*. *ubianum* (MPN94). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Melomastia puerensis R.F. Xu & Tibpromma, MycoKeys 103:75 (2024) Figure 3.3

Index Fungorum number: IF901419; Facesoffungi number: FoF15195

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 480–650 μm wide, 482–670 μm high, solitary to gregarious or confluent, black, erumpent to superficial, unilocular, glabrous, coriaceous to carbonaceous, subglobose to pyriform, with the ruptured host tissue around the surface of the ascomata, papillate, ostiolate. *Ostiole* 84–121 μm wide, 200–249 μm high, single, subcylindrical, straight or curved, central. *Peridium* 53–90 μm wide, brittle when dry, composed of thick-walled dark brown cells of *textura angularis* or *textura epidermoidea*. *Hamathecium* 1.5–3.3 μm wide, composed of dense, numerous, filiform, unbranched, septate, constricted at the septum, hyaline, pseudoparaphyses, longer than asci. *Asci* 190–240 × 7–9 μm ($\bar{x}$ = 209 × 8 μm; n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 23–30 × 6–8 μm ($\bar{x}$ = 26 × 7 μm; n = 30), uniseriate, partially overlapping, straight or slightly curved, hyaline, fusiform, obtuse or conical ends, narrow towards the apex, 3-septate, constricted at the septa, with guttules in each cell, the lower cell slightly wider than the upper cell, without sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 25–27 mm diam. after two weeks at 25°C in dark, circular to irregular, felty and cottony, raised, yellowish white, dry, cottony to filiform towards the margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL38 (HUEST XX), living culture UESTCC XX.

Hosts – *Hevea brasiliensis* (Xu et al., 2024), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Melomastia puerensis* was collected from *Hevea brasiliensis* and illustrated by Xu et al. (2024). According to the guidelines of Jeewon and Hyde (2016), I identified my collection as *M. puerensis*, since the difference of molecular DNA data compared to the type species is not enough to support it as a new species. The LSU, SSU and *tef1α* sequences of my collection showed five bp (890/895 bp), four bp (1095/1099 bp) and three bp (900/903 bp) differences from *M. puerensis* (ZHKUCC 23-0802, ex-type strain), respectively. Morphologically, my collection is similar to *M. puerensis* with the dimensions of microscopic features as described by Xu et al. (2024). I herein provide a new host record for *M. puerensis* from *Rosa roxburghii* in China.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 200 µm; f, g = 30 µm; h–j = 50 µm; k–r = 10 µm

Figure 3.3 *Melomastia puerensis* (HUEST SL38, new host record)

Melomastia sichuanensis W.L. Li, Maharachch. & Jian K. Liu, Journal of Fungi 8(1, no. 76): 12 (2022) Figure 3.4

Index Fungorum number: IF841501; Facesoffungi number: FoF10535

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 275–553 μm wide, 290–730 μm high, solitary to gregarious, sometimes confluent, dark brown to black, coriaceous to carbonaceous, semi-immersed to erumpent, visible as raised, dark spots on host surface, unilocular, glabrous, globose to oval or pyriform, papillate. ostiolate. *Ostiole* 90–128 μm wide, 250–297 μm high, single, subcylindrical, straight or curved, central. *Peridium* 60–95 μm wide, composed of dark brown to black cells of *textura angularis* to *textura intricata*. *Hamathecium* 1.5–3 μm wide, composed of dense, numerous, filiform, unbranched, aseptate, hyaline, pseudoparaphyses, longer than asci. *Asci* 80–125 × 6–8 μm ($\bar{x}$ = 103 × 7 μm; n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 14–18 × 4.5–6 μm ($\bar{x}$ = 16 × 5 μm; n = 30), uniseriate, partially overlapping, straight or slightly curved, hyaline, fusiform, obtuse or conical ends, narrow towards the apex, 3-septate, constricted at the septa, with guttules in each cell, smooth-walled, with mucilaginous sheath. Asexual morph: Undetermined.

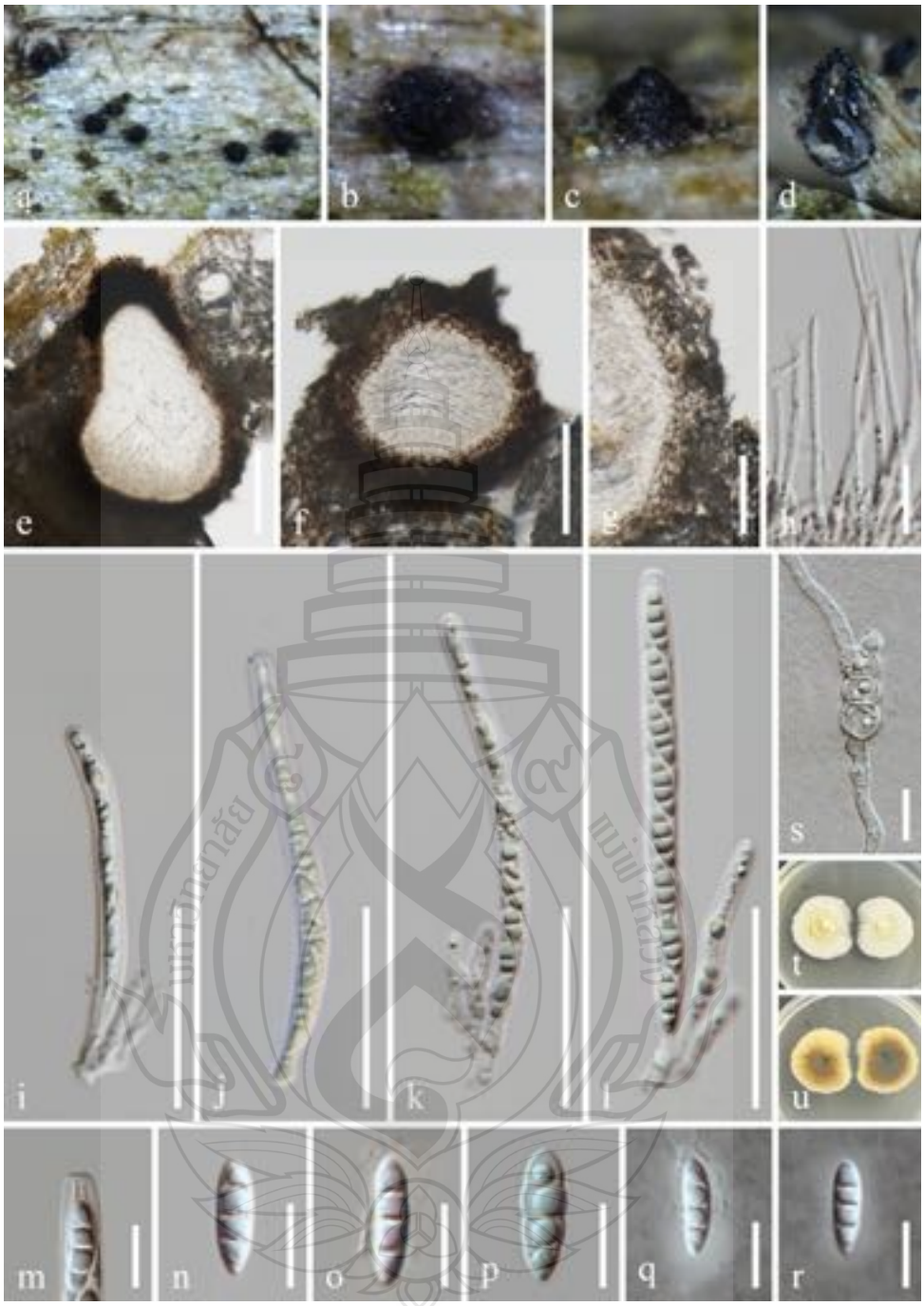
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 33–35 mm diam. after two weeks at 25℃ in dark, circular, dense, yellow in the inner ring and white at the edge; in reverse, brown in the middle with an orange ring, dark yellow radiating outwardly.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL64 (HUEST XX), living culture UESTCC XX.

Host: *Olea europaea* (Li et al., 2022b).

Known geographical distribution – China.

Notes – Based on a BLAST search in NCBI GenBank, the LSU, SSU and *tef1α* sequences of my collection are 99.65%, 99.71% and 99.44% identical to *Melomastia sichuanensis* (CGMCC3.20620), respectively. Phylogenetic analysis showed that my new collection clustered with *M. sichuanensis* (CGMCC 3.20620 and UESTCC 21.0008) (Figure 3.2). My collection matches with the holotype of *M. sichuanensis* in morphology and by dimensions (Li et al., 2022b). Thus, I recognize my collection as *M. sichuanensis*, which was recollected in China, and extend its host to *Rosa roxburghii*.



Note a–c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Peridium. h Pseudoparaphyses. i–l Asci. m Ascus ocular chamber. n–p Ascospores. q, r Ascospores stained with Indian ink. s Germinating ascospore. t, u Colony on PDA, above (t), below (u). Scale bars: e, f = 100 μm; g, i–l = 40 μm; h = 20 μm; m–s = 10 μm

Figure 3.4 *Melomastia sichuanensis* (HUEST SL64, new host record)

Monoblastiales Lücking, M.P. Nelsen & K.D. Hyde

Eriomycetaceae Huanraluek & Hyde

Type genus – *Eriomyces* Huanraluek, Thambugala & K.D. Hyde

Notes – Eriomycetaceae was established by Hyde et al. (2020a) to accommodate five non-lichenized genera, viz., *Eriomyces* (type genus), *Funbolia*, *Heleiosa*, *Phellinocrescentia* and *Pseudopassalora*, which were placed in Dothideomycetes, families *incertae sedis*. Hongsanan et al. (2020b) presented a revised and updated report on orders and families *incertae sedis* of Dothideomycetes, and treated Eriomycetaceae as a synonym of Monoblasticaceae. However, Zhang et al. (2023) resurrected this family and accommodated it within Monoblastiales based on morphological characteristics and multi-gene phylogenetic analysis. Currently, eight genera are listed within Eriomycetaceae, viz., *Eriomyces*, *Funbolia*, *Haudseptoria*, *Heleiosa*, *Italiofungus*, *Karstiomyces*, *Phellinocrescentia* and *Pseudopassalora* (Kohlmeyer et al., 1996; Crous et al., 2011a, b, 2014, 2020c; Hyde et al., 2020a, 2024).

Heleiosa Kohlm., Volkm.-Kohlm. & O.E. Erikss., Can. J. Bot. 74(11): 1830 (1996)

Type species – *Heleiosa barbatula* Kohlm., Volkm.-Kohlm. & O.E. Erikss

Notes – *Heleiosa* was introduced to accommodate its type species *H. barbatula* by Kohlmeyer et al. (1996). Due to lack of molecular data, *Heleiosa* was placed in Dothideales and Pleosporales *incertae sedis*, respectively, based on morphology (Kohlmeyer et al., 1996; Jones et al., 2009). Suetrong et al. (2009) provided LSU and SSU gene sequence data for the type species *H. barbatula*. Subsequently, Mortimer et al. (2021) introduced *Neoheleiosa*, which is monotypic and formed a sister clade to *Heleiosa*. Morphologically, *Neoheleiosa* is similar to *Heleiosa* in having bitunicate, fissitunicate, pedicellate, with an ocular chamber, cylindric asci with uniseriate, hyaline to brown, 1-septate, guttulate, faintly longitudinally striated, ellipsoidal or ovoid ascospores, only differs from latter in ascospores lack of numerous cilia-like sub-apical appendages. In the phylogenetic analysis, *Neoheleiosa* and *Heleiosa* formed an

independent clade and clustered with *Phellinocrescentia guianensis*, where *Heleiosa* is congeneric with the genus *Neoheleiosa*. The same tree topology also appeared in previous literatures (Zhang et al., 2023; Du et al., 2025; Sun et al., 2025).

Suetrong et al. (2009) indicated that some species form ascospore appendages by fragmentation of a sheath, e.g., *Capronia ciliomaris*, an intertidal marine fungus from San Juan Island (Au et al., 1999) and *Tirisporella beccariana*, an ascomycete from the mangrove palm *Nypa fruticans* (Jones et al., 1996). An analogous mechanism of appendages unfolding appears to be present in *Heleiosa barbatula* (Kohlmeyer et al., 1996). *Heleiosa barbatula* was first collected from *Juncus roemerianus* in salt marshes of the United States east coast, and its ascospores had cilia-like appendages (Kohlmeyer et al., 1996). Recently, Yang et al. (2023a) recollected this species on dead branches of *Mangifera indica* in terrestrial habitat, but its ascospores lacked cilia-like appendages. My collection is also similar to *Heleiosa* and *Neoheleiosa*, but lack ascospore appendages. This indicates that the appendage is not enough to distinguish *Heleiosa* and *Neoheleiosa*, as the same species may exhibit certain morphological variations depending on the host and habitat. In the present study, I follow the recent updates of these two genera (Sun et al., 2025) and propose to transfer *Neoheleiosa ellipsoidispora*, *N. septata* and *N. verrucosispora* to the genus *Heleiosa*. A new species, *H. rosae*, is introduced based on morphological and phylogenetic analysis. Morphological descriptions of the asexual morph of this genus are provided. Additionally, the link between the asexual and sexual morphs of *Heleiosa* species is established by molecular DNA data.

Heleiosa ellipsoidispora (N. Wu, H.Z. Du & Jian K. Liu) N. Wu, K.D. Hyde & Jian K. Liu, comb. nov. Figure 3.5

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Basionym – *Neoheleiosa ellipsoidispora* N. Wu, H.Z. Du & Jian K. Liu XX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: See Du et al. (2025). Asexual morph: Coelomycetous. *Conidiomata* 120–146 μm wide, 100–175 μm

high, solitary or confluent, dark brown, semi-immersed to superficial, visible as black dots on the host, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, ostiolate. *Ostiole* 53–63 μm wide, 63–80 μm high, single, central. *Conidiomatal wall* 13–25 μm wide, composed of brown to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–13 × 2–3.5 μm ($\bar{x}$ = 8.7 × 2.8 μm; n = 30), hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical, and arising from the inner layers of conidiomata. *Conidia* 40–51 × 3.5–5 μm ($\bar{x}$ = 45 × 4 μm; n = 30), hyaline, acerose to elongate fusiform, with a narrow and obtuse apex, and a truncate and rounded base, straight or slightly curved, 7–11-septate, slightly constricted at the septum, smooth-walled, guttulate.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium reaching 22–24 mm diam. after two weeks at 25°C in dark, circular, slightly raised, surface rough, dry, grayish green; in reverse, grayish brown with an entire margin.

Materials examined – CHINA, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna tropical rain forest South Medicine Garden, 22°0′25″ N, 100°47′20″ E, on dead stems of medicinal plant *Uncaria rhynchophylla* (Miq.) Miq. (Rubiaceae), 11 November 2022, N. Wu & H.Z. Du, W327 (HKAS XX, **holotype**); ex-type living culture CGMCC XX; *ibid.*, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL11 (HUEST XX); living culture UESTCC XX.

Notes – The phylogenetic tree (Figure 3.6) showed that my newly obtained isolate clustered together with *Heleiosa ellipsoidispora* (≡ *Neoheleiosa ellipsoidispora*), and I identified it as *H. ellipsoidispora*. Only the sexual morph was provided when Du et al. (2025) described this species, and here I illustrate the asexual morph of *H. ellipsoidispora* and report it as a new host record from *Rosa roxburghii*. In addition, for detailed diagnostic notes of *H. ellipsoidispora*, see above.



Note a Host: *Rosa roxburghii*. b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j–p Conidia. q Germinating conidium. r, s Colony on PDA, above (r), below (s). Scale bars: d, e = 50 μm; f–q = 20 μm

Figure 3.5 *Heleiosa ellipsoidispora* (HUEST SL11, new host record)

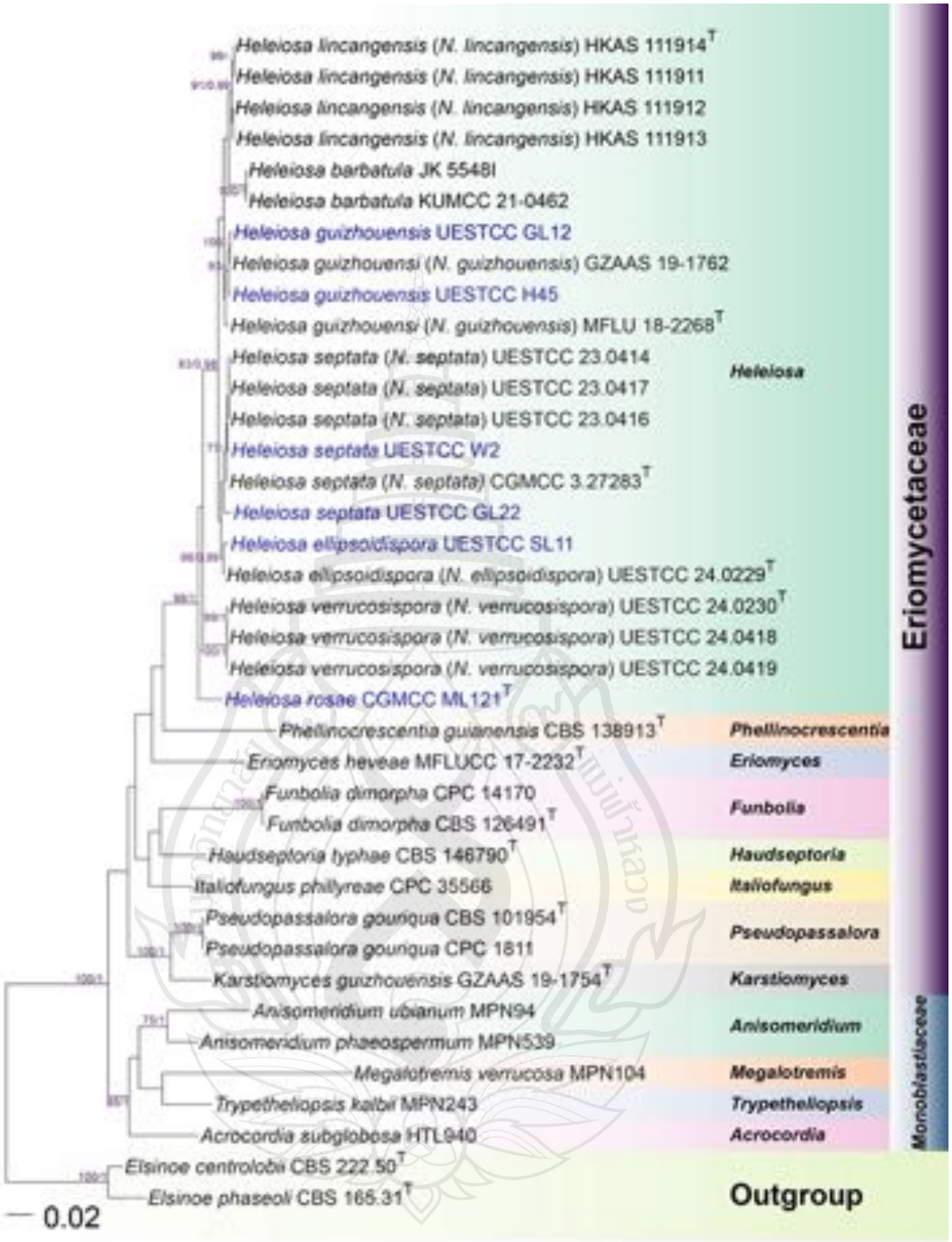


Figure 3.6 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of *Heleiosa*

Figure 3.6 The tree is rooted with *Elsinoe centrolobii* (CBS 222.50) and *E. phaseoli* (CBS 165.31). Bootstrap values for maximum likelihood (ML) equal to or

greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Heleiosa guizhouensis (Jin F. Zhang & K.D. Hyde) Y.R. Sun, Yong Wang bis & K.D. Hyde, Fungal Diversity 131: 128 (2025) Figure 3.7

Index Fungorum number: IF903099; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 170–225 μm wide, 185–320 μm high, solitary to gregarious, sometimes confluent, dark brown to black, immersed to semi-immersed, oval or globose to subglobose, unilocular, glabrous, coriaceous, ostiolate. *Ostiole* 53–83 μm wide, 89–127 μm high, single, central. *Peridium* 18–35 μm wide, composed of dark brown to black cells of *textura angularis*. *Hamathecium* 1–2.5 μm wide, branched, septate, hyaline, trabecular pseudoparaphyses. *Asci* 105–125 × 9–12 μm ($\bar{x}$ = 114 × 10 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 14–18 × 6.5–9 μm ($\bar{x}$ = 16 × 7 μm; n = 30), uniseriate, guttulate, aseptate, ovoid or ellipsoidal, rounded at both ends or sometimes with truncate bases, hyaline to pale yellowish, becoming pale brown and 1-septate with age, with two equal cells, constricted in the middle, straight or slightly curved, smooth-walled, with longitudinal striate ornamentation. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25℃ in dark, circular, slightly raised, surface rough, dry, grayish green; in reverse, grayish brown with an entire margin.

Materials examined – CHINA, Guizhou Province, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL12 (HUEST XX), living culture UESTCC XX; *ibid.*, Sichuan Province, Leshan City, Huangdan

Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H45 (HUEST XX), living culture UESTCC XX.

Notes – I identified my isolates as *Heleiosa guizhouensis* (≡ *Neoheleiosa guizhouensis*) based on morphology and phylogeny (Figure 3.6). This is the first record of *H. guizhouensis* found on *Rosa roxburghii* and *R. sterilis* in China (Zhang et al., 2023a).



Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–q Ascospores. r Germinating ascospore. Scale bars: d, e = 100 μm; h–j = 30 μm; f, g, k–r = 10 μm.

Figure 3.7 *Heleiosa guizhouensis* (HUEST H45, new host record)

Heleiosa rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.8

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML121

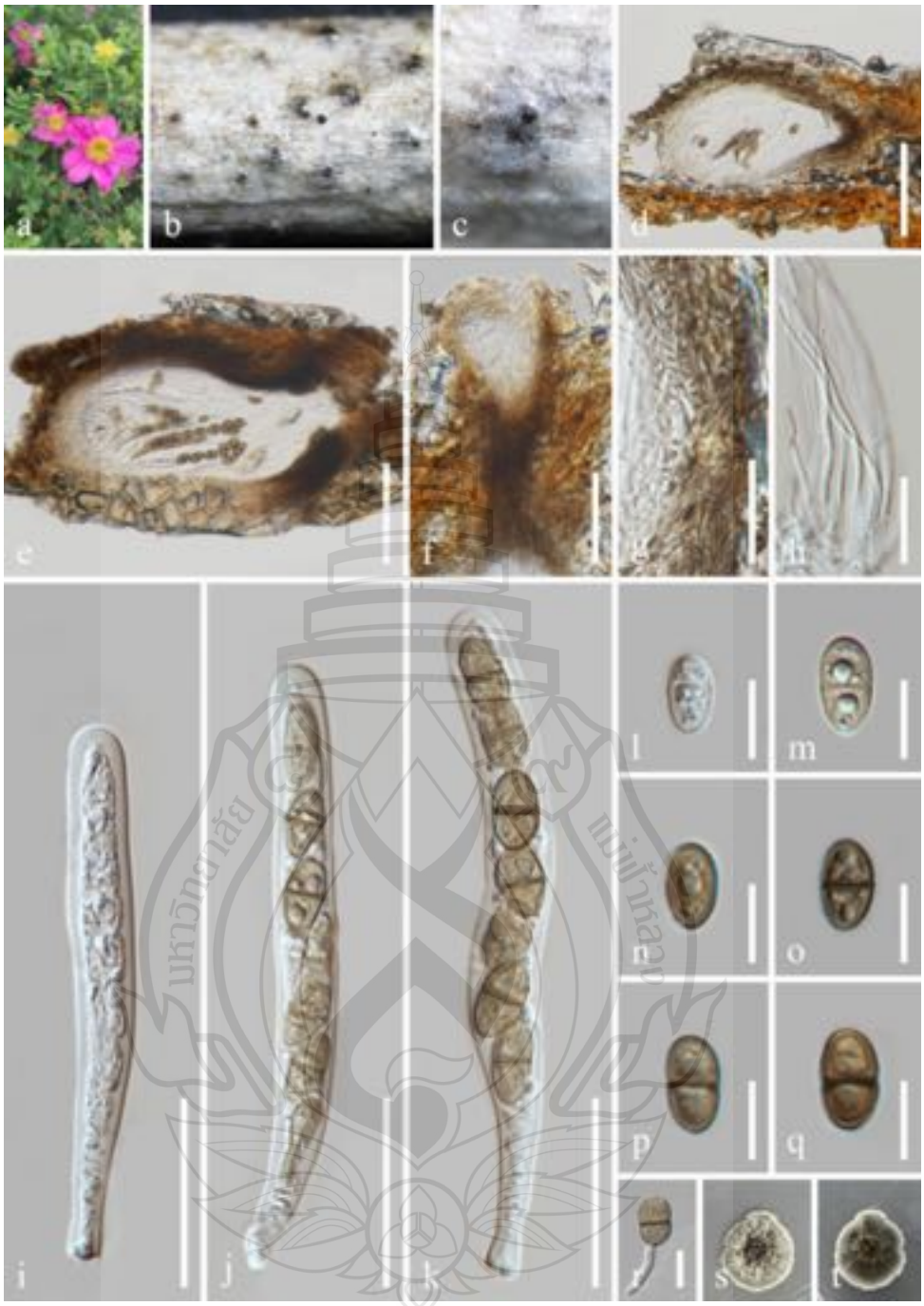
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 230–265 μm long, 115–155 μm high, mostly solitary, occasionally gregarious, dark brown to black, immersed to superficial or erumpent through bark, irregularly pyriform, not upright, laid on the substrate, unilocular, glabrous, coriaceous, ostiolate. *Ostiole* 47–61 μm wide, 70–85 μm high, single, central or laterally located, long, subcylindrical, straight or curved, composed of thick-walled cells of *textura intricata* to *textura oblita*. *Peridium* 18–35 μm wide, poorly developed, composed of dark brown to black cells of *textura angularis*, fusing with the host tissue outwardly. *Hamathecium* 1.5–2 μm wide, composed of dense, numerous, filamentous, branched, septate, hyaline, trabecular pseudoparaphyses. *Asci* 95–130 × 8.5–11 μm ($\bar{x}$ = 105 × 10 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 11–15 × 5–7.5 μm ($\bar{x}$ = 12.5 × 6.5 μm; n = 30), uniseriate, guttulate, hyaline, aseptate, ovoid or ellipsoidal, rounded at both ends or sometimes with truncate bases, becoming pigmented brown and one septate at maturation, constricted in the middle, smooth-walled, without longitudinal striations or mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25℃ in dark, circular, flattened, slightly raised, dry, grayish green; in reverse, grayish brown with an entire margin.

Material examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on

decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML121 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – *Heleiosa rosae* matches the generic concept of *Heleiosa*. It resembles *H. barbatula*, *H. brownie*, *H. ellipsoidispora*, *H. guizhouensis*, *H. lincangensis* and *H. septate* in having bitunicate, fissitunicate, cylindrical asci and ovoid or ellipsoidal, brown, 1-septate ascospores (Kohlmeyer et al., 1996; Mortimer et al., 2021; Yang et al., 2023; Zhang et al., 2023a; Sun et al., 2025; Du et al., 2025). However, *H. rosae* differs from the others by mostly immersed, irregularly pyriform ascomata, not upright, laid on the substrate, with a relatively long neck. In the ITS-LSU-SSU-*tef1α* phylogenetic tree, *H. rosae* (CGMCC ML121) formed a basal branch within *Heleiosa* clade (Figure 3.6). Based on the morphology and molecular data, I recognize *H. rosae* as a new species.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Pseudoparaphyses. i–k Asci. l–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 80 μm; f = 50 μm; g, h = 20 μm; i–k = 30 μm; l–r = 10 μm.

Figure 3.8 *Heleiosa rosae* (HKAS ML121, holotype)

Heleiosa septata (H.Z. Du & Jian K. Liu) N. Wu, K.D. Hyde & Jian K. Liu, comb. nov. Figure 3.9; Figure 3.10

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Basionym – *Neoheleiosa septata* H.Z. Du & Jian K. Liu XX

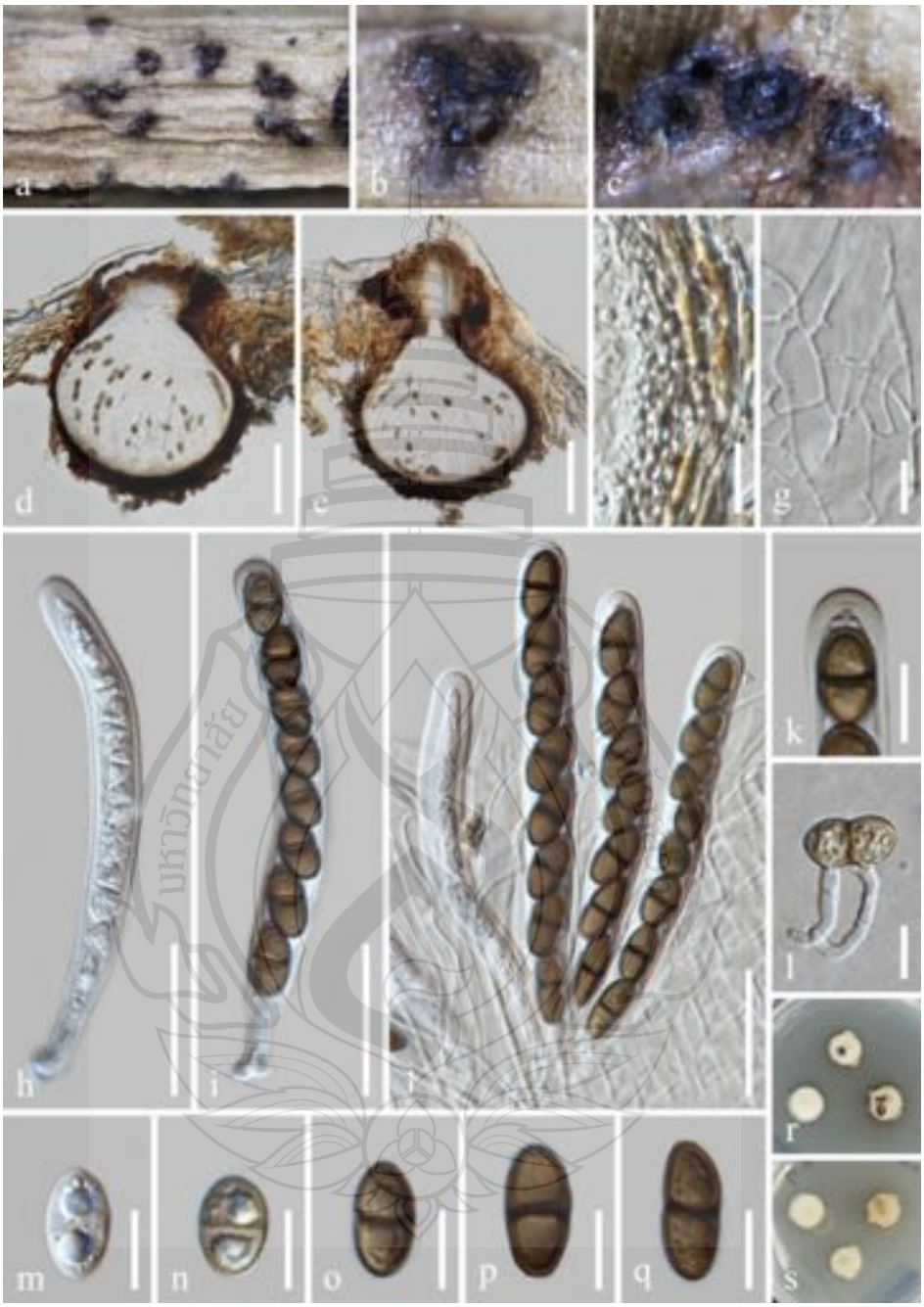
Saprobic on dead branches of *Rosa roxburghii and R. sterilis*. Sexual morph: *Ascomata* 177–300 μm wide, 220–360 μm high, solitary, scattered, dark brown to black, immersed to semi-immersed, pyriform, unilocular, glabrous, coriaceous, papillate, ostiolate. *Ostiole* 50–92 μm wide, 82–140 μm high, single, centric or eccentric, long, subcylindrical, straight or curved. *Peridium* 12–35 μm wide, composed of dark brown to black cells of *textura angularis*. *Hamathecium* 1.5–2 μm wide, composed of dense, numerous, anastomosing, filamentous, branched, septate, hyaline, trabecular pseudoparaphyses. *Asci* 118–145 × 10–13 μm ($\bar{x}$ = 128 × 12 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 15–18 × 7–9 μm ($\bar{x}$ = 17 × 8 μm; n = 30), uniseriate, guttulate, straight or slightly curved, hyaline to brown, aseptate or 1-septate, constricted in the middle, ovoid or ellipsoidal, rounded at both ends or sometimes with truncate bases, smooth-walled, without longitudinal striations or mucilaginous sheath. Asexual morph: Coelomycetous. *Conidiomata* 94–140 μm wide, 75–151 μm high, mostly solitary, occasionally gregarious, dark brown, semi-immersed to superficial, visible as black dots on the host, pycnidial, oval or globose to subglobose, mostly unilocular, occasionally multi-locular, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Conidiomatal wall* 11–25 μm wide, composed of hyaline to brown compressed cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–11 × 2–4 μm ($\bar{x}$ = 8.5 × 2.5 μm; n = 30), hyaline, enteroblastic, phialidic, aseptate, smooth, thin-walled, cylindrical to subcylindrical or irregular, determinate, and arising from the inner layers of conidiomata. *Conidia* 37–45 × 3–4.5 μm ($\bar{x}$ = 44 × 3.5 μm; n = 30), hyaline, elongate fusiform, with a narrow apex, and a truncate base, straight or slightly curved, 7–12-septate, slightly constricted at the septum, smooth-walled, guttulate.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from every cell. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, dry, milky white in the whole colony. Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium reaching 15–18 mm diam. after two weeks at 25°C in dark, circular, slightly raised, surface rough, dry, grayish green; in reverse, grayish brown with an entire margin.

Materials examined – CHINA, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 25°8′27″ N, 102°44′24″ E, elevation 1,922 m, on dead stems of medicinal plant *Helwingia chinensis* Batalin, 11 November 2022, H.Z. Du, S718 (HKAS 132391, holotype); ex-type living culture CGMCC S718; *ibid.*, S750 (HUEST 23.0417, paratype), living culture UESTCC 23.0416; *ibid.*, Dongchuan District, Tuobuka Town, 103°2′32″E, 26°19′20″N, elevation 2,348 m, on dead branches of medicinal plant *Taxus wallichiana* var. *chinensis* (Pilg.) Florin, 29 March 2022, Q. J. Shang, S515 (HUEST 23.0415), living culture UESTCC 23.0414; *ibid*., Sichuan Province, Guangyuan City, Chaotian District, Qingquan Village, 32°41′32″ N, 105°58′35″ E, elevation 820 m, on dead stems of medicinal plant *Lonicera japonica* Thunb. (Caprifoliaceae), 19 April 2021, H.Z. Du, S224 (HKAS 132392), living culture UESTCC 23.0417; *ibid*., Guizhou Province, Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *Rosa roxburghii*, 6 February 2023, N. Wu, W2 (HUEST XX), living culture UESTCC XX; *ibid*., Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL22 (HUEST XX), living culture UESTCC XX.

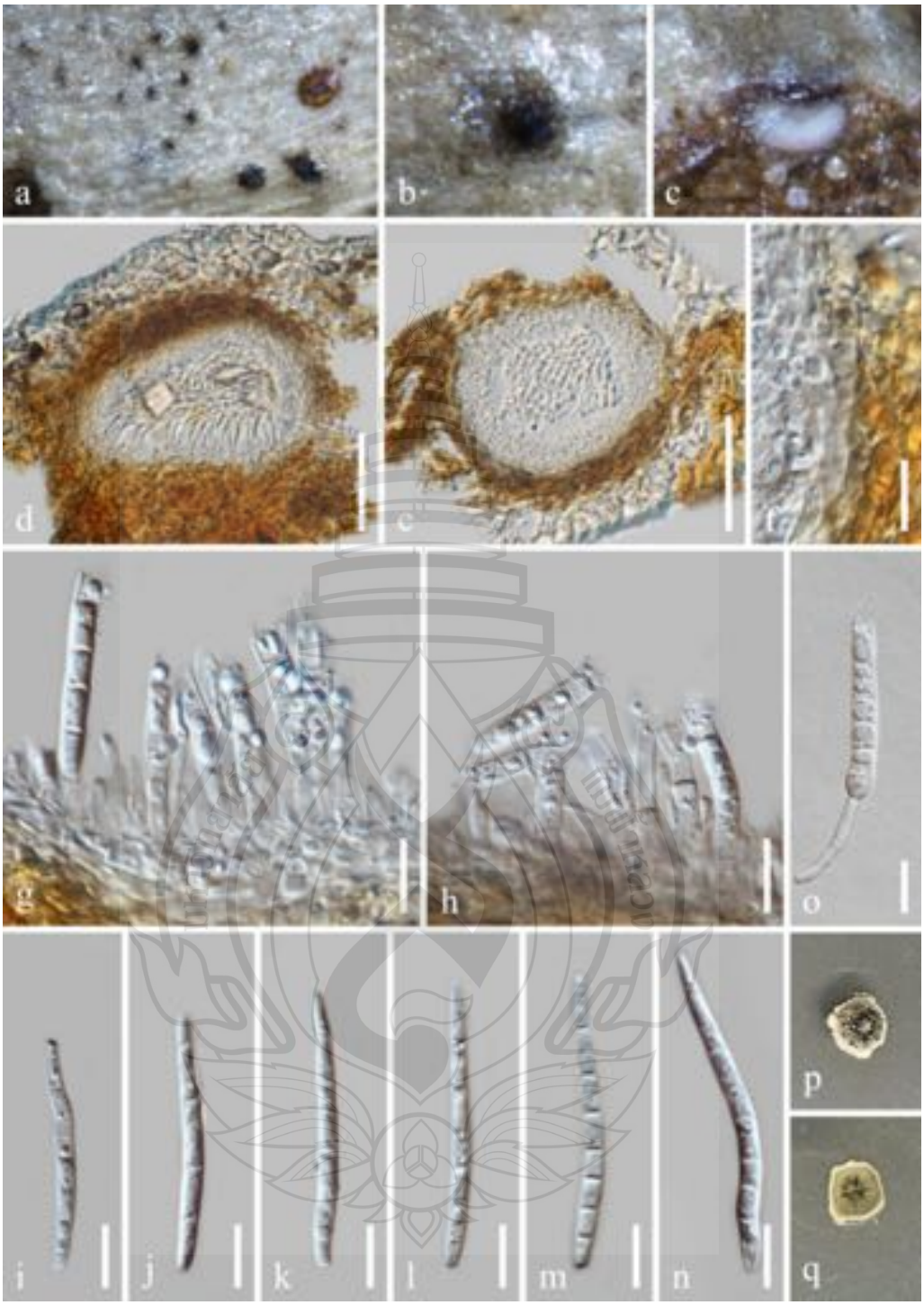
Notes – *Heleiosa septata* (≡ *Neoheleiosa septata*) is a holomorphic species. This species with both asexual and sexual morphs was isolated from *Helwingia chinensis* and *Lonicera japonica*, respectively (Du et al., 2025). In the present study, I also isolated the asexual and sexual morphs of *H. septata* from *Rosa sterilis* and *R. roxburghii*, respectively.

The phylogenetic tree indicate that these two isolates are identical and belong to the same species (Figure 3.6).



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k Ascus ocular chamber. l Germinating ascospore. m–q Ascospores. r, s Colony on PDA, above (r), below (s). Scale bars: d, e = 100 µm; h–j = 30 µm; f, g, k–q = 10 µm.

Figure 3.9 *Heleiosa septata* (HUEST W2; sexual morph, new host record)



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g, h Conidiogenous cells and developing conidia. i–n Conidia. o Germinating conidium. p, q Colony on PDA, above (p), below (q). Scale bars: d, e = 50 μm; f–o = 10 μm.

Figure 3.10 *Heleiosa septata* (HUEST GL22; asexual morph, new host record)

Muyocopronales Mapook, Boonmee & K.D. Hyde

Muyocopronaceae K.D. Hyde

Type genus – *Muyocopron* Speg.

Notes – Muyocopronaceae was originally proposed as 'Myiocopronaceae' by Luttrell (1951) and was included in the order Hemisphaeriales. This family was formally introduced by Hyde et al. (2013) as an *incertae sedis* family in Dothideomycetes to accommodate the monotypic genus *Muyocopron*. Subsequently, Mapook et al. (2016) reappraised the genus *Muyocopron* and established the order Muyocopronales to accommodate Muyocopronaceae based on the distinct phylogeny and unique morphological characteristics. Phylogenetically, the order is closely related to Acrospermales and Dyfrolomycetales (Mapook et al., 2016). Currently, ten genera are accepted in the family, *Arxiella*, *Leptodiscella*, *Muyocopron*, *Muyocopromyces*, *Mycoleptodiscus*, *Neocochlearomyces*, *Neomycoleptodiscus*, *Paramycoleptodiscus*, *Pseudopalawania* and *Setoapiospora* (Crous et al., 2018a; Hernández-Restrepo et al., 2019; Mapook et al., 2020b).

Muyocopron Speg., Anales Soc. Ci. Argent. 12 (3): 113 (1881)

Type species – *Muyocopron corrientinum* Speg.

Notes – Spegazzini (1881) established *Muyocopron* based on *M. corrientinum*, which was collected from dead leaves of *Oncidium* sp. in Argentina. The genus is characterized by superficial, pseudo-thyriothecial, flattened, carbonaceous, black ascomata, as well as clavate to saccate or obclavate asci with hyaline, unicellular verruculose, ellipsoidal to ovate ascospores. Asexual morphs are not known. Members of *Muyocopron* are usually found as saprobes on dead plant substrates (Tian et al., 2024a; Zhang et al., 2024a; Manawasinghe et al., 2025). Over 80 epithets are listed in Index Fungorum (2025, June), but only a few species with molecular data.

Muyocopron lithocarpi Mapook, Boonmee & K.D. Hyde, Phytotaxa 265(3): 235 (2016) Figure 3.11

Index Fungorum number: IF551618; Facesoffungi number: FoF01890

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* superficial, solitary to gregarious, scutate, flattened, dark spots, covering the host, without a subiculum, with a poorly developed basal layer and an irregular margin, unilocular, coriaceous, glabrous; in section 185–290 μm wide, 135–160 μm high, short papillate, ostiolate. *Ostiole* 290–405 μm wide, 60–100 μm high, single, short-cylindrical, central or laterally located. *Peridium* 13–25 μm wide at the side, carbonaceous to coriaceous, outer layer composed of dark brown to black pseudoparenchymatous, occluded cells of *textura epidermoidea*, inner layer comprising hyaline to light brown cells of *textura angularis*, thinner at the base, 15–20 μm wide. *Hamathecium* 2.5–3.5 μm wide, composed of dense, rarely branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 53–65 × 14–19 μm ($\bar{x}$ = 59.5 × 16.3 μm; n = 20), 6–8-spored, bitunicate, saccate or broadly obpyriform, straight or slightly curved, slightly narrowing to rounded thickened apex, short pedicel. *Ascospores* 14.5–16.5 × 5.5–7.5 μm ($\bar{x}$ = 15.5 × 6.5 μm; n = 30), irregularly arranged or crowded, hyaline, oval to obovoid with obtuse ends, aseptate, smooth-walled, with granular appearance. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h and germ tube produced from the apex. Colonies on PDA medium reaching 12–15 mm diam. after two weeks at 25°C in dark, circular or irregular, slightly raised, with velvety, white, sparse mycelium on surface initially, becoming dense, gray from middle to the edge with age; in reverse, dark green with white undulate margin.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Guiding County, Yunwu Town, elevation 1,071 m, 26°12′36″ N, 107°6′36″ E, on dead branches of *Rosa roxburghii*, 6 February 2023, N. Wu, ML01 (HUEST XX), living culture UESTCC XX; *ibid.*, Bijie City, Dafang County, Wenge Town, Anqing

Village, elevation 1496 m, 27°8′60″ N, 105°25′48″ E, on dead branches of *R. roxburghii*, 2 February 2023, N. Wu, ML152 (HUEST XX), living culture UESTCC XX; *ibid.*, Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on dead branches of *R. roxburghii*, 6 February 2023, N. Wu, ML164 (HUEST XX), living culture UESTCC XX; *ibid.*, Anshun City, Xixiu District, Ninggu Town, Shangwan Village, elevation 1,400 m, 26°12′32″ N, 105°58′36″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL66 (HUEST XX), living culture UESTCC XX; *ibid.*, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H46 (HUEST XX), living culture UESTCC XX; *ibid.*, H52 (HUEST XX), living culture UESTCC XX.

Hosts – *Cercis chinensis* (Phookamsak et al., 2019), *Chromolaena odorata* (Mapook et al., 2020a), *Coffea* sp. (Lu et al., 2025), *Lithocarpus lucidus* (Mapook et al., 2016), *Paeonia suffruticosa* (Li et al., 2023b), *Peltophorum* sp. (Phookamsak et al., 2019), *Trachycarpus fortunei* (Zhang et al., 2024a), *Rosa roxburghii* and *R. sterilis* (present study).

Known geographical distribution – China, Thailand.

Notes – *Muyocopron lithocarpi* was introduced by Mapook et al. (2016) based on specimens collected from fallen leaves of *Lithocarpus lucidus* in Thailand. In the present study, six of my isolates clustered with several strains of *M. lithocarpi* with strong statistical support (Figure 3.12). Among these, one specimen was found on *Rosa sterilis* in Guizhou Province, while the others were collected from *Rosa roxburghii* in Guizhou and Sichuan Provinces, China. The ITS and LSU sequences of my specimens are identical to the type material of *M. lithocarpi* (MFLUCC 14-1106). Therefore, I identified my collection as *M. lithocarpi*, representing the first report of this species on *Rosa roxburghii* and *R. sterilis*.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–n Ascospores. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: d = 50 µm; e, h–k = 30 µm; f, g, l–o = 10 µm.

Figure 3.11 *Muyocopron lithocarpi* (HUEST ML01, new host record)

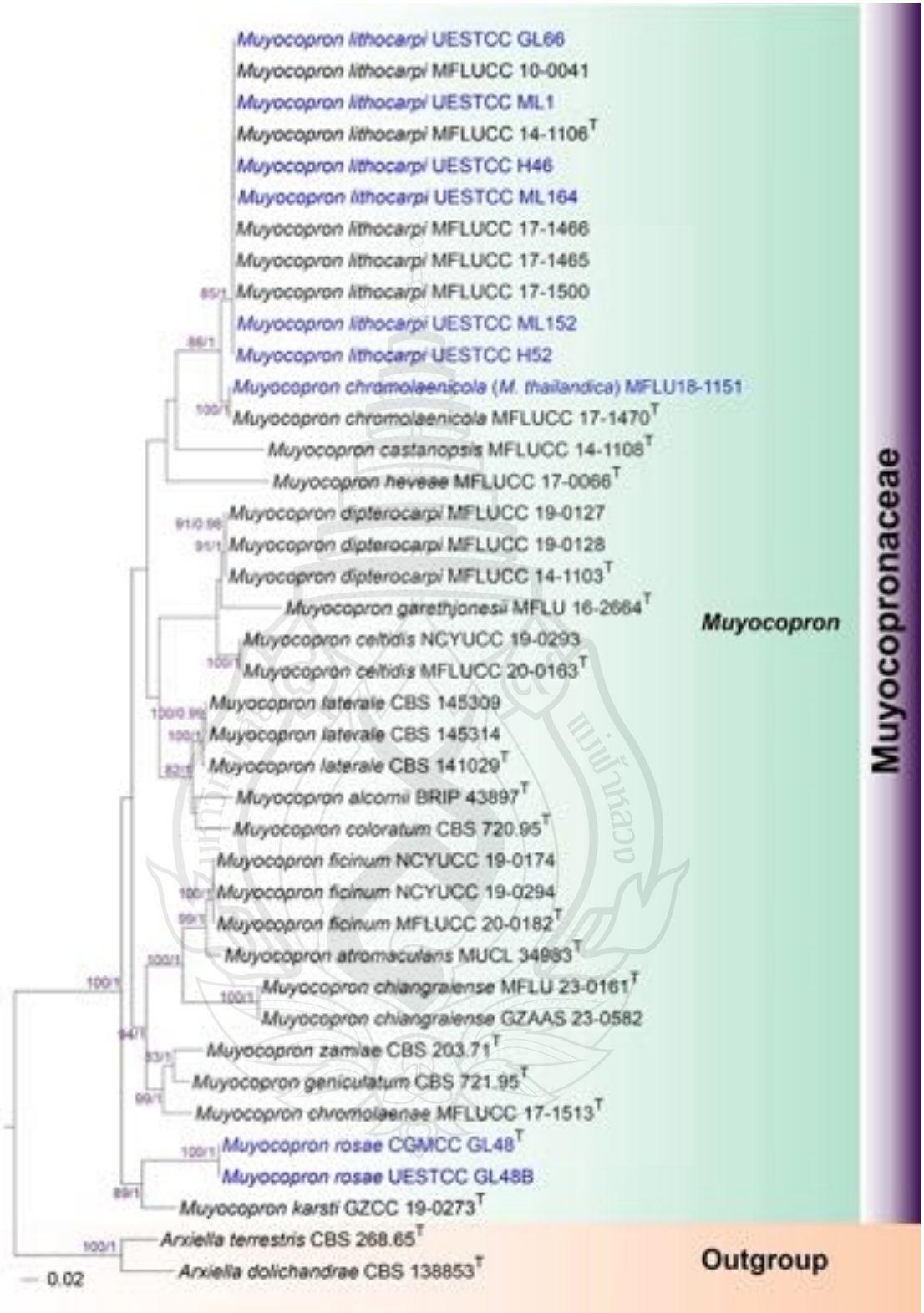


Figure 3.12 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tef1α* sequence data of *Muyocopron*

Figure 3.12 The tree is rooted with *Arxiella dolichandrae* (CBS 138853) and *A. terrestris* (CBS 268.65). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Muyocopron rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.13

Index Fungorum number: IFXX; Facesoffungi number: FoFXX; Figure 39

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS GL48

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: *Ascomata* 220–330 µm wide, 75–95 µm high, mostly solitary, occasionally gregarious, coriaceous, unilocular, glabrous, black spots, pseudostromatic, dimidiate, scutate, covering the host, without a subiculum, poorly developed basal layer and irregular margin, with an ostiole. *Ostiole* raised, central, single. *Peridium* or *scutellum*, 15–25 µm wide at the side, composed of *textura prismatica* to *textura porrecta* cells radiating to the margin, carbonaceous to coriaceous, outer layer composed of dark brown to black pseudoparenchymatous, occluded cells of *textura epidermoidea*, inner layer composed of hyaline to light brown cells of *textura angularis*, thinner at the base, 7–10 µm wide. *Hamathecium* 2–3 µm wide, filamentous, rarely branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 53–70 × 25–37 µm ($\bar{x}$ = 64 × 33 µm; n = 20), 8-spored, bitunicate, ovoid or clavate, sessile or subsessile. *Ascospores* 18–22 × 13–16 µm ($\bar{x}$ = 19.5 × 14.5 µm; n = 30), irregularly arranged or crowded, hyaline, ellipsoid to ovoid, externally smooth, internally verruculose, unicellular, guttulate. Asexual morph: Undetermined.

Materials examined – CHINA, Guizhou Province, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N,

105°19′21″ E, on decaying branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL48 (HKAS XX, holotype); *ibid*., CDW33 (HUEST XX, paratype).

Notes – *Muyocopron rosae* (CGMCC GL48 and HUEST CDW33) and *M. karsti* (GZCC 19-0273) formed a sister clade with a good support (Figure 3.12). Morphologically, *M. rosae* is similar to *M. karsti* in having 8-spored, bitunicate asci and unicellular, guttulate, verruculose, hyaline ascospores (Zhang et al., 2023). However, *M. rosae* has smaller asci (53–70 × 25–37 μm vs. 118.5–179.5 × 21–24.5 μm) and wider ascospores (18–22 × 13–16 μm vs. 18–22.5 × 10–12.5 μm) than those of *M. karsti*. In addition, the asci of *M. rosae* are sessile or subsessile and ovoid or clavate, while those of *M. karsti* are clavate with a distinct pedicel. The ascospores of *M. rosae* are ellipsoid to ovoid, while those of *M. karsti* are obovoid to pyriform and tapered towards the basal end. In addition, the LSU and *tef1α* sequences of *M. rosae* and *M. karsti* showed 16 bp (831/847 bp, 3 gaps) and 73 bp (764/837 bp, 2 gaps) differences, respectively. Therefore, I introduce *M. rosae* as a new species based on the molecular evidence and morphological characters.



Note a Host: *Rosa sterilis*. b, c Appearance of ascomata on host surface. d Ascoma as seen from above in squash mount. e Vertical section of ascomata. f Peridium. g–i Asci. j–m Ascospores. Scale bars: d, e = 100 μm; f–i = 30 μm; j–m = 10 μm.

Figure 3.13 *Muyocopron rosae* (HKAS GL48, holotype)

Mycosphaerellaceae Lindau, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 421 (1897)

Type genus – *Mycosphaerella* Johanson

Notes – Mycosphaerellaceae was introduced by Lindau (1897), with *Mycosphaerella* as the type genus, typified by *M. punctiformis*. As the largest family in Capnodiales (Dothideomycetes), it currently comprises 134 accepted genera and over 6000 species (Videira et al., 2017; Hongsanan et al., 2020a; Hyde et al., 2024; Zhang et al., 2024a).

Virosphaerella Videira & Crous, Stud. Mycol. 87: 377 (2017)

Type species – *Virosphaerella pseudomarksii* (Cheew., K.D. Hyde & Crous) Videira & Crous

Notes – Based on morphological and molecular evidence, Videira et al. (2017) introduced *Virosphaerella* to accommodate two new combinations that were initially identified as *Mycosphaerella irregularis* and *M. pseudomarksii* (Cheewangkoon et al., 2008). Although Guatimosim et al. (2016) had previously synonymized these two species under *Paramycosphaerella*. Subsequently, Huang et al. (2024) introduced the third member, *V. gleicheniacearum*, from living leaves (*Diplopterygium blotianum*, *D. chinense* and *Dicranopteris tetraphylla*), and distinguished *V. gleicheniacearum* from *V. irregularis* and *V. pseudomarksii* based on molecular data and ascospore shape. *Virosphaerella* is characterized by black, globose or subglobose ascomata, non-paraphyses, sessile or subsessile, cylindric-obclavate asci and hyaline, 1-septate, constricted at the septum, upper cell slightly wider than lower cell, verrucose, smooth-walled, ellipsoid-fusiform ascospores with a thin mucilaginous sheath, but no known sexual morphs have been reported for this genus (Cheewangkoon et al., 2008; Videira et al., 2017; Huang et al., 2024). Videira et al. (2017) emphasized that the mucilaginous sheath around ascospores is a key diagnostic feature of *Virosphaerella*; however, this structure was not observed in *V. gleicheniacearum* (Huang et al., 2024).

Virosphaerella rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.14

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

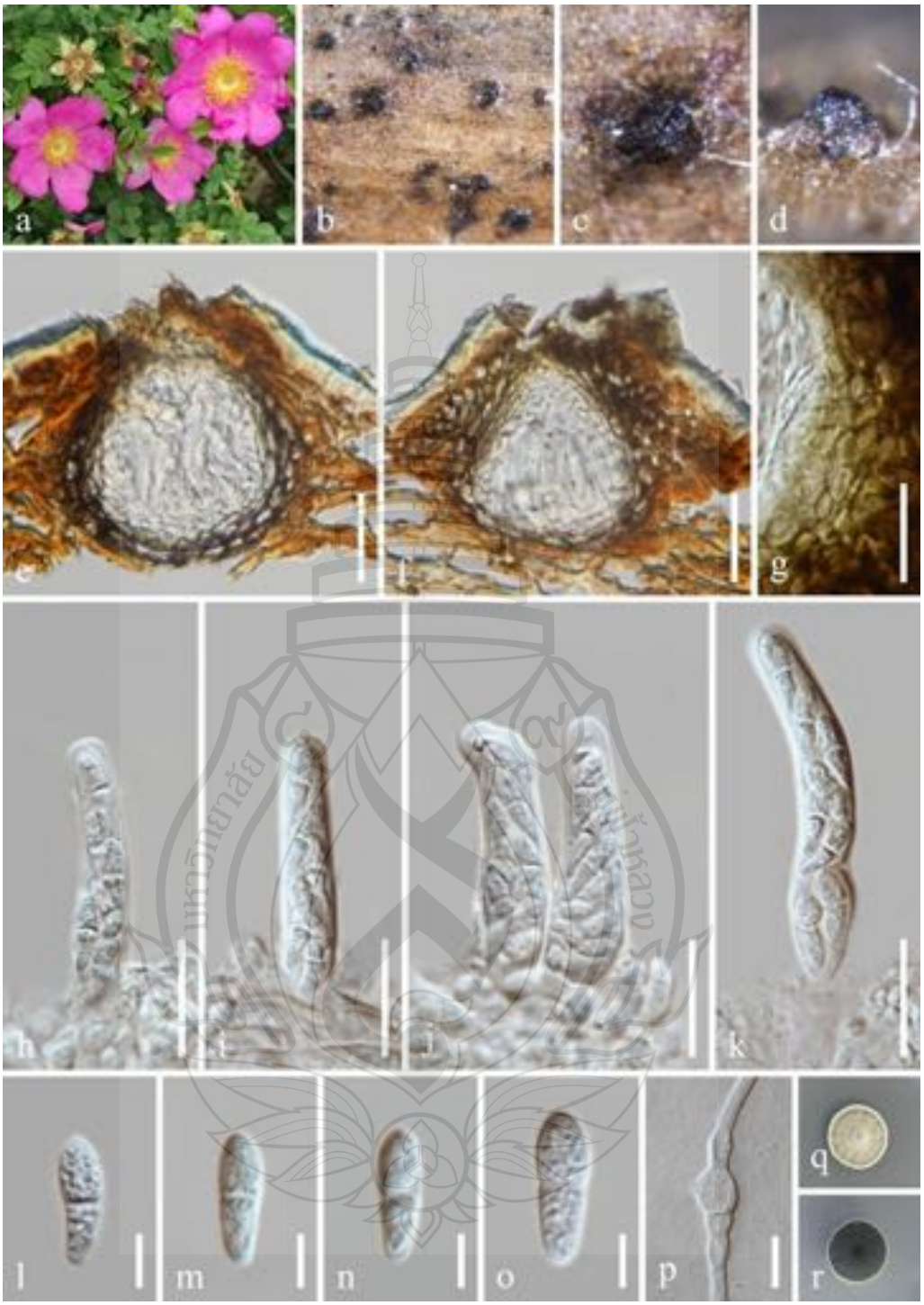
Holotype – HKAS ML96

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 75–140 μm wide, 76–166 μm high, solitary, black, initially immersed, becoming erumpent through bark fissures, visible as black dots on the host when mature, subglobose to pyriform, unilocular, glabrous, coriaceous, short papillate, ostiolate. *Ostiole* 20–40 μm wide, 30–45 μm high, single, straight or curved, central or laterally located. *Peridium* 12–18 μm wide, composed of thick-walled, dark brown to pale brown cells of *textura angularis*. *Asci* 42–65 × 6.5–10 μm ($\bar{x}$ = 50 × 8 μm; n = 20), 8-spored, aparaphysate, cylindric-obclavate, straight to slightly curved, sessile or subsessile, slightly narrowing to rounded thickened apex, with an ocular chamber. *Ascospores* 12–14 × 3–5 μm ($\bar{x}$ = 13 × 4 μm; n = 30), uniseriate, usually overlapping or biseriate towards the base, hyaline, ellipsoid-fusiform, slightly acute at both ends, inequilateral, straight to slightly curved, 1-septate, slightly constricted at the septum, upper cell slightly wider than lower cell, verrucose, smooth-walled, occasionally with a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, cottony, flat, pale greenish gray in central, white at the edge; in reverse, dull green with an entire margin.

Materials examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML96 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid*., ML405 (HUEST XX, paratype), living culture UESTCC XX.

Notes – Based on a blast search of ITS sequence of *Virosphaerella rosae* in NCBI GenBank, the closest hit is *V. gleicheniacearum* (R. Kirschner 5776, Query cover 100%, identities 97.31%); the closest hits based on *rpb2* sequence is *V. irregularis* (CBS:123242, Query cover 91%, identities 88.43%). The multi-gene phylogenetic tree showed that *V. gleicheniacearum*, *V. irregularis*, *V. pseudomarksii* and *V. rosae* formed a monophyletic clade (Figure 3.15). In addition, the germinating hyphae of *V. gleicheniacearum* and *V. rosae* are relatively regular, whereas those of *V. irregularis* are highly contorted (Cheewangkoon et al., 2008; Videira et al., 2017; Huang et al., 2024).



Note a Host: *Rosa roxburghii*. b–d Appearance of ascomata on host surface. e, f Vertical sections of ascomata. g Peridium. h–k Asci. l–o Ascospores. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: e, f = 30 μm; g–k = 15 μm; l–o = 5 μm; p = 10 μm.

Figure 3.14 *Virosphaerella rosae* (HKAS ML96, holotype)

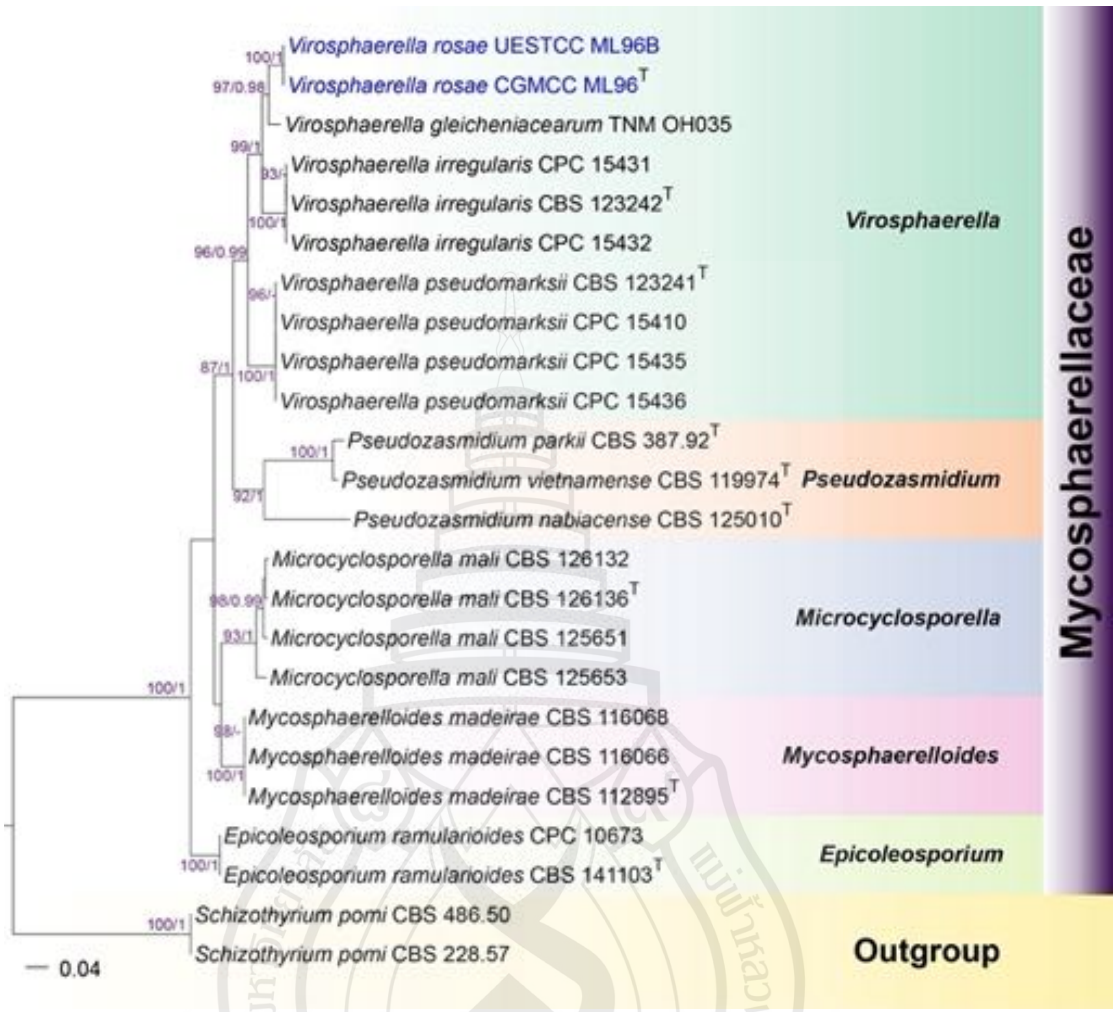


Figure 3.15 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *rpb2* sequence data of *Virosphaerella*

Figure 3.15 The tree is rooted with *Schizothyrium pomi* (CBS 228.57 and CBS 486.50). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Pleosporales Luttrell ex M.E. Barr

Acrocalymmaceae Crous & Trakun.

Type genus – *Acrocalymma* Alcorn & J.A.G. Irwin

Notes – Trakunyingcharoen et al. (2014b) established Acrocalymmaceae to accommodate a monotypic genus *Acrocalymma*. This family comprises plant pathogens, endophytes and saprobes on leaf litter, seed pods, stems or branches from various hosts in terrestrial or freshwater habitats (Alcorn & Irwin, 1987; Shoemaker et al., 1991; Zhang et al., 2012a, b; Trakunyingcharoen et al., 2014b; Jayasiri et al., 2019; Dong et al., 2020; Mortimer et al., 2021; Liu et al., 2022; Konta et al., 2023; Zhang et al., 2023a). The sexual morphs of Acrocalymmaceae are characterized by globose to oval, unilocular, ostiolate ascomata with bitunicate, 1–8-spored, cylindrical to clavate asci, and hyaline to brown or pale reddish-brown, fusiform, 1–3-septate ascospores which are surrounded by a thick, distinct mucilaginous sheath, while the asexual morphs are characterized by superficial to subepidermal, spherical to oval or pyriform, with a short to long papillate conidiomata, enteroblastic, phialidic, hyaline, subcylindrical to ampulliform conidiogenous cells with hyaline to brown, aseptate or 1–3-septate, guttulate, apex rounded, base obtuse, cylindrical to fusiform conidia, bearing flabellate or irregular, mucilaginous appendage at one or both ends (Alcorn & Irwin, 1987; Shoemaker et al., 1991; Trakunyingcharoen et al., 2014b; Dong et al., 2020; Liu et al., 2022; Li et al., 2023b).

Acrocalymma Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2): 163 (1987)

Type species – *Acrocalymma medicaginis* Alcorn & J.A.G. Irwin

Notes – Alcorn and Irwin (1987) introduced the genus *Acrocalymma* to accommodate a plant pathogen *A. medicaginis*, which was known only from its asexual morph. Currently, the genus comprises 18 species, among which only *A. arengae*, *A. chuxiongense*, *A. hongheense*, *A. medicaginis*, *A. pterocarpi* and *A. walkeri* have been reported with sexual morphs (Shoemaker et al., 1991; Jayasiri et al., 2019;

Mapook et al., 2020a; Mortimer et al., 2021; Liu et al., 2022; Konta et al., 2023; Zhang et al., 2023a).

Acrocalymma hyalinum N. Wu, Jian K. Liu & K.D. Hyde [as '*hyalina*'], Asian Journal of Mycology 6(2): 102 (2023) Figure 3.16

Index Fungorum number: IF663478; Facesoffungi number: FoF14276

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 171–220 μm wide, 160–210 μm high, solitary to gregarious, sometimes confluent, dark brown to brown, at first immersed, eventually erumpent and appearing superficial, pycnidial, oval or globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Ostiole* single. *Conidiomatal wall* 15–25 μm wide, composed of 5–6 layers of dark brown to black cells of *textura angularis*, outer 3–4 layers of brown and thicker cells, inner 1–3 layers of hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–12 × 4–6 μm ($\bar{x}$ = 11 × 5 μm; n = 30), cylindrical, sometimes slightly curved, phialidic, hyaline. *Conidia* 25–35 × 5–8 μm ($\bar{x}$ = 30 × 7 μm; n = 30), hyaline, cylindrical, with a rounded or obtuse apex and a truncate base, straight or slightly curved, aseptate, smooth-walled, guttulate, not constricted or slightly constricted at the middle, bearing a flabellate or funneled, mucilaginous appendage at apex, with an irregular or less conspicuous, mucilaginous, basal appendage.

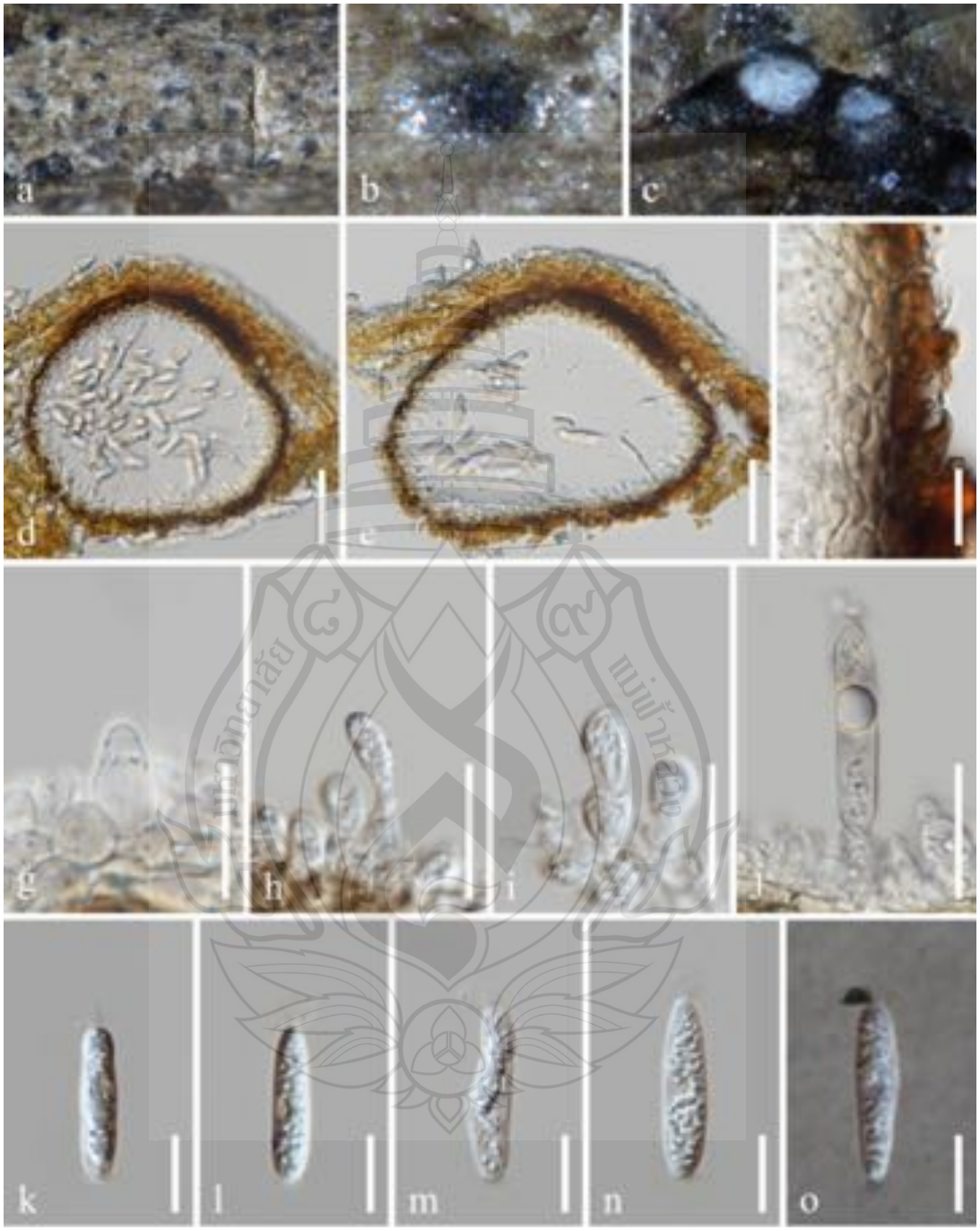
Material examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H09 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), Unidentified dead wood (Chethana et al., 2023).

Known geographical distribution – China, Thailand.

Notes – *Acrocalymma hyalinum* was described by Chethana et al. (2023) based on morphological and molecular analysis. The phylogenetic tree (Figure 3.17) showed that my new collection (HUEST H09) clustered with *A. hyalinum* (GZCC 23-0590 and

GZCC 23-0591). Therefore, I identified my collection as *A. hyalinum*, representing a new geographical and host record for the species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k–n Conidia; o Conidium stained with Indian ink. Scale bars: d, e = 50 µm; f–j = 20 µm; k–o = 10 µm.

Figure 3.16 *Acrocalymma hyalinum* (HUEST H09, new geographical and host record)

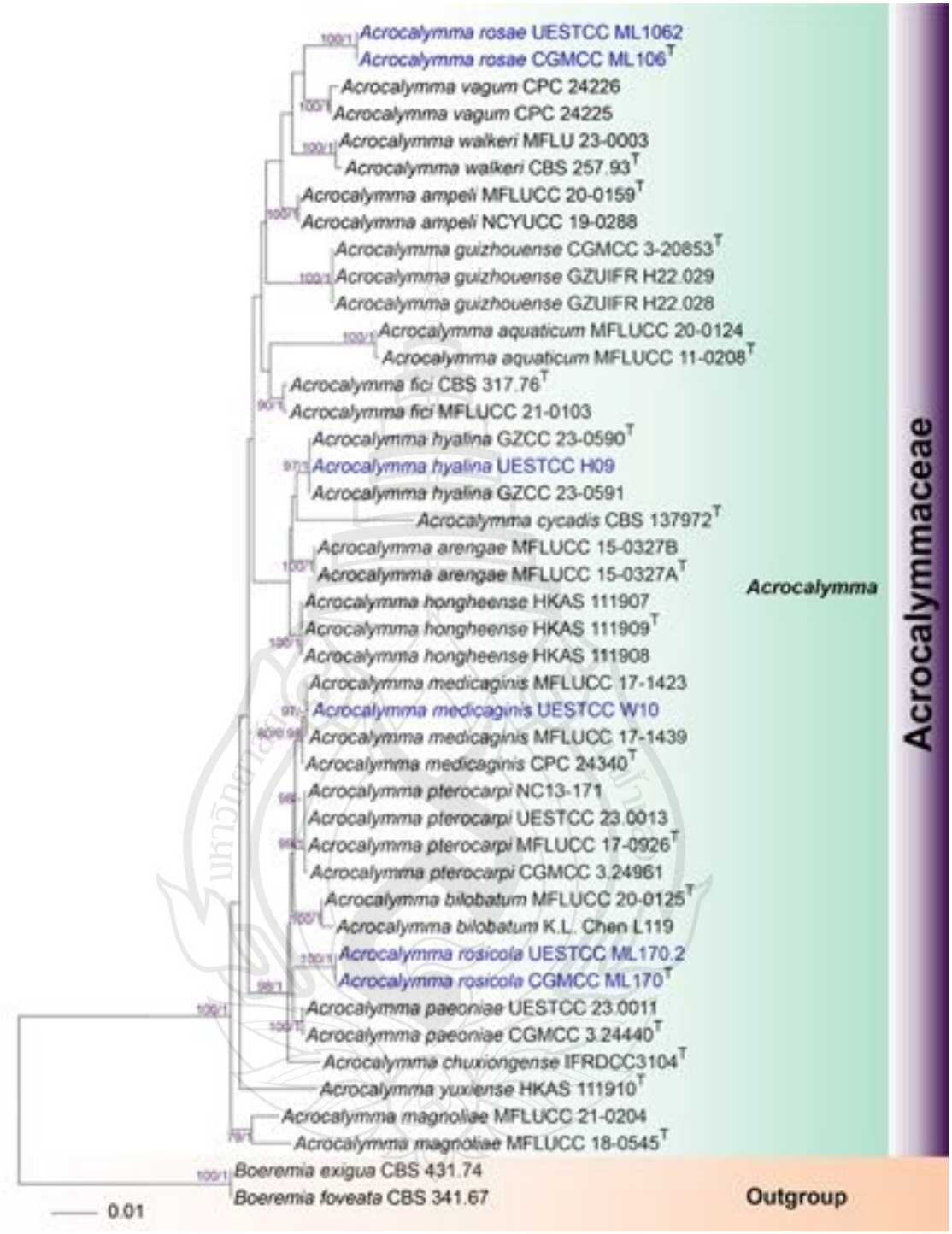


Figure 3.17 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data of *Acrocalymma*

Figure 3.17 The tree is rooted with *Boeremia exigua* (CBS 431.74) and *B. foveata* (CBS 341.67). Bootstrap values for maximum likelihood (ML) equal to or greater than 75

and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Acrocalymma medicaginis Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2): 163 (1987) Figure 3.18

Index Fungorum number: IF130085; Facesoffungi number: FoF07099

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 177–290 μm wide, 110–280 μm high, solitary to gregarious, sometimes confluent, dark brown to black, semi-immersed, visible as erumpent, unilocular, glabrous, coriaceous, depressed subglobose to conical, ostiolate. *Ostiole* 40–68 μm wide, 70–86 μm high, single, eccentric, long, subcylindrical, straight or curved. *Peridium* 12–35 μm wide, composed of dark brown to black cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide, composed of dense, numerous, filamentous, branched, septate, constricted at the septum, hyaline, trabecular pseudoparaphyses. *Asci* 75–92 × 9–11 μm ($\bar{x}$ = 84 × 9.5 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 14–25 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, guttulate, straight or slightly curved, hyaline, aseptate or 1-septate, constricted in the middle, broadly fusiform with obtuse to slightly obtuse ends, surrounded by a hyaline gelatinous sheath. Asexual morph: see Alcorn and Irwin (1987).

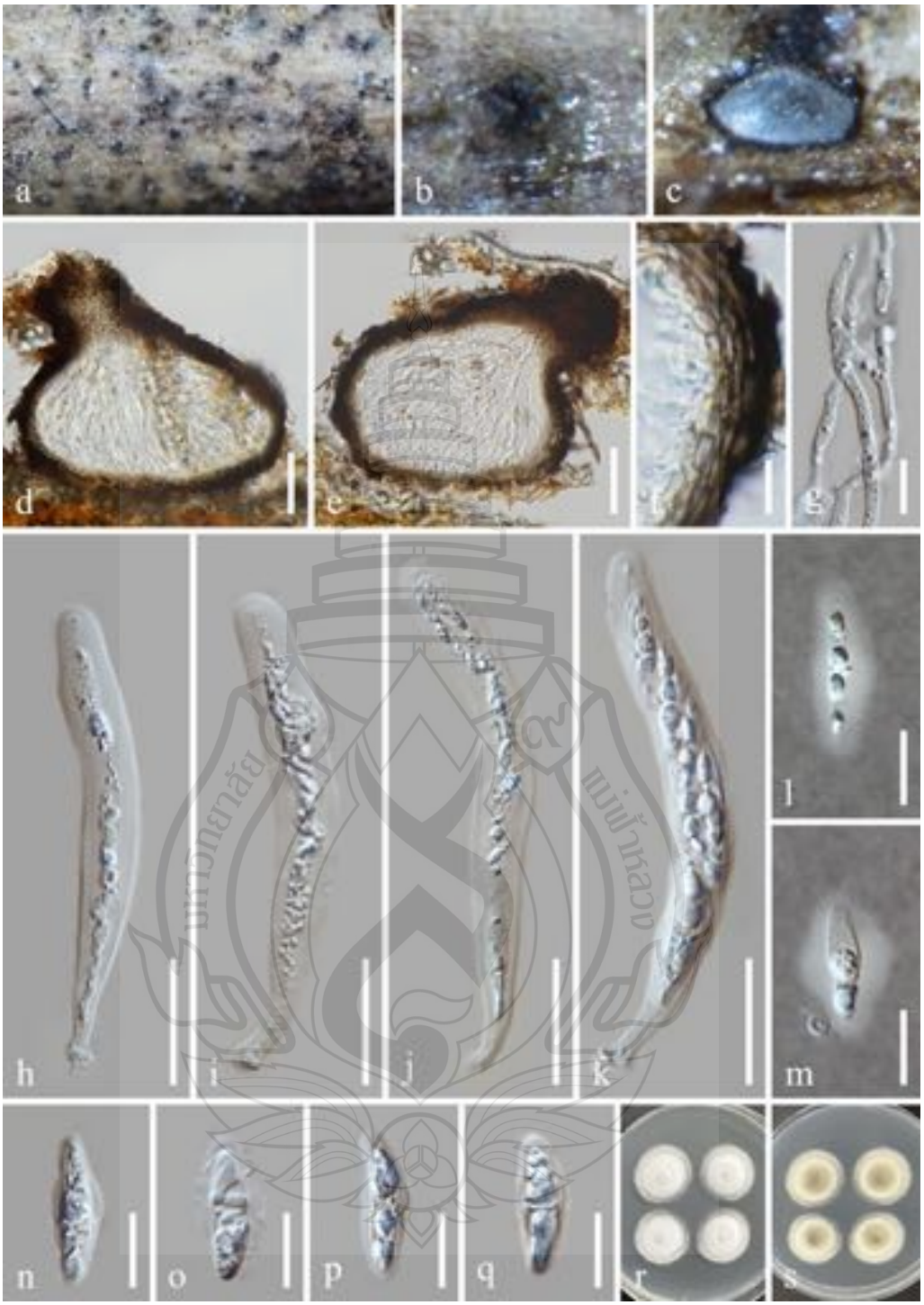
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25℃ in dark, circular, velvety, white; in reverse, grayish green to pale brown in the middle, white mycelium in the outer ring.

Material examined – CHINA, Guizhou Province, Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *Rosa roxburghii*, 6 February 2023, N. Wu, W10 (HUEST XX), living culture UESTCC XX.

Hosts – *Chromolaena odorata* (Mapook et al., 2020a), *Eleiodoxa conferta* (Pinnoi et al., 2006), *Medicago sativa* (Alcorn & Irwin, 1987; Nikandrow, 1990), *Rosa roxburghii* (present study), *Trachycarpus fortunei* (Taylor & Hyde, 2003), Unidentified herbaceous plant (Zhang et al., 2023a).

Known geographical distribution – Australia, China, Thailand.

Notes – *Acrocalymma medicaginis* was introduced by Alcorn and Irwin (1987) based on its asexual morph, which was collected from *Medicago sativa* in Australia. Nikandrow (1990) isolated *A. medicaginis* from three-year-old lucerne plants and identified it as a causal agents of crown rot of Lucerne in Australia. The sexual morph of *A. medicaginis* was subsequently reported by Mapook et al. (2020a) and Zhang et al. (2023). The phylogenetic tree (Figure 3.17) showed that my newly obtained isolate (UESTCC W10) clustered with *A. medicaginis* (CPC 24340, MFLUCC 17-1423 and MFLUCC 17-1439). Morphologically, my specimen also matches the sexual morph of *A. medicaginis* as described by Mapook et al. (2020a) and Zhang et al. (2023). Therefore, this represents a new host record of *A. medicaginis* from *Rosa roxburghii*.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l, m Ascospores stained with Indian ink. n–q Ascospores. r, s Colony on PDA, above (r), below (s). Scale bars: d, e = 50 µm; h–k = 20 µm; f, g, l–q = 10 µm.

Figure 3.18 *Acrocalymma medicaginis* (HUEST W10, new host record)

Acrocalymma rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.19

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML106

Saprobic or *parasitic* on branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 121–152 μm wide, 106–159 μm high, solitary to gregarious, dark brown to black, immersed to erumpent, pycnidial, globose to oval or pyriform, unilocular, glabrous, coriaceous, smooth-walled, short papillate, ostiolate. *Ostiole* 30–43 μm wide, 32–45 μm high, single, short-cylindrical, central. *Conidiomatal wall* 12–20 μm wide, composed of dark brown to brown cells of *textura angularis* in outer several layers, gradually merging with hyaline cells in inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–10 × 3–5 μm, hyaline, enteroblastic, phialidic, subcylindrical to ampulliform, determinate, smooth, periclinal thickening thin to thick, channel broad, collarette sometimes present, and arising from the inner layers of conidiomata. *Conidia* 14–18 × 3–5 μm ($\bar{x}$ = 16 × 4 μm; n = 30), hyaline, cylindrical to fusiform, with a rounded or obtuse apex and a truncate base, straight, aseptate, or 1–3-septate, slightly constricted at septa, smooth-walled, guttulate, bearing a flabellate, mucilaginous appendage (2–3 μm diam.) at apex, or sometimes, with an irregular or less conspicuous, mucilaginous, basal appendage.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25℃ in dark, surface rough, dry, flat, entire, white to grayish; in reverse, grayish to dull brown in the middle, white mycelium in the outer ring.

Materials examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML106 (HKAS

XX, holotype); ex-type living culture CGMCC XX; *ibid.*, ML301 (HUEST XX, paratype), living culture UESTCC XX.

Notes – In the phylogenetic analysis inferred from a combined ITS-LSU-SSU sequence dataset, *Acrocalymma rosae* (CGMCC ML106 and UESTCC ML301) was positioned as a sister taxon to *A. vagum* (CPC 24225 and CPC 24226) and *A. walkeri* (CBS 257.93 and MFLU 23-0003) (Figure 3.17). Morphologically, *A. rosae* and *A. vagum* (≡ *Rhizopycnis vagum*) share the characters in having pycnidial, superficial to subepidermal, spherical to oval or pyriform, with a short to long papilla conidiomata, enteroblastic, phialidic, hyaline, subcylindrical to ampulliform conidiogenous cells with septate, guttulate, apex rounded, base obtuse, cylindrical to fusiform conidia (Farr et al., 1998; Trakunyingcharoen et al., 2014b). However, *A. rosae* has narrower conidiomata (121–152 μm vs. 200–400 μm) and smaller conidia (14–18 × 3–5 μm vs. 18–25 × 4.5–6 μm) than *A. vagum* (Farr et al., 1998). Moreover, conidia of *A. rosae* are hyaline throughout the life cycle and bearing mucilaginous appendages at both ends, while in *A. vagum* they are hyaline to brown and without appendages. It is unable to compare the morphology between *A. rosae* and *A. walkeri* (≡ *Massarina walkeri*) since the asexual morph of the latter is unknown (Shoemaker et al., 1991; Trakunyingcharoen et al., 2014b).



Note a Host: *Rosa roxburghii*. b, c Conidiomata on natural substrate. d Vertical section of conidiomata. e–j Conidiogenous cells and developing conidia. k–o Conidia with mucoid appendages; p, q Conidia stained with Indian ink. r Germinating conidium. s, t Colony on PDA, above (s), below (t). Scale bars: d = 50 μm; e = 15 μm; f–r = 10 μm.

Figure 3.19 *Acrocalymma rosae* (HKAS ML106, holotype)

Acrocalymma rosicola N. Wu & Jian K. Liu, sp. nov. Figure 3.20

Index Fungorum number: IFXXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosicola*" refers to the host genus, *Rosa*, on which the species was isolated.

Holotype – HKAS ML170

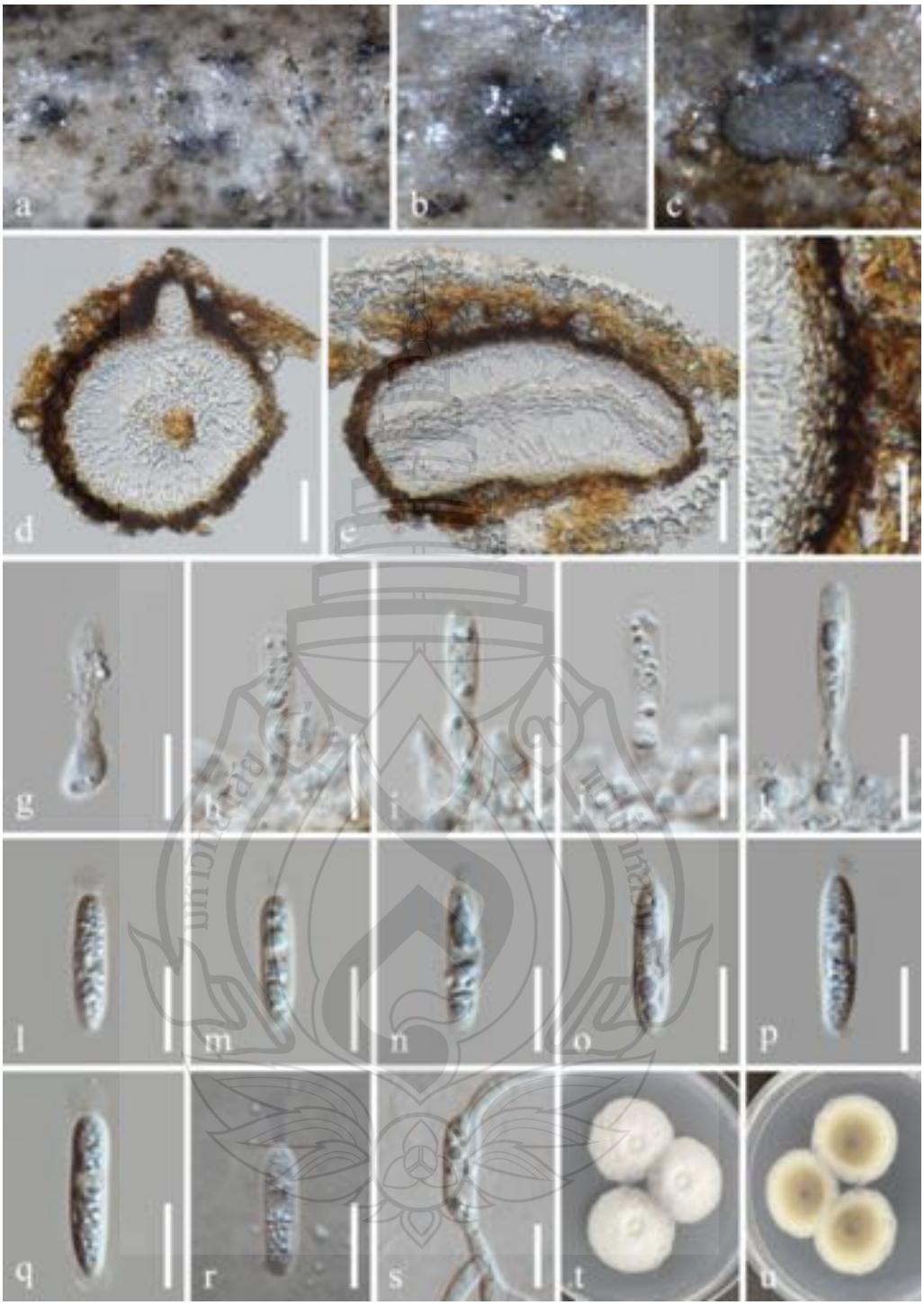
Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 165–247 μm wide, 129–222 μm high, solitary to gregarious, dark brown to black, immersed to partly erumpent, pycnidial, pyriform or irregular in shape, unilocular, glabrous, coriaceous, smooth-walled, papillate, ostiolate. *Ostiole* 35–41 μm wide, 45–59 μm high, single, cylindrical, central. *Conidiomatal wall* 16–30 μm wide, composed of several layers of dark brown to black cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–10.5 × 3–5 μm ($\bar{x}$ = 9 × 4 μm; n = 30), hyaline, enteroblastic, phialidic, cylindrical or ampulliform, smooth-walled, periclinal thickening thin to thick, and arising from the inner layers of conidiomata. *Conidia* 11–18 × 3.5–5 μm ($\bar{x}$ = 15 × 4 μm; n = 30), hyaline, cylindrical, with a rounded or obtuse apex and a truncate base, straight, aseptate or 1-septate, smooth-walled, guttulate, bearing a flabellate or funneled, mucilaginous appendage (1.5–2 μm diam.) at apex, with an irregular or less conspicuous, mucilaginous, basal appendage.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 33–35 mm diam. after two weeks at 25°C in dark, circular, flat, felty, white, velvety; in reverse, brown in the middle, white mycelium in the outer ring.

Materials examined – CHINA, Guizhou Province, Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *Rosa roxburghii*, 6 February 2023, N. Wu, ML170 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of

R. *roxburghii*, 3 February 2023, N. Wu, ML311 (HUEST XX, paratype), living culture UESTCC XX.

Notes – *Acrocalymma rosicola* was recognized as a new species, since it forms a single branch sister to *A*. *paeoniae* (CGMCC 3.24440 and UESTCC 23.0011), based on phylogenetic analysis of combined ITS, LSU and SSU sequence data (Figure 3.17). Comparisons of the ITS, LSU and SSU sequences of *A*. *rosicola* and *A*. *paeoniae* revealed 98.04% (451/460 bp, 0 gap), 99.53% (844/848 bp, 2 gaps) and 99.48% (962/967 bp, 5 gaps) similarities, respectively. Morphologically, *A*. *rosicola* is similar to *A*. *paeoniae* in having hyaline, subcylindrical conidia with mucoid appendages at both ends (Li et al., 2023b). However, *A*. *rosicola* differs from *A*. *paeoniae* by its 1-septate with age and constricted at the median and smaller conidia (12–15 × 3.5–5 μm vs. 19–21 × 4–5 μm). Thus, *A*. *rosicola* and *A*. *paeoniae* can be regarded as two different species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–k Conidiogenous cells and developing conidia. l–q Conidia; r Conidium stained with Indian ink. s Germinating conidium. t, u Colony on PDA, above (t), below (u). Scale bars: d, e = 50 µm; f = 20 µm; g–s = 10 µm.

Figure 3.20 *Acrocalymma rosicola* (HKAS ML170, holotype)

Amorosiaceae Thambug. & K.D. Hyde

Type genus – *Amorosia* Mantle & D. Hawksw.

Notes – The holomorphic family Amorosiaceae was introduced by Thambugala et al. (2015) to accommodate *Amorosia* (Mantle et al., 2006) and its sister taxon *Angustimassarina*. Subsequently, five new genera *Alfoldia* (Crous et al., 2019a), *Amorocoelophoma* (Jayasiri et al., 2019), *Neothyrostroma*, *Podocarpomyces* (Crous et al., 2019c) and *Neoangustimassarina* (Yu et al., 2022) were included in Amorosiaceae. Only *Angustimassarina* and *Neoangustimassarina* are known to exhibit sexual morphs (Yu et al., 2022; Zhang et al., 2024a).

Amorocoelophoma Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 25 (2019)

Type species – *Amorocoelophoma cassiae* Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – Based on the phylogeny inferred from combined ITS-LSU-SSU-*tef1α* sequences, Jayasiri et al. (2019) established the genus *Amorocoelophoma* to accommodate the coelomycetous fungus *A. cassiae*, which was collected from a decaying pod of *Cassia* sp. in Thailand. The genus is phylogenetically close to the type species (*Amorosia littoralis*) of the family Amorosiaceae (Thambugala et al., 2015; Jayasiri et al., 2019). Ariyawansa et al. (2020a) introduced *A. camelliae*, which was associated with leaf lesions of *Camellia sinensis*. However, it was subsequently transferred to *Neoamorocoelophoma* (as *N. camelliae*) supported by a multi-gene phylogeny including ITS, LSU, SSU, *rpb2*, and *tef1α* sequences (Lu et al., 2025). *Amorocoelophoma neoregeliae* was isolated from leaf spots of *Neoregelia* sp. in New Zealand (Crous et al., 2021a). More recently, *A. sinensis* was isolated from soil in China by Zhang et al. (2024b). *Amorocoelophoma* species are characterized by immersed to semi-immersed conidiomata, aseptate, ampulliform to cylindrical conidiogenous cells and hyaline, aseptate, straight, guttulate, cylindrical to subcylindrical conidia with rounded ends (Jayasiri et al., 2019; Ariyawansa et al., 2020a; Crous et al., 2021a; Zhang et al., 2024b). The sexual morph remains unknown in this genus.

Amorocoelophoma guizhouensis N. Wu & Jian K. Liu, sp. nov. Figure 3.21

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*guizhouensis*" refers to Guizhou Province where the fungus was collected.

Holotype – HKAS ML100

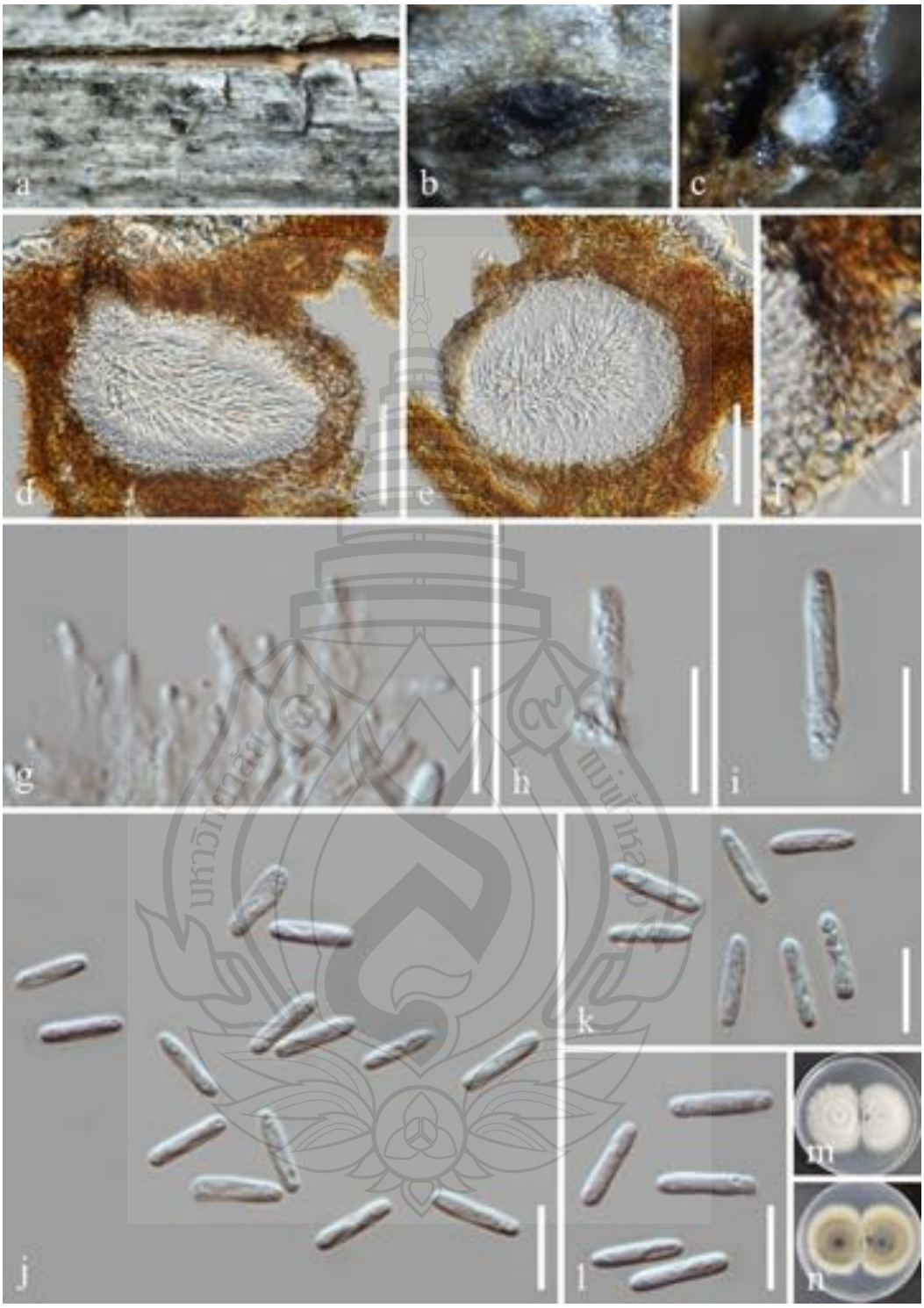
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 125–158 μm wide, 94–115 μm high, scattered or gregarious, semi- immersed to superficial, brown, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, papillate, ostiolate. *Ostiole* single, straight or curved, central or laterally located. *Conidiomatal wall* 10–18 μm wide, composed of thick-walled, brown cells of *textura angularis*, becoming hyaline cells towards inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 1.5–3 μm ($\bar{x}$ = 5 × 2.6 μm; n = 30), enteroblastic, phialidic, hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical or lageniform. *Conidia* 8–10 × 2–2.5 μm ($\bar{x}$ = 9 × 2.2 μm; n = 30), hyaline, aseptate, cylindrical to subcylindrical, rounded at both ends, straight, guttulate concentrated at ends.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 35–37 mm diam. after two weeks at 25℃ in dark, circular to irregular, dense, flat to slightly raised, dry, white; in reverse, yellowish brown in the middle and white at the margin.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML100 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – *Amorocoelophoma cassiae* was introduced as the type species of the genus *Amorocoelophoma* by Jayasiri et al. (2019) based on the way of fungus sporulating in culture, which was collected from a fallen pod of *Cassia* sp. (Fabaceae) in Thailand. In the phylogenetic analysis (Figure 3.22), *A. guizhouensis* formed a sister

clade to *A*. *cassiae* with a moderate support (78% MLBS/1.0 PP). Morphologically, *A*. *guizhouensis* differs from *A*. *cassiae* by its thinner conidiomatal wall (10–18 μm vs. 17–22 μm) and smaller conidiogenous cells (4–6 × 1.5–3 μm vs. 6–8 × 2.3–3.7 μm) and conidia (8–10 × 2–2.5 μm vs. 9–11 × 2–3 μm) (Jayasiri et al., 2019). Therefore, I introduced *A*. *guizhouensis* as a novel species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j–l Conidia. m, n Colony on PDA, above (m), below (n). Scale bars: d, e = 50 μm; f–l = 10 μm.

Figure 3.21 *Amorocoelophoma guizhouensis* (HKAS ML100, holotype)

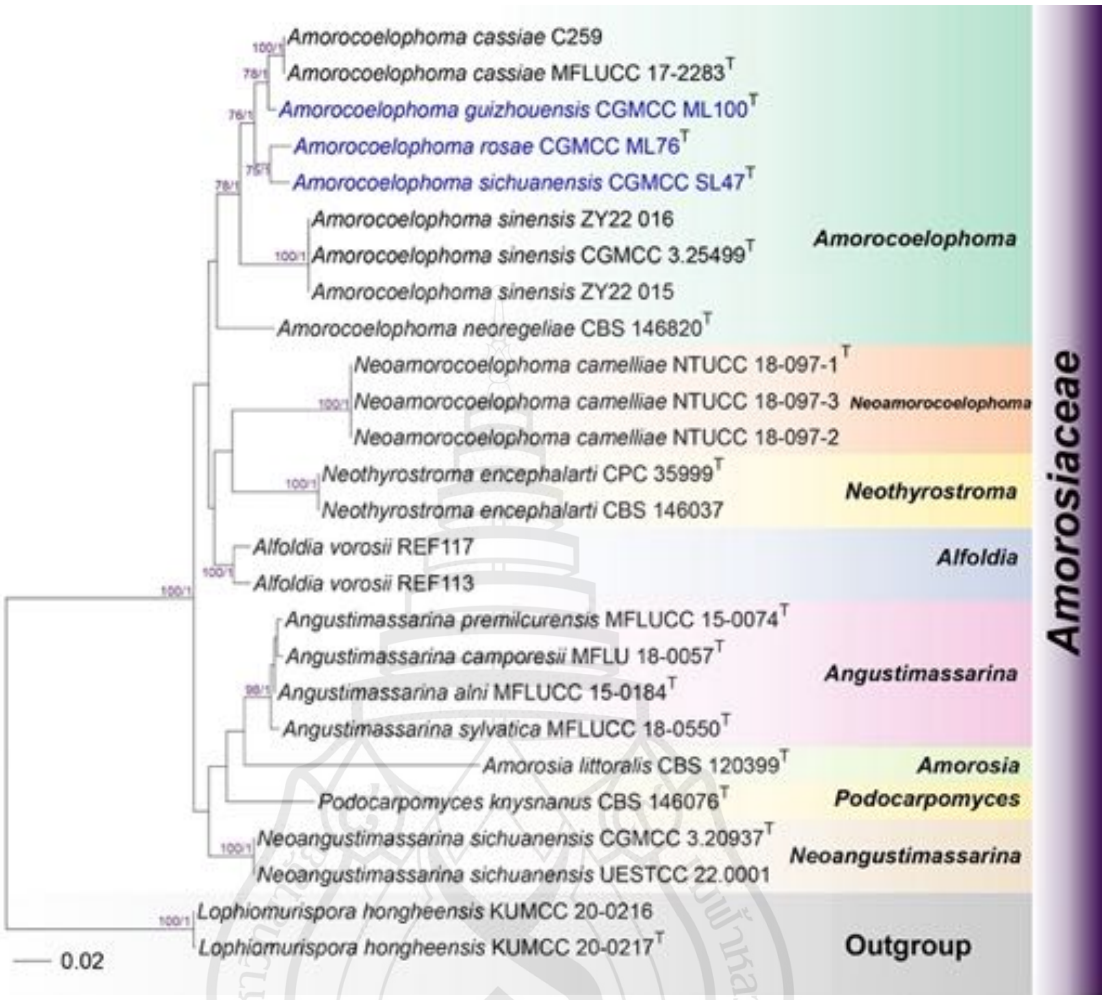


Figure 3.22 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Amorosiaceae

Figure 3.22 The tree is rooted with *Lophiomurispora hongheensis* (KUMCC 20-0216 and KUMCC 20-0217). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Amorocoelophoma rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.23

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML76

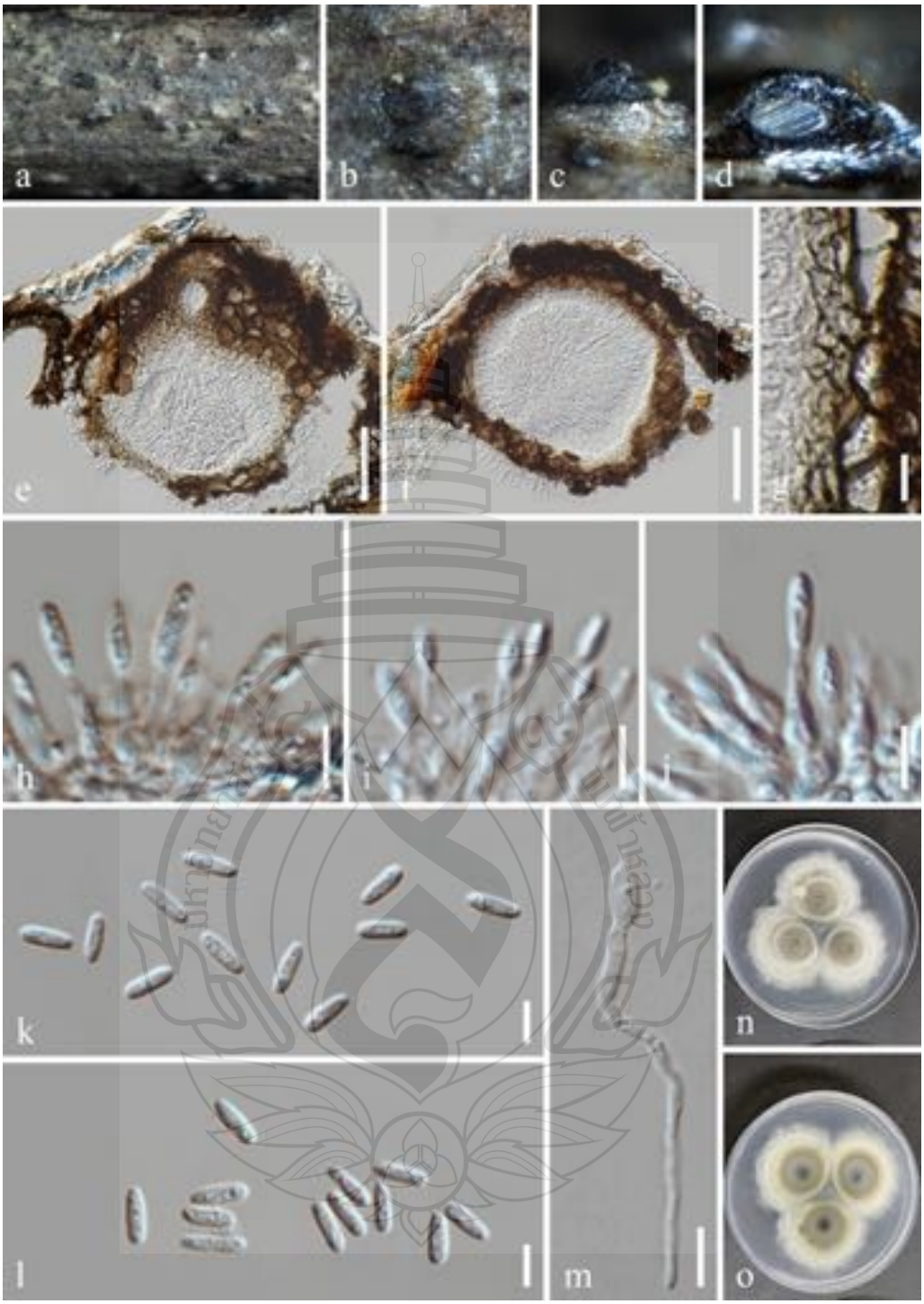
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 185–230 μm wide, 140–250 μm high, mostly solitary, occasionally gregarious, black to dark brown, immersed to partly erumpent through bark, visible as black dots on the host, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, ostiolate. *Ostiole* single, short, central. *Conidiomatal wall* 25–40 μm wide, composed of several layers of small, flattened, brown to dark brown cells, towards the inside lightly pigmented, arranged with *textura angularis* cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7.5–15 × 2.2–4.5 μm ($\bar{x}$ = 10.5 × 3.4 μm; n = 30), hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical or lageniform, and arising from the inner layers of conidiomata. *Conidia* 7.5–10 × 2–3.6 μm ($\bar{x}$ = 8.4 × 2.8 μm; n = 30), hyaline, aseptate, cylindrical to subcylindrical, rounded at both ends, straight, guttulate.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 33–35 mm diam. after two weeks at 25°C in dark, circular to irregular, dense, flat to slightly raised, dry, dark green mycelium in the middle and white mycelium in the outer ring; in reverse, yellowish brown in the middle and white at the margin.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML76 (HKAS XX, **holotype**); ex-type living culture CGMCC XX.

Notes – *Amorocoelophoma rosae* clusters with *A. sichuanensis* in my phylogenetic tree (Figure 3.22) but can be recognized as distinct species with 2.9%

(14/467) nucleotide differences in the ITS region. These two species share similar morphological characters, including hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical conidiogenous cells and hyaline, aseptate, cylindrical to subcylindrical conidia. However, *A*. *rosae* can be distinguished from *A*. *sichuanensis* by its longer conidiogenous cells (7.5–15 × 2.2–4.5 µm vs. 5.5–7.3 × 2.3–3.4 µm) and larger conidia (7.5–15 × 2.2–4.5 µm vs. 5.2–7 × 1.8–2.5 µm). I followed the guidelines of Jeewon and Hyde (2016) when introducing *A*. *rosae* as a new species.



Note a–c Conidiomata on natural substrate. d–f Vertical sections of conidiomata. g Conidiomatal wall. h–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: e, f = 50 μm; g, m = 10 μm; h–l = 5 μm.

Figure 3.23 *Amorocoelophoma rosae* (HKAS ML76, holotype)

Amorocoelophoma sichuanensis N. Wu & Jian K. Liu, sp. nov. Figure 3.24

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*sichuanensis*" refers to Sichuan Province where the fungus was collected.

Holotype – HKAS SL47

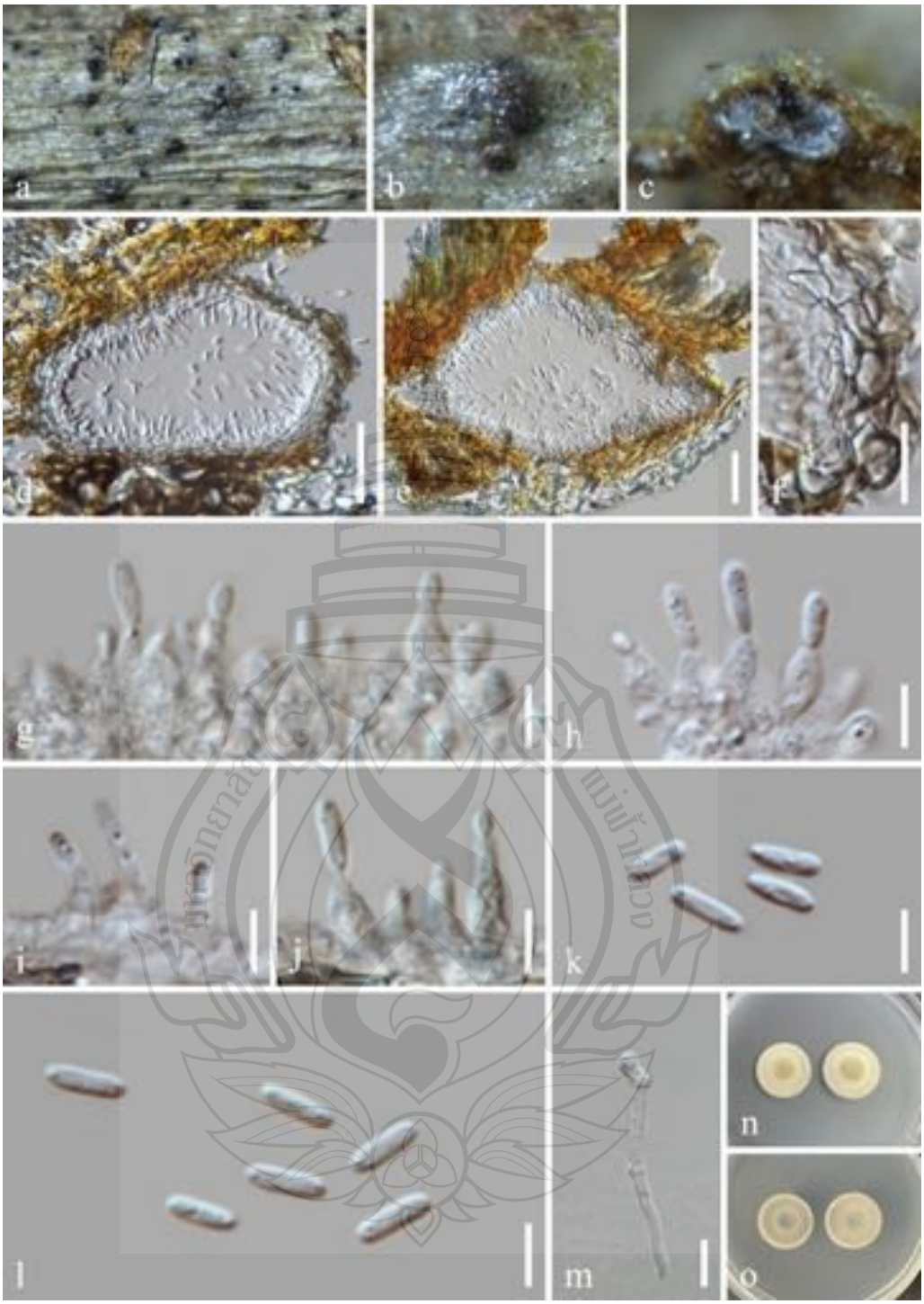
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 125–210 μm wide, 70–120 μm high, solitary to gregarious, sometimes confluent, dark brown to black, at first immersed, eventually erumpent and appearing superficial, visible as black dots on the host, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, ostiolate. *Ostiole* single, short, central. *Conidiomatal wall* 9–19 μm wide, composed of thick-walled, hyaline to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–7.3 × 2.3–3.4 μm ($\bar{x}$ = 6 × 3 μm; n = 30), hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical, and arising from the inner layers of conidiomata. *Conidia* 5.2–7 × 1.8–2.5 μm ($\bar{x}$ = 6.4 × 2 μm; n = 30), hyaline, cylindrical to subcylindrical, rounded at both ends, straight or slightly curved, smooth-walled, aseptate, guttules concentrated at ends.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, dense, flat to slightly raised, dry, pale brown; in reverse, yellowish brown in the middle and white at the margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL47 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – The morphology of *Amorocoelophoma sichuanensis* fits well with the asexual morph of other species in this genus. I recognize my isolate (CGMCC SL47) as a novel species, since it forms a sister branch to *A. rosae* (CGMCC ML76) in the phylogenetic tree (Figure 3.22). Morphologically, *A. sichuanensis* differs from *A. rosae* in

the size of conidiogenous cells and conidia. It is interesting to note that *A*. *guizhouensis*, *A*. *rosae* and *A*. *sichuanensis* were isolated from *Rosa roxburghii* and share coelomycetous asexual morphs characterized by hyaline, aseptate, cylindrical to subcylindrical conidia with guttules concentrated at both ends.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 30 μm; f, m = 10 μm; g–l = 5 μm.

Figure 3.24 *Amorocoelophoma sichuanensis* (HKAS SL47, holotype)

Anteagloniaceae K.D. Hyde, J.K. Liu & A. Mapook

Type genus – *Anteaglonium* Mugambi & Huhndorf

Notes – Hyde et al. (2013) reappraised the genus *Anteaglonium*, and established the family Anteagloniaceae to accommodate *Anteaglonium* as the type genus, based on a multigene phylogeny and previous studies (Mugambi & Huhndorf, 2009a; Schoch et al., 2009; Zhang et al., 2012b, 2023). Subsequently, three genera were included into this family, viz. *Flammeascoma*, *Neolophiotrema* and *Purpureofaciens* (Liu et al., 2015b; Dong et al., 2020; Ren et al., 2021; Hyde et al., 2024).

Anteaglonium Mugambi & Huhndorf, Syst. Biodiv. 7(4): 460 (2009)

Type species – *Anteaglonium abbreviatum* (Schwein.) Mugambi & Huhndorf

Notes – Mugambi and Huhndorf (2009a) introduced a monophyletic hysterothecial group within Pleosporales to accommodate *Anteaglonium abbreviatum* (≡ *Glonium abbreviatum*), *A. globosum*, *A. latirostrum* and *A. parvulum* (≡*G. parvulum*). Members of *Anteaglonium* are usually found on dead plant substrates. Index Fungorum lists twelve epithets of *Anteaglonium* (2025, June).

Anteaglonium rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.25

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL35

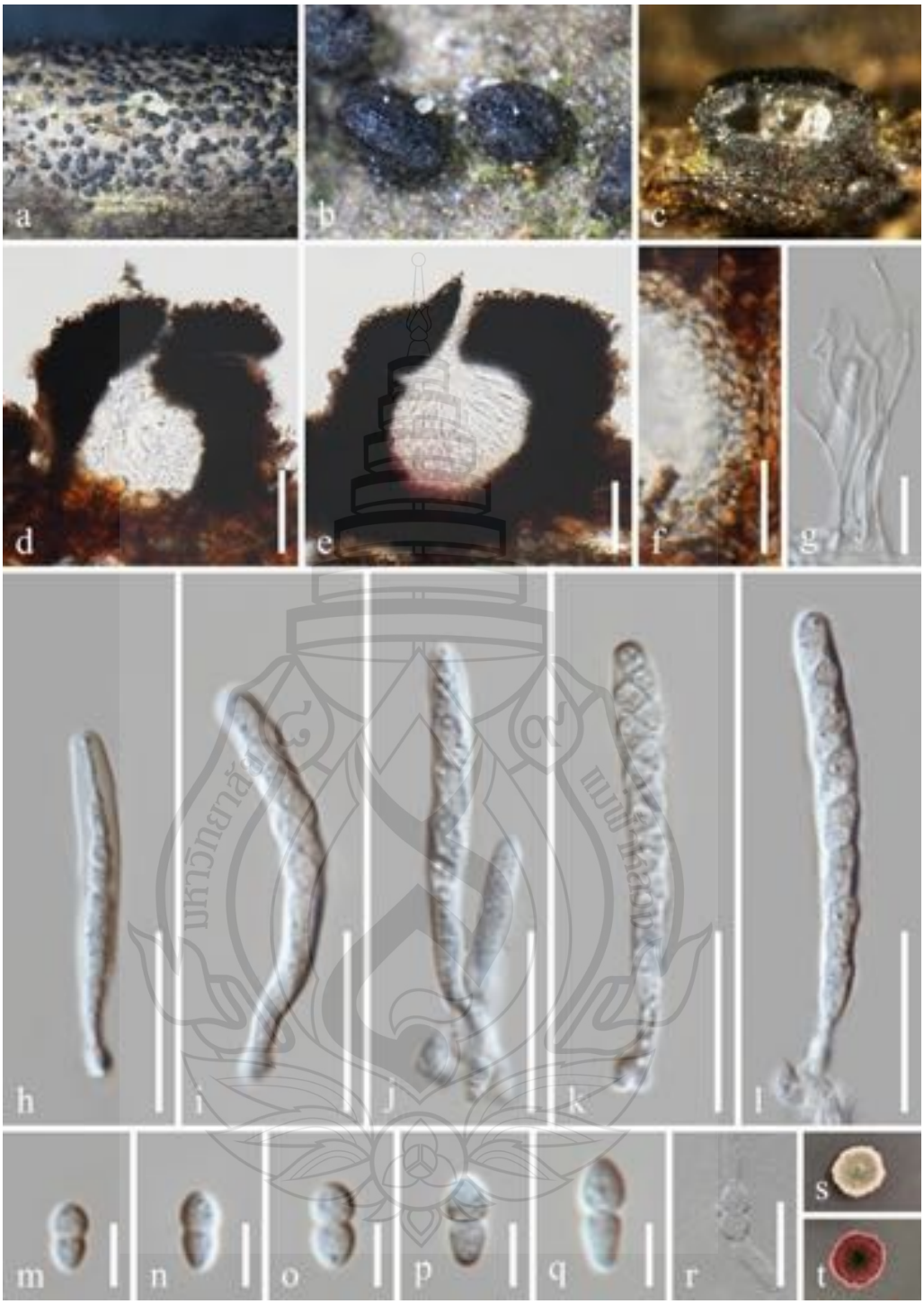
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* hysterothecioid, solitary to gregarious or confluent, erumpent to superficial with base immersed, black, glabrous, coriaceous to carbonaceous, oval or navicular to elongated with obtuse ends, opening by a longitudinal slit, subglobose in vertical section, 160–200 µm wide, 135–200 µm high. *Peridium* 45–60 µm wide, carbonaceous and brittle when dry, wider in the middle and at the apical end, and at the base thinner, composed of thick-walled brown cells of *textura epidermoidea* in a thin section. *Pseudoparaphyses* 1.5–2 µm wide, filiform, dense, septate, branched and anastomosed,

embedded in a gelatinous matrix. *Asci* 47–58 × 4–5.5 µm ($\bar{x}$ = 52 × 5 µm; n = 20), 8-spored, bitunicate, cylindrical to clavate, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 6–9.2 × 2.7–3.8 µm ($\bar{x}$ = 7.7 × 3.4 µm; n = 30), obliquely to irregularly uniseriate, hyaline, fusoid with subobtuse apices, straight, 1-septate, strongly constricted at the septum, upper cell slightly wider than lower cell, granular, small guttulate, smooth-walled, without a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25℃ in dark, circular, flat, velvety to somewhat viscid, olive green in central, yellowish white at the edge; in reverse, dark brown to black in the center, red towards the margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL35 (HKAS XX, holotype); ex-type living culture CGMCC XX; ibid., SL103 (HUEST XX, paratype), living culture UESTCC XX.

Notes – *Anteaglonium rosae* was isolated from dead branches of *Rosa roxburghii*. In the phylogenetic tree inferred from ITS, LSU, SSU, *tef1α* and *rpb2* gene regions, *A. rosae* (CGMCC SL35 and UESTCC SL103) clustered within *Anteaglonium*, formed a sister group to *A. lusitanicum* (AMI-SPL647) (Figure 3.26). *Anteaglonium rosae* resembles *A. lusitanicum* in having black ascomata with a longitudinal slit and hyaline, 1-septate, fusoid ascospores (Tan et al., 2022). However, the asci of *A. lusitanicum* are larger than *Anteaglonium rosae* ((51.7–)53.4–66.8–86.1(–90) × 4–4.7–5.6(–5.7) µm vs. 47–58 × 4–5.5 µm). In addition, *A. rosae* differs from *A. lusitanicum* by 18 bp (461/479 bp, 3 gaps) in the ITS sequence. Therefore, I recognize *A. rosae* as a new species following the guidelines of Jeewon and Hyde (2016).



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 50 μm; f–l, r = 20 μm; m–q = 5 μm.

Figure 3.25 *Anteaglonium rosae* (HKAS SL35, holotype)

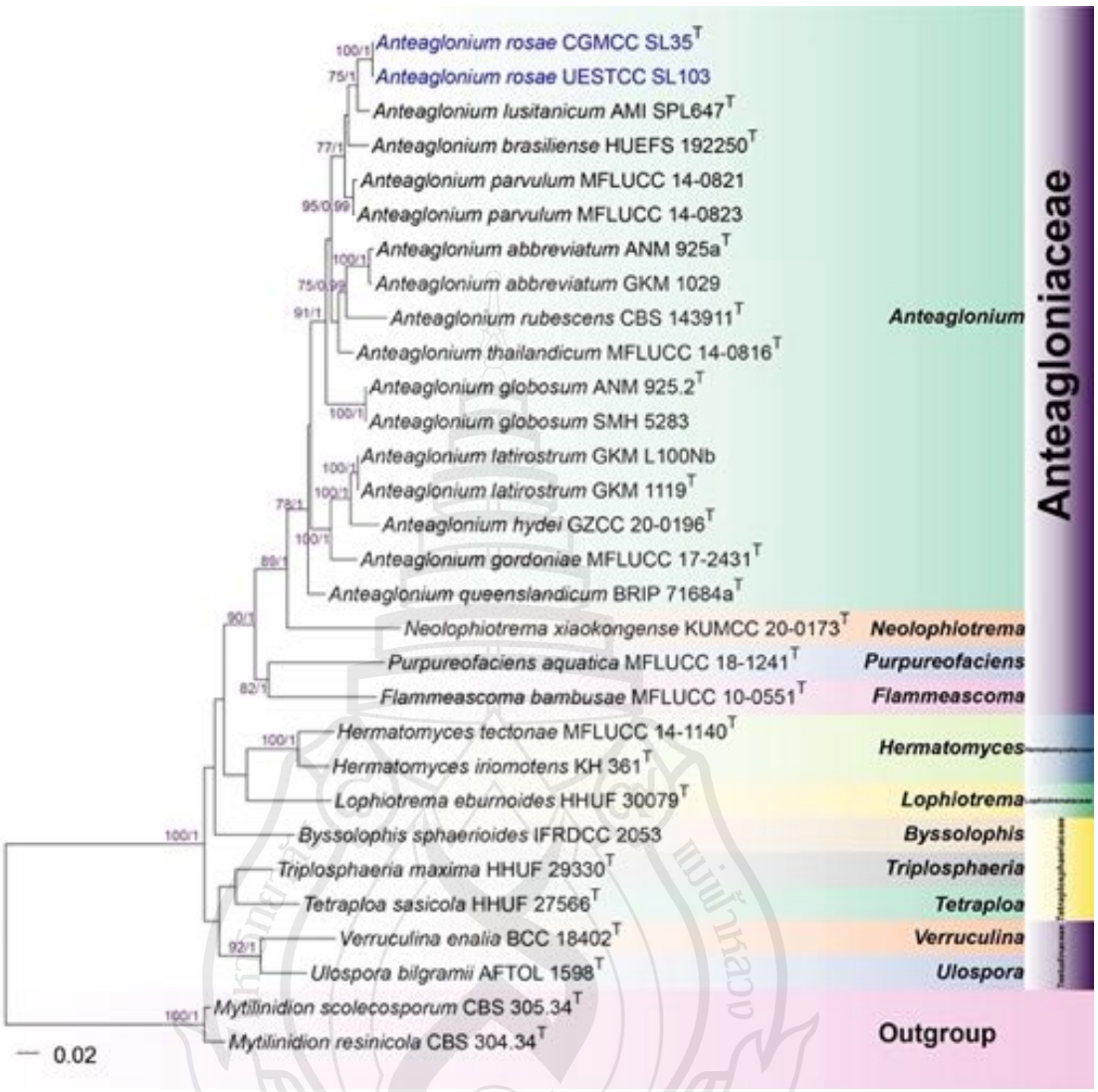


Figure 3.26 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Anteagloniaceae

Figure 3.26 The tree is rooted with *Mytilinidion resinicola* (CBS 304.34) and *M. scolecosporum* (CBS 305.34). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Bambusicolaceae D.Q. Dai & K.D. Hyde

Type genus – *Bambusicola* D.Q. Dai & K.D. Hyde

Notes – Bambusicolaceae was established by Hyde et al. (2013) to accommodate *Bambusicola* as the type genus. Currently, Bambusicolaceae comprises five genera: *Bambusicola*, *Corylicola*, *Leucaenicola*, *Neopalmiascoma* and *Palmiascoma* (Wijayawardene et al., 2022; Hyde et al., 2024). Morphologically, the sexual morphs are characterized by having immersed to erumpent, globose to subglobose ascomata, cylindrical, bitunicate asci with a well-developed ocular chamber and short furcate pedicel, and fusiform, hyaline or yellowish to brown, didymosporous ascospores with or without a gelatinous sheath (Hongsanan et al., 2020a; Wijesinghe et al., 2020). The asexual morphs are characterized by pycnothyrial conidiomata, and holoblastic, annelidic or phialidic conidiogenous cells, producing cylindrical, globose or oblong to ellipsoidal, pale to dark brown, aseptate or 1–3-septate conidia (Wijesinghe et al., 2020; Phukhamsakda et al., 2022). The exterior appearance of ascomata, as well as the shape of ascospores and/or conidia, are diagnostic features to distinguish genera within this family (Hongsanan et al., 2020; Wijesinghe et al., 2020; Phukhamsakda et al., 2022).

Corylicola Corylicola Wijes., Camporesi, Yong Wang bis & K.D. Hyde, Biodiversity Data Journal 8(e55957): 7 (2020)

Type species – The genus *Corylicola* was introduced by Wijesinghe et al. (2020) and typified by *C. italica*. Zhang et al. (2023) introduced the second species, *C. hydei*, which is phylogenetically closely related to *C. italica*, but is obviously different from *C. italica* in having smooth ascospores and smaller asci and spores. Subsequently, Zhang et al. (2024a) recovered type species *C. italica* from *Trachycarpus fortunei* in China and observed verrucose ornamented ascospores surrounded by a thin gelatinous sheath. This genus is characterized by dark brown to black, immersed to semi-immersed, subglobose to pyriform ascomata, bitunicate, short pedicellate, cylindric-clavate asci and hyaline to yellowish or brown, 1-septate, verrucose, fusiform ascospores, with or

without gelatinous sheath; solitary to gregarious, semi-immersed to superficial, globose to subglobose conidiomata, holoblastic, phialidic, ampulliform, hyaline to yellowish or pale brown, aseptate conidiogenous cells with hyaline to pale brown, aseptate, guttulated, globose or oblong to ellipsoid conidia (Wijesinghe et al., 2020; Zhang et al., 2023a, 2024a).

Corylicola italica Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde, Biodiversity Data Journal 8(e55957): 8 (2020) Figure 3.27; Figure 3.28

Index Fungorum number: IF 512742; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 170–266 µm wide, 140–170 µm high, solitary, dark brown to black, immersed to semi-immersed, subglobose to pyriform, unilocular, glabrous, coriaceous, short papillate, ostiolate. *Ostiole* 30–50 µm wide, 50–65 µm high, single, short-cylindrical, central or eccentric, filled with hyaline periphyses. *Peridium* 13–17 µm wide, composed of thick-walled, brown cells of *textura angularis* on the exterior, gradually merging with hyaline cells of *textura prismatica* in inner layers. *Hamathecium* 1.5–2.5 µm wide, comprising of numerous, filamentous, branched, septate, not constricted at the septa, hyaline pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 43–58 × 7–9 µm ($\bar{x}$ = 49 × 8 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 9–14 × 3.3–4.6 µm ($\bar{x}$ = 11.8 × 4 µm; n = 30), uniseriate or overlapping biseriate, fusiform, initially hyaline, guttulate, aseptate, becoming yellowish to brown at maturity, slightly curved, 1-septate, slightly constricted at septum, upper cell slightly wider than lower cell, verrucose. Asexual morph: Coelomycetous. *Conidiomata* 130–220 µm wide, 105–165 µm high, pycnidial, solitary to gregarious or confluent, black, immersed to partly erumpent, globose to subglobose, unilocular or multilocular, glabrous, coriaceous, ostiolate. *Ostiole* 17–23 µm wide, 35–45 µm high, single, short-cylindrical, eccentric. *Conidiomatal wall* 12–20 µm wide, composed of thick-walled, hyaline to brown *textura angularis* cells merged

with the plant tissue outwardly. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Conidiogenous cells* 3–11 × 2–3.5 μm ($\bar{x}$ = 5.6 × 2.8 μm; n = 20), hyaline to pale brown, holoblastic, phialidic, ampulliform to subcylindrical, smooth, arising from the inner layer of the pycnidium wall. *Conidia* 4–5 × 2–3 μm ($\bar{x}$ = 4.7 × 2.5 μm; n = 30), globose to ellipsoid, rounded or obtuse ends, hyaline to pale brown, aseptate, smooth, guttulate.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies growing on PDA reached 25–27 mm in diam. after three weeks at 25℃ in the dark, circular, dry, dense, flat, whitish-gray; in reverse, pale brown with a milky white margin. Conidia germinated on PDA within 12 h and germ tubes produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 ℃ in the dark, circular, dry, milky white to yellowish; in reverse, pale brown in the centre and yellow at the margin.

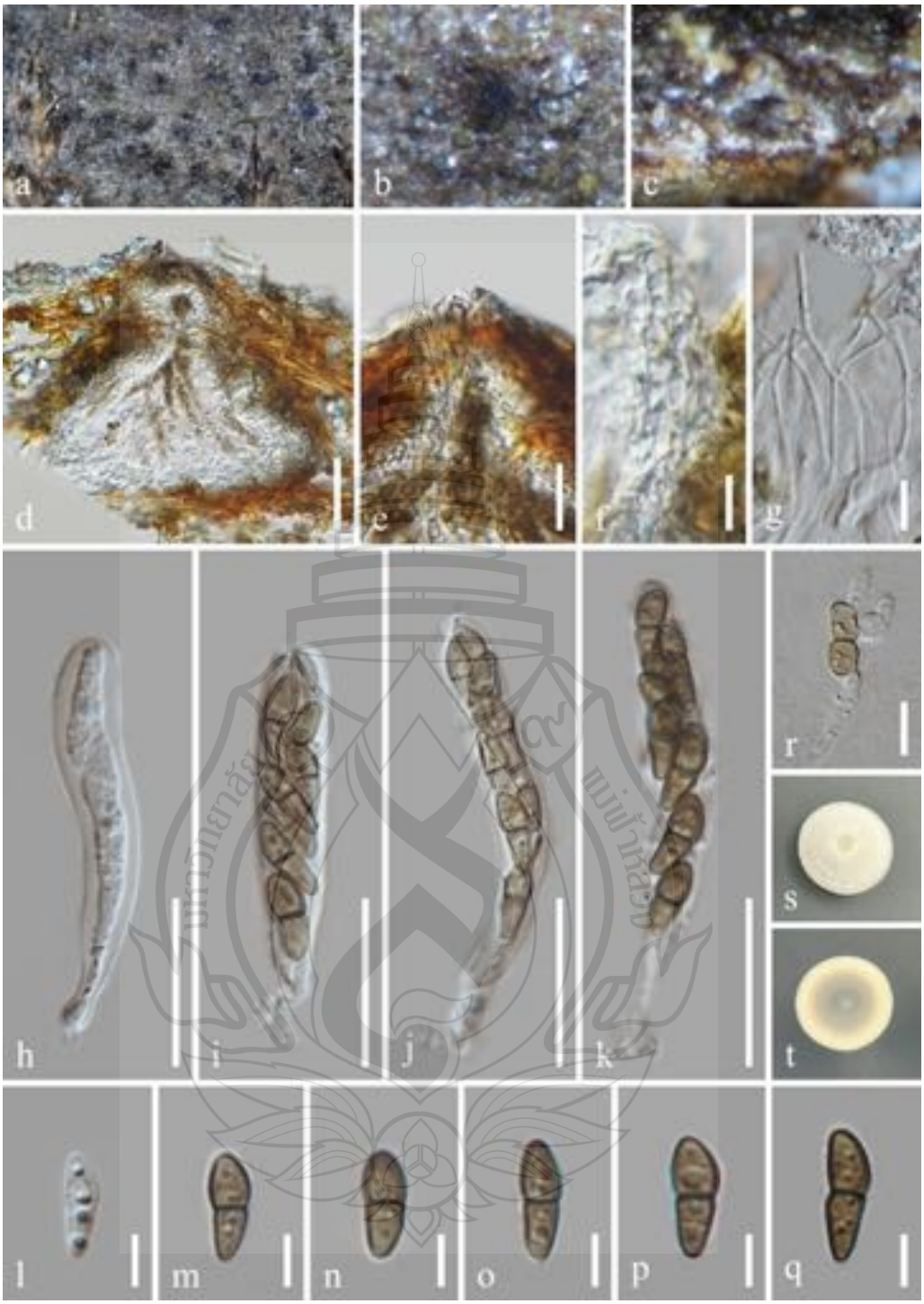
Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL02 (HUEST XX), living culture UESTCC XX; *ibid.*, SL66 (HUEST XX), living culture UESTCC XX; *ibid.*, SL34 (HUEST XX), living culture UESTCC XX; *ibid.*, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H11 (HUEST XX), living culture UESTCC XX; *ibid.*, H31 (HUEST XX), living culture UESTCC XX; *ibid.*, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML04 (HUEST XX), living culture UESTCC XX; *ibid.*, ML21 (HUEST XX), living culture UESTCC XX; *ibid.*, Guiyang City, Xifeng County, elevation 1,233 m, 27° 5′ 24″ N, 106° 45′ 36″ E, on decaying branches of *R. roxburghii*, Tratt., 6 February 2023, N. Wu, W16 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL54 (HUEST XX), living culture UESTCC XX; *ibid.*,

Danxia Town, Danxia Mountain, elevation 1,760 m, 25° 39′ 46″ N, 104° 37′ 28″ E, on branches of *R. roxburghii* Tratt., 9 July 2022, N. Wu, GL116 (HUEST XX), living culture UESTCC XX; *ibid.*, GL144 (HUEST XX), living culture UESTCC XX.

Hosts – *Corylus avellana* (Wijesinghe et al., 2020), *Rosa roxburghii* and *R. sterilis* (present study), *Rubus* sp. (Rosaceae) (Jayawardena et al., 2022), *Trachycarpus fortunei* (Zhang et al., 2024a).

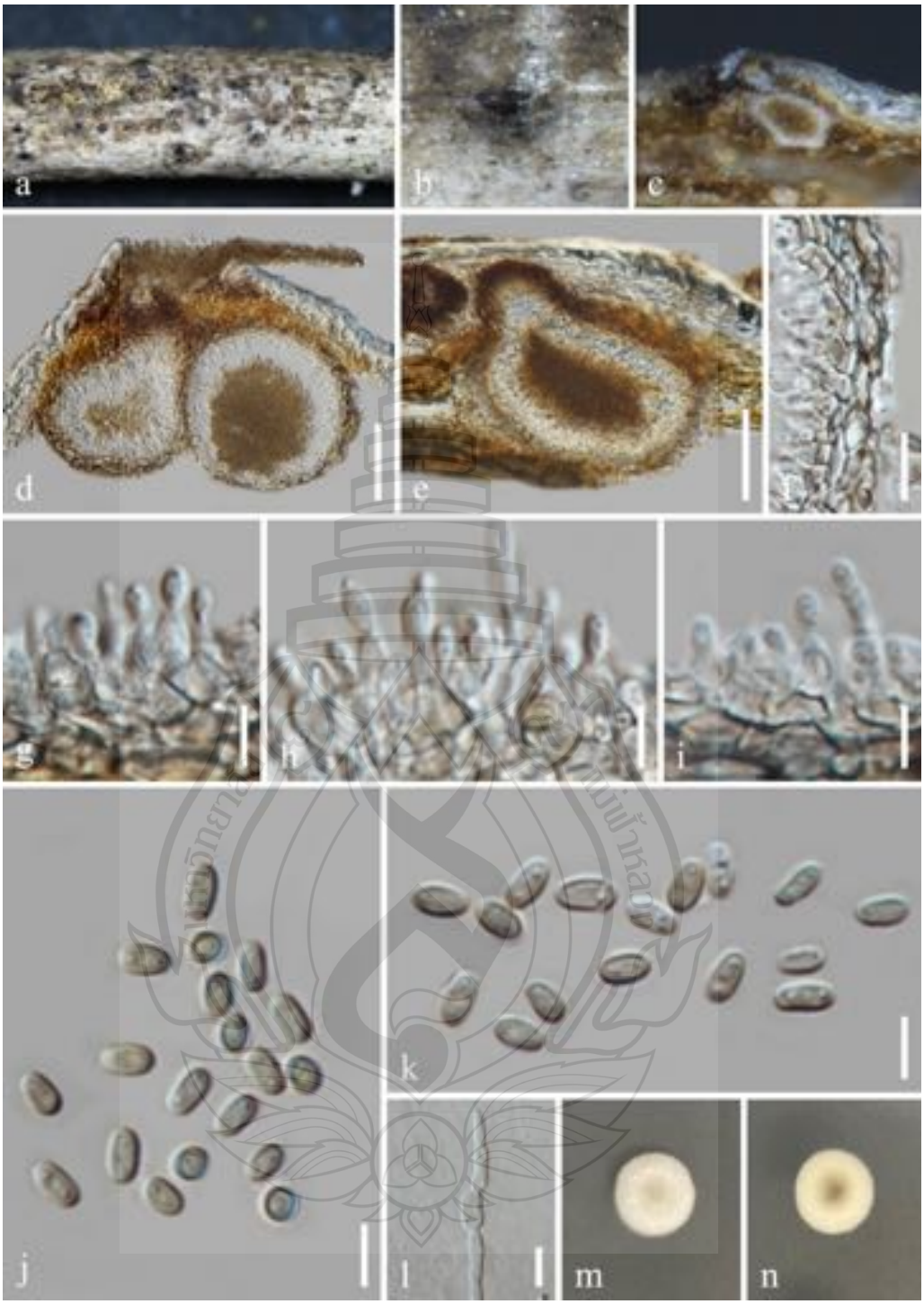
Known geographical distribution – China, Italy.

Notes – Wijesinghe et al. (2020) introduced *Corylicola italica* from a dead hanging branch of *Corylus avellana* in Italy, which was represented by both sexual morph (on the natural substrate) and asexual morph (on PDA). In this study, I isolated the asexual and sexual morphs of a *Corylicola* species from *Rosa roxburghii* and *R. sterilis*. My collections are similar to *C. italica* in the morphology of asci, ascospores, conidiophores and conidia with comparable dimensions. Multi-locus phylogenetic analysis showed that my collection (UESTCC SL02, UESTCC SL66, UESTCC SL34, UESTCC H11, UESTCC H31, UESTCC ML04, UESTCC ML21, UESTCC GL116, UESTCC GL144, UESTCC W16 and UESTCC CL54) is identical and clustered with *C. italica* (MFLUCC 20-0111 and MFLU 19-0500) (Figure 3.29). Therefore, I identify my collection as *C. italica*, with *Rosa roxburghii* and *R. sterilis* representing new host records.



Note a–c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d = 50 µm; e, h–k = 20 µm; f, g, r = 10 µm; l–q = 5 µm.

Figure 3.27 *Corylicola italica* (HUEST SL02; sexual morph, new host record)



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j, k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: d, e = 50 μm; f, l = 10 μm; g–k = 5 μm.

Figure 3.28 *Corylicola italica* (HUEST SL66; asexual morph, new host record)

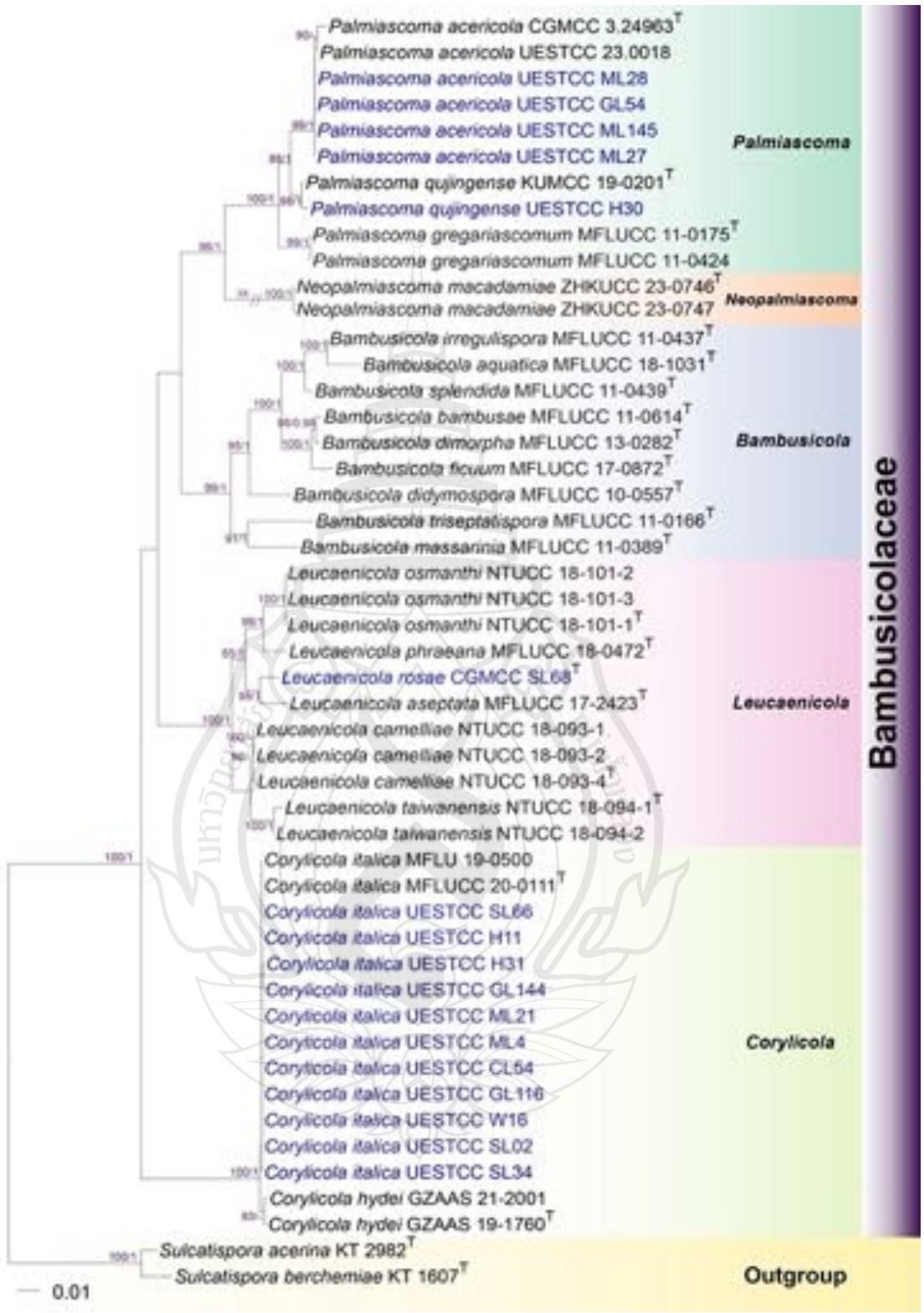


Figure 3.29 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Bambusicolaceae

Figure 3.29 The tree is rooted with *Sulcatispora acerina* (KT 2982) and *S. berchemiae* (KT 1607). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Leucaenicola Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 37 (2019)

Type species – *Leucaenicola aseptata* Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – *Leucaenicola* was introduced by Jayasiri et al. (2019) to accommodate *Leucaenicola aseptata* as the type species. The genus is characterized by globose to subglobose, ostiolate conidiomata, enteroblastic, phialidic, globose to flask-shaped conidiogenous cells, and one-celled, hyaline to brown, oblong to ellipsoidal, aseptate, smooth-walled conidia (Jayasiri et al., 2019). Currently, *Leucaenicola* comprises five species, namely *L. aseptata*, *L. camelliae*, *L. osmanthi*, *L. phraeana* and *L. taiwanensis* (Jayasiri et al., 2019; Ariyawansa et al., 2020a, 2020b).

Leucaenicola rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.30

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL68

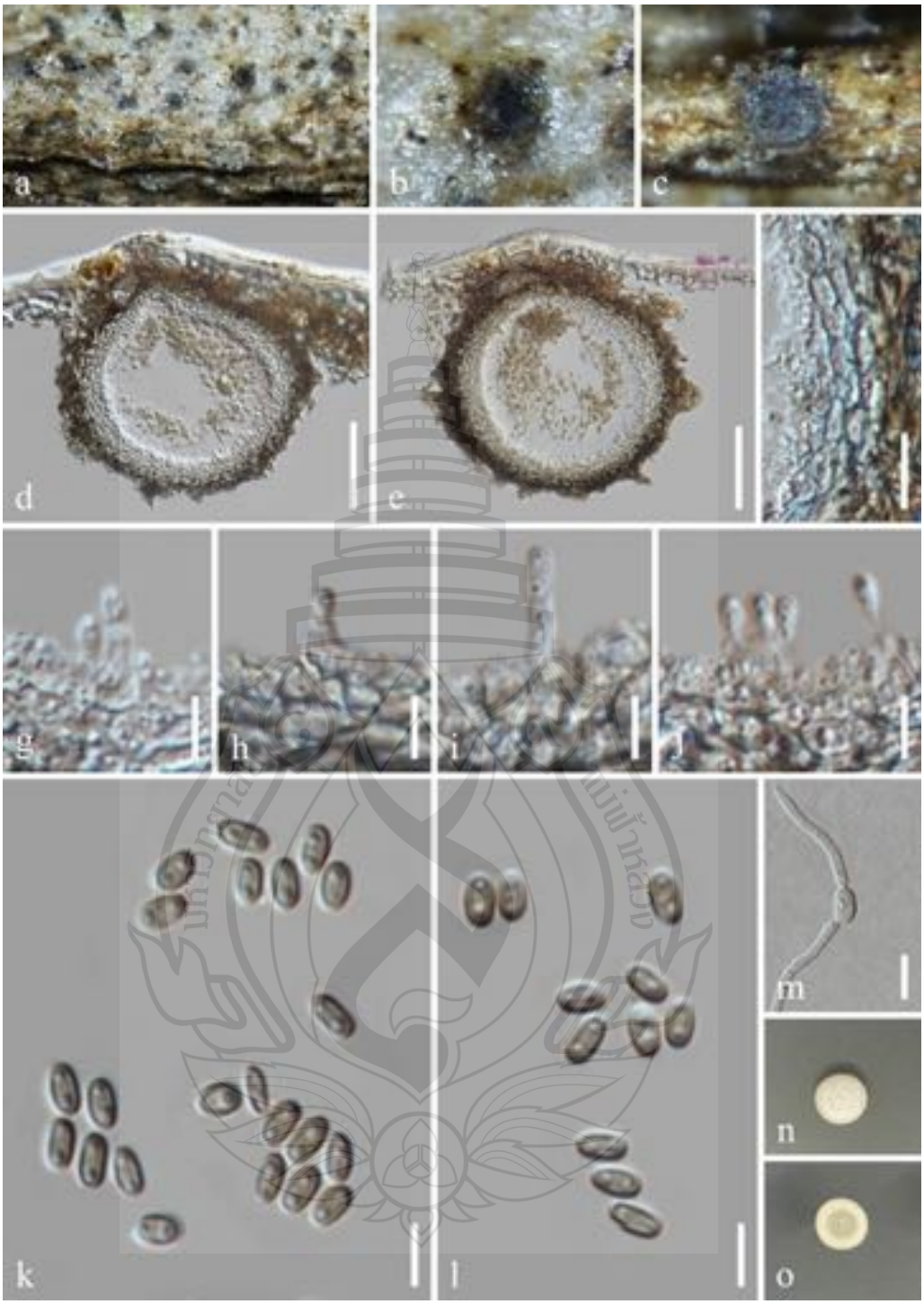
Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 95–160 µm wide, 95–165 µm high, solitary, pycnidial, immersed to erumpent, visible as black dots covered by epidermal tissues, uniloculate, globose to subglobose, glabrous. *Conidiomatal wall* 12–20µm wide, thin-walled, composed of several layers of hyaline to brown, pseudoparenchymatous cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–7 × 2–3 µm ($\bar{x}$ = 6 × 2.3 µm; n = 20),

phialidic, enteroblastic, hyaline, smooth, ampulliform to doliiform or cylindrical, aseptate, lining the conidiomatal cavity. *Conidia* 4–5 × 2–3 µm ($\bar{x}$ = 4.5 × 2.5 µm; n = 30), ellipsoidal to cylindrical, initially hyaline, after secession olivaceous-brown or pale brown to brown, thin-walled, smooth, aseptate, mostly with two polar oil-droplets.

Culture characteristics – Conidia germinated on PDA medium within 24 h and germ tubes produced from both ends. Colonies growing on PDA reached 15–17 mm in diam. after three weeks at 25℃ in the dark. Colonies from above, white, circular, dense, dull with entire edge, center slightly elevated; in reverse, pale gray in the center, white at the margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL68 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – Multi-locus phylogenetic analysis showed that my isolate (CGMCC SL68) clustered together with *Leucaenicola aseptata* (MFLUCC 17-2423) and formed a sister lineage (Figure 3.29). Morphologically, *L. rosae* is similar to *L. aseptata* in having pycnidial conidiomata, ampulliform to cylindrical conidiogenous cells, oblong to ellipsoidal conidia (Jayasiri et al., 2019). However, *L. rosae* can be distinguished from *L. aseptata* (MFLUCC 17-2423, ex-type strain) by the nucleotide base pair differences of 2.0% (18/922 bp, 3 gaps) in *tef1α* and 5.7% (50/883 bp, 2 gaps) in *rpb2* sequence data. Therefore, *L. rosae* is introduced as a new species based on phylogenetic evidence which is associated with *Rosa roxburghii* in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 50 μm; f, m = 10 μm; g–l = 5 μm.

Figure 3.30 *Leucaenicola rosae* (HKAS SL68, holotype)

Palmiascoma Phook. & K.D. Hyde, Fungal Diversity 72: 65 (2015)

Type species – *Palmiascoma gregariascomum* Phook. & K.D. Hyde

Notes – *Palmiascoma* was introduced as a monotypic genus to accommodate *P. gregariascomum*, which was collected from dead palm fronds in Thailand (Liu et al., 2015b). Two additional species, *P. acericola* and *P. qujingense*, were subsequently discovered and included in this genus (Monkai et al., 2021; Li et al., 2023b). *Palmiascoma* species commonly appears as saprobes on woody hosts but are rarely pathogens (Wang et al., 2022).

Palmiascoma acericola W.L. Li & Jian K. Liu, Mycosphere 14(1): 1450 (2023) Figure 3.31; Figure 3.32

Index Fungorum number: IF849144; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 210–300 µm wide, 150–270 µm high, solitary to gregarious, sometimes confluent, dark brown to black, immersed to erumpent, dissilient the host epidermis, subglobose to pyriform, unilocular, glabrous, coriaceous to carbonaceous, short papillate, ostiolate. *Ostiole* 70–100 µm wide, 72–105 µm high, single, short-cylindrical, central or eccentric, filled with hyaline periphyses. *Peridium* 15–22 µm wide, composed of several layers of brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, comprising of numerous, branched, septate, not constricted at the septa, hyaline pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 62–72 × 8.5–13 µm ($\bar{x}$ = 68 × 10 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with a short, furcate pedicel, rounded and thick-walled at the apex. *Ascospores* 13–15.5 × 4–6 µm ($\bar{x}$ = 14 × 5 µm; n = 30), uniseriate or irregularly arranged, fusiform, with rounded ends, slightly curved, hyaline to brown, 1-septate, slightly constricted at septum, upper cell slightly wider than lower cell, guttulate. Asexual morph: Coelomycetous. *Conidiomata* 195–365 µm wide, 130–230 µm high, pycnidial, solitary to gregarious or confluent, dark brown to black, immersed to erumpent, dissilient the host epidermis, globose to subglobose, mostly unilocular, occasionally multi-locular,

glabrous, coriaceous, ostiolate. *Ostiole* 50–62 µm wide, 60–88 µm high, single, inconspicuous, circular, central or laterally located. *Conidiomatal wall* 15–22 µm wide, 5–8-layered, thin-walled cells of *textura angularis*, hyaline to brown, lined with 3–5 inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–9 × 2–5 µm ($\bar{x}$ = 7 × 3.5 µm; n = 20), hyaline to pale brown, holoblastic, phialidic, subcylindrical to doliiform, smooth, arising from the inner layer of the pycnidium wall. *Conidia* 4.5–6.2 × 2.3–3 µm ($\bar{x}$ = 5.2 × 2.6 µm; n = 30), globose to ellipsoid, rounded or obtuse ends, hyaline to pale brown, aseptate, smooth, guttulate.

Culture characteristics – Ascospores and conidia germinated on PDA within 12 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 25–27 mm in diam. after three weeks at 25°C in the dark, circular, dense, whitish-gray, fluffy; in reverse, pastel yellow, with a milky white margin.

Materials examined – CHINA, Guizhou Province, Zunyi City, Bozhou District, Tuanxi Town, Ximashui Village, elevation 990.6 m, 27°27′36″ N, 107°4′12″ E, on dead branches of *Rosa roxburghii*, 2 February 2023, N. Wu, ML145 (HUEST XX), living culture UESTCC XX; *ibid.*, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML27 (HUEST XX), living culture UESTCC XX; *ibid.*, ML28 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL54 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer truncatum*, *Pistacia chinensis* and *Vernicia fordii* (Li et al., 2023b), *Rosa roxburghii* and *R. sterilis* (present study).

Known geographical distribution – China.

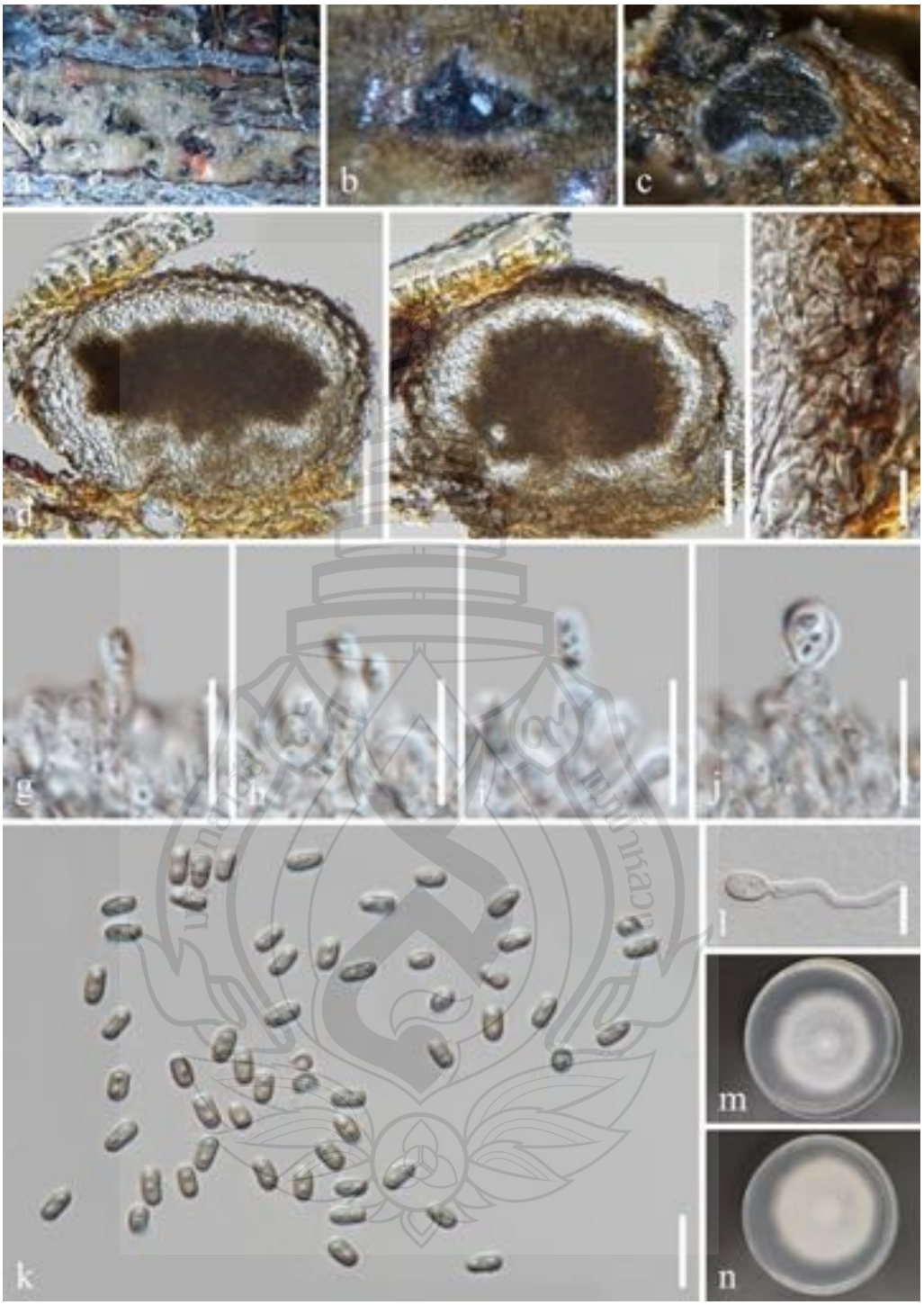
Notes – Li et al. (2023b) introduced *Palmiascoma acericola* as a sexual morph, which was originally discovered on three different oil plants. My collection is similar to *P. acericola* in the morphology of asci and ascospores with comparable dimensions.

The multi-locus phylogenetic analysis revealed that my collection (UESTCC ML145, UESTCC ML27, UESTCC ML28 and UESTCC GL54) is identical and clustered with *P*. *acericola* (CGMCC 3.24963 and UESTCC 23.0018) (Figure 3.29). The ITS sequences of my isolates are identical to the type material of *P*. *acericola*. Therefore, I recognize my collections as *P*. *acericola*, while two new host records are provided. In addition, I isolated both the asexual and sexual morphs of *P*. *acericola* from *Rosa roxburghii* and *R*. *sterilis*, with the asexual morph reported for the first time.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–l Asci. m–p Ascospores. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 100 μm; e, h–l = 30 μm; f, g, m–q = 10 μm.

Figure 3.31 *Palmiascoma acericola* (HUEST ML145; sexual morph, new host record)



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: d, e = 50 μm; f–l = 10 μm.

Figure 3.32 *Palmiascoma acericola* (HUEST GL54; asexual morph, new host record)

Palmiascoma qujingense Monkai & Phookamsak, Mycol. Progr. 20: 727 (2021) Figure 3.33

Index Fungorum number: IF556132; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 150–250 μm wide, 130–300 μm high, solitary to gregarious, sometimes confluent, black, immersed to partly erumpent, globose to subglobose, unilocular or multilocular, glabrous, coriaceous, short papillate, ostiolate. *Ostiole* 55–80 μm wide, 80–95 μm high, single, well-developed, subcylindrical, central or laterally located. *Conidiomatal wall* 15–22 μm wide, composed of thick-walled cells of *textura angularis*, with brown to dark brown cells in outer several layers, gradually merging with thin-walled, hyaline cells in innermost layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–10 × 2–3.2 μm ($\bar{x}$ = 6.7 × 2.7 μm; n = 20), hyaline, holoblastic, phialidic, subcylindrical, smooth, arising from the inner layer of the pycnidium wall. *Conidia* 4.5–6.3 × 2.2–3.4 μm ($\bar{x}$ = 5.3 × 2.7 μm; n = 30), globose to ellipsoid, obtuse ends, hyaline to pale brown, aseptate, guttulate, straight or sometimes slightly curved, smooth-walled.

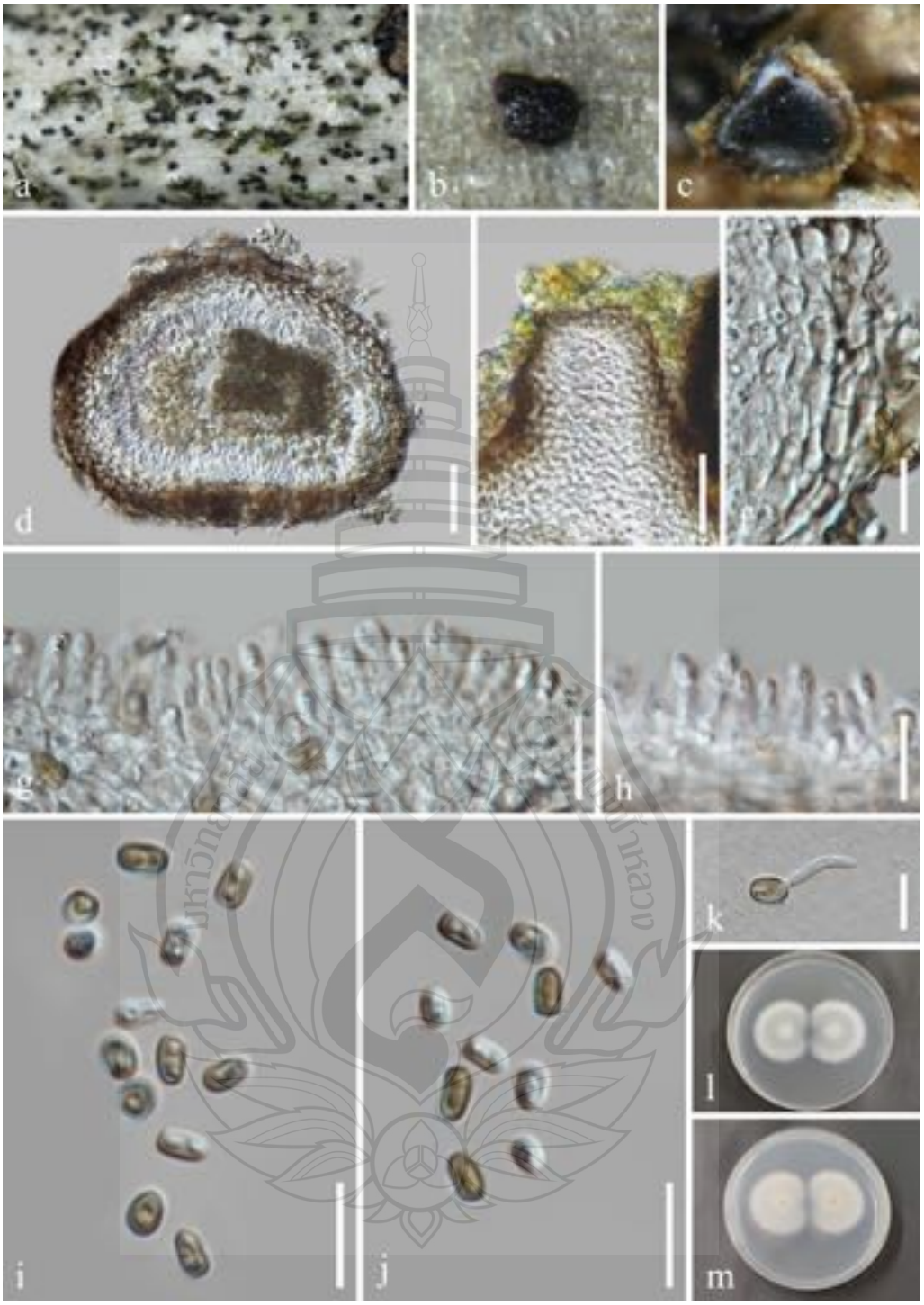
Culture characteristics – Conidia germinated on PDA medium within 24 h and germ tube produced from one end. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25°C in dark, circular, dry, dense, flat mycelium velvety towards the margin, initially off-white, becoming olivaceous-gray; in reverse, pastel yellow with grayish white margin.

Material examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H30 (HUEST XX), living culture UESTCC XX.

Hosts – *Fagaceae* sp. (Monkai et al., 2021), *Juglans regia* (Wang et al., 2022), *Myristica yunnanensis* (Ren et al., 2024a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Monkai et al. (2021) introduced *Palmiascoma qujingense* as a saprobic species associated with Fagaceae sp. Subsequently, *P*. *qujingense* was reported as a pathogen causing branch blight in *Juglans regia* (Wang et al., 2022). In the multi-gene phylogenetic analysis (Figure 3.29), my isolate (UESTCC H30) clustered with *P*. *qujingense* (KUMCC 19-0201) showing no nucleotide differences in the ITS region. Based on the phylogenetic and morphological evidence, I identify my collection as *P*. *qujingense*, and report *Rosa roxburghii* as a new host record.



Note a, b Conidiomata on natural substrate. c, d Vertical sections of conidiomata. e Ostiole. f Conidiomata wall. g, h Conidiogenous cells and developing conidia. i, j Conidia. k Germinating conidium. l, m Colony on PDA, above (l), below (m). Scale bars: d, e = 30 μm; f–k =10 μm.

Figure 3.33 *Palmiascoma qujingense* (HUEST H30, new host record)

Dictyosporiaceae Boonmee & K.D. Hyde

Type genus – *Dictyosporium* Corda

Notes – The family Dictyosporiaceae, which was originally proposed as Dictyosporaceae by Liu et al. (2015b), was introduced by Boonmee et al. (2016) within the order Pleosporales and class Dothideomycetes. Although Hyde et al. (2024) listed 21 genera in Dictyosporiaceae but without the inclusion of the genera *Pseudocyclothyriella* and *Neoxylochrysis* (Jiang et al., 2021b; Wu et al., 2024). Moreover, the genus *Paradictyocheirospora* has already been synonymized with *Digitodesmium* by Tian et al. (2022). In the present study, a new genus, *Neohysterium*, is introduced based on morphological characteristics and multi-locus phylogenetic analysis.

Neohysterium N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX.

Etymology – "*Neohysterium*" refers to the resemblance of its ascosporic morphology to the genus *Hysterium*.

Type species – *Neohysterium rosae* N. Wu & Jian K. Liu

Saprobic on dead branches of *Coffea arabica* var. *catimor* (Rubiaceae) and *Rosa roxburghii*. Sexual morph: *Ascomata* solitary or confluent, brown to black, immersed to semi-immersed, unilocular, subglobose to pyriform, with the ruptured host tissue around the surface of the ascomata. *Peridium* coriaceous. *Hamathecium* trabeculate pseudoparaphyses, longer than asci. *Asci* 8-spored, bitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* uniseriate to overlapping or crowded, hyaline to yellowish brown, ellipsoid or oblong, septate, constricted at the septa, guttulate. Asexual morph: Undetermined.

Notes – *Neohysterium* is introduced as a segregated genus from *Pseudocoleophoma* to accommodate *N. puerensis* (≡ *P. puerensis*) and *N. rosae.* Fourteen *Pseudocoleophoma* species are listed in Index Fungorum (2025, June). However, *P. clematidis* and *P. typhicola* were transferred to *Pseudocyclothyriella* and

Neoxylochrysis, respectively (Jiang et al., 2021b; Wu et al., 2024). *Pseudocoleophoma* currently comprises 12 species, although the placement of some remains questionable, such as *P. guizhouensis* (Zhang et al., 2023a) and *P. puerensis* (Lu et al., 2022b). In my phylogenetic tree, I observed that *P. guizhouensis* clustered with *Neoxylochrysis typhicola*, while *N. puerensis* and *N. rosae* clustered with *Pseudoconiothyrium broussonetiae*, and they all are separated from *Pseudocoleophoma*. My tree topology is similar to Feng et al., (2024) and Wu et al., (2024). As there were no fresh specimens, previous studies did not address the phylogenetic issues with *P. guizhouensis* and *N. puerensis*. *Neohysterium* is similar to *Hysterium* in their sexual morphs. However, *Hysterium* belongs to Hysteriaceae (Hysteriales), whereas *Neohysterium* belongs to Dictyosporiaceae (Pleosporales). In addition, *Neohysterium* differs from other genera within Dictyosporiaceae by its immersed to semi-immersed, unilocular, subglobose to pyriform ascomata and bitunicate, cylindrical, short pedicellate asci with hyaline to yellowish brown, 1–3-septate, constricted at the septa, guttulate, ellipsoid or oblong ascospores without any gelatinous sheath or appendages (Tanaka et al., 2015; Atienza et al., 2021; Lu et al., 2022b; Zhang et al., 2023a; Feng et al., 2024; Wu et al., 2024).

I rechecked the BLASTn search result based on ITS sequence of *Pseudocoleophoma guizhouensis* (MFLU 18-2262; type strain) available in GenBank and noted that *P. guizhouensis* is similar to the Pleosporales sp. strain ZHKUCC 24-0827 (PQ605120) with 87.25% similarity, *Dictyosporium nigroapice* strain MFLU 18-1043 (MH381768) with 87.25% similarity, and match with *P. rosae* isolate HKAS 131315 (PP925615) with 89.61% similarity, which is far from *Pseudocoleophoma*. In addition, the BLASTn search result based on LSU, SSU, *tef1α* and *rpb2* sequences showed that the species is not closely related to *Pseudocoleophoma*, exposing these results may be erroneous. It seems that *P. guizhouensis* could be segregated from *Pseudocoleophoma*, but due to the lack of resequencing and the absence of fresh specimens, I retain it within the genus *Pseudocoleophoma* until new collections are found.

Neohysterium puerensis (L. Lu & Tibpromma) N. Wu & Jian K. Liu, comb. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Basionym – *Pseudocoleophoma puerensis* L. Lu & Tibpromma, Journal of Fungi, J. Fungi 8(no. 1113): 6 (2022)

Holotype – CHINA, Yunnan Province, Pu'er City, elevation 1,090.5 m, 22°40′28″ N, 100°56′9″ E, on a decaying branch of *Coffea arabica* var. *catimor*, 16 September 2021, L. Lu, Pu'er 3-2 (ZHKU 22-0118, holotype), living culture ZHKUCC 22-0204 = ZHKUCC 22-0205.

Notes – *Neohysterium puerensis* was previously placed in *Pseudocoleophoma* based on molecular phylogenetic analysis and morphological characteristics by Lu et al. (2022b). *Neohysterium puerensis* differs from the other *Pseudocoleophoma* species in having hyaline to yellowish brown, 1–3-septate, constricted at the septa, guttulate, ellipsoid or oblong ascospores without any gelatinous sheath or appendages (Lu et al., 2022b), while in *Pseudocoleophoma* the ascospores are hyaline, 1-septate, constricted at the septum, fusiform with a conspicuous sheath (Tanaka et al., 2015; Wu et al., 2024). Based on morphology and molecular evidence, I transfer *Pseudocoleophoma puerensis* to the genus as *Neohysterium puerensis*. In the phylogenetic analysis (Figure 3.34), *N. puerensis* and *N. rosae* formed distinct clades in Dictyosporiaceae, being sister to *Pseudoconiothyrium broussonetiae*. The hyaline to yellowish brown, ellipsoid or oblong ascospores of *Neohysterium* extended the concept of Dictyosporiaceae.

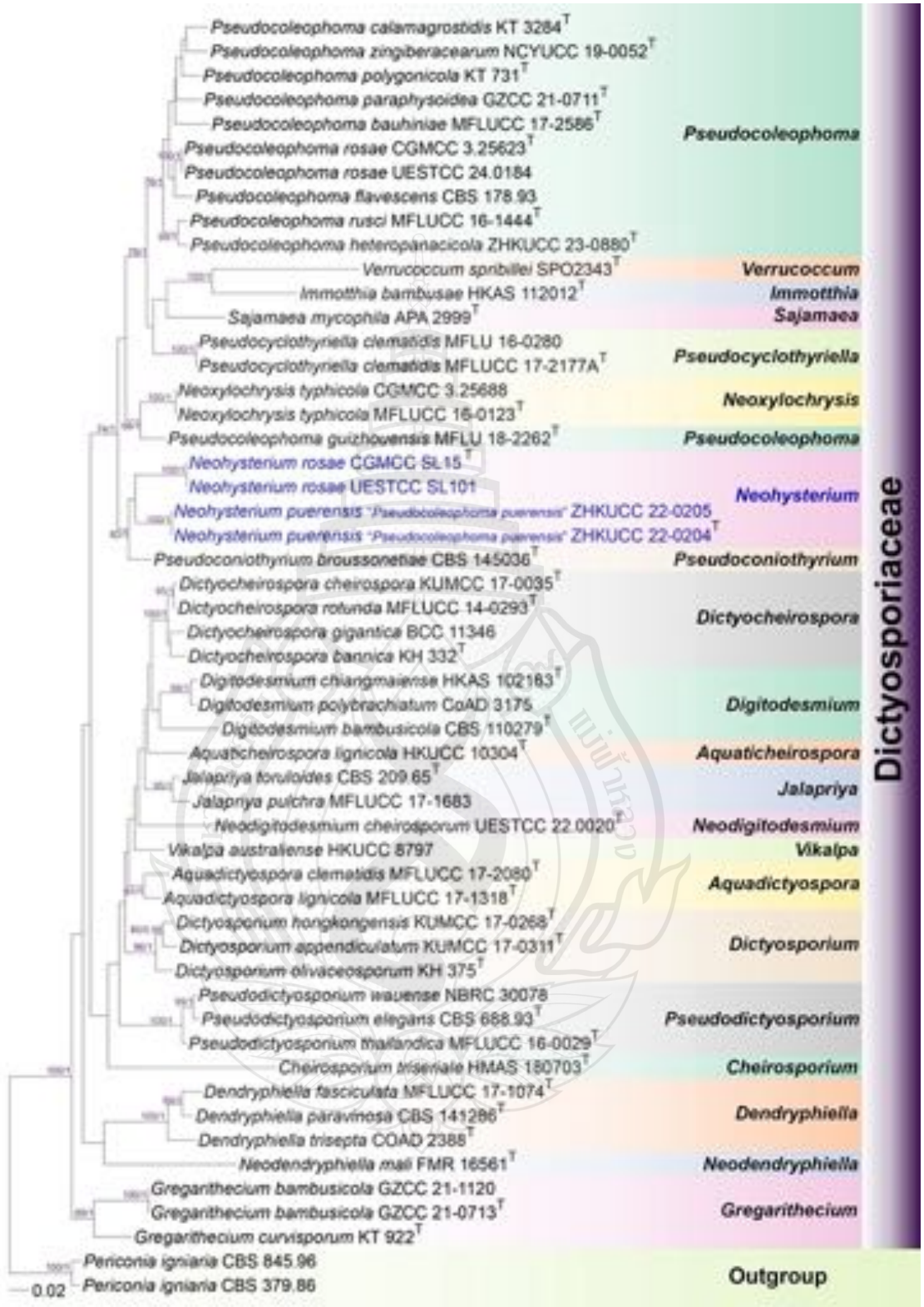


Figure 3.34 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of *Neohysterium*

Figure 3.34 The tree is rooted with *Periconia igniaria* (CBS 379.86 and CBS 845.96). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Neohysterium rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.35

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL15

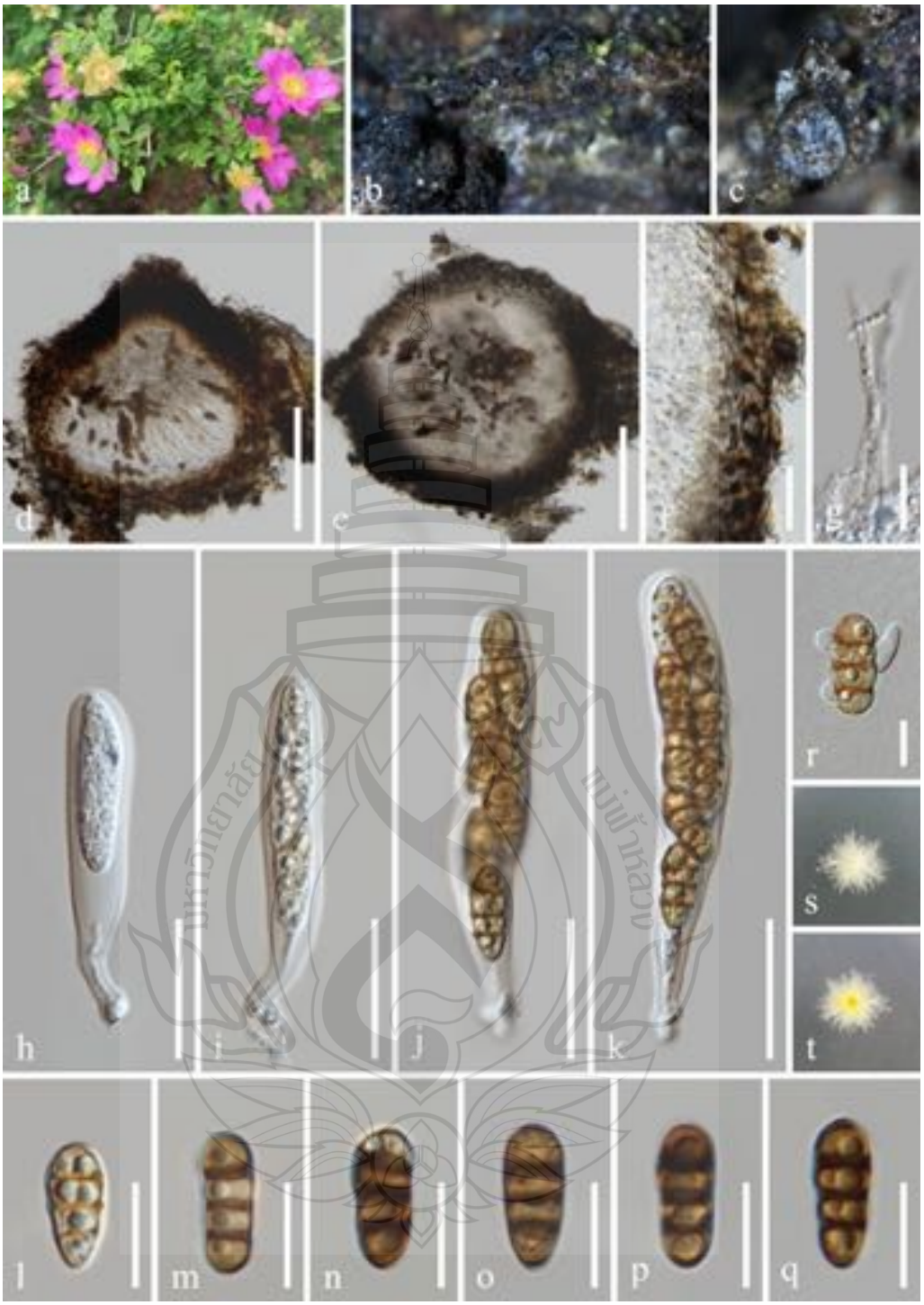
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 200–315 μm wide, 190–270 μm high, solitary or confluent, brown to black, immersed to semi-immersed, unilocular, subglobose to pyriform, coriaceous, with the ruptured host tissue around the surface of the ascomata, papillate, ostiolate. *Ostiole* 74–90 μm wide, 70–85 μm high, single, subcylindrical, straight or curved, central. *Peridium* 23–53 μm wide, composed of 3–5 layers of *textura angularis* or *textura epidermoidea* cells, brown to dark brown. *Hamathecium* 2.5–3 μm wide, composed of dense, numerous, filiform, branched, septate, hyaline, guttulate, pseudoparaphyses, longer than asci. *Asci* 57–75 × 9–12 μm ($\bar{x}$ = 66 × 11 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 12–15 × 5–7.5 μm ($\bar{x}$ = 14 × 6 μm; n = 30), overlapping to crowded, straight or slightly curved, hyaline to yellowish brown, ellipsoid or oblong, inequilateral 3-septate, constricted at the septa, lower cell smaller, with guttules in each cell, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25°C in dark,

irregular, cottony, velvety, white, the margin filamentous; in reverse, pale yellow in the middle and white at the margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL15 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid*., SL101 (HUEST XX, paratype), living culture UESTCC XX.

Notes – *Neohysterium rosae* is similar to *N. puerensis* in the morphology of the ascomata, asci and ascospores (Lu et al., 2022b). However, ascospores of *Neohysterium rosae* are often 3-septate with the apical cell broader than the basal cell, while in *N. puerensis* they are mostly 1–3-septate, symmetrically narrower at both ends. Additionally, the ITS, LSU, SSU and *tef1α* sequences of *N. rosae* (CGMCC SL15, ex-type) and *N. puerensis* (ZHKUCC 22-0204, ex-type) showed 86.82% (448/516 bp, 22 gaps), 96.99% (839/865 bp, two gaps), 98.51% (1057/1073 bp, eleven gaps) and 94.67% (905/956 bp, one gap) similarities, respectively. Phylogenetically, they formed a distinct sister clade in Dictyosporiaceae (Figure 3.34). Therefore, herein I introduce *N. rosae* as a new species in *Neohysterium*.



Note a Host: *Rosa roxburghii*. b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 100 μm; f, h–k = 20 μm; g, l–r = 10 μm.

Figure 3.35 *Neohysterium rosae* (HKAS SL15, holotype)

Pseudocoleophoma rosae N. Wu & Jian K. Liu, J. Fungi 10: 15 (2024) Figure 3.36; Figure 3.37

Index Fungorum number: IF902297; Faces of Fungi number: FoF16020

Etymology – Referring to the host genus *Rosa* from which the fungus was collected.

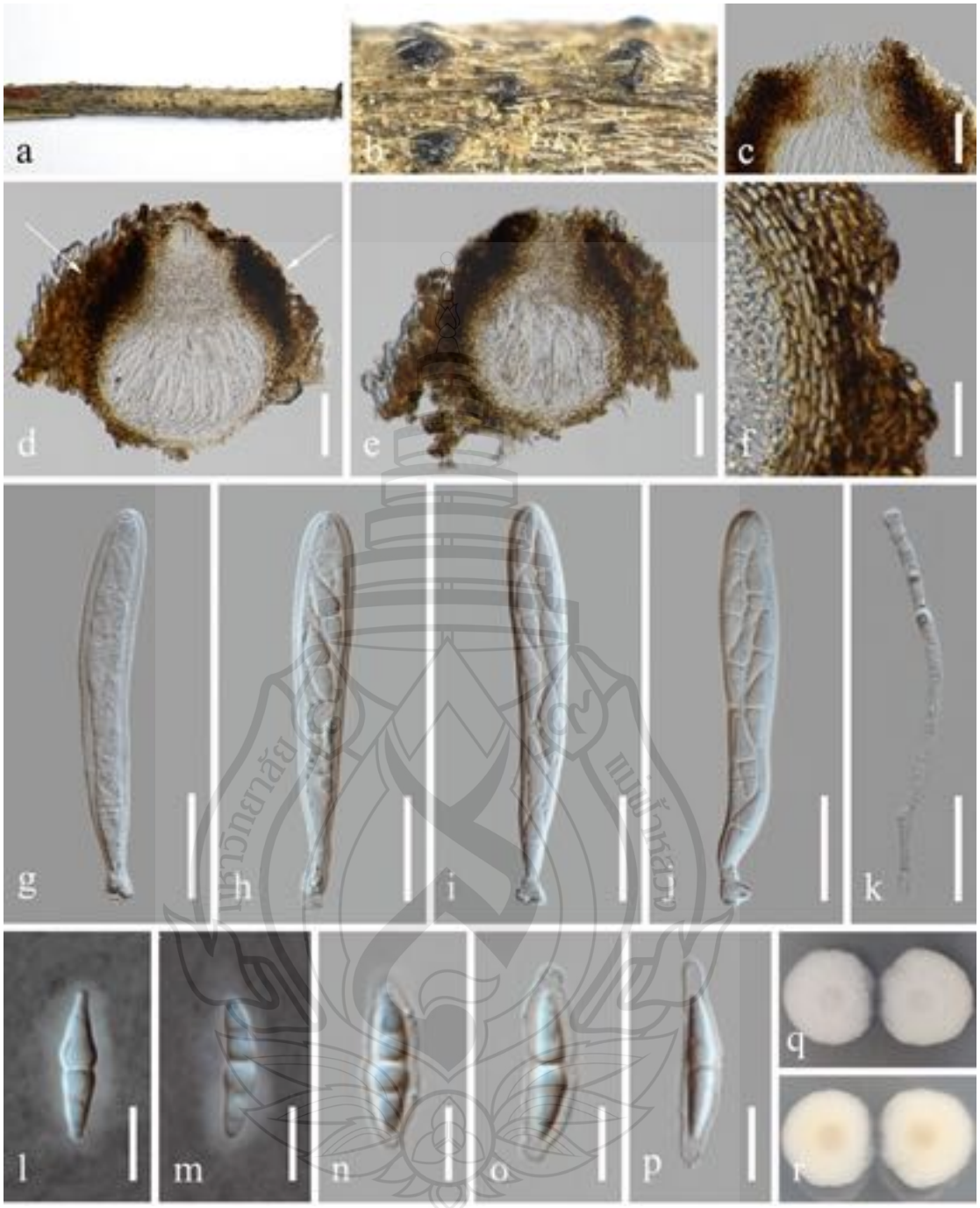
Holotype – HKAS 131315

Saprobic on dead twigs of *Rosa roxbunghii* Tratt. Sexual morph: *Ascomata* 170–210 µm high × 175–220 µm diam. ($\bar{x}$ = 196 × 188 µm, n = 20), semi-immersed or immersed in the substrate, dark brown, globose to subglobose, unilocular, glabrous, thick-walled, thickened at the apex, visible as black dots or papilla on the host, ostiolate. *Ostiole* neck central, 59–71 µm long, 49–71 µm wide. *Peridium* up to 12–35 µm wide, composed of thick-walled, dark brown to pale brown or hyaline cells of *textura angularis*. *Hamathecium* up to 2–3 µm wide, hyaline, septate, branched. *Asci* 55–70 × 7–10 µm ($\bar{x}$ = 65 × 8 µm, n = 20), 8-spored, cylindrical to clavate, some slightly curved, with an ocular chamber, short-stalked with club-shape pedicel. *Ascospores* 12–20 × 3–6 µm ($\bar{x}$ = 16 × 4 µm, n = 50), hyaline, smooth-walled, fusiform with acute ends, 1-septate, slightly constricted at the septum, occasionally 2–4-guttulate when young, surrounded by a mucilaginous sheath; 1–2 µm wide at sides, 2–3 µm at each end. Asexual morph: Coelomycetous. *Conidiomata* 100–184 µm high × 98–215 µm diam. ($\bar{x}$ = 140 × 148 µm, n = 10), dark brown to black, visible as black dots covered by epidermal tissues, solitary to gregarious, globose to sub- globose, pyriform or irregular in shape, unilocular, glabrous, ostiolate. *Ostiole* 30–40 µm long, 30–50 µm wide, cylindrical, centrally or laterally located. *Conidiomatal wall* 8–20 µm wide ($\bar{x}$ = 15 µm, n = 20), composed of thick-walled, dark brown to hyaline cells of textura angularis. Conidiophores reduced to conidiogenous cells. Conidiogenous cells 3–5 × 4–7 µm ($\bar{x}$ = 4 × 6 µm, n = 30), phialidic, aseptate, smooth-walled, hyaline. Conidia 6–9 × 2–4 µm ($\bar{x}$ = 8 × 3 µm, n = 50), hyaline, aseptate, oblong to cylindrical, smooth, thin-walled, guttules concentrated to ends.

Culture characteristics – Ascospores and conidia germinated on PDA within 12 h. Colonies on PDA reaching 30–40 mm diam. after two weeks at 25°C in natural light. Mycelium superficial, with regular margins, slightly raised, fluffy, moderate aerial mycelium on the surface, underneath pale yellow.

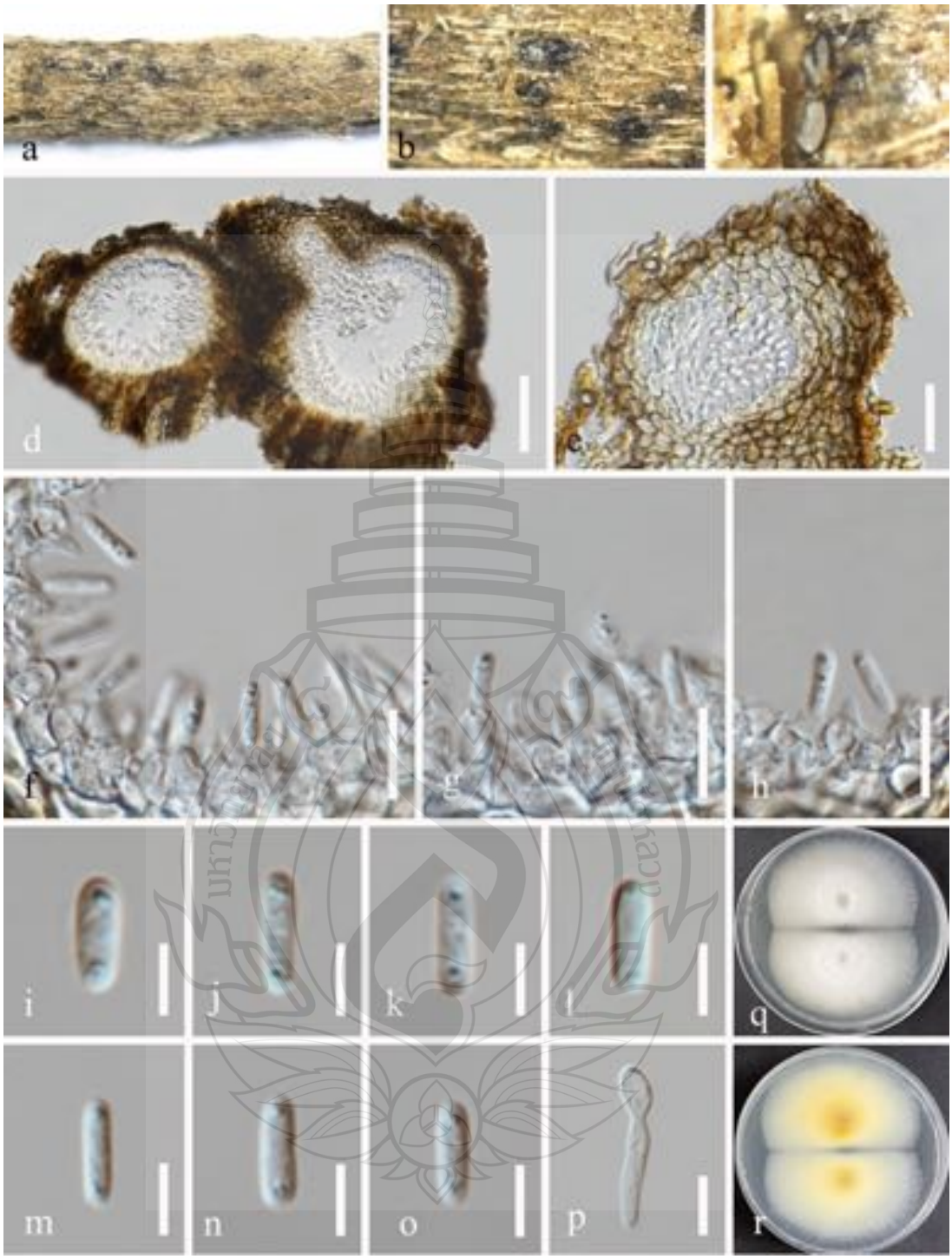
Material examined – China, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, on dead twigs of *Rosa roxbunghii*, 30 October 2021, Na Wu, H54 (HKAS 131315, holotype), ex-type living culture CGMCC 3.25623 = UESTCC 23.0220; *ibid*., H245 (HUEST 24.0201), living culture UESTCC 24.0184.

Notes – I isolated the asexual and sexual morphs of *Pseudocoleophoma rosae* from the same substrate, *Rosa roxbunghii*. The phylogeny indicates that these two isolates are identical (Figure 3.38). The multi-locus phylogenetic result (Figure 3.38) clearly showed that these two iso- lates are identical. And these two isolates constitute a distinct lineage but clustered close to *P. rhapidis* and *P. yunnanensis*. The sexual morph of *P. rosae* differs from *P. yunnanensis* by having smaller ascomata (170–210 × 175–220 μm vs. 160–280 × 200–280 μm), asci (55–70 × 7–10 μm vs. 65–90 × 8–11 μm) and ascospores (12–20 × 3–6 μm vs. 16–26 × 4–8 μm). Ascospores of *P. rosae* have guttules when young that disappear at maturity. The asexual morph of *P. rosae* differs from *P. rhapidis* by its smaller conidiomata (100–184 × 98–215 μm vs. 150–225 × 225–300 μm), narrower conidiogenous cells (3–5 × 4–7 μm vs. 7–10 × 13–17 μm), and smaller conidia (6–9 × 2–4 μm vs. 20–25 × 10–15 μm). In addition, the conidia of *P. rosae* have guttules concentrated at the ends, while *P. rhapidis* lacks guttules. Therefore, I introduce *P. rosae* as a new species based on the morphology and phylogeny.



Note a, b Appearance of thallus and ascomata on the host surface. c Vertical section through an ostiole. d, e Vertical section through ascomata. f Structure of peridium. g–j Asci. k Pseudoparaphyses. l–p Ascospores, l,m in Indian ink showing the sheath. q, r Colonies on PDA, from above (q), from be-low (r). Scale bars: c, f–k = 20 µm, d, e = 50 µm, l–p = 10 µm.

Figure 3.36 *Pseudocoleophoma rosae* (HKAS 131315, holotype; sexual morph)



Note a–c Conidiomata on the host substrate. d Vertical section of conidiomata. e Structure of the peridium. f–h Conidiogenous cells and developing conidia. i–o Conidia. p Germinated conidium. q, r Colonies on PDA, from above (q), from below (r). Scale bars: d = 50 µm, e = 20 µm, f–h = 10 µm, i–o = 5 µm, p = 10 µm.

Figure 3.37 *Pseudocoleophoma rosae* (HUEST 24.0201, asexual morph)

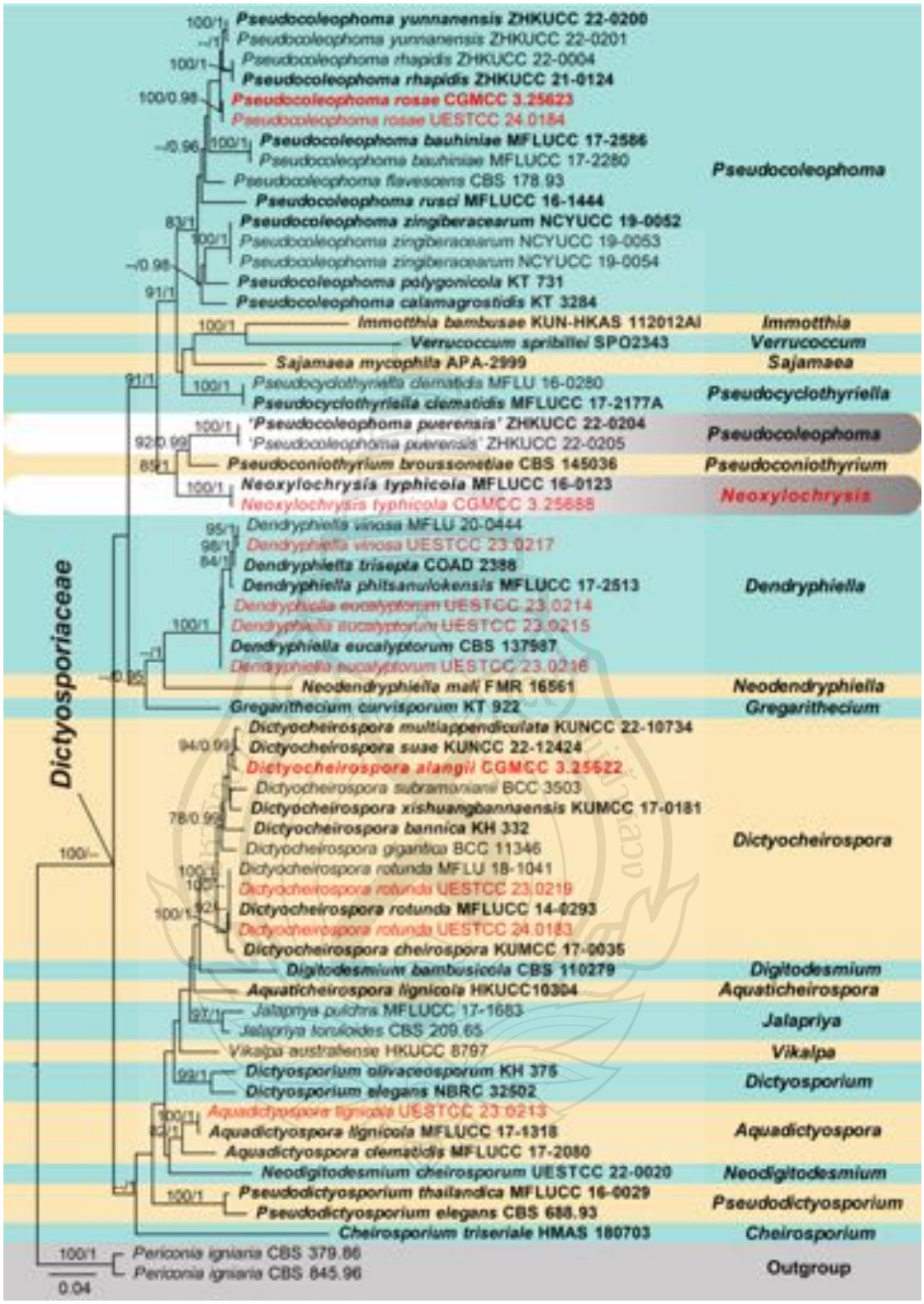


Figure 3.38 Phylogenetic tree generated from the maximum likelihood analysis based on the com-bined ITS, LSU, SSU and *tef1α* sequence data of Dictyosporiaceae

Figure 3.38 The tree is rooted with Periconia igniaria (CBS 379.86 and CBS 845.96). The ML (≥75%) and BI (≥95%) bootstrap supports are given near the nodes, respectively. The new isolates obtained in this study are indicated in red and ex-type strains are in bold.

Didymosphaeriaceae Munk

Type genus – *Didymosphaeria* Fuckel

Notes – Munk (1953) established Didymosphaeriaceae with *Didymosphaeria* Fuckel as the type genus. Currently, 38 genera are accepted in this family, most of which are saprobic on leaves, stems or branches in aquatic, mangroves, marine and terrestrial habitats, and even human pathogens (Ariyawansa et al., 2013, 2014; Hyde et al., 2013; Liu et al., 2015b; Wanasinghe et al., 2016; Nakashima et al., 2019; Afshan et al., 2020; Wijayawardene et al., 2022; Liu et al., 2023b). Most members of the Didymosphaeriaceae are sexual species and characterized by cylindro-clavate to clavate asci with septate, brown ascospores, viz., *Barria*, *Bimuria*, *Didymocrea*, *Didymosphaeria*, *Julella*, *Kalmusia*, *Karstenula*, *Montagnula*, *Neokalmusia*, *Paraconiothyrium*, *Paraphaeosphaeria*, *Phaeodothis* and *Trematеia* (Ariyawansa et al., 2014; Hongsanan et al., 2020a; Lu et al., 2022b; Tennakoon et al., 2022). A few genera have coelomycetous asexual morphs, viz., *Alloconiothyrium*, *Letendraea*, *Paraconiothyrium* and *Paraphaeosphaeria*, while the genus *Spegazzinia* has hyphomycetes asexual morphs (Ariyawansa et al., 2014; Hongsanan et al., 2020a; Xiong et al., 2024).

Austropleospora R.G. Shivas & L. Morin, Fungal Diversity 40(1): 70 (2010)

Type species – *Austropleospora osteospermi* R.G. Shivas & L. Morin

Notes – *Austropleospora* was established by Morin et al. (2010) to accommodate *A*. *osteospermi* as the type species. The sexual morph has scattered and immersed, ostiolate ascomata, 6–8-spored, clavate to cylindrical asci, and ellipsoidal, yellowish brown ascospores (Morin et al., 2010; Ariyawansa et al., 2015; Dissanayake et al., 2021c). The asexual morph is primarily characterized by pycnidial and globose

conidiomata with a central ostiole, and brown to yellowish brown, globose to obovate conidia (Morin et al., 2010; Jayasiri et al., 2019). Currently, four species, *A. osteospermi* (sexual and asexual morphs), *A. archidendri* (asexual morph), *A. keteleeriae* (asexual morph), *A. ochracea* (sexual morph), are listed in Index Fungorum (2025, June). Notably, *A. osteospermi* lacks the molecular data.

Austropleospora keteleeriae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 65 (2019) Figure 3.39

Index Fungorum number: IF 555541; Facesoffungi number: FoFXX

Saprobic on dead twigs of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 242–281 μm wide, 190–221 μm high, pycnidial, solitary, immersed, globose to subglobose or obpyriform, unilocular, ostiolate. *Ostiole* 27–33 μm wide, 34–41 μm high, central, papillate, dark brown. *Conidiomatal wall* 14–19 μm wide, thin-walled, composed of *textura angularis* cells, 3–4-layered, hyaline to brown, lined with 1–2 hyaline layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Conidiogenous cells* 4.3–7 × 3.4–5.3 μm ($\bar{x}$ = 5.8 × 4.3 μm; n = 20), phialidic, enteroblastic, determinate, ampulliform, arising from the inner layer of the pycnidium wall, hyaline, smooth, thin walled. *Conidia* 5.3–6.7 × 2.8–3.6 μm ($\bar{x}$ = 6 × 3.2 μm; n = 30), solitary, subglobose to obovate, aseptate, thick and smooth-walled, and some cells containing 1–3-minute guttules, with obtuse apex and base bluntly rounded, hyaline when young, becoming brown to dark brown at maturity.

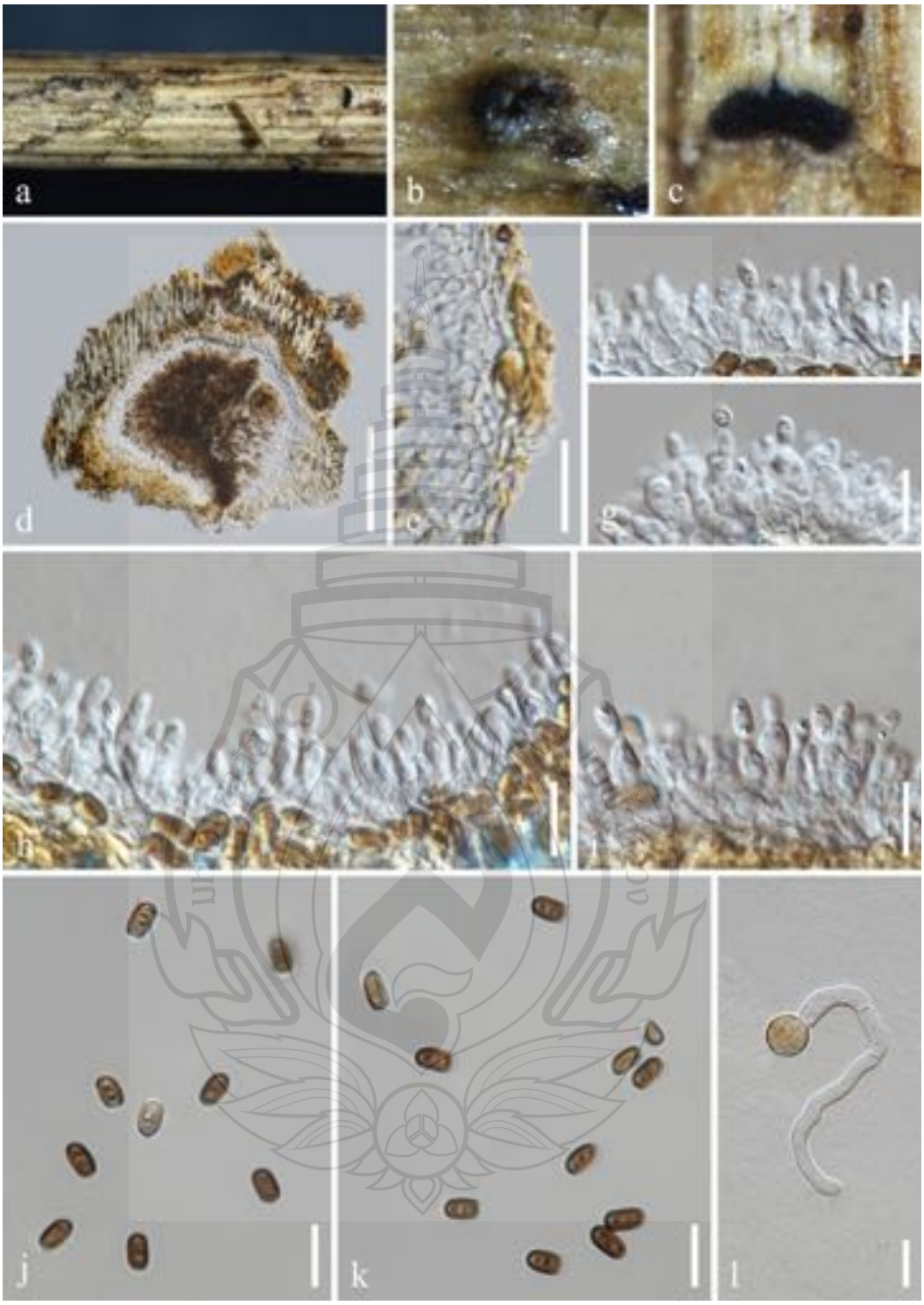
Culture characteristics – Conidia germinated on PDA within 24 h and germ tube produced from one end. Colonies growing on PDA reached 30–32 mm in diam. after three weeks at 25℃ in the dark, circular, irregular margin, fluffy, grayish brown in the center, grayish white at the edge; in reverse, brown in the center, and middle off white at the edge.

Material examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H51 (HUEST XX), living culture UESTCC XX.

Hosts – *Austropleospora keteleeriae* (Jayasiri et al., 2019), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Austropleospora keteleeriae* was introduced by Jayasiri et al. (2019) based on its asexual morph and was isolated from *Keteleeria fortunei* (Pinaceae) in China. My collection matches well with the holotype of *A. keteleeriae* in morphology. The phylogenetic analysis revealed my collection (HUEST H51) clustered together with *A. keteleeriae* (MFLUCC 18-1551) with a strong support (Figure 3.40). In addition, comparisons of the ITS, LSU, SSU and *tef1α* sequences of my collection and the holotype of *A. keteleeriae* revealed 100%, 100%, 99.57%, 100% and 99.6% similarities, respectively. Thus, my collection is identified as *A. keteleeriae* based on morphology and molecular evidence. This study extends the known host record of this species to *Rosa roxburghii*.



Note a, b Conidiomata on natural substrate. c, d Vertical section of conidiomata. e Conidiomatal wall. f–i Conidiogenous cells and developing conidia. j, k Conidia. l Germinating conidium. Scale bars: d = 100 µm; e = 20 µm; f–l = 10 µm.

Figure 3.39 *Austropleospora keteleeriae* (HUEST H51, new host record)

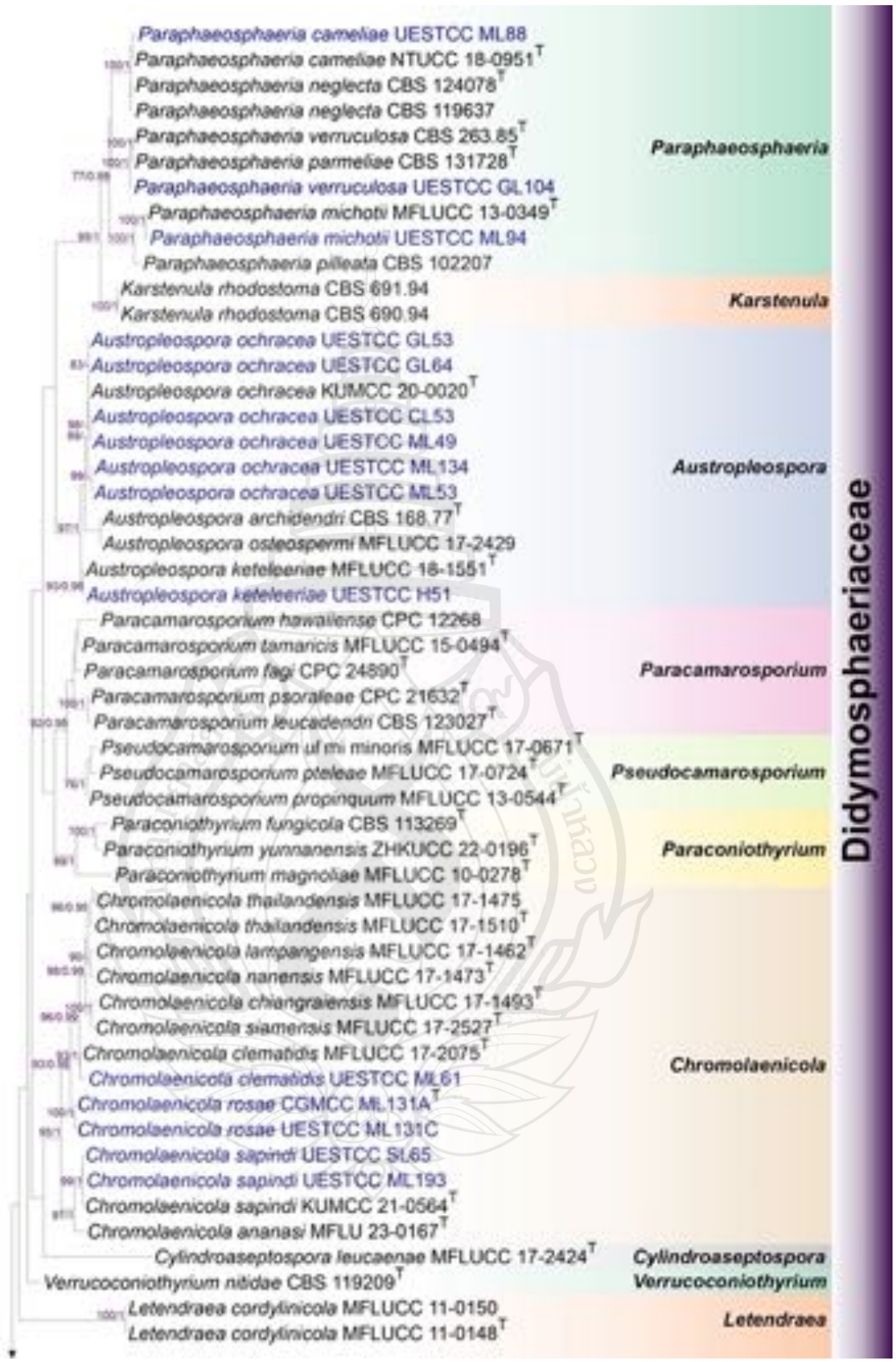


Figure 3.40 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1α* sequence data of Didymosphaeriaceae

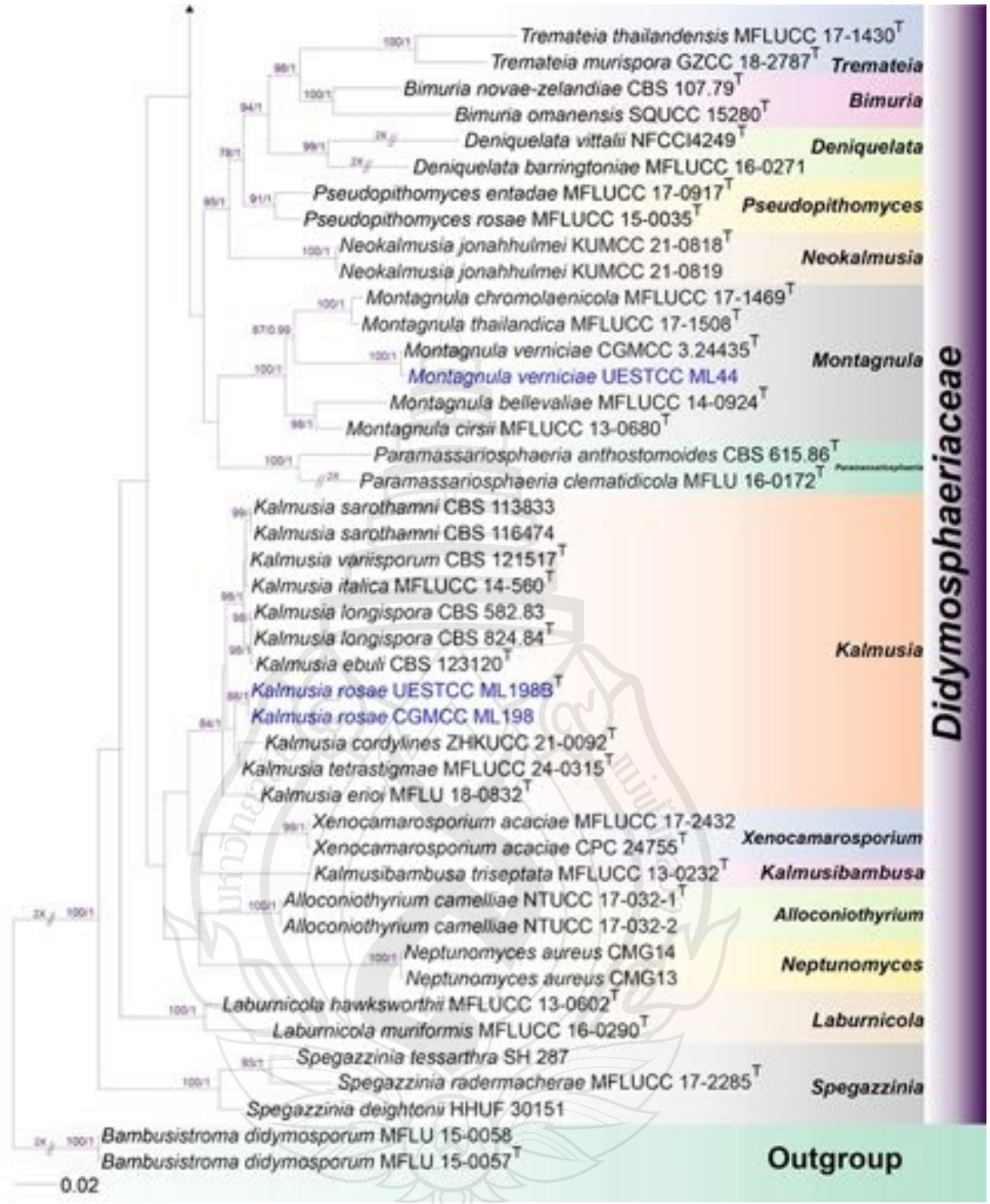


Figure 3.40 (continued)

Figure 3.40 The tree is rooted with *Bambusistroma didymosporum* (MFLU 15-0057 and MFLU 15-0058). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for

Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Austropleospora ochracea L.S. Dissan, J.C. Kang & K.D. Hyde, Phytotaxa 491(3): 223 (2021) Figure 3.41; Figure 3.42

Index Fungorum number: IF 512742; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 304–402 µm wide, 224–300 µm high, scattered, solitary to gregarious, immersed to erumpent, dark brown to black, globose to subglobose, uni-loculate, coriaceous, ostiolate, with short papilla. *Ostiole* 103–133 µm wide, 109–156 µm high, central or eccentric, filled with periphyses. *Peridium* 26–38 µm wide, coriaceous, composed of several layers of thin to thick-walled of *texutura angularis* cells, flattened, hyaline to brown. *Hamathecium* 2–3 µm wide, comprising numerous, filamentous, septate, cellular, hyaline pseudoparaphyses, intermixed with asci. *Asci* 110–137 × 10–12 µm ($\bar{x}$ = 119 × 11 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with a short, furcate pedicel, rounded and thick-walled at the apex. *Ascospores* 15–19 × 7.5–9 µm ($\bar{x}$ = 17 × 8 µm; n = 30), overlapping uniseriate, ovoid to ellipsoidal, with 3 transverse septa, constricted at the medium septum, and 0–1-longitudinal septa, initially hyaline to pale brown, becoming yellowish-brown to dark brown at maturity, asymmetrical, conical and narrowly rounded at the ends, smooth walled, without appendages. Asexual morph: Coelomycetous, *Conidiomata* 180–235 µm wide, 110–260 µm high, pycnidial, solitary, immersed, globose to subglobose, unilocular, ostiolate. *Ostiole* 55–80 µm wide, 70–80 µm high, central, papillate, blackish brown. *Conidiomatal wall* 12–20 µm wide, 3–4-layered, thin-walled cells of *textura angularis*, hyaline to brown, lined with 1–2 inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Conidiogenous cells* 5–10 × 3.5–6 µm ($\bar{x}$ = 7 × 4.5 µm; n = 20), phialidic, determinate, with minute collarette, globose to doliiform, arising from the inner layer of the pycnidium wall, hyaline, smooth, thin walled. *Conidia* 6.5–8.5 × 3–4 µm ($\bar{x}$ = 6.8

× 3.5 μm; n = 30), globose to obovate, solitary, aseptate, thick and smooth-walled, hyaline when young, becoming brown to dark brown at maturity.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tube produced from one end. Colonies growing on PDA reached 48–50 mm in diam. after three weeks at 25℃ in the dark, circular, dense, regular edge, white, center slightly elevated, and the reverse is similar in color, except for the pale-yellow center. Conidia germinated on PDA within 12 h and germ tubes produced from one end. Colonies growing on PDA reached 30–34 mm in diam. after three weeks at 25℃ in the dark. Colonies from above, white, irregular edge, medium dense, fluffy, covered with white aerial mycelium; in reverse, brown at the center, pale yellowish-white at the edge.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML134 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL53 (HUEST XX), living culture UESTCC XX; *ibid.*, Anshun City, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL64 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL53 (HUEST XX), living culture UESTCC XX; *ibid.*, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML49 (HUEST XX), living culture UESTCC XX; *ibid.*, ML53 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer palmatum* and *Nandina domestica* (Du et al., 2025), *Rosa roxburghii* and *R. sterilis* (present study).

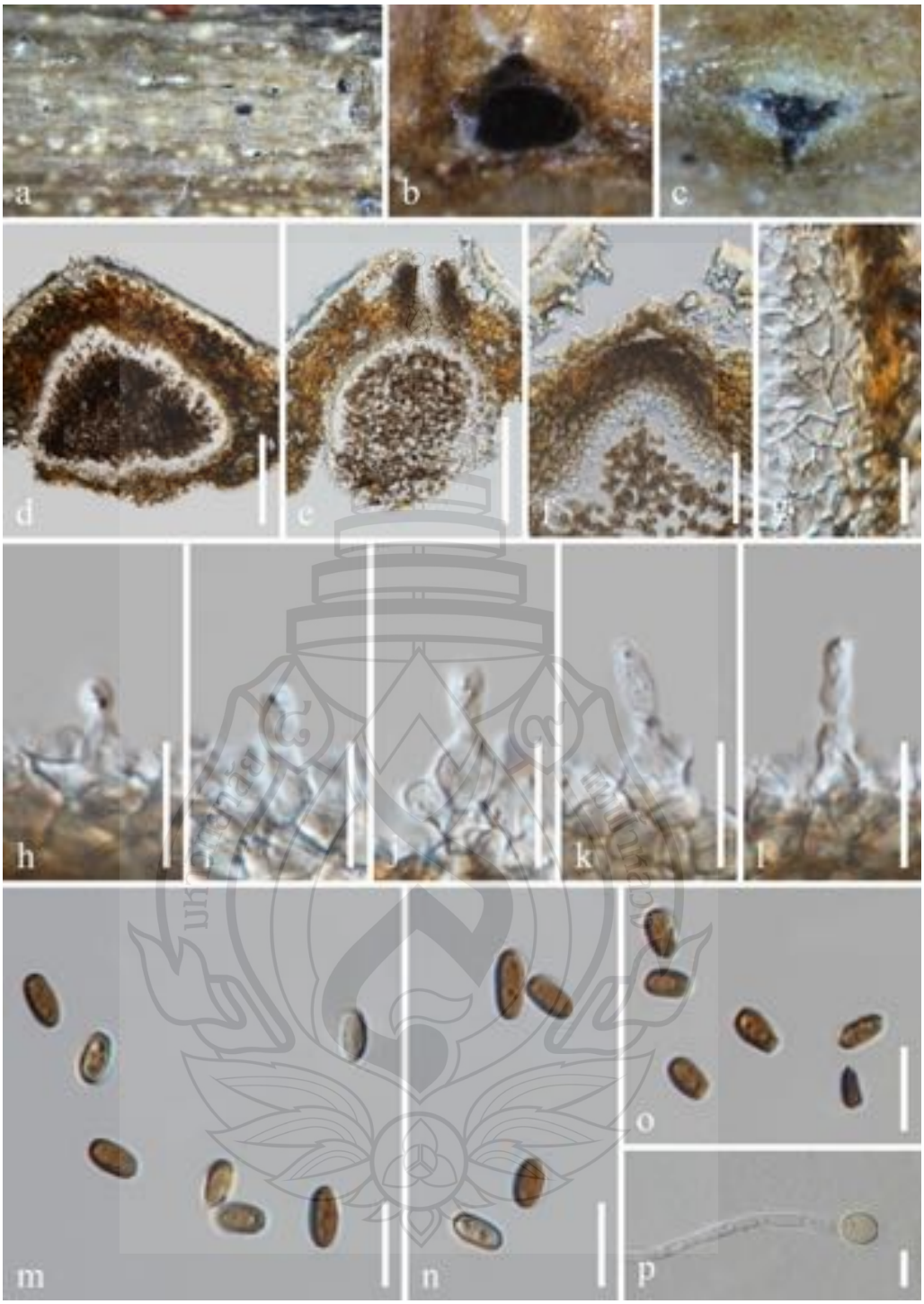
Known geographical distribution – China.

Notes – Dissanayake et al. (2021c) described the sexual morph of *Austropleospora ochracea* based on a collection of dead twigs from an undetermined plant in China. Subsequently, Yang et al. (2023b) reported this species from freshwater habitats, and Du et al. (2025) reported its asexual morph from medicinal plants *Acer palmatum* and *Nandina domestica* in China. Multi-locus phylogeny indicated that my isolates clustered together with *A. ochracea* (KUMCC 20-0020, ex-type strain) with a good support (Figure 3.40). I recognize my collection as *A. ochracea*, which is morphologically similar to the taxa as of Dissanayake et al. (2021c) and Du et al. (2025). In the present study, representatives of both asexual and sexual morphs of *A. ochracea* were collected from *Rosa roxburghii* and *R. sterilis*.



Note a, b Appearance of ascomata on host surface. c–e Vertical section of ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–r Ascospores. s Germinating ascospore. t, u Colonies on PDA, above (t), below (u). Scale bars: d, e = 100 μm; f, h–j = 30 μm; g, k–s = 10 μm.

Figure 3.41 *Austropleospora ochracea* (HUEST ML134; sexual morph, new host record)



Note a–c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Ostiole. g Conidiomatal wall. h–l Conidiogenous cells and developing conidia. m–o Conidia. p Germinating conidium. Scale bars: d, e = 100 μm; f = 30 μm; g–p = 10 μm.

Figure 3.42 *Austropleospora ochracea* (HUEST GL53; asexual morph, new host record)

Chromolaenicola Mapook & K.D. Hyde, Fungal Diversity 101: 20 (2020)

Type species – *Chromolaenicola nanensis* Mapook & K.D. Hyde

Notes – *Chromolaenicola* was classified under Didymospheriaceae by Mapook et al. (2020a) with *C. nanensis* as the type species. The sexual morph of *Chromolaenicola* is characterized by immersed to semi-immersed ascomata, cylindrical asci, and uniseriate, ellipsoid, muriform ascospores (Mapook et al., 2020a). The asexual morph is characterized by pycnidial conidiomata, phialidic, enteroblastic conidiogenous cells, and oblong, oval to ellipsoid, or globose to subglobose conidia (Jayasiri et al., 2019; Mapook et al., 2020a). Currently, eight species are listed in Index Fungorum (2025, June). All species of *Chromolaenicola* are reported as saprobic fungi from terrestrial habitats in China and Thailand (Mapook et al., 2020a; Phukhamsakda et al., 2020; Ren et al., 2022; Du et al., 2025).

Chromolaenicola clematidis Phukhams. & K.D. Hyde, Fungal Diversity 102: 31 (2020) Figure 3.43

Index Fungorum number: IF 557133; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 237–368 µm wide, 183–290 µm high, pycnidial, solitary or scattered, uniloculate, immersed, globose to subglobose, coriaceous, thin, brown to dark brown, ostiolate. *Ostiole* 78–85 µm wide, 94–104 µm high, central or eccentric, blackish brown, opening by a pore. *Conidiomatal wall* 16–22 µm wide, uniform, wider at apex, composed of 4–5 layers of brown to dark brown thin-walled cells of *textura angularis*, lined with 1–2 hyaline inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.4–6.4 × 4.5–6 µm ($\bar{x}$ = 5.5 × 5.2 µm; n = 20), phialidic, enteroblastic, determinate, discrete, truncate, arising from the inner layer of the pycnidium wall, hyaline, smooth, thin walled. *Conidia* 9–13 × 5.5–7.5 µm ($\bar{x}$ = 11 × 6.5 µm; n = 30), broad oblong to oval or obovate, rounded ends, hyaline when immature, reddish brown at maturity, 1-septate,

not constricted at the septum, with minute guttules in each cell, rough-walled, verruculose.

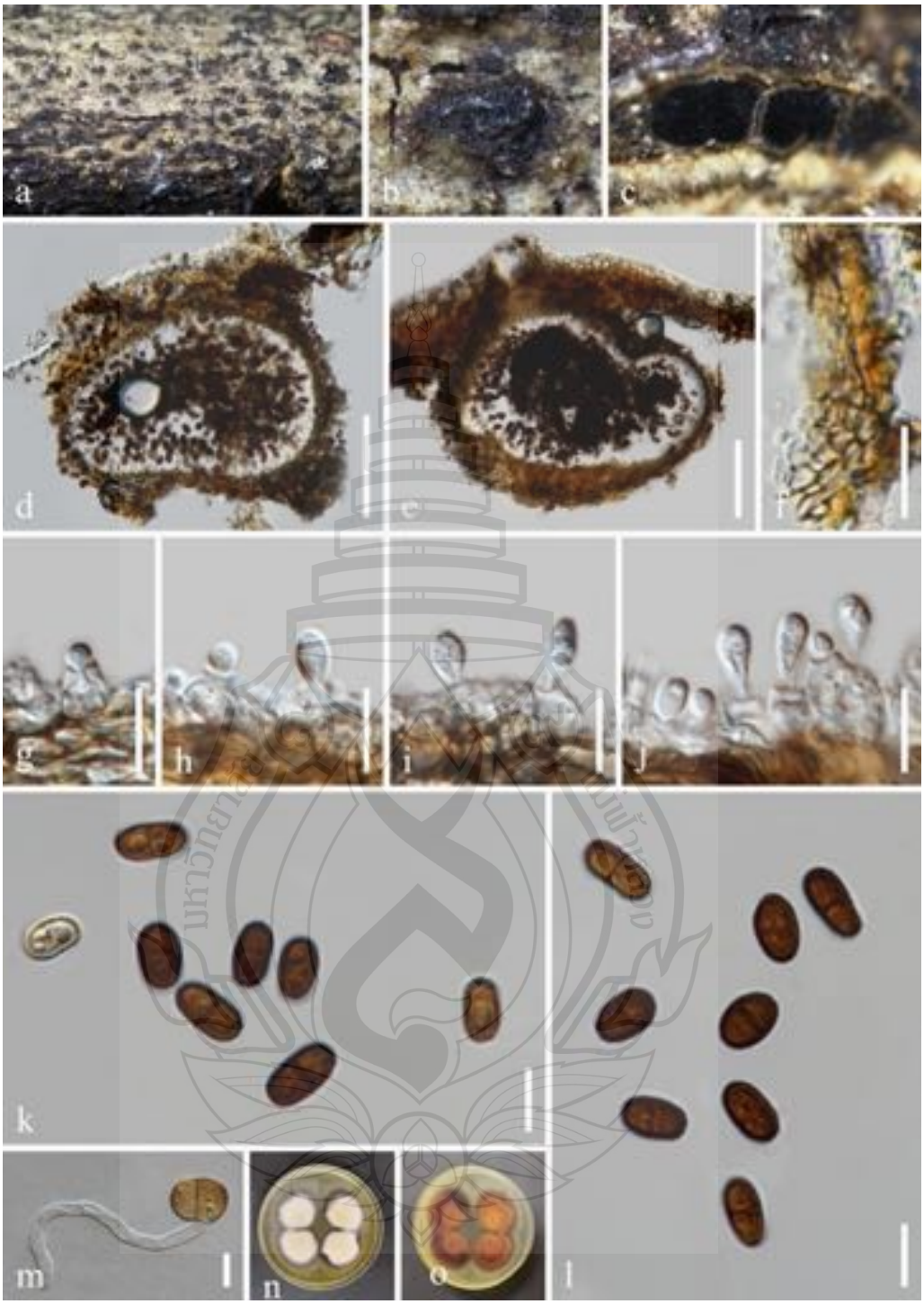
Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 32–34 mm in diam. after three weeks at 25℃ in the dark, circular, dense, covered with off-white aerial mycelium, with filamentous margin; in reverse, brown in the center, yellowish brown at the edge, with concentric rings.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa roxburghii*, 1 February 2023, N. Wu, ML61 (HUEST XX), living culture UESTCC XX.

Hosts – *Clematis subumbellata* (Phukhamsakda et al., 2020), *Rosa roxburghii* (present study).

Known geographical distribution – China, Japan, Thailand.

Notes – Multi-locus phylogenetic analysis (Figure 3.40) showed that my isolate (UESTCC ML61) clustered with *Chromolaenicola clematidis*. Morphologically, my collection (HUEST ML61) is similar to *C. clematidis* (MFLU 17-1483, holotype) in having pycnidial, solitary, immersed, globose to subglobose conidiomata, phialidic and enteroblastic conidiogenous cells, and broad oblong to oval, 1-septate, reddish brown, verruculose conidia with guttules, without significant differences (Phukhamsakda et al., 2020). Therefore, I identify my collection as *C. clematidis*, and report *Rosa roxburghii* as a new host record in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 100 μm; f = 20 μm; g–m = 10 μm.

Figure 3.43 *Chromolaenicola clematidis* (HUEST ML61, new host record)

Chromolaenicola rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.44

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

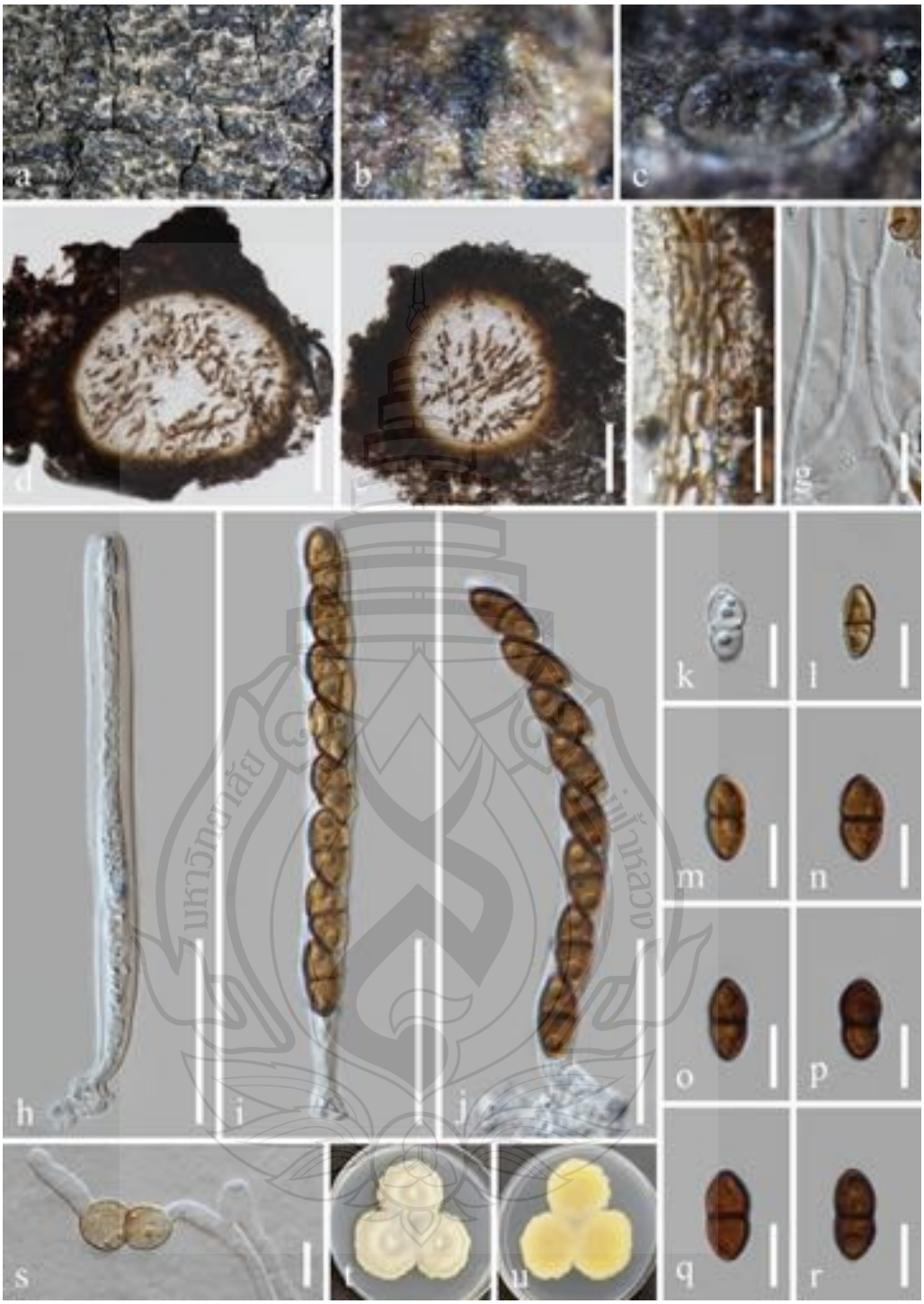
Holotype – HKAS ML131

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 292–434 µm wide, 243–329 µm high, immersed to erumpent, solitary or scattered, appearing as dark spots, coriaceous, black, globose to subglobose. *Ostiole* single, straight, central or laterally located. *Peridium* 16–25 µm wide, consisting of 3–5 layers, thin-walled cells of *textura angularis*, inner layers comprising hyaline to pale brown, and outer layers brown to dark brown cells. *Hamathecium* comprising 2.5–4.5 µm wide, cylindrical to filiform, septate, branched pseudoparaphyses, intermixed with asci. *Asci* 99–115 × 7.5–9 µm ($\bar{x}$ = 107 × 8 µm; n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, pedicellate with an ocular chamber. *Ascospores* 12–16.5 × 5.5–8.3 µm ($\bar{x}$ = 14 × 6.7 µm; n = 30), uniseriate, initially hyaline, 1-septate when immature, becoming reddish brown to brown at maturity, ellipsoid to broadly fusiform with slightly acute ends, muriform, guttulate, smooth-walled, 1-transversely septate, constricted at the central septum, straight. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 35–37 mm in diam. after three weeks at 25℃ in the dark, circular, dense, and have a regular edge, appearing yellowish white from above; in reverse, yellowish brown in the middle and white at the margin.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML131 (HKAS XX, **holotype**); ex- type living culture CGMCC XX; *ibid*., ML133A (HUEST XX), living culture UESTCC XX.

Notes – In the phylogenetic analysis, *Chromolaenicola rosae* formed a distinct branch within *Chromolaenicola* with a strong support (Figure 3.40). Based on a megablast search of the NCBI GenBank nucleotide sequence database using the ITS sequence of *C. rosae*, the highest similarity (97.34%) is with *C. clematidis* (MFLUCC 17-2075) with 16 base pair differences (586/602 bp, three gaps). Thus, I recognize *C. rosae* as a new species following the guidelines of Jeewon and Hyde (2016).



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–r Ascospores. s Germinating ascospore. t, u Colonies on PDA, above (t), below (u). Scale bars: d, e = 100 μm; f = 20 μm; h–j = 30 μm; g, k–s = 10 μm.

Figure 3.44 *Chromolaenicola rosae* (HKAS ML131, holotype)

Chromolaenicola sapindi G.C. Ren & K.D. Hyde, Biology 11(no. 1660): 13(2022) Figure 3.45

Index Fungorum number: IF 559806; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 297–336 µm wide, 425–447 µm high, immersed to erumpent, solitary or scattered, coriaceous, appearing as dark spots, ampulliform or obovoid, dark brown to black. *Ostiole* 125–147 µm wide, 108–129 µm high, central, filled with periphyses. *Peridium* 17–26 µm wide, multi-layered, thin-walled, composed of *textura angularis* cells, inner layers hyaline to pale brown, and outer layers brown to dark brown. *Hamathecium* comprising 1.5–2.8 µm wide, filiform, septate, branched pseudoparaphyses, embedded in a hyaline, gelatinous matrix. *Asci* 107–119 × 11.5–14 µm ($\bar{x}$ = 114 × 13 µm; n = 20), 8-spored, bitunicate, cylindrical to clavate, straight or slightly curved, apically rounded, pedicellate, with an ocular chamber. *Ascospores* 15–20 × 7.8–9 µm ($\bar{x}$ = 17 × 8.5 µm; n = 30), overlapping, uniseriate, initially hyaline, aseptate or 1-septate, guttulate when immature, becoming reddish brown to brown at maturity, ellipsoid to broadly fusiform, guttulate, and 1-septate, slightly constricted at the central septum, straight, thick and smooth-walled, without gelatinous sheath. Asexual morph: undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 20–22 mm in diam. after three weeks at 25°C in the dark, circular, dense, regular edge, covered with pale yellowish-white aerial mycelium, in reverse, yellowish brown in the centre, light yellow ring at the edge.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL65 (HUEST XX), living culture UESTCC XX; *ibid.*, Guizhou Province, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of

R. *roxburghii*, 4 February 2023, N. Wu, ML193 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), *Sapindus rarak* (Ren et al., 2022).

Known geographical distribution – China.

Notes – *Chromolaenicola sapindi* was introduced by Ren et al. (2022) and isolated from *Sapindus rarak* in China. Multi-locus phylogenetic analysis (Figure 3.40) showed that my isolates (UESTCC SL65 and UESTCC ML193) clustered with *C*. *sapinda* (KUMCC 21-0564). Morphologically, my collection is similar to *C*. *sapindi* (HKAS 122789, holotype) in having immersed to erumpent, ampulliform or obovoid ascomata, 8-spored, bitunicate, cylindrical to clavate asci with an ocular chamber, and septate, reddish brown to brown, ellipsoid to broadly fusiform ascospores without gelatinous sheath, without significant differences. Therefore, I identify my collection as *C*. *sapindi*, while *Rosa roxburghii* is a new host record.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–l Asci. m–s Ascospores. t Germinating ascospore. u, v Colony on PDA, above (u), below (v). Scale bars: d = 100 μm; e = 50 μm; f, h–l = 30 μm; g, t = 15 μm; m–s = 10 μm.

Figure 3.45 *Chromolaenicola sapindi* (HUEST SL65, new host record)

Kalmusia Niessl, Verh. Naturf. Vereins Brünn 10: 204 (1872)

Type species – *Kalmusia ebuli* Niessl

Notes – *Kalmusia* was established by Niessl (1872) with *K. ebuli* as the type species. Most species are described based on their sexual morph, which is characterized by septate pseudoparaphyses, narrowly ovoid to clavate asci, and 3-septate ascospores (Ariyawansa et al., 2014; Zhang et al., 2014; Hyde et al., 2020a). The asexual morphs are coniothyrium-like and have been reported in *K. araucariae*, *K. italica*, *K. longispora*, and *K. spartii* (Tennakoon et al., 2016).

Kalmusia rosae N. Wu, Hong-Zhi Du & Jian K. Liu, sp. nov. Figure 3.46

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML198

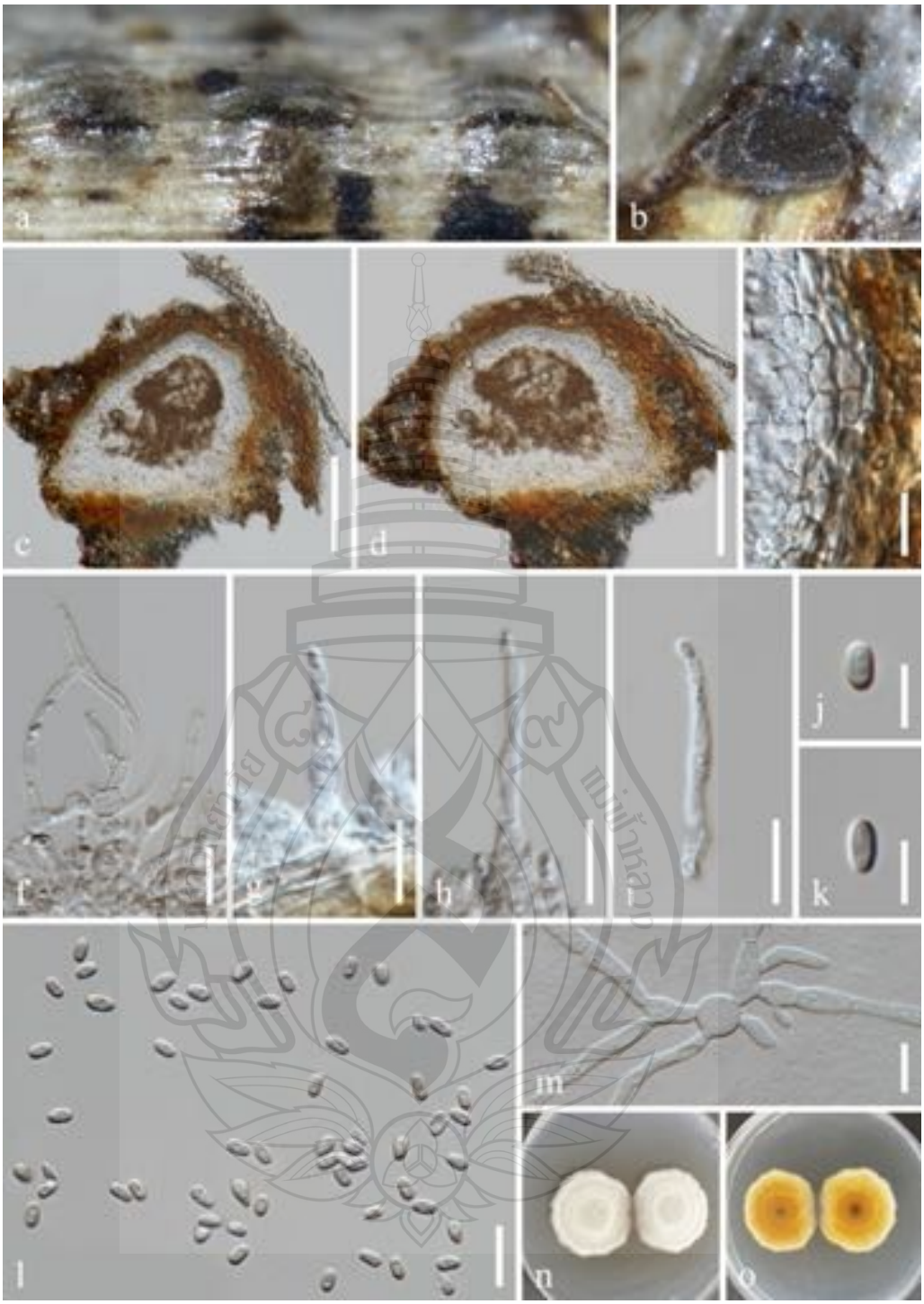
Saprobic on dead twigs of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 215–276 μm wide, 256–314 μm high, pycnidial, solitary, immersed to erumpent, apapillate, brown to dark brown, globose to subglobose or oblate-spheroid, coriaceous, ostiolate. *Ostiole* central, apapillate. *Conidiomatal wall* 14.5–17 μm wide, comprising several layers of *textura angularis* cells, the outer layer consists of thick-walled, brown to dark brown cells, while the inner layer is mostly composed of hyaline to pale brown, thin-walled cells, with bearing conidiogenous cells. *Paraphyses* 1.7–2.6 μm wide, hyaline, arising from the inner wall layer of locules, septate, branched, filiform. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* 14–20 × 2.5–3.5 μm ($\bar{x}$ = 18.5 × 3 μm; n = 20), phialidic, hyaline, discrete, determinate, cylindrical and smooth-walled. *Conidia* 3.6–4.7 × 1.9–2.5 μm ($\bar{x}$ = 4.1 × 2.2 μm; n = 30), hyaline to pale brown, ellipsoidal to oval with rounded ends, aseptate, smooth-walled, with two small polar guttules.

Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 30–32 mm

diam. after three weeks at 25°C in the dark, circular, regular, dense mycelium, white, entire edge; in reverse, dark brown at the central point, yellowish brown in the middle, and pale yellowish white at the edge.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML198 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, ML198B (HUEST XX), living culture UESTCC XX.

Notes – Multi-locus phylogenetic analysis (Figure 3.40) revealed that *Kalmusia rosae* (CGMCC ML198 and UESTCC CMD18) formed a distinct clade, which is sister to *K. cordylines* (ZHKUCC 21-0092, ex-type strain). Morphologically, my new collection resembles *K. cordylines* (ZHKU 21-0003, holotype) in having pycnidial, solitary, globose to subglobose conidiomata, phialidic, hyaline, cylindrical conidiogenous cells, and aseptate, ellipsoidal to oval conidia with two-minute polar guttules (Manawasinghe et al., 2022). However, *K. rosae* differs from *K. cordylines* by its smaller conidiomata (215–276 × 256–314 μm vs. 280–350 × 380–440 μm), and longer conidiogenous cells (14–20 × 2.5–3.5 μm vs. 5–10 × 5–6 μm) (Manawasinghe et al., 2022). Additionally, comparison of the nucleotide base pairs between ex-type strains showed that *K. rosae* can be distinguished from *K. cordylines* by 10/516 bp (1.9%) in ITS, 12/884 bp (1.4%) in LSU, and 20/959 bp (2.1%) in SSU sequence data. Therefore, *K. rosae* is introduced as a new species based on morphological and phylogenetic evidence.



Note a Conidiomata on natural substrate. b–d Vertical sections of conidiomata. e Conidiomatal wall. f Paraphyses. g–i Conidiogenous cells and developing conidia. j–l Conidia. m Germinating conidium. n, o Colonies on PDA, above (n), below (o). Scale bars: c, d = 50 μm; e–i, l–m = 10 μm; j–k = 5 μm.

Figure 3.46 *Kalmusia rosae* (HKAS ML198, holotype)

Montagnula Berl., Icon. fung. (Abellini) 2: 68 (1896)

Type species: *Montagnula infernalis* (Niessl) Berl.

Notes: *Montagnula* was established by Berlese (1896), with *M. infernalis* as the type species. Barr (2001) introduced the family Montagnulaceae in Pleosporales with three genera *Kalmusia*, *Montagnula*, and *Didymosphaerella*. Subsequently, Montagnulaceae was synonymized with Didymosphaeriaceae, and *Montagnula* was transferred to Didymosphaeriaceae (Ariyawansa et al., 2014). The sexual morph of *Montagnula* is characterized by immersed, globose or spherical ascomata, claviform asci, and fusoid to ellipsoid ascospores of three different types (dictyospore, didymospore and phragmospore), with transverse and one or more longitudinal septa (Tanaka et al., 2015). The asexual morph is characterized by solitary, brown to dark brown, globose to subglobose conidiomata, hyaline, phialidic, ampulliform to doliiform conidiogenous cells, and hyaline, aseptate, cylindrical conidia (Crous et al., 2020b). Currently, 61 epithets are listed in Index Fungorum (2025, June), but only 34 species have molecular data.

Montagnula verniciae W.L. Li & Jian K. Liu, Mycosphere 14(1): 1464 (2023) Figure 3.47

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: *Ascomata* 462–489 µm wide, 483–492 µm high, immersed to erumpent, solitary or scattered, globose to subglobose, coriaceous, dark brown to black, with wide papilla, ostiolate. *Ostiole* 156–176 µm wide, 168–188 µm high, papillate, central or eccentric, filled with periphyses. *Peridium* 23–27 µm wide, comprising 4–5 layers, fused with host tissues, thick-walled, brown to reddish-brown cells of *textura angularis*. *Hamathecium* 1.5–2.7 µm wide, hyaline, septate, cylindrical to filiform, branched, anastomosing at the apex, filamentous pseudoparaphyses. *Asci* 88.5–126 × 19–24 µm ($\bar{x}$ = 107 × 22 µm; n = 30), 8-spored, bitunicate, fissitunicate, elongate clavate, slightly curved, with a long pedicel with knob-like to furcate base, apically rounded, with a small ocular chamber.

Ascospores 20.5–26 × 7.3–10.5 µm ($\bar{x}$ = 23 × 8.8 µm; n = 30), overlapping, uni- to bi-seriate, straight to slightly curved, ellipsoidal to fusiform with rounded and subhyaline ends, aseptate and hyaline when immature, 1-septate, 2-celled and becoming brown to reddish-brown when mature, constricted at the septum, slightly widest at the upper cell and tapering towards ends, smooth-walled, guttulate, surrounded by irregular mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 45–48 mm in diam. after three weeks at 25℃ in the dark, white, medium dense, superficial, circular with erose edge, covered with white aerial mycelium; in reverse, grayish brown in the center, and grayish white ring at the edge.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″N, 105°30′54″E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML44 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa sterilis* (present study), *Vernicia fordii* (Li et al., 2023b).

Known geographical distribution – China.

Notes – *Montagnula verniciae* isolated from *Vernicia fordii* in China was introduced by Li et al. (2023b) with the sexual morph. Multi-gene phylogenetic analysis showed that my isolate (UESTCC ML44) clustered with *M. verniciae* (CGMCC 3.24435) with a strong statistical support (Figure 3.40). Morphologically, my collection (HUEST ML44) is similar to *M. verniciae* in having immersed, solitary or scattered, globose to subglobose ascomata, 8-spored, bitunicate, fissitunicate, clavate asci, and ellipsoidal to fusiform, septate, guttulate, hyaline to reddish-brown ascospores, without significant differences. Therefore, I identify my collection as *M. verniciae*, with *Rosa sterilis* as a new host record.



Note a Appearance of ascomata on host surface. b–d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: c, d=200 µm; e = 100 µm; f, g = 20 µm; h–j = 30 µm; k–q = 10 µm.

Figure 3.47 *Montagnula verniciae* (HUEST ML44, new host record)

Paraconiothyrium Verkley, Stud. Mycol. 50(2): 327 (2004)

Type species – *Paraconiothyrium estuarinum* Verkley & Manuela Silva

Notes – Verkley et al. (2004) established the genus *Paraconiothyrium* to accommodate four coelomycetous taxa, *P. brasiliense*, *P. cyclothyrioides*, *P. estuarinum* and *P. fungicola*, and transferred *Coniothyrium minitans* and *C. sporulosum* to the genus *Paraconiothyrium*. Currently, 36 epithets are registered in Index Fungorum (2025, June). Among them, *P. africanum*, *P. fungicola* and *P. hawaiiense* were transferred to the genus *Pseudocamarosporium* by Crous et al. (2015b) and Wijayawardene et al. (2016). *Paraconiothyrium minitans* and *P. sporulosum* were transferred to the genus *Paraphaeosphaeria* by Verkley et al. (2014). *Paraconiothyrium flavescens* was transferred to the genus *Pseudocoleophoma* by Li et al. (2020). *Paraconiothyrium rosae* was synonymized with *P. fuckelii* (Tennakoon et al., 2022) and *P. variabile* was transferred to the genus *Didymosphaeria* by Ariyawansa et al. (2014).

Most members of *Paraconiothyrium* have coelomycetous asexual morphs and are characterized by eustromatic to pycnidial conidiomata, phialidic or annelidic conidiogenous cells, and hyaline to brown conidia (Verkley et al., 2004, 2014; Hongsanan et al., 2020a; Xiong et al., 2024). A few species have sexual morphs, viz., *P. fuckelii*, *P. iridis*, *P. magnoliae*, *P. thysanolaenae*, *P. yunnanense* and *P. zingiberacearum*, and are characterized by immersed to semi-immersed, globose to sub-globose ascomata and bitunicate, 8-spored, fissitunicate, clavate to cylindrical asci with fusiform to ellipsoidal, septate, hyaline to brown ascospores (Ariyawansa et al., 2014; Liu et al., 2015a; Lu et al., 2022b; Tennakoon et al., 2022).

Paraconiothyrium brasiliense Verkley, Stud. Mycol. 50(2): 329 (2004) Figure 3.48

Index Fungorum number: IF500082; Facesoffungi number: FoF10757

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 80–110 µm wide, 75–100 µm high, solitary to gregarious, dark brown, immersed to semi-immersed, visible as black dots

on the host, pycnidial, globose to subglobose, mostly unilocular, occasionally multi-locular, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Conidiomatal wall* 8–15 μm wide, comprising 3–5 layers, hyaline to brown, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–8.5 × 2–3.5 μm ($\bar{x}$ = 5.8 × 2.8 μm; n = 30), hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical, and arising from the inner layers of conidiomata. *Conidia* 3–4.5 × 1.5–2 μm ($\bar{x}$ = 4 × 1.8 μm; n = 30), initially hyaline, brown after secession, oval or globose to subglobose, rounded at both ends, or with a rounded apex and a truncate base, straight, aseptate, smooth-walled, guttulate.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 43–45mm diam. after two weeks at 25℃ in dark, circular, velvety, entire, white aerial mycelium mixed with yellow; in reverse, pale brown with yellow in the middle, yellowish white at periphery, becoming lighter towards the borders.

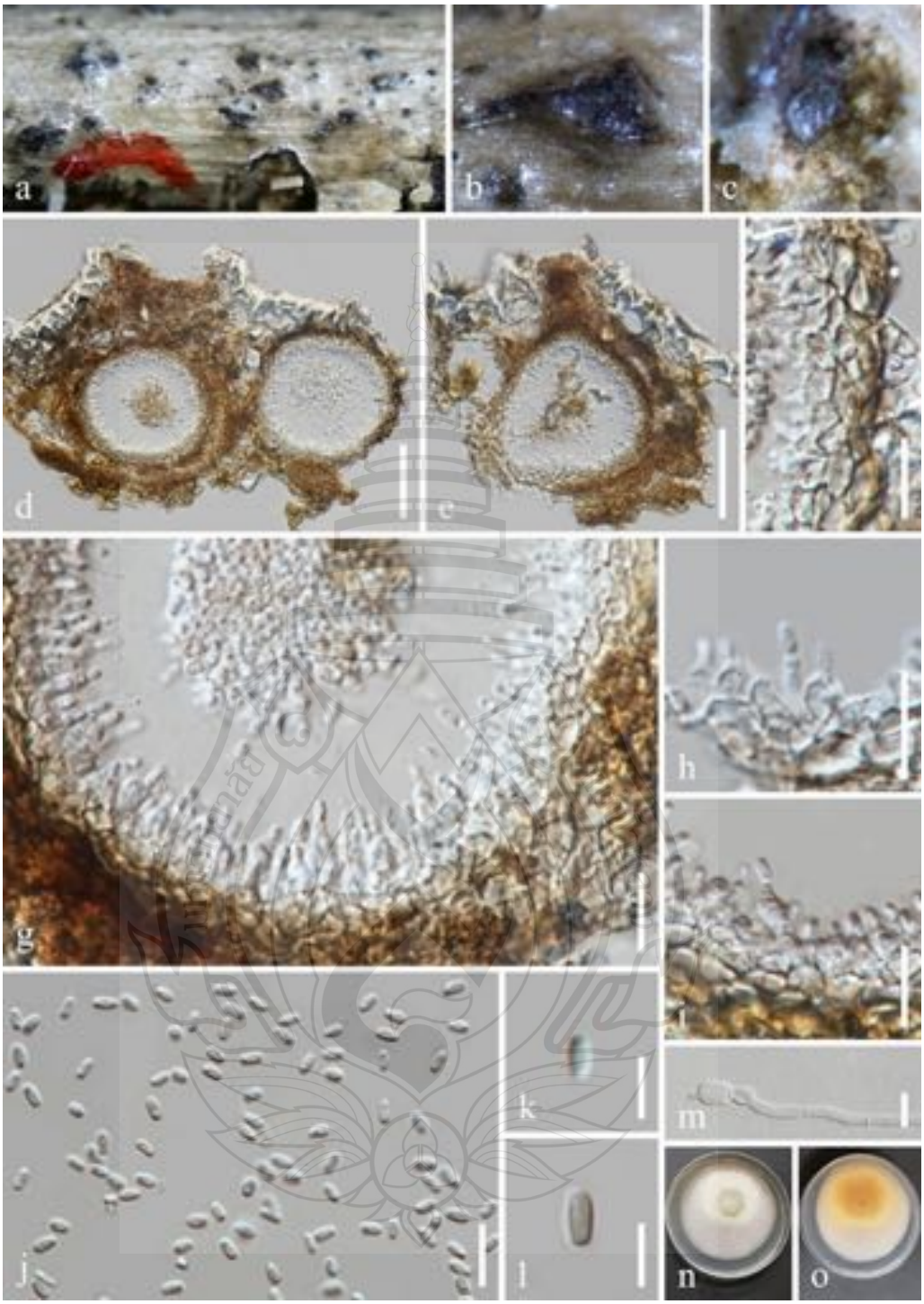
Material examined – CHINA, Guizhou Province, Anshun City, Zhenning County, Baima Village, elevation 1,280 m, 26°2′35″ N, 105°44′12″ E, on dead branches of *Rosa roxburghii*, 3 July 2022, N. Wu, GL94 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer truncatum*, *Aesculus* sp., *Coffea arabica*, *Gleditsia* sp., *Magnolia* sp., *Pachysandra terminalis*, *Phoradendron perrottettii*, *Prunus persica*, *P. salicina*, *Quercus prinoides*, *Rosa roxburghii*, *Sarcococca saligna*, *Tapirira guianensis* and *Vitis vinifera* (Verkley et al., 2004; Choi et al., 2014; Afshan et al., 2020; NCBI; present study).

Known geographical distribution – Brazil, Canada, China, Italy, Korea, Pakistan, South Africa, Spain.

Notes – Verkley et al. (2004) introduced *Paraconiothyrium brasiliense*, which was originally isolated from the fruits of *Coffea arabica* in Brazil. This species has a worldwide distribution and occurs on various substrates, functioning as a saprobe, plant

pathogen, endophyte, and even as a human pathogen (Nakashima et al., 2019; Afshan et al., 2020; Liu et al., 2023b). It has also been reported to exhibit diverse biological activities (Liu et al., 2015b; Arredondo-Santoyo et al., 2018). In the present study, my strain (UESTCC GL94) clustered with *P. brasiliense* (CB 100299 and CBS 115.92) (Figure 3.49), and the morphology of my collection is similar to the original description of *P. brasiliense* (Verkley et al., 2004). Therefore, I identify my collection as *P. Brasiliense* and extend the known host range of this species to *Rosa roxburghii*.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j–l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 50 μm; f–j, m = 10 μm; k–l = 5 μm.

Figure 3.48 *Paraconiothyrium brasiliense* (HUEST GL94, new host record)

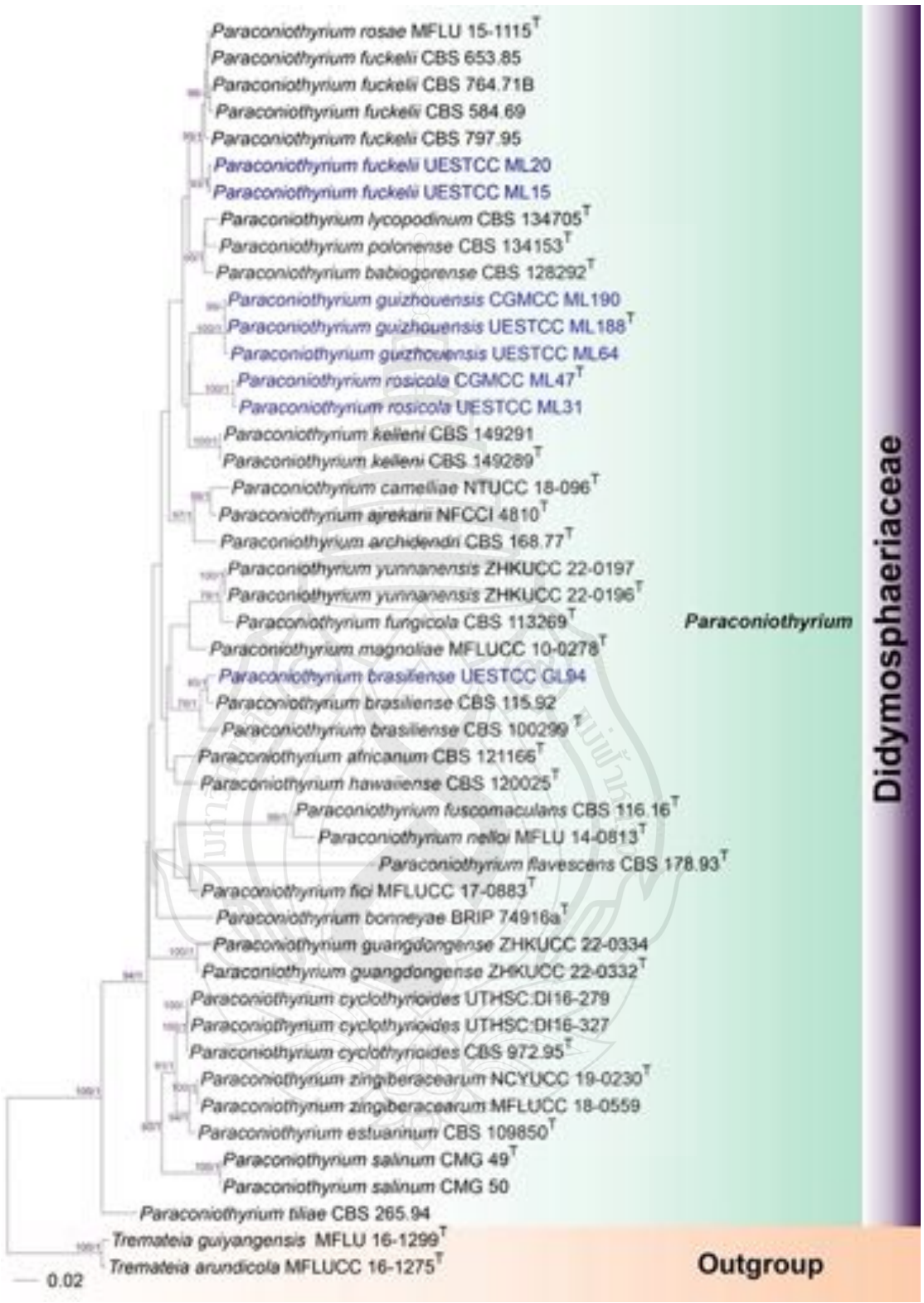


Figure 3.49 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α* and *tub2* sequence data of *Paraconiothyrium*

Figure 3.49 The tree is rooted with *Trematеia arundicola* (MFLUCC 16-1275) and *T. guiyangensis* (MFLU 16-1299). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Paraconiothyrium fuckelii Verkley & Gruyter, Stud. Mycol. 75: 25 (2012) [2013] Figure 3.50

Index Fungorum number: IF564787; Facesoffungi number: FoF00055

Saprobic on dead branches of *Rosa sterilis*. Sexual morph: see Ariyawansa et al. (2014). Asexual morph: Coelomycetous. *Conidiomata* 208–272 μm wide, 126–223 μm high, solitary or confluent, dark brown, immersed to semi-immersed, visible as black dots on the host, pycnidial, globose to pyriform, mostly unilocular, occasionally multi-locular, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. Ostiole central, single. *Conidiomatal wall* 13–27 μm wide, composed of thick-walled, brown cells of *textura globulosa* on the exterior, gradually merging with hyaline cells of *textura prismatica* in inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.8–7 × 2.5–5 μm ($\bar{x}$ = 5.4 × 3.5 μm; n = 30), hyaline, aseptate, smooth, thin-walled, cylindrical to lageniform, determinate, formed from inner layers of conidiomata. *Conidia* 3–4.2 × 2.3–2.8 μm ($\bar{x}$ = 3.6 × 2.5 μm; n = 30), initially hyaline, brown after secession, subglobose to obovoid, rounded at both ends, or with a rounded apex and a truncate base, straight, aseptate, smooth-walled, guttulate.

Culture characteristics: Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 35–40 mm diam. after two weeks at 25°C in dark, circular, velvety, entire, white.

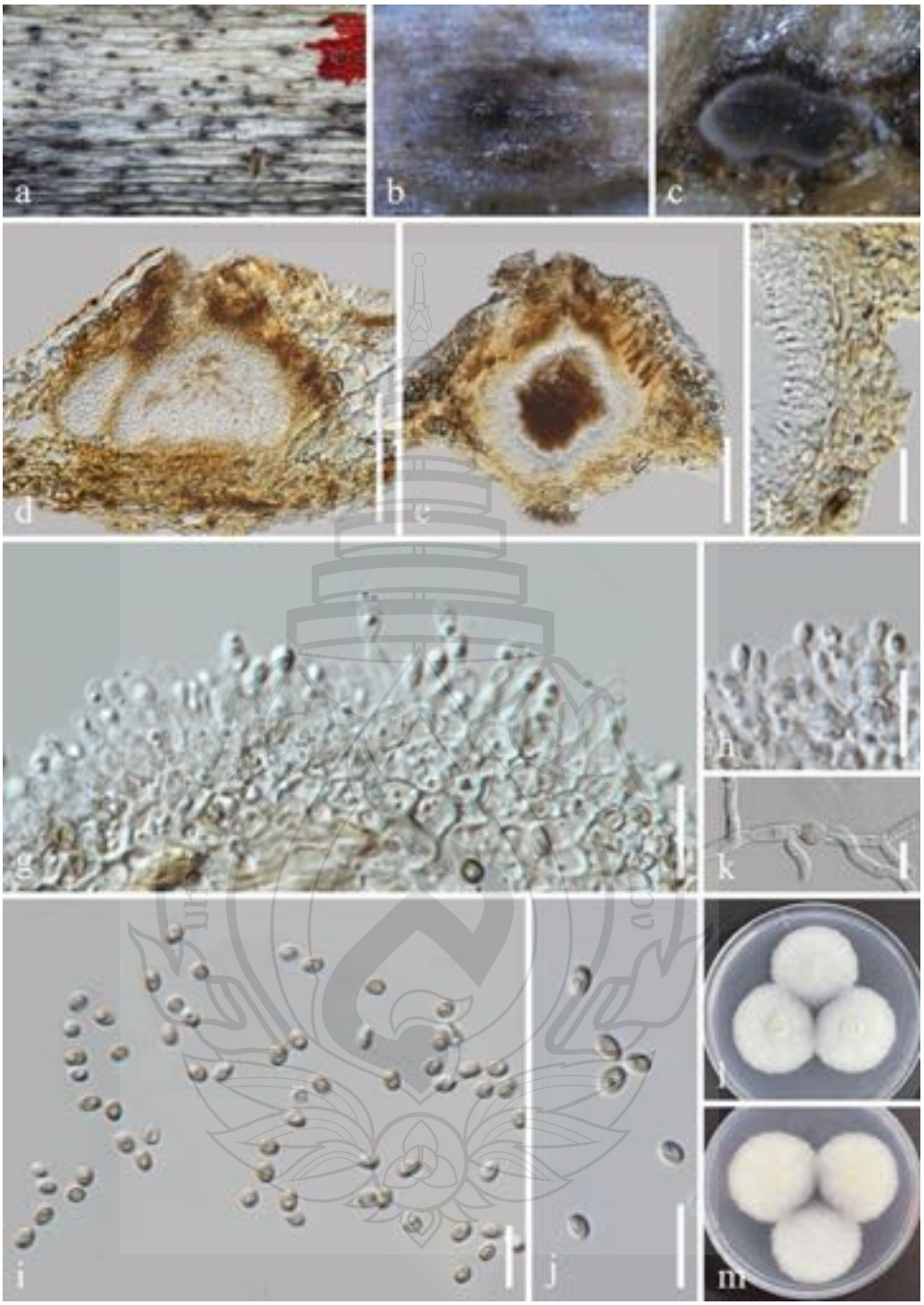
Materials examined: CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead

branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML15 (HUEST XX), living culture UESTCC XX, *ibid*., ML20 (HUEST XX), living culture UESTCC XX.

Hosts: *Dimocarpus longan*, *Picea abies*, *Prunus* sp., *Punica granatum*, *Rosa hybrid*, and *Rubus* sp. (de Gruyter et al., 2013; Verkley et al., 2014; Gafforov, 2017; Jamali, 2020; present study).

Known geographical distribution: China, Denmark, Germany, Iran, Netherlands, Thailand and Uzbekistan.

Notes: de Gruyter et al. (2013) transferred several Phoma-like species, which grouped outside the Pleosporineae to the genera *Aposphaeria*, *Paraconiothyrium* and *Westerdykella*, based on the LSU sequence analysis. For instance, *Coniothyrium fuckelii* has been transferred to *Paraconiothyrium*. Ariyawansa et al. (2014) provided a detailed description of the sexual and asexual morphs of *P. fuckelii* collected from dead wood in Thailand. Tennakoon et al. (2022) synonymized *P. rosae* under *P. fuckelii* based on the morphological and phylogenetic evaluation. In the phylogenetic tree, my isolates (UESTCC ML15 and UESTCC 20) cluster with *Paraconiothyrium fuckelii* (Figure 3.49). My collection is morphologically almost identical to *P. fuckelii* as provided by Ariyawansa et al. (2014) and confirmed with molecular comparisons. *Paraconiothyrium fuckelii* has been reported as a serious plant pathogen of Rosaceae (Horst & Cloyd, 2007) as well as an opportunistic human pathogen (de Hoog et al., 2000). In the present study, my collection was obtained from *Rosa sterilis*, and is reported as a new host record in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. Conidiomatal wall. g, h Conidiogenous cells and developing conidia. i, j Conidia. k Germinating conidium. l, m Colony on PDA, above (l), below (m). Scale bars: d, e = 100 μm; f = 20 μm; g–k = 10 μm.

Figure 3.50 *Paraconiothyrium fuckelii* (HUEST ML15, new host record)

Paraconiothyrium guizhouense N. Wu & Jian K. Liu, sp. nov. Figure 3.51; Figure 3.52

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*guizhouensis*" refers to the holotype being collected from Guizhou Province.

Holotype – HKAS ML188

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 128–190 µm wide, 206–258 µm high, solitary to gregarious, brown to dark brown, initially immersed, raising host surface, ellipsoid to subglobose, unilocular, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Peridium* 15–27 µm wide, composed of brown to hyaline cells of *textura angularis*, gradually merging with cells in inner layers. *Hamathecium* 1.5–2.2 µm wide, composed of numerous, filamentous, rarely branched and anastomosed, septate, hyaline, cellular pseudoparaphyses. *Asci* 80–102 × 11–15 µm ($\bar{x}$ = 88 × 13 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short and furcate pedicel, apically rounded, with a minute ocular chamber. *Ascospores* 17–28 × 5–10 µm ($\bar{x}$ = 21 × 7 µm; n = 30), biseriate, narrowly ovoid to clavate, the upper cell slightly wider than the lower cell, hyaline, becoming pale brown at maturity, paler towards the base, 1–3-septate, constricted at the middle septum, smooth-walled, without a sheath or appendages. Asexual morph: Coelomycetous. *Conidiomata* 197–290 µm wide, 222–300 µm high, solitary to gregarious or confluent, dark brown, semi-immersed to superficial, visible as black dots on the host, pycnidial, globose to pyriform, unilocular, glabrous, coriaceous, smooth-walled, short papillate, with rounded or cylindrical, inconspicuous ostiolate. *Conidiomatal wall* 18–37 µm wide, 6–9 layers, consisting of brown and small-celled *textura angularis*, becoming hyaline towards the inner region. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.2–5.4 × 2.7–4.8 µm, hyaline, aseptate, sometimes 1-septate, smooth, thin-walled, ampulliform to subcylindrical, and arising from the inner layers of conidiomata. *Conidia* 3.7–5 × 2.7–4.8 µm ($\bar{x}$ = 4.3 × 3 µm; n = 30), hyaline when liberated, later brown, narrowly ellipsoidal or short-cylindrical,

rounded at both ends, or with a rounded apex and a truncate base, straight, aseptate, smooth-walled, guttulate.

Culture characteristics – Ascospores and conidia germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25°C in dark, circular, flat, dry, white; in reverse, pale brown in the middle, white mycelium in the outer ring.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML188 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, ML190 (HUEST XX), living culture UESTCC XX; *ibid*., Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML64 (HUEST XX, paratype), living culture UESTCC XX.

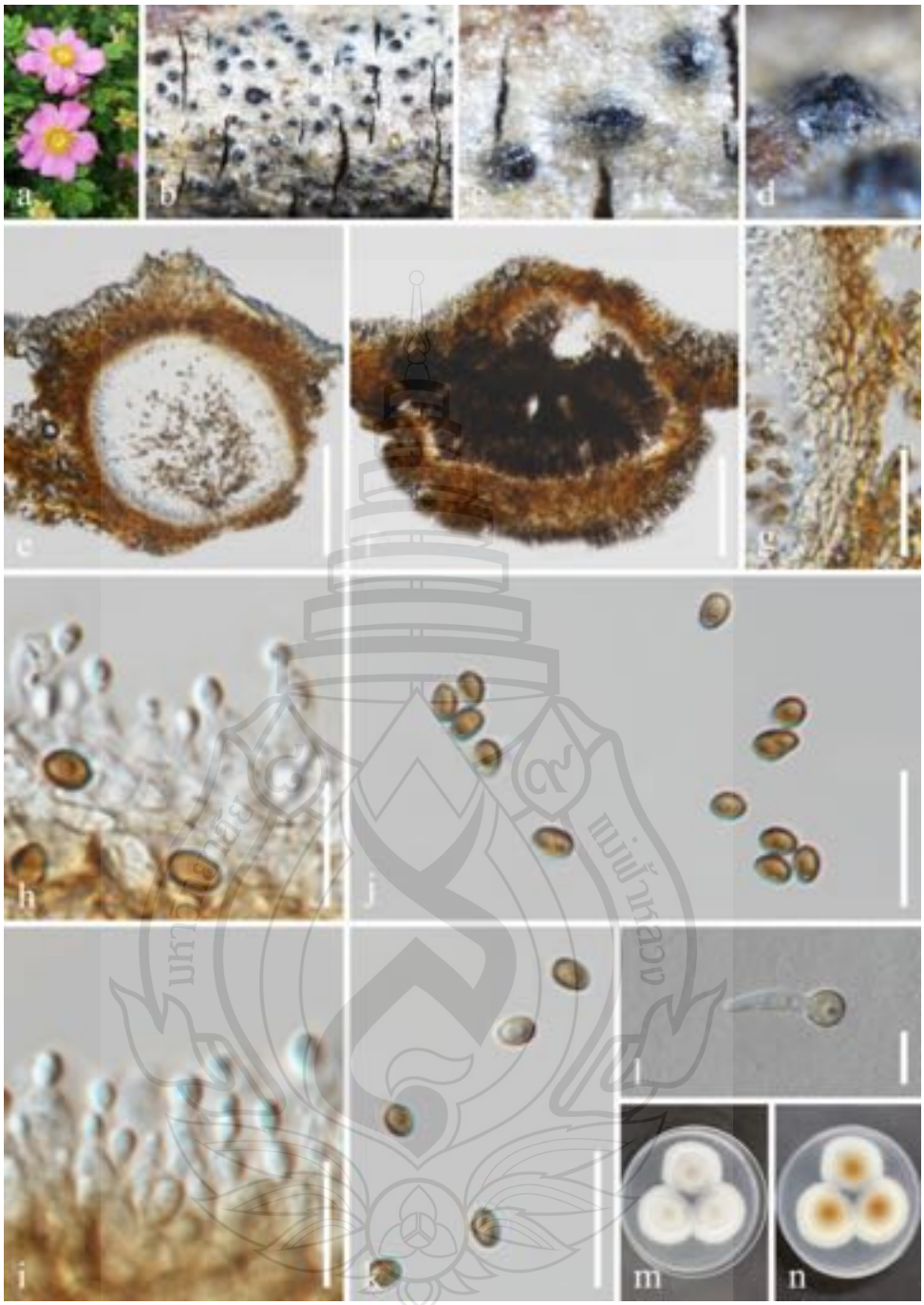
Notes – I isolated both the asexual and sexual morphs of *Paraconiothyrium guizhouense* from *Rosa roxburghii* and *R. sterilis*. Phylogenetic analysis revealed that *P. guizhouense* (CGMCC ML188, UESTCC ML190 and UESTCC ML64) forms a distinct lineage that clusters closely with *P. rosicola* (CGMCC ML47 and UESTCC ML31) (Figure 3.49). Morphologically, *P. guizhouense* shares similar characters with the sexual morphs of *P. fuckelii*, *P. iridis*, *P. magnoliae*, *P. thysanolaenae*, *P. yunnanense* and *P. zingiberacearum* in having bitunicate, 8-spored, fissitunicate, clavate to cylindrical asci and brown ascospores (Ariyawansa et al., 2014; Lu et al., 2022b; Tennakoon et al., 2022). However, they can be distinguished by the shape and dimensions of the ascospores. Since *P. rosicola* lacks a sexual morph, it cannot be compared morphologically with *P. guizhouense.* The asexual morph of *P. guizhouense* differs from that of *P. rosicola* by having larger conidiomata (197–290 × 222–300 μm vs. 182–238 × 187–210 μm) and conidia (3.7–5 × 2.7–4.8 μm vs. 2.8–4.8 × 2.8–3.6 μm), while they differ in shape of the conidia (ellipsoidal to short-cylindrical vs. subglobose to obovoid). Based on both

morphological and phylogenetic evidence, *P. guizhouense* and *P. rosicola* can be regarded as different species.



Note a Host: *Rosa roxburghii*. b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–s Ascospores. t Germinating ascospore. u, v Colony on PDA, above (u), below (v). Scale bars: d, e = 80 μm; f–l = 20 μm; m–t = 10 μm.

Figure 3.51 *Paraconiothyrium guizhouense* (HKAS ML188; sexual morph**,** holotype)



Note a Host: *Rosa sterilis*. b–d Conidiomata on natural substrate. e, f Vertical sections of conidiomata. g Conidiomatal wall. h, i Conidiogenous cells and developing conidia. j, k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: e = 100 µm; f = 150 µm; g = 30 µm; h, i, l = 10 µm; j–k = 15µm.

Figure 3.52 *Paraconiothyrium guizhouense* (HKAS ML64; asexual morph)

Paraconiothyrium rosicola N. Wu & Jian K. Liu, sp. nov. Figure 3.53

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosicola*" refers to the host genus, *Rosa*, on which the species was isolated.

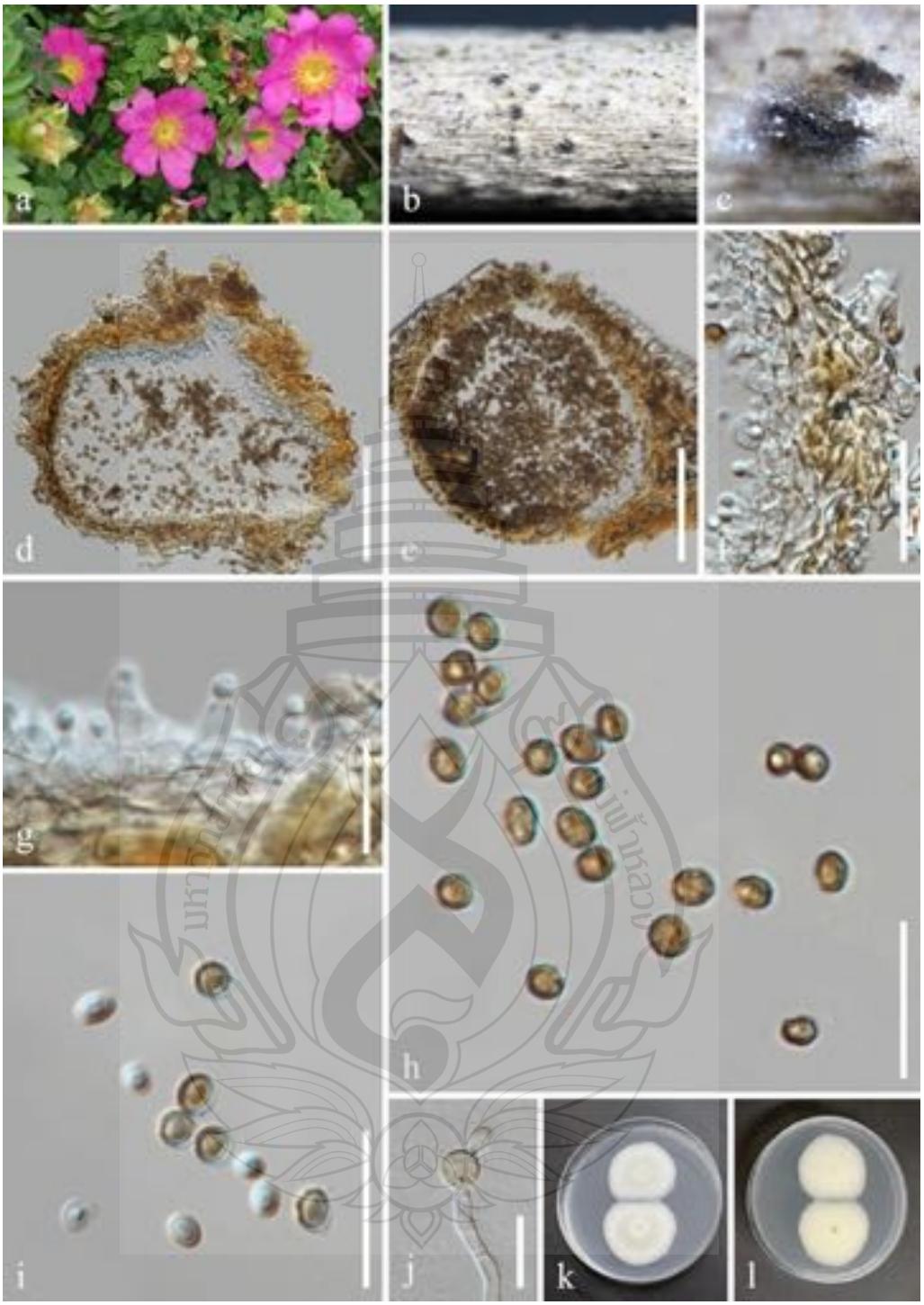
Holotype – HKAS ML47

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 182–238 μm wide, 187–210 μm high, mostly solitary, occasionally gregarious, dark brown, immersed to partly erumpent, visible as black dots on the host, pycnidial, globose to pyriform, mostly unilocular, occasionally multi-locular, glabrous, coriaceous, smooth-walled, short papillate, inconspicuous ostiole. *Conidiomatal wall* 15–24 μm wide, composed of 4–6 layers, brown, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.2–5.4 × 2.7–4.8 μm, hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical, and arising from the inner layers of conidiomata. *Conidia* 2.8–4.8 × 2.8–3.6 μm ($\bar{x}$ = 3.7 × 3 μm; n = 30), initially hyaline, brown after secession, subglobose to obovoid, rounded at both ends, or with a rounded apex and a truncate base, straight, aseptate, smooth-walled, thickened and darkened, rarely guttulate.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 35–37 mm diam. after two weeks at 25℃ in dark, pale yellow to white, dry, flattened, dense, entire; in reverse, white to yellow with an entire margin.

Materials examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML47 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, ML31 (HUEST XX, paratype), living culture UESTCC XX.

Notes – In the phylogenetic tree constructed from ITS, LSU, *tef1α* and *tub2* gene regions, *Paraconiothyrium rosicola* (CGMCC ML47 and UESTCC ML31) nested within *Paraconiothyrium*, closer to *P. guizhouense* (CGMCC ML188, UESTCC ML190 and UESTCC ML64) and *P. kelleni* (CBS 149289 and CBS 149291) (Figure 3.49). Comparisons of the ITS, LSU, *tef1α* and *tub2* sequences of *P. rosicola* and *P. guizhouense* revealed 92.08% (535/581 bp, 23 gaps), 99.42% (862/867 bp, 2 gaps), 95.80% (935/976 bp, 1 gap) and 90.29% (372/412 bp, 0 gap) similarities, respectively. Comparisons of the ITS, LSU, *tef1α* and *tub2* sequences of *P. rosicola* and *P. kelleni* revealed 91.81% (538/586 bp, 24 gaps), 99.42% (850/855 bp, 2 gaps), 95.15% (922/969 bp, 4 gaps) and 89.95% (367/408 bp, 4 gaps) similarities, respectively. Morphologically, *P. rosicola* fits the descriptions of asexual morphs in *Paraconiothyrium*, characterized by smaller, hyaline conidia when liberated, which later turn brown and are aseptate (Verkley et al., 2004; Ariyawansa et al., 2014; Tennakoon et al., 2022; Xiong et al., 2024). However, they can be distinguished by the conidial shapes and dimensions of conidia (Tan et al., 2022). Considering the morpho-molecular data, here I introduced *P. rosicola* as a new species.



Note a Host: *Rosa sterilis*. b, c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Conidiomatal wall. g Conidiogenous cells and developing conidia. h, i Conidia. j Germinating conidium. k, l Colony on PDA, above (k), below (l). Scale bars: d, e = 80 µm; f = 20 µm; g = 10 µm; h–j = 15 µm.

Figure 3.53 *Paraconiothyrium rosicola* (HKAS ML47, holotype)

Paraphaeosphaeria O.E. Erikss., Ark. Bot., Ser. 2 6: 405 (1967)

Type species – *Paraphaeosphaeria michotii* (Westend.) O.E. Erikss.

Notes – *Paraphaeosphaeria* was established by Eriksson (1967), and Ariyawansa et al. (2014) reconfirmed the phylogenetic placement of *Paraphaeosphaeria* within Didymosphaeriaceae. The sexual morph of *Paraphaeosphaeria* is characterized by immersed to semi-immersed ascomata, bitunicate asci with a short pedicel, and broadly elliptical, yellowish-brown, multi-septate ascospores (Wong et al., 2000; Du et al., 2025). The asexual morph is characterized eustromatic or pycnidial conidiomata, phialidic or annelidic conidiogenous cells and aseptate or 1-septate conidia (Verkley et al., 2014; Wanasinghe et al., 2018; Hongsanan et al., 2020a). In recent years, most species of *Paraphaeosphaeria* have been reported as saprobes (Zhang et al., 2021d; Tennakoon et al., 2022; Absalan et al., 2024, Du et al., 2025).

Paraphaeosphaeria camelliae Ariyaw., I. Tsai & Thambug., Sci. Rep. 10 (no. 12762): 15 (2020) Figure 3.54

Index Fungorum number: IF 834509; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 155–216 μm wide, 117–187 μm high, pycnidial, solitary, scattered, immersed to slightly erumpent, with dark brown mature conidia, uniloculate, globose to subglobose, glabrous, ostiolate. *Ostiole* 41–62 μm wide, 59–75 μm high, central, dark brown, slightly papillate. *Conidiomatal wall* 15.5–19 μm wide, multi-layered, composed of 3–4 outer layers of brown to yellowish brown thick-walled cells of *textura angularis*, lined with 1–2 hyaline and thin-walled inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.3–4.2 × 3.1–4.9 μm ($\bar{x}$ = 3.2 × 4 μm; n = 20), phialidic, hyaline, discrete or positioned on clumps of cells that protrude into the cavity, smooth, ampulliform to doliiform or cylindrical, arising from the inner layer of pycnidium wall. *Conidia* 4.1–5.5 × 2.2–3 μm ($\bar{x}$ = 4.7 × 2.6 μm; n = 30), ellipsoidal to cylindrical,

initially hyaline, after secession olivaceous-brown or pale brown to brown, thin-walled, smooth, aseptate, mostly with two polar oil-droplets (1–1.5 µm diam.).

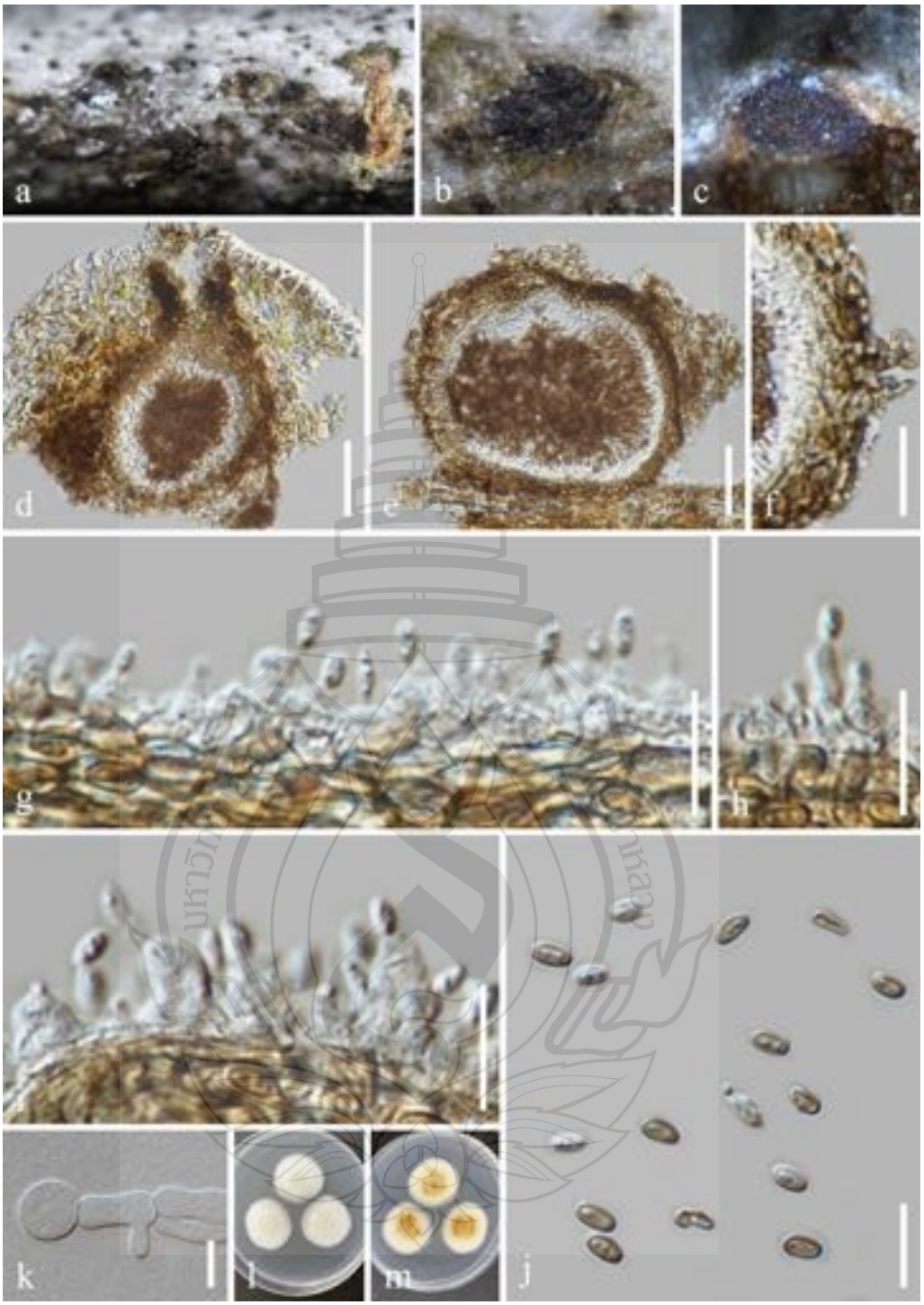
Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25℃ in the dark. Colonies from above, circular, regular, dense, entire edge, white to creamy white on surface; in reverse, yellowish brown in the center, and white at the edge.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,280 m, 28°23′24″ N, 107°2′24″ E, on dead branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML88 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia sinensis* (Ariyawansa et al., 2020b), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Paraphaeosphaeria camelliae* was established by Ariyawansa et al. (2020b) based on its asexual morph and was isolated from *Camellia sinensis* in China. In this study, multi-locus phylogenetic analysis showed that my isolate (UESTCC ML88) clustered with *P. camelliae* (NTUCC 18-0952, ex-type strain) (Figure 3.40). In addition, my collection shares similar morphological characteristics with the original description of *P. camelliae*. Sequence comparison between UESTCC ML88 and NTUCC 18-0952 showed high similarities by 99.9% in LSU, 99.4% in ITS, and 99.5% in SSU. Therefore, I identify my collection as *P. camelliae*, and report *Rosa roxburghii* as a new host record for this species in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j Conidia. k Germinating conidium. l, m Colonies on PDA, above (l), below (m). Scale bars: d, e = 100 µm; f = 20 µm; g–k = 10 µm.

Figure 3.54 *Paraphaeosphaeria camelliae* (HUEST ML88, new host record)

Paraphaeosphaeria michotii (Westend.) O.E. Erikss., Arch. Botan. 6: 405 (1967) Figure 3.55

Index Fungorum number: IF 335615; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 160–193 μm wide, 102–139 μm high, pycnidial, solitary, immersed to erumpent, globose to subglobose, brown to dark brown. *Ostiole* apapillate, opening with a pore. *Conidiomatal wall* 13–18 μm, composed of 3–4 layers of *textura angularis* cells, thin-walled, outer layer brown, hyaline towards inner layer. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.9–4.8 μm × 4.9–6 μm ($\bar{x}$ = 4.4 × 5.5 μm; n = 20), lining the inner cavity, phialidic, short, discrete, hyaline, smooth, globose to ampulliform. *Conidia* 6.4–8.3 μm × 3.9–4.6 μm ($\bar{x}$ = 7.5 × 4.2 μm; n = 20), aseptate, oval to ellipsoid with obtuse ends, initially hyaline, becoming brown to golden brown, thick-walled, with some small oil-droplets.

Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes produced from the basal cells. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25°C in the dark, circular, regular, dense, covered with white aerial mycelium, filamentous, fluffy, white to creamy white on surface; in reverse, yellow in the center, and pale yellowish white at the edge.

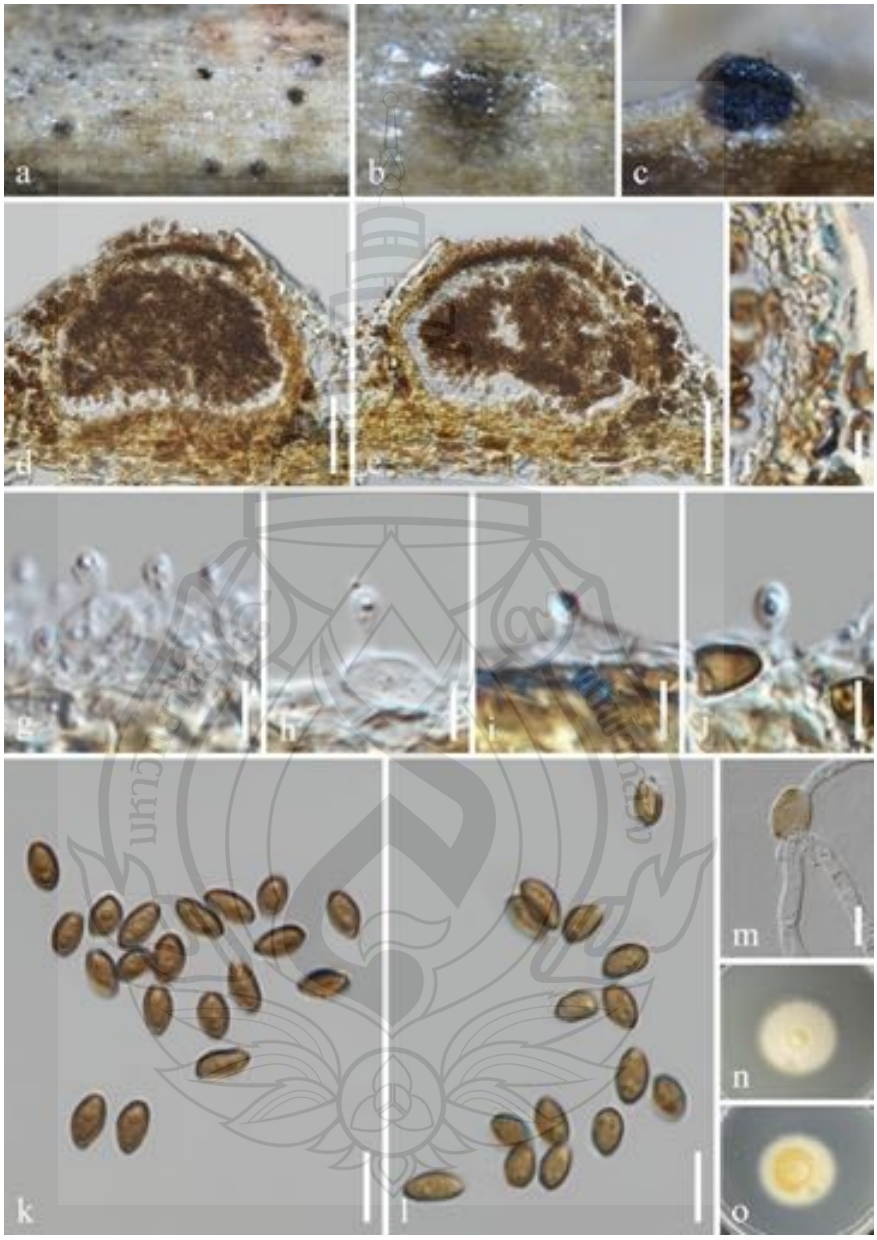
Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML94 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa canina* (Wanasinghe et al., 2018), *Rosa roxburghii* (present study).

Known geographical distribution – China, France, Italy, Switzerland.

Notes – *Paraphaeosphaeria michotii* was earlier recorded in marine environments (Jones et al., 2019). In the phylogenetic tree, my isolate (UESTCC ML94) clustered with *P. michotii* (MFLUCC 13-0349) with a strong statistical support (Figure 3.55). Morphologically, the description of my collection (HUEST ML94) did not differ with the

definitions of *P. michotii* and hence considered my species to be the same. Therefore, I identify my collection as *P. michotii* and report *Rosa roxburghii* as a new host record for this species in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 50 μm; f, k–m = 10 μm; g–j = 5 μm.

Figure 3.55 *Paraphaeosphaeria michotii* (HUEST ML94, new host record)

Paraphaeosphaeria verruculosa Verkley, Göker & Stielow, Persoonia 32: 48 (2014) Figure 3.56

Index Fungorum number: IF 800770; Facesoffungi number: FoFXX

Synonym – *Paraphaeosphaeria parmeliae* Crous & Trakun., IMA Fungus 5(2): 401 (2014)

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 98–173 μm wide, 90–138 μm high, pycnidial, solitary, immersed, globose to subglobose, dark brown to black, ostiolate. *Ostiole* indistinct or absent, apapillate. *Conidiomatal wall* 14–19 μm wide, 2–3 outer layers of pale brown to brown thick-walled cells of *textura angularis* and lined with 1–2 hyaline and thin-walled inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.1–4.8 × 3.5–4.4 μm ($\bar{x}$ = 4.1 × 3.9 μm; n = 20), phialidic, hyaline, discrete or positioned on clumps of cells that protrude into the cavity, smooth, globose to broadly ampulliform, arising from the inner layer of pycnidial wall. *Conidia* 4.1–5.3 × 3.5–4.7 μm ($\bar{x}$ = 4.7 × 3.9 μm; n = 30), globose, subglobose to ellipsoid, initially hyaline with some minute oil-droplets (< 1 μm diam.), after secession olivaceous-brown to brown with fewer but larger oil-droplets (1.5–2 μm diam.), mature conidial wall orange-brown, verruculose, aseptate.

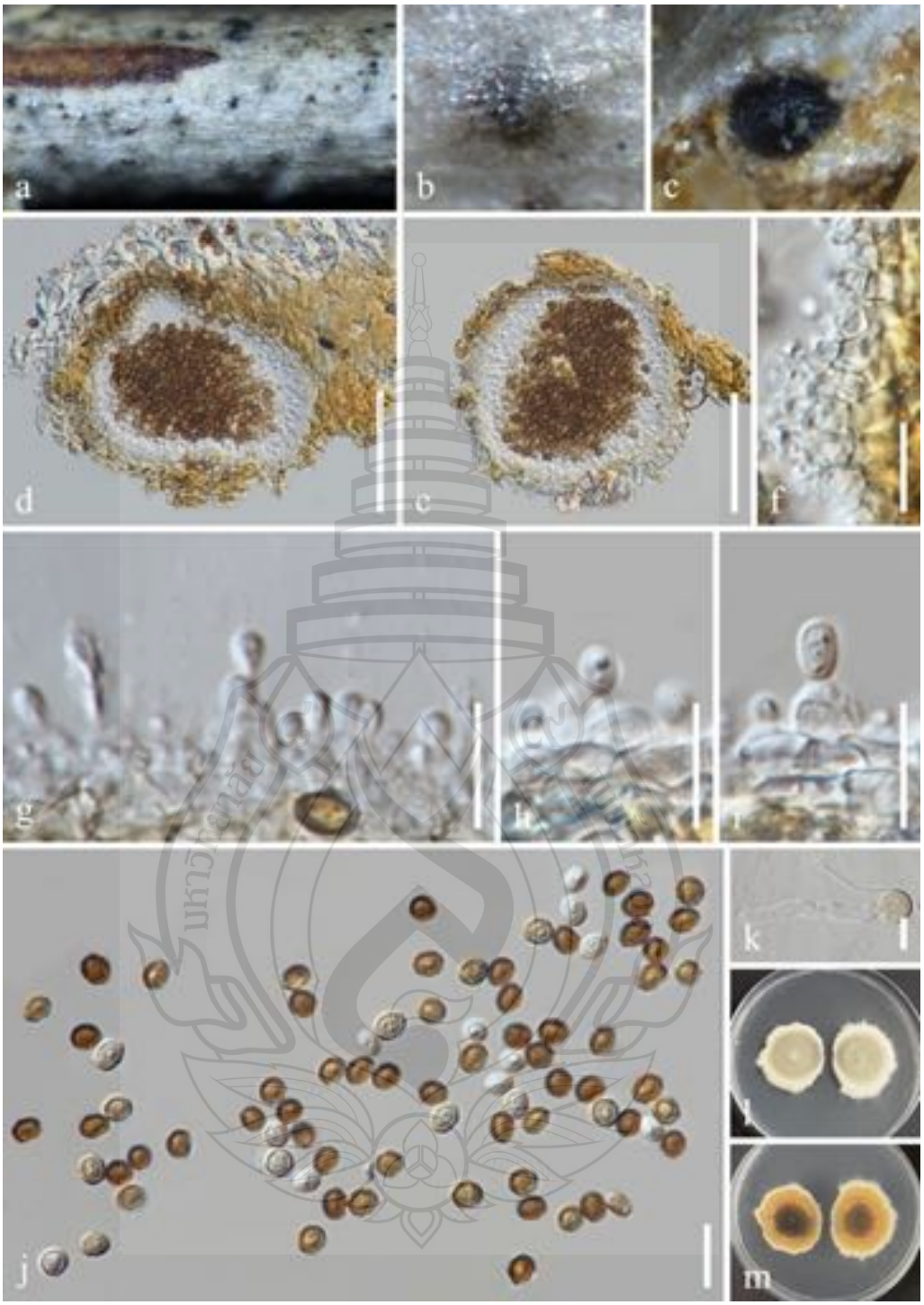
Culture characteristics – Conidia germinated on PDA medium within 24 h and germ tube produced from one end. Colonies growing on PDA reached 25–28 mm in diam. after three weeks at 25°C in the dark, circular, cottony, filamentous edge, olivaceous-gray in the center, and white at the edge; in reverse, dark brown in the center, following the yellowish brown in the middle with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Anshun City, Zhenning County, Baima Village, elevation 1,280 m, 26°2′35″ N, 105°44′12″ E, on dead branches of wild *Rosa roxburghii*, 3 July 2022, N. Wu, GL104 (HUEST XX), living culture UESTCC XX.

Hosts – *Parmelia sulcata* (Trakunyingcharoen et al., 2014b), *Picea abies*, *Pinus radiata* and páramo soil after burning (Verkley et al., 2014), *Rosa roxburghii* (present study).

Known geographical distribution – Belgium, Chile, China, Colombia, Germany.

Notes – *Paraphaeosphaeria verruculosa* was introduced by Verkley et al. (2014), and subsequently, *P. parmeliae* was introduced by Trakunyingcharoen et al. (2014b). Multi-locus phylogenetic analysis revealed that *P. parmeliae* (CBS 131728), *P. verruculosa* (CBS 263.85) and my isolate (UESTCC GL104) clustered together with a good support (Figure 3.40). Morphologically, *P. parmeliae* is similar to *P. verruculosa* in having pycnidial, globose conidiomata, discrete, ampulliform conidiogenous cells, and globose, brown, aseptate, thick and rough-walled conidia. In addition, nucleotide comparisons between *P. verruculosa* and *P. parmeliae* showed high similarities as 100% (560/560 bp) in ITS, 100% (845/845 bp) in LSU and 99.8% (427/428 bp, 1 gap) in *tub2* sequence. Therefore, I synonymize *P. parmeliae* under *P. verruculosa* and regard them as one species. In the present study, my collection is morphologically similar to *P. verruculosa* without significant differences in the shape and color of conidiomata, conidiogenous cells, and conidia. Sequence comparisons between my isolate (UESTCC GL104) and *P. verruculosa* (CBS 263.85) showed high similarities of 99.5%, 100% in ITS and LSU. Therefore, I identify my collection as *P. verruculosa*, reporting first time from *Rosa roxburghii* in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j Conidia. k Germinating conidium. l, m Colonies on PDA, above (l), below (m). Scale bars: d, e = 50 μm; f–k = 10 μm.

Figure 3.56 *Paraphaeosphaeria verruculosa* (HUEST GL104, new host record)

Lophiostomataceae Luerss.

Type genus – *Lophiostoma* Ces. & De Not.

Notes – The family Lophiostomataceae was first mentioned by Nitschke (1869), and later validly introduced by Sbaccardo (1883) based on type genus, *Lophiostoma*. Thambugala et al. (2015) provided a key to genera of Lophiostomataceae and accepted 16 genera wirhin the family. Thirteen more genera were subsequently introduced in this family, *Crassiclypeus*, *Flabellascoma*, *Lentistoma*, *Leptoparies*, *Neovaginatispora*, *Parapaucispora*, *Pseudopaucispora* (Hashimoto et al., 2018), *Desertiserpentica* (Maharachchikumbura et al., 2021), *Kiskunsagia* (Crous et al., 2019), *Lophiomurispora*, *Neopaucispora* (Wanasinghe et al., 2018, 2021), *Magnopulchromyces* (Yuan et al., 2020), and *Pseudocapulatispora* (Mapook et al., 2020). Members of Lophiostomataceae are reported as saprobes on twigs, stems or bark of woody plants and herbaceous plants from terrestrial and aquatic habitats worldwide (Holm, 1988; Thambugala et al., 2015). I obtained several lophiostomataceous collections from *Rosa roxburghii* and *R. sterilis*, including one new genus, three new species and six new host records.

Biappendiculispora Thambug., Kaz. Tanaka & K.D. Hyde, Fungal Diversity 74: 214 (2015)

Type species – *Biappendiculispora japonica* Thambug., Wanas., Kaz. Tanaka & K.D. Hyde

Notes – Thambugala et al. (2015) established a monotypic genus, *Biappendiculispora*, to accommodate *B. japonica* (≡ *Lophiostoma caulium* "var. f") (Tanaka & Harada, 2003), based on its distinct morphological features and phylogenetic analyses of a combined LSU, SSU, ITS, and *tef1α* dataset. Andreasen et al. (2021) later synonymized *Biappendiculispora* with *Lophiostoma* according to multigene phylogenetic analyses of ITS, LSU, *tef1α*, and *rpb2* sequences. However, their interpretation relied solely on molecular data and overlooked clear morphological distinctions between the two genera. In the present study, my new collection of

Biappendiculispora from *Rosa sterilis* further supports its recognition as an independent genus. Phylogenetically, *Biappendiculispora* forms a well-supported and distinct clade within *Lophiostomataceae*, separate from *Lophiostoma*. Morphologically, *Biappendiculispora* can be readily distinguished from *Lophiostoma* by its immersed, coriaceous ascomata, bitunicate, cylindric-clavate asci with a distinct ocular chamber, and fusiform, 7–9-septate, hyaline to brown ascospores bearing appendages at both ends (Li et al., 2023b; Ren et al., 2024c).

Biappendiculispora japonica Thambug., Wanas., Kaz. Tanaka & K.D. Hyde, Fungal Diversity, 74: 214 (2015) Figure 3.57

Index Fungorum number: IF 838983; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, solitary to gregarious or confluent, dark brown to black, immersed to partly erumpent, visible as black dots on the host, subglobose or pyriform, unilocular, thick-walled, glabrous, papillate, ostiolate. *Ostiole* 55–67 μm wide, 107–115 μm high, single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 20–30 μm wide, composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with an elongate and cylindrical pedicel, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, fusiform with acute ends, 6–7-septate, slightly constricted at the septa, guttulate, smooth-walled, initially hyaline, becoming yellowish-brown at maturity, with a narrow sheath drawn out 5–10 μm long at both ends. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from both ends. Colonies on PDA reaching 15–17 mm diam. after 2

weeks at 25°C in dark, circular or irregular, flat to slightly raised, white; in reverse, greyish-green with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML 26 (HUEST XX), living culture UESTCC XX.

Hosts – *Camphora glandulifera* (Ren et al., 2024c); *Dactylis glomerata* (Thambugala et al., 2015); *Paeonia suffruticosa* (Li et al., 2023b); *Rosa sterilis* (present study); Unidentified herbaceous plant (Zhang et al., 2023a).

Known geographical distribution – China, Japan.

Notes – My collection is similar to *Biappendiculispora japonica* in having coriaceous ascomata, bitunicate, cylindric-clavate asci, and fusiform, multi-septate, hyaline to brown ascospores with appendages at both ends (Thambugala et al., 2015; Li et al., 2023b; Ren et al., 2024c). Moreover, comparison of the available sequence data between my isolate and the type strain of *B. japonica* revealed only two nucleotide substitutions in the ITS region. Therefore, I identify my collection as *B. japonica* and report it here as a new host record on *Rosa sterilis*.



Note a Host: *Rosa sterilis*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Pseudoparaphysis. h–l Asci. m–p Ascospores. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 150 µm; e = 60 µm; f–l = 30 µm; m–q = 15 µm.

Figure 3.57 *Biappendiculispora japonica* (HUEST ML26, new host record)

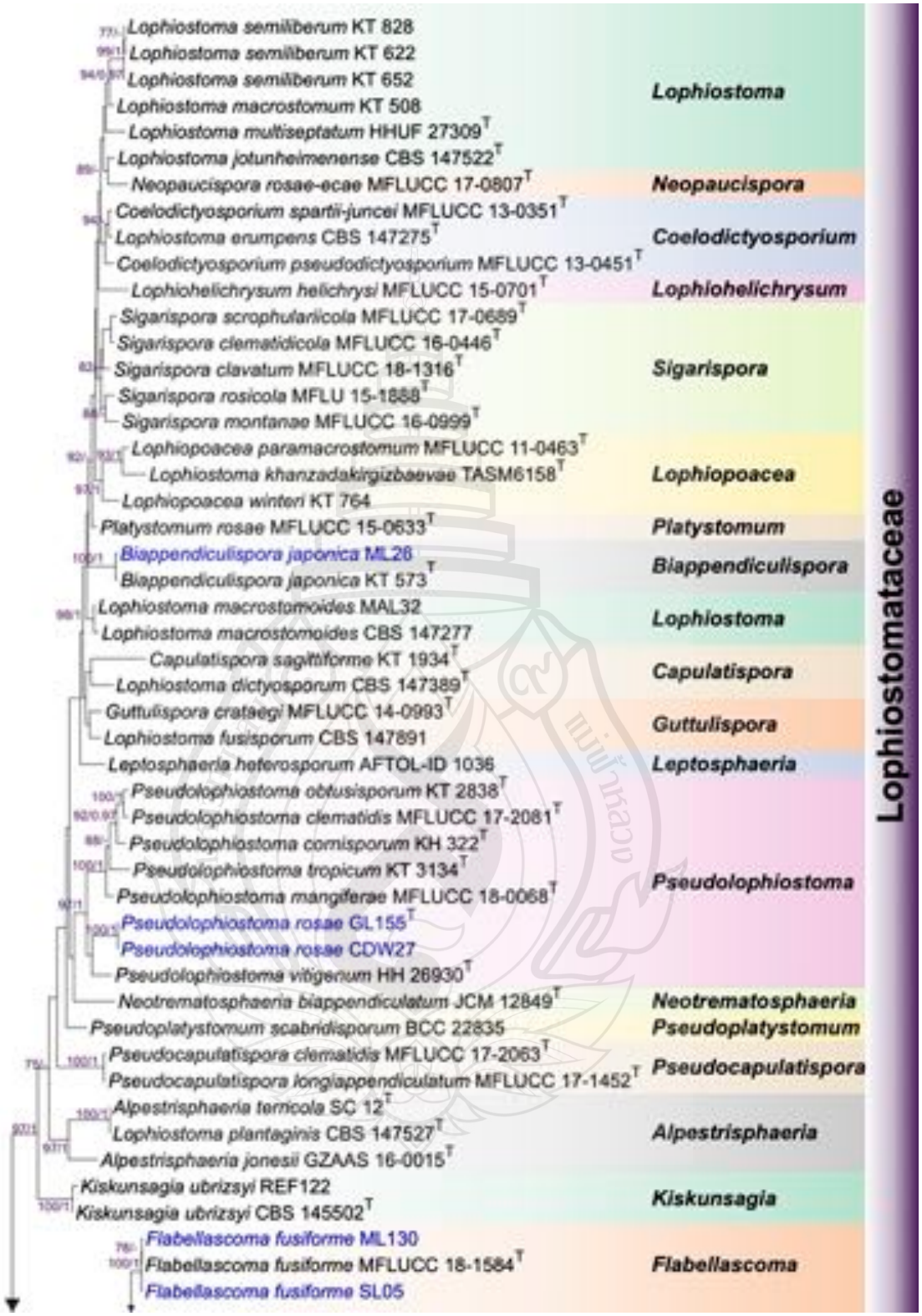


Figure 3.58 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Lophiostomataceae

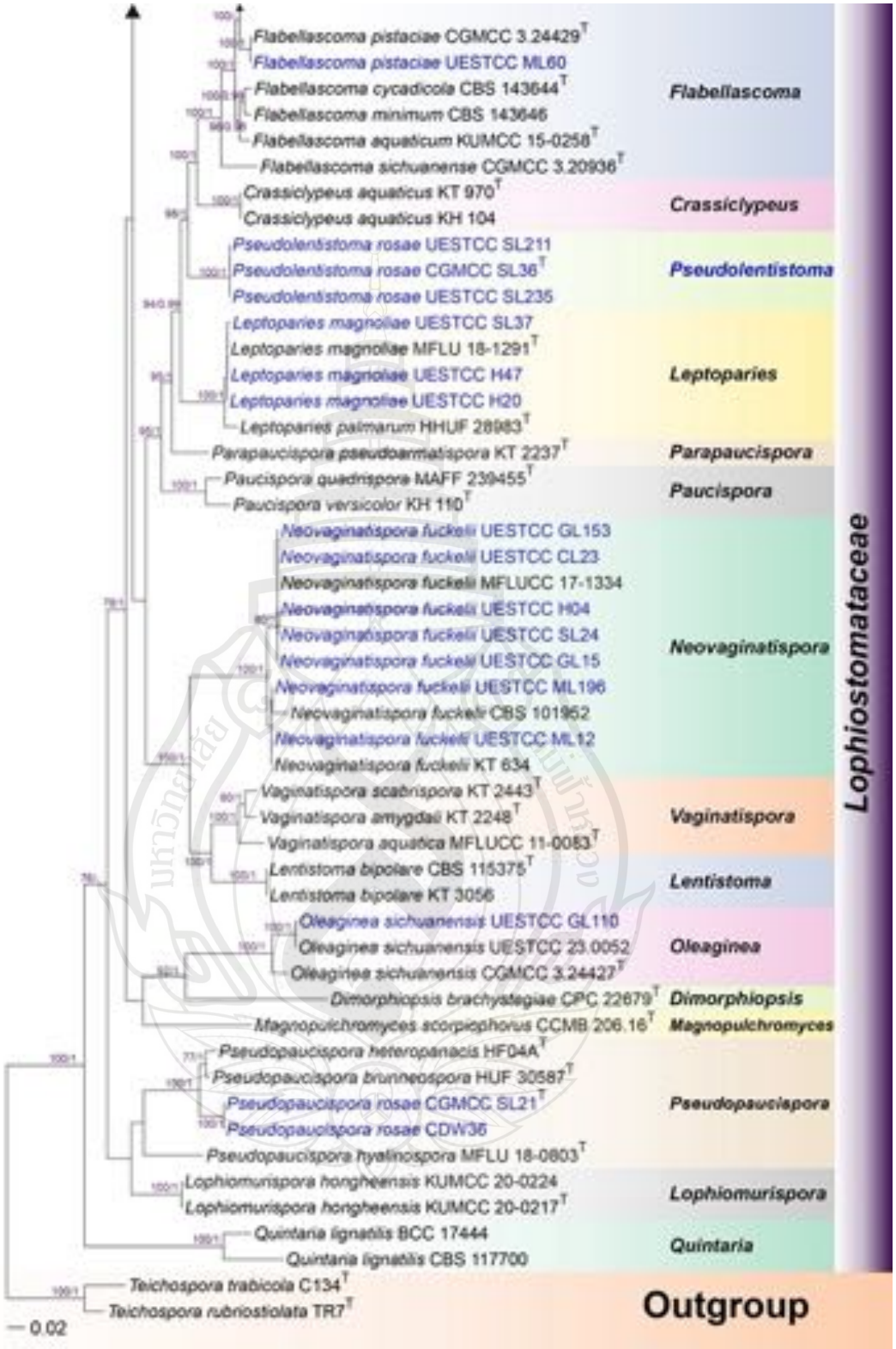


Figure 3.58 (continued)

Figure 3.58 The tree is rooted with *Teichospora rubriostiolata* (TR7) and *T. trabicola* (C134). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Flabellascoma A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 167 (2018)

Type species – *Flabellascoma minimum* A. Hashim., K. Hiray. & Kaz. Tanaka

Notes – Hashimoto et al., (2018) introduced the genus *Flabellascoma* to accommodate two species, *F. cycadicola* and the type species *F. minimum*, which are characterized by immersed to semi-immersed ascomata with a well-developed, crest-like ostiolar neck, and a peridium of uniform thickness. Subsequently, five more species were accepted in this genus, *F. aquaticum*, *F. fusiforme* (Bao et al., 2019), *F. coffeae* (Lu et al., 2025), *F. pistaciae* (Li et al., 2023b), and *F. sichuanense* (Yu et al., 2022). In the present study, I isolated *F. fusiforme* from *Rosa roxburghii* and *F. pistaciae* from *R. sterilis* in China.

Flabellascoma fusiforme D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su, Mycosphere 10(1): 1089 (2019) Figure 3.59

Index Fungorum number: IF556721; Facesoffungi number: FoF06213

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, semi-immersed, solitary to gregarious, visible as erumpent, crest-like, black, laterally compressed ostiole on host substrate, ampulliform or subglobose with an ostiolar neck, unilocular, glabrous, coriaceous to carbonaceous, thick-walled. *Ostiole* 55–67 μm wide, 107–115 μm high, single, long, straight or curved, central or laterally located, periphysate. *Peridium* 20–30 μm wide, composed of two strata, the outer stratum comprising black, indistinguishable cells fusing with the host tissue, the inner stratum comprising several layers of brown cells of *textura angularis*,

thinner at the base. *Hamathecium* 1.5–3 μm wide, numerous, filamentous, septate, branched, cellular pseudoparaphyses. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate with a furcate pedicel, apically rounded with a broad ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform with narrow and obtuse to acute ends, 1-septate, slightly constricted at the septum, asymmetrical, upper cell mostly slightly wider and longer, 4-guttules, 2 middle guttules larger than others, smooth- and thin-walled, with a narrow sheath drawn out 7.5–11 μm long at both ends, sheath with a lateral pad-like structure; sometimes with an internal, inconspicuous, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25°C in dark, circular, raised, cottony, producing mucus, glistening, yellowish white; in reverse, pastel yellow, with a milky white margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL05 (HUEST XX), living culture UESTCC XX; *ibid.*, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on dead branches of *R. roxburghii*, 4 February 2023, N. Wu, ML130 (HUEST XX), living culture UESTCC XX.

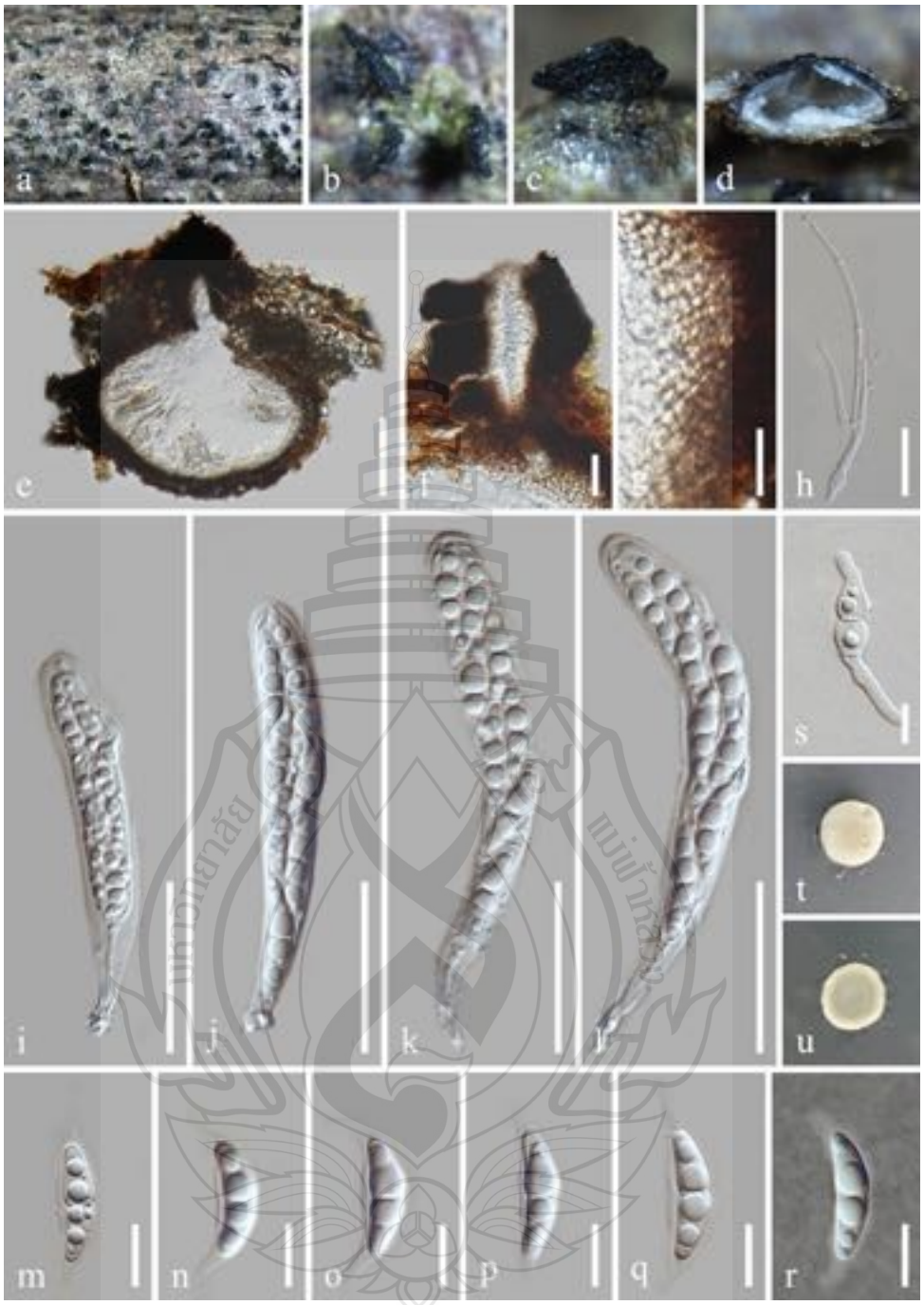
Host – *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Bao et al. (2019) introduced *Flabellascoma fusiforme* based on multi-gene phylogeny, identifying it as sister to *F. aquaticum* (KUMCC 15–0258), both of which were collected from freshwater habitats. In the phylogenetic analysis, my collection clustered with the type material of *F. fusiforme* (MFLUCC 18-1584) with a good statistical support (Figure 3.58). Sequence similarities of the ITS, LSU and *tef1α*

gene regions between UESTCC SL05 and the type material (MFLUCC 18-1584) is 99.58% (475/477 bp), 99.88% (815/816 bp) and 100% (839/839 bp), respectively. Furthermore, morphology of my collections matches well with the holotype of *F. fusiforme* (Bao et al., 2019). I therefore identify my collection as *F. fusiforme*, representing a new host record of *Rosa roxburghii*.





Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Pseudoparaphyses. i–l Asci. m–q Ascospores. r Ascospore stained with Indian ink. s Germinating ascospore. t, u Colony on PDA, above (t), below (u). Scale bars: e = 100 μm; f, i–l = 30 μm; g, h = 20 μm; m–s = 10 μm.

Figure 3.59 *Flabellascoma fusiforme* (HUEST SL05, new host record)

Flabellascoma pistaciae W.L. Li & Jian K. Liu, Mycosphere 14(1): 1474 (2023) Figure 3.60

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, semi-immersed, solitary to gregarious, visible as erumpent, crest-like, black, laterally compressed ostiole on host substrate, pyriform or subglobose with an ostiolar neck, unilocular, glabrous, coriaceous to carbonaceous, thick-walled. *Ostiole* 55–67 μm wide, 107–115 μm high, single, long, straight or curved, central or laterally located, periphysate. *Peridium* 20–30 μm wide, composed of 7–8 layers of brown-walled cells of *textura angularis*, thinner at the base. *Hamathecium* 1.5–3 μm wide, numerous, filamentous, septate, branched, cellular pseudoparaphyses. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate with a furcate pedicel, apically rounded with a broad ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, hyaline, broadly fusiform with narrow and obtuse to acute ends, 1-septate, slightly constricted at the septum, asymmetrical, upper cell mostly slightly wider and longer, 4-guttules, 2 middle ones larger than end ones, smooth- and thin-walled, with a narrow sheath drawn out 7.5–11 μm long at both ends, with a lateral pad-like structure within the sheath; sometimes with an internal, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, velvety to woolly, white grayish to gray; in reverse, white grayish to gray in the centre, dark gray to blackish in the middle, white-brown to light brown at the margin.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead

branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML60 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia oleifera* and *Pistacia chinensis* (Li et al., 2023b); *Rosa sterilis* (present study).

Known geographical distribution – China, Germany, Japan, Sweden, Switzerland, UK.

Notes – Based on the morphological traits and molecular evidence (Figure 3.58), my strain (UESTCC ML 60) is identified as *Flabellascoma pistaciae* which was described by Li et al. (2023b), and isolated from decaying branches of *Pistacia chinensis* in China. In this study, I report a new host record of *F. pistaciae*, isolated from *Rosa sterilis.*



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f Pseudoparaphyses. g Germinating ascospore. h, i Colony on PDA, above (h), below (i). j–n Asci. o–s Ascospores. t Ascospore stained with Indian ink. Scale bars: d = 100 µm; e–g, o–t = 10 µm; j–n = 30 µm.

Figure 3.60 *Flabellascoma pistaciae* (HUEST ML60, new host record)

Leptoparies A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 171 (2018)

Type species – *Leptoparies palmarum* A. Hashim., K. Hiray. & Kaz. Tanaka

Notes – Hashimoto et al. (2018) established the genus *Leptoparies* to accommodate *L. palmarum*, which is characterized by a relatively thinner, non-carbonised peridium and ascospores with the drawn-out sheaths. de Silva et al. (2022) introduced the second member, *L. magnoliae*, from *Magnolia* species in Thailand, and distinguished it from *L. palmarum* based on molecular data, as well as its smaller asci and ascospores.

Leptoparies magnoliae N.I. de Silva & S. Lumyong, Journal of Fungi, J. Fungi 8(no. 1094): 11 (2022) Figure 3.61

Index Fungorum number: IF559914; Facesoffungi number: FoF12709

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, semi-immersed, solitary to gregarious, visible as erumpent, crest-like, black, laterally compressed ostioles on host substrate, ampulliform or subglobose with an ostiolar neck, unilocular, glabrous, coriaceous to carbonaceous, thick-walled. *Ostiole* 55–67 μm wide, 107–115 μm high, single, long, straight or curved, central or laterally located, periphysate. *Peridium* 20–30 μm wide, composed of two strata, the outer stratum comprising black, indistinguishable cells fusing with the host tissue, the inner stratum comprising several layers of brown cells of *textura angularis*, thinner at the base. *Hamathecium* 1.5–3 μm wide, numerous, filamentous, septate, cellular pseudoparaphyses, anastomosing at the apex. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform with obtuse ends, 1-septate, slightly constricted at the septum, asymmetrical, upper cell mostly slightly wider and longer, guttulate, smooth- and thin-walled, with a narrow sheath drawn out 7.5–11 μm long at both ends, sheath with a lateral pad-like structure;

sometimes with an internal, inconspicuous, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25°C in dark, circular, flat, dry, velvety, mycelium initially creamy-white, becoming yellowish; in reverse, orange to brown in the centre, yellowish towards the margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL37 (HUEST XX), living culture UESTCC XX; *ibid.*, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H20 (HUEST XX), living culture UESTCC XX; *ibid.*, H47 (HUEST XX), living culture UESTCC XX.

Hosts – *Magnolia* sp. (de Silva et al., 2022); *Rosa roxburghii* (present study).

Known geographical distribution – China, Thailand

Notes – *Leptoparies magnoliae* was introduced by de Silva et al. (2022) which was collected from dead twigs of *Magnolia* sp. In this study, my isolates (HUEST SL37, HUEST H20 and HUEST H47) showed morphological similarity to the holotype (MFLU 18-1291) of *L. magnoliae*. Multi-locus phylogeny revealed that my isolates (UESTCC SL37, UESTCC H20 and UESTCC H47) clustered with the type strain of *L. magnoliae* (MFLU 18-1291) (Figure 3.58) representing a new geographical and host record.



Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Pseudoparaphyses. i–l Asci. m–q Ascospores. r Ascospore stained with Indian ink. s Germinating ascospore. t, u Colony on PDA, above (t), below (u). Scale bars: e = 100 μm; f = 50 μm; g–l = 20 μm; m–s = 10 μm.

Figure 3.61 *Leptoparies magnoliae* (HUEST SL37, new host record)

Neovaginatispora A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 188 (2018)

Type species – *Neovaginatispora fuckelii* (Sacc.) A. Hashim., K. Hiray. & Kaz. Tanaka

Notes – *Neovaginatispora* was introduced by Hashimoto et al. (2018) with *N. fuckelii* as the type species. There are four epithets listed in Index Fungorum (2025, June), viz., *N. aquadulcis*, *N. clematidis*, *N. fuckelii* and *N. mangiferae*. *Neovaginatispora aquadulcis* is the only holomorphic species in the genus, while the other three species are known only from the sexual morph, and their asexual morphs have yet to be discovered (Phukhamsakda et al., 2020; Magaña-Dueñas et al., 2022; Jayawardena et al., 2022). Magaña-Dueñas et al. (2022) redefined the genus *Neovaginatispora* and established the link between its sexual and asexual morphs based on morphological and molecular evidence. In the present study, I report *N. fuckelii* on *Rosa roxburghii* and *R. sterilis*. A phylogenetic tree based on combined dataset of ITS, LSU, SSU, *tef1α* and *rpb2* sequence data is presented in Figure 3.58.

Neovaginatispora fuckelii (Sacc.) A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 188 (2018) Figure 3.62

Index Fungorum number: IF551535; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 272–381 µm wide, 237–361 µm high, immersed, initially intraepidermal, visible as black dots on the host when mature, scattered, dark brown to black, subglobose to pyriform, unilocular, solitary, thick-walled, glabrous, ostiolate. *Ostiole* 55–67 µm wide, 107–115 µm high, single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 20–30 µm wide, composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 µm ($\bar{x}$ = 87 × 15 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short

pedicellate, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 µm ($\bar{x}$ = 20 × 6 µm; n = 30), overlapping to bi-seriate, hyaline, narrowly fusiform to fusiform with obtuse ends, 1-septate, slightly constricted at the septum, enlarged near the septum at the upper cell, mostly with 4 guttules, smooth-walled, with rounded cap-like appendages at both ends. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, with velvety, dark grayish green mycelium; in reverse, dark green to black with an entire margin.

Materials examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 6 February 2023, N. Wu, ML 12 (HUEST XX), living culture UESTCC XX; *ibid.*, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of *R. roxburghii*, 5 February 2023, N. Wu, ML 196 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL15 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL23 (HUEST XX), living culture UESTCC XX; *ibid.*, Jichangping Town, Songhe Township, elevation 1,800 m, 26°3′7″ N, 104°35′36″ E, on branches of *R. roxburghii*, 10 July 2022, N. Wu, GL153 (HUEST XX), living culture UESTCC XX; *ibid.*, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *R. roxburghii*, 19 January 2024, N. Wu, SL24 (HUEST XX), living culture UESTCC XX; *ibid.*, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H04 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia oleifera*, *Idesia polycarpa*, *Juglans nigra* and *Paeonia suffruticosa* (Li et al., 2023b); *Mangifera indica* (Tennakoon et al., 2018); *Pelagia noctiluca* (Pasqualetti et al., 2024); *Phoenix canariensis* (Yang et al., 2021b); *Phoenix dactylifera* (Zhang et al., 2024a); *Prunus* sp. (Hyde et al., 2020); *Rosa chinensis* (Han et al., 2021); *Rosa roxburghii* and *R. sterilis* (present study); *Rosa* sp. (Hyde et al., 2016); *Vitis coignetiae* (Thambugala et al., 2015).

Known geographical distribution – China, Germany, Japan, Sweden, Switzerland, UK.

Notes – *Neovaginatispora fuckelii* is the most common species of the genus, but its taxonomic placement has been continuously revised. *Neovaginatispora fuckelii* was initially identified as *Lophiostoma fuckelii* (Saccardo, 1878). Later, Thambugala et al. (2015) transferred *L. fuckelii* to the genus *Vaginatispora* as *V. fuckelii*. However, Hashimoto et al. (2018) excluded *V. fuckelii* from *Vaginatispora* and established a new genus, *Neovaginatispora*, to accommodate *N. fuckelii*. *Neovaginatispora fuckelii* is distributed worldwide and has been recorded in China, Germany, Japan, Sweden, Switzerland and UK. It has been reported from *Camellia oleifera*, *Idesia polycarpa*, *Juglans nigra* and *Paeonia suffruticosa*, *Mangifera indica*, *Pelagia noctiluca*, *Phoenix canariensis*, *Phoenix dactylifera*, *Prunus* sp., *Rosa chinensis*, *Rosa* sp. and *Vitis coignetiae* in terrestrial and freshwater habitats (Tennakoon et al., 2018; Bao et al., 2019; Li et al., 2023b). In the present study, seven strains isolated from *Rosa roxburnhii* and *R. sterilis* clustered with *N. fuckelii*, and these strains could be recognized as conspecific (Figure 3.58). Morphologically, my new collection is similar to *N. fuckelii* in having cylindrical to clavate asci, and 1-septate, hyaline, fusiform ascospores with rounded cap-like appendages at both ends. My collection represents two new host and habitat records for this fungus. In addition, *N. fuckelii* has a wide distribution in southwestern China, including Bijie City, Liupanshui City, Qiandongnan Autonomous Prefectures and Qianxinan Autonomous Prefectures in Guizhou Province, as well as in Chengdu City and Leshan City in Sichuan Province.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–p Ascospores. q Ascospore stained with Indian ink. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d = 100 μm; e, f, h–k = 20 μm; g, l–r = 10 μm.

Figure 3.62 *Neovaginatispora fuckelii* (HUEST ML12, new host record)

Oleaginea W.L. Li & Jian K. Liu, Mycosphere 14(1): 1484 (2023)

Type species – *Oleaginea sichuanensis* W.L. Li & Jian K. Liu

Notes – *Oleaginea* is a monotypic genus typified by *O. sichuanensis* (Li et al., 2023b). The genus is characterized by immersed to semi-immersed, uniloculate, coriaceous ascomata, 8-spored, bitunicate, fissitunicate, clavate asci and biseriate, hyaline, septate, deeply constrict at the septum, with large guttules in each cell, fusiform to ellipsoid ascospores, without known asexual morph.

Oleaginea sichuanensis W.L. Li & Jian K. Liu, Mycosphere 14(1): 1485 (2023) Figure 3.63

Index Fungorum number: IF849151; Facesoffungi number: FoF14412

Saprobic on decaying branches of *Rosa sterilis*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, solitary to gregarious, initially immersed, becoming erumpent through bark fissures, visible as black dots on the host, dark brown to black, globose or subglobose, unilocular, thick-walled, glabrous, coriaceous or carbonaceous, ostiolate. *Ostiole* 55–67 μm wide, 107–115 μm high, single, central. *Peridium* 20–30 μm wide, composed of dark brown to black compressed cells of *textura angularis*, thicker near the ostiole, thinner at the base. *Hamathecium* 1.5–3 μm wide, composed of dense, filamentous, branched, septate, constricted at the septa, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 4-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded and thickened with an ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), uniseriate or overlapping uniseriate, hyaline, fusiform with acute ends, slightly curved, 1-septate, constricted at the septum, upper cell slightly swollen towards the medial septum, guttulate, smooth-walled, surrounded by a gelatinous sheath and thickened at both ends; sheath drawn out 3–7 μm long at both ends. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17

mm diam. after two weeks at 25℃ in dark, circular, velvety to woolly, grayish green; in reverse, pale brown with white entire margin.

Material examined – CHINA, Guizhou Province, Anshun City, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL110 (HUEST XX), living culture UESTCC XX.

Hosts – *Mahonia fortune* (Sun et al., 2025), *Olea europaea* (Li et al., 2023b), *Rosa sterilis* (present study).

Known geographical distribution – China.

Notes – Li et al. (2023b) introduced *Oleaginea sichuanensis* (from decaying branches of *Olea europaea*) in China, which is typical in having broad fusiform to ellipsoid, 1-septate, hyaline ascospores containing four refractive globules. Sun et al. (2025) reported this species from *Mahonia fortune*. However, the ascospores of *O. sichuanensis* in Sun et al. (2025) differ from the type, being hyaline with an inconspicuous terminal appendage when young, and brown without a terminal appendage at mature. I herein provide a new host record for this species based on a collection from *Rosa sterilis* in China, of which the gelatinous sheath was observed.



Note a–c Appearance of ascomata on host surface. d Vertical section of ascomata. e Peridium. f Pseudoparaphyses. g Germinating ascospore. h, i Colony on PDA, above (h), below (i). j–n Asci. o–s Ascospores. t Ascospore stained with Indian ink. Scale bars: d = 100 µm; e = 60 µm; f, g, j–n = 20 µm; e, o–t = 10 µm.

Figure 3.63 *Oleaginea sichuanensis* (HUEST GL110, new host record)

Pseudolentistoma N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*Pseudolentistoma*" refers to the similarity to the genus "*Lentistoma*".

Type species – *Pseudolentistoma rosae* N. Wu & Jian K. Liu

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* solitary to gregarious, immersed to superficial or erumpent through bark, subglobose to pyriform, unilocular, glabrous, coriaceous to carbonaceous, papillate, ostiolate. *Ostiole* single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* composed of few layers of hyaline to dark brown cells of *textura angularis*. *Hamathecium* composed of dense, filamentous, rarely branched, septate, constricted, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* uniseriate or overlapping biseriate, hyaline, widely fusiform to fusiform with obtuse ends, 1-septate, slightly constricted at the septum, upper cell slightly swollen towards the medial septum, guttulate, smooth-walled, with a curved, wide bipolar sheath, and forming a rounded cap-like structure at the tips of the sheath, sometimes with an internal, inconspicuous, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Notes – Phylogenetic analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data shows that *Pseudolentistoma* represents a distinct lineage closely related to *Crassiclypeus* and *Flabellascoma* with a good statistical support (Figure 3.58). Morphologically, *P. rosae* is characterized by hyaline, 1-septate, fusiform ascospores with a curved and wide bipolar sheath, forming a rounded cap-like structure at the tips of the sheath. In contrast, *Crassiclypeus* and *Flabellascoma* have hyaline, 1-septate, fusiform ascospores with a narrow bipolar sheath (Hashimoto et al., 2018). Therefore, I introduce *Pseudolentistoma* as a new genus with a new species, *P. rosae* based on morphology and phylogeny.

Pseudolentistoma rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.64

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

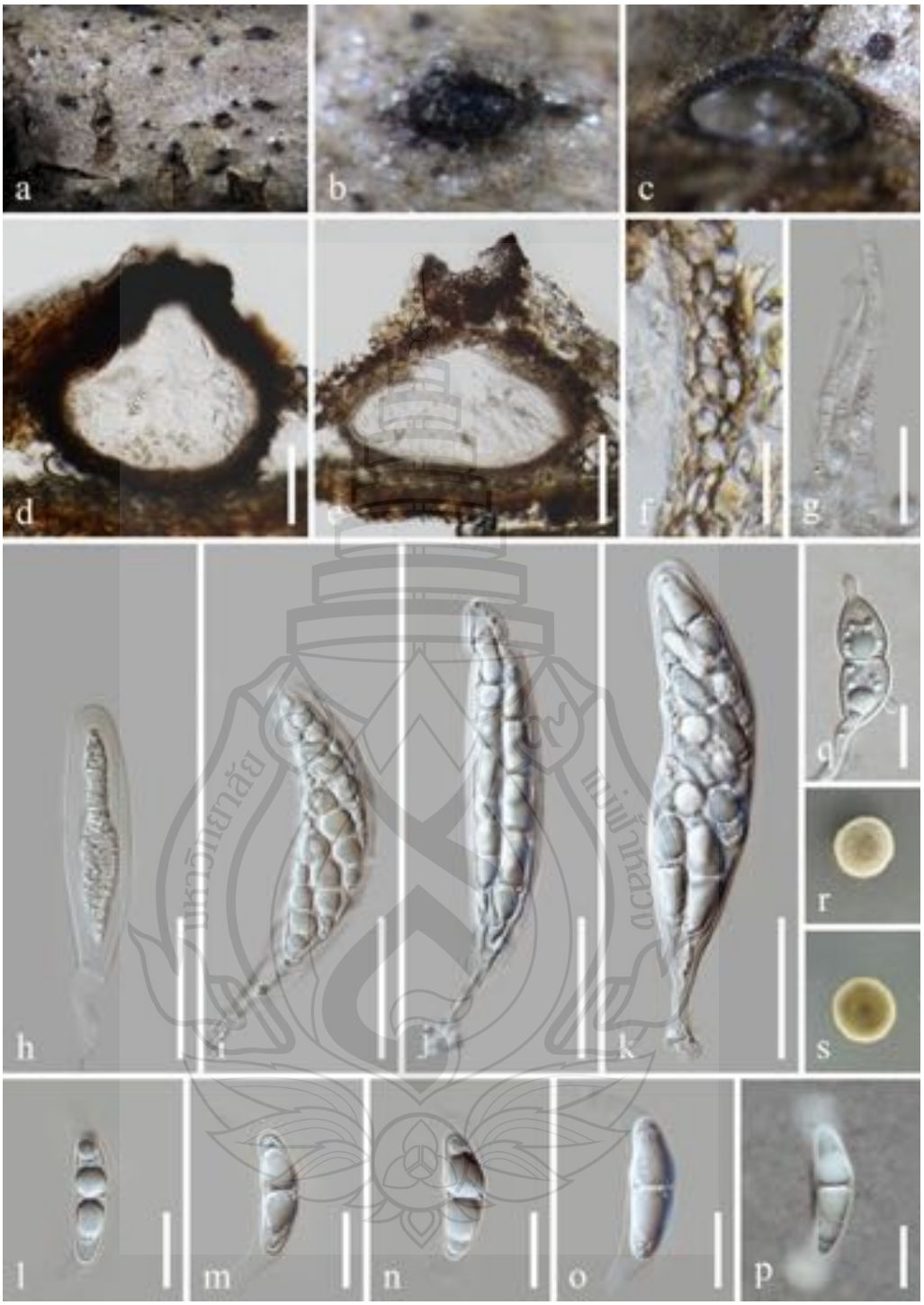
Holotype – HKAS SL36

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 272–381 µm wide, 237–361 µm high, solitary to gregarious, immersed to superficial or erumpent through bark, visible as black dots on the host, subglobose to pyriform, unilocular, glabrous, coriaceous to carbonaceous, thick- and smooth-walled, papillate, ostiolate. *Ostiole* 55–67 µm wide, 107–115 µm high, single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 20–30 µm wide, composed of few layers of hyaline to dark brown cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide, composed of dense, filamentous, rarely branched, septate, constricted at the septum, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 µm ($\bar{x}$ = 87 × 15 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 µm ($\bar{x}$ = 20 × 6 µm; n = 30), uniseriate or overlapping biseriate, hyaline, widely fusiform to fusiform with obtuse ends, 1-septate, slightly constricted at the septum, upper cell slightly swollen towards the medial septum, guttulate, smooth-walled, with a curved and wide bipolar sheath; sheath is drawn out 7.5–15 µm long at both ends, forming a rounded cap-like structure at the tips of the sheath, sometimes with an internal, inconspicuous, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25℃ in dark, circular, velvety to woolly, grayish green; in reverse, pale brown with white entire margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL36 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid*., SL211 (HUEST XX, paratype), living culture UESTCC XX; *ibid*., SL235 (HUEST XX), living culture UESTCC XX.

Notes – Three isolates of my lentistoma-like collection, having hyaline, 1-septate, fusiform ascospores with curved and wide bipolar sheaths, and forming rounded cap-like structures at the tips of the sheath, are different from other Lophiostomataceae species (Hashimoto et al., 2018; Andreasen et al., 2021; Zhang et al., 2023, 2024a). The phylogenetic tree based on multi-gene dataset showed that the three isolates form a distinct clade in Lophiostomataceae (Figure 3.58). Therefore, I introduced *Pseudolentistoma* to accommodate *P. rosae*.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d, e = 100 µm; f = 20 µm; h–k = 30 µm; g, l–q = 15 µm.

Figure 3.64 *Pseudolentistoma rosae* (HKAS SL36, holotype)

Pseudolophiostoma Thambug., Kaz. Tanaka & K.D. Hyde, Fungal Diversity 74: 235 (2015)

Type species – *Pseudolophiostoma vitigenum* (Kaz. Tanaka & Y. Harada) Thambug., Kaz. Tanaka & K.D. Hyde

Notes – Thambugala et al. (2015) established *Pseudolophiostoma* with *P. vitigenum* as the type species, which was previously described as *Lophiotrema vitigenum* (≡ *Lophiostoma vitigenum*). Seven more species were subsequently introduced, *P. chiangraiense* and *P. clematidis* (Phukhamsakda et al., 2020), *P. cornisporum*, *P. obtusisporum* and *P. tropicum* (Hashimoto et al., 2018), *P. lincangense* (Ren et al., 2024b) and *P. mangiferae* (Tennakoon et al., 2018). Five of which were transferred to *Lophiostoma* by Andreasen et al. (2021) and Li et al. (2023b). The hyaline, 1-septate ascospores with two eusepta and a narrow mucilaginous sheath, lacking terminal appendages, are considered key characteristics for delimiting genera in Lophiostomataceae (Thambugala et al., 2015). In the present study, I retain all accepted species of *Pseudolophiostoma* within the genus and introduce a new species based on both morphological and phylogenetic evidence.

Pseudolophiostoma rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.65

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS GL155

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 270–490 μm wide, 400–700 μm high, solitary or confluent, semi-immersed, globose or subglobose, unilocular, glabrous, coriaceous or carbonaceous, thick-walled, visible as an erumpent, crest-like, black, laterally compressed ostiolar neck on host substrate. *Ostiole* 125–145 μm wide, 200–260 μm high, single, long, subcylindrical, straight, central or laterally located, periphysate. *Peridium* 15–30 μm wide, composed of thick-walled brown cells of *textura angularis*, gradually paler and thinner inwardly, thicker

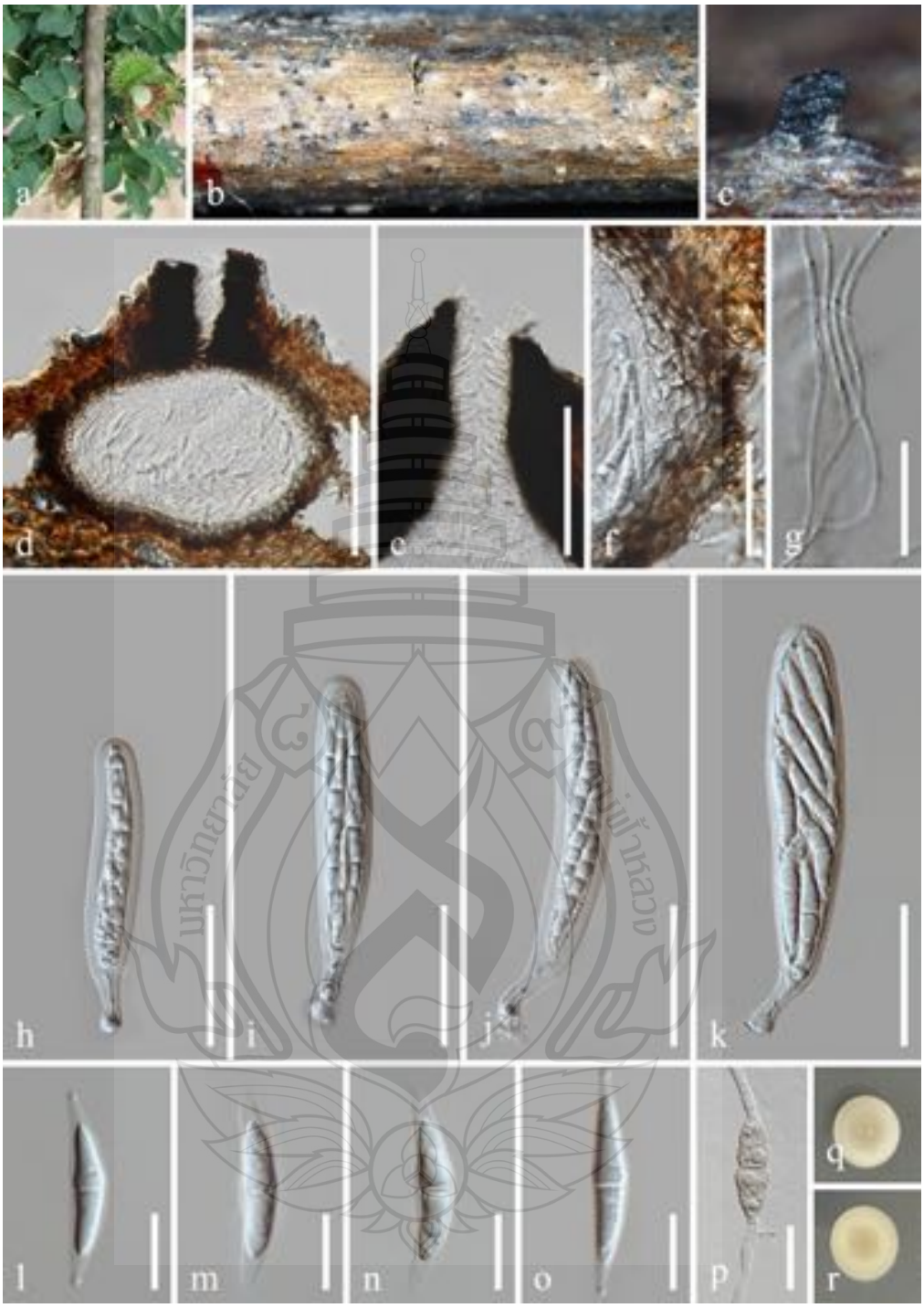
near the ostiole, thinner at the base. *Hamathecium* 2–2.5 μm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses, anastomosing and embedded in a gelatinous matrix. *Asci* 80–120 × 12–19 μm ($\bar{x}$ = 95 × 16 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, pedicellate, apically rounded with an ocular chamber. *Ascospores* 27–38 × 5.5–7.5 μm ($\bar{x}$ = 30 × 6.5 μm; n = 30), uniseriate or overlapping biseriate, hyaline, widely fusiform with acute ends, 1-septate, becoming 3-septate at germination, slightly constricted at the septum, upper cell slightly swollen towards the medial septum, guttulate, smooth-walled, with a straight or slightly curved and wide bipolar sheath, drawn out 5–7 μm long at both ends, forming a rounded cap-like structure at the tips; with a lateral pad-like structure within the sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, flat to slightly raised, mycelium velvety, initially creamy-white, becoming yellowish; in reverse, orange to brown in the centre, yellowish towards the margin.

Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Jichangping Town, Songhe Township, elevation 1,800 m, 26°3′7″ N, 104°35′36″ E, on branches of *Rosa roxburghii*, 10 July 2022, N. Wu, GL155 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Bijie City, Qixingguan District, Salaxi Town, Longfeng Village, elevation 1,869 m, 27°13′22″ N, 105°3′7″ E, on dead branches of *R. roxburghii*,1 February 2023, N. Wu, CDW27 (HUEST XX, paratype), living culture UESTCC XX.

Notes – *Pseudolophiostoma rosae* (CGMCC GL155 and UESTCC CDW27) formed a sister clade to *P. vitigenum* (HH 26930) with a high support in the phylogenetic tree (Figure 3.58). However, *P. rosae* is distinctive in its widely fusiform ascospores with straight or slightly curved and wide bipolar sheaths; the sheath is drawn out 5–7 μm long at both ends, forming a rounded cap-like structure at the tips of the

sheath. The ascospores of *P*. *vitigenum* are fusiform with narrow sheaths; the sheath drawn out at the ends, 3–12µm long at both ends (Thambugala et al., 2015). In addition, *P*. *rosae* has smaller asci (average: 95 × 16 µm vs. 129.8 × 20.1 µm) and ascospores (average: 30 × 6.5 µm vs. 38.5 × 10.5 µm) than *P*. *vitigenum*.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: d, e = 100 μm; f, h–k = 30 μm; g, p = 20 μm; l–o = 15 μm.

Figure 3.65 *Pseudolophiostoma rosae* (HKAS GL155, holotype)

Pseudopaucispora A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 175 (2018)

Type species – *Pseudopaucispora brunneospora* A. Hashim., K. Hiray. & Kaz. Tanaka

Notes – Hashimoto et al. (2018) established the genus *Pseudopaucispora* to accommodate *P. brunneospora*, which is characterized by small brown ascospores and pseudopycnidial conidiomata. Brahmanage et al. (2020) introduced the second member, *P. hyalinospora*, from a terrestrial habitat, and distinguished it from *P. brunneospora* based on molecular data, as well as its larger ascomata, asci and ascospores. Subsequently, *P. heteropanacis* was added to the genus from *Heteropanax fregans* in China (Dong et al., 2023). Herein, a new species, *P. rosae*, is introduced and illustrated.

Pseudopaucispora rosae N. Wu & Jian K. Liu, sp. nov. Figure 3. 66

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL21

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 210–330 μm wide, 295–360 μm high, immersed to erumpent throughout the host, subglobose or pyriform, dark brown to black, unilocular, glabrous, coriaceous or carbonaceous, thick-walled, elongated papillate, ostiolate. *Ostiole* 62–158 μm wide, 118–151 μm high, single, long, cylindrical to subcylindrical, straight or curved, central or laterally located, with a pore-like opening, and usually a pruinose layer of yellow to orange-brown material appearing around the apices of the ostiole. *Peridium* 15–30 μm wide, composed of dark brown to black compressed cells of *textura angularis*, pale pigmented to hyaline towards inwardly, thicker near the ostiole, thinner at the base. *Hamathecium* 1.5–2 μm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 60–69 × 8–10 μm ($\bar{x}$ = 65 × 8.5 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical,

short pedicellate, apically rounded with an ocular chamber. *Ascospores* 11–15.5 × 3.5–4.7 μm ($\bar{x}$ = 13 × 4.3 μm; n = 30), uniseriate or overlapping biseriate, fusiform with obtuse ends, slightly curved, 1–3-septate, slightly constricted at the septum, asymmetrical, upper cell mostly slightly wider and shorter, hyaline when young, becoming brown to dark brown, or reddish brown when mature, guttulate, smooth- and thin-walled, with a curved and bipolar sheath; sheath is drawn out 3–6 μm long at both ends, forming a rounded cap-like structure at the tips of the sheath, sometimes with an internal, inconspicuous, chamber-like, small appendage at both ends of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from the apex. Colonies on PDA medium reaching 7–9 mm diam. after two weeks at 25℃ in dark, circular, flat, dry, mycelium mostly immersed in the culture, orange brown; in reverse, brown at the margin, reddish brown in the middle. Producing yellow water-solute pigment.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL21 (HKAS XX, holotype); ex-type living culture CGMCC XX. *ibid.*, Bijie City, Qixingguan District, Salaxi Town, Longfeng Village, elevation 1,869 m, 27°13′22″ N, 105°3′7″ E, on dead branches of *R. roxburghii*,1 February 2023, N. Wu, CDW36 (HUEST XX, paratype), living culture UESTCC XX.

Notes – Multi-locus phylogenetic analysis revealed that *Pseudopaucispora rosae* (CGMCC SL21 and UESTCC CDW36) forms a distinct lineage, clustering with *P. brunneospora* (CBS 609.86) and *P. heteropanacis* (ZHKUCC 23-0881) with a strong support (Figure 3.58). Morphologically, *P. rosae* is similar to *P. brunneospora* and *P. heteropanacis* in having bitunicate, fissitunicate, cylindrical-clavate asci and brown, septate, fusiform ascospores with a sheath (Hashimoto et al., 2018; Dong et al., 2023). However, asci of *P. brunneospora* are longer (67–89 × 7–10.5 μm) than those of *P. heteropanacis* (65–80 × 8–10.5 μm) and *P. rosae* (60–69 × 8–10 μm). Ascospores

of *P. brunneospora* are also longer (14–17 × 3.5–4.5 µm) than *P. heteropanacis* (12.5–15.5 × 3.5–4.5 µm) and *P. rosae* (11–15.5 × 3.5–4.7 µm). The rounded cap-like structure at the tips of the sheath is present in *P. rosae* but absent in *P. brunneospora* and *P. heteropanacis*. Comparisons of the ITS, LSU, SSU, *tef1α* and *rpb2* sequences of *P. rosae* (CGMCC SL21) and *P. brunneospora* (CBS 143661) revealed 90.37% (535/592 bp), 97.27% (784/806 bp), 99.01% (1000/1010 bp), 98.44% (881/895 bp) and 96.37% (849/881 bp) similarities, respectively. Furthermore, *P. rosae* shows 88.81% similarity (627/706 bp) in the ITS sequence, 96.93% (820/846 bp) in the LSU sequence and 98.76% (956/968 bp) in the SSU sequence when compared to *P. heteropanacis* (CBS 609.86). Therefore, I recognize my collection as a new species, *P. rosae*.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Peridium. h Pseudoparaphysis. i–l Asci. m–q Ascospores. r Ascospore stained with Indian ink. s Germinating ascospore. t, u Colony on PDA, above (t), below (u). Scale bars: e, f = 100 μm; g–l = 20 μm; m–s = 10 μm.

Figure 3.66 *Pseudopaucispora rosae* (HKAS SL21, holotype)

Lophiotremataceae K. Hiray. & Kaz. Tanaka

Type genus – *Lophiotrema* Sacc.

Notes – Lophiotremataceae was introduced by Hirayama and Tanaka (2011) to accommodate the holomorphic genus *Lophiotrema* based on the phylogeny inferred from combined LSU and SSU gene regions. Currently, eight genera, *Atrocalyx*, *Crassimassarina*, *Cryptoclypeus*, *Decaisnella*, *Galeaticarpa*, *Koordersiella*, *Lophiotrema* and *Pseudocryptoclypeus*, are included in the family Lophiotremataceae (Hashimoto et al., 2017; Hongsanan et al., 2020a; Hyde et al., 2024). Members of the Lophiotremataceae are mostly saprobes on herbaceous or woody plants in terrestrial habitats (Boonmee et al., 2021; Zhang et al., 2023a).

Lophiotrema Sacc., Michelia 1(no. 3): 338 (1878)

Type species – *Lophiotrema nucula* (Fr.) Sacc.

Notes – Saccardo (1878) introduced this genus and placed it in Lophiostomataceae, as it was phylogenetically closely related to Lophiostoma and shared similar morphological characteristics. Hirayama and Tanaka (2011) re-evaluated these two genera and confirmed that *Lophiostoma* and *Lophiotrema* are distinct genera belonging to different families. They established the family Lophiotremataceae to accommodate *Lophiotrema*. Members of *Lophiotrema* are usually found on dead plant substrates and Index Fungorum lists approximately 171 epithets (2025, June). The morphology of *Lophiotrema* is unique, and is characterized by immersed to semi-immersed, globose to pyriform ascomata, 8-spored, bitunicate, fissitunicate, cylindrical to clavate asci and hyaline, guttulate, 3-septate, fusiform ascospores, surrounded by a mucilaginous sheath or not (Zhang et al., 2009, 2023a); the coleomycetous asexual morph produces hyaline, aseptate or 1-septate, ellipsoid to short-cylindrical conidia, with or without a sheath (Sun et al., 2025). In the present study, previously known *Lophiotrema hydei*, *L. karsti* and *L. rubusiicola* were isolated from *Rosa roxburghii*, while two new species were introduced, namely *L. rosicola* and *L. rosae.*

Lophiotrema hydei J.F. Zhang, J.K. Liu & Z.Y. Liu, Phytotaxa 379(2): 172 (2018) Figure 3.67

Index Fungorum number: IF 555333; Facesoffungi number: FoF04941

Synonym – *Lophiotrema mucilaginosum* Raza & L. Cai [as '*mucilaginosis*'], Fungal Diversity 95: 32 (2019)

Saprobic on branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 165–270 μm wide, 165–225 μm high, solitary to gregarious or confluent, semi-immersed to superficial, pyriform to subglobose, unilocular, thick-walled, glabrous, coriaceous to carbonaceous, papillate, ostiolate. *Ostiole* 50–70 μm wide, 65–95 μm high, single, straight or curved, central or laterally located. *Peridium* 20–30 μm wide, composed of thick-walled cells of *textura angularis*, with brown to dark brown cells in outer several layers, gradually merging with hyaline cells lining the cavity. *Hamathecium* 2–3 μm wide, unbranched, rarely septate, cellular pseudoparaphyses, anastomosing among and between the asci, embedded in a gelatinous matrix. *Asci* 60–75 × 5.5–7 μm ($\bar{x}$ = 68 × 6 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 16–22 × 2.7–3.8 μm ($\bar{x}$ = 19 × 3 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform, 1–3-septate, slightly constricted at the septa, guttulate, smooth-walled, surrounded by a thin distinct mucilaginous sheath. Asexual morph: Undetermined.

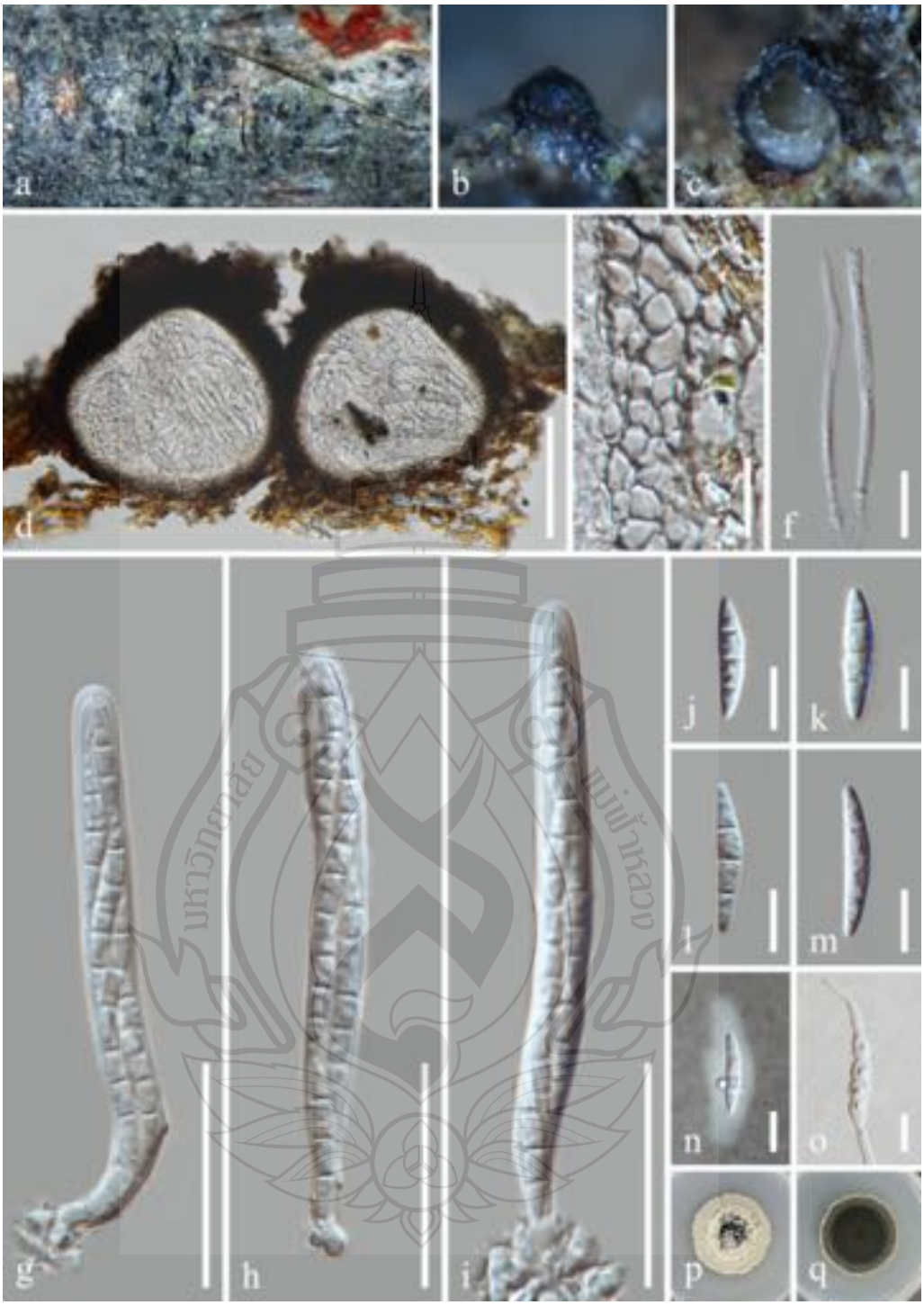
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 25–27 mm diam. after two weeks at 25°C in dark, circular, dense, cottony, grayish; in reverse, olive-green with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Huopu Town, on branches of *Rosa roxburghii*, 28 September 2021, N. Wu, CL24 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), *Rosa* sp. (Boonmee et al., 2021), Unidentified herbaceous plant (Zhang et al., 2018), Wood litter (Phookamsak et al., 2019).

Known geographical distribution – China.

Notes – My collection is phylogenetically most closely related to *Lophiotrema hydei* (99.36% ITS identities to MK108982, the type material, GZCC 18-0016) and *L. mucilaginosum* (98.99% ITS identities to MH822889, the type material, HMAS 255437). In the multi-locus phylogeny (Figure 3.68), my collection (UESTCC CL24) clustered with *L. hydei* (GZCC 18-0016) and *L. mucilaginosum* (HMAS 255437). In addition, my collection matches well in morphology with *L. hydei* and *L. mucilaginosum*, but a mucilaginous sheath surrounding the ascospores was observed in both my collection and *L. mucilaginosum*. This may be because the fungus was still young when observed, or it could be due to host variation. Phookamsak et al. (2019) introduced *L. mucilaginosum*, which forms a well-supported lineage and is sister to *L. hydei.* These two species were collected from wood litter and unidentified herbaceous plants in China, respectively (Zhang et al., 2018). When comparing the ITS, LSU and SSU regions, there were no base pair differences (0%) between *L. hydei* (GZCC 19-0273) and *L. mucilaginosum* (HMAS 255437). Therefore, I synonymize *L. mucilaginosum* under *L. hydei* based on my phylogenetic analysis, while recognizing my collection as *L. hydei* which is a new host record on *Rosa roxburghii*.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f Pseudoparaphyses. g–i Asci. j–m Ascospores. n Ascospore stained with Indian ink. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: d = 100 µm; g–i = 30 µm; e, f, j–o = 10 µm.

Figure 3.67 *Lophiotrema hydei* (HUEST CL24, new host record)

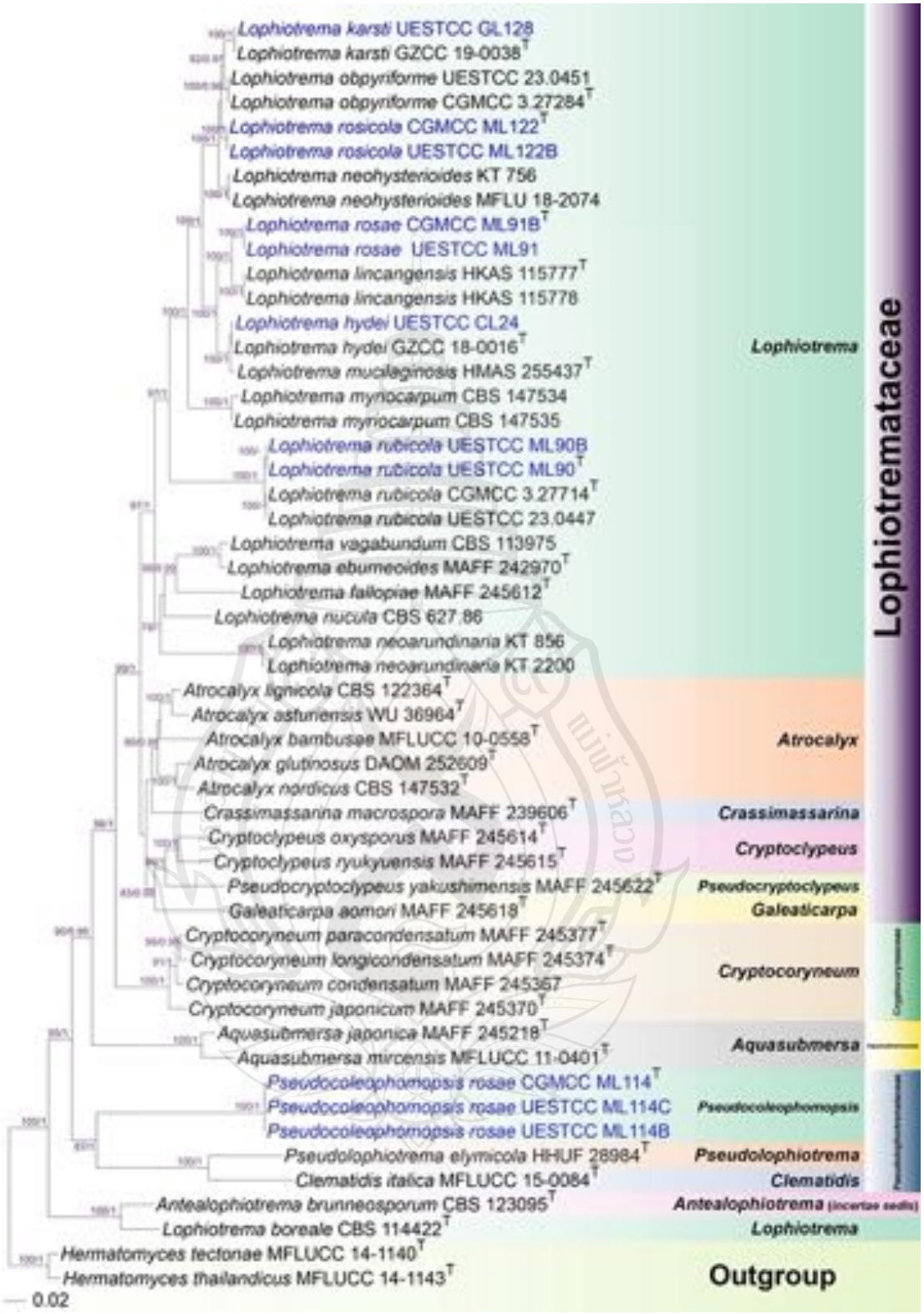


Figure 3.68 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Lophiotremataceae

Figure 3.68 The tree is rooted with *Hermatomyces tectonae* (MFLUCC 14-1140) and *H. thailandicus* (MFLUCC 14-1143). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Lophiotrema karsti J.F. Zhang & Jian K. Liu, Fungal Diversity 122: 41 (2023) Figure 3.69

Index Fungorum number: IF900705; Facesoffungi number: FoFXX

Saprobic on branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 165–270 μm wide, 165–225 μm high, solitary to gregarious, immersed to superficial or erumpent through bark, visible as black dots on the host when mature, pyriform to subglobose, unilocular, thick-walled, glabrous, coriaceous to carbonaceous, papillate, ostiolate. *Ostiole* 50–70 μm wide, 65–95 μm high, single, long, circular, cylindrical, straight, central. *Peridium* 20–30 μm wide, composed of several layers of dark brown to black, thick-walled pseudoparenchymatous cells of *textura angularis*, fusing with host tissue at the outermost layer, and become pale pigmented inwardly, thicker near the ostiole, thinner at the base. *Hamathecium* 2–3 μm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 60–75 × 5.5–7 μm ($\bar{x}$ = 68 × 6 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 16–22 × 2.7–3.8 μm ($\bar{x}$ = 19 × 3 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform, 1–3-septate, slightly constricted at the septa, narrower towards both ends, guttulate, smooth-walled, surrounded by a thin distinct mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17

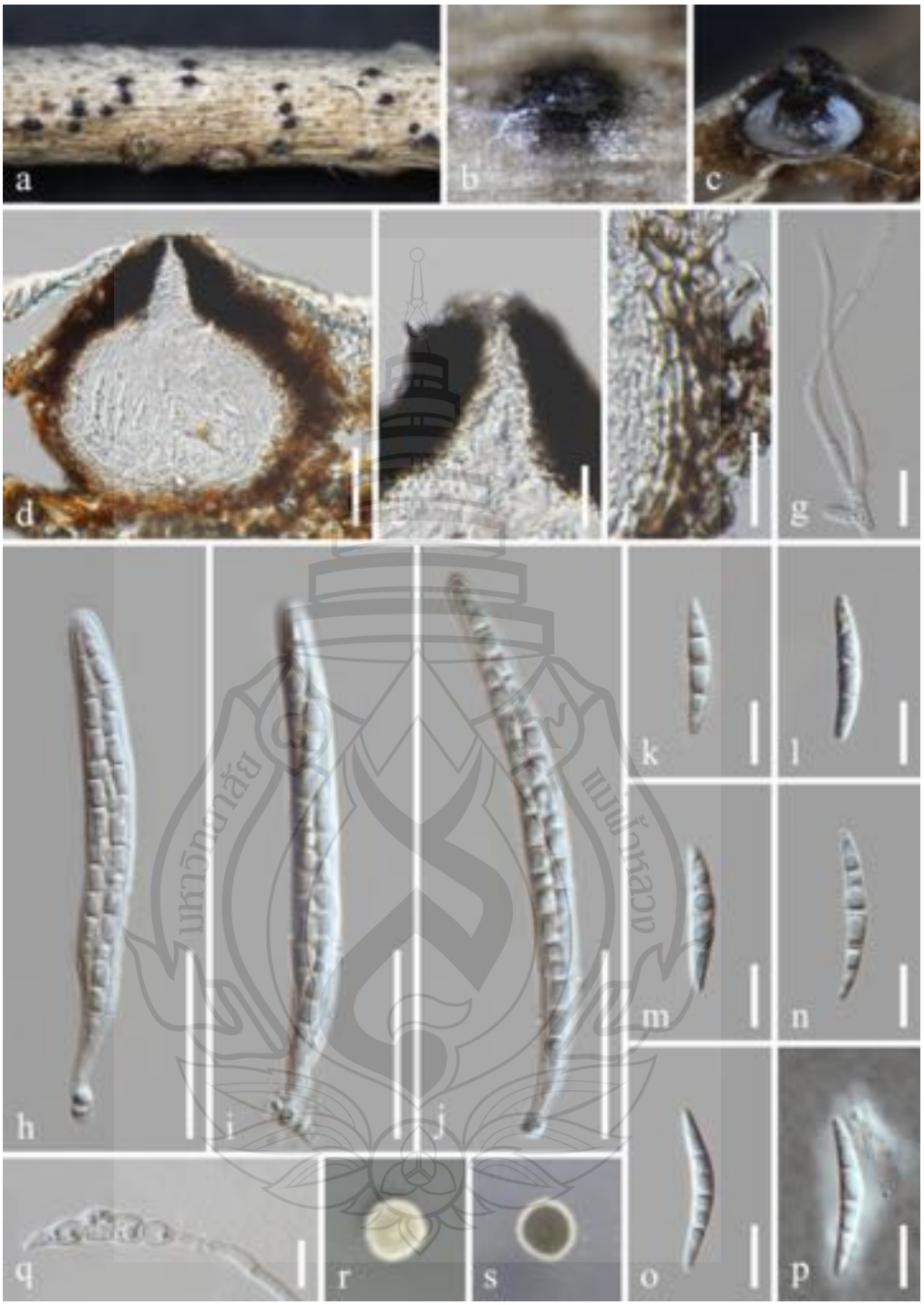
mm diam. after two weeks at 25℃ in dark, circular, dense, initially white and become grayish; in reverse, grayish brown with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *Rosa roxburghii*, 9 July 2022, N. Wu, GL128 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), Unidentified herbaceous plant (Zhang et al., 2023a).

Known geographical distribution – China.

Notes – Zhang et al. (2023) introduced *Lophiotrema karsti* (on dead culm of an unidentified herbaceous plant) from China, which was represented by its sexual morph. Based on a BLAST search of the ITS sequence of my collection in NCBI GenBank, the closest hit is *L. karsti* (GZCC 19-0038, identity 99.79%). In the present phylogenetic analysis, my collection (UESTCC GL128) clusters with *L. karsti* (GZCC 19-0038) with a high bootstrap support (Figure 3.68). My collection matches well with *L. karsti* in morphology, except that a thin mucilaginous sheath surrounding the ascospores was observed in my specimen. This feature might be due to the fungus was still young when observed due to host variation. Therefore, I identified my collection as *L. karsti* based on morphology and phylogeny and provide a new host record for this species from *Rosa roxburghii* in China.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 50 µm; e, f = 20 µm; g, k–q = 10 µm; h–j = 30

Figure 3.69 *Lophiotrema karsti* (HUEST GL128, new host record)

Lophiotrema rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.70

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

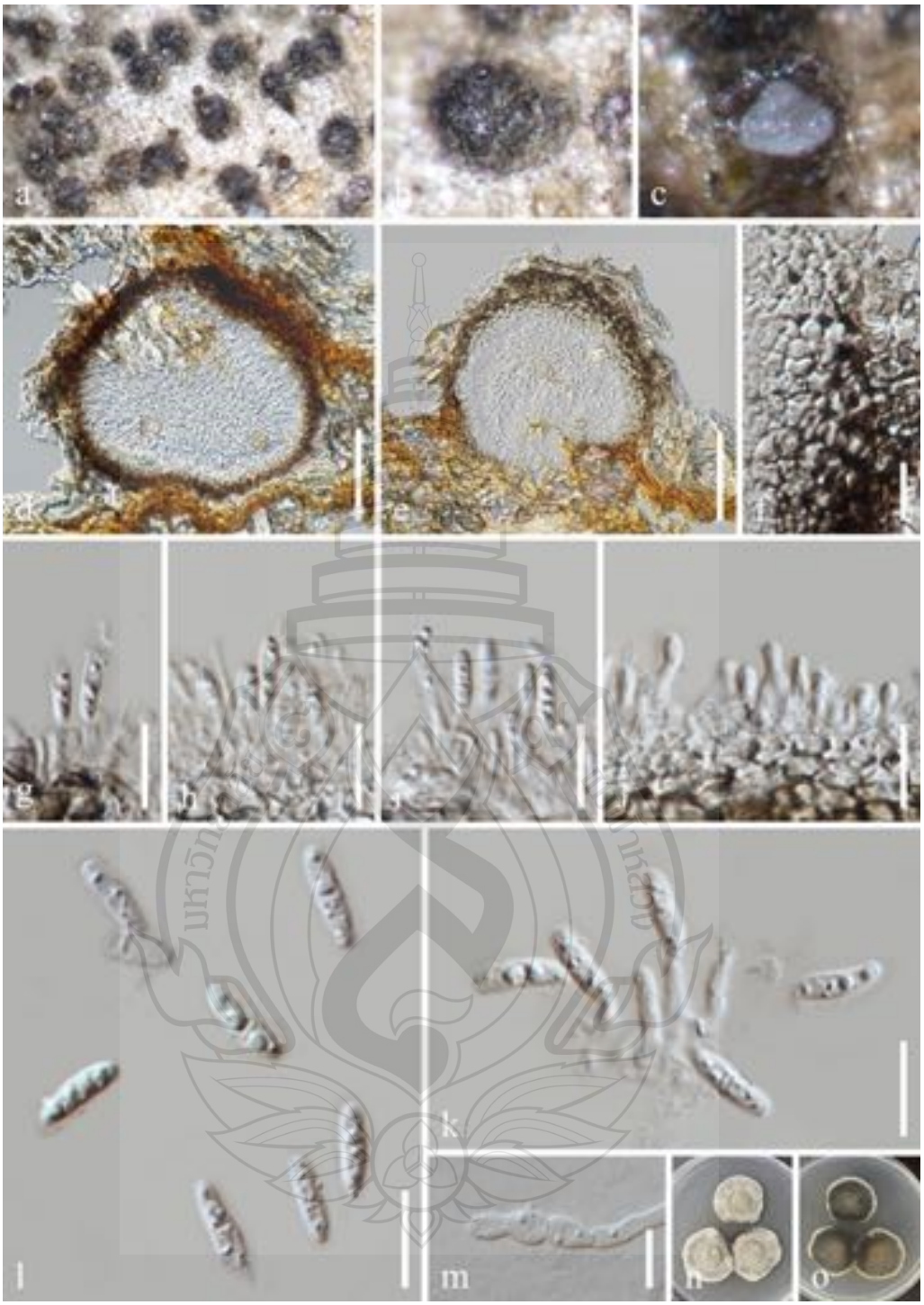
Holotype – HKAS ML91

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 125–160 μm wide, 105–155 μm high, solitary to gregarious, semi-immersed to superficial, visible as black dots on host substrate, pycnidial, globose to subglobose, unilocular, coriaceous or carbonaceous, glabrous, short papillate, inconspicuous ostiolate. *Ostiole* single, central. *Conidiomatal wall* 10–30 μm wide, composed of dark brown to brown cells of *textura angularis* in outer several layers, gradually merging with hyaline cells in inner layers, thicker near the ostiole, thinner at the base. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–11 × 1.5–3 μm ($\bar{x}$ = 9 × 2 μm; n = 30), hyaline, enteroblastic, phialidic, cylindrical to doliiform, determinate, smooth-walled, and arising from the inner layers of conidiomata. *Conidia* 8.5–12 × 2.5–3.5 μm ($\bar{x}$ = 10 × 3 μm; n = 30), hyaline, ellipsoid to short-cylindrical with rounded to obtuse ends, straight or slightly curved, 0–1-septate, with two unequal cells, lower cell smaller, granulate, smooth-walled, with a thin mucilaginous sheath.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25℃ in dark, circular or irregular, cottony, producing mucus, glistening, raised or convex, grayish green; in reverse, olive-green to dark brown with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML91 (HKAS XX, **holotype**); ex-type living culture CGMCC XX.

Notes – I recognize *Lophiotrema rosae* as a new species, as it phylogenetically forms a separate clade that is sister to *L. lincangensis* (HKAS 115777 and HKAS 115778) (Figure 3.68), based on the phylogeny inferred from ITS-LSU-SSU-*tef1α*-*rpb2* sequences. However, *L. lincangensis* is a sexual morph species (Boonmee et al., 2021), while *L. rosae* is represented by an asexual morph. Comparisons of the ITS, LSU, SSU, *tef1α* and *rpb2* sequence from the ex-type isolates of *L. rosae* (CGMCC ML91) and *L. lincangensis* (HKAS 115777) revealed 98% (490/500 bp), 99.51% (817/821 bp), 99.68% (945/948 bp), 98.54% (876/889 bp), and 96.17% (955/993 bp) similarities, respectively. Therefore, based on the criteria established by Jeewon and Hyde (2016), *L. rosae* and *L. lincangensis* can be regarded as two different species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 50 μm; f–m = 10 μm.

Figure 3.70 *Lophiotrema rosae* (HKAS ML91, holotype)

Lophiotrema rosicola N. Wu & Jian K. Liu, sp. nov. Figure 3.71

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosicola*" refers to the host genus, *Rosa*, on which the species was isolated.

Holotype – HKAS ML122

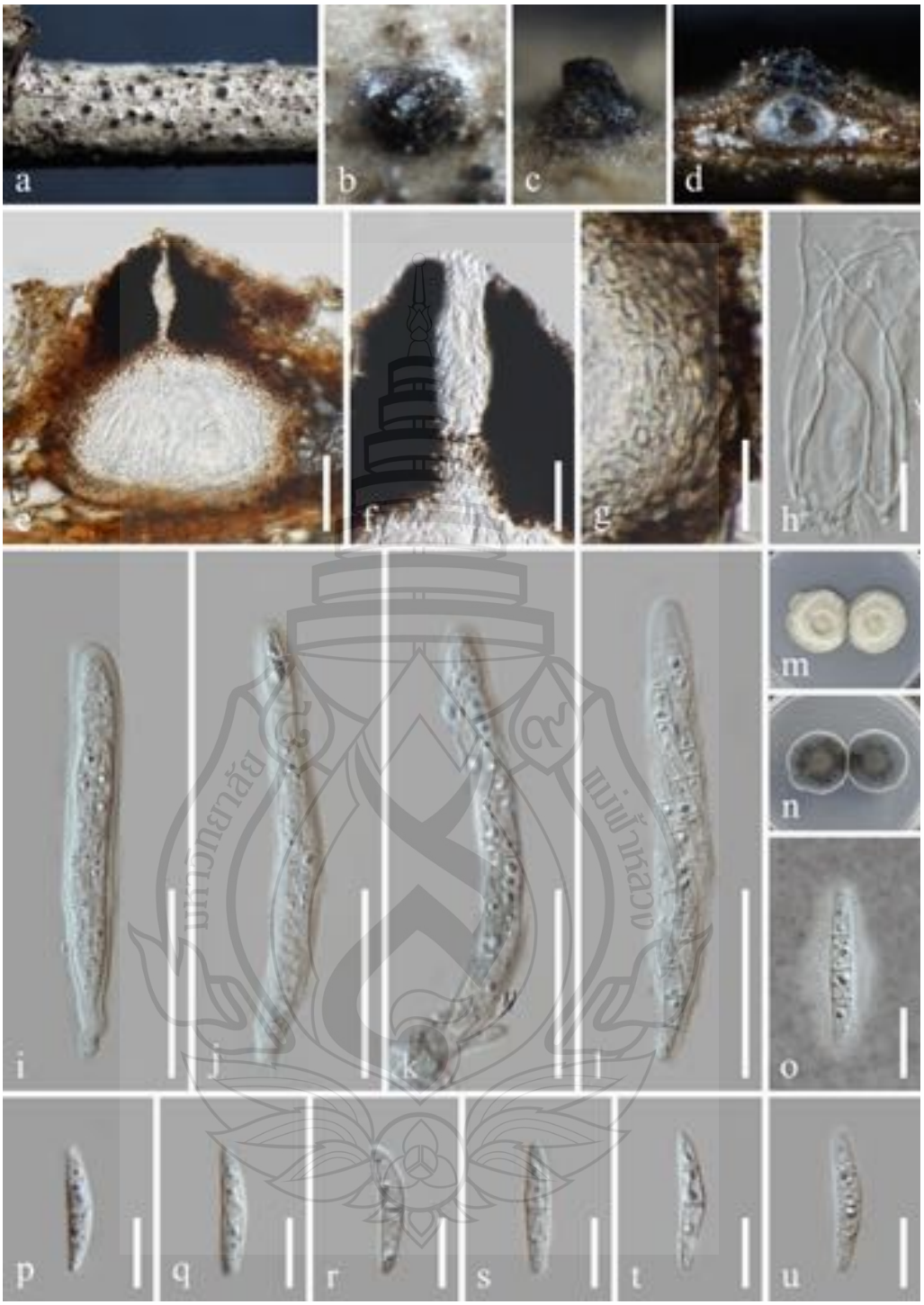
Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 165–270 μm wide, 165–225 μm high, solitary to gregarious or confluent, immersed to superficial or erumpent through bark, visible as black dots on the host when mature, pyriform to subglobose, unilocular, thick-walled, glabrous, coriaceous to carbonaceous, papillate, ostiolate. *Ostiole* 50–70 μm wide, 65–95 μm high, single, long, circular, cylindrical, straight, central. *Peridium* 20–30 μm wide, composed of several layers of dark-brown to black, thick-walled pseudoparenchymatous cells of *textura angularis*, fusing with host tissue at the outermost layer, and become pale pigmented inwardly, thicker near the ostiole, thinner at the base. *Hamathecium* 2–3 μm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 60–75 × 5.5–7 μm ($\bar{x}$ = 68 × 6 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 16–22 × 2.7–3.8 μm ($\bar{x}$ = 19 × 3 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform, 1–3-septate, slightly constricted at the septa, narrower towards both ends, guttulate, smooth-walled, surrounded by a thin distinct mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 hand germ tubes produced from both ends. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25℃ in dark, circular or irregular, cottony, producing mucus, glistening, raised or convex, grayish green; in reverse, olive-green to dark brown with white mycelium of the outer ring.

Materials examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″

E, on decaying branches of *Rosa roxburghii*, 3 February 2023, ML122 (HKAS XX, holotype); ex-type living culture CGMCC XX; ML12B (HUEST XX, paratype), living culture UESTCC XX.

Notes – In a BLASTn search of NCBI GenBank, the closest match of the ITS and LSU sequences of *Lophiotrema rosicola* (CGMCC ML122, ex-holotype) is *L. mucilaginosum* with 97.16% (isolate M37-21, OQ779068) and 99.66% (strain HMAS 255437, NG_066426) similarities, respectively, while the closest match with the SSU, *tef1α* and *rpb2* sequences is *L. neohysterioides* with 99.89% (isolate SNC97, PP627299), 97.24% (isolate SNC97, PP740446) and 97.34% (isolate SNC97, PP780224) similarities, respectively. In the present phylogenetic analysis, *L. rosicola* is closely related to *L. karsti* and *L. obpyriforme* (Figure 3.68). Morphologically, *L. rosicola* resembles *L. karsti* and *L. obpyriforme* with overlapping sizes of asci and ascospores. However, they can be distinguished by comparisons of each partial gene region (Zhang et al., 2023; Du et al., 2025). Therefore, *L. rosicola* is described as a new species based on phylogeny and morphological comparison.



Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Pseudoparaphyses. i–l Asci. m, n Colony on PDA, above (m), below (n). o Ascospore stained with Indian ink. p–u Ascospores. Scale bars: e = 50 μm; f, i–l = 30 μm; g, h = 20 μm; o–u = 10

Figure 3.71 *Lophiotrema rosicola* (HKAS ML122, holotype)

Lophiotrema rubicola H.Z. Du & Jian K. Liu, Mycosphere X(X): XX (2025) Figure 3.72

Index Fungorum number: IF 555333; Facesoffungi number: FoF04941

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 165–270 μm wide, 165–225 μm high, solitary to gregarious or confluent, immersed to superficial or erumpent through bark, visible as black dots on the host when mature, pyriform to subglobose, unilocular, thick-walled, glabrous, coriaceous, papillate, ostiolate. *Ostiole* 50–70 μm wide, 65–95 μm high, single, conical, slightly curved, centric or eccentric. *Peridium* 20–30 μm wide, composed of thick-walled, hyaline to brown cells of *textura angularis*, thicker near the ostiole, thinner at the base. *Hamathecium* 2–3 μm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 60–75 × 5.5–7 μm ($\bar{x}$ = 68 × 6 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded. *Ascospores* 16–22 × 2.7–3.8 μm ($\bar{x}$ = 19 × 3 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform, slightly curved, 1–3-septate, slightly constricted at the septa, narrower towards both ends, guttulate, smooth-walled, surrounded by a thin distinct mucilaginous sheath. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25°C in dark, circular, dense, cottony, grayish; in reverse, olive-green with white mycelium of the outer ring.

Materials examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML90 (HUEST XX), living culture UESTCC XX; ibid., ML90B (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), *Rubus corchorifolius* (Du et al., 2025).

Known geographical distribution – China.

Notes – *Lophiotrema rubicola* was introduced by Du et al. (2025) based on collections from *Rubus corchorifolius* in China. In the phylogenetic analysis (Figure 3.68), my collection (UESTCC ML90 and UESTCC ML90b) clustered with the type strain of *L. rubicola* (xxx) and showed nearly identical in the ITS gene sequence (only 4 nucleotide differences). Therefore, I report a new host record of *L. rubicola* on *Rosa roxburghii*.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–p Ascospores. q Ascospore stained with Indian ink. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 50 µm; f, g, l–r = 10 µm; h–k = 20 µm.

Figure 3.72 *Lophiotrema rubicola* (HUEST ML90, new host record)

Melanommataceae G. Winter [as 'Melanommeae']

Type genus: *Melanomma* Nitschke ex Fuckel

Notes: Melanommataceae was introduced by Winter (1885) with *Melanomma* as the type genus. The taxonomic history of the members in Melanommataceae has been reappraised and updated by Tian et al. (2015) and Hongsanan et al. (2020a). Currently, 35 genera are accepted within Melanommataceae, of which 17 genera are supported by molecular data (Hyde et al., 2024). Molecular data are still lacking for the genera *Asymmetricospora*, *Bicrouania*, *Calyptronectria*, *Exosporiella*, *Mamillisphaeria*, *Melanocamarosporium*, *Navicella* and *Nigrolentilocus*. Members of this family are known as saprobes or hyperparasites occurring in terrestrial, marine or freshwater habitats. They are characterized by immersed to semi-immersed, globose or depressed perithecial ascomata with or without a subiculum, trabeculate pseudoparaphyses, bitunicate and fissitunicate asci, and hyaline or pigmented, aseptate to septate, fusoid to ellipsoidal ascospores, with or without a mucilaginous sheath, as well as coelomycetous or hyphomycetous asexual morphs (Barr ME 1990a; Wanasinghe et al., 2018; Hongsanan et al., 2020a; Gao et al., 2023).

Magnitheca N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology: The epithet "*Magnitheca*" refers to the larger ascospores having a clear sheath; the Latin words "*magni*" and "*thecae*" mean large and sheath, respectively.

Type species: *Magnitheca rosae* N. Wu & Jian K. Liu

Saprobic on dead branches in terrestrial habitats. Sexual morph: *Ascomata* solitary to gregarious, immersed to semi-immersed, subglobose to pyriform, unilocular, glabrous, coriaceous, thick- and smooth-walled, papillate, ostiolate. *Ostiole* single, centric or eccentric, the region between the perithecial necks were occupied by hyaline to pale brown pseudoparenchymatous tissue. *Peridium* 5–7 layers, comprising hyaline to dark brown cells of *textura angularis* to *textura intricata*. *Hamathecium* numerous, filamentous, trabeculate pseudoparaphyses, septate, branched, anastomosing and

embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, cylindrical, short sessile or subsessile, apically rounded with an indistinct ocular chamber. *Ascospores* uniseriate or overlapping uniseriate, fusiform to oblong or oval, rounded or obtuse ends, 0–1-septate, constricted at the septum, guttulate, smooth and thick-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Notes: In the phylogenetic analysis based on ITS, LSU, SSU, *tef1α* and *rpb2* sequence data, *Magnitheca rosae* formed a sister clade to *Neobyssosphaeria clematidis* in Melanommataceae, with a high bootstrap support (Figure 3.74). *Magnitheca* differs from *Neobyssosphaeria* in having smaller ascomata, non-pigmented tissue around the ostiole, uniseriate ascospores that are fusiform to oblong or oval with rounded ends, 0–1-septate with large guttules in each cell, surrounded by a mucilaginous sheath, while *Neobyssosphaeria* has biseriate ascospores that are fusiform with acute ends, 7-septate, without gelatinous sheaths (Phukhamsakda et al., 2020). Therefore, I introduce *Magnitheca* as a new genus with a new species, *M. rosae* based on morphology and phylogeny.

Magnitheca rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.73

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology: The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype: HKAS ML68

Saprobic on dead branches of *Rosa sterilis*. Sexual morph: *Ascomata* 300–720 μm wide, 230–400 μm high, solitary to gregarious, immersed to semi-immersed, visible as black domes, subglobose or pyriform, or rarely irregular, unilocular, glabrous, coriaceous, thick- and smooth-walled, short papillate, ostiolate. *Ostiole* 40–70 μm wide, 45–65 μm high, single, centric or eccentric, circular to oval, the region between the perithecial necks were occupied by hyaline to pale brown pseudoparenchymatous tissue. *Peridium* 30–45 μm wide, carbonaceous and brittle when dry, with 5–7 layers, outer layer heavily pigmented, comprising black to dark brown cells of *textura intricata*,

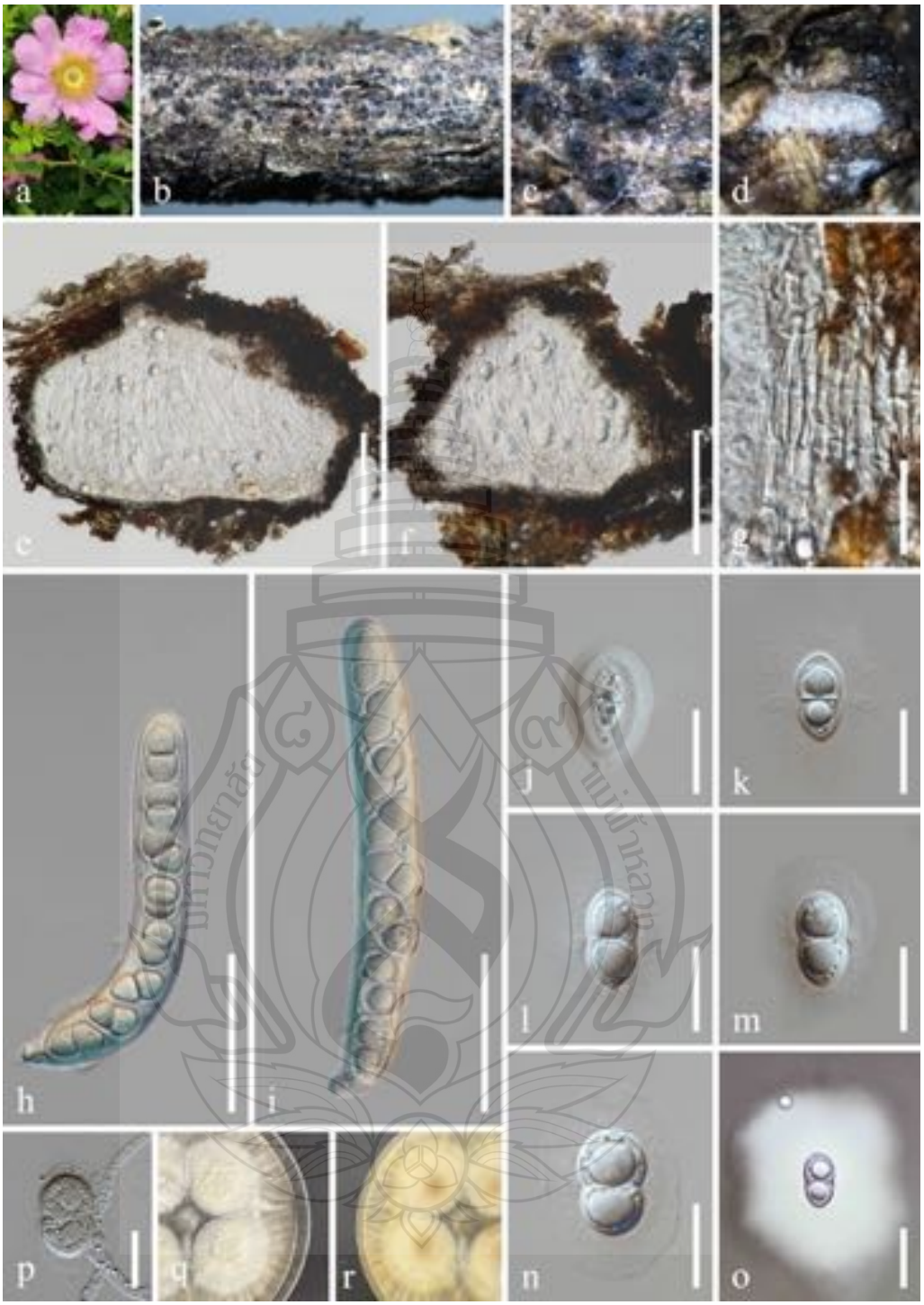
inner layer composed of hyaline thin-walled cells of *textura angularis*, thinner at the base. *Hamathecium* 1.5–2 µm wide, numerous, filamentous, trabeculate pseudoparaphyses, septate, branched, anastomosing and embedded in a gelatinous matrix. *Asci* 160–200 × 22–25 µm ($\bar{x}$ = 180 × 23 µm; n = 20), 8-spored, bitunicate, cylindrical, short sessile or subsessile, apically rounded with an indistinct ocular chamber. *Ascospores* 24–31 × 12.5–19 µm ($\bar{x}$ = 28 × 17 µm; n = 30), uniseriate or overlapping uniseriate, hyaline, initially fusiform with acute ends, 1-septate, verrucose, becoming oblong or oval, rounded at ends, deeply constricted at the septum, with large guttules in each cell at maturity, upper cell slightly wider than lower cell, smooth and thick-walled, surrounded by a 7–10 µm wide mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics: Ascospores germinated on PDA medium within 24 h and germ tubes produced from every cells. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular or irregular, dry, dense, flat and central slightly raised, mycelium velvety towards the margin, initially off-white, becoming olivaceous-gray; in reverse, yellowish brown in center, grayish white in the middle and yellowish at the entire margin.

Materials examined: CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML68 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, CDW03 (HUEST XX, paratype), living culture UESTCC XX.

Notes: *Magnitheca rosae* is a sexual morph species, which was collected from *Rosa sterilis* in China. In my phylogenetic analysis, *M. rosae* (CGMCC ML68 and UESTCC CDW03) clustered closer to *Neobyssosphaeria clematidis* (MFLUCC 17–0794), forming an independent clade within Melanommataceae (Figure 3.74). Sequence comparisons between the ex-type isolates of *M. rosae* (CGMCC ML68) and

N. clematidis (MFLUCC 17–0794) revealed a less similarity of 95.51% (809/847 bp) in the LSU region. The SSU sequence of *N. clematidis* (MFLUCC 17-0794) is too short to compare with my collection, but the available sequence showed only 96.83% (244/252 bp) similarity. Morphologically, *Magnitheca rosae* is clearly distinguished from other species in Melanommataceae by its immersed to semi-immersed ascomata, hyaline to pale brown pseudoparenchymatous tissue in the ostiole, uniseriate or overlapping uniseriate, short sessile or subsessile asci, and large, hyaline, thick-walled, fusiform to oblong or oval ascospores with rounded ends, 1-septate, constricted at the septum, large guttules in each cell, and surrounded by a distinctive thick mucilaginous sheath (Hongsanan et al., 2020a; Phukhamsakda et al., 2020). I therefore introduced the genus *Magnitheca* to accommodate *M. rosae* as a new species.



Note a Host: *Rosa sterilis*. b, c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Ostiole. h, i Asci. j–n Ascospores. o Ascospore stained with Indian ink. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: e = 150 μm; f = 120 μm; g, j–p = 20 μm; h–i = 60 μm.

Figure 3.73 *Magnitheca rosae* (HKAS ML68, holotype)

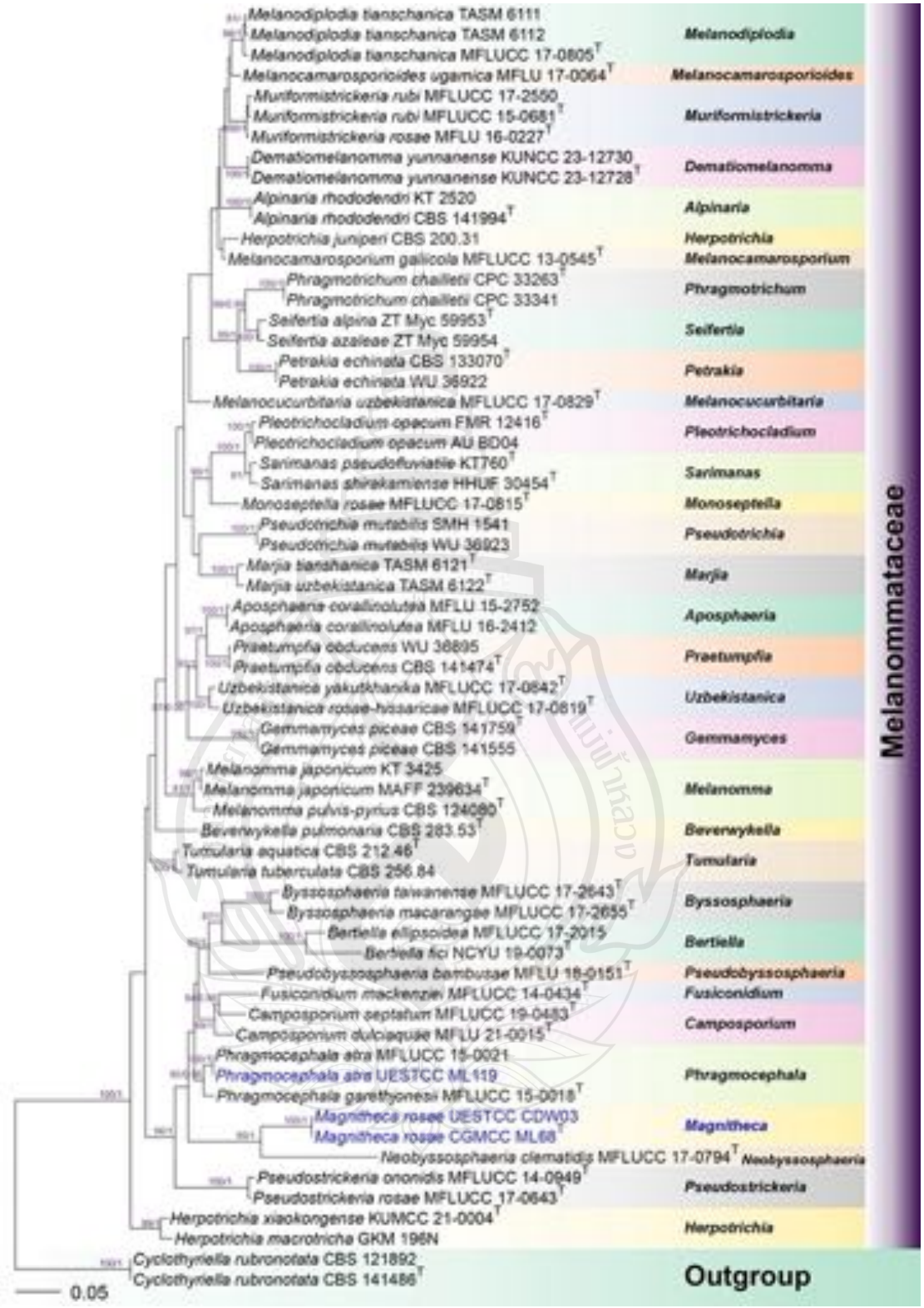


Figure 3.74 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Melanommataceae

Figure 3.74 The tree is rooted with *Cyclothiyriella rubronotata* (CBS 121892) and *C. rubronotata* (CBS 141486). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Phragmocephala E.W. Mason & S. Hughes, Naturalist (Hull), ser. 3, 1951: 97 (1951)

Type species – *Phragmocephala elliptica* (Berk. & Broome) S. Hughes

Notes – The genus *Phragmocephala* was established by Mason and Hughes (1951) and typified by *P. elliptica* (= *P. cookei*), along with two other species, *P. atra* and *P. minima*. Su et al. (2015) rediscovered *P. atra* from decaying wood in a stream in China and described a new species, *P. garethjonesii*. They also provided the first molecular sequence data for the genus, confirming its phylogenetic placement in the family Melanommataceae within Dothideomycetes (Su et al., 2015). *Phragmocephala* is characterized by macronematous, mononematous or synnematous, septate, unbranched, brown to pale brown conidiophores, holoblastic, monoblastic, terminal, pale brown, integrated conidiogenous cells, and ellipsoidal to subglobose, 4–6-septate, brown, paler at both ends, with middle cells dark brown, rounded at apex, truncate at base, versicoloured conidia (Su et al., 2015; Crous et al., 2024; Zhang et al., 2025a).

Phragmocephala atra (Berk. & Broome) E.W. Mason & S. Hughes, Naturalist: 97 (1951) Figure 3.75

Index Fungorum number: IF303243; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii*. Asexual morph: Hyphomycetous. *Colonies* effuse, scattered, erect, dark brown to black, glistening. *Mycelium* partly superficial, partly immersed, septate, branched. *Conidiophores* 125–185 × 6–8.5 μm ($\bar{x}$ = 159 × 7 μm; n = 30), synnematous, macronematous, cylindrical, straight or slightly curved, unbranched, 5–8-septate, slightly constricted at some septa, erect, dark brown at

the base, pale brown at fertile, flared apex, sometimes proliferating. *Conidiogenous cells* 10–14.5 × 7.5–10 µm ($\bar{x}$ = 12.5 × 9 µm; n = 30), monoblastic, integrated, terminal, elongated, pale brown. *Conidial secession* schizolytic. *Conidia* 30–43.5 × 18.5–25.5 µm ($\bar{x}$ = 39 × 21 µm; n = 30), ellipsoidal to subglobose, 3–5-septate, dark brown, paler at both ends, middle cells dark brown, rounded at apex, truncate at base, sometimes, after release, tubular part of conidiogenous cell remains attached to conidium. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA medium within 12 h. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25°C in dark, circular, cottony, umbonate, velvety, dense, dry, surface folded, smooth, lobate margin, yellowish brown in the middle, pale yellow at the edge; in reverse, orange to sienna with yellowish mycelium of the outer ring.

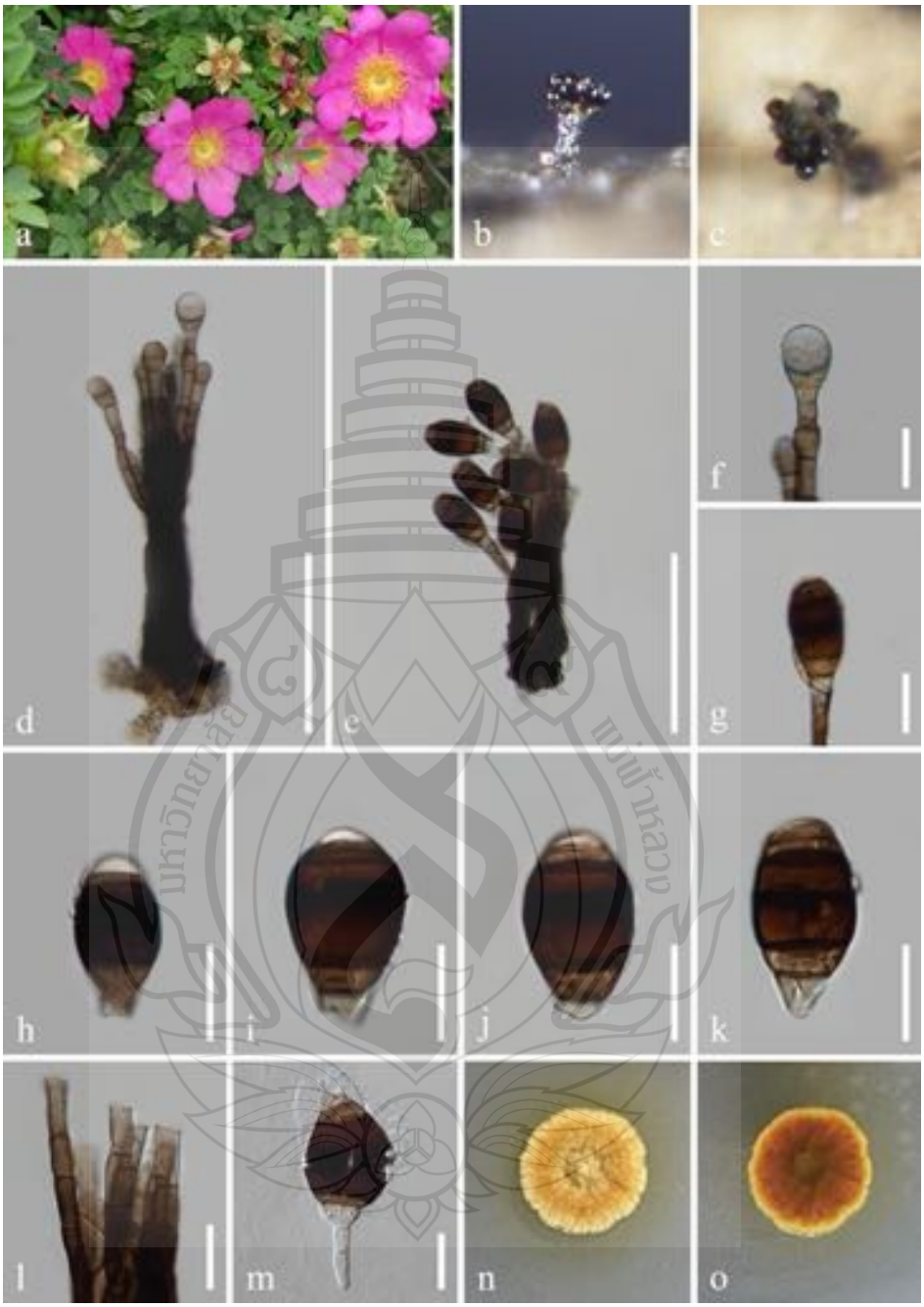
Materials examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML119 (HUEST XX), living culture UESTCC XX.

Hosts – Coffee plants (Lu et al., 2025), *Cryptomeria fortunei* and *Cryptomeria japonica* (Tian et al., 2024c), *Pteris vittata* and *Woodwardia unigemmata* (Zhang et al., 2025a), *Ripogonum scandens* (NCBI), *Rosa roxburghii* (present study), *Urtica dioica* (Ellis 1959).

Known geographical distribution – China, Italy, New Zealand, UK.

Notes – Based on a BLAST search of the ITS sequence of my collection in NCBI GenBank, the closest match is *Phragmocephala atra* (LCGS09_2, OR887408, identities 99.80%), and the closest match for the LSU sequence is also *P. atra* (LC3-1-9, PQ608162, identities 99.77%). In the phylogenetic tree, my collection clusters with *P. atra* (MFLUCC 15-0021) with a strong statistical support (Figure 3.74). My collection is similar to *P. atra* in the morphology of conidiophores and conidia with comparable dimensions (Su et al.,

2015; Zhang et al., 2025a). Therefore, I recognize my collection as *P. atra* and report a new host record, *Rosa roxburghii.*



Note a Host: *Rosa roxburghii*. b, c Colonies on substrate. d, e Conidiophores with conidia. f, g Conidiogenous cells with conidia. h–k Conidia. l Apex of conidiophores. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 100 μm; f–m = 20 μm.

Figure 3.75 *Phragmocephala atra* (HUEST ML119, new host record)

Neomassariaceae H.A. H.A. Ariy., Jaklitsch & Voglmayr

Type genus – *Neomassaria* Mapook, Camporesi & K.D. Hyde

Notes – Neomassariaceae was established by Ariyawansa et al. (2018), with *Neomassaria* as the type genus (type species *N. fabacearum*). Morpho-phylogenetic evidence supported the acceptance of three genera in this family, *Neomassaria*, *Pigmentatineomassaria* and *Pseudoneohendersonia* (Wijesinghe et al., 2023; Yang et al., 2024). Members of Neomassariaceae are characterized by immersed to erumpent ascomata, 8-spored, bitunicate, oblong to cylindrical, pedicellate asci, and hyaline to brown, septate, ellipsoid to fusiform ascospores with or without a gelatinous sheath, and its asexual morphs are characterized by macronematous, mononematous, unbranched, brown conidiophores, and monoblastic, holoblastic, terminal, brown conidiogenous cells, and acrogenous, solitary, pale brown to brown, 4–30-septate, smooth-walled, obclavate conidia (Hyde et al., 2016; Ariyawansa et al., 2018; de Silva et al., 2022; Hu et al., 2022; Yang et al., 2022a, 2024; Wijesinghe et al., 2023; Zhang et al., 2024a; Wu et al., 2025).

Neomassaria Mapook, Camporesi & K.D. Hyde, Fungal Diversity 80: 74 (2016)

Type species – *Neomassaria fabacearum* Mapook, Camporesi & K.D. Hyde

Notes – Hyde et al. (2016) introduced the genus *Neomassaria* to accommodate a single species, *N. fabacearum*, and placed it in Massariaceae based on LSU and SSU sequence data. Subsequently, Ariyawansa et al. (2018) recognized the second *Neomassaria* species, *N. formosana*, and introduced the family Neomassariaceae to accommodate *N. fabacearum* and *N. formosana*. Currently, 13 epithets of *Neomassaria* are listed in Index Fungorum (2025, June). *Neomassaria* was known only from sexual morphs until Zhang et al. (2024a) introduced an asexual morph species, *N. thailandense*, collected from *Rhapis excelsa* in China. Wu et al. (2025) presented the first documentation of *Neomassaria* associated with *Camellia sinensis* and introduced two

new asexual morph species, *N. camelliae* and *N. sichuanensis.* In the present study, I isolated *N. formosana* from *Rosa roxburghii* in China.

Neomassaria formosana H.A. H.A. Ariy., Jaklitsch & Voglmayr, Cryptog. Mycol. 39(3): 368 (2018) Figure 3.76

Index Fungorum number: IF827114; Facesoffungi number: FoF17579

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 140–190 μm wide, 170–210 μm high, solitary to gregarious, black, immersed to semi-immersed, unilocular, coriaceous, pyriform to subglobose, glabrous, papillate, ostiolate. *Ostiole* 50–75 μm wide, 60–70 μm high, single, long, subcylindrical, central or laterally located, periphysate. *Peridium* 30–45 μm wide, composed of thick-walled dark brown cells of *textura angularis*. *Hamathecium* 1.5–2 μm wide, trabecular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 85–100 × 7.5–9 μm ($\bar{x}$ = 95 × 8 μm; n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, slightly curved, short pedicellate, apically rounded. *Ascospores* 20–26 × 4–6 μm ($\bar{x}$ = 23.5 × 5 μm; n = 30), overlapping biseriate, straight or slightly curved, hyaline, fusiform, guttulate, the upper cell slightly wider than the lower cell, obtuse or conical ends, 1-septate, slightly constricted at the median septum, smooth-walled, surrounded by a thin gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, umbonate, radially striate, with a slightly lobate edge; surface smooth, with cottony texture, green to light green or gray-white; in reverse, dark green expanding from the center.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL33 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia sinensis* (Wu et al., 2025), *Coffea* sp. (Lu et al., 2025), *Rhododendron* sp. (Ariyawansa et al., 2018), *Trachycarpus fortunei* (Zhang et al., 2024a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Neomassaria formosana* was introduced by Ariyawansa et al. (2018) from dead stems of *Rhododendron* sp. in Taiwan Province, China. My collection matches the holotype of *N. formosana* in the morphology and dimensions of ascomata, asci and ascospores. Phylogenetic analysis supports the identification of my collection as *N. formosana* (Figure 3.77) and this is the first record of *N. formosana* found on *Rosa roxburghii* in China.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–j Asci. k–m Ascospores. n Ascospore stained with Indian ink. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: d = 50 μm; e, h–j = 30 μm; f, g, k–o = 10 μm.

Figure 3.76 *Neomassaria formosana* (HUEST SL33, new host record)

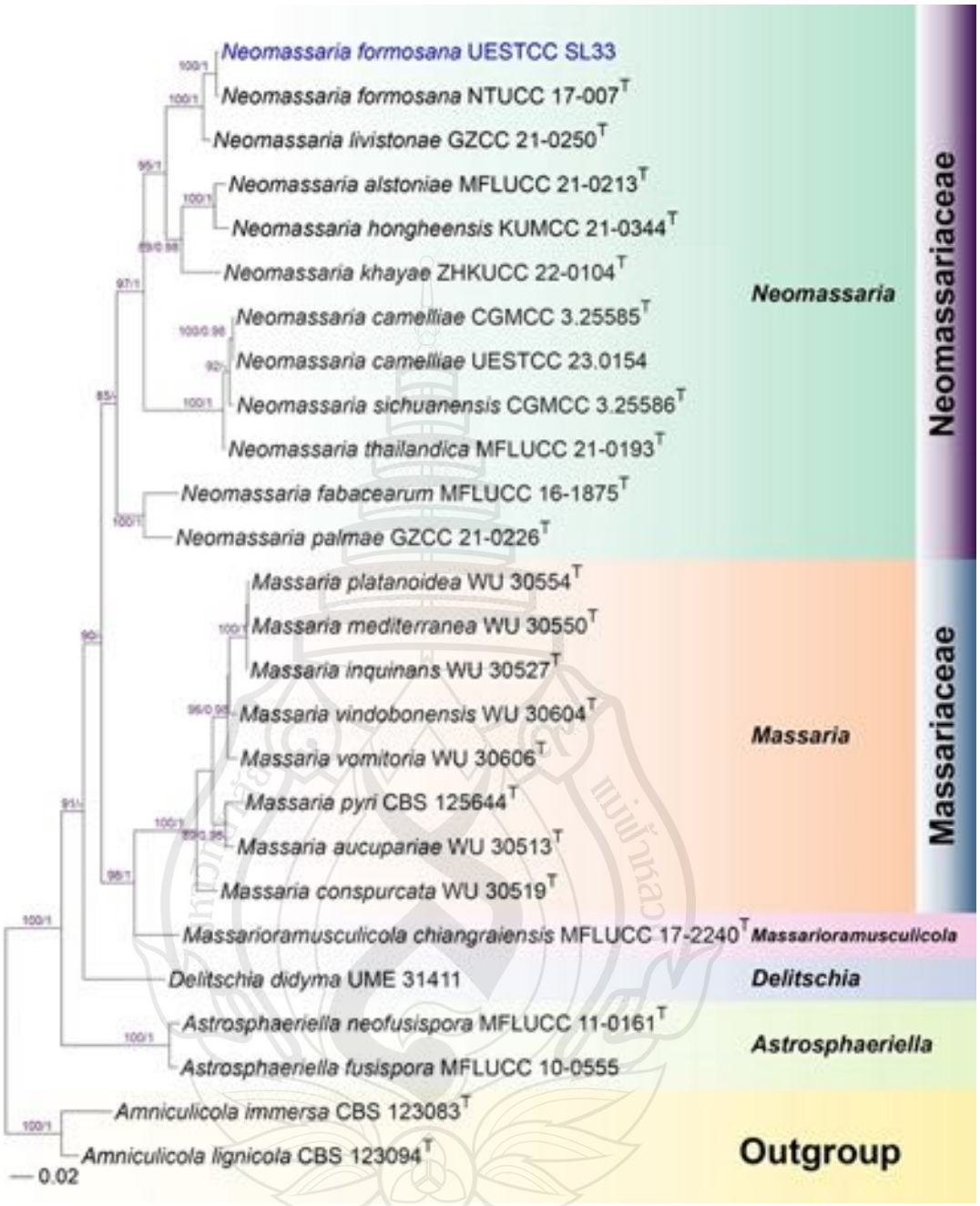


Figure 3.77 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, *tef1α* and *rpb2* sequence data of *Neomassaria*

Figure 3.77 The tree is rooted with *Amniculicola immersa* (CBS 123083) and *A. lignicola* (CBS 123094). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian.

The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "[T]" after the strain number.

Nigrogranaceae Jaklitsch & Voglmayr

Type genus – *Nigrograna* Gruyter, Verkley & Crous

Notes – Nigrogranaceae is a monotypic family with *Nigrograna* as the holomorphic type genus (Jaklitsch & Voglmayr, 2016c). This family comprises saprobic, pathogenic and endophytic species associated with a wide variety of substrates mainly from aquatic, terrestrial and marine habitats, as well as human superficial tissue (Hyde et al., 2017; Tibpromma et al., 2017; Kolařík 2018; Zhao et al., 2018; Dayarathne et al., 2020; Li et al., 2023b; Du et al., 2024a).

Nigrograna Gruyter, Verkley & Crous, Stud. Mycol. 75: 31 (2012) [2013]

Type species – *Nigrograna mackinnonii* (Borelli) Gruyter, Verkley & Crous

Notes – de Gruyter et al. (2013) introduced *Nigrograna* to accommodate the human pathogen *N. mackinnonii* (≡ *Pyrenochaeta mackinnonii*) with its asexual morph. There are about 45 *Nigrograna* epithets listed in Index Fungorum (2025, June). *Nigrograna* is a holomorphic genus characterized by immersed to semi-immersed, perithecial, ostiolate ascomata, cylindrical or clavate, bitunicate, fissitunicate asci with subsessile or short-pedicellate and fusiform, hyaline to brown, straight or curved, aseptate or 1–3-septate ascospores, slightly constricted at the septum, with or without a mucilaginous sheath; asexual morphs hyphomycetous, possessing hyaline, aseptate, ellipsoidal or cylindrical conidia or coelomycetous with phialidic conidiogenous cells and ellipsoidal, unicellular, aseptate conidia (Dong et al., 2020; Li et al., 2023b; Du et al., 2024a; Ren et al., 2024a; Yu et al., 2024).

Nigrograna camelliae Y.H. Lu, H.Z. Du & Jian K. Liu, MycoKeys 110: 15 (2024) Figure 3.78

Index Fungorum number: IF 854178; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 170–270 μm wide, 145–365 μm high, solitary to gregarious, black, immersed to semi-immersed,

unilocular, long necks, bursting through the bark of host, coriaceous to carbonaceous, globose to subglobose, papillate, ostiolate. *Setae* 2–3 μm wide, sparse, septate, brown. *Ostiole* 70–90 μm wide, 142–205 μm high, single, long, subcylindrical, central or laterally located. *Peridium* 19–30 μm wide, composed of thick-walled dark brown cells of *textura angularis* or *textura epidermoidea*. *Hamathecium* 2–2.5 μm wide, composed of numerous, filiform, hyaline, aseptate or septate, smooth-walled pseudoparaphyses. *Asci* 75–100 × 9–13 μm ($\bar{x}$ = 84 × 10.5 μm; n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 14–18 × 4.5–6.5 μm ($\bar{x}$ = 15 × 5 μm; n = 30), uniseriate or overlapping to crowded, straight or slightly curved, fusiform, guttulate, the upper cell slightly wider than the lower cell, obtuse or conical ends, initially hyaline and aseptate, becoming pale brown to dark brown and 1-septate when mature, slightly constricted at the median septum, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25°C in dark, circular, dense, velvety; in reverse, yellowish brown in the middle, white mycelium in the outer ring.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML84 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia sinensis* (Du et al., 2024a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Du et al. (2024a) introduced *Nigrograna camelliae*, which is phylogenetically separated from *N. coffeae* and has immersed, subglobose ascomata with long neck and brown setae, and 1-septate, ellipsoid ascospores. The morphology and dimensions of my collection well matches with the holotype *N. camelliae* (Du et al., 2024a).

I therefore identify my collection as *N. camelliae* and report it as a new host record on *Rosa roxburghii* in China.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Setae. i–l Asci. m Pseudoparaphyses. n–q Ascospores. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 100 μm; f = 60 μm; g, i–l = 30 μm; h–m = 20 μm; n–r = 10 μm.

Figure 3.78 *Nigrograna camelliae* (HUEST ML84, new host record)

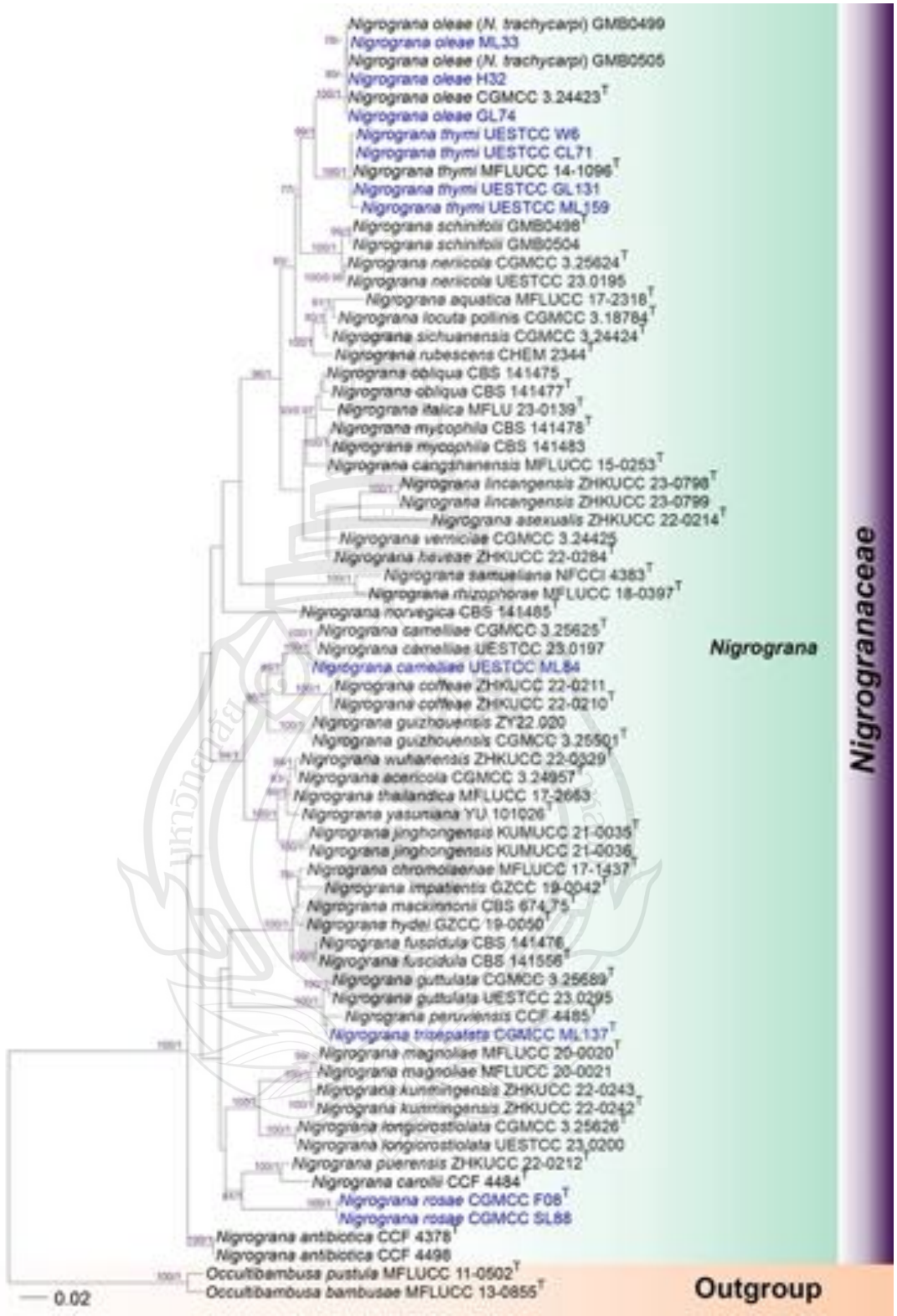


Figure 3.79 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of *Nigrograna*

Figure 3.79 The tree is rooted with *Occultibambusa bambusae* (MFLUCC 13-0855) and *O. pustula* (MFLUCC 11-0502). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Nigrograna oleae W.L. Li & Jian K. Liu, Mycosphere 14(1): 1503 (2023) Figure 3.80

Index Fungorum number: IF849157; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 220–330 μm wide, 165–230 μm high, solitary to gregarious or confluent, brown to dark brown, immersed to semi-immersed, unilocular, glabrous, coriaceous, subglobose to obpyriform, ostiolate. *Ostiole* single, centric or eccentric. *Peridium* 25–40 μm wide, composed of several layers of thick-walled, brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 μm wide, composed of dense, numerous, filiform, branched, septate, constricted at the septum, hyaline, pseudoparaphyses. *Asci* 70–86 × 12–18 μm ($\bar{x}$ = 78 × 15 μm; n = 20), 8-spored, bitunicate, cylindrical to clavate, straight or slightly curved, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 16–20 × 6–8 μm ($\bar{x}$ = 19 × 7 μm; n = 30), irregularly arranged or crowded, straight or slightly curved, fusoid to clavate, apical cell mostly obtuse, narrow towards the base, initially hyaline and 1-septate, becoming pale brown to dark brown and 2–3-septate when mature, slightly constricted at the septa, smooth-walled. Asexual morph: Undetermined.

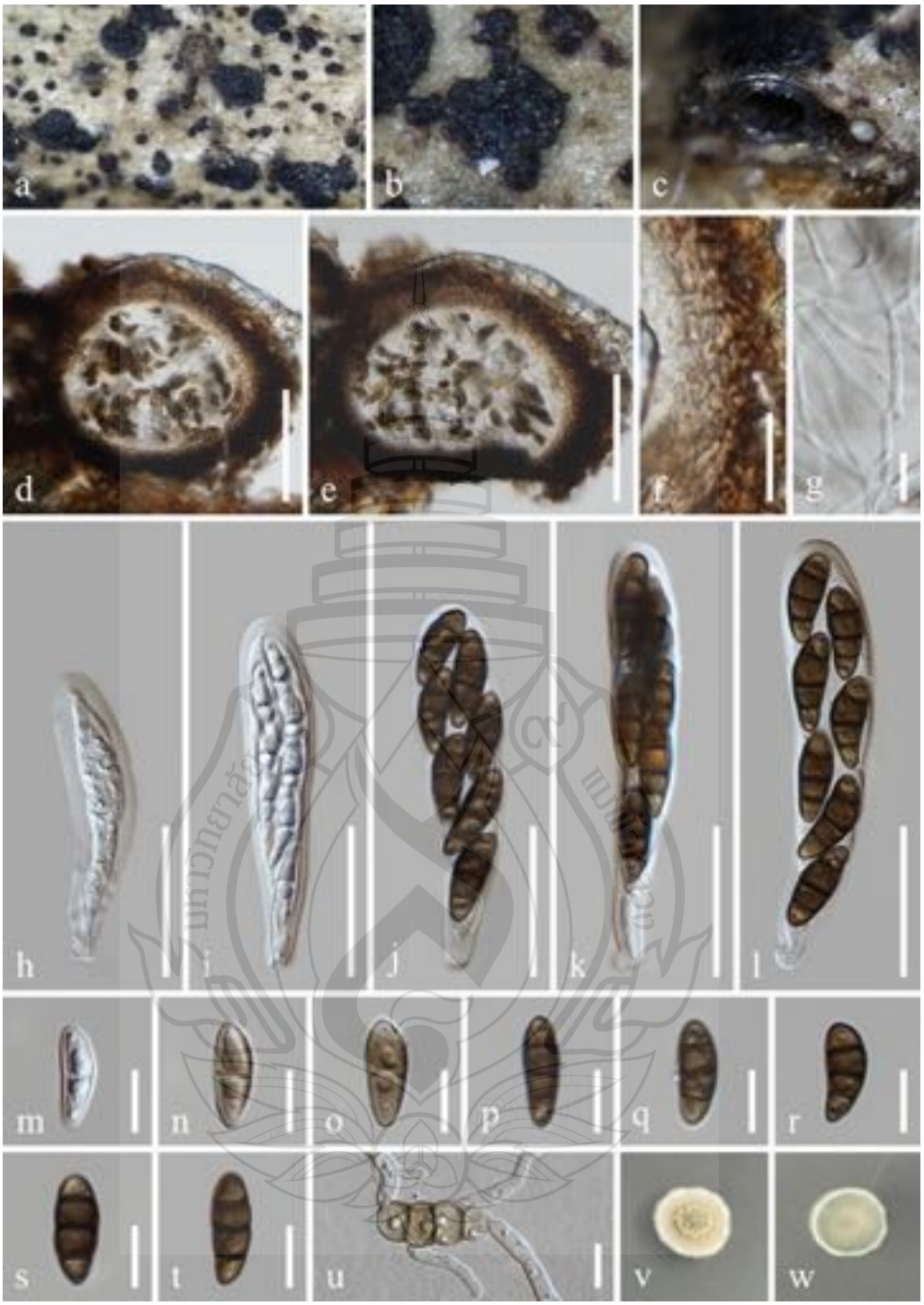
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25℃ in dark, circular, dense, velvety, cream white, pale brown in the middle; in reverse, brown to green, white at the margin.

Materials examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 6 February 2023, N. Wu, ML33 (HUEST XX), living culture UESTCC XX; *ibid*., Anshun City, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL74 (HUEST XX), living culture UESTCC XX; *ibid*., Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H32 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer truncatum* and *Olea europaea* (Li et al., 2023b), *Ardisia crenata* and *Camellia sinensis* (Du et al., 2024a), *Rosa roxburghii* and *R. sterilis* (present study), *Trachycarpus* sp. (Hu et al., 2023).

Known geographical distribution – China.

Notes – This species was first described by Li et al. (2023b) based on specimens collected from *Acer truncatum* and *Olea europaea* in China. Subsequently, Du et al. (2024a) recollected this species from *Ardisia crenata* and *Camellia sinensis*, and synonymized *Nigrograna trachycarpi* with *N. oleae* based on morphology and phylogeny. In this study, three isolates obtained from *Rosa roxburghii* and *R. sterilis* clustered with other strains of *N. oleae* in the multi-gene phylogenetic tree (Figure 3.79). Morphologically, the new collection share similar characteristics with the type species of *N. oleae*. Therefore, I identify my collection as *N. oleae*, which is reported for the first time from *R. roxburghii* and *R. sterilis*.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–t Ascospores. u Germinating ascospore. v, w Colony on PDA, above (v), below (w). Scale bars: d, e = 100 μm; f, h–l = 30 μm; g, m–u = 10 μm.

Figure 3.80 *Nigrograna oleae* (HUEST ML33, new host record)

Nigrograna rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.81

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS MF08

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 202–250 μm wide, 195–315 μm high, solitary to gregarious, sometimes confluent, deeply immersed or immersed to semi-immersed, black, unilocular, glabrous, coriaceous, globose to subglobose to pyriform, papillate, ostiolate. *Ostiole* 49–55 μm wide, 78–90 μm high, single, cylindrical to subcylindrical, straight or curved, central or laterally located, periphysate. *Peridium* 12–25 μm wide, composed of thick-walled, hyaline to dark brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 μm wide, composed of dense, numerous, filiform, unbranched, septate, hyaline, tapering at the apex, pseudoparaphyses, longer than asci. *Asci* 54–70 × 7–9 μm ($\bar{x}$ = 62 × 8 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or slightly curved, short pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 11–14 × 3–4 μm ($\bar{x}$ = 13 × 3.5 μm; n = 30), uniseriate or overlapping biseriate, fusiform, smooth-walled, straight or slightly curved, 1-septate, slightly constricted at the septum, upper cell swollen towards the central septum, and longer than the lower cell, slightly acute at both ends, initially hyaline and guttulate, becoming pale brown when mature, surrounded by a thin gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 10–12 mm diam. after two weeks at 25℃ in dark, circular, dense, dry, white; in reverse, dark brown in the middle and white at the margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024,

N. Wu, MF08 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid*., SL88 (HUEST XX, paratype), living culture UESTCC XX.

Notes – *Biatriospora carollii* was initially reported as an endophytic fungus from the living sapwood of wild *Hevea brasiliensis* in Peru (Kolařík et al., 2017). However, Kolařík (2018) transferred *B*. *carollii* to *Nigrograna* as *N*. *carollii* based on the phylogenetic analysis inferred from ITS sequences. Subsequently, Lu et al. (2022a) introduced *N*. *puerensis* as a sister taxon to *N*. *carollii* based on nucleotide differences of ITS, LSU, SSU and *tef1α* sequences and colony morphology, as sufficient morphological data was not available to compare. In my phylogenetic analysis, *N*. *rosae* (CGMCC MF08 and UESTCC SL88) formed a sister branch to *N*. *carollii* (CCF 4484, ex-type strain) and *N*. *puerensis* (ZHKUCC 22-0212, ex-type strain) with a good support (Figure 3.79). *Nigrograna rosae* and *N*. *puerensis* both have immersed ascomata, clavate and short pedicellate asci, and hyaline to pale brown, 1-septate ascospores. However, the latter has wider asci (54–70 × 7–9 μm vs. 50–80 × 8–11 μm) and larger ascospores (11–14 × 3–4 μm vs. 15–18 × 4–5 μm) (Lu et al., 2022a) and lacks the gelatinous sheath. Therefore, *N*. *rosae* is introduced as a new species based on morpho-molecular analysis.



Note a Appearance of ascomata on host surface. b–d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–l Asci. m–p Ascospores. q Ascospore stained with Indian ink. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: c, d = 50 μm; e, g, h–l = 20 μm; f, m–r = 10 μm.

Figure 3.81 *Nigrograna rosae* (HKAS MF08, holotype)

Nigrograna thymi Mapook, Camporesi & K.D. Hyde, Fungal Diversity 87: 68 (2017) Figure 3.82

Index Fungorum number: IF827557; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 125–260 μm wide, 145–365 μm high, solitary or confluent, black, at first immersed, eventually erumpent and appearing superficial, unilocular, glabrous, coriaceous to carbonaceous, subglobose to pyriform, not upright, laid on the substrate, papillate, ostiolate. *Ostiole* 145–160 μm wide, 80–95 μm high, single, cylindrical to subcylindrical, curved, central or laterally located. *Peridium* 15–30 μm wide, composed of thick-walled hyaline to dark brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 μm wide, composed of dense, numerous, filiform, branched, aseptate, hyaline, pseudoparaphyses. *Asci* 49–65 × 8–10 μm ($\bar{x}$ = 56 × 9.5 μm; n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with a poorly developed ocular chamber. *Ascospores* 13–16 × 4.5–6 μm ($\bar{x}$ = 15 × 5.5 μm; n = 30), uniseriate or overlapping biseriate, straight or slightly curved, fusiform, conical ends, guttulate, initially hyaline and septate, becoming pale brown and 3-septate when mature, slightly constricted at the septa. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 10–15 mm diam. after two weeks at 25°C in dark, circular, dry, raised, white; in reverse, grayish green to white.

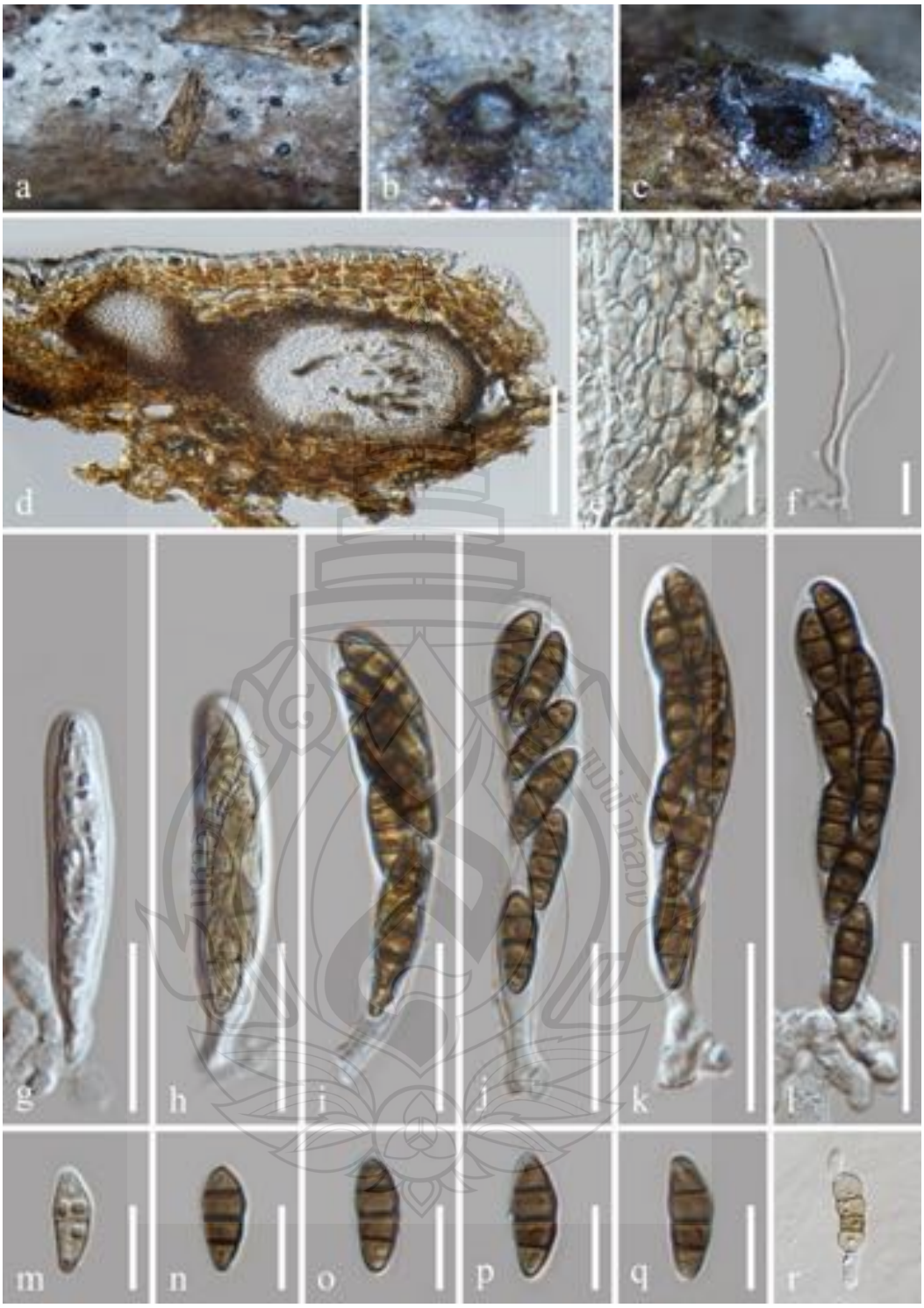
Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Huopu Town, on branches of *Rosa roxburghii*, 28 September 2021, N. Wu, CL71 (HUEST XX), living culture UESTCC XX; *ibid*., Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *R. roxburghii*, 9 July 2022, N. Wu, GL131 (HUEST XX), living culture UESTCC XX; *ibid*., Bijie City, Dafang County, Wenge Township, Anqing Village, elevation 1,496 m, 27°8′60″ N, 105°25′48″ E, on branches of *R. roxburghii*, 2 July 2023, N. Wu, ML159 (HUEST XX),

living culture UESTCC XX; *ibid*., Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *Rosa roxburghii*, 6 February 2023, N. Wu, W6 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia sinensis* and *Huangtcia renifolia* (Du et al., 2024a), *Rosa roxburghii* (present study), *Thymus oenipontanus* (Hyde et al., 2017).

Known geographical distribution – China, Italy.

Notes – *Nigrograna thymi* was collected from a dead aerial stem of *Thymus oenipontanus* by Hyde et al. (2017). This species can be distinguished from other species in the genus by its 4–5-septate ascospores. Du et al. (2024a) provided new host records of *N. thymi* from medicinal plants *Camellia sinensis* and *Huangtcia renifolia* in China, but they only observed 3-septate ascospores. My collection is similar to *N. thymi* as described by Du et al. (2024a), possessing 3-septate ascospores, but differ from the type species, which composed 4–5-septate ascospores. This difference may be attributed to variations in host and geographical location, as the multigene phylogenetic analysis does not support their classification as two distinct species. I followed the guidelines in Jeewon and Hyde (2016) and identified my collection of *N. thymi* as a new host record associated with *Rosa roxburghii*.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f Pseudoparaphyses. g–l Asci. m–q Ascospores. r Germinating ascospore. Scale bars: d = 100 µm; e, f, m–r = 10 µm; g–l = 20 µm.

Figure 3.82 *Nigrograna thymi* (HUEST CL71, new host record)

Nigrograna triseptata N. Wu & Jian K. Liu, sp. nov. Figure 3.83

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*triseptata*" refers to its 3-septate ascospores.

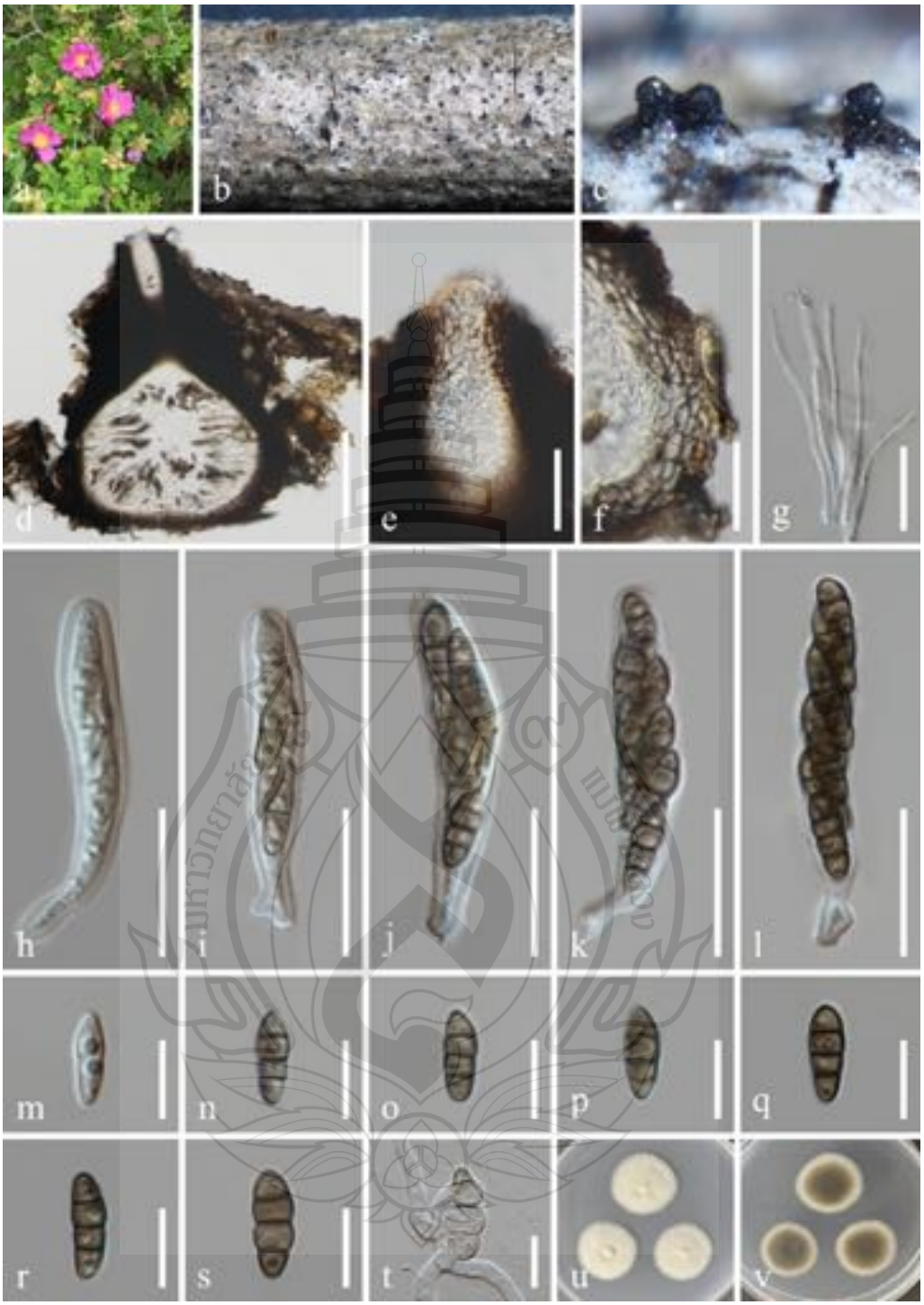
Holotype – HKAS ML137

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 265–385 μm wide, 260–416 μm high, solitary to gregarious or confluent, immersed to semi-immersed, black, glabrous, unilocular, long necks, bursting through the bark of host, coriaceous to carbonaceous, pyriform or irregular in shape, papillate, ostiolate. *Ostiole* 85–95 μm wide, 205–287 μm high, single, long, cylindrical to subcylindrical, straight or curved, centric or eccentric. *Peridium* 21–39 μm wide, brittle when dry, composed of thick-walled dark brown cells of *textura angularis*. *Hamathecium* 1.5–3.3 μm wide, composed of dense, numerous, filiform, unbranched, aseptate, hyaline, pseudoparaphyses, longer than asci. *Asci* 44–80 × 8–12 μm ($\bar{x}$ = 55 × 8.5 μm; n = 20), 8-spored, bitunicate, cylindrical to clavate, straight or slightly curved, short pedicel, apically rounded with a poorly developed ocular chamber. *Ascospores* 13–16 × 4–6 μm ($\bar{x}$ = 15 × 4.5 μm; n = 30), overlapping to crowded, straight or slightly curved, fusoid with subobtuse apices, guttulate, second cell from apex slightly swollen towards the middle, sometimes the upper cell slightly wider than the lower cell, initially hyaline and aseptate, becoming pale brown to dark brown and 3-septate when mature, slightly constricted at the septa, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from every cell. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25℃ in dark, circular, dense, felty and cottony, dry, white; in reverse, yellowish brown in the middle and white at the margin.

Material examined – CHINA, Guizhou Province, Qiannan Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on branches of *Rosa roxburghii*, 5 February 2023, N. Wu, ML137 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – *Biatriospora peruviensis* was initially reported as an endophytic fungus in living sapwood of wild *Virola* sp. in Peru (Kolařík et al., 2017). Subsequently, *B. peruviensis* was transferred to *Nigrograna* as *N. peruviensis* by Kolařík (2018). The phylogenetic analysis of this study revealed that the isolate of *N. triseptata* (CGMCC ML137) formed a sister branch to *N. peruviensis* (CCF 4885), and they clustered closer to *N. guttulata* (CGMCC 3.25689 and UESTCC 23.0295) (Figure 3.79). *Nigrograna triseptata* is morphologically similar to *N. guttulata* in having bitunicate, clavate asci and fusoid to ellipsoid, 3-septate, brown ascospores (Du et al., 2024a). However, *N. triseptata* is distinguished from *N. guttulata* by its larger ascomata (265–385 × 260–416 μm vs. 182–283 × 106–276 μm) with a long ostiolar neck (205–287 × 85–95 μm vs. 35–61 × 15–30 μm) and multi-layered peridium, and longer asci (44–80 × 8–12 μm vs. 35–70 × 7–12 μm) with larger ascospores (13–16 × 4–6 μm vs.10–13 × 3–5 μm) (Du et al., 2024a). Due to the lack of morphological data on *N. peruviensis* in previous studies, comparison of above two species was not possible. Therefore, I follow the guidelines of Jeewon and Hyde (2016) and introduce *N. triseptata* as a new species.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–l Asci. m–s Ascospores. t Germinating ascospore. u, v Colony on PDA, above (u), below (v). Scale bars: d = 100 μm; e–f = 30 μm; g–l = 20 μm; m–t = 10 μm.

Figure 3.83 *Nigrograna triseptata* (HKAS ML137, holotype)

Occultibambusaceae D.Q. Dai & K.D. Hyde

Type genus – *Occultibambusa* D.Q. Dai & K.D. Hyde

Notes – Dai et al. (2017) introduced this family to accommodate *Neooccultibambusa*, *Occultibambusa* (type genus), *Seriascoma* and *Versicolorisporium*. Subsequently, *Brunneofusispora* was accepted in this family (Phookamsak et al., 2019).

Brunneofusispora S.K. Huang & K.D. Hyde, Fungal Diversity 95: 36 (2019)

Type species – *Brunneofusispora sinensis* S.K. Huang & K.D. Hyde

Notes – Phookamsak et al. (2019) introduced *Brunneofusispora* to accommodate the type species *B. sinensis*, which was collected from a woody plant in China. *Brunneofusispora* is a holomorphic genus characterized by subglobose to pyriform, unilocular, glabrous ascomata with a long neck, 8-spored, bitunicate, fissitunicate, short pedicellate, cylindrical-clavate asci, and broadly fusiform, uniseptate, guttulate, hyaline ascospores, surrounded by a mucilaginous sheath; asexual morphs coelomycetous possessing hyaline, guttulate, oblong to cylindrical conidia (Wanasinghe et al., 2020; Calabon et al., 2021; Liu et al., 2024b). *Brunneofusispora* contains six species, *B. baoshanensis* (Liu et al., 2024b), *B. clematidis* (Phukhamsakda et al., 2020), *B. hyaline* (Calabon et al., 2021), *B. inclinatiostiola* (Yu et al., 2021), *B. sennae-torae* (Tan et al., 2021) and *B. sinensis* (Phookamsak et al., 2019), and all are supported with molecular data.

Brunneofusispora rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.84

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML123

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 220–280 μm wide, 175–245 μm high, mostly solitary, occasionally gregarious, black, immersed to superficial or erumpent through bark, visible as small black dots on host surface, subglobose to pyriform, unilocular, glabrous, coriaceous, thick-walled,

papillate, ostiolate. *Ostiole* 43–60 μm wide, 80–120 μm high, single, long, subcylindrical, straight or slightly curved, central or laterally located, periphysate. *Peridium* 25–40 μm wide, carbonaceous and brittle when dry, composed of 5–9 layers of brown to dark brown cells of *textura angularis*, gradually paler and thinner inwardly, thicker near the ostiole. *Hamathecium* 2–3 μm wide, composed of dense, filamentous, branched, septate, hyaline, slightly swollen at the base, longer than asci, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 65–87 × 11–13 μm ($\bar{x}$ = 71 × 12 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 16.5–21.5 × 5–6.5 μm ($\bar{x}$ = 19 × 5.5 μm; n = 30), uniseriate or overlapping biseriate, hyaline, widely fusiform with obtuse ends, uniseptate, slightly constricted at the septum, apical cell usually slightly broader and longer than the basal cell, smooth-walled, straight or slightly curved, verruculose, guttulate, surrounded by a fusiform, 2–5 μm wide mucilaginous sheath; and the sheath becoming constricted at the septum. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, flat to slightly raised, velvety, dry, grayish white in the middle, olivaceous-gray at edge; in reverse, dull green to black in the middle, grayish green in the outer ring with smooth margin.

Material examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML123 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – *Brunneofusispora rosae* (CGMCC ML123) formed a sister clade to *B*. *sinensis* (KUMCC 17-0030) with a good statistical support in the phylogenetic tree (Figure 3.85). Comparisons of the ITS, LSU, *tef1α* and *rpb2* sequences of *B*. *rosae* and *B*. *sinensis* revealed 95.14% (489/514 bp), 98.85% (772/781 bp), 95.67% (905/946 bp), 91.34% (949/1039 bp) similarities, respectively. *Brunneofusispora rosae* is distinctive

in its widely fusiform, hyaline ascospores surrounded by a mucilaginous sheath, and the sheath becoming constricted at the septum. In contrast, the ascospores of *B*. *sinensis* are light brown to brown at maturity (Phookamsak et al., 2019). I therefore introduce *B*. *rosae* as a new species based on the morphology and molecular evidence.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–n Ascospores. o Ascospore stained with Indian ink. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: d, e = 100 μm; f, h–k = 20 μm; g, l–p = 10 μm.

Figure 3.84 *Brunneofusispora rosae* (HKAS ML123, holotype)

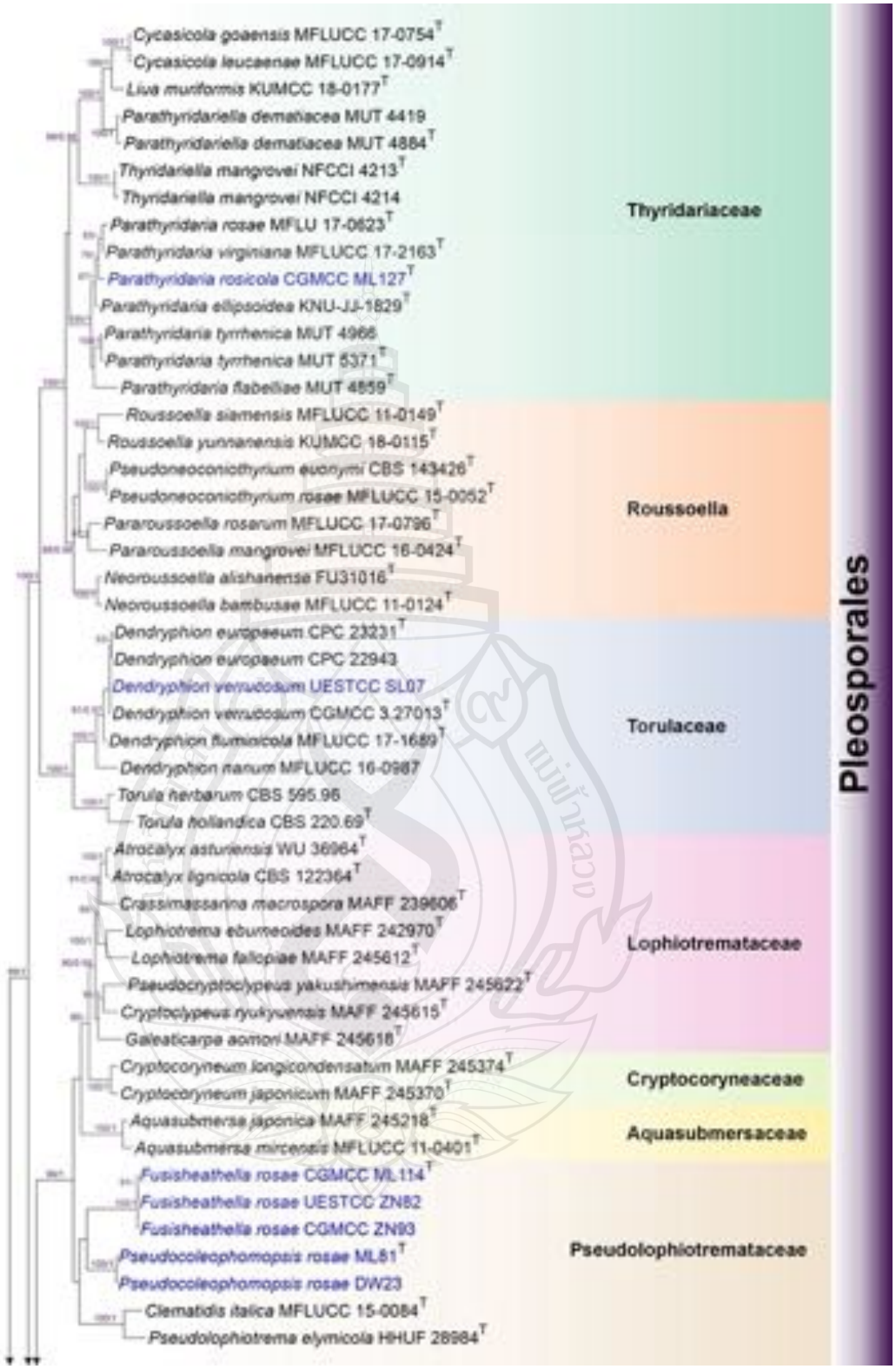


Figure 3.85 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Pleosporales

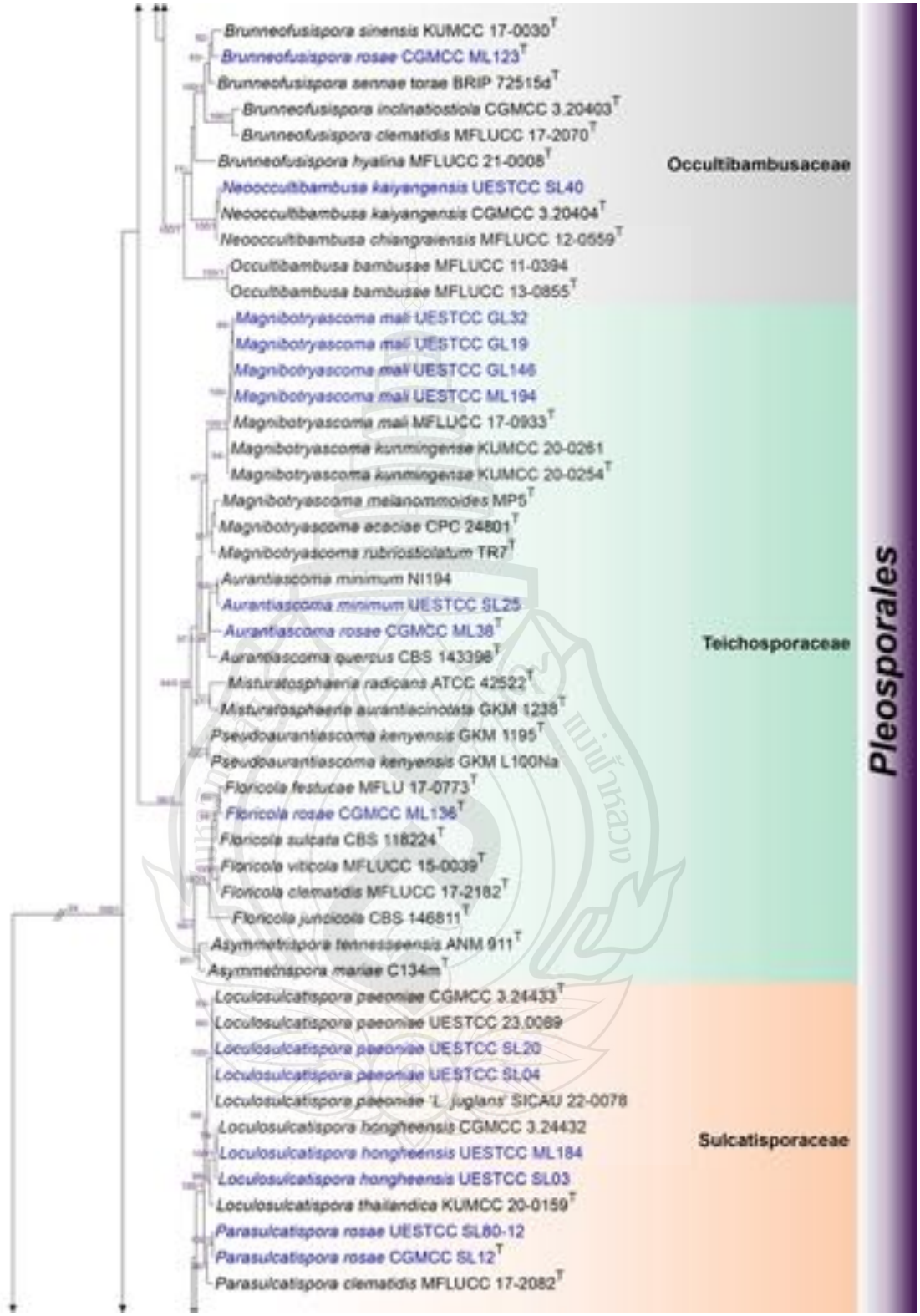


Figure 3.85 (continued)

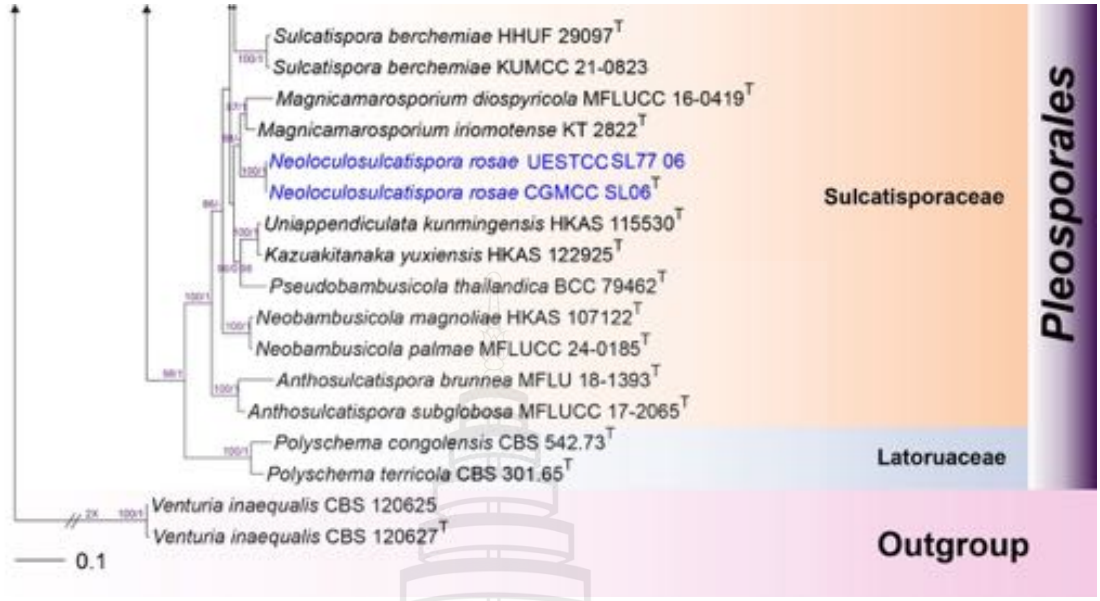


Figure 3.85 (continued)

Figure 3.85 The tree is rooted with *Venturia inaequalis* (CBS 120625 and CBS 120627). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Neooccultibambusa Doilom & K.D. Hyde, Fungal Diversity 82: 126 (2017)

Type species – *Neooccultibambusa chiangraiensis* Doilom & K.D. Hyde

Notes – Doilom et al. (2017) established *Neooccultibambusa* to accommodate two species, *N. chiangraiensis* (MFLUCC 12-0559), and *Neooccultibambusa* sp. (MFLUCC 12-0564). *Neooccultibambusa* is similar to *Occultibambusa* in having brown, septate, fusiform ascospores surrounded by a gelatinous sheath. However, *Neooccultibambusa* has subcylindrical asci and ascospores with 1–3 transverse septa, whereas *Occultibambusa* produces broadly cylindrical to clavate asci and ascospores with only one transverse septum (Doilom et al., 2017; Yu et al., 2022). Currently, *Neooccultibambusa* contains seven species, *N. chiangraiensis* (Doilom et al., 2017),

N. coffeae (Lu et al., 2025), *N. jonesii* (Jayasiri et al., 2016), *N. kaiyangensis* and *N. trachycarpi* (Yu et al., 2022), *N. pandanicola* and *N. thailandensis* (Tibpromma et al., 2018), all of which are supported by molecular data. In the present study, I recovered *N. kaiyangensis* from *Rosa roxburghii*.

Neooccultibambusa kaiyangensis X.D. Yu, S.N. Zhang & Jian K. Liu, Diversity 13(11, no. 516): 516 (2021) Figure 3.86

Index Fungorum number: IF841010; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 210–300 μm wide, 200–380 μm high, solitary, immersed to partly erumpent, visible as small black dots on host surface, subglobose to pyriform, not upright, laid on the substrate, unilocular, glabrous, coriaceous, thick-walled, ostiolate. *Ostiole* 60–75 μm wide, 150–180 μm high, single, long, straight or slightly curved, central or laterally located, periphysate. *Peridium* 18–25 μm wide, composed of 5–8 layers of brown to dark brown cells of *textura angularis*, gradually paler and thinner inwardly, thicker near the ostiole. *Hamathecium* 2–3.5 μm wide, numerous, filamentous, septate, branched, cellular pseudoparaphyses, anastomosing above asci, embedded in a gelatinous matrix. *Asci* 100–140 × 18–22.5 μm ($\bar{x}$ = 111 × 20 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 31–41 × 5.5–8.5 μm ($\bar{x}$ = 36 × 7.5 μm; n = 30), crowded or irregularly arranged in asci, hyaline, fusiform with slightly acute ends, 1-septate, not constricted at the septa, apical cell usually slightly broader and longer than the basal cell, smooth-walled, straight or slightly curved, verruculose, guttulate, surrounded by a 3–5 μm wide mucilaginous sheath. Asexual morph: Undetermined.

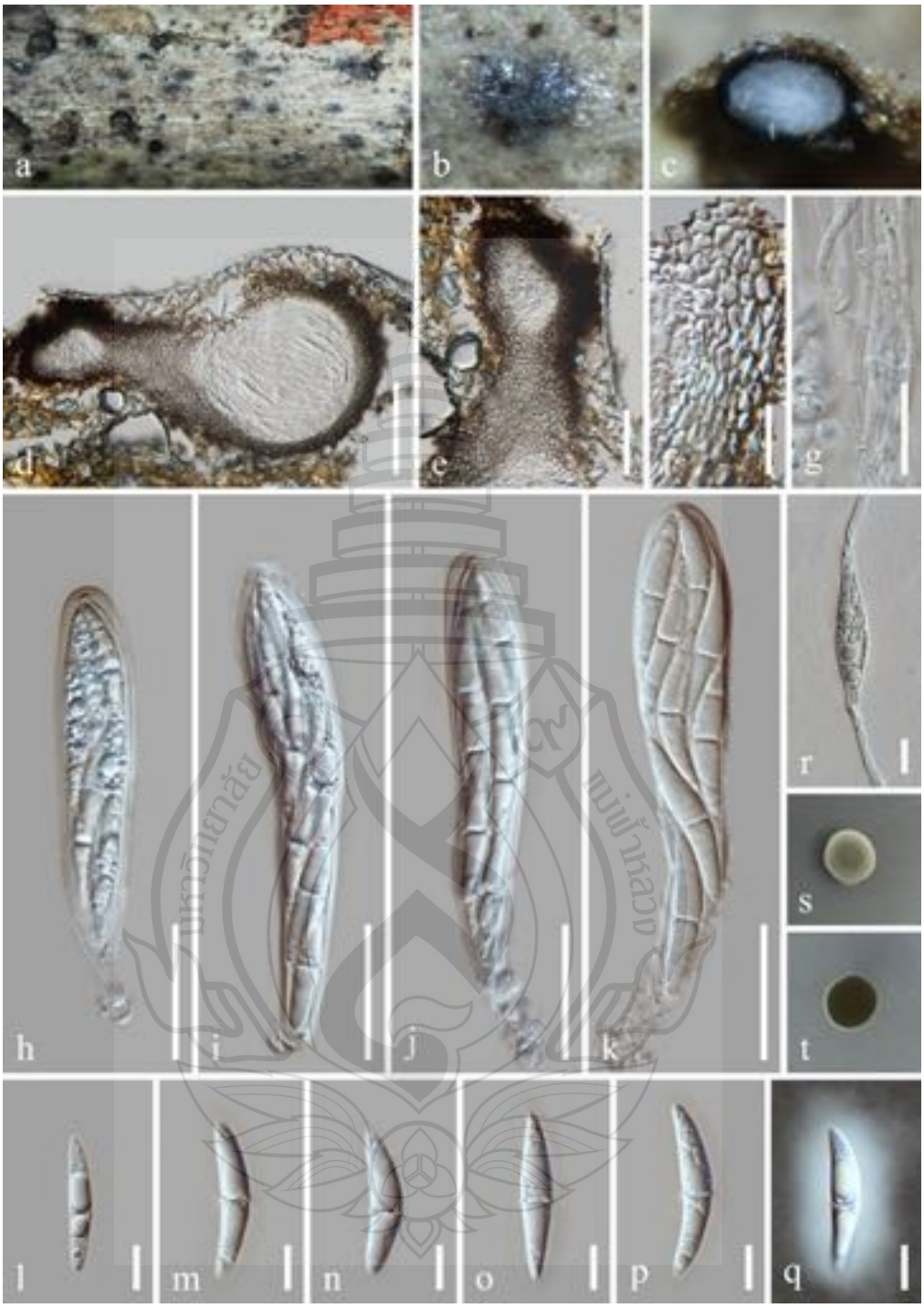
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, dry, velvety, slightly raised, dark grayish green mycelium on the surface; in reverse, dark green to black with an entire margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL40 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), *Trachycarpus fortunei* (Yu et al., 2022).

Known geographical distribution – China.

Notes – *Neoocculitibambusa kaiyangensis* was introduced by Yu et al. (2021) from decaying petioles of *Trachycarpus fortunei* in China. My collection matches the type material of *N. kaiyangensis* in the morphology of ascomata, asci and ascospores. However, my collection has slightly longer asci (100–140 × 18–22.5 μm vs. 70–108 × 7.5–11.0 μm) and larger ascospores (31–41 × 5.5–8.5 μm vs. 16.0–23.5 × 3.0–5.5 μm) than the holotype (Yu et al., 2021). In the phylogenetic analysis, my collection (UESTCC SL40) clustered with *N. kaiyangensis* (CGMCC 3.20404) as a sister taxon with a good statistical support (Figure 3.85). I therefore recognize my collection as *N. kaiyangensis* based on the molecular evidence and extend the known host of this fungus to *Rosa roxburghii*.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–p Ascospores. q Ascospore stained with Indian ink. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d = 100 µm; e = 50 µm; f, g = 20 µm; h–k = 30 µm; l–r = 10 µm.

Figure 3.86 *Neooccultibambusa kaiyangensis* (HUEST SL40, new host record)

Pseudolophiotremataceae K.D. Hyde & Hongsanan

Type genus – *Pseudolophiotrema* A. Hashim. & Kaz. Tanaka

Notes – *Clematidis* and *Pseudolophiotrema* were introduced and treated as Pleosporales genus *incertae sedis* by Li et al. (2016b) and Hashimoto et al. (2017), respectively. Hongsanan et al. (2018) established the family Pseudolophiotremataceae to accommodate *Pseudolophiotrema*. Subsequently, Phukhamsakda et al. (2020) placed *Clematidis* within Pseudolophiotremataceae based on the phylogenetic analysis of combined LSU, SSU, ITS, *tef1α* and *rpb2* sequence data. Members of this family are only known from their sexual morphs. In the present study, two new genera are recognized based on morphology and multi-gene phylogeny. Therefore, the family currently comprises four genera: *Clematidis*, *Fusivaginella*, *Pseudocoleophomopsis*, and *Pseudolophiotrema* among which *Pseudocoleophomopsis* is represented by a coelomycetous asexual morph.

Fusivaginella N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*Fusivaginella*" refers to the fusiform ascospores surrounded by a mucilaginous sheath.

Type species – *Fusivaginella rosae* N. Wu & Jian K. Liu

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* immersed to semi-immersed, initially intraepidermal, visible as black dots on the host when mature, scattered, subglobose to pyriform, unilocular, solitary, thick-walled, glabrous, ostiolate. *Ostiole* single, cylindrical to subcylindrical. *Peridium* composed of brown cells of *textura angularis*, thicker near the ostiole, thinner at the base. *Hamathecium* composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 8-spored, bitunicate, obclavate, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* uniseriate or overlapping biseriate, fusiform, hyaline, 1–3-septate, constricted at each septum, cells

above central septum often broader than the lower ones, guttulate, smooth-walled, surrounded by a thick mucilaginous sheath. Asexual morph: Undetermined.

Notes – *Fusivaginella* is introduced as a monotypic genus to accommodate the sexual morph of, *F. rosae*, which was collected from decaying branches of *Rosa roxburghii. Fusivaginella* is distinguished from members of Pseudolophiotremataceae by its solitary, scattered, subglobose to pyriform, unilocular, immersed to semi-immersed ascomata, bitunicate, obclavate asci, and hyaline, fusiform, guttulate, septate ascospores with a thick mucilaginous sheath (Li et al., 2016b; Hashimoto et al., 2017; Hongsanan et al., 2018; Phukhamsakda et al., 2020). Phylogenetic analysis indicated that *Fusivaginella* does not belong to any other existing genera.

Fusivaginella rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.87

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML114

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 272–381 µm wide, 237–361 µm high, immersed to semi-immersed, initially intraepidermal, visible as black dots on the host when mature, scattered, dark brown to black, subglobose to pyriform, unilocular, solitary, thick-walled, glabrous, ostiolate. *Ostiole* single, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 20–30 µm wide, composed of brown celled *textura angularis*, thicker near the ostiole, thinner at the base. *Hamathecium* 1.5–3 µm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 µm ($\bar{x}$ = 87 × 15 µm; n = 20), 8-spored, bitunicate, obclavate, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 µm ($\bar{x}$ = 20 × 6 µm; n = 30), uniseriate or overlapping biseriate, fusiform with obtuse ends, hyaline, 1–3-septate, constricted at each septum, cells above central

septum often broader than the lower ones, with large guttules in each cell, smooth-walled, surrounded by a thick mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from the apex. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular or irregular, off-white, flat, dry; in reverse, off-white at the center, with grayish brown ring in the middle, off-white ring at the edge.

Materials examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML114 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid*., Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *R. roxburghii*, 6 February 2023, N. Wu, ZN82 (HUEST XX, paratype), living culture UESTCC XX; *ibid*., ZN93 (HUEST XX), living culture UESTCC XX.

Notes – Multi-gene phylogenetic analysis showed that *Fusivaginella rosae* (CGMCC ML114, UESTCC ZN82 and UESTCC ZN93) formed a sister clade to *Pseudocoleophomopsis rosae* (CGMCC ML81 and UESTCC DW23) in the family Pseudolophiotremataceae (Figure 3.85). Since *P. rosae* is only known from its asexual morph, its morphology cannot be compared with *F. rosae*, since it possess the sexual morph. The ascospores of *F. rosae* are similar to *Clematidis italica* and *Pseudolophiotrema elymicola*, both of which belong to the family Pseudolophiotremataceae. Among species of Pseudolophiotremataceae, *F. rosae*, *C. italica* and *P. elymicola* share the characters in having semi-immersed, subglobose ascomata, bitunicate, cylindrical to cylindric-clavate asci, and hyaline, septate, fusiform ascospores (Li et al., 2016b; Hashimoto et al., 2017). However, the ascospores of *F. rosae* are uniseriate or overlapping biseriate, fusiform with obtuse ends, 1–3-septate, constricted at each septum, cells above central septum often broader than the lower ones, surrounded by a thick mucilaginous sheath. In *C. italica*, the ascospores are overlapping

2–3-seriate, without sheaths and are mostly 1-septate at the center (Hashimoto et al., 2017). In *P*. *elymicola*, the ascospores are fusiform with acute ends, 1-septate, strongly constricted at the septum and midpoint of each cell and are surrounded by a gelatinous sheath (Hashimoto et al., 2017). I therefore identify *F*. *rosae* as a new species and introduce the genus *Fusivaginella* to accommodate it.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d, e = 50 μm; f–k = 30 μm; l–q = 15 μm.

Figure 3.87 *Fusivaginella rosae* (HKAS ML114, holotype)

Pseudocoleophomopsis N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*Pseudocoleophomopsis*" refers to the morphology resembling the genus "*Pseudocoleophoma*", with the Latin suffix "-*opsis*" meaning like, similar.

Type species – *Pseudocoleophomopsis rosae* N. Wu & Jian K. Liu

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* solitary, scattered, immersed to semi-immersed, pycnidial, globose to subglobose, unilocular, coriaceous, glabrous, ostiolate. *Ostiole* single. *Conidiomatal wall* composed of thick-walled, hyaline to dark brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, enteroblastic, phialidic, cylindrical to subcylindrical. *Conidia* hyaline, aseptate, oblong to ellipsoidal, straight, smooth-walled, with guttules.

Notes – I introduce a new genus *Pseudocoleophomopsis* to accommodate the type species *P. rosae* based on morphology and multi-gene phylogeny. *Pseudocoleophomopsis* is characterized by solitary, scattered, pycnidial, globose to subglobose, unilocular, immersed to semi-immersed conidiomata, hyaline, enteroblastic, phialidic, cylindrical to subcylindrical conidiogenous cells and hyaline, straight, guttulate, aseptate, oblong to ellipsoidal conidia with rounded to obtuse ends. In the combined gene sequences of ITS-LSU-SSU-*tef1α-rpb2* phylogenetic tree, *Pseudocoleophomopsis* was placed within Pseudolophiotremataceae, and it formed a distinct clade closely related to the genus *Fusivaginella* (Figure 3.85). The morphological comparison between *Pseudocoleophomopsis* and *Fusivaginella* is not possible, as the asexual morph of the latter is unknown.

Pseudocoleophomopsis rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.88

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML81

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 125–160 μm wide, 105–155 μm high, solitary, scattered, immersed to semi-immersed, visible as black dots on host substrate, pycnidial, globose to subglobose or irregular in shape, unilocular, coriaceous, glabrous, inconspicuous ostiolate. *Ostiole* single, central. *Conidiomatal wall* 10–30 μm wide, two layered, outer layer composed of 2–3 layers of dark brown to black, thick-walled *textura angularis* cells, inner layer composed of hyaline to lightly pigmented cells of *textura prismatica. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–11 × 1.5–3 μm ($\bar{x}$ = 9 × 2 μm; n = 30), hyaline, enteroblastic, phialidic, cylindrical to subcylindrical, determinate, smooth-walled, and arising from the inner layers of conidiomata. *Conidia* 8.5–12 × 2.5–3.5 μm ($\bar{x}$ = 10 × 3 μm; n = 30), hyaline, solitary, aseptate, oblong to ellipsoidal, straight, with rounded to obtuse ends, smooth-walled, with guttules.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular to irregular, cottony, producing mucus, glistening, raised or convex, grayish white in the middle, dark olivaceous at edge; in reverse, olive-green to dark brown with white mycelium of the outer ring.

Materials examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML81 (HKAS XX, **holotype**); ex-type living culture CGMCC XX; *ibid*., Guiyang City, Xifeng County, elevation

1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *R. roxburghii*, 6 February 2023, N. Wu, DW23 (HUEST XX, **paratype**), living culture UESTCC XX.

Notes – *Pseudocoleophomopsis rosae* is an asexual morph species collected from *Rosa roxburghii* in China. In my phylogenetic analysis, *P. rosae* (CGMCC ML81 and UESTCC DW23) clustered with *Fusivaginella rosae* (CGMCC ML114, UESTCC ZN82 and UESTCC ZN93), forming an independent clade within Pseudolophiotremataceae (Figure 3.85). Sequence comparisons between the ex-type strains of *P. rosae* (CGMCC ML81) and *F. rosae* (CGMCC ML114) revealed similarities of 90.20% (414/459 bp) in the ITS region, 93.98% (827/880 bp) in the LSU region, 97.13% (542/558 bp) in the SSU region, and 92.39% (898/972 bp) in the *tef1α* region. *Pseudocoleophomopsis* is similar to *Pseudocoleophoma* in its asexual morphs (Jayasiri et al., 2019; Li et al., 2020; Wu et al., 2024). However, *Pseudocoleophoma* belongs to Dictyosporiaceae, whereas *Pseudocoleophomopsis* is classified in Pseudolophiotremataceae. As the sexual morph of *Pseudocoleophomopsis* has not been discovered, it is currently impossible to compare its sexual morphology with members of Pseudolophiotremataceae. I therefore identify *P. rosae* as a new species and introduce the genus *Pseudocoleophomopsis* to accommodate it.



Note a Host: *Rosa roxburghii*. b, c Conidiomata on natural substrate. d–f Vertical sections of conidiomata. g Conidiomatal wall. h–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: e, f = 100 μm; g, k, l = 20 μm; h–j, m = 10 μm.

Figure 3.88 *Pseudocoleophomopsis rosae* (HKAS ML81, holotype)

Sulcatisporaceae Kazu. Tanaka & K. Hiray.

Type genus – *Sulcatispora* Kaz. Tanaka & K. Hiray.

Notes – Tanaka et al. (2015) introduced the family Sulcatisporaceae to accommodate the genera *Magnicamarosporium*, *Neobambusicola* and *Sulcatispora* (type genus), based on morphological characteristics and multi-gene analysis. Subsequent studies introduced additional genera into the family, including *Anthosulcatispora*, *Kazuakitanaka*, *Loculosulcatispora*, *Parasulcatispora*, *Pseudobambusicola* and *Uniappendiculata* (Rupcic et al., 2018; Phukhamsakda et al., 2020; Ren et al., 2020; Wanasinghe et al., 2022). However, Zhang et al. (2024a) synonymized *Kazuakitanaka* with *Uniappendiculata* based on nomenclatural priority. Members of this family mainly inhabit dead wood, twigs, branches, and stems as saprobes. They are characterized by immersed ascomata, cellular or trabeculate pseudoparaphyses and uniseriate or overlapping uniseriate, cylindrical to cylindric-clavate asci, and fusiform or oblong to ellipsoidal, septate, hyaline or brown to dark brown ascospores, with or without sheath (Tanaka et al., 2015; Phukhamsakda et al., 2020; Wanasinghe et al., 2022; Zhang et al., 2024a). The asexual morphs are characterized by pycnidial conidiomata, cylindrical to doliiform, annellidic or phialidic conidiogenous cells and ellipsoid to subglobose, hyaline to dark brown, aseptate or 1- to multi-septate (occasionally muriform) conidia, with or without striate ornamentation (Tanaka et al., 2015; Ren et al., 2020).

Loculosulcatispora G.C. Ren & K.D. Hyde, Phytotaxa 475(2): 70 (2020)

Type species – *Loculosulcatispora thailandica* G.C. Ren & K.D. Hyde

Notes – Ren et al. (2020) conducted a phylogenetic study on selected representative families within *Massarineae* and comprehensively analyzed all families of Sulcatisporaceae. As a result, they introduced a new monotypic coelomycetous genus, *Loculosulcatispora* (type species *L. thailandica*), in Sulcatisporaceae. Subsequently, three additional species, *L. hongheensis*, *L. juglandis* and *L. paeoniae*, were introduced to this genus based on morph-phylogenetic evidence (Wanasinghe et al., 2022; Li et al.,

2023b; Wang et al., 2023b). Based on the high sequence similarity and morphological resemblance between *L. juglandis* and *L. paeoniae* (Wang et al., 2023b), I treat *L. juglandis* as a synonym for *L. paeoniae*.

Loculosulcatispora hongheensis Wanas., Journal of Fungi 8(4, no. 375): 14 (2022) Figure 3.89

Index Fungorum number: IF843434; Facesoffungi number: FoFXX

Saprobic or *parasitic* on branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 334–384 μm wide, 153–246 μm high, solitary to gregarious or confluent, brown to dark brown, initially immersed, eventually erumpent and appearing superficial, pycnidial, globose or oval to irregular, mostly multi-locular, convoluted, occasionally unilocular, *locules* 105–170 μm diam., 80–160 μm high, ovoid to subglobose, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Conidiomatal wall* 15–36 μm wide, composed of dark brown to brown cells of *textura angularis* in outer several layers, gradually merging with hyaline cells in inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.5–9× 1.5–3 μm ($\bar{x}$ = 6 × 2 μm; n = 30), hyaline, enteroblastic, phialidic, subcylindrical, indeterminate, smooth-walled, and arising from the inner layers of conidiomata. *Conidia* 7–12 × 3–5 μm ($\bar{x}$ = 10 × 3.5 μm; n = 30), hyaline, ellipsoid to short-cylindrical or obovoid, aseptate, with rounded to obtuse ends, smooth-walled, with guttules.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25℃ in dark, circular, floccose, umbonate, entire edge, pale brown in the middle with white margin; in reverse, olive-green to dark brown with white mycelium of the outer ring.

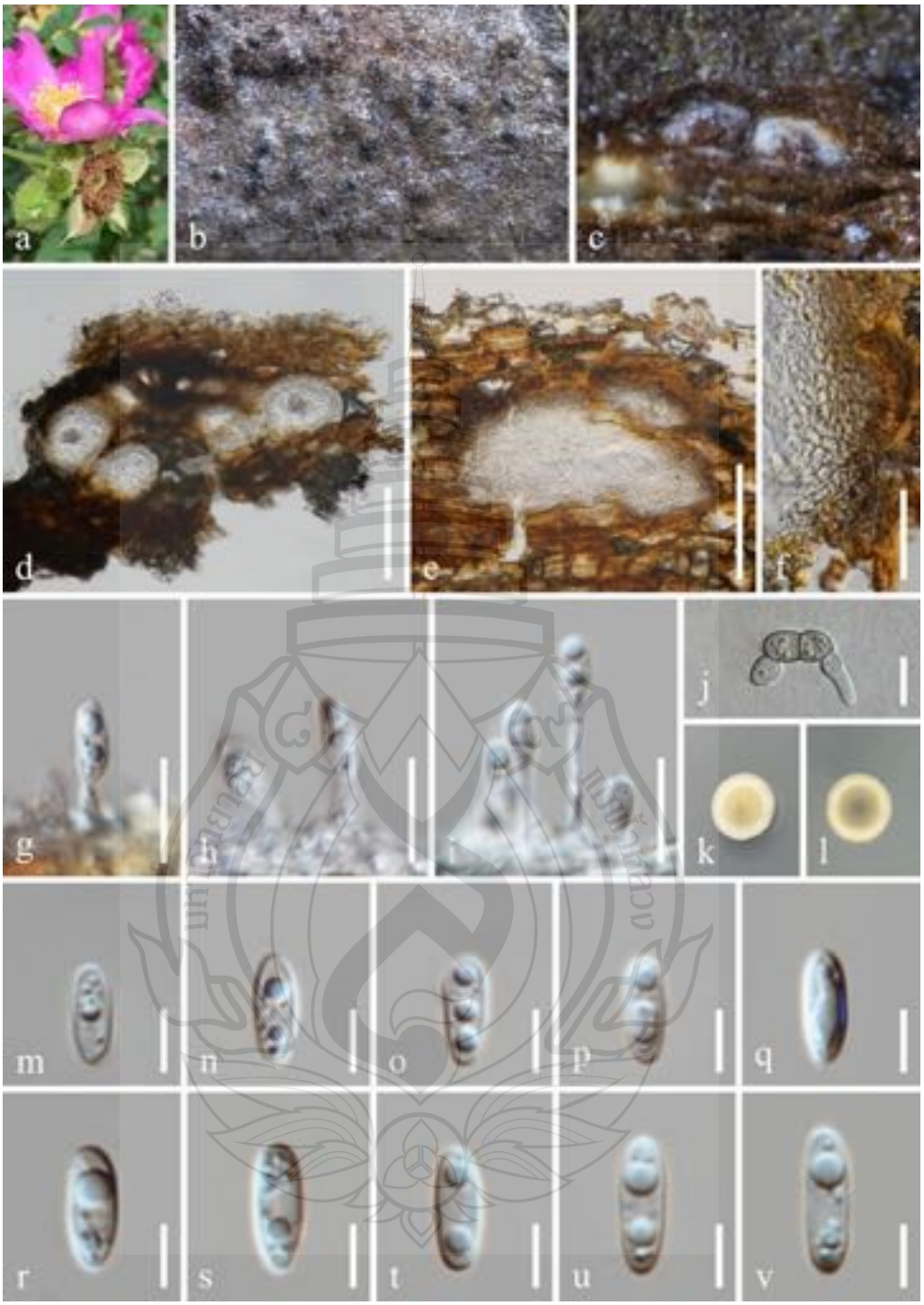
Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL03 (HUEST XX), living culture UESTCC XX; *ibid.*, Guizhou Province,

Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on branches of *R. roxburghii*, 4 February 2023, N. Wu, ML184 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), Unidentified dead wood litter (Wanasinghe et al., 2022), *Vernicia fordii* (Li et al., 2023b).

Known geographical distribution – China.

Notes – *Loculosulcatispora hongheensis* was introduced by Wanasinghe et al. (2022) based on its sexual morph, collected from unidentified dead wood litter in China. The asexual morph of *L. hongheensis* was described by Li et al. (2023b) from decaying branches of *Vernicia fordii* Hemsl in China. My collection matches well with the asexual morph of *L. hongheensis*, though the conidiomata are multi-locular and slightly larger (Li et al., 2023b). In the phylogenetic analysis, my collection (UESTCC SL03 and UESTCC ML184) clustered with *L. hongheensis* (CGMCC 3.24432) as sister taxa with a good statistical support (Figure 3.85). Sequence similarities of the ITS, LSU, *tef1α* and *tub2* gene regions between UESTCC SL03 and the type of strain (HKAS 122920) is 99.89% (873/874 bp, 1 gap), 99.57% (694/697 bp), 99.67% (903/906 bp, 1 gap) and 99.62% (777/780 bp, 1 gap), respectively. I therefore identify my collection as *L. hongheensis* based on the morphology and molecular evidence. My specimens were collected in China, same as the holotype (Wanasinghe et al., 2022). However, this is the first report of *L. hongheensis* from *Rosa roxburghii*.



Note a Host: *Rosa roxburghii*. b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j Germinating conidium. k, l Colony on PDA, above (k), below (l). m–v Conidia. Scale bars: d = 100 µm; e = 50 µm; f = 30 µm; g–j = 10 µm; m–v = 5 µm.

Figure 3.89 *Loculosulcatispora hongheensis* (HUEST SL03, new host record)

Loculosulcatispora paeoniae W.L. Li & Jian K. Liu, Mycosphere 14(1): 1514 (2023) Figure 3.90

Index Fungorum number: IF849160; Facesoffungi number: FoFXX

Synonym – *Loculosulcatispora juglandis* F.H. Wang & C.L. Yang [as '*juglans*'], Phytotaxa 620(4): 268 (2023)

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* dark brown to black, solitary to gregarious or confluent, deeply immersed or immersed to semi-immersed, unilocular or irregularly plurilocular, *locules* 156–194 μm diam., 159–210 μm high, ellipsoid to subglobose, glabrous, coriaceous, smooth-walled, inconspicuous ostiolate. *Peridium* 15–29 μm wide, composed of several layers of *textura angularis*, merged with the host tissues. *Hamathecium* 1.5–2.5 μm wide, composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses. *Asci* 64–76 × 11–13 μm ($\bar{x}$ = 68 × 12 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a short and furcate pedicel, apically rounded. *Ascospores* 16–22 × 4–7 μm ($\bar{x}$ = 19 × 6 μm; n = 30), overlapping biseriate or obliquely uniseriate, fusiform, with obtuse ends, slightly curved, the upper cell slightly wider than the lower cell, hyaline, 1–2-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a thick distinct mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 25–27 mm diam. after two weeks at 25℃ in dark, circular, umbonate, dense, gray in the middle with white margin; in reverse, olive-green in the middle with white mycelium of the outer ring.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL04 (HUEST XX), living culture UESTCC XX; *ibid.*, SL20 (HUEST XX), living culture UESTCC XX.

Hosts – *Juglans regia* (Wang et al., 2023b); *Paeonia suffruticosa* (Li et al., 2023b); *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – In the phylogenetic analysis, my collection (UESTCC SL04 and UESTCC SL20) clustered together with *Loculosulcatispora juglans* (SICAU 22-0078) and *L. paeoniae* (CGMCC 3.24433 and UESTCC 23-0089) (Figure 3.85). Comparisons of the ITS, LSU, SSU and *tef1α* gene regions between *L. juglans* (SICAU 22-0078, ex-type strain) and *L. paeoniae* (CGMCC 3.24433, ex-type strain) show that only the ITS gene region has two nucleotide differences. The ascospore size of *L. juglans* is comparable with *L. paeoniae* but differs in lacking a mucoid sheath (Li et al., 2023b; Wang et al., 2023b). Therefore, I synonymize *L. juglans* under *L. paeoniae* based on the molecular evidence and overlapping morphological characteristics. Additionally, my collection is identical to *L. paeoniae* based on morphology and phylogeny. In the present study, I provide a new host record for this species from *Rosa roxburghii* in China.



Note a Host: *Rosa roxburghii*. b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 100 μm; e, g–k, q = 20 μm; f, l–p = 10 μm.

Figure 3.90 *Loculosulcatispora paeoniae* (HUEST SL04, new host record)

Neoloculosulcatispora N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*Neoloculosulcatispora*" refers to its resemblance to the genus *Loculosulcatispora*.

Type species – *Neoloculosulcatispora rosae* N. Wu & Jian K. Liu

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* immersed, visible as black dots on the host when mature, dark brown to black, globose or subglobose, unilocular, glabrous, ostiolate. *Ostiole* single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* composed of dense, filamentous, branched, septate, hyaline, cellular pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* overlapping to bi-seriate, hyaline, fusiform, with obtuse ends, septate, slightly constricted at the septum, guttulate, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Notes – *Neoloculosulcatispora* is established to accommodate a sexual species, *N. rosae*, which was isolated from *Rosa roxburghii* in China. This genus is characterized by semi-immersed to superficial, subglobose ascomata, bitunicate, fissitunicate, cylindrical asci, and hyaline, 1-septate, fusiform ascospores, surrounded by a mucilaginous sheath. *Neoloculosulcatispora* is similar to *Loculosulcatispora*, but the ascospores of *Neoloculosulcatispora* are constricted at the central septum, while the upper and lower cells of the ascospores in *Loculosulcatispora* are swollen towards the central septum (Ren et al., 2020; Wanasinghe et al., 2020; Wang et al., 2023b). In the phylogenetic analysis inferred from a combined ITS, LSU, *tef1α* and *rpb2*, two strains of *N. rosae* were nested within Sulcatisporaceae and formed an independent clade close to *Magnicamarosporium* with a strong statistical support (Figure 3.85). However, I cannot compare the morphological characteristics of *N. rosae* with *Magnicamarosporium* species, as the latter is only known from its asexual morph. Based on morpho-

phylogenetic evidence, *Neoloculosulcatispora* is introduced as a new genus to accommodate the type species *N. rosae*.

Neoloculosulcatispora rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.91

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL06

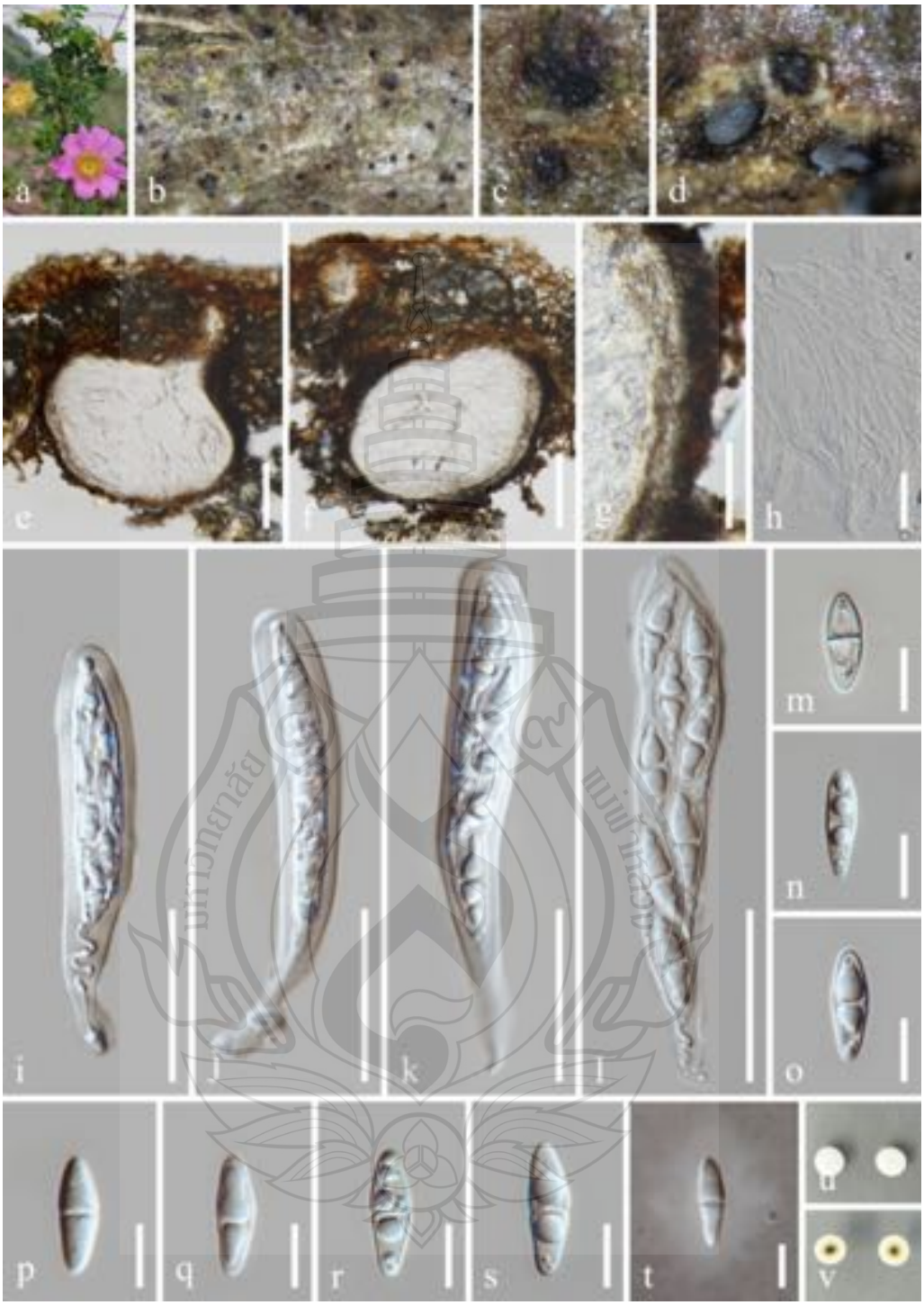
Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 272–381 μm wide, 237–361 μm high, immersed, initially intraepidermal, visible as black dots on the host when mature, scattered, dark brown to black, globose or subglobose, unilocular, solitary, thick-walled, glabrous, ostiolate. *Ostiole* 55–67 μm wide, 107–115 μm high, single, long, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 20–30 μm wide, composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide, composed of dense, filamentous, rarely branched, remotely separate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 78–100 × 12–17 μm ($\bar{x}$ = 87 × 15 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 17–24 × 5–7 μm ($\bar{x}$ = 20 × 6 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform, with obtuse ends, 1-septate, slightly constricted at the septum, guttulate, smooth-walled, surrounded by a thick distinct mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from the apex. Colonies on PDA medium reaching 15–17 mm diam. after two weeks at 25°C in dark, circular, velvety to woolly, entire and the margin filiform, white; in reverse, grayish green to pale yellowish with white mycelium of the outer ring.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January

2024, N. Wu, SL06 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, SL77 (HUEST XX, paratype), living culture UESTCC XX

Notes – The phylogenetic analysis revealed that two isolates of *Neoloculosulcatispora rosae* (CGMCC SL06 and UESTCC SL77) constitute a distinct lineage within Sulcatisporaceae, clustering closer to *Magnicamarosporium diospyricola* (MFLUCC 16-0419) and *M. iriomotense* (KT 2822) (Figure 3.85). Comparisons of the ITS, LSU, *rpb2* and *tef1α* sequence of *N. rosae* (CGMCC SL06) and *M. diospyricola* (MFLUCC 16-0419) showed 86.13% (323/375 bp, 10 gaps), 95.61% (850/889 bp, 2 gaps), 92.41% (694/751 bp) and 93.77% (858/915 bp) similarity, respectively. Comparisons of the ITS, LSU and *tef1α* sequence of *N. rosae* (CGMCC SL06) and *M. iriomotense* (KT 2822) showed 89.16% (469/526 bp, 12 gaps), 97.53% (830/851 bp, 1 gap) and 94.17% (872/926 bp) similarity, respectively. The *rpb2* sequence is unavailable for *M. iriomotense*. Based on the molecular evidence, I recognize my collections as a new species.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Peridium. h Pseudoparaphyses. i–l Asci. m–s Ascospores. t Ascospore stained with Indian ink. u, v Colony on PDA, above (u), below (v). Scale bars: e, f = 100 μm; g–l = 30 μm; m–t = 10 μm.

Figure 3.91 *Neoloculosulcatispora rosae* (HKAS SL06, holotype)

Parasulcatispora Phukhams. & K.D. Hyde, Fungal Diversity 102: 119 (2020)

Type species – *Parasulcatispora clematidis* Phukhams. & K.D. Hyde

Notes – *Parasulcatispora* was introduced by Phukhamsakda et al. (2020) as a monotypic genus from dead stems of *Clematis fulvicoma*, with *P. clematidis* as the type species. The genus is characterized by immersed ascomata, short ostioles, branched, septate, trabeculate pseudoparaphyses, bitunicate, fissitunicate, cylindrical-clavate to clavate, asymmetric asci, and broad fusiform, 1-euseptate, constricted at the septum, guttulate, hyaline ascospores with mucilaginous sheath, without known asexual morph.

Parasulcatispora rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.92

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL12

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 169–275 μm wide, 146–260 μm high, immersed to erumpent, solitary to gregarious, dark brown to black, globose or subglobose, unilocular, thin-walled, glabrous, ostiolate. *Ostiole* 40–45 μm wide, 47–55 μm high, single, central, smooth-walled, filled with hyaline periphyses. *Peridium* 10–16 μm wide, poorly developed, composed of 4–5 layers of dark brown to black cells of *textura angularis*, fusing with the host tissue outwardly. *Hamathecium* 1.5–2 μm wide, composed of dense, numerous, filamentous, rarely branched, remotely septate, hyaline, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 50–65 × 10–12 μm ($\bar{x}$ = 57 × 11 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 16–22 × 4–7 μm ($\bar{x}$ = 20 × 5 μm; n = 30), overlapping to crowded, hyaline, fusiform, with obtuse ends and slightly tapering, 1–3-septate, slightly constricted at the septum, upper cell broader than lower cell, guttulate, smooth-walled, surrounded by a thick distinct mucilaginous sheath (6–10 μm). Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, umbonate, papillate, fluffy, grayish green; in reverse, dark brown in the middle, light brown radiating outwardly.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL12 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, SL80 (HUEST XX, paratype), living culture UESTCC XX.

Notes – In the phylogenetic analysis (Figure 3.85), *Parasulcatispora rosae* (CGMCC SL12 and UESTCC SL80) clustered with *P. clematidis* (MFLUCC 17-2082), and they nested within Sulcatisporaceae. *Parasulcatispora rosae* is morphologically similar to *P. clematidis* in having immersed to erumpent, dark brown to black, subglobose ascomata with bitunicate, fissitunicate, cylindrical asci, and fusiform, hyaline ascospores with a mucilaginous sheath (Phukhamsakda et al., 2020). However, *P. rosae* differs in having 3-septate ascospores with a slightly wider mucoid sheath. Comparisons of the ITS, LSU and *tef1α* sequences of my isolates and *P. clematidis* (MFLUCC 17-2082) revealed 97.36% (443/455 bp), 99.42% (857/862 bp) and 97.09% (867/893 bp) sequence similarities, respectively.



Note a Host: *Rosa roxburghii*. b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–r Ascospores. s Ascospore stained with Indian ink. t Germinating ascospore. u, v Colony on PDA, above (u), below (v). Scale bars: d, e = 100 μm; f–l = 20 μm; m–t = 10 μm.

Figure 3.92 *Parasulcatispora rosae* (HKAS SL12, holotype)

Teichosporaceae M.E. Barr

Type genus – *Teichospora* Fuckel

Notes – Barr (2002) established Teichosporaceae (Pleosporales) to accommodate eight genera. Most members of Teichosporaceae were previously assigned to the lichenicolous Dacampiaceae. Hyde et al. (2024) listed 17 genera in Teichosporaceae, viz., *Asymmetrispora*, *Aurantiascoma*, *Chaetomastia*, *Floricola*, *Lendemeriella*, *Loculohypoxylon*, *Magnibotryascoma*, *Misturatosphaeria*, *Parateichospora*, *Paulkirkia*, *Pseudoaurantiascoma*, *Pseudocyclothyriella*, *Pseudomisturatosphaeria*, *Pseudoteichospora*, *Ramusculicola*, *Sinodidymella* and *Teichospora*.

Aurantiascoma Thambug. & K.D. Hyde, Fungal Diversity 74: 249 (2015)

Type species – *Aurantiascoma minimum* (Mugambi, A.N. Mill. & Huhndorf) Thambug. & K.D. Hyde

Notes – *Aurantiascoma* was established by Thambugala et al. (2015) to accommodate the type species *A. minimum* (≡*Misturatosphaeria minima*), which phylogenetically formed a separate clade within Floricolaceae. Jaklitsch et al. (2016b) reappraised the genus *Teichospora* and its related genera and proposed the new combination *Teichospora parva* to accommodate *A. minimum* within Teichosporaceae. However, Tennakoon et al. (2021b) resurrected *Aurantiascoma* as a distinct genus in Teichosporaceae and transferred *T. nephelii* (Crous et al., 2016) and *T. quercus* (Crous et al., 2018b) to *Aurantiascoma* based on morphological and phylogenetic evidence. The genus is characterized by globose to subglobose condiomata, subcylindrical, hyaline, branched or unbranched conidiophores, phialidic, ampulliform to subcylindrical conidiogenous cells and ellipsoid, aseptate, hyaline conidia with an apex obtuse, base truncate. The sexual morph is characterized by superficial, coriaceous, dark brown ascomata and unitunicate, short pedicel, cylindrical asci and hyaline, fusiform, septate, constricted at the septum, guttulate ascospores with mucilaginous sheath (Crous et al., 2016, 2018b; Tennakoon et al., 2021b; Ren et al., 2024a). In the present study,

I introduce a new species of *Aurantiascoma* and report the asexual morph of *A*. *minimum*, both isolated from *Rosa roxburghii*.

Aurantiascoma minimum (Mugambi, A.N. Mill. & Huhndorf) Thambug. & K.D. Hyde, Fungal Diversity 74: 249 (2015) Figure 3.93

Index Fungorum number: IF551263; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 160–210 μm wide, 150–185 μm high, solitary to gregarious, dark brown to black, at first immersed, eventually erumpent and appearing superficial, visible as black dots on the host, shiny, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, ostiolate. *Ostiole* single, short, central. *Conidiomatal wall* 15–30 μm wide, composed of thick-walled, dark brown to brown cells of *textura angularis*. *Conidiophores* 7–22 × 1.5–3.2 μm ($\bar{x}$ = 13 × 2 μm; n = 30), hyaline, subcylindrical, smooth, septate, branched. *Conidiogenous cells* 8.5–13 × 1.7–3.5 μm ($\bar{x}$ = 11 × 2.5 μm; n = 30), enteroblastic, phialidic, cylindrical, septate, usually integrated, smooth-walled, and arising from the inner layers of conidiomata. *Conidia* 3.7–5 × 2.6–3.3 μm ($\bar{x}$ = 4.5 × 3 μm; n = 30), hyaline, ellipsoid, straight, smooth-walled, truncate at base, slender and rounded at apex, aseptate, guttulate.

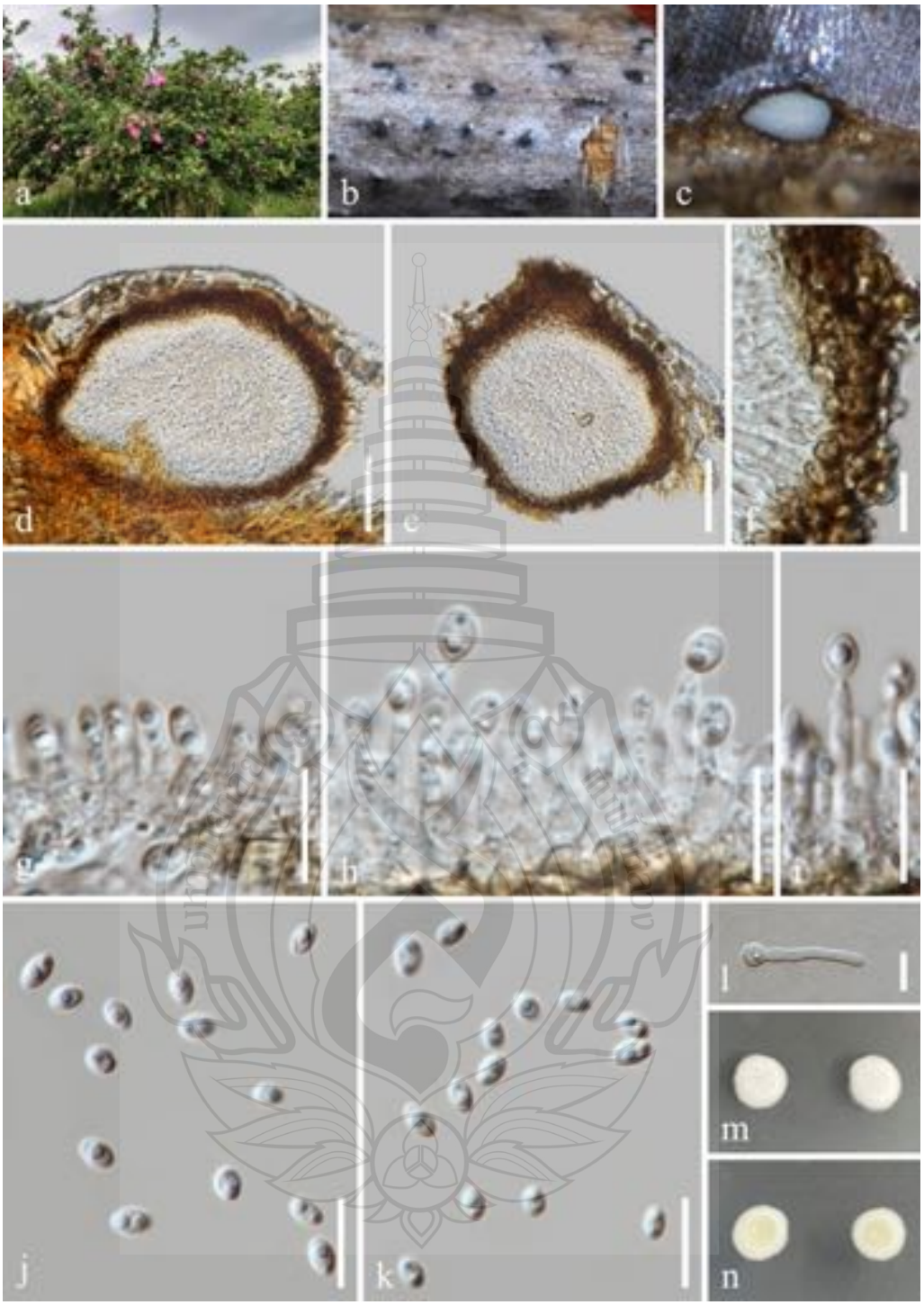
Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, dense, dry, white on the surface becoming yellow with age; in reverse, white to yellow with an entire margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL25 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study); *Shorea assamica* (Ren et al., 2024a).

Known geographical distribution – China, Costa Rica, Kenya, USA.

Notes – Multi-gene phylogenetic analysis revealed that my newly obtained isolate (UESTCC SL25) clustered with *Aurantiascoma minimum* (NI194) (Figure 3.85). There was only the sexual morph provided when Thambugala et al. (2015) and Ren et al. (2024a) described this species. In the present study, I illustrate the asexual morph of *A*. *minimum* and reported it as a new host record from *Rosa roxburghii*.



Note a Host: *Rosa roxburghii*. b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j, k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: d, e = 50 µm; f–l = 10 µm.

Figure 3.93 *Aurantiascoma minimum* (HUEST SL25, new host record)

Aurantiascoma rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.94

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML38

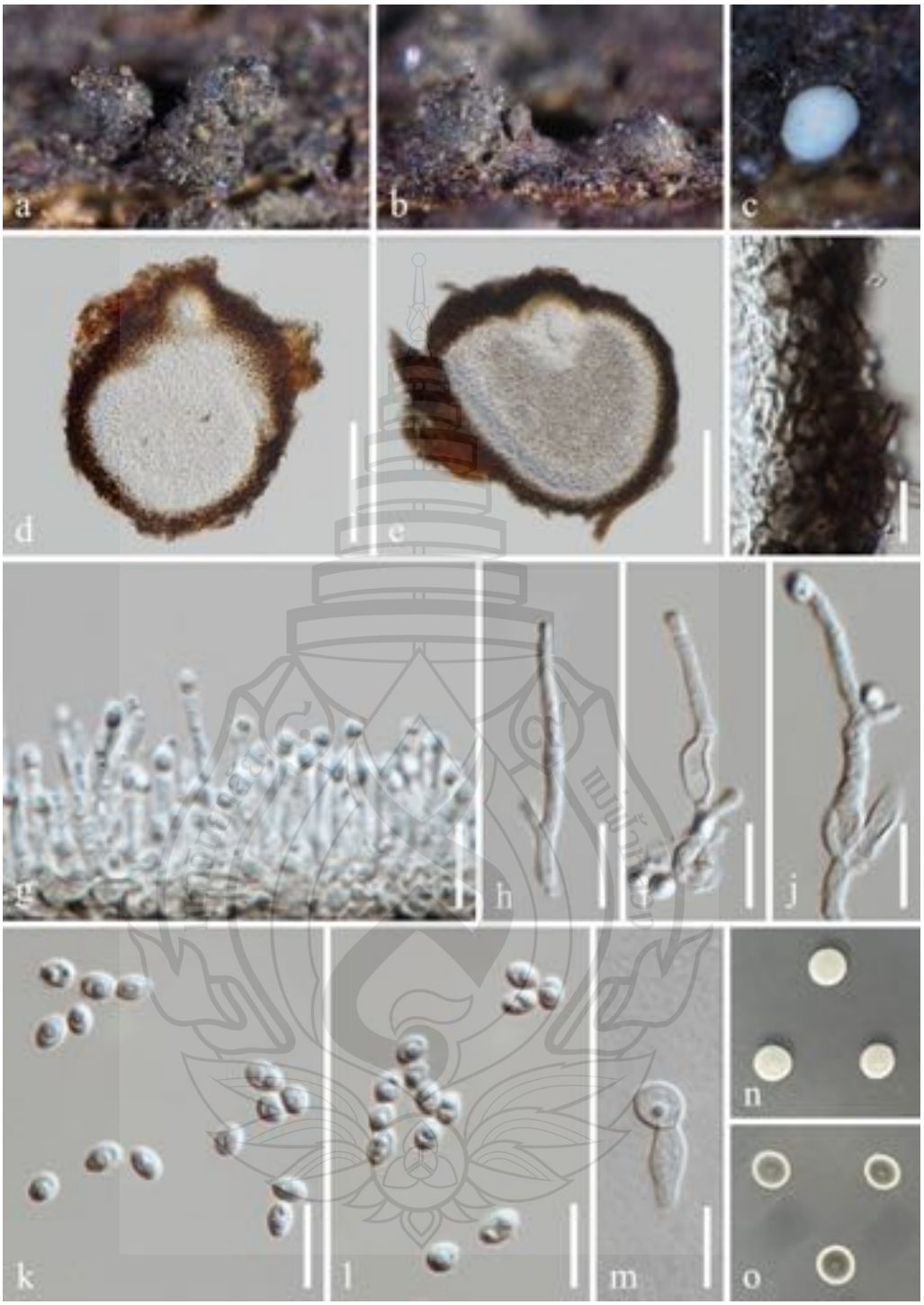
Saprobic on dead branches of *Rosa sterilis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 190–235 μm wide, 225–255 μm high, erumpent to superficial, dark brown to black, solitary, scattered, with a small, papilla-like black dot in the central, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, smooth-walled, ostiolate. *Ostiole* single, short, central. *Conidiomatal wall* 16–32 μm wide, composed of thick-walled cells of *textura angularis*, with dark brown to black cells in outer several layers, gradually merging with hyaline cells lining the cavity. *Conidiophores* 21–44 × 1.5–3.5 μm ($\bar{x}$ = 30 × 2.5 μm; n = 30), hyaline, subcylindrical, smooth, septate, branched. *Conidiogenous cells* 10.5–15 × 1.5–2.3 μm ($\bar{x}$ = 11.5 × 2 μm; n = 30), intercalary to terminal, cylindrical, aseptate, phialidic, smooth-walled. *Conidia* 3.2–5 × 2.9–4.3 μm ($\bar{x}$ = 4.4 × 3.3 μm; n = 30), hyaline, ellipsoid, straight, smooth-walled, truncate at base, slender and rounded at apex, aseptate, guttulate.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 10–12 mm diam. after two weeks at 25℃ in dark, circular, dense, flat to slightly raised, dry, grayish green; in reverse, dark green in the middle and white at the margin.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML38 (HKAS XX, **holotype**); ex-type living culture CGMCC XX.

Notes – Tennakoon et al. (2021b) transferred *Teichospora quercus* to *Aurantiascoma* based on a well-resolved phylogeny and morphological evidence. In the

phylogenetic analysis, *A*. *rosae* (CGMCC ML38) was positioned as a sister taxon to *A*. *quercus* (CBS 143396) with a strong statistical support (Figure 3.85). *Aurantiascoma rosae* and *A*. *quercus* share the characters in having subcylindrical conidiophores, intercalary to terminal, phialidic, cylindrical conidiogenous cells with hyaline, ellipsoid, straight, guttulate, smooth-walled, aseptate conidia (Crous et al., 2018b; Tennakoon et al., 2021b). However, *A*. *rosae* differs from *A*. *quercus* by having longer but narrower conidiophores (21–44 × 1.5–3.5 μm vs. 10–20 × 3–5 μm), longer conidiogenous cells (10.5–15 × 1.5–2.3 μm vs. 5–10 × 2–4 μm), and slightly wider conidia with distinct guttules (3.2–5 × 2.9–4.3 vs. 4–6 × 2.5–3 μm). The ITS and LSU sequences of *A*. *rosae* and *A*. *quercus* exhibit 96.65% (549/568 bp) and 99.18% (847/854 bp) sequence similarities, respectively. Based on different morphology and molecular evidence, I propose *A*. *rosae* as a new species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k, l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d, e = 100 μm; f–m = 10 μm.

Figure 3.94 *Aurantiascoma rosae* (HKAS ML38, holotype)

Floricola Kohlm. & Volkm.-Kohlm., Bot. Mar. 43(4): 385 (2000)

Type species – *Floricola striata* Kohlm. & Volkm.-Kohlm.

Notes – Kohlmeyer and Volkmann-Kohlmeyer (2000) introduced the coelomycetous genus *Floricola* to accommodate *F. striata*, which was found on dead standing leaves and inflorescences of *Juncus roemerianus* in the USA. Thambugala et al. (2015) established the family Floricolaceae to accommodate *Floricola* and seven other new genera, based on morphological characteristics and phylogenetic affinities. Subsequently, Ariyawansa et al. (2015) introduced the second member, *F. viticola*, from a dead branch of *Vitis vinifera* in Italy. Based on molecular phylogenetic analysis and morphological comparisons, Jaklitsch et al. (2016b) synonymized *Asymmetrispora*, *Aurantiascoma*, *Floricola*, *Magnibotryascoma*, *Misturatosphaeria*, *Neocurreya*, *Pseudoaurantiascoma*, *Pseudomisturatosphaeria* and *Ramusculicola* under *Teichospora*, and placed them all within the family Teichosporaceae. However, Boonmee et al. (2019) rejected this treatment, as they recognized 14 genera in the family. Thus, *F. clematidis* and *F. juncicola* were later introduced to the genus by Phukhamsakda et al. (2020) and Crous et al. (2021b), respectively. Tennakoon et al. (2021b) formally resurrected the genus *Floricola* and updated the generic description, as well as described the first sexual morph species, *F. festucae*. Seven epithets of *Floricola* are listed in Index Fungorum (2025, June). The sexual morph of *Floricola* is characterized by cylindrical asci and fusiform, apically conical, narrow towards the apex, guttulate, septate, constricted at the septa, hyaline to yellowish brown ascospores surrounded by a mucilaginous sheath. The asexual morph is characterized by subcylindrical, hyaline to golden brown conidia with roughened striations (Kohlmeyer & Volkmann-Kohlmeyer, 2000; Ariyawansa et al., 2015; Phukhamsakda et al., 2020; Crous et al., 2021b, 2022; Tennakoon et al., 2021b).

Floricola rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.95

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML136

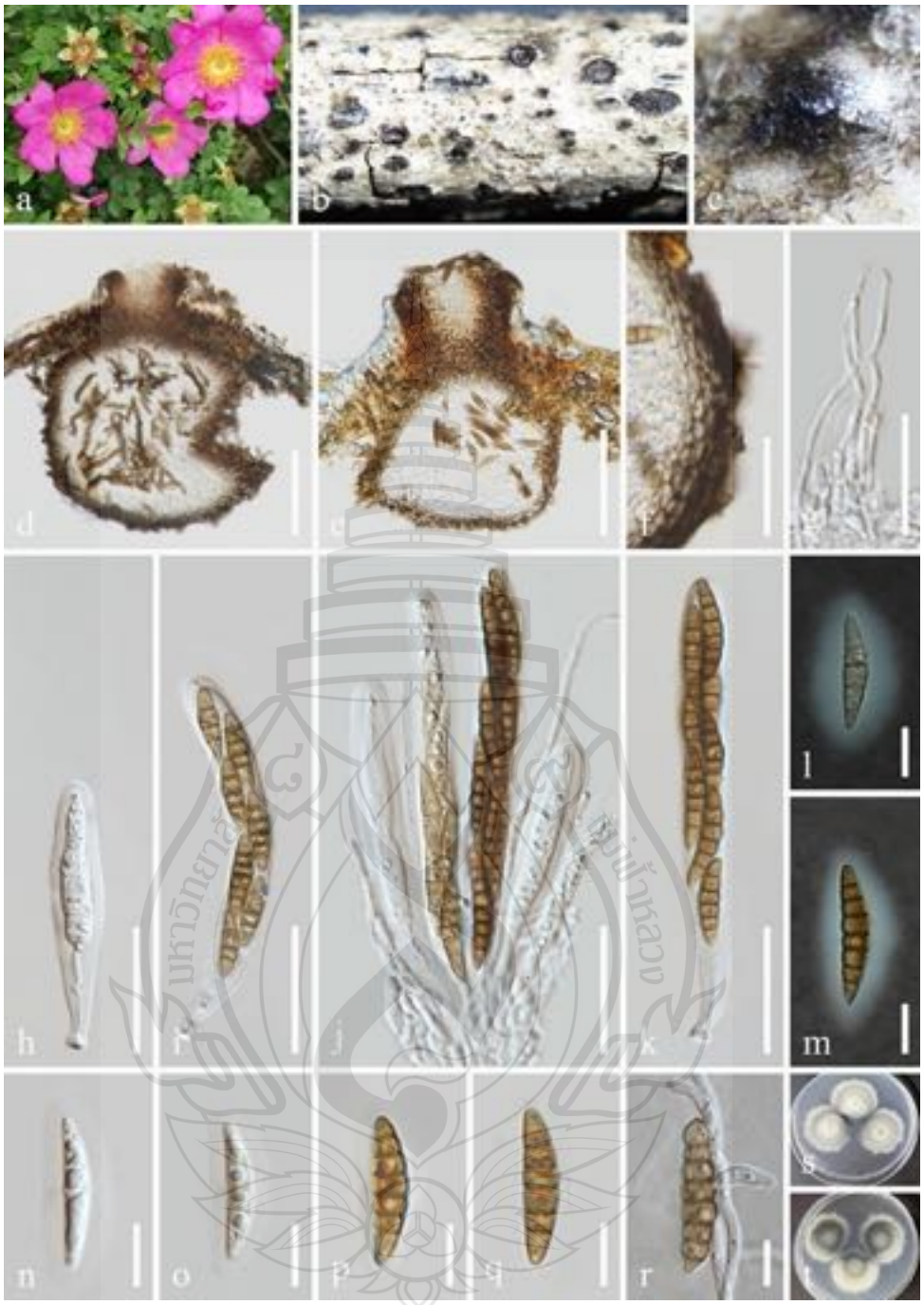
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 170–400 μm wide, 200–360 μm high, solitary, black, immersed to semi-immersed, unilocular, glabrous, coriaceous to carbonaceous, subglobose to pyriform, with the ruptured host tissue around the surface of the ascomata, papillate, ostiolate. *Ostiole* 70–120 μm wide, 75–140 μm high, single, subcylindrical, straight or curved, central. *Peridium* 22–35 μm wide, brittle when dry, composed of thick-walled dark brown cells of *textura angularis* or *textura epidermoidea*, thickened and fusing with host tissue near the ostiole, up to 50 μm wide. *Hamathecium* 2–2.5 μm wide, composed of dense, numerous, filiform, branched, septate, hyaline, guttulate, pseudoparaphyses, longer than asci. *Asci* 112–140 × 9–12 μm ($\bar{x}$ = 121 × 11 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 24–33 × 5.5–7 μm ($\bar{x}$ = 27 × 6 μm; n = 30), overlapping to crowded, straight or slightly curved, hyaline to yellowish brown, fusiform, with a swollen supra-median cell, (1–)5–7(–9)-septate, constricted at the septa, with guttules in each cell, apically conical, narrow towards the apex, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h. Colonies on PDA medium reaching 30–33 mm diam. after two weeks at 25°C in dark, circular to irregular, felty and cottony, flat to slightly raised, dry, white mycelium in the middle and dark green to white mycelium in the outer ring; in reverse, olive to gray green in the middle and white at the margin.

Material examined – CHINA, Qiannan Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on branches of *Rosa roxburghii*,

5 February 2023, N. Wu, ML136 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – Tennakoon et al. (2021b) introduced *Floricola festucae* from *Festuca arundinacea* in China, which was reported as a sexual morph and distinguished it from the type species of *Teichospora* (*T. trabicola*) by its cylindric-fusiform ascospores with 5–6-septa. Molecular evidence confirmed that my collection grouped as sister to *F. festucae* (MFLU 17-0773) with a good statistical support (Figure 3.85). The two species share similar ascomata morphology and guttulate, septate, fusiform ascospores. However, my collection is easily distinguished from *F. festucae* by its thicker peridium (22–35 µm vs. 10–20 µm), longer asci (112–140 × 9–12 µm vs. 100–125 × 6–10 µm) and mostly (1–)5–7(–9)-septate, larger ascospores (24–33 × 5.5–7 µm vs. 20–25 × 5–6 µm) with a mucilaginous sheath, whereas ascospores in *F. festucae* are 5–6-septate and lack a sheath. Therefore, I propose my collection as a new species, namely *F. rosae*.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–q Ascospores. l, m Ascospores stained with Indian ink. r Germinating ascospore. s, t Colony on PDA, above (s), below (t). Scale bars: d = 100 μm; e = 80 μm; f–k = 30 μm; l–r = 10 μm.

Figure 3.95 *Floricola rosae* (HKAS ML136, holotype)

Magnibotryascoma Thambug. & K.D. Hyde, Fungal Diversity 74: 249 (2015)

Type species – *Magnibotryascoma uniseriatum* (Mugambi, A.N. Mill. & Huhndorf) Thambugala & K.D. Hyde

Notes – Thambugala et al. (2015) introduced the genus *Magnibotryascoma* to accommodate *M. uniseriatum*, which was previously known as *Misturatosphaeria uniseriata* (Mugambi & Huhndorf, 2009b). Currently, six species are accepted in *Magnibotryascoma*, viz., *M. acaciae*, *M. kungmingense*, *M. mali*, *M. melanommoides*, *M. rubriostiolata* and *M. uniseriata* (Hyde et al., 2017, Tennakoon et al., 2021b, Crous et al., 2022).

Magnibotryascoma mali Phukhams., Wanas. & K.D. Hyde, Fungal Diversity 87: 105 (2017) Figure 3.96

Index Fungorum number: IF553255; Facesoffungi number: FoF003387

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 155–220 µm wide, 130–180 µm high, solitary, immersed to erumpent, visible as black dots on the host, pycnidial, globose to subglobose, unilocular, glabrous, coriaceous, thick- and smooth-walled, ostiolate. *Ostiole* single, short, central. *Conidiomatal wall* 22–25 µm wide, composed of hyaline to brown compressed cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–13 × 1.5–4.5 µm ($\bar{x}$ = 8 × 3.5 µm; n = 30), hyaline, aseptate, smooth, thin-walled, ampulliform to subcylindrical or lageniform, and arising from the inner layers of conidiomata. *Conidia* 3.5–4.5 × 2.8–3.5 µm ($\bar{x}$ = 4 × 3.2 µm; n = 30), subglobose or ellipsoidal, aseptate, straight, guttulate, truncate at base, rounded at apex, initially hyaline, becoming brown when mature, smooth-walled.

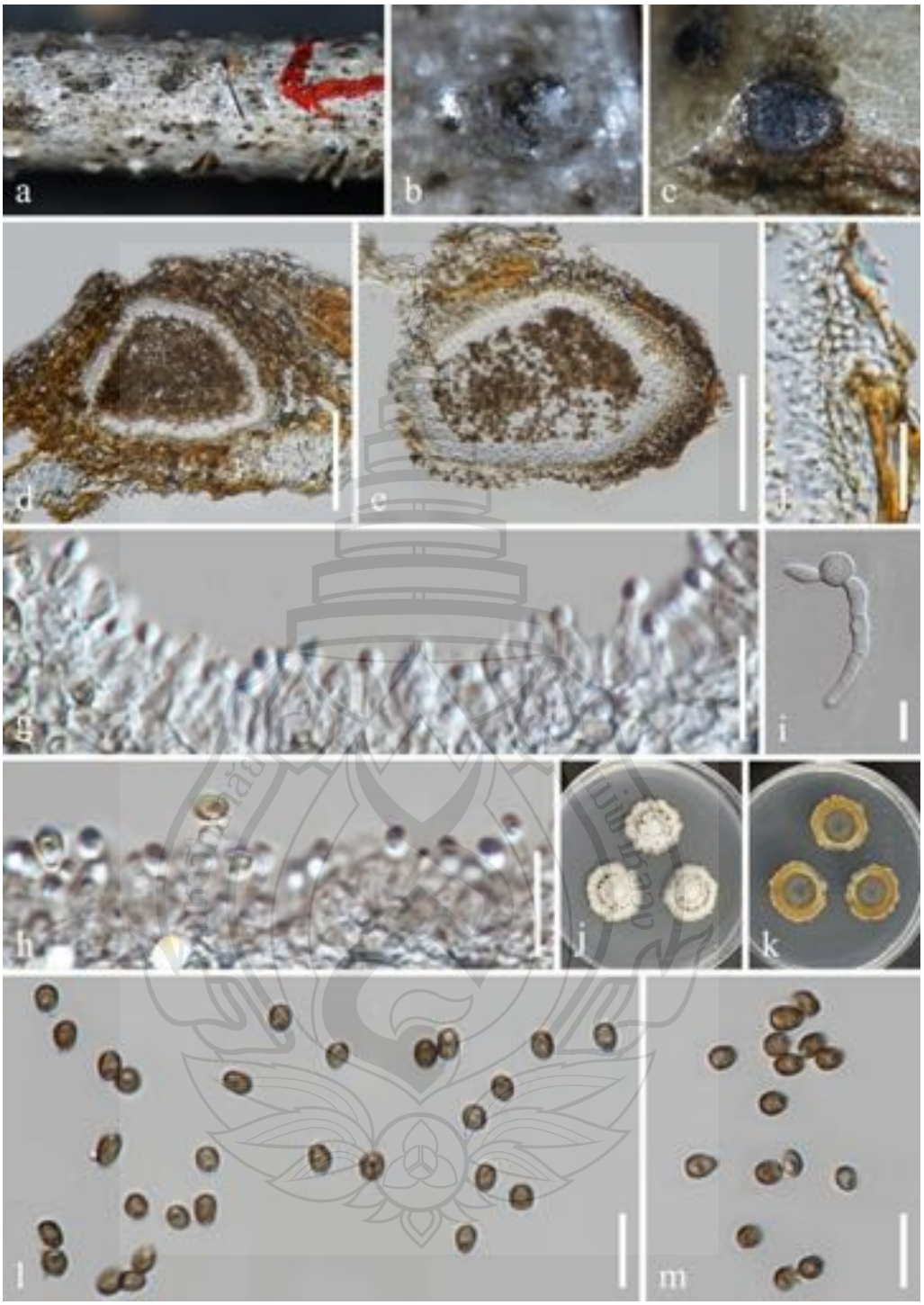
Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 23–25 mm diam. after two weeks at 25°C in dark, circular to irregular, dense, flat to slightly raised, producing mucus, white; in reverse, dark olive-green in the middle and yellowish brown at the margin.

Materials examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML194 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *R. roxburghii*, 9 July 2022, N. Wu, GL146 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL19 (HUEST XX), living culture UESTCC XX; *ibid.*, GL32 (HUEST XX), living culture UESTCC XX.

Hosts – *Malus halliana* (Hyde et al., 2017); *Osmanthus fragrans* (Chethana et al., 2023); *Rosa roxburghii* and *R. sterilis* (present study); *Shorea assamica* (Ren et al., 2024a).

Known geographical distribution – China.

Notes – *Magnibotryascoma mali* was introduced by Hyde et al. (2017) based on morphological and phylogenetic evidence. In the present study, four of my isolates (UESTCC GL32, UESTCC GL19, UESTCC GL146 and UESTCC ML149) clustered with the ex-type strain of *M. mali* (MFLUCC 17-0933) (Figure 3.85), three of which were found on *Rosa roxburghii* from China, and the other on *R. sterilis*. My collection matches well with the holotype of *M. mali* in the morphology and dimensions of conidiogenous cells and conidia. Therefore, I identify my collection as *M. mali* and extend the known hosts of this fungus to *Rosa roxburghii* and *R. sterilis.*



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g, h Conidiogenous cells and developing conidia. i Germinating conidium. j, k Colony on PDA, above (j), below (k). l, m Conidia. Scale bars: d, e = 100 μm; f = 20 μm; g–m = 10 μm.

Figure 3.96 *Magnibotryascoma mali* (HUEST ML194, new host record)

Thyridariaceae Q. Tian & K.D. Hyde, Fungal Diversity 63: 254 (2013)

Type genus – *Thyridaria* Sacc.

Notes – Thyridariaceae was introduced by Hyde et al. (2013) to accommodate the type genus *Thyridaria* based on its unique morphology and a well-resolved phylogeny. Presently, nine genera are accepted in Thyridariaceae, *Chromolaenomyces*, *Cycasicola*, *Liua*, *Parathyridaria*, *Parathyridariella*, *Pseudothyridariella*, *Thyridaria*, *Thyridariella* and *Vaginospora* (Hyde et al., 2024; Tian et al., 2024b, 2024c).

Parathyridaria Jaklitsch & Voglmayr, Stud. Mycol. 85: 48 (2016)

Type species – *Parathyridaria ramulicola* Jaklitsch, J. Fourn. & Voglmayr

Notes – Jaklitsch and Voglmayr (2016c) introduced this genus to accommodate the type species *Parathyridaria ramulicola* and a new combination, *P. percutanea* (≡ *Roussoella percutanea*). Subsequently, ten species were included into this genus, viz. *P. clematidis*, *P. ellipsoidea*, *P. ephedrae*, *P. flabelliae*, *P. philadelphi*, *P. robiniae*, *P. rosae*, *P. serratifoliae*, *P. tyrrhenica* and *P. virginianae* (Tibpromma et al., 2017; Crous et al., 2018b; Wanasinghe et al., 2018; Phukhamsakda et al., 2020; Poli et al., 2020; Das et al., 2021; Mattoo et al., 2022). Members of this genus are commonly found as saprobes in terrestrial habitats or as human pathogens. They are characterized by immersed to erumpent, subglobose to pyriform ascomata, with multi-septate, fusoid, hyaline to brown ascospores surrounded by a mucilaginous sheath. The asexual morphs are coelomycetes, and are characterized by globose to subglobose conidiomata, phialidic conidiogenous cells, ellipsoid, aseptate, guttulate, hyaline to brown conidia (Jaklitsch & Voglmayr, 2016c; Wanasinghe et al., 2018; Du et al., 2025).

Parathyridaria rosicola N. Wu & Jian K. Liu, sp. nov. Figure 3.97

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosicola*" refers to the host genus, *Rosa*, on which the species was isolated.

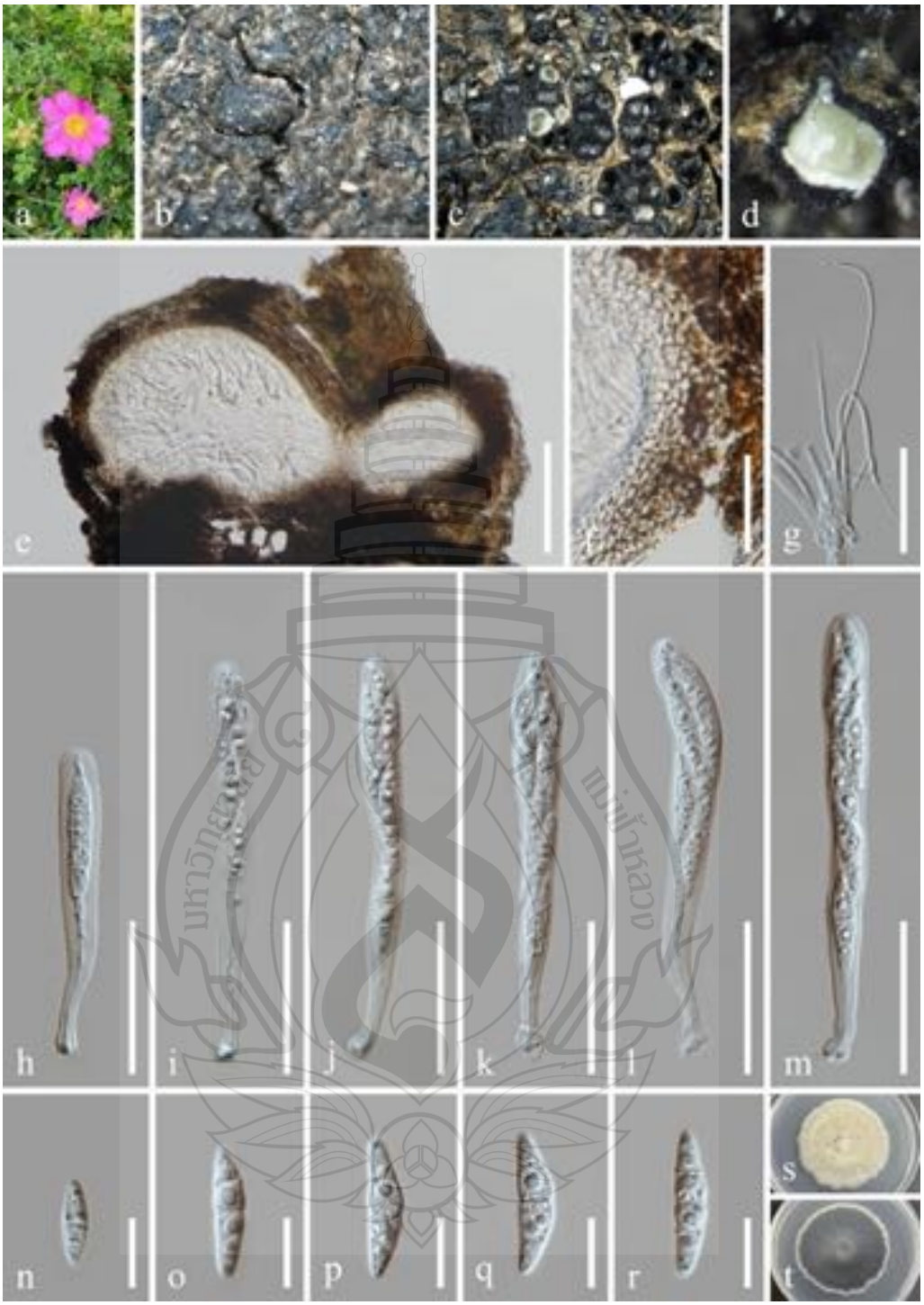
Holotype – HKAS ML127

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 190–320 μm wide, 180–300 μm high, gregarious, dark brown to black, semi-immersed to superficial or erumpent through bark, subglobose to pyriform, sometimes not upright, laid on the substrate, unilocular, glabrous, coriaceous, thick-walled, short papillate, ostiolate. *Ostiole* 60–70 μm wide, 100–112 μm high, single, cylindrical to subcylindrical, straight or curved, central or laterally located, lined with numerous periphyses in the ostiolar canal. *Peridium* 18–30 μm wide, carbonaceous and brittle when dry, composed of several layers of hyaline to brown cells of *textura angularis*, gradually paler and thinner inwardly. *Hamathecium* 1.5–3 μm wide, composed of dense, filamentous, branched, hyaline, slightly swollen at the base, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 100–140 × 11–13.5 μm ($\bar{x}$ = 113 × 12.5 μm; n = 20), 8-spored, bitunicate, cylindric-clavate, short pedicellate, straight or slightly curved, apically rounded with an ocular chamber. *Ascospores* 22–27 × 5–7.2 μm ($\bar{x}$ = 24.5 × 6.2 μm; n = 30), overlapping to bi-seriate, hyaline, fusiform with acute ends, initially 1-septate, not constricted at the septum, guttulate, becoming 2–3-septate, occasionally 3-septate, deeply constricted at middle septum, cell above middle septum widest, verrucose, smooth-walled, surrounded by an inconspicuous gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 43–45 mm diam. after two weeks at 25℃ in dark, circular, cottony, dense, grayish green; in reverse, olive-green to dark brown in the middle and grayish green at the undulate margin.

Material examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML127 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – Multi-gene phylogenetic analysis showed that *Parathyridaria rosicola* (CGMCC ML127) formed a sister clade to *P. ellipsoidea* (KNU-JJ-1829) (Figure 3.85). *Parathyridaria ellipsoidea* was initially introduced based on its asexual morph produced in culture (Das et al., 2021). Du et al. (2025) reported both asexual and sexual morphs of *P. ellipsoidea* from *Buxus sinica* and *Mahonia bealei*, respectively. *Parathyridaria rosicola* resembles *P. ellipsoidea* in having dark brown to black, subglobose to pyriform ascomata, bitunicate, short pedicellate, cylindric-clavate asci, and septate, guttulate, hyaline ascospores (Du et al., 2025). However, *P. rosicola* possesses 3-septate, verrucose, fusiform ascospores with inconspicuous sheaths that are larger than the 1-septate, small guttuled, fusoid ascospores of *P. ellipsoidea* (22–27 × 5–7.2 μm vs. 15– 21 × 3–6 μm). Asci of *P. rosicola* are longer than *P. ellipsoidea* (100–140 × 11–13.5 μm vs. 48–76 × 5.5–9.5 μm). Comparisons of the ITS, LSU, and *tef1α* sequences of *P. rosicola* and *P. ellipsoidea* revealed 95.20% (496/521 bp), 99.76% (835/837 bp) and 98.14% (952/970 bp) sequence similarities, respectively. The SSU and *rpb2* sequences are unavailable for the latter. I therefore identify *P. rosicola* as a new species based on the morphology and molecular evidence (Jeewon & Hyde, 2016).



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–m Asci. n–r Ascospores. s, t Colony on PDA, above (s), below (t). Scale bars: e = 80 μm; f–m = 30 μm; n–r = 10 μm.

Figure 3.97 *Parathyridaria rosae* (HKAS ML127, holotype)

Torulaceae Corda

Type genus – *Torula* Pers.

Notes – Torulaceae was introduced by Sturm (1829) based on the hyphomycetous genus *Torula*. Currently, the family comprises seven genera, *Cylindrotorula*, *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides* and *Torula* (Crous et al., 2015a, 2020a; Li et al., 2016a; Su et al., 2016, 2018; Boonmee et al., 2021; Hyde et al., 2024). Among them, *Cylindrotorula* and *Sporidesmioides* are monotypic genera (Li et al., 2016a; Boonmee et al., 2021). However, the taxonomic placements of *Neopodoconis*, *Rostriconidium* and *Sporidesmioides* are unstable within Torulaceae. Qiu et al. (2022) synonymized *Rostriconidium* and *Sporidesmioides* with *Neopodoconis* based on morpho-phylogenetic evidence. Subsequently, in the phylogenetic tree presented by Wang et al. (2023a), *Neopodoconis* formed two distinct clades, one of which formed a monophyletic clade basal to Torulaceae, while the other was located outside the family. A similar phylogenetic arrangement was also observed in the study by the He et al. (2024). The sexual state of the family is still unknown. Members of the family are mainly lignicolous saprobic fungi from freshwater and terrestrial habitats (Boonmee et al., 2021; Li et al., 2024; Wang et al., 2024a, 2024b).

Dendryphion Wallr., Fl. crypt. Germ. (Norimbergae) 2: 300 (1833)

Type species – *Dendryphion comosum* Wallr.

Notes – Wallroth (1833) introduced this genus based on a hyphomycetous species, *Dendryphion comosum*. *Dendryphion* is the second largest genus in Torulaceae with 86 species registered in Index Fungorum (2025, June), of which only eight species have molecular data (Wang et al., 2024a, 2024b). Members of this genus are known as saprobes from freshwater and terrestrial habitats, and characterized by macronematous, mononematous, brown to black conidiophores branched at the apex forming a stipe and a head, monotretic or polytretic, integrated or discrete, cicatrized, clavate, cylindrical or doliiform conidiogenous cells, and acropleurogenous, catenate or solitary, cylindrical with rounded ends or obclavate, sometimes cheiroid, multi-septate, simple

or branched, pale to olivaceous brown conidia (Ellis, 1971; Su et al., 2016; Dong et al., 2020; Zhang et al., 2025a).

Dendryphion verrucosum S. Luan, H.W. Shen & Z.L. Luo, Phytotaxa 676(1): 69 (2024) Figure 3.98

Index Fungorum number: IF902832; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Asexual morph: Hyphomycetous. *Colonies* on natural substrates effuse, hairy, scattered or in small groups, brown to dark brown, with glistening conidial masses at apex. *Mycelium* partly superficial, partly immersed, composed of septate, branched, pale brown to brown hyphae. *Conidiophores* 100–166 × 5.5–7.5 μm ($\bar{x}$ = 136 × 6.7 μm; n = 30), macronematous, mononematous, erect, cylindrical, straight or slightly flexuous, dark brown, 5–7-septate, branched in the upper part, thick-walled. *Conidiogenous cells* polytretic, integrated, terminal or intercalary, pale brown. *Conidia* 12.5–31 × 6–10 μm ($\bar{x}$ = 21.5 × 7.8 μm; n = 30), pale brown to brown, sometimes solitary, mostly catenate to branched, monilioid, composed of subglobose to globose cells, (1–)2–6-septate, constricted at the septa, straight or slightly curved, rounded at the apex, rounded or truncate at the base, verrucose, sometimes central cells wider than end cells. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from the basal cell. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, cottony, slightly raised, with sparse pale-yellow mycelium in the middle and dense white mycelium towards the edge; in reverse, black in the middle, dark brown in the inner ring and pale yellow at the entire margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL07 (HUEST XX), living culture UESTCC XX.

Hosts – *Coffea arabica* (Lu et al., 2025); *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Dendryphion verrucosum* was introduced by Wang et al. (2024b) based on a specimen collected from a submerged decaying wood in a freshwater habitat in China. Subsequently, Lu et al. (2025) reported this species from *Coffea arabica* in a terrestrial habitat. My collection matches with the original diagnosis of *D. verrucosum* (Wang et al., 2024b). In the phylogenetic analysis (Figure 3.85), my collection (UESTCC SL07) clustered with type strain of *D. verrucosum* (CGMCC 3.27013). The comparison of their ITS, LSU, *tef1α* and *rpb2* sequences showed 99.80% (493/494 bp), 99.76% (817/819 bp) and 99.55% (880/884 bp) sequence similarities, respectively. Such difference is not enough to distinguish them as different species. Hence, I recognize my collection as *D. verrucosum* and a new host record of this species from *Rosa roxburghii* is provided.



Note a Host: *Rosa roxburghii*. b–d Colonies on substrate surface. e, f Conidiophores with conidia. g, h Conidiogenous cells with conidia. i–p Conidia. q Germinating conidium. r, s Colony on PDA, above (r), below (s). Scale bars: e, f = 50 μm; g, h = 20 μm; i–q = 10 μm.

Figure 3.98 *Dendryphion verrucosum* (HKAS SL07, new host record)

Dothideomycetes families *incertae sedis*

Pseudorobillardaceae Crous

Type genus – *Pseudorobillarda* M. Morelet

Notes – The family Pseudorobillardaceae was formally introduced by Crous et al. (2019) to accommodate members of *Pseudorobillarda* and placed it in Dothideomycetes. The taxonomic placement of Pseudorobillardaceae is unclear. Until now, this family is consisted with only *Pseudorobillarda* and has been classified within Dothideomycetes *incertae sedis* (Li et al., 2020; Hyde et al., 2024).

Pseudorobillarda M. Morelet, Bull. Soc. Sci. nat. Arch. Toulon et du Var 175: 5 (1968)

Type species – *Pseudorobillarda phragmitis* (Cunnell) M. Morelet

Notes – *Pseudorobillarda* was established by Morelet (1968) to accommodate *P. muhlenbergiae* (= *Robillarda muhlenbergiae*) and *P. phragmitis* (= *R. phragmitis*). Crous et al. (2018a) showed that *Pseudorobillarda* taxa are related to Pleosporales. However, the phylogenetic analysis of LSU sequence data showed that *Pseudorobillarda* is distinct from Pleosporales (Li et al., 2020). Members of this genus are coelomycetes, which are characterized by immersed to semi-immersed, globose to subglobose conidiomata, phialidic or annellidic, cylindrical to ampulliform conidiogenous cells, and subcylindrical to fusiform, aseptate or septate conidia with appendages at the one end (Tangthirasunun et al., 2014; Li et al., 2020; Song et al., 2022; Wang et al., 2024a). Up to date, there are 22 species of *Pseudorobillarda*, listed in Index Fungorum (2025, June).

Pseudorobillarda camelliae-sinensis Rathnayaka, C.H. Kuo & K.D. Hyde, Phytotaxa 516(2): 122 (2021) Figure 3.99

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 165–260 μm wide, 160–200 μm high, pycnidial, scattered, slightly erumpent, multilocular or unilocular, coriaceous, subcylindrical, black, glabrous, ostiolate. *Ostiole* in the center of the pileus, circular, dark brown, ostiolar

canal filled with hyaline cells, apapillate. *Conidiomatal wall* 15–20 µm wide, composed of thin-walled, 3–5 layers, pale brown to hyaline cells of *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.5–9.5 × 3–6 µm ($\bar{x}$ = 6.5 × 5 µm; n = 20), hyaline, enteroblastic, phialidic, subcylindrical, thick- and smooth-walled. *Conidia* 18–22 × 4.5–6 µm ($\bar{x}$ = 20 × 5 µm; n = 30), hyaline, aseptate, subcylindrical, rounded at apex, truncated at base, thick-walled, smooth, bearing 4–5-unbranched, flexuous, extracellular, apical appendages (15–22 µm long).

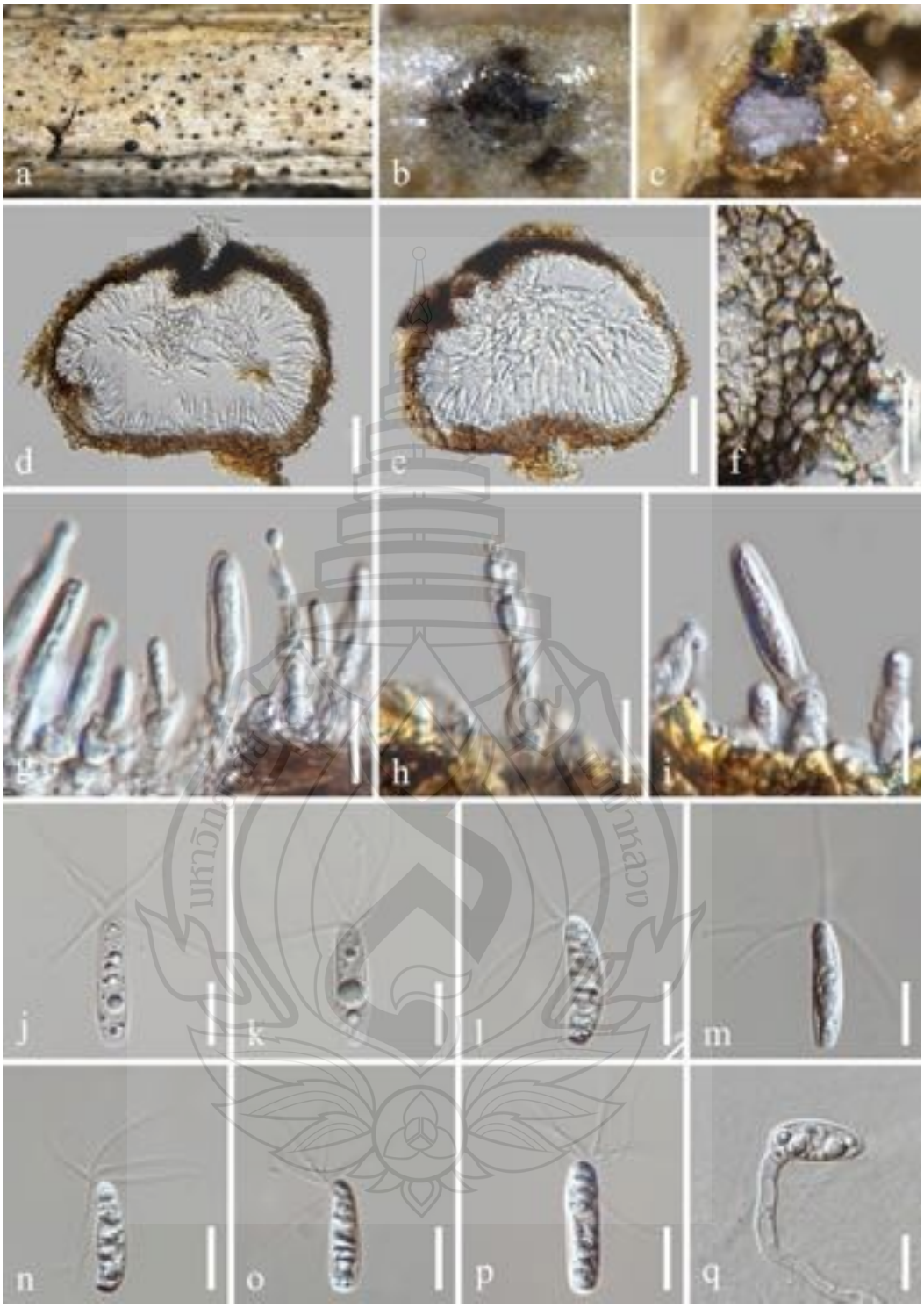
Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 20–22 mm diam. after two weeks at 25°C in dark, circular or irregular, cottony, flat, initially white, gradually becoming pale gray to orange in middle and gray at the margin; in reverse, filamentous, pale brown at the middle, and dark gray at the margin.

Material examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H43 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia sinensis* (Rathanyaka et al., 2021); *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Pseudorobillarda camelliae-sinensis* was introduced by Rathanyaka et al. (2021) with an asexual morph, which was isolated from *Camellia sinensis* in China. Multi-locus phylogenetic analysis showed that my isolate (UESTCC H43) clustered together with *P. camelliae-sinensis* (NCYUCC 10-0408) with a strong statistical support (Figure 3.100). Morphologically, my collection is similar to *P. camelliae-sinensis* in having pycnidial, scattered, slightly erumpent conidiomata, hyaline, enteroblastic, phialidic conidiogenous cells, and hyaline, aseptate, subcylindrical conidia with apical appendages. No significant morphological differences were observed between my collection and the type strain. Therefore, I identify my collection as *P. camelliae-sinensis* and report a new host record from *Rosa roxburghii* in China.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j–p Conidia. q Germinating conidium. Scale bars: d, e = 50 μm; f = 20 μm; g–q = 10 μm.

Figure 3.99 *Pseudorobillarda camelliae-sinensis* (HUEST H43, new host record)

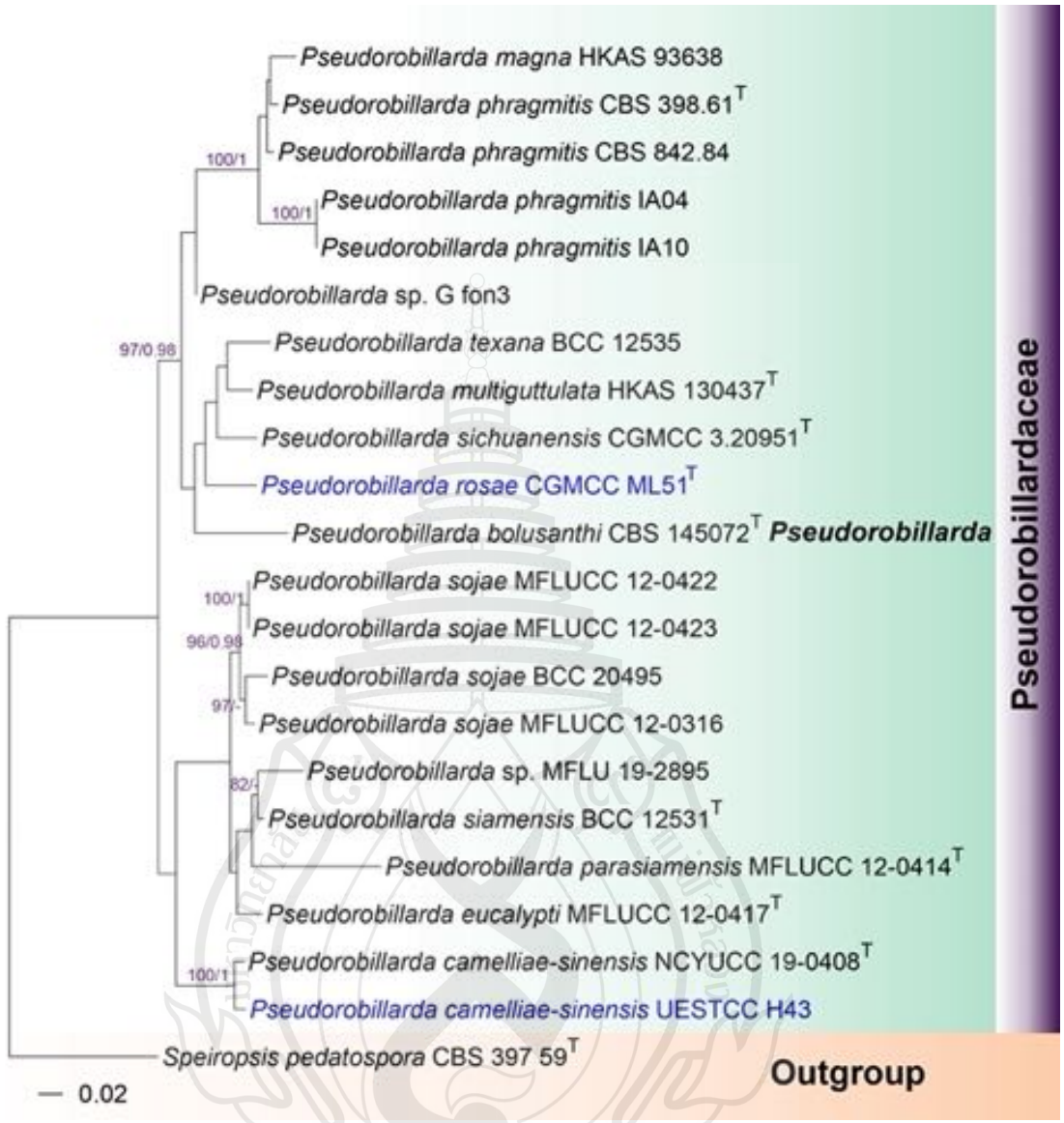


Figure 3.100 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU, sequence data of Pseudorobillardaceae

Figure 3.100 The tree is rooted with *Speiropsis pedatospora* (CBS 397.59). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Pseudorobillarda rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.101

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

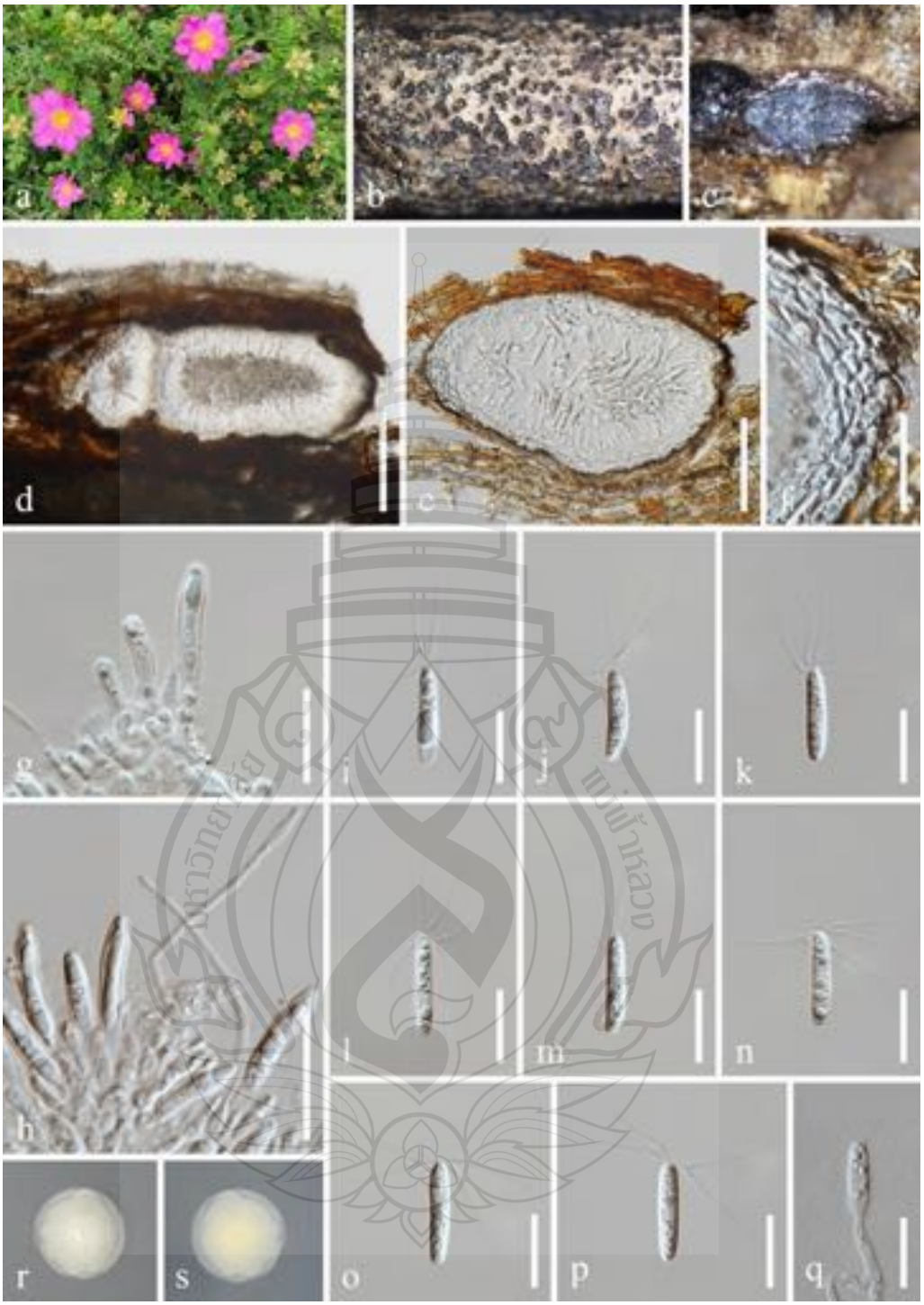
Holotype – HKAS ML51

Saprobic on decaying branches of *Rosa roxburghii*. Forming black, lenticular spots on the host surface. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 180–320 μm wide, 120–165 μm high, pycnidial, scattered, immersed to slightly erumpent, multilocular or unilocular, coriaceous, subcylindrical, black, without a ostiole. *Conidiomatal wall* 12–20 μm wide, consisting of 3–5-layered cells of *textura angularis*, outer layers with brown to black, oblong, thick-walled cells, inner layers with subhyaline, ovoid, thin-walled cells. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Paraphyses* 2–2.5 μm wide, hyaline, unbranched, narrowly cylindrical, aseptate, smooth-walled, rounded at the apex. *Conidiogenous cells* 5.5–8 × 2–3.5 μm ($\bar{x}$ = 7 × 3 μm; n = 20), enteroblastic, monophialidic, integrated, cylindrical, hyaline, straight, smooth-walled. *Conidia* 18.5–21.5 × 3.7–4.5 μm ($\bar{x}$ = 20.5 × 4 μm; n = 30), subcylindrical, hyaline, rounded or sharp at the apex, straight or slightly curved, aseptate, multi-guttulate, smooth-walled, with 4–5 unbranched, filiform, flexuous, attenuated, supple apical appendages (17–21 μm long).

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25℃ in the dark. Colonies from above, circular, cottony, dense, regular edge, white, center slightly elevated.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa roxburghii*, 1 February 2023, N. Wu, ML51 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – Multi-locus phylogenetic analysis revealed that *Pseudorobillarda rosae* (CGMCC ML51) is nested within the genus *Pseudorobillarda*, forming a well-supported monophyletic lineage sister to *P. sichuanensis* (CGMCC 3.20951) (Figure 3.100). Morphologically, *P. rosae* differs from *P. sichuanensis* by having slightly longer and broader conidia (18.5–21.5 × 3.7–4.5 μm vs. 12–17 × 2.5–4 μm), and by a greater number of apical appendages (4–5 vs. 3–4) (Song et al., 2022). Additionally, the ITS and LSU sequences of my isolate (CGMCC ML51) and the ex-type of *P. sichuanensis* (CGMCC 3.20951) showed 79 bp (396/475 bp, 28 gaps) and 24 bp (815/839 bp) differences, respectively. Based on both molecular phylogenetic evidence and morphological distinctions, I introduce *P. rosae* as a novel species collected from *Rosa roxburghii* in China.



Note a Host *Rosa roxburghii*. b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g, h Conidiogenous cells and developing conidia. i–p Conidia. q Germinating conidium. r, s Colony on PDA, above (r), below (s). Scale bars: d = 100 μm; e = 60 μm; f, h, q = 20 μm; g, i–p = 15 μm.

Figure 3.101 *Pseudorobillarda rosae* (HKAS ML51, holotype)

Sordariomycetes O.E. Erikss. & Winka

Pseudoneodictyosporiaceae N. Wu & Jian K. Liu, fam. nov.

Index Fungorum number:XXX; Facesoffungi number:XX

Etymology – Name refers to "*Pseudoneodictyosporium*".

Type genus – *Pseudoneodictyosporium* N. Wu & Jian K. Liu

Notes – A new family, Pseudoneodictyosporiaceae is established here to accommodate the new genus *Pseudoneodictyosporium* in the order Amphisphaeriales, Sordariomycetes, based on its unique morphology of xxx and due to the formation of a distinct lineage in the phylogenetic analysis.

Pseudoneodictyosporium N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IFxx; Facesoffungi number: FoFxx

Etymology – Name refers to the similarity to the genus "*Neodictyosporium*".

Type species – *Pseudoneodictyosporium rosae* N. Wu & Jian K. Liu

Saprobic on dead wood. Sexual morph: *Ascomata* solitary to gregarious, immersed to semi-immersed, subglobose to pyriform or irregular in shape, unilocular or multilocular, glabrous, smooth, coriaceous, short papillate, ostiolate. *Ostiole* single, periphysate, cylindrical to subcylindrical, straight or curved, centric or eccentric. *Peridium* composed of elongated pale brown cells of *textura angularis*, thicker near the ostiole, thinner at the base, and cells of *textura oblita* between each locule when stromatic. *Paraphyses* hyaline, hypha-like, septate, unbranched, guttulate, wider at base, tapering at the apex, numerous between asci and embedded in a gelatinous matrix. *Asci* 8-spored, unitunicate, long-cylindrical, straight or slightly curved, short pedicellate or lacking, apically obtuse, with a J− subapical ring at apex. *Ascospores* uniseriate or overlapping biseriate, fusiform with obtuse ends, hyaline, 3-septate, not constricted at the septa, straight to slightly curved, guttulate, verrucose, smooth-walled, surrounded by a thick mucilaginous sheath. **Asexual morph**: Undetermined.

Notes – *Pseudoneodictyosporium* is a monotypic genus collected from a terrestrial habitat, and its asexual morph is undetermined. The genus is characterized by solitary to

gregarious, immersed to semi-immersed, unilocular or multilocular, subglobose to pyriform ascomata, septate, guttulate, unbranched paraphyses, 8-spored, unitunicate, long-cylindrical asci with a J− subapical ring at apex, and hyaline, 3-septate, guttulate, smooth-walled, fusiform ascospores, surrounded by a thick mucilaginous sheath. Its ascospore morphology resembles the genus *Neodictyosporium* (Tennakoon et al., 2021a; Yu et al., 2024). However, *Neodictyosporium* belongs to Neodictyosporiaceae, whereas *Pseudoneodictyosporium* belongs to Pseudoneodictyosporiaceae. Multi-gene phylogenetic analysis based on combined ITS, LSU, *rpb2* and *tub2* sequence data (Figure 3.103) showed that *Pseudoneodictyosporium* forms a distinct clade, closer to members of *Amphisphaeria* and *Neoarthrinium*. Therefore, I introduce a new genus *Pseudoneodictyosporium* to accommodate the type species *Pse. rosae* based on morphology and multi-gene phylogeny.

Pseudoneodictyosporium rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.102

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS SL14

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 265–360 μm wide, 125–345 μm high, mostly solitary, occasionally gregarious, immersed to semi-immersed, visible as raised, dome-shaped, black spots, with a small central papilla, subglobose to pyriform or irregular in shape, unilocular or multilocular, glabrous, smooth, coriaceous, ostiolate. *Ostiole* 63–108 μm wide, 110–150 μm high, single, periphysate, cylindrical to subcylindrical, straight or curved, centric or eccentric. *Peridium* 15–20 μm wide, composed of elongated pale brown cells of *textura angularis*, thicker near the ostiole, thinner at the base, and cells of *textura oblita* between each locule when stromatic. *Paraphyses* 2.5–4.5 μm wide, hypha-like, septate, unbranched, guttulate, wider at base, tapering at the apex, numerous between asci and embedded in a gelatinous matrix. *Asci* 98–120 × 7.5–12 μm ($\bar{x}$ = 108× 9 μm; n = 20), 8-spored, unitunicate, long-cylindrical, straight or slightly curved, short pedicellate or lacking,

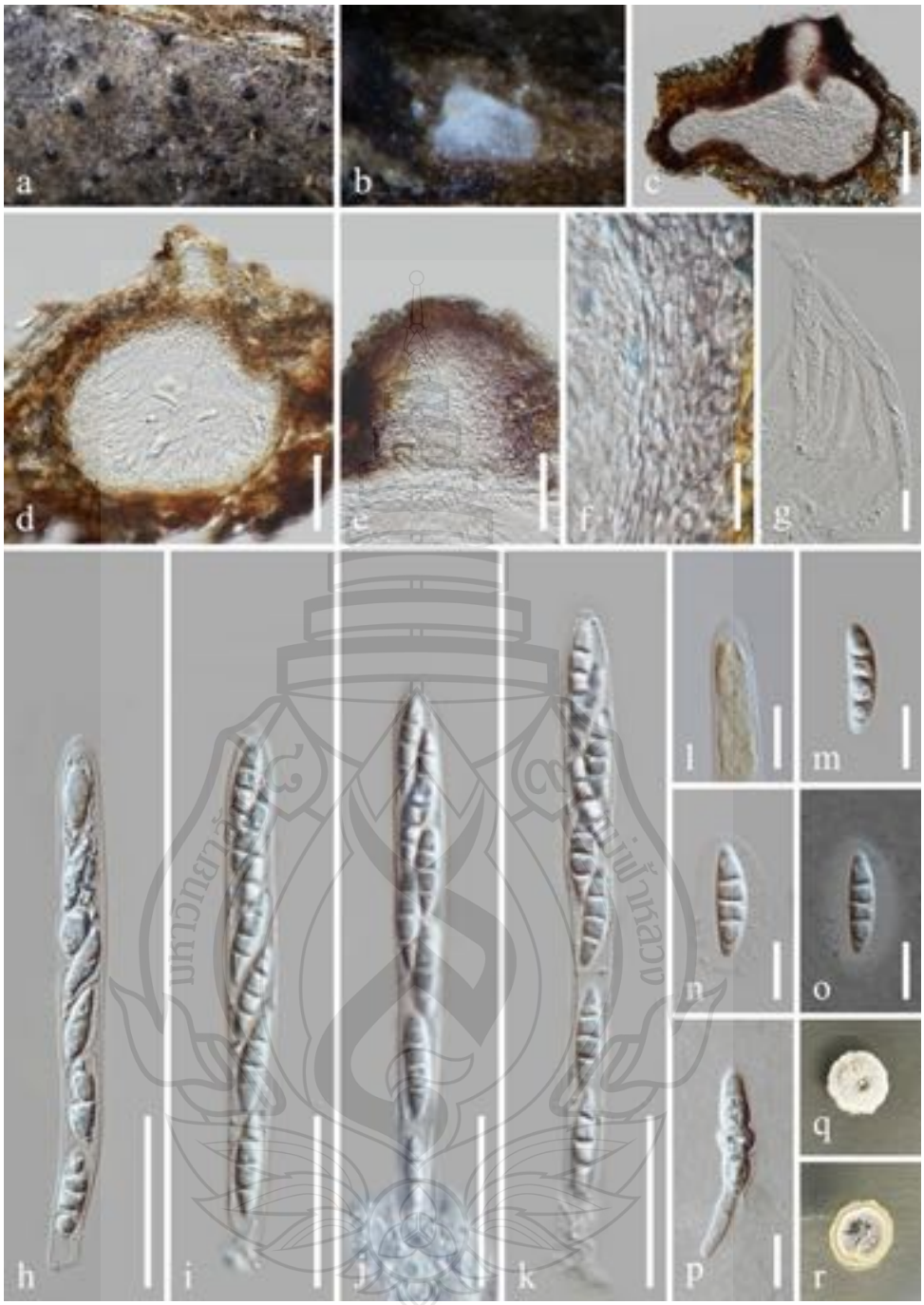
apically obtuse, with a J− subapical ring at apex. *Ascospores* 16–20 × 4–5.5 µm ($\bar{x}$ = 18 × 4.6 µm; n = 30), uniseriate or overlapping biseriate, narrowly fusiform with obtuse ends, hyaline, 3-septate, not constricted at the septa, end cells often slightly longer, straight to slightly curved, guttulate when young, verrucose when old, smooth-walled, surrounded by a 4–9 µm wide mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, off-white or grayish green and central light-colored, stiff, brittle, from the side view, raised or convex; in reverse, smoke-gray to grayish white in the center, yellowish towards the margin.

Materials examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL14 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″ E, on dead branches of *R. roxburghii*, 4 February 2023, N. Wu, ML132 (HUEST XX, paratype), living culture UESTCC XX; *ibid.*, Bijie City, Dafang County, Wenge Town, Anqing Village, elevation 1496 m, 27°8′60″ N, 105°25′48″ E, on dead branches of *R. roxburghii*, 2 February 2023, N. Wu, ML156 (HUEST XX), living culture UESTCC XX; *ibid.*, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *R. roxburghii*, 3 February 2023, N. Wu, ML108 (HUEST XX), living culture UESTCC XX; *ibid.*, ML124 (HUEST XX), living culture UESTCC XX.

Notes – *Pseudoneodictyosporium rosae* is a sexual morph species, which was collected from *Rosa roxburghii* in Guizhou and Sichuan Provinces, China. Based on a blast search of ITS sequence of *Pse. rosae* the closest hit in NCBI GenBank, is *Amphisphaeria qujingensis* (≡ *Lepteutypa qujingensis*) (KUMCC 19-0187, Query cover 74%, identities 89.67%); the closest hits based on LSU sequence is

Amphisphaeria curvaticonidia (MFLU 18-0789, Query cover 94%, identities 92.57%); the closest hits based on *rpb2* sequence is *Amphisphaeria* sp. (MC22-002, Query cover 94%, identities 81.02%) and the closest hits based on *tub2* sequence is *Amphisphaeria camelliae* (MFLU 20-0181, Query cover 87%, identities 82.84%). The multi-gene phylogenetic result showed that *Pse*. *rosae* (CGMCC SL14, UESTCC ML132, UESTCC ML156, UESTCC ML108 and UESTCC ML124) formed a distinct well-supported clade within Amphisphaeriales (Figure 3.103). Morphology of *Pse*. *rosae* resembles *Neodictyosporium bambusae* in having hyaline, 3-septate, fusiform ascospores with a mucilaginous sheath (Yu et al., 2024). Nevertheless, *Pse*. *rosae* differs from the latter in its larger ascomata (265–360 × 125–345 μm vs. 110–190 × 100–200 μm) and longer ascospores (16–20 × 4–5.5 μm vs. 13.5–16.5 × 4.5–5.5 μm). I therefore identify *Pse*. *rosae* as a new species and introduce *Pseudoneodictyosporium* to accommodate it.



Note a Appearance of ascomata on host surface. b–d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l Ascus apex with a J− subapical ring. m Ascospore. n, o Ascospores stained with Indian ink. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: c = 100 µm; d, e = 50 µm; h–k = 30 µm; f, g, l–p = 10 µm.

Figure 3.102 *Pseudoneodictyosporium rosae* (HKAS SL14, holotype)

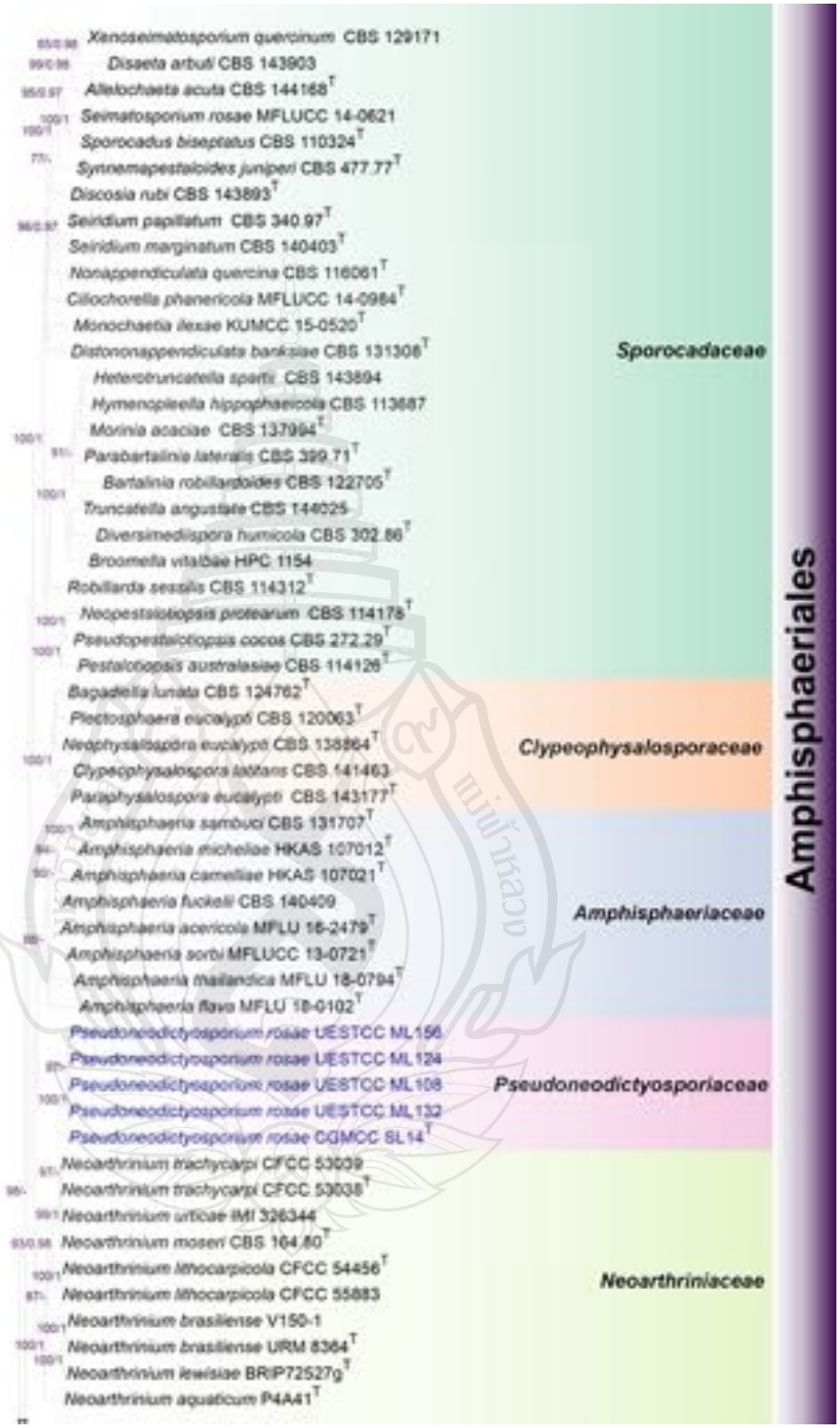


Figure 3.103 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tub2* sequence data of Amphisphaeriales

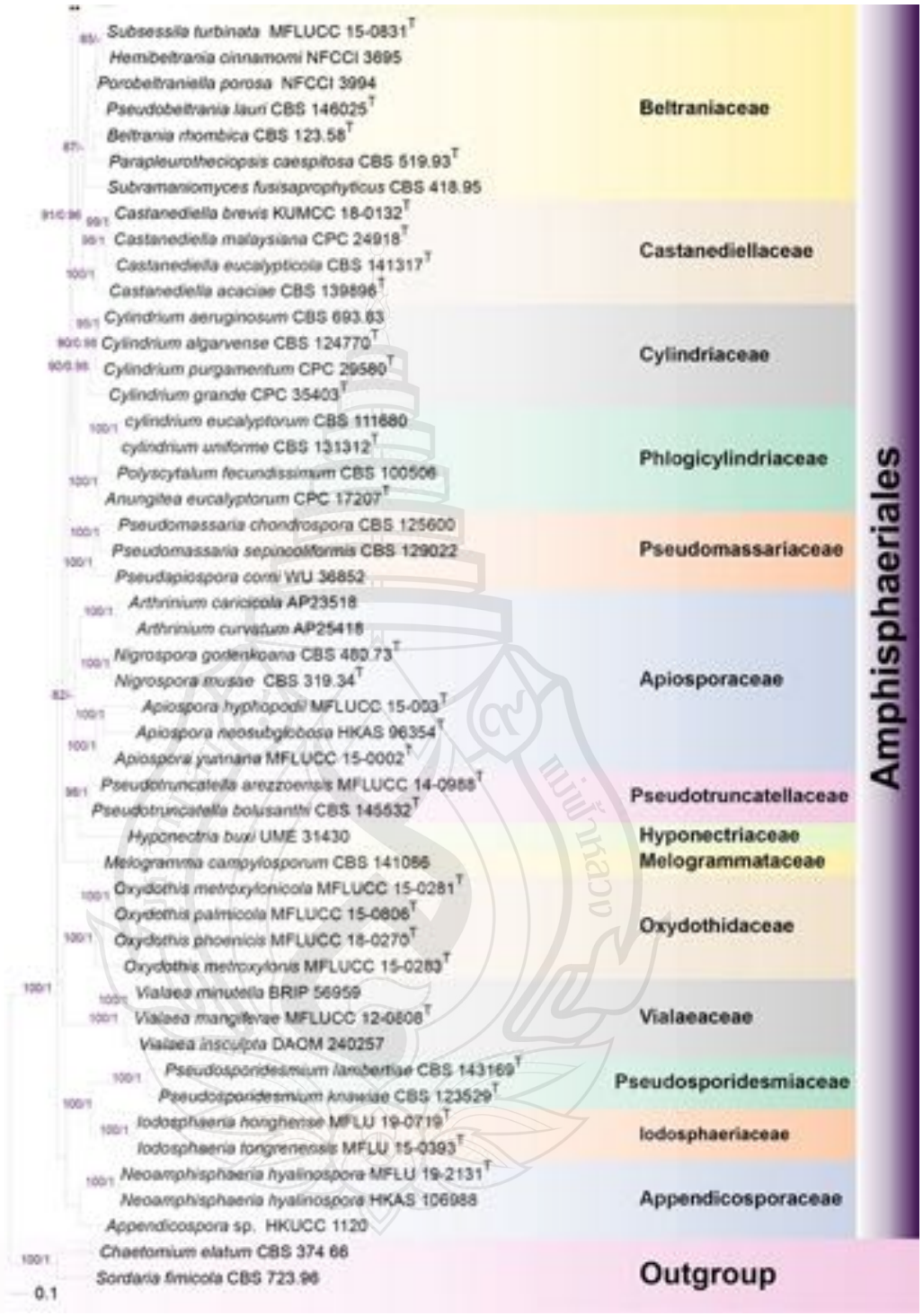


Figure 3.103 (continued)

Figure 3.103 The tree is rooted with *Chaetomium elatum* CBS 374.66) and *Sordaria fimicola* (CBS 723.96). Bootstrap values for maximum likelihood (ML) equal to

or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "[T]" after the strain number.

Sporocadaceae Corda [as 'Sporocadeae']

Type genus – *Sporocadus* Corda

Notes – Corda (1842) introduced Sporocadaceae with *Sporocadus* as the type genus. Sporocadaceae comprises saprobic, endophytic and pathogenic fungi on stems or branches from various hosts (Tanaka et al., 2011; Maharachchikumbura et al., 2016; Hyde et al., 2020b). Currently, 35 genera are accepted in Sporocadaceae (Hyde et al., 2024).

Discosia Lib. ex Durieu & Mont., Fl. d'Algérie, Cryptog. 1(15): 587 (1849) [1846-49]

Type species – *Discosia artocreas* (Tode) Fr.

Notes – *Discosia* was introduced by Libert (1837) although no type species was originally designated. *Discosia strobilina* was later selected as the lectotype of the genus (Subramanian & Reddy, 1974; Nag Raj, 1993; Tanaka et al., 2011). However, *Sphaeria artocreas* was transferred to the genus *Discosia* and recombined as *D. artocreas*, which was later designated as the lectotype of the genus (Fries, 1849; Vanev, 1991). The type species, *D. artocreas*, along with *D. neofraxinea*, *D. pini* and *D. pseudopleurochaeta* were initially placed in Discosiaceae (Senanayake et al., 2015), but later synonymized under Sporocadaceae based on nomenclatural priority and supported by DNA sequence analyses (Bundhun et al., 2021; Hyde et al., 2024). Sexual morphs are known for *D. ascidiata*, *D. tricellularis* (≡ *Discostroma tricellulare*), *D. yakushimensis* and *D. kaki*, all of which are characterized by immersed to semi-immersed, subglobose ascomata, unitunicate, cylindrical asci with a J+ or J- subapical ring, and fusiform, septate, guttulate, hyaline ascospores (Okane et al., 1996; Tanaka et al., 2011; Yamamoto et al., 2012; Liu et al., 2019; Razaghi et al., 2024). Asexual morph of this genus generally comprises coelomycetous species, which are characterized by semi-immersed to superficial conidiomata, holoblastic,

phialidic, subcylindrical conidiogenous cells, and hyaline to yellowish, septate, verrucose, cylindrical to subcylindrical conidia with filiform appendages at both ends (Li et al., 2015; Jiang et al., 2021a; Razaghi et al., 2024).

Discosia castaneae C.M. Tian & N. Jiang, J. Fungi 7(1, no. 64): 15 (2021) Figure 3.104

Index Fungorum number: IF837794; Facesoffungi number: FoFXX

Synonym – *Discosia celtidis* Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity 108: 108 (2021)

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 180–250 μm wide, 95–190 μm high, pycnidial, solitary to gregarious, semi-immersed to superficial, black, shiny, conical or trapezoid, base flattened, unilocular or multilocular, with locules separated by cells of *textura porrecta*, glabrous, coriaceous to carbonaceous, short papillate, ostiolate. *Ostiole* 18–28 μm wide, 30–40 μm high, single, central, cylindrical, straight. *Conidiomatal wall* composed of several layers of small, flattened, dark brown to black pseudoparenchymatous cells, thicker at the base, 20–40 μm wide, cells towards the inside light brown, arranged in a *textura angularis*, fusing and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–9.5 × 1.5–3.5 μm ($\bar{x}$ = 6 × 2.2 μm; n = 20), holoblastic, phialidic, subcylindrical, ampulliform, integrated, smooth-walled. *Conidia* 15.5–21.5 × 2.4–3.2 μm ($\bar{x}$ = 19.5 × 2.7 μm; n = 50), cylindrical to subcylindrical, straight or slightly curved, verrucose, smooth-walled, 3-septate, not constricted at the septa, hyaline to pale brown, basal cell obconic, with a truncate base; 2 median cells subcylindrical, second cell adjacent to the base 5.5–9 μm ($\bar{x}$ = 7.5 μm) long, the third cell adjacent to the apex 4–5.5 μm ($\bar{x}$ = 4.7 μm) long; apical cell subconical with a rounded apex; apical and basal cells each with a subapical and suprabasal, unbranched, filiform, flexuous or straight appendage, 8–15 μm.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from the basal cells. Colonies on PDA medium reaching 38–40 mm

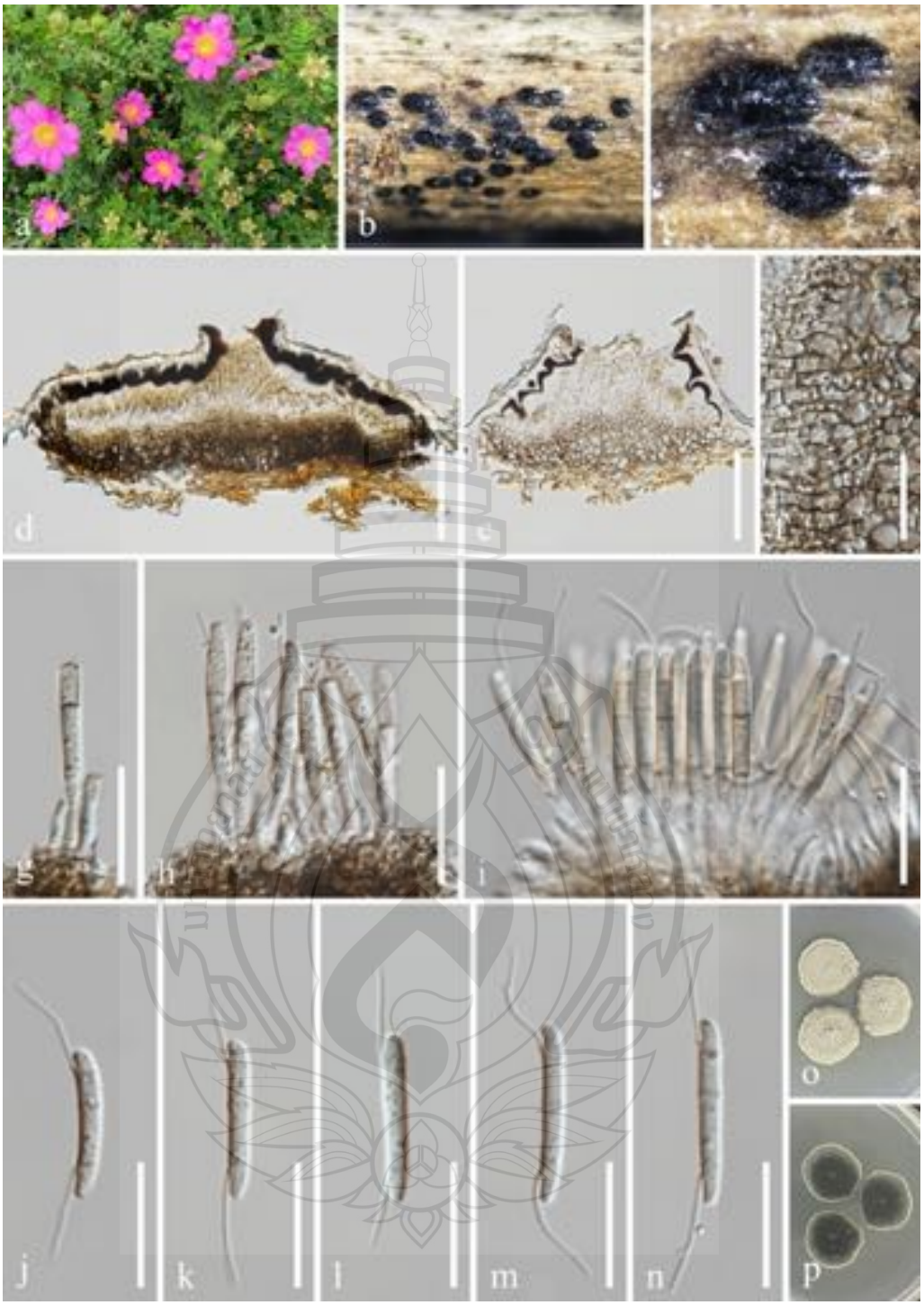
diam. after two weeks at 25°C in dark, circular, cottony, umbonate, velvety, dense, grayish green; in reverse, olive-green to dark brown with an entire margin.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML93 (HUEST XX), living culture UESTCC XX.

Hosts – *Castanea mollissima* (Jiang et al., 2021a), *Celtis formosana* (Tennakoon et al., 2021a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – In the phylogenetic analysis, my collection (UESTCC ML93) clustered with *Discosia castaneae* isolate (CFCC 54088) (Figure 3.105). Morphologically, my collection shares similar characteristics with the holotype, such as erumpent, globose to subglobose, solitary or gregarious conidiomata, holoblastic to phialidic, ampulliform conidiogenous cells, and cylindrical, 3-septate, hyaline to pale brown conidia with filamentous appendage at the ends (Jiang et al., 2021a). However, my collection has larger conidiomata (180–250 × 95–190 μm vs. 100–170 × 20–40 μm) and slightly longer conidia (15.5–21.5 × 2.4–3.2 μm vs. 14.1–18.7 × 2.9–3.9 μm). Based on morpho-molecular evidence, I conclude that my collection represents a new host record on *Rosa roxburghii* in China. Tennakoon et al. (2021a) introduced *D. celtidis* as a new species of *Discosia*, based on isolates MFLUCC 19-0058, NCYUCC 19-0101 and NCYUCC 19-0291. However, comparison of the ITS and LSU regions revealed no nucleotide differences between *D. celtidis* (MFLUCC 19-0058, NCYUCC 19-0101 and NCYUCC 19-0291) and *D. castaneae* (CFCC 54088, CFCC 54352 and CFCC 54584). According to my phylogenetic analysis, *D. celtidis* clusters with *D. castaneae* isolate (Figure 3.105). Therefore, I synonymize *D. celtidis* under *D. castaneae*.



Note a Host: *Rosa roxburghii*. b, c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j–n Conidia. o, p Colony on PDA, above (o), below (p). Scale bars: d, e = 50 μm; f–n = 15 μm.

Figure 3.104 *Discosia castaneae* (HUEST ML93, new host record)

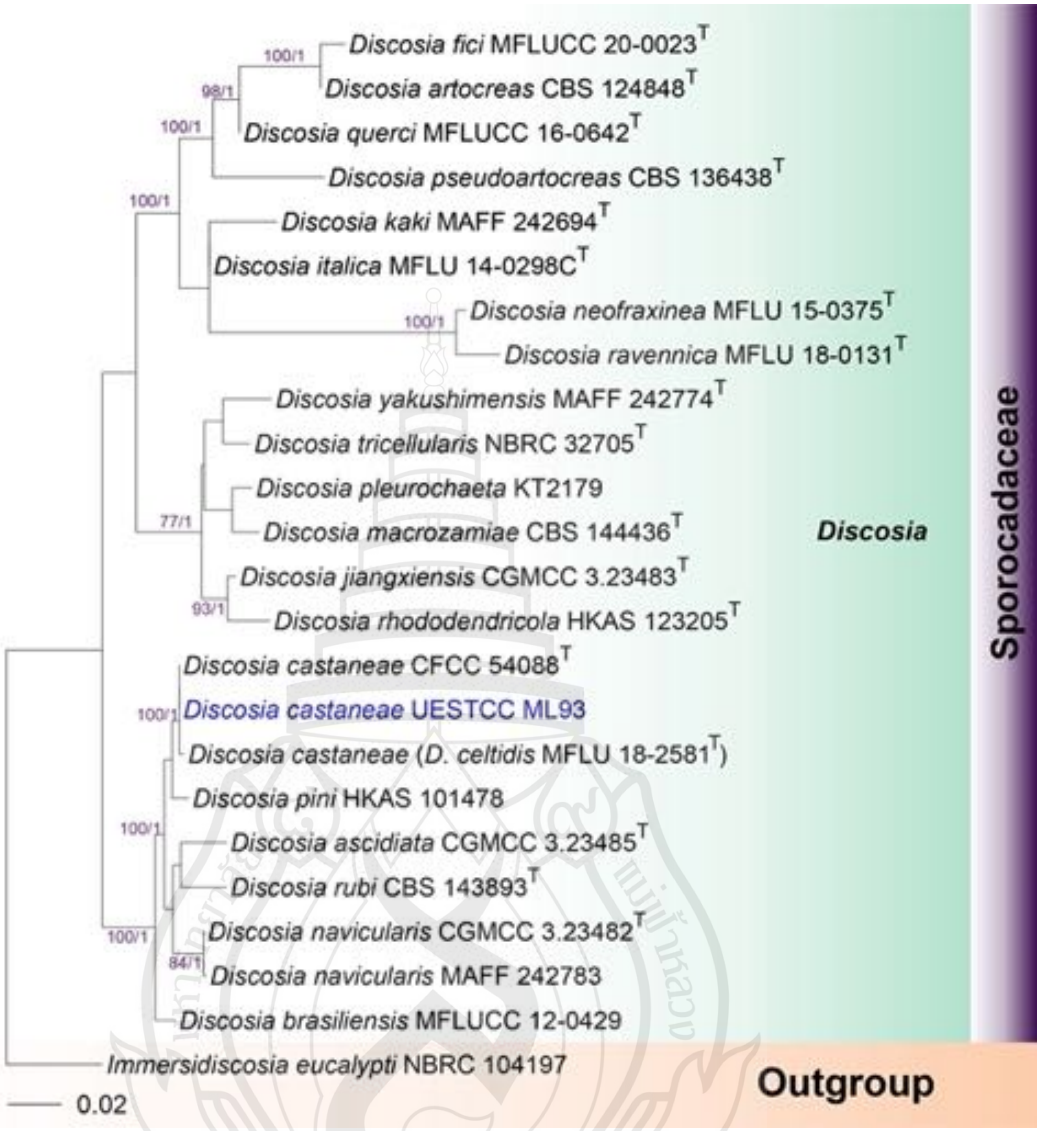


Figure 3.105 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α*, *rpb2* and *tub2* sequence data of *Discosia*

Figure 3.105 The tree is rooted with *Immersidiscosia eucalypti* (NBRC 104197). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Type genus – *Chaetosphaeria* Tul. & C. Tul.

Notes – The family Chaetosphaeriaceae was proposed by Locquin (1984) and formally introduced by Réblová et al. (1999). Chaetosphaeriaceae is the largest family in Chaetosphaeriales, comprising 107 genera (Hyde et al., 2024), some of which are polyphyletic, such as *Chaetosphaeria*, *Codinaea*, *Dictyochaeta* and *Tainosphaeria* (Réblová et al., 2020, 2021a, 2021b, 2021c; Wu & Diao, 2022). In the present study, I identified one new species, *Chaetosphaeria rosae*, from *Rosa sterilis*, and isolated *Pseudodinemasporium fabiforme* and *Stilbochaeta sinensis* from *Rosa roxburghii*.

Pseudodinemasporium A. Hashim. & Kaz. Tanaka, Mycologia 107(2): 390 (2015)

Type species – *Pseudodinemasporium fabiforme* A. Hashim., G. Sato & Kaz. Tanaka

Notes – *Pseudodinemasporium* was introduced by Hashimoto et al. (2015) with *P. fabiforme* as the type species. It is represented by a coelomycetous asexual morph collected from *Betula platyphylla*. Two more species were subsequently accepted in this genus, *P. elegans* and *P. minimum* (Wu & Diao, 2022). *Pseudodinemasporium* is a monophyletic genus that resembles *Dinemasporium* in producing setose conidiomata and hyaline, aseptate, smooth-walled, ovoid to reniform conidia with a single setula at each end.

Pseudodinemasporium fabiforme A. Hashim., G. Sato & Kaz. Tanaka, Mycologia 107(2): 390 (2015) Figure 3.106

Index Fungorum number: IF808708; Facesoffungi number: FoFxx

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 150–200 µm wide, 105–130 µm high, stromatic, acervular, cupulate, solitary to gregarious, superficial, globose or ellipsoid, dark brown to black, with white to orange conidial mass in center, setose. *Setae* 220–300 mm long, 7–8 mm wide, arising from outer elements of excipulum,

septate, brown, unbranched, smooth, thick-walled. *Conidiomatal wall* 25–45 μm wide, composed of a basal stroma of *textura angularis* with thick-walled, pale brown to hyaline cells; and a well-developed excipulum of *textura porrecta* with dark brown to hyaline cells. *Conidiophores* 13–19 mm long, 1.5–2.5 mm wide, lining the basal stroma, cylindrical, septate, smooth, hyaline, branched. *Conidiogenous cells* 8–14 × 1.2–2 μm ($\bar{x}$ = 10.3 × 1.5 μm; n = 30), phialidic, cylindrical, hyaline, smooth. *Conidia* 4–5.2 × 1.5–2 μm ($\bar{x}$ = 4.6 × 1.8 μm; n = 30), hyaline, aseptate, smooth-walled, ovoid to reniform, obtuse at the apex, slightly truncate at the base, with an unbranched appendage at each end, 1.5–3 μm long.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, flat, filamentous, creamy-white; in reverse, central yellowish white.

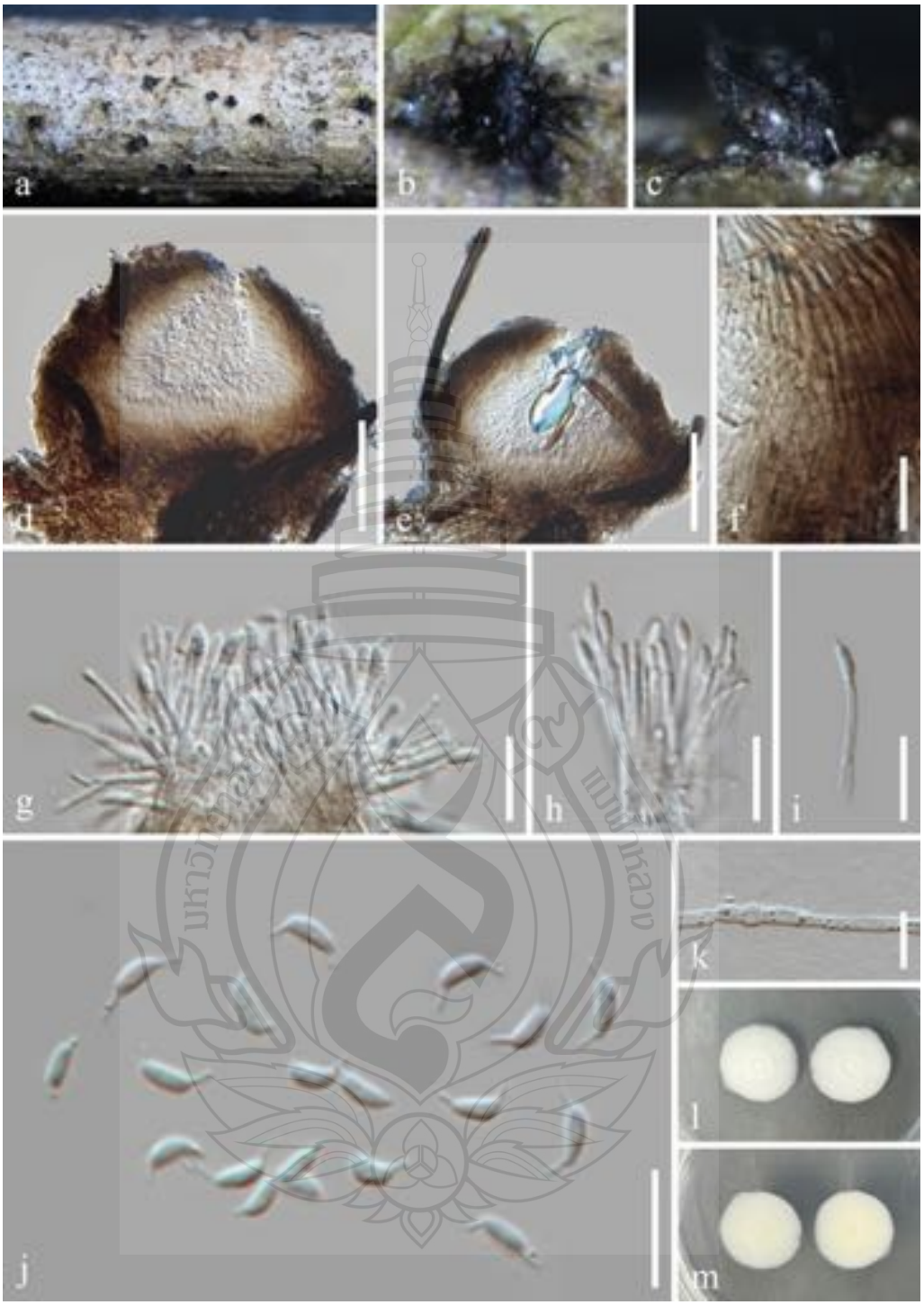
Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL58 (HUEST XX), living culture UESTCC XX.

Hosts – *Acacia mangium* (Crous et al., 2015b), *Betula platyphylla* (Hashimoto et al., 2015), *Rosa roxburghii* (present study).

Known geographical distribution – China, Japan, Malaysia.

Notes – *Pseudodinemasporium fabiforme* was introduced by Hashimoto et al. (2015) based on a specimen collected from dead twigs of *Betula platyphylla* in Japan. Subsequently, Crous et al. (2015b) recollected and described it in Malaysia, where it was found on leaves of *Acacia mangium*. I recognize my collection (HUEST SL58) as *P. fabiforme* as it clustered with *P. fabiforme* (CBS 140010) in a multi-gene phylogeny (Figure 3.107). *Pseudodinemasporium fabiforme* is characterized by superficial, cupulate, dark brown to black, globose or ellipsoid conidiomata, with a white to orange conidial mass in center, brown setae arising from the excipulum, and phialidic, cylindrical conidiogenous cells, and hyaline, reniform conidia, bearing an appendage

at each end (Crous et al., 2015b; Hashimoto et al., 2015). My collection morphologically fits well with *P. fabiforme*, and the dimensions of conidia (115–150 × 10–12 μm vs. 130–140 × 11–13 μm) are also comparable with the type (Hashimoto et al., 2015). Therefore, a new host (*Rosa roxburghii*) and geographical record (China) for *P. fabiforme* is provided in the present study.



Note a–c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and developing conidia. j Conidia. k Germinating conidium. l, m Colony on PDA, above (l), below (m). Scale bars: d, e = 50 μm; f–k = 10 μm.

Figure 3.106 *Pseudodinemasporium fabiforme* (HUEST SL58, new host record)

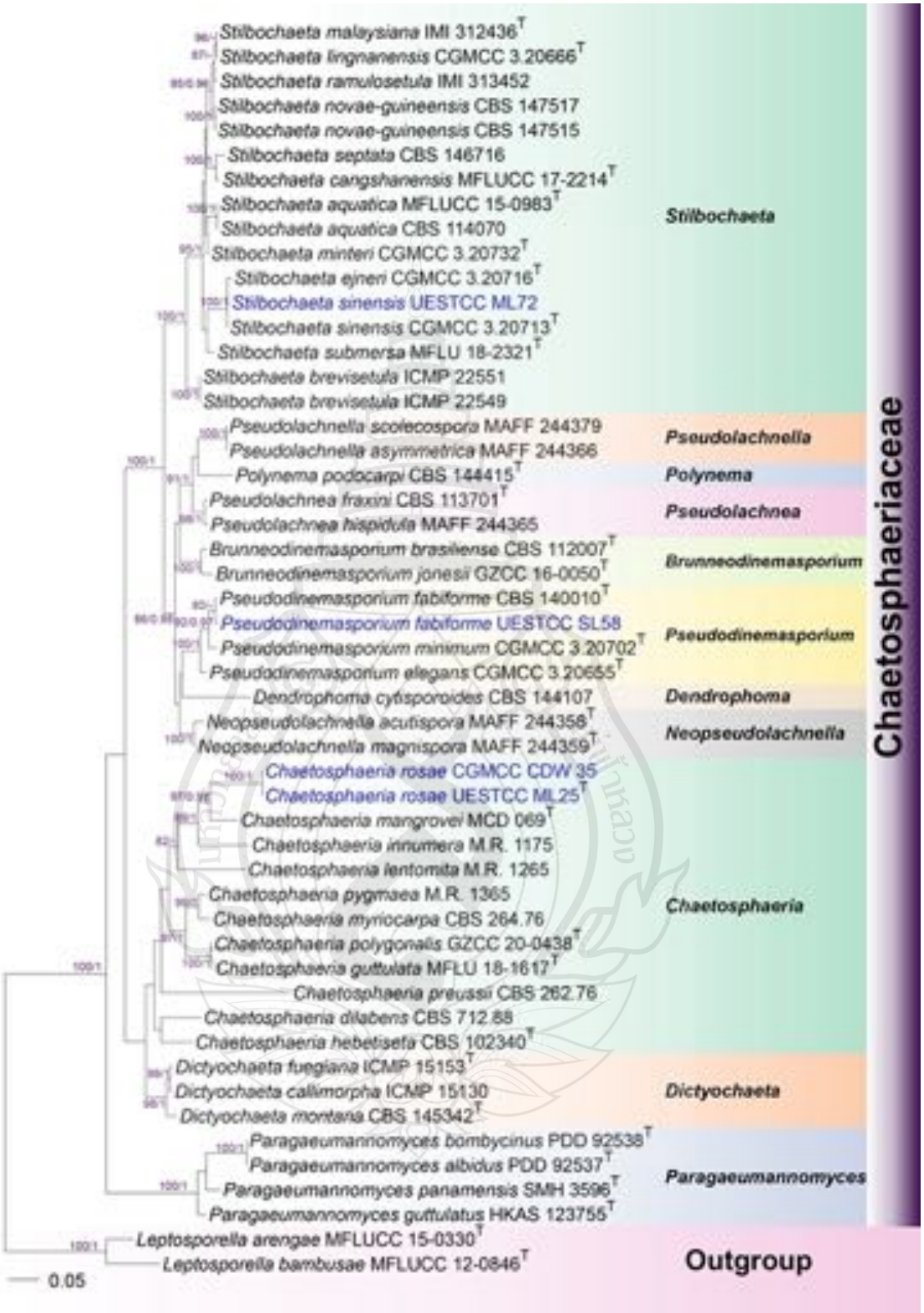


Figure 3.107 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of Chaetosphaeriaceae

Figure 3.107 The tree is rooted with *Leptosporella arengae* (MFLUCC 15-0330) and *L. bambusae* (MFLUCC 12-0846). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Stilbochaeta Réblová & Hern.-Restr., J. Fungi 7(12, no. 1097): 68 (2021)

Type species – *Stilbochaeta malaysiana* (Kuthub.) Réblová & Hern.-Restr.

Notes – Based on molecular evidence and morphological differences, Réblová et al. (2021a) introduced *Stilbochaeta* to accommodate eight new combinations that were initially identified as *Codinaea novae-guineensis*, *C. septata*, *Dictyochaeta aquatica*, *D. brevisetula*, *D. cangshanensis*, *D. malaysiana*, *D. ramulosetula* and *D. submersa*. Subsequently, Wu and Diao (2022) reviewed the genus and added one new combination and three new species, viz., *S. ejneri*, *S. jianfenglingensis* (≡ *C. jianfenglingensis*), *S. minteri* and *S. sinensis*. Additionally, they provided a key to the accepted *Stilbochaeta* species and to other known *Codinaea* and *Dictyochaeta* species that might belong to *Stilbochaeta*. *Stilbochaeta* is a holomorphic genus characterized by dark brown, superficial, globose to subglobose ascomata, usually with sterile setae rounded at the apex, and unitunicate, shortly-stipitate, cylindrical-clavate asci, and fusiform, hyaline, septate ascospores without gelatinous sheath or appendages. The hyphomycetous asexual morphs are charactered by brown, septate, unbranched, sterile setae in fascicles with brown, septate, unbranched conidiophore, and mono- or polyphialidic conidiogenous cells with funnel-shaped collarettes and hyaline, falcate, oblong to falcate, ellipsoidal to fusiform, septate conidia with a setula at both ends (Réblová et al., 2021a; Wu & Diao, 2022).

Stilbochaeta sinensis W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 204 (2022) Figure 3.108

Index Fungorum number: IF841589; Facesoffungi number: FoFxx

Saprobic on decaying branches of *Rosa roxburghii*. Asexual morph: Hyphomycetous. *Colonies* on natural substrates effuse, hairy, brown, with glistening conidial masses at apex. *Mycelium* partly superficial, partly immersed, composed of septate, smooth, brown hyphae. *Setae* 88–150 × 4.2–6 μm ($\bar{x}$ = 125 × 5 μm; n = 10), sterile, erect, arising mostly single, straight, or slightly flexuous, cylindrical, smooth-walled, 6–8-septate, thick-walled, dark brown at the base, paler towards the apex, apex swollen and rounded. *Conidiophores* 43–86 × 3.2–5.5 μm ($\bar{x}$ = 60.5 × 4 μm; n = 10), macronematous, straight, or slightly flexuous, cylindrical, smooth-walled, 2–5-septate, unbranched, brown at the base, pale brown to hyaline towards the apex, paler than setae, 4–6 around the base of 1–2 setae. *Conidiogenous cells* 19.5–44 × 3.5–5 μm ($\bar{x}$ = 30 × 4 μm; n = 10), integrated, terminal, monophialidic, cylindrical, pale brown or subhyaline, thin-walled, extending sympodially, with a funnel-shaped collarette 3.5–5 μm wide, 3–5 μm high. *Conidia* 18–21 × 3–3.5 μm ($\bar{x}$ = 19.5 × 3.3 μm; n = 10), holoblastic, acrogenous, solitary, formed in droplet surrounding the tips of conidiogenous cells, falcate to lunate, slightly curved, 1-septate, hyaline, thin-walled, smooth, apex obtuse, base slightly truncate to obtuse, guttulate, with a 7.5–9.5 μm long filiform appendage at both ends. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, irregular, producing brown pigment, velvety, white, sparse mycelium on surface initially, becoming dense, gray from middle to the edge with age; in reverse, dark brown to brown with white undulate margin.

Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on

branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML72 (HUEST XX), living culture UESTCC XX.

Hosts – *Cyclobalanopsis* sp. and *Eucalyptus* sp. (Wu and Diao 2022), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Stilbochaeta ejneri*, *S. jianfenglingensis* (≡*Codinaea jianfenglingensis*), *S. minteri* and *S. sinensis* were recently introduced into the genus *Stilbochaeta* by Wu and Diao (2022). In the phylogenetic tree constructed by Wu and Diao (2022), based on ITS and LSU gene regions, showed that the type strain of *S. ejneri* was nested among four *S. sinensis* strains, and these two species formed a sister clade to the monotypic genus *Falholtia*. I compared the nucleotide differences between *S. ejneri* and *S. sinensis* and found only 1.3% (6/458 bp) nucleotide differences in the ITS gene region. The LSU sequence is unavailable for *S. sinensis*. According to the recommendations of Jeewon and Hyde (2016), such difference is insufficient to delineate them as separate species. However, they exhibit significant morphological differences. *Stilbochaeta sinensis* is characterized by brown, septate, unbranched, cylindrical sterile setae that are hyaline towards the apex, which is swollen and rounded. Its conidiophores are pale brown, becoming hyaline towards the apex, septate, unbranched, and mono- or polyphialidic, cylindrical conidiogenous cells with funnel-shaped collarettes, and hyaline, falcate, slightly curved, 1-septate conidia with a setula at both ends. In contrast, *S. ejneri* lacks setae, has longer (180–285 × 4–7 μm vs. 30–60 × 3–4 μm), 10–14-septate conidiopores (vs. 2–3-septate in *S. sinensis*), and larger conidia (30–32 × 4–4.5 μm vs. 13–17 × 2–2.5 μm) with longer setulae (5–12.5 μm vs. 4–8 μm). Following Wu and Diao (2022), I continue to treat *S. ejneri* and *S. sinensis* as distinct species until further collections and protein-coding genes confirm their relationship. In the present study, my collection (UESTCC ML72) clustered with *S. ejneri* and *S. sinensis* (Figure 3.107). However, based on morphology, it more closely resembles *S. sinensis* than *S. ejneri*, as my collection has sterile setae and hyaline, falcate, slightly curved, 1-septate conidia with

a setula at both ends. The ITS sequences of my collection differ by eight base pairs (450/458 bp) from *S. ejneri* (CGMCC 3.20716, ex-type) and by three base pair (455/458 bp) from *S. sinensis* (CGMCC 3.20713, ex-type). Therefore, I identify my collection as *S. sinensis*, representing a new host record.



Note a Host: *Rosa roxburghii*. b, c Colonies on substrate surface. d–f Conidiophores, sterile setae and conidiogenous cells. g, h Conidiogenous cells with conidia. i–k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: d = 50 μm; e, f, l = 20 μm; g–k = 10 μm.

Figure 3.108 *Stilbochaeta sinensis* (HUEST ML72, new host record)

Diaporthales Nannf.

Cytosporaceae Fr. [as '*Cytisporei*'], Syst. orb. veg. (Lundae): 118 (1825)

Type genus – *Cytospora* Ehrenb.

Notes – Cytosporaceae was introduced by Fries (1825) but was later synonymized with Valsaceae, which was originally named "*Valsarum*" by Tulasne and Tulasne (1863). However, Cytosporaceae was recommended for use rather than Valsaceae based on its priority (Fan et al., 2015a, b, Rossman et al., 2015). Currently, the family comprises *Cryptascoma*, *Cytospora*, *Pachytrype*, *Paravalsa*, *Waydora* and *Xenotypa*, of which only *Cytospora*, *Pachytrype* and *Waydora* have molecular data available (Hyde et al., 2024; Lin et al., 2024).

Cytospora Ehrenb., Sylv. mycol. berol. (Berlin): 28 (1818)

Type species – *Cytospora chrysosperma* (Pers.) Fr.

Notes – *Cytospora* was established by Ehrenberg (1818) to accommodate four species, *C. betulina*, *C. epimyces*, *C. resinae* and *C. ribis*. Later, Donk (1964) designated the anamorphic species *C. chrysosperma* of *Valsa sordida* as the type species of the genus. Since *Cytospora* is the older name and should take priority, the four related sexual genera, *Leucostoma*, *Valsa*, *Valsella* and *Valseutypella*, were synonymized with *Cytospora* (Adams et al., 2005; Fan et al., 2015a, b; Rossman et al., 2015). Members of *Cytospora* are cosmopolitan and comprise saprobic, pathogenic, and endophytic species, which have been found across Africa, Asia, Europe, and South America (Adams et al., 2005; Wang et al., 2015; Lawrence et al., 2018; Fan et al., 2020; Zhu et al., 2020; Lin et al., 2024). Over 770 morphological species related to *Cytospora* are listed in Index Fungorum (2025, June), most of which were described in the nineteenth century and lack herbarium materials, ex-type cultures and DNA sequence data (Kirk et al., 2008). *Cytospora* is characterized by diaporthalean-like perithecia, clavate to obovoid asci with hyaline, aseptate, straight or slightly curved, smooth-walled, allantoid ascospores; the asexual morph produces single or labyrinthine pycnidial locules, branched at base, filamentous conidiophores, enteroblastic, phialidic,

cylindrical to subcylindrical conidiogenous cells and hyaline, aseptate, straight or slightly curved, guttulate, allantoid conidia (Adams et al., 2005; Zhu et al., 2020; Lin et al., 2024).

Cytospora rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.109

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

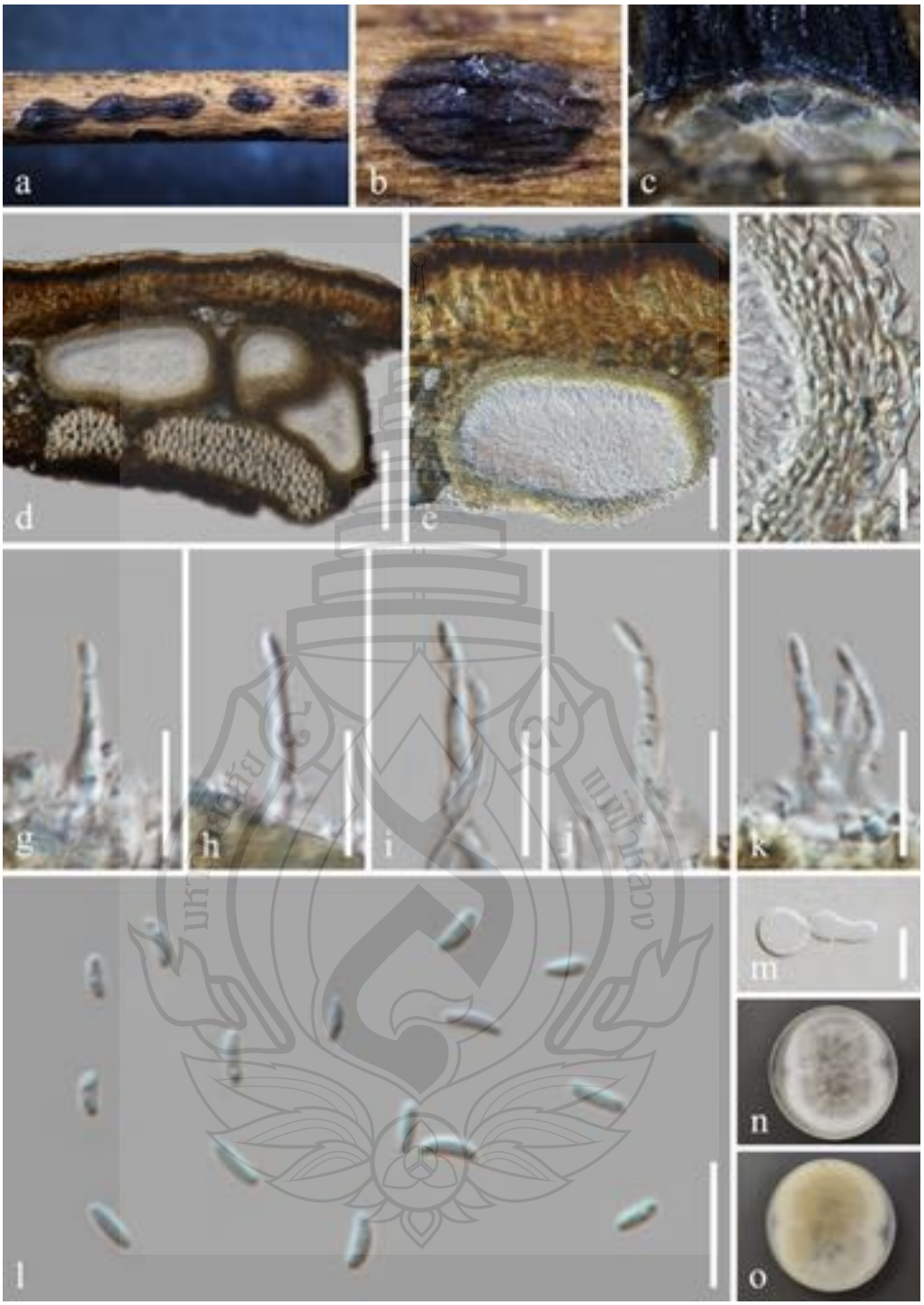
Holotype – HKAS GL45

Saprobic on dead branches of *Rosa sterilis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 850–950 μm wide, 160–260 μm high, eustromatic, pycnidial, immersed to erumpent, producing black area on bark, mostly solitary, occasionally gregarious, conical to subglobose, multilocular, with locules 120–240 μm diam., 120–225 μm high, circular to ovoid, separated by inner walls, but uniting in the ostiolar region, thick-walled, glabrous, ostiolate. *Ostiole* single, cylindrical, prominent, central. *Conidiomatal wall* 15–22 μm wide, composed of brown, thick-walled cells of *textura angularis* to *textura intricta* in outer layer, becoming hyaline towards conidial hymenium. *Conidiophores* arising from inner wall layer of locules, hyaline, straight or flexuous, cylindrical to subcylindrical, occasionally branched at base, smooth-walled. *Conidiogenous cells* 9–13 × 1.5–1.9 μm ($\bar{x}$ = 11 × 1.7 μm; n = 30), hyaline, enteroblastic, phialidic, determinate, smooth-walled, cylindrical to subcylindrical, tapering towards apices. *Conidia* 4.2–5 × 1.2–1.8 μm ($\bar{x}$ = 4.7 × 1.3 μm; n = 30), hyaline, cylindrical or allantoid, with obtuse ends, straight or curved, unicellular, smooth-walled, with small guttules near each end.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 35–37 mm diam. after two weeks at 25℃ in dark, circular, with sparse aerial mycelium, cottony, dense, white; in reverse, pale brown in central, off-white at the edge.

Material examined – CHINA, Guizhou Province, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL45 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – In the phylogenetic analysis, *Cytospora rosae* (CGMCC GL45) and *C. tamaricicola* (CFCC 50508) formed a sister clade (Figure 3.110). Morphologically, *C. rosae* is similar to *C. tamaricicola* in having branched conidiophores with phialidic conidiogenous cells, and hyaline, cylindrical or allantoid, obtuse ends, straight or curved, aseptate conidia with small guttules near each end (Fan et al., 2020). However, *C. rosae* has smaller conidia than *C. tamaricicola* (4.2–5 × 1.2–1.8 μm vs. (5–)5.5–6(–6.5) × 1–1.5 μm). The conidia of *C. rosae* usually have small guttules near each end, while those of *C. tamaricicola* rarely with guttules at each end. In addition, the ITS and *rpb2* sequences of *C. rosae* and *C. tamaricicola* showed 10 bp (485/495 bp) and 27 bp (709/727 bp) differences, respectively. Therefore, I introduce *C. rosae* as a new species.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–k Conidiogenous cells and developing conidia. l Conidia. m Germinating conidium. n, o Colony on PDA, above (n), below (o). Scale bars: d = 100 μm; e = 50 μm; f–m = 10 μm.

Figure 3.109 *Cytospora rosae* (HKAS GL45, holotype)

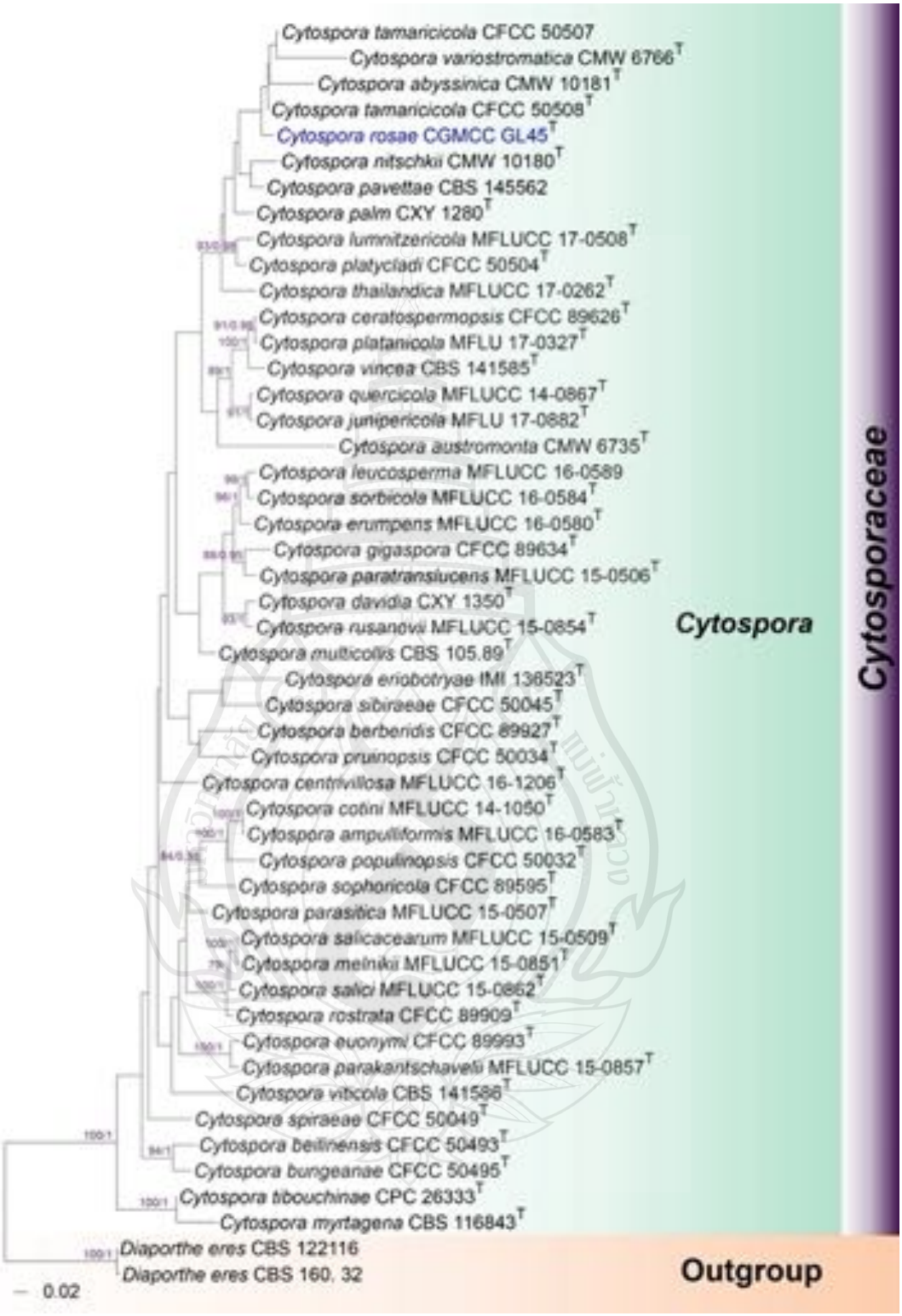


Figure 3.110 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, *tef1α* and *tub2* sequence data of *Cytospora*

Figure 3.110 The tree is rooted with *Diaporthe eres* (CBS 122116 and CBS 160.32). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

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

Distoseptisporaceae K.D. Hyde & McKenzie

Type genus – *Distoseptispora* K.D. Hyde, McKenzie & Maharachch.

Notes – Distoseptisporaceae is a monotypic family with *Distoseptispora* as the type genus (Su et al., 2016). In the present study, I recovered two sporidesmium-like taxa from *Rosa roxburghii*, which represent new host records for *D. alangii* and *D. sinensis*.

Distoseptispora K.D. Hyde, McKenzie & Maharachch., Fungal Diversity 80: 402 (2016)

Type species – *Distoseptispora fluminicola* McKenzie, Hong Y. Su, Z.L. Luo & K.D. Hyde

Notes – Su et al. (2016) established *Distoseptispora* with *D. fluminicola* as the type species, which was one of the sporidesmium-like genera. In recent years, the generic circumscription has undergone continuous revisions with the frequent introduction of new members into the genus. *Distoseptispora* was initially introduced based on hyphomycetous asexual morphs until Yang et al. (2021a) recognized a new species, *D. hyaline*, and provided the first description of a sexual morph for the genus based on molecular DNA data. Subsequently, two species, *D. bambusae* and *D. licualae*, were described from their sexual morphs (Konta et al., 2023; Sun et al., 2025). There are 94 epithets listed in Index Fungorum (2025, June). Liu et al. (2023a) and Liao et al. (2024) sequentially listed a total of 87 recognized *Distoseptispora* species, providing their major morphological features, habitat, host, and distribution. Members of this

genus are known as saprobes from freshwater and terrestrial habitats, and characterized by immersed to semi-immersed, subglobose to ellipsoidal ascomata, septate, branched paraphyses, unitunicate, 8-spored, short pedicellate, cylindrical asci with hyaline, 0–3-septate, smooth-walled, guttulate, thin-walled, fusiform ascospores, surrounded by a mucilaginous sheath; the asexual morphs are sporidesmium-like hyphomycetes (Xia et al., 2017; Luo et al., 2018b; Dong et al., 2021a).

Distoseptispora alangii H.Z. Du & Jian K. Liu, XX Figure 3.111

Index Fungorum number: IF855440; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse, hairy, scattered or in small groups, brown to dark brown. *Mycelium* partly superficial, partly immersed, composed of septate, branched, dark brown hyphae. *Conidiophores* 20–45 × 5–8.5 μm ($\bar{x}$ = 36 × 6.8 μm; n = 30), macronematous, mononematous, erect, solitary or in small groups, straight or flexuous, cylindrical, smooth-walled, septate, unbranched, brown to dark brown. *Conidiogenous cells* 5–10 × 4–6 μm ($\bar{x}$ = 8 × 5 μm; n = 30), monoblastic, integrated, terminal, determinate, cylindrical, brown to dark brown, truncated at the apex. *Conidia* 122–300 × 13–16.5 μm ($\bar{x}$ = 207 × 14.3 μm; n = 30), acrogenous, solitary, rostrate, cylindrical or obclavate, 20–35-distoseptate, verrucose, yellowish brown, pale brown at the apex, rounded at the apex and truncated at the base, straight or curved, thick-walled.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from the basal cell. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, cottony, grayish green; in reverse, dark brown with white entire margin.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL01 (HUEST XX), living culture UESTCC XX.

Hosts – *Alangium chinense* (Du et al., 2025), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Distoseptispora alangii* was introduced by Du et al. (2025) based on a specimen collected from dead twigs of medicinal plant *Alangium chinense* in China. My collection matches the type material of *D. alangii* in the morphology of conidiophores, conidiogenous cells and conidia, but shows minor differences in the sizes of conidiophores (15–30 × 5–9 μm vs. 20–45 × 5–8.5 μm), conidiogenous cells (4.5–7 × 4–5.5 μm vs. 5–10 × 4–6 μm) and conidia (122–367 × 10–15 μm vs. 122–300 × 13–16.5 μm). In the phylogenetic tree, my isolate (UESTCC SL01) was sister to the ex-type strain of *D. alangii* (HKAS 132478) with a strong support (Figure 3.112). The comparison of their ITS, LSU, *rpb2* and *tef1α* sequences showed 100% (490/490 bp), 97.56% (800/820 bp, 16 gaps), 99.54% (862/866 bp, 3 gaps) and 99.89% (907/908 bp) sequence similarities, respectively. Since, such differences are not enough to distinguish them as different species, I recognize my collection as *D. alangii* and provide a new host record. This is the second time this species has been collected in China, and the first host record from the medicinal plant *Rosa roxburghii*.



Note a Host: *Rosa roxburghii*. b, c Colonies on the host surface. d, g Conidiogenous cells with conidia. e Conidiophores with conidia. f, h, i, m–q Conidia. j Germinating conidium. k, l Colony on PDA, above (k), below (l). Scale bars: d–g = 30 μm; j, m–q = 50 μm.

Figure 3.111 *Distoseptispora alangii* (HUEST SL01, new host record)

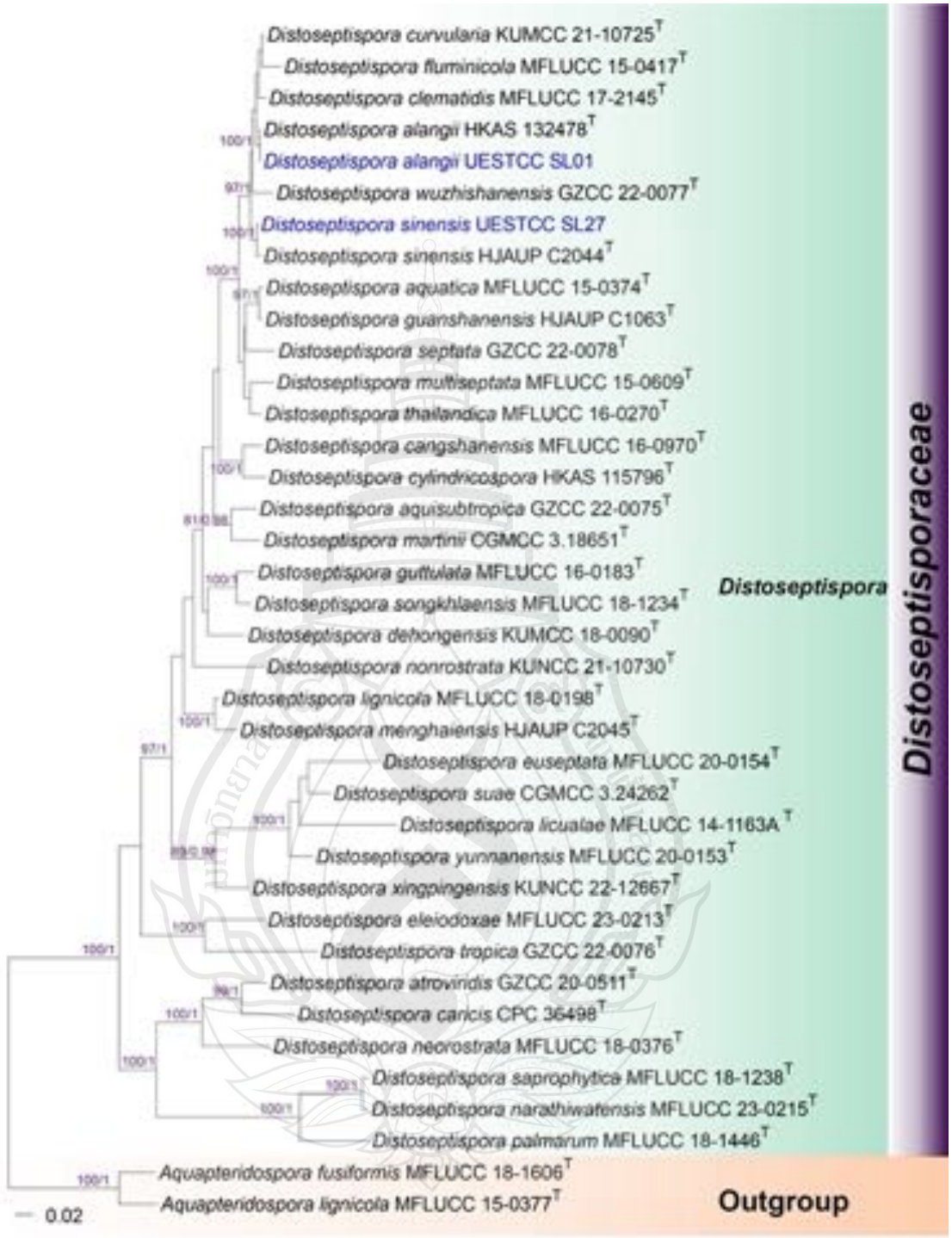


Figure 3.112 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2* and *tef1α* sequence data of *Distoseptispora*

Figure 3.112 The tree is rooted with *Aquapteridospora fusiformis* (MFLUCC 18-1606) and *A. lignicola* (MFLUCC 15-0377). Bootstrap values for maximum

likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Distoseptispora sinensis Jing W. Liu, X.G. Zhang & Jian Ma, J. Fungi 9(no. 470): 8 (2023) Figure 3.113

Index Fungorum number: IF900055; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse, hairy, scattered or in small groups, erect, brown to dark brown. *Mycelium* partly superficial, partly immersed, composed of septate, branched, dark brown hyphae. *Conidiophores* 40–76 × 5.8–7.8 μm ($\bar{x}$ = 57 × 6.9 μm; n = 30), macronematous, mononematous, cylindrical, 4–7-septate, unbranched, solitary, smooth, thick-walled, straight or slightly flexuous, brown to dark brown. *Conidiogenous cells* 8–12 × 5–7.8 μm ($\bar{x}$ = 10 × 6.5 μm; n = 30), monoblastic, integrated, terminal, determinate, cylindrical, brown to dark brown, truncated at the apex. *Conidial secession* schizolytic. *Conidia* 82–120 μm ($\bar{x}$ = 103 μm; n = 30) long (rostrum included), 13–17.5 μm ($\bar{x}$ = 15.3 μm; n = 30) wide at the widest part, 8–12 μm ($\bar{x}$ = 10 μm; n = 30), wide at middle part, acrogenous, solitary, rostrate, obclavate, elongated, 7–22-distoseptate, verrucose, dark brown, pale brown at the apex, straight or curved, thick-walled, rounded or truncated at the apex, truncated at the base, often with percurrent regeneration forming a secondary conidium from the conidial apex.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 38–40 mm diam. after two weeks at 25℃ in dark, circular, cottony, umbonate, velvety, dense, grayish green; in reverse, yellow mycelium in centre, olive-green to dark brown in the middle ring and white at the edge.

Material examined – CHINA, Sichuan Province, Chengdu City, Tianfu New Area, 30°41′26″ N, 103°48′13″ E, on dead branches of *Rosa roxburghii*, 19 January 2024, N. Wu, SL27 (HUEST XX), living culture UESTCC XX.

Hosts – An unidentified broadleaf tree (Liu et al., 2023a), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Based on a blast search of the ITS sequence of my isolate UESTCC SL27, the closest hits are *Distoseptispora sinensis* (HJAUP C2044, identities 99.44%) and *D. tectonae* (MFLUCC 12-0291, identities 98.89%). Among *Distoseptispora* species, my collection more closely resembles *D. mengsongensis* than *D. sinensis* in having brown to dark brown, multi-septate conidia that are sometimes constricted at the septa, especially in proximal parts, and often exhibiting percurrent regeneration, forming a secondary conidium from the conidial apex (Liu et al., 2023a). In the phylogenetic tree, my isolate (UESTCC SL27) was sister to the ex-type strain of *D. sinensis* (HJAUP C2044) with a strong support (Figure 3.112). The comparison of their ITS, LSU and *tef1α* sequences showed 99.44% (535/538 bp), 98.80% (576/583 bp, five gaps) and 99.25% (923/930 bp, two gaps) sequence similarities, respectively. I therefore recognize my collection as *D. sinensis* based on the molecular evidence. *Distoseptispora sinensis* was introduced by Liu et al. (2023a) based on a specimen collected from dead branches of an unidentified broadleaf tree in China. This study extends the known host range of *D. sinensis* to *Rosa roxburghii* and provides *rpb2* gene sequence data for the first time.



Note a Host: *Rosa roxburghii*. b, c Colonies on substrate surface. d–i Conidiophores with conidia. j–m Conidia. n, o Conidiogenous cells with conidia. p Germinating conidium. q, r Colony on PDA, above (q), below (r). Scale bars: d–i = 50 μm; j–p = 30 μm.

Figure 3.113 *Distoseptispora sinensis* (HUEST SL27, new host record)

Glomerellales Chadef. ex Réblová, W. Gams & Seifert

Reticulascaceae Réblová & W. Gams

Type genus – R*eticulascus* Réblová & W. Gams

Notes – The family was established by Réblová et al. (2011) based on multi-gene phylogeny to accommodate *Porosphaerellopsis* and *Reticulascus*. Additionally, the genera *Cylindrotrichum*, *Kylindria* and *Sporoschismopsis* are linked as asexual genera with the Reticulascaceae (Réblová et al., 2011; Maharachchikumbura et al., 2018).

Cylindrotrichum Bonord., Handb. Allgem. Mykol. (Stuttgart): 88 (1851)

Type species – *Cylindrotrichum oligospermum* (Corda) Bonord.

Notes – Members of *Cylindrotrichum* are usually found as hyphomycetous asexual morphs and characterized by macronematous, mononematous, cylindrical, brown conidiophores, monophialidic or polyphialidic conidiogenous cells and elongated, cuneiform, cylindrical, rounded at apex, obtuse at base, 0–3-septate, not constricted, guttulate and hyaline conidia (Hyde et al., 2016; Crous et al., 2022; Luo et al., 2019). There are 26 epithets in Index Fungorum (June 2025), but some species were transferred to other genera. Only seven species have available sequence data, including the taxon introduced in the present study. Among *Cylindrotrichum* species, *C. clavatus* and *C. tulasneorum* are sexual morphs, which were transferred from *Reticulascus* (Réblová et al., 2011; Luo et al., 2019). The sexual morphs are characterized by subglobose to conical ascomata, unitunicate, cylindrical-clavate, short-stipitate asci and ellipsoidal to fusiform, septate, hyaline ascospores (Réblová et al., 2011).

Cylindrotrichum rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.114

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML147

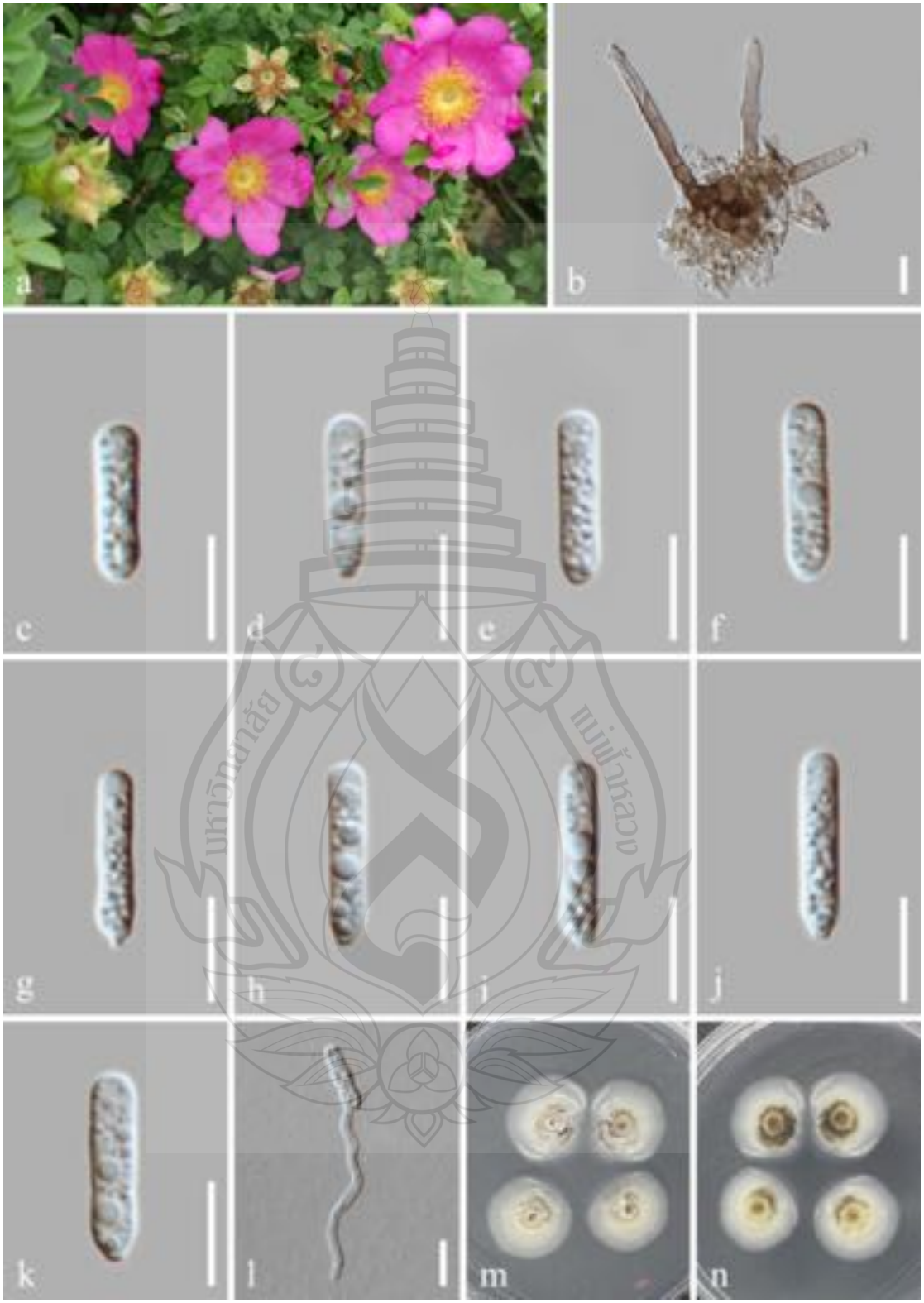
Saprobic on dead branches of *Rosa roxburghii*. Asexual morph: Hyphomycetous. *Colonies* on natural substrates effuse, hairy, scattered or in small groups, brown to dark brown. *Mycelium* mostly immersed and partly superficial, composed of septate, branched, pale brown to brown hyphae. *Conidiophores* 35–68 × 3–5 μm ($\bar{x}$ = 60 × 4 μm; n = 30), macronematous, mononematous, erect, cylindrical, straight or slightly flexuous, dark brown, paler towards the apex, 3–5-septate, unbranched, tapering distally, verrucose, thick-walled. *Conidiogenous cells* monophialidic, integrated, terminal, cylindrical, pale brown at the base and subhyaline above, smooth-walled. *Conidia* 15–18.5 × 3.5–4.5 μm ($\bar{x}$ = 17 × 3.7 μm; n = 30), acrogenous, hyaline, cylindrical or clavate, rounded at apex, narrowed towards the flattened base, guttulate, verrucose, aseptate, smooth-walled. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, with rough surface, pale brown in the middle, white at the edge; in reverse, dark brown in the middle and white with smooth margin.

Material examined – CHINA, Guizhou Province, Zunyi City, Bozhou District, Tuanxi Town, Ximashui Village, elevation 990.6 m, 27°27′36″ N, 107°4′12″ E, on dead branches of *Rosa roxburghii*, 2 February 2023, N. Wu, ML147 (HKAS XX, **holotype**); ex-type living culture CGMCC XX.

Notes – Based on a blast search of ITS sequence of *Cylindrotrichum rosae* in NCBI GenBank, the closest hits are *C. submersum* (MFLU 18-2320, Query cover 99%, identities 91.92%) and *C. aquaticum* (MFLUCC 15-0264, Query cover 100%, identities 91.46%). The multi-gene phylogenetic tree showed that *C. rosae* (CGMCC ML147) formed a sister branch to *C. aquaticum* (Figure 3.115), which was transferred from *Blastophorum* by Luo et al. (2019). *Cylindrotrichum rosae* shares similar conidiophores, conidiogenous cells and conidia morphology with *C. aquaticum* (Hyde et al., 2016; Luo

et al., 2019) and *C. submersum* (Luo et al., 2019). However, the conidiophores of *C. rosae* (35–68 × 3–5 µm) are shorter and narrower than *C. aquaticum* (190–250 × 6–8 µm) and *C. submersum* (77–135(–148) × 4–6 µm). Conidia of *C. rosae* are cylindrical or clavate, rounded at apex, narrowed towards the flattened base, guttulate, verrucose and aseptate; in contrast, conidia of *C. aquaticum* are elongated, cuneiform, 1–3-septate, rounded at the tip and narrowed towards the flattened base. In addition, *C. aquaticum* and *C. submersum* have been found in aquatic habitats, whereas *C. rosae* was collected from a terrestrial habitat. I therefore identify *C. rosae* as a new species based on morphology and available molecular data.



Note a Host: *Rosa roxburghii*. b Conidiophores. c–k Conidia. l Germinating conidium. m, n Colony on PDA, above (m), below (n). Scale bars: b–l = 10 μm.

Figure 3. 114 *Cylindrotrichum rosae* (HKAS ML147, holotype)

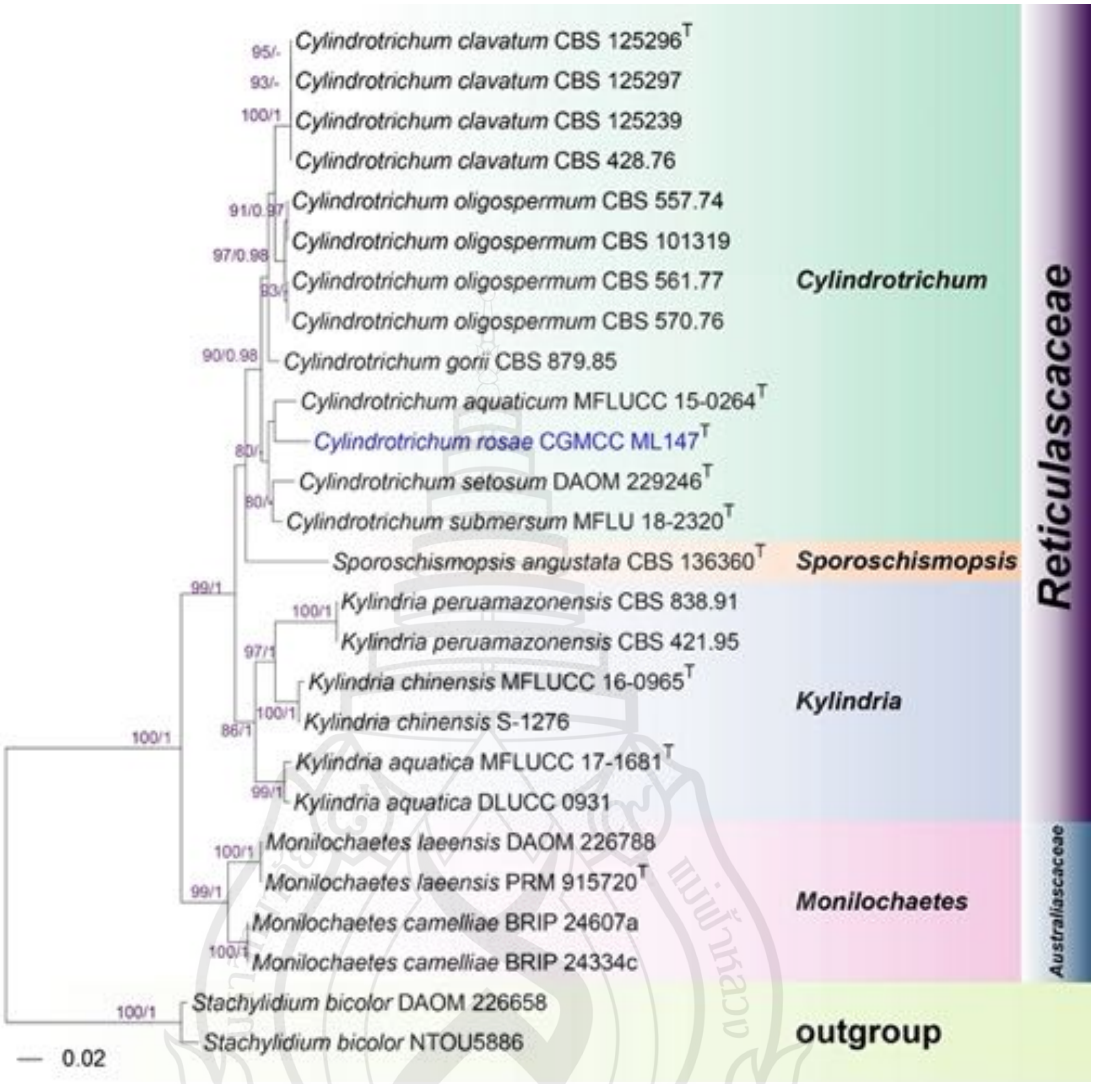


Figure 3.115 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of Reticulascaceae

Figure 3.115 The tree is rooted with *Stachylidium bicolor* (DAOM 226658 and NTOU5886). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Pararamichloridiales Crous

Woswasiaceae Huang Zhang, K.D. Hyde & Maharachch.

Type genus – *Woswasia* Jaklitsch, Réblová & Voglmayr

Notes – Woswasiaceae was established by Zhang et al. (2017a) to accommodate the genera *Cyanoannulus*, *Woswasia* and *Xylochrysis* (type genus). It was originally listed as families *incertae sedis* within Diaporthomycetidae, until Hyde et al. (2021) presented a multi-gene phylogenetic analysis combined with divergence time estimation, which supported the placement of Woswasiaceae in Pararamichloridiales, as proposed by Crous et al. (2017).

Xylochrysis Réblová, Mycologia 106(3): 567 (2014)

Type species – *Xylochrysis lucida* Réblová, V. Štěpánek & R.K. Schumach.

Notes – Réblová et al. (2014) introduced the monotypic genus *Xylochrysis* to accommodate a single species *X. lucida*, which is closely related to the genera *Ceratolenta*, *Cyanoannulus* and *Woswasia*. Song et al. (2023) introduced the second member *X. aquatica* from a freshwater habitat, and distinguished *X. aquatica* from *X. lucida* based on the morphology and phylogeny evidence. Subsequently, *X. guttulata* was described from *Camellia sinensis* by Xiao et al. (2025). The morphology of *Xylochrysis* is unique, and is characterized by solitary to gregarious, immersed to semi-immersed ascomata, 8-spored, unitunicate, long pedicellate, cylindrical asci with uniseriate, hyaline, aseptate, straight, guttulate, ellipsoidal ascospores (Réblová et al., 2014, Song et al., 2023, Xiao et al., 2025); the coleomycetous asexual morph produces hyaline, aseptate, guttulate, ellipsoid to obovoid conidia (Réblová et al., 2014).

Xylochrysis asexualis N. Wu & Jian K. Liu, sp. nov. Figure 3.116

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*asexualis*" refers to the asexual morph of this species.

Holotype – HKAS ML189

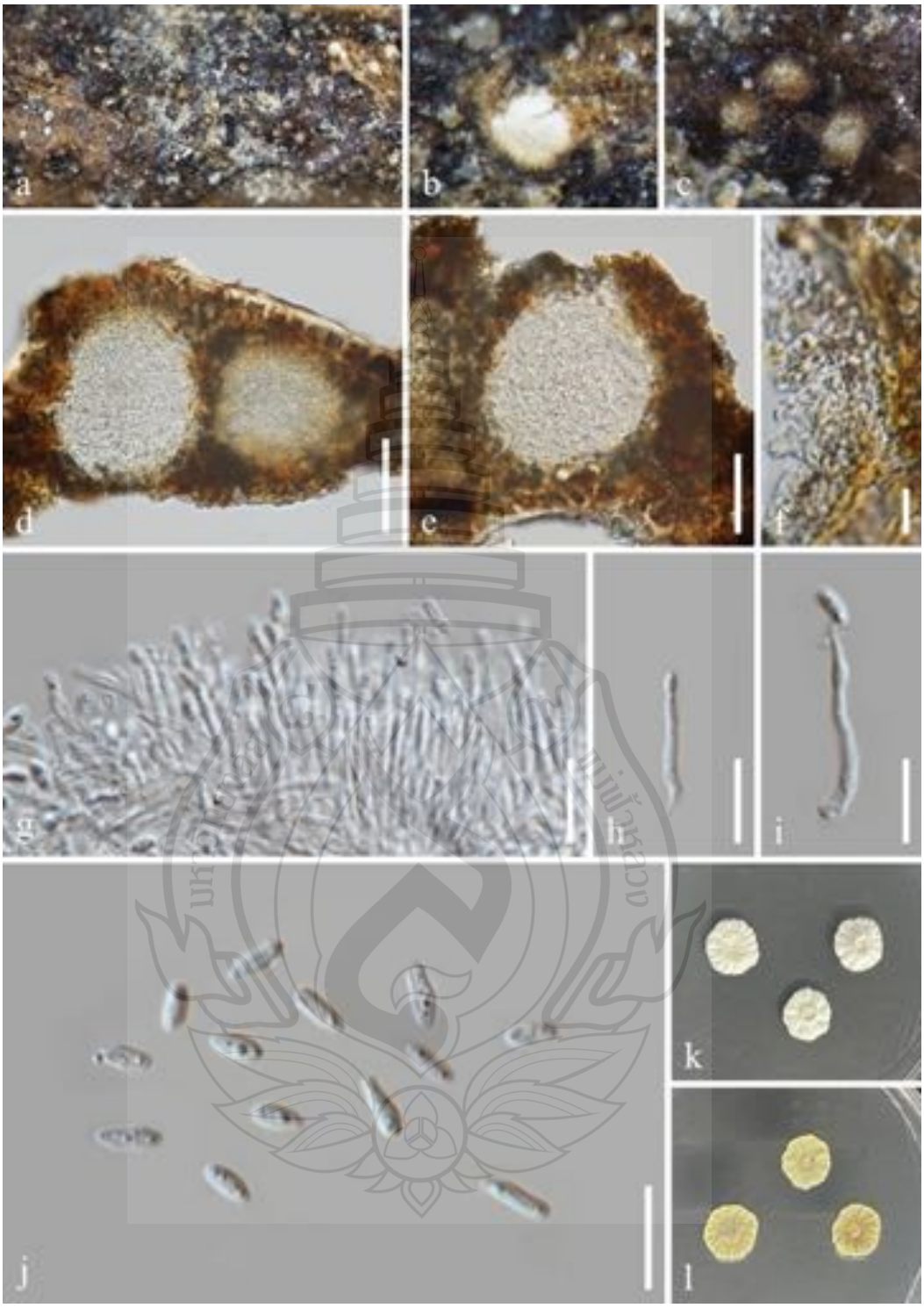
Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 90–183 μm wide, 106–172 μm high,

solitary to gregarious, immersed to erumpent, globose or subglobose to obpyriform, unilocular, glabrous, coriaceous, ostiolate. *Ostiole* single, centrical. *Conidiomatal wall* 10–15 μm wide, composed of thick-walled, brown cells of *textura globulosa* to *textura intricata*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 14–25 × 1.7–2.5 μm ($\bar{x}$ = 19 × 2 μm; n = 30), hyaline, monoblastic, cylindrical to subcylindrical, determinate, straight or slightly curved, smooth-walled. *Conidia* 5–7.5 × 2–2.6 μm ($\bar{x}$ = 6.4 × 2.3 μm; n = 30), hyaline, aseptate, guttulate, smooth-walled, ellipsoid to obovoid, slightly curved, rounded at apex, sometimes slightly tapering with truncate at base, without mucilaginous sheath or appendages.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 15 mm diam. after one week at 25°C in dark, circular, flattened, slightly raised, mycelium dry, white; in reverse, olivaceous gray to brown.

Material examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Duyun City, Mochong Town, Xinmeng Village, elevation 1,001 m, 25°55′12″ N, 107°23′24″ E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML189 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – In the molecular analysis, my collection (CGMCC ML189) grouped with *Xylochrysis aquatica* (CGMCC 3.23639) and *X. rosae* (CGMCC H36 and UESTCC H08) (Figure 3.117). However, *X. aquatica* and *X. rosae* are sexually typified thus, morphologically, cannot be compared with the new collection as it is represented only by its asexual morph. The comparison of nucleotide substitutions between my collection and *X. aquatica* (CGMCC 3.23639) showed 2.8% (27/935) differences in the *tef1α* gene region. Therefore, I recognize my collection as a new species, namely *X. asexualis*.



Note a Conidiomata on natural substrate. b–e Vertical sections of conidiomata. f Peridium. g–i Conidiogenous cells and developing conidia. j Conidia. k, l Colony on PDA, above (k), below (l). Scale bars: d, e = 50 μm; f–j = 10 μm.

Figure 3.116 *Xylochrysis asexualis* (HUEST ML189, holotype)

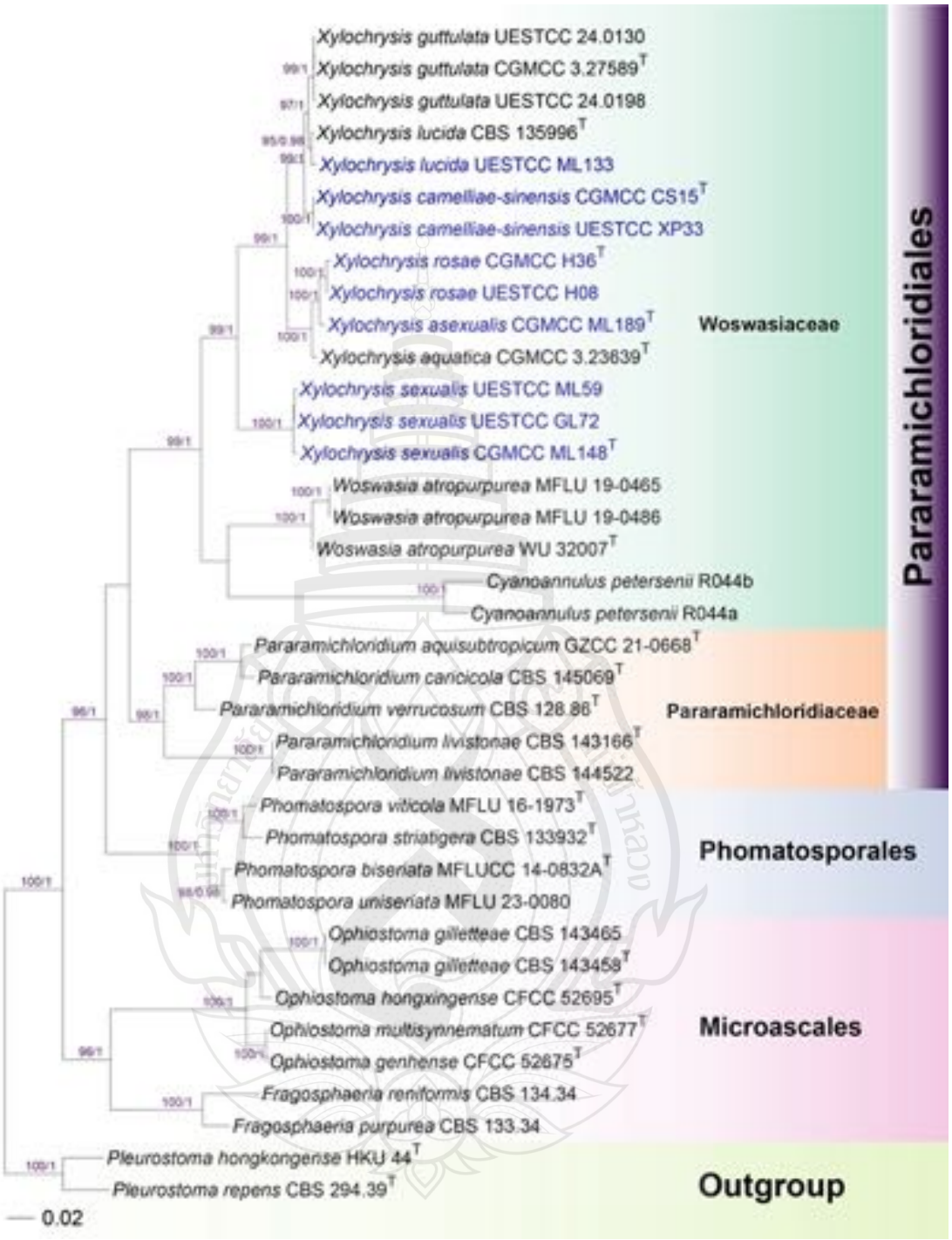


Figure 3.117 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1α* and *rpb2* sequence data of Pararamichloridiales

Figure 3.117 The tree is rooted with *Pleurostoma hongkongense* (HKU 44) and *P. repens* (CBS 294.39). Bootstrap values for maximum likelihood (ML) equal to or

greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Xylochrysis lucida Réblová, V. Štěpánek & R.K. Schumach., Mycologia 106(3): 567 (2014) Figure 3.118

Index Fungorum number: IF805254; Facesoffungi number: FoFXX

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 210–290 μm wide, 315–335 μm high, solitary to gregarious or confluent, dark, immersed to superficial or erumpent through bark, subglobose to pyriform, unilocular, glabrous, coriaceous, thick- and smooth-walled, short papillate, ostiolate. *Ostiole* 66–100 μm wide, 106–120 μm high, well-developed, subcylindrical, straight or curved, sulcate, periphysate, central or laterally located. *Peridium* 15–25 μm wide, composed of cells of *textura angularis*, outer layer brown and thicker, inner layer hyaline. *Hamathecium* 3–5 μm wide, cellular pseudoparaphyses, septate, constricted at the septum, rarely branched. *Asci* 85–140 × 4.5–5 μm ($\bar{x}$ = 120 × 4.6 μm; n = 20), 8-spored, unitunicate, cylindrical, slightly curved, apex wide and slightly square, tapering gradually to a long pedicel. *Ascospores* 6–7.5 × 2.5–3.3 μm ($\bar{x}$ = 6.5 × 3 μm; n = 30), uniseriate, hyaline, ellipsoidal, rounded at both ends, sometimes slightly tapering with truncate at base, aseptate, straight, guttulate, smooth-walled, without mucilaginous sheath or appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores and conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 20 mm diam. after two weeks at 25℃ in dark, circular, flattened, slightly raised, mycelium dry, white; in reverse, pastel yellow.

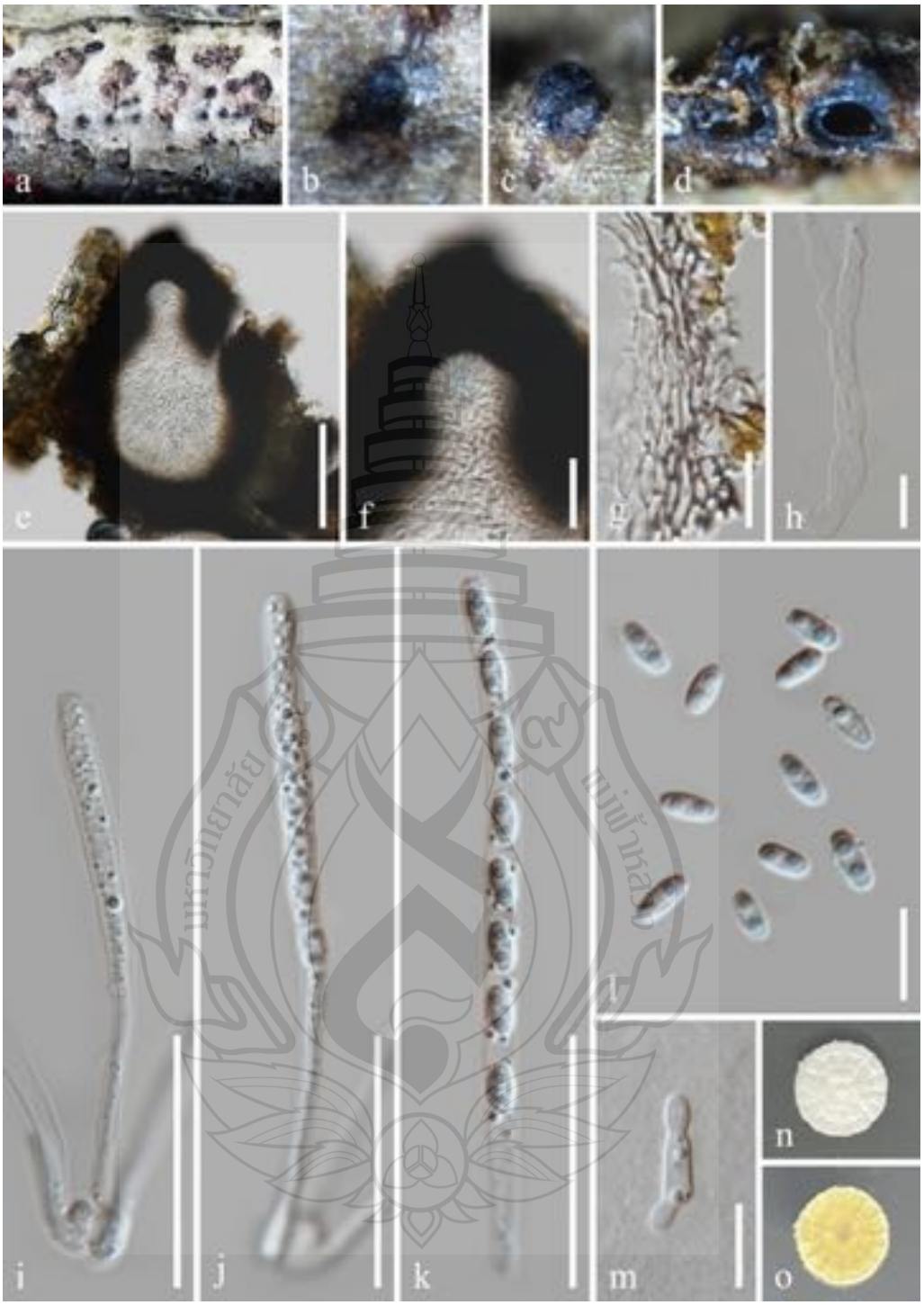
Material examined – CHINA, Guizhou Province, Qiannan Autonomous Prefecture, Pingtang County, Dalai Village, elevation 804 m, 25°56′24″ N, 107°18′36″

E, on dead branches of *Rosa roxburghii*, 4 February 2023, N. Wu, ML133 (HUEST XX), living culture UESTCC XX.

Hosts – *Rhododendron* sp. (Réblová et al., 2014), *Rosa roxburghii* (present study).

Known geographical distribution – China, Germany.

Notes – Réblová et al. (2014) introduced the sexual morph of *Xylochrysis lucida* from decaying wood and bark of a twig of a cultivated shrubby *Rhododendron* sp. in Germany, with the asexual morph produced in culture. My specimen (HUEST ML133) resembles *X. lucida* in having aggregated or confluent ascomata with the base slightly immersed and seated on a small, basal stroma, and unitunicate, long pedicellate, cylindrical asci with uniseriate, hyaline, aseptate, straight, guttulate, ellipsoidal ascospores. In the phylogenetic tree (Figure 3.117), my strain (UESTCC ML133) formed a sister clade to the ex-type strain of *X. lucida* (CBS 135996). The ITS, LSU, SSU and *tef1α* sequences of my collection and the type material of *X. lucida* exhibit 99.4%, 100%, 99.4% and 99.6% similarities, respectively. Therefore, I recognize my collection as *X. lucida*, while a new host record (*Rosa roxburghii*) and a geographical record (China) is provided.



Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Ostiole. g Peridium. h Pseudoparaphyses. i–k Asci. l Ascospores. m Germinating ascospore. n, o Colony on PDA, above (n), below (o). Scale bars: e = 100 μm; f, i–k = 30 μm; g, h, l, m = 10 μm.

Figure 3.118 *Xylochrysis lucida* (HUEST ML133, new host record)

Xylochrysis rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.119

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

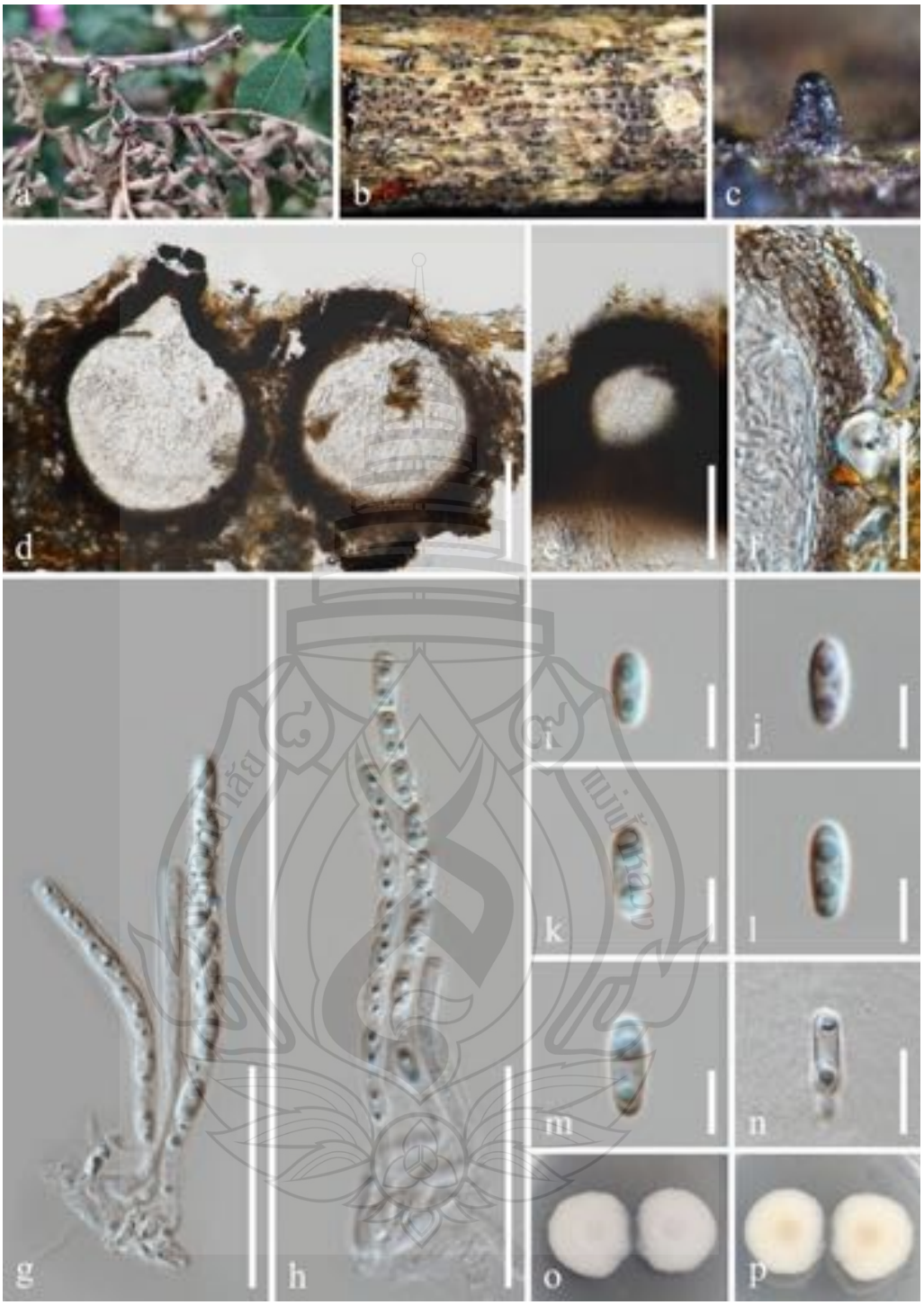
Holotype – HKAS H36

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 170–340 μm wide, 230–346 μm high, solitary to gregarious, deeply immersed, and erumpent through host epidermis, visible as raised, black ostiolar dots or papilla on host surface, subglobose, with a long immersed ostiolar neck, glabrous. *Ostiole* 70–124 μm wide, 95–149 μm high, single, well-developed, subcylindrical, straight or curved, centric or eccentric, periphysate. *Peridium* 19–25 μm wide, outer layer carbonaceous composed of black, thick-walled cells, inner layer comprising hyaline to brown cells of *textura angularis*. *Hamathecium* 4–4.5 μm wide, sparse, septate, slightly constricted or not constricted, hyaline, pseudoparaphyses. *Asci* 85–136 × 4.5–5.8 μm ($\bar{x}$ = 106 × 5 μm; n = 20), 8-spored, unitunicate, cylindrical, long pedicellate, slightly curved, apically rounded with an apical ring. *Ascospores* 6–7.7 × 2.7–3.3 μm ($\bar{x}$ = 7 × 3 μm; n = 30), uniseriate, ellipsoidal, rounded at both ends, hyaline, aseptate, straight, guttulate, smooth-walled, without mucilaginous sheaths or appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and produced germ tube from one end. Colonies on PDA medium reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, slightly raised, velvety, white; in reverse, pastel yellow, with a milky white margin.

Materials examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H36 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, H08 (HUEST XX), living culture UESTCC XX.

Notes – *Xylochrysis rosae* matches the generic circumscription of *Xylochrysis* (Réblová et al., 2014; Song et al., 2023). Phylogenetically, *X. rosae* forms a sister clade to *X. asexualis* (HKAS ML189) with a strong support (Figure 3.117). However, *X. asexualis* is an asexual morph species (in this study), whereas *X. rosae* is represented by a sexual morph. The comparison of nucleotide substitutions between *X. rosae* (CGMCC H36) and *X. asexualis* (CGMCC ML189) showed 2.4% (23/935) differences in the *tef1α* gene region. Thus, *X. rosae* and *X. asexualis* can be regarded as different species.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g, h Asci. i–m Ascospores. n Germinating ascospore. o, p Colony on PDA, above (o), below (p). Scale bars: d = 100 μm; e = 60 μm; f–h = 30 μm; i–m = 5 μm; n = 10 μm.

Figure 3.119 *Xylochrysis rosae* (HKAS H36, holotype)

Xylochrysis sexualis N. Wu & Jian K. Liu, sp. nov. Figure 3.120

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*sexualis*" refers to the sexual morph.

Holotype – HKAS ML148

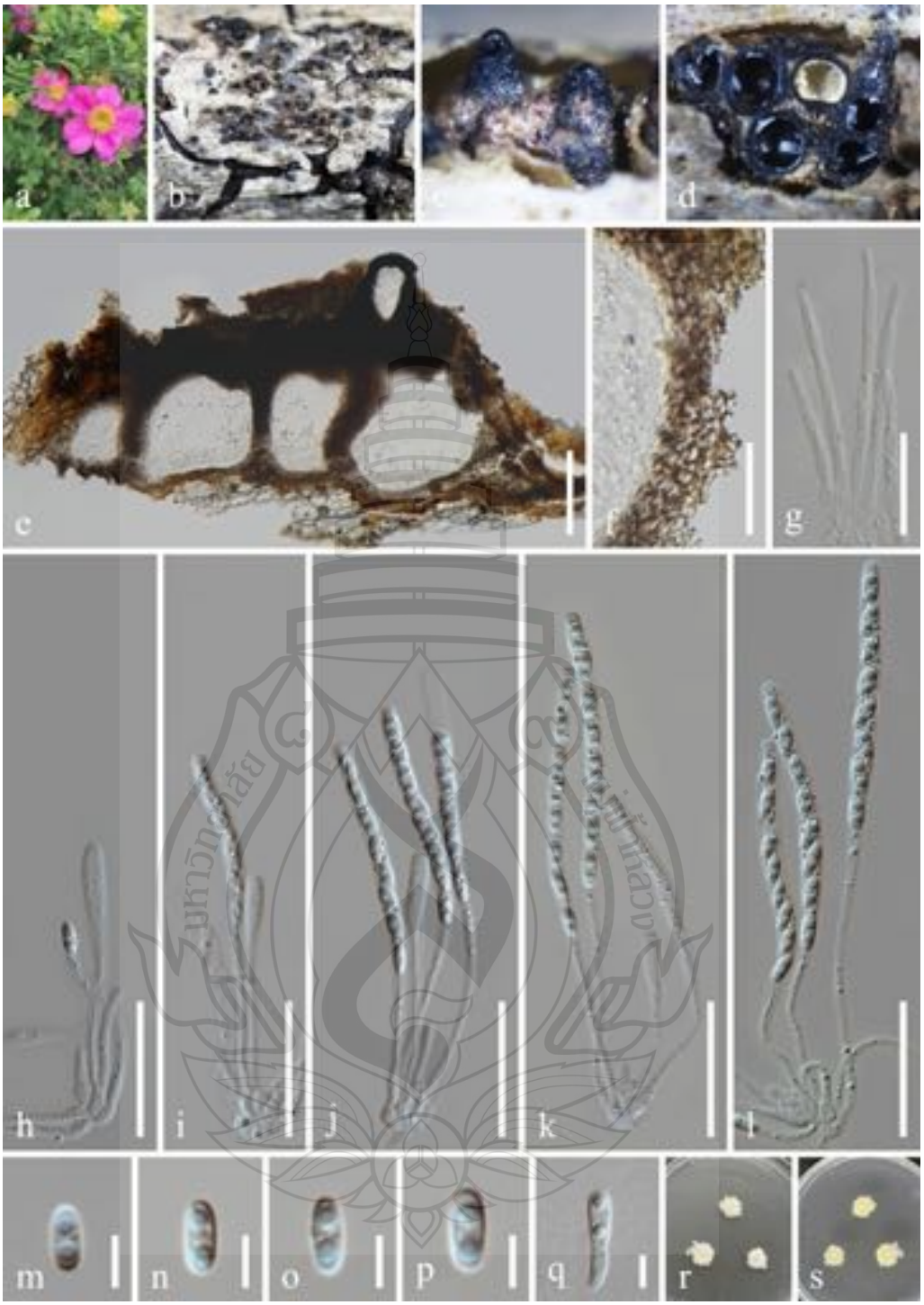
Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Stromata* 470–530 μm wide, 300–330 μm high, solitary to gregarious, with a well-developed interior, at first immersed, eventually erumpent and appearing superficial, black, glabrous, circular to irregular in shape, pustulate, bi- to multi-ascoma, with umbilicate ostioles appearing on the surface of stroma. *Ascomata* 135–275 μm wide, 190–320 μm high, perithecial, immersed to semi-immersed in stroma, delimited by a black zone in host tissues, subglobose to pyriform, glabrous, thick-walled, ostioles individual, with long necks. *Ostiole* 65–73 μm wide, 111–150 μm high, subcylindrical, straight or curved, centric or eccentric, sulcate, periphysate. *Peridium* 15–20 μm wide, composed of thick-walled, brown to dark brown cells of *textura angularis* in the outer layers, becoming hyaline cells towards conidial hymenium. *Hamathecium* 3.5–6 μm wide, narrowly cylindrical to filiform, rarely branched, septate, constricted at the septum, hyaline, not embedded in a gelatinous matrix, pseudoparaphyses. *Asci* 105–155 × 4.5–5.5 μm ($\bar{x}$ = 123 × 5 μm; n = 20), 8-spored, unitunicate, cylindrical, slightly curved, apex wide and slightly square, tapering gradually to a long pedicel. *Ascospores* 6.5–9 × 3–4 μm ($\bar{x}$ = 7.5 × 3.5 μm; n = 30), uniseriate, ellipsoidal, rounded at both ends, hyaline, aseptate, straight, guttulate, smooth-walled, without mucilaginous sheaths or appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one end. Colonies on PDA medium reaching 8–10 mm diam. after two weeks at 25°C in dark, irregular, flat to raised, mycelium dry, white; in reverse, pastel yellow, with a milky white margin.

Materials examined – CHINA, Guizhou Province, Zunyi City, Bozhou District, Tuanxi Town, Ximashui Village, elevation 990.6 m, 27°27′36″ N, 107°4′12″ E, on dead

branches of *Rosa roxburghii*, 2 February 2023, N. Wu, ML148 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML59 (HUEST XX), living culture UESTCC XX; *ibid.*, Anshun City, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL72 (HUEST XX), living culture UESTCC XX.

Notes – In the ITS-LSU-SSU-*rpb2*-*tef1α* phylogenetic tree, *Xylochrysis sexualis* formed a basal branch of the *Xylochrysis* clade (Figure 3.117). Morphologically, *X. sexualis* resembles *X. aquatica* (Song et al., 2023) and *X. lucida* (Réblová et al., 2014) in the size of the ascomata, asci, as well as in having uniseriate, hyaline, aseptate, straight, 2-guttulate, ellipsoidal ascospores. However, the ascomata of *X. lucida* and *X. sexualis* are often aggregated or confluent, whereas *X. aquatica* are solitary and scattered. The asci of *X. sexualis* (105–155 × 4.5–5.5 μm) are longer than those of *X. aquatica* (68–120 × 3–6.5 μm) and wider than those of *X. lucida* (105–135 × 4–4.6 μm). The ascospores of *X. sexualis* (6.5–9 × 3–4 μm) are longer than those of *X. aquatica* (4.5–6.5 × 2.5–4 μm) and *X. lucida* (6.5–7.5 × 2.5–3 μm). Based on morphological and phylogenetic evidence, *X. sexualis* is hereby introduced as a novel species.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–p Ascospores. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: e = 100 μm; f–l = 30 μm; m–q = 5 μm.

Figure 3.120 *Xylochrysis sexualis* (HUEST ML148, holotype)

Pleurotheciales Réblová & Seifert

Pleurotheciaceae Réblová & Seifert, Persoonia 37: 63 (2015) [2016]

Type genus – *Pleurothecium* Höhn.

Notes – Réblová et al. (2016) introduced Pleurotheciaceae with *Pleurothecium* as the type genus. Currently, the family comprises *Adelosphaeria*, *Anapleurothecium*, *Coleodictyospora*, *Dematipyriforma*, *Helicoascotaiwania*, *Melanotrigonum*, *Monotosporella*, *Neomonodictys*, *Phaeoisaria*, *Phragmocephala*, *Pleurotheciella*, *Pleurothecium*, *Pseudosaprodesmium*, *Saprodesmium* and *Sterigmatobotrys* (Hernández-Restrepo et al., 2017; Sun et al., 2017; Dayarathne et al., 2019; Dong et al., 2021b; Hyde et al., 2024; Tian et al., 2024a).

Phaeoisaria Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 118: 330 (1909)

Type species – *Phaeoisaria bambusae* Höhn.

Notes – *Phaeoisaria* was introduced by Höhnel (1909) based on a collection from *Gigantochloa* sp. and is typified by *P. bambusae*. Several species have been reported from freshwater habitats and collected from southwestern China (Hyde et al., 2018; Luo et al., 2018a). This genus is characterized by superficial to immersed, globose to elongate ascomata with a long neck, branched, septate paraphyses, unitunicate, cylindrical asci with filiform, guttulate, tapered at both ends, septate, smooth-walled, hyaline ascospores (Luo et al., 2019); asexual morphos hyphomycetous, possessing brown to dark brown synnemata with parallelly adpressed conidiophores, polyblastic, sympodial, denticulate, recurved conidiogenous cells, and small, hyaline, guttulate, ellipsoidal or obovoidal conidia (Crous et al., 2022; Jayawardena et al., 2022).

Phaeoisaria clematidis (Fuckel) S. Hughes, Can. J. Bot. 36: 794 (1958) Figure 3.121

Index Fungorum number: IF302703; Facesoffungi number: FoFxx

Saprobic on decaying branches of *Rosa sterilis*. Asexual morph: Hyphomycetous. *Colonies* effuse, scattered, hairy, visible as solitary, brown conidiophores with white

conidial masses at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, branched, smooth, pale brown hyphae. *Synnemata* solitary, erect or slanted, rigid, subulate, sometimes flared at the apex, tapering towards the apex, brown to dark brown, paler towards the apex, composed of compact appressed conidiophores, 250–290 µm long, 40–80 µm wide at middle part, 13–27 µm wide near the base. *Conidiophores* 40–280 × 1.8–2.7 µm ($\bar{x}$ = 205 × 2.4 µm; n = 10), macronematous, synnematous, cylindrical, reddish brown, pale pigment at the apex, straight or sometimes slightly, smooth-walled. *Conidiogenous cells* 7.5–21 × 2–3.2 µm ($\bar{x}$ = 13 × 2.6 µm; n = 10), polyblastic, integrated, terminal or intercalary, curved to recurved, longer at the apex of synnema, smooth at the base, cylindrical or tapering towards the tip, pale brown near the base, becoming hyaline towards the apex, with several small denticulate conidiogenous cells. *Conidia* 6.4–8.8 × 2.2–3.3 µm ($\bar{x}$ = 7.3 × 2.7 µm; n = 50), subcylindrical to ellipsoidal, rounded apical and obtuse basal, aseptate, smooth-walled, hyaline, straight, guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, cottony, raised or convex, dark olivaceous in the middle, grayish white at edge; in reverse, olive-green to dark brown with white mycelium of the outer ring.

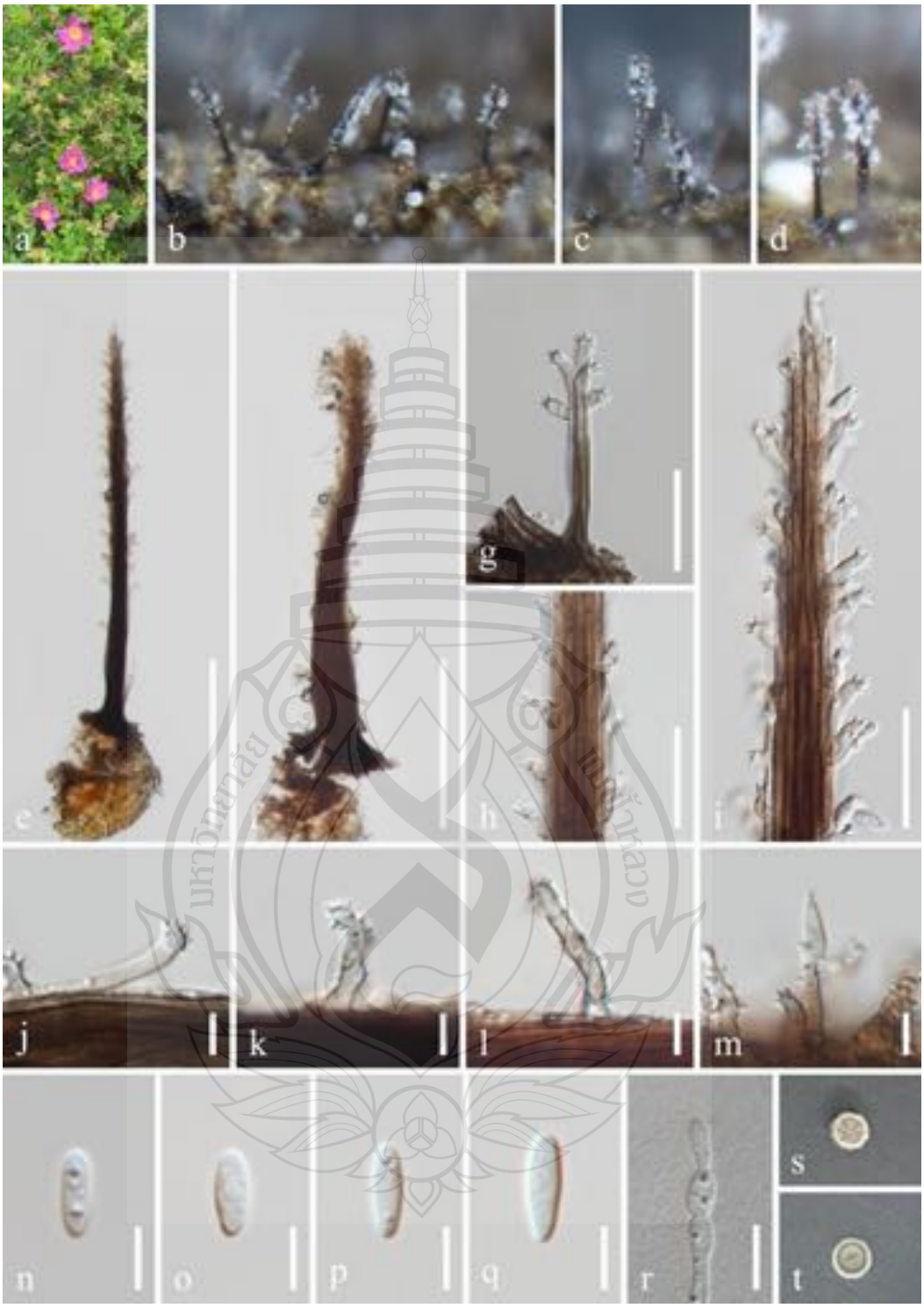
Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML32 (HUEST XX), living culture UESTCC XX.

Hosts – *Protea neriifolia* (NCBI), *Rosa sterilis* (present study), *Sambucus nigra* (Crous et al., 2022).

Known geographical distribution – China, Netherlands, South Africa.

Notes – Based on a BLAST search in NCBI GenBank, the ITS sequence of my collection shares 99.63% identity with *Phaeoisaria clematidis* (MFLUCC 17-1968).

Phylogenetic tree showed that my collection clustered with *P. clematidis* (MFLUCC 17-1968) (Figure 3.122). The morphology of my collection closely matches the description of *P. clematidis* as in Crous et al. (2022). Thus, I recognize my collection as *P. clematidis* and provide a new host record from *Rosa sterilis*.



Note a Host: *Rosa sterilis*. b–d Colonies on substrate surface. e–g Conidiophores. h–m Conidiogenous cells. n–q Conidia. r Germinating conidium. s, t Colony on PDA, above (s), below (t). Scale bars: d = 50 μm; e, m = 20 μm; f–l = 10 μm.

Figure 3.121 *Phaeoisaria clematidis* (HUEST ML32, new host record)

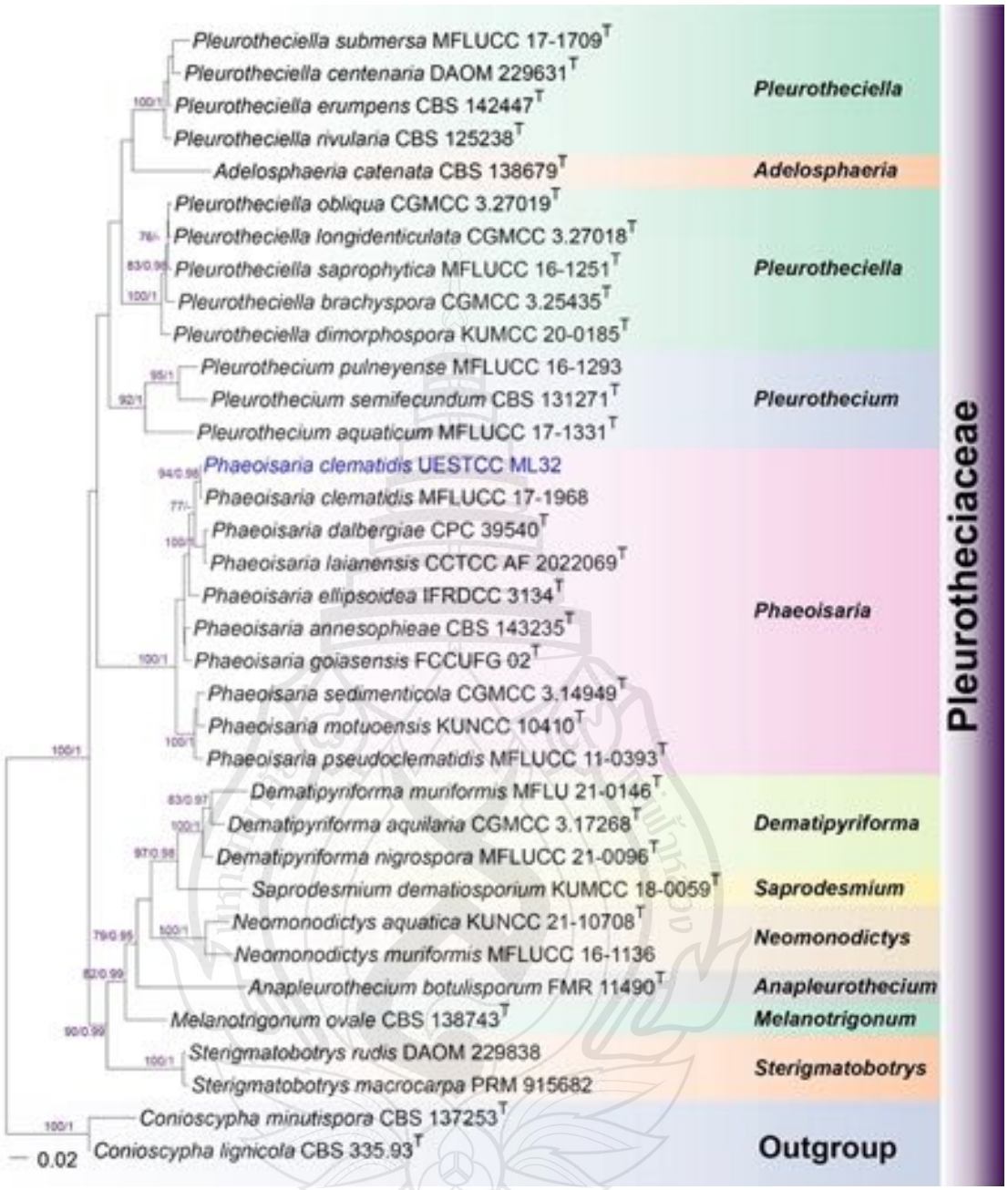


Figure 3.122 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data of Pleurotheciaceae

Figure 3.122 The tree is rooted with *Conioscypha lignicola* (CBS 335.93) and *C. minutispora* (CBS 137253). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for

Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "[T]" after the strain number.

Togniniales Senan., Maharachch. & K.D. Hyde

Togniniaceae Réblová, L. Mostert, W. Gams & Crous

Type genus – *Togninia* Berl.

Notes – Based on a single gene phylogeny of LSU and SSU sequences, Réblová et al. (2004) introduced Togniniaceae to accommodate *Togninia* with its *Phaeoacremonium* anamorph. Togniniaceae was initially placed within Diaporthales with four species, *P. aleophilum*, *T. minima*, *T. fraxinopennsylvanica* and *T. novaezealandiae*. Later, Maharachchikumbura et al., (2015) excluded Togniniaceae from Diaporthales based on phylogeny and morphology and established the monotypic order Togniniales to accommodate Togniniaceae. The family currently contains only one genus, *Phaeoacremonium*. (Hyde et al., 2024).

Phaeoacremonium W. Gams, Crous & M.J. Wingf., Mycologia 88(5): 789 (1996)

Type species – *Phaeoacremonium parasiticum* (Ajello, Georg & C.J.K. Wang) W. Gams, Crous & M.J. Wingf.

Notes – *Phaeoacremonium* was initially described by Crous et al. (1996) as a dematiaceous hyphomycete genus and is typified by *P. parasiticum*. Its sexual state was previously known as *Togninia* (Mostert et al., 2006), which was erected by Berlese (1900) with *T. minima* as the type species. This continued until the dual nomenclature system was abolished and replaced by the "one fungus, one name" principle (Hawksworth 2011; Wingfield et al., 2012). Subsequently, Gramaje et al. (2015) reviewed the genera and synonymized *Togninia* under *Phaeoacremonium*. Although *Togninia* is the older name and should take priority, *Phaeoacremonium* accommodates more species and is widely used by researchers. To minimize nomenclatural changes, *Phaeoacremonium* is therefore retained. *Phaeoacremonium* is characterized by black, long-necked perithecial ascomata, hyaline ascogenous hyphae with cylindrical to

clavate asci, and hyaline, aseptate, guttulate, oblong-ellipsoidal to allantoid ascospores; the hyphomycetous asexual morph produces hyaline, cylindrical-ellipsoidal to allantoid conidia (Shang et al., 2021; Phukhamsakda et al., 2022; Senanayake et al., 2023; Calabon et al., 2024; Zhang et al., 2025b).

Phaeoacremonium argentinense L. Mostert, W. Gams & Crous, Stud. Mycol. 54: 45 (2006) Figure 3.123

Index Fungorum number: IF500228; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 159–174 μm wide, 334–365 μm high, immersed in the host, solitary to gregarious, upright or laid on the substrate, unilocular, glabrous, thick-walled, long necks, bursting through the bark of host, coriaceous to carbonaceous. *Ostiole* 70–75 μm wide, 125–160 μm high, single, periphysate. *Peridium* 17–22 μm wide, composed of several layers of brown to black cells of *textura angularis*. *Hamathecium* 2.5–4 μm wide, dense, hyaline, unbranched, septate, slightly constricted at septa, swollen at the base, gradually narrowing towards the apex, longer than asci. *Asci* 16–20 × 4.3–5 μm ($\bar{x}$ = 18 × 4.5 μm; n = 20), 6–8-spored, arising in acropetal succession, unitunicate, cylindrical to clavate, apex wide and slightly square, apedicellate, with a nonamyloid apical ring. *Ascogenous hyphae* hyaline, branched, smooth-walled. *Ascospores* 3.8–4.3 × 1.3–2 μm ($\bar{x}$ = 4 × 1.6 μm; n = 30), overlapping biseriate, hyaline, oblong, straight, aseptate, smooth-walled, with small guttules near each end. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h and germ tubes produced from both ends. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25°C in dark, irregular, flattened, grayish brown mycelium in the middle and white mycelium in the outer ring on the surface; in reverse, brown in the centre and white undulate margin.

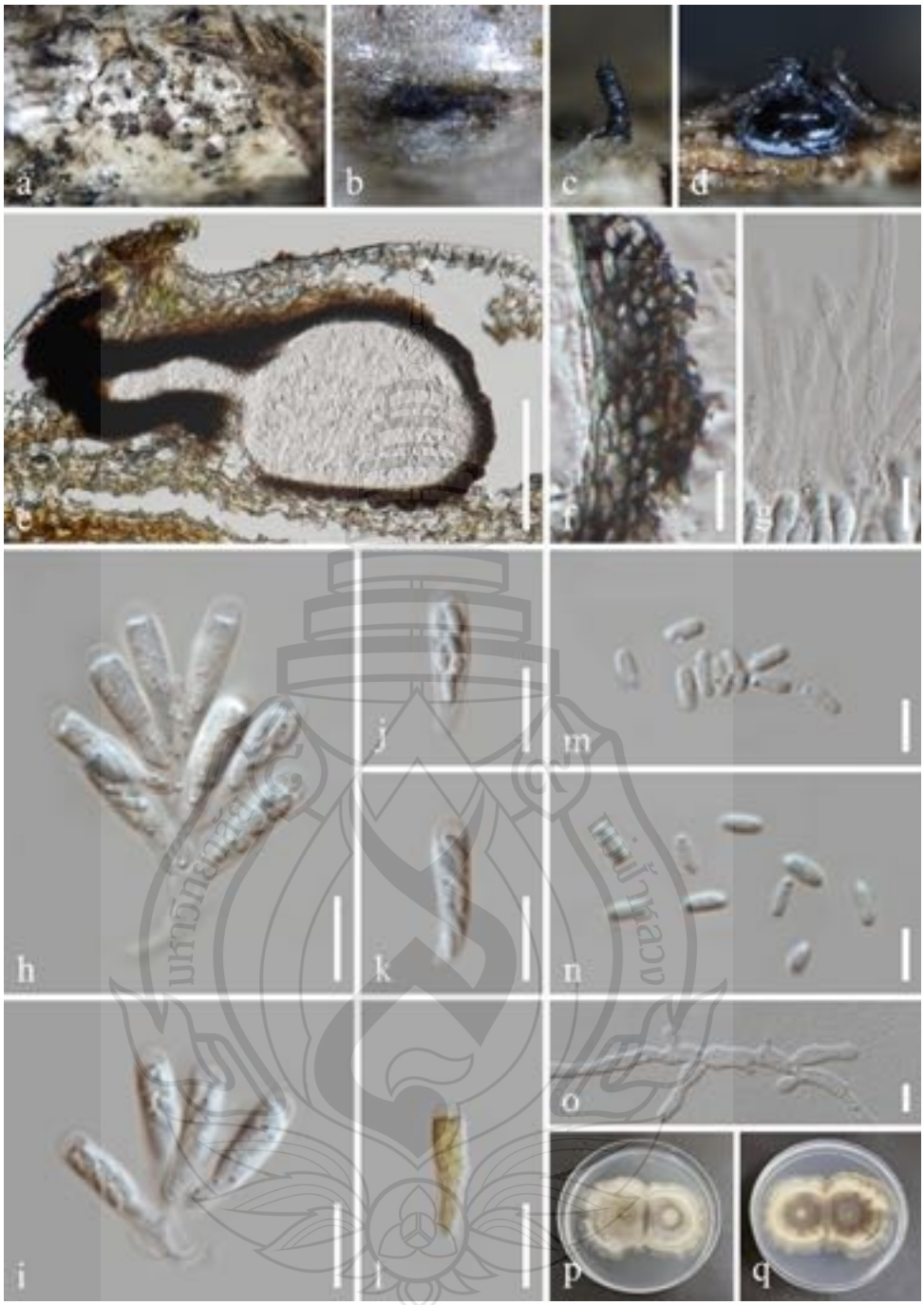
Material examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on

branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML83 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* (present study), *Vitis vinifera* canes (Mostert et al., 2006).

Known geographical distribution – Argentina, China.

Notes – Mostert et al., (2006) introduced *Togninia argentinensis* and its anamorph *Phaeoacremonium argentinense*. Gramaje et al. (2015) synonymized *T. argentinensis* under *P. argentinense* based on the one fungus-one name policy (Hawksworth et al., 2011). The morphological characteristics of my collection resemble *P. argentinense* in having subglobose ascomata with long necks, branched, hyaline ascogenous hyphae, cylindrical to clavate asci with a nonamyloid apical ring, and biseriate, small, hyaline, aseptate, oblong ascospores with small guttules near each end. The comparison of nucleotide substitutions between my collection and the ex-type of *P. argentinense* (CBS 777.83) revealed 0.8% (4/524), 1.7% (4/233) and 0.4% (2/529) differences in the ITS, ACT and *tub2* gene regions, respectively. Therefore, I report my collection as a new geographical and new host record of *P. argentinense* from *Rosa roxburghii* in China.



Note a–c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h, i Ascogenous hyphae with asci attached. j, k Asci. l Ascus stained in Melzer's reagent. m, n Ascospores. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: e = 100 μm; f–l = 10 μm; m–o = 5 μm.

Figure 3.123 *Phaeoacremonium argentinense* (HUEST ML83, new host record)

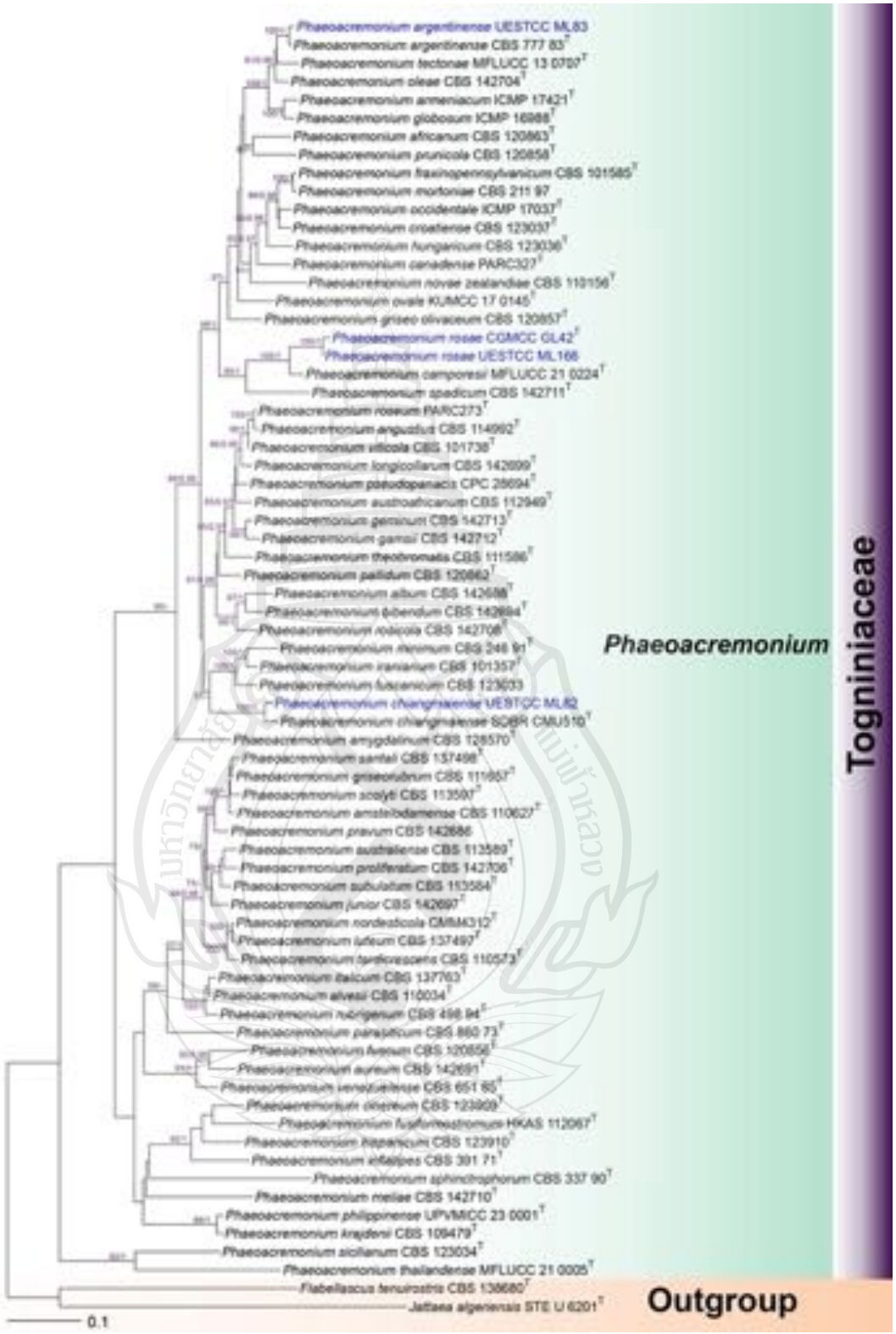


Figure 3.124 Phylogram generated from maximum likelihood analysis based on combined act and *tub2* sequence data of *Phaeoacremonium*

Figure 3.124 The tree is rooted with *Flabellascus tenuirostris* (CBS 138680) and *Jattaea algeriensis* (STE-U 6201). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Phaeoacremonium chiangmaiense X. Zhang & Suwannar., MycoKeys 113: 8 (2025) Figure 3.125

Index Fungorum number: IF903217; Facesoffungi number: FoF17085

Saprobic on dead branches of *Rosa sterilis*. Sexual morph: *Ascomata* 265–320 μm wide, 160–230 μm high, solitary to gregarious or confluent, dark, immersed to erumpent, dissilient the host epidermis, globose to subglobose, unilocular, glabrous, coriaceous to carbonaceous, thick-walled, ostiolate. *Ostiole* 35–45 μm wide, 65–75 μm high, single. *Peridium* 18–33 μm wide, comprising 6–9 layers, dark brown to black cells of *textura prismatica* to *textura angularis*. *Hamathecium* 4–6 μm wide, dense, hyaline, septate, slightly constricted at septa, swollen at the base, gradually narrowed towards the apex, longer than asci. *Asci* 18–23 × 5–6.5 μm ($\bar{x}$ = 20 × 5.5 μm; n = 20), arising in acropetal succession, 6–8-spored, unitunicate, cylindrical to clavate, apex wide and slightly square, apedicellate. *Ascogenous hyphae* septate, hyaline. *Ascospores* 5.5–6.5 × 1.2–2 μm ($\bar{x}$ = 6 × 1.6 μm; n = 30), overlapping biseriate, hyaline, oblong to allantoid, straight or slightly curved, aseptate, smooth-walled, with small guttules near each end. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h and germ tubes produced from both ends. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25°C in dark, circular, flat, filamentous, creamy-white; in reverse, central yellowish white.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead

branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML62 (HUEST XX), living culture UESTCC XX.

Hosts – *Macadamia* sp. (Zhang et al., 2025b); *Rosa sterilis* (present study).

Known geographical distribution – China, Thailand.

Notes – *Phaeoacremonium chiangmaiense* was introduced by Zhang et al. (2025b) and isolated from *Macadamia* sp. in Thailand. I recognize my collection (HUEST ML62) as *P. chiangmaiense* since it clustered with the type isolate (CMUB 40065) in the multi-gene phylogeny (Figure 3.124). Morphologically, my collection is similar to *P. chiangmaiense* in having unitunicate, cylindrical to clavate asci and oblong to allantoid, aseptate, guttulate, hyaline ascospores, without significant differences. Therefore, a new host (*Rosa sterilis*) and a new geographical record (China) is provided in the present study.



Note a, b Appearance of ascomata on host surface. c–e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h, i Ascogenous hyphae with asci attached. j–l Asci. m, n Ascospores. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: d, e=100 μm; f, g=20 μm; h–o=10 μm.

Figure 3.125 *Phaeoacremonium chiangmaiense* (HUEST ML62, new host record)

Phaeoacremonium rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.126

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS GL42

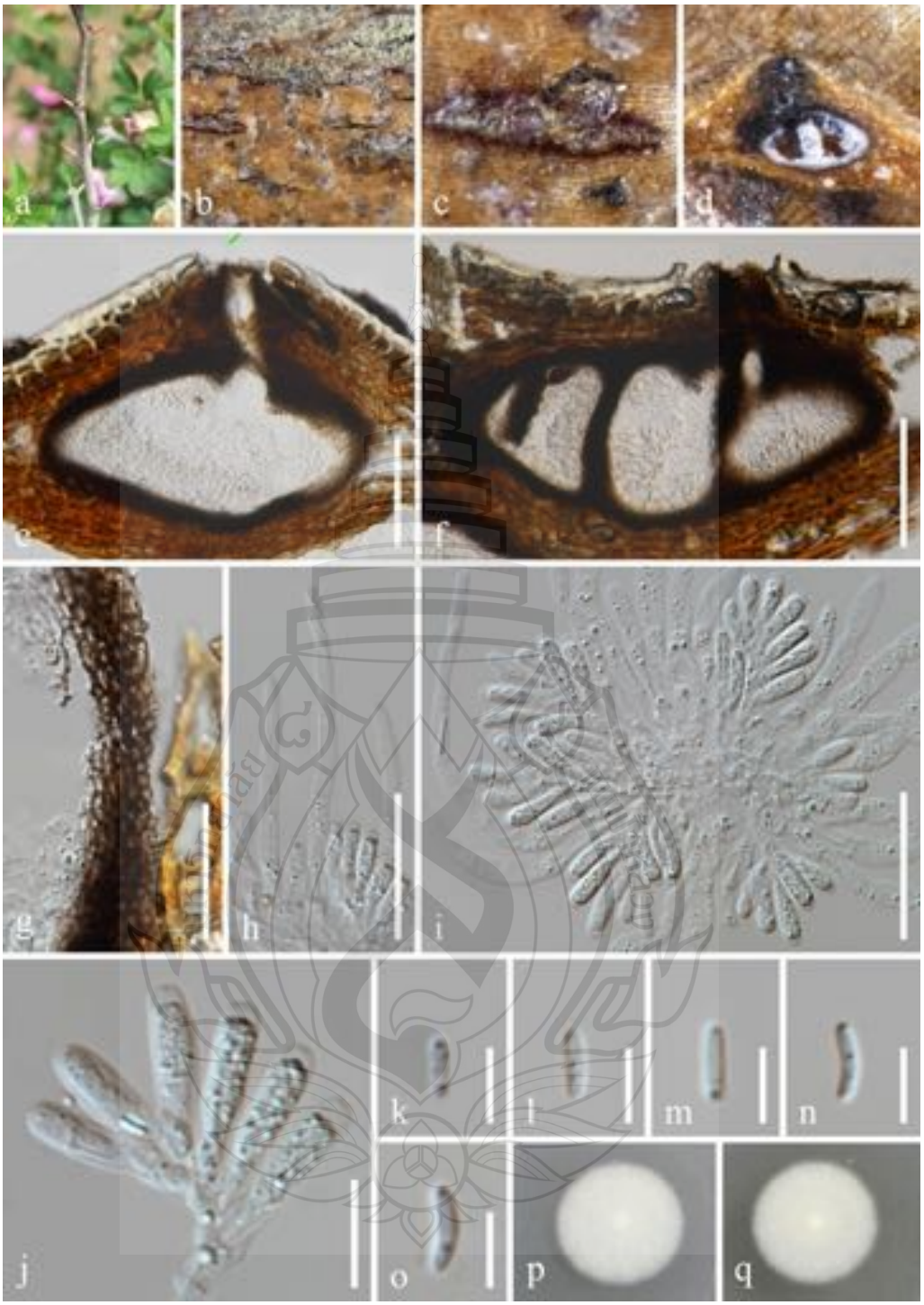
Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 230–320 μm wide, 190–250 μm high, perithecial, solitary to gregarious or confluent, dark brown to black, immersed to superficial or erumpent through bark, subglobose to irregular, unilocular or multilocular, glabrous, thick-walled, long necks, coriaceous to carbonaceous. *Ostiole* 53–60 μm wide, 90–100 μm high, single, cylindrical, slightly curved, periphysate. *Peridium* 14–20 μm wide, composed of several layers of brown to black cells of *textura angularis*. *Hamathecium* 3.3–5 μm wide, dense, hyaline, unbranched, septate, slightly constricted at septa, swollen at the base, gradually narrowed towards the apex, longer than asci. *Asci* 15.5–20 × 3.5–5 μm ($\bar{x}$ = 18 × 4.3 μm; n = 20), arising in acropetal succession, 6–8-spored, unitunicate, cylindrical to clavate, apex wide and slightly square, apedicellate. *Ascogenous hyphae* septate, hyaline, branched. *Ascospores* 4.4–5.7 × 1–1.5 μm ($\bar{x}$ = 5 × 1.3 μm; n = 30), overlapping biseriate, hyaline, oblong to allantoid, straight or slightly curved, aseptate, smooth-walled, with small guttules near each end. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h and germ tubes produced from both ends. Colonies on PDA medium reaching 28–30 mm diam. after two weeks at 25°C in dark, circular, flat, filamentous, creamy-white; in reverse, central yellowish white.

Materials examined – CHINA, Guizhou Province, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL42 (HKAS XX, holotype); ex-type living culture CGMCC XX; *ibid.*, Guiyang City, Xifeng County,

elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *R. roxburghii*, 6 February 2023, ML166 (HUEST XX), living culture UESTCC XX.

Notes – In the phylogenetic analysis (Figure 3.124), *Phaeoacremonium rosae* (CGMCC GL42 and UESTCC ML166) formed a different branch closely related to *P. camporesii* (MFLUCC 21-0024) and *P. spadicum* (CBS 142711). *Phaeoacremonium rosae* resembles *P. camporesii* with dark brown to black, immersed to semi-immersed, globose to subglobose, perithecial ascoma, septate, hyaline ascogenous hyphae with unitunicate, clavate asci spicately arranged, and biseriate, hyaline, aseptate, allantoid ascospores (Phukhamsakda et al., 2022). However, *P. rosae* can be distinguished from *P. camporesii* by its long neck in the ascomata and oblong ascospores. *Phaeoacremonium spadicum* is an asexual morph species (Spies et al., 2018), whereas *P. rosa* is represented by a sexual morph. In addition, the *act* and *tub2* sequences of *P. rosae* and *P. spadicum* showed 25 bp (204/236 bp, 7 gaps) and 75 bp (586/686 bp, 25 gaps) differences, respectively. Therefore, I introduce *P. rosae* as a new species.



Note a Host: *Rosa sterilis*. b, c Appearance of ascomata on host surface. d–f Vertical sections of ascomata. g Peridium. h Paraphyses. i, j Ascogenous hyphae with asci attached. k–o Ascospores. p, q Colony on PDA, above (p), below (q). Scale bars: e, f = 100 μm; g–i = 30 μm; j = 10 μm; k–o = 5 μm.

Figure 3.126 *Phaeoacremonium rosae* (HKAS GL42, holotype)

Xylariales Nannf.

Diatrypaceae Nitschke [as 'Diatrypeae']

Type genus – *Diatrype* Fr.

Notes – Nitschke (1869) introduced the family Diatrypaceae with *Diatrype* as the type genus. Members of this family are characterized by immersed to partly erumpent, solitary to gregarious, dark brown to black stromata, unitunicate, clavate to elongate obovoid, polysporous or octosporous asci, and subhyaline to pale yellowish, elongate-allantoid, aseptate ascospores (Mehrabi et al., 2015; Du et al., 2022; Zhang et al., 2024a). Previous phylogenetic studies mainly used the entire internal transcribed spacer (ITS) region and partial ß-tubulin gene (tub2) to determine the systematic placement of new taxa within this family (Senwanna et al., 2017; Phookamsak et al., 2019; Konta et al., 2020; Zhu et al., 2021; Yang et al., 2022b; Li et al., 2023c; Ma et al., 2023; Lu et al., 2025). Currently, 31 genera are accepted within Diatrypaceae (Hyde et al., 2024), most of which are saprobic on woody plants (Shang et al., 2017; Zhang et al., 2023a).

Allocryptovalsa Senwanna, Phookamsak & K.D. Hyde, Mycosphere 8(10): 1839 (2017)

Type species – *Allocryptovalsa polyspora* Senwanna, Phookamsak & K.D. Hyde

Notes – This genus was introduced by Senwanna et al. (2017) to accommodate cryptovalsa-like species, *Allocryptovalsa cryptovalsoidea* (≡*Eutypella cryptovalsoidea*) *A. polyspora* and *A. rabenhorstii* (≡*Cryptovalsa rabenhorstii*). Several new species were subsequently introduced (Hyde et al., 2020b; Konta et al., 2020; Zhu et al., 2021; Samarakoon et al., 2022; Chethana et al., 2023; Senanayake et al., 2023), and 11 species epithets are recorded in Index Fungorum (2025, June). The collection from *Rosa sterilis* was recognized as *A. xishuangbanica* and is illustrated here.

Allocryptovalsa xishuangbanica Maharachch. & Wanas., Life 12(5, no. 635): 9 (2022) Figure 3.127

Index Fungorum number: IF843438; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa sterilis*. Sexual morph: *Stromata* solitary to gregarious, immersed to semi-immersed, visible as slightly raised blackened domes. *Ascomata* 230–370 μm wide, 350–400 μm high, perithecial, dark brown to black, globose to subglobose, glabrous, coriaceous or carbonaceous, individual ostioles with long necks. *Ostiole* 65–80 μm wide, 135–195 μm high, numerous, gregarious, umbilicate, dark brown to black, periphysate. *Peridium* 15–35 μm wide, composed of thick-walled, dark brown cells of *textura angularis* on the exterior, gradually merging with light brown to hyaline cells of *textura prismatica* in inner layers. *Hamathecium* 4–5.5 μm wide, dense, filamentous, unbranched, septate, hyaline, paraphyses, embedded in a mucilaginous matrix. *Asci* 110–140 × 5.5–8 μm ($\bar{x}$ = 120 × 7 μm; n = 20), 8-spored, unitunicate, clavate to elongate obovoid, sessile, apically rounded to truncate, with long and fragile pedicels. *Ascospores* 8–10 × 2.3–2.8 μm ($\bar{x}$ = 9 × 2.5 μm; n = 30), irregularly arranged or crowded, subhyaline to pale yellowish, elongate-allantoid, aseptate, usually slightly curved, with small guttules near each end, smooth-walled. Asexual morph: Undetermined.

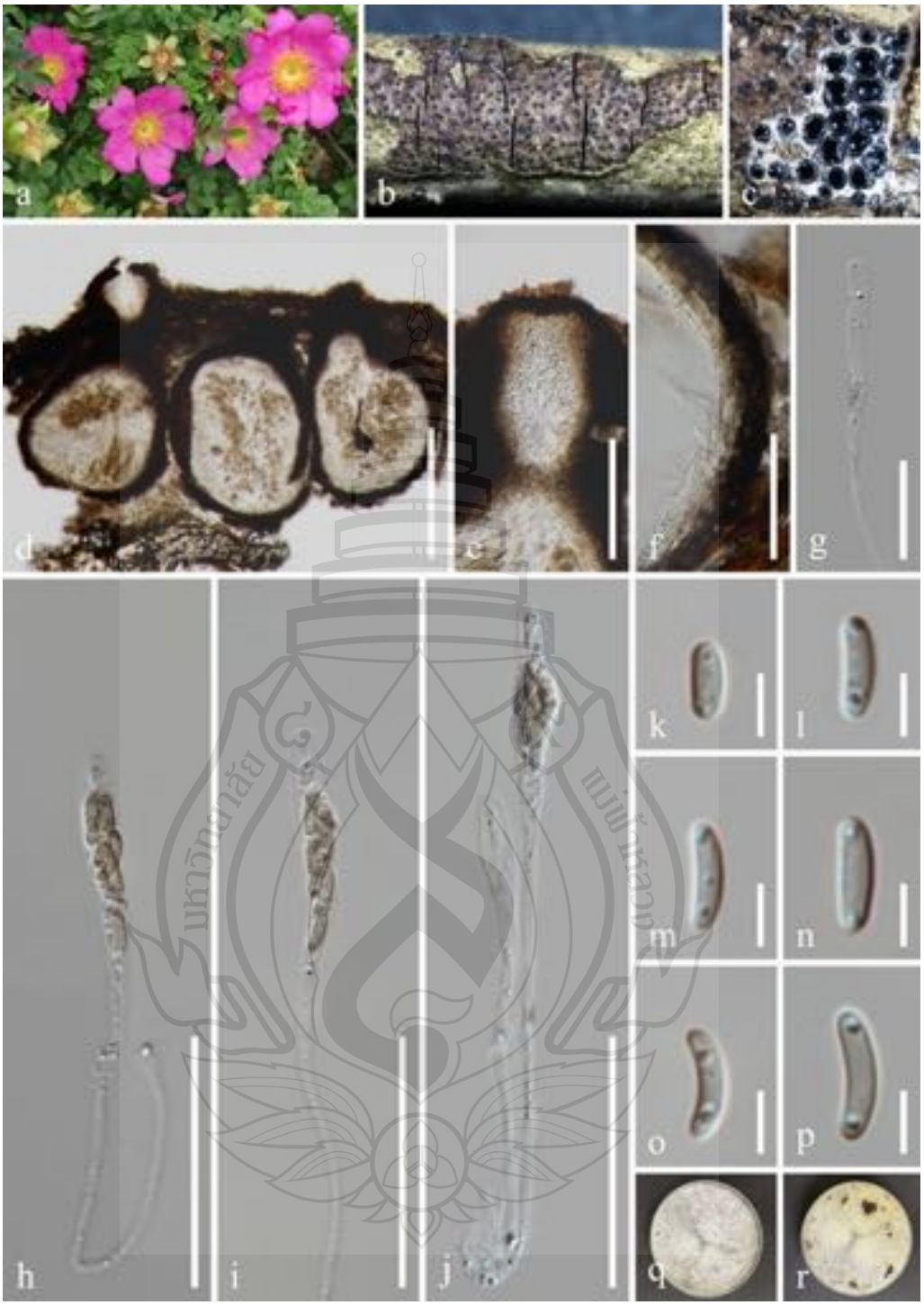
Culture characteristics – Ascospores germinated on PDA medium within 24 h and germ tubes produced from one end. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25℃ in dark, circular, medium dense, flat or effuse, slightly raised, fluffy, white at the beginning and becoming cream-colored after two weeks with reverse cream-orange.

Material examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML63 (HUEST XX), living culture UESTCC XX.

Hosts – *Bombax ceiba* (Li et al., 2023c); *Coffea arabica* (Lu et al., 2025); *Rosa sterilis* (present study).

Known geographical distribution – China.

Notes – *Allocryptovalsa xishuangbanica* was frequently collected from different plant hosts in China (Maharachchikumbura et al., 2022; Li et al., 2023c; Lu et al., 2025). My specimen matches with *A. xishuangbanica* in morphology, based on the holotype description provided by Maharachchikumbura et al. (2022). The multi-gene phylogenetic tree showed that my specimen (UESTCC ML63) clustered with *A. xishuangbanica* (KUMCC 21-0830 and KUMCC 21-0825) (Figure 3.128). The comparison of nucleotide substitutions between my collection and the type collection of *A. xishuangbanica* (KUMCC 21-0830) showed 1.0% (5/469) and 2.4% (9/364) differences (without gaps) in the ITS and *tub2* gene region, respectively. Therefore, I identify my specimen as *A. xishuangbanica* and report *Rosa sterilis* as a new host for this species in China.



Note a Host: *Rosa sterilis*. b Appearance of stromata on host surface. c Cross-section through stroma. d Vertical section of stroma. e Ostiole. f Peridium. g Paraphyses. h–j Asci. k–p Ascospores. q, r Colony on PDA, above (q), below (r). Scale bars: d = 200 µm; e = 80 µm; f, h–j = 40 µm;g = 20 µm; k–p = 5 µm.

Figure 3.127 *Allocryptovalsa xishuangbanica* (HUEST ML63, new host record)

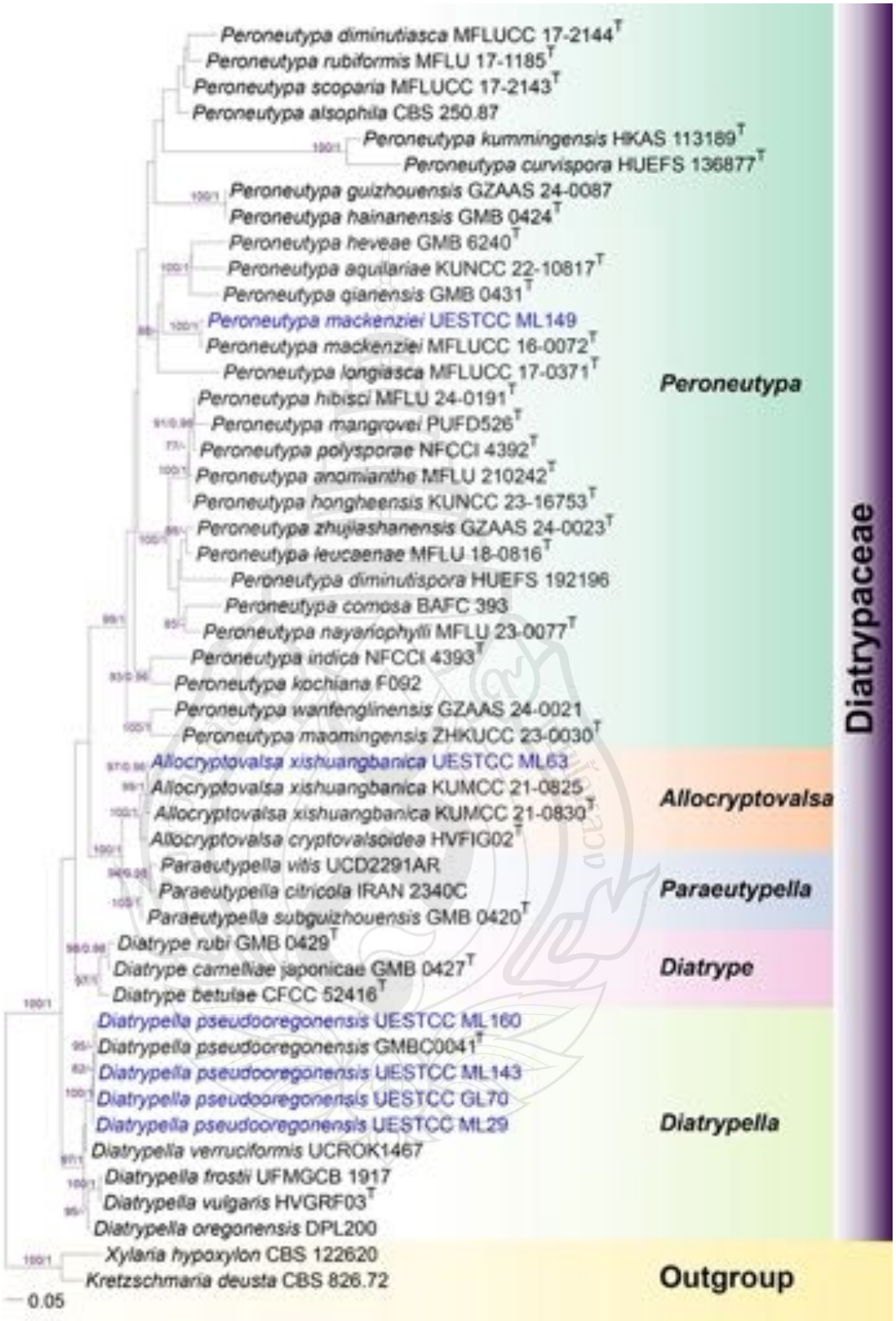


Figure 3.128 Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data of Diatrypaceae

Figure 3.128 The tree is rooted with *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122620). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Diatrypella (Ces. & De Not.) De Not., Sfer. Ital.: 29 (1863)

Type species – *Diatrypella verruciformis* (Ehrh. ex Pers.) Nitschke

Notes – The genus *Diatrypella* was introduced by Cesati and De Notaris (1863) and typified by *D. verruciformis*. Over 160 epithets are listed in Index Fungorum (2025, June), but only 100 species were accepted in the latest outline of fungi (Hyde et al., 2024). However, few have available molecular data. *Diatrypella* is characterized by pustule-like stromata erumpent through the host surface, unitunicate, clavate to cylindrical, polysporous asci and subhyaline to pale yellowish, elongate-allantoid, aseptate ascospores and libertella-like asexual morphs (Senanayake et al., 2015; Hyde et al., 2017; Shang et al., 2017; Long et al., 2021; Dissanayake et al., 2024). The collection from *Rosa roxburghii* and *R. sterilis* were recognized as *D. pseudooregonensis* and are illustrated here.

Diatrypella pseudooregonensis S.H. Long & Q.R. Li, MycoKeys 83: 14 (2021) Figure 3.129

Index Fungorum number: IF839656; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Stromata* solitary to gregarious, immersed to erumpent, dissilient the host epidermis, with groups of 6–10 perithecia. *Ascomata* 350–450 μm wide, 460–540 μm high, perithecial, dark brown to black, globose to subglobose, glabrous, coriaceous or carbonaceous, individual ostiole with long neck. *Ostiole* 60–105 μm wide, 205–235 μm high, opening separately, subcylindrical, centric or eccentric, periphysate. *Peridium* 70–85 μm wide, composed of brown cells of *textura angularis*. *Hamathecium* not observed. *Asci* 100–130 × 6.5–9 μm ($\bar{x}$ = 110 × 7.5 μm; n = 20), 8-spored, unitunicate, clavate to cylindrical, apically

rounded to truncate, with long and fragile pedicels. *Ascospores* 11–16 × 2.3–3.8 µm ($\bar{x}$ = 12.5 × 3 µm; n = 30), irregularly arranged or crowded, subhyaline to pale yellowish, elongate-allantoid, aseptate, usually slightly curved, with small guttules near each end, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one or both ends. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25°C in dark, circular, dense, first white, becoming ash-gray on the surface after one week and finally pale brown after two weeks.

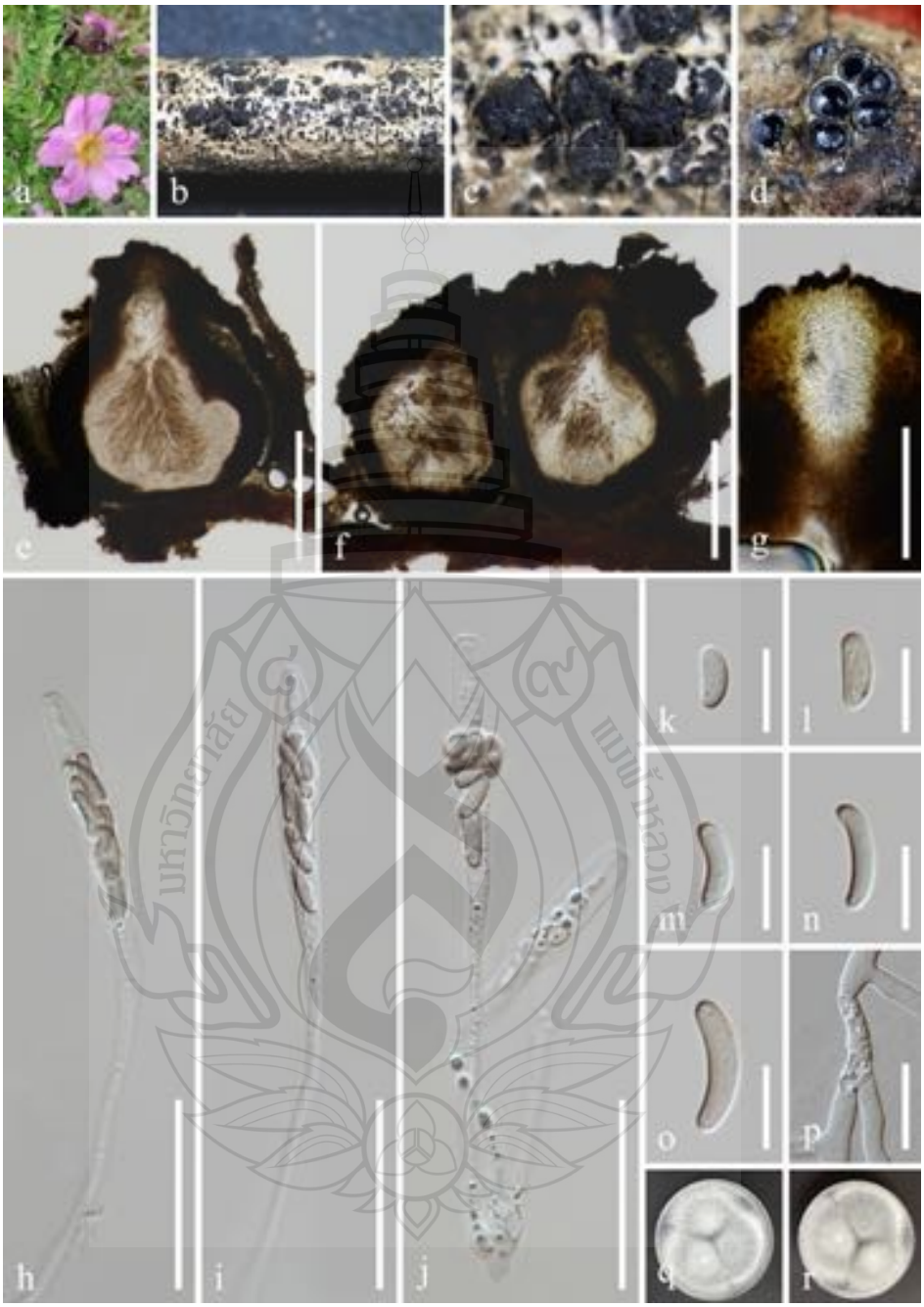
Materials examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML29 (HUEST XX), living culture UESTCC XX; *ibid.*, Dafang County, Wenge Town, Anqing Village, elevation 1496 m, 27°8′60″ N, 105°25′48″ E, on dead branches of *R. roxburghii*., 2 February 2023, N. Wu, ML160 (HUEST XX), living culture UESTCC XX; *ibid.*, Zunyi City, Bozhou District, Tuanxi Town, Ximashui Village, elevation 990.6 m, 27°27′36″ N, 107°4′12″ E, on dead branches of *R. roxburghii*, 2 February 2023, N. Wu, ML143 (HUEST XX), living culture UESTCC XX; *ibid.*, Anshun City, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL70 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* and *R. sterilis* (present study).

Known geographical distribution – China.

Notes – Long et al. (2021) provided several isolates of *Diatrypella pseudooregonensis* from China. In the phylogenetic analysis (Figure 3.130), my isolates (UESTCC ML29, UESTCC ML160, UESTCC ML143 and UESTCC GL70) clustered with the ex-type strain of *D. pseudooregonensis* (GMBC0041) as sister taxa. The comparison of available ITS gene sequences indicated that these taxa can be recognized as the same species. My collection also matches with the holotype of *D. pseudooregonensis* in the morphology and dimensions of ascomata, asci and ascospores (Long et al., 2021).

Therefore, I identify my isolates as *D. pseudooregonensis*, and expand the known host range of this species to *Rosa roxburghii* and *R. sterilis* in China.



Note a Host: *Rosa sterilis*. b, c Appearance of stromata on host surface. d Cross-section through stroma. e, f Vertical sections of stroma. g Ostiole. h–j Asci. k–o Ascospores. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: e, f = 250 µm; g = 100 µm; h–j = 30 µm; k–o = 10 µm; p = 20 µm.

Figure 3.129 *Diatrypella pseudooregonensis* (HUEST ML29, new host record)

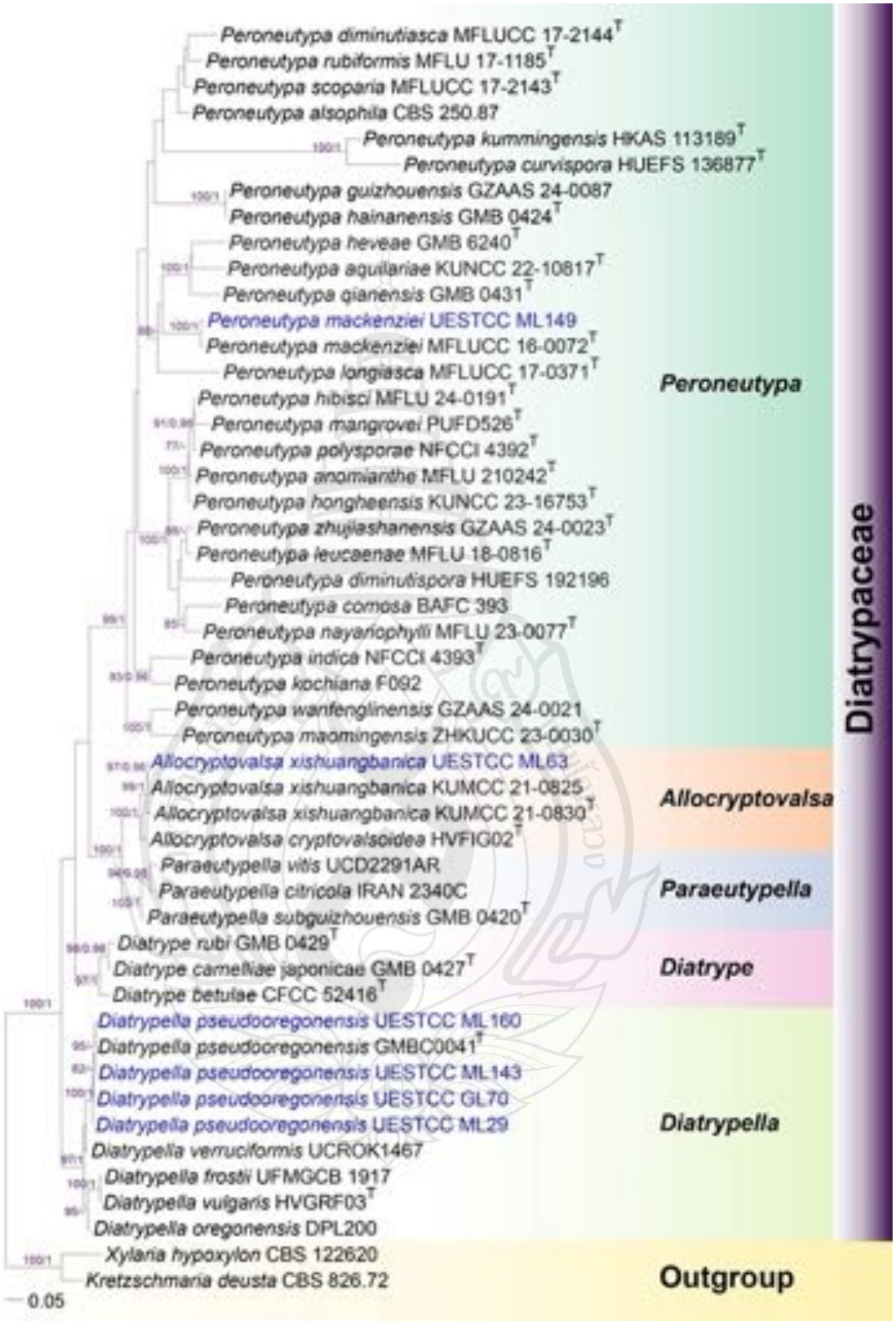


Figure 3.130 Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data of Diatrypaceae

Figure 3.130 The tree is rooted with *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122620). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Peroneutypa Berl., Icon. fung. (Abellini) 3(3-4): 80 (1902)

Type species – *Peroneutypa bellula* (Desm.) Berl.

Notes – Berlese (1902) introduced the genus *Peroneutypa* to accommodate *P. bellula*, *P. corniculata* and *P. heteracantha*, but without designating the type species. Subsequently, *P. bellula* was designated as the genetic type and synonymized under *Eutypella* due to nomenclatural priority (Rappaz, 1987). Carmarán et al. (2006) resurrected the genus *Peroneutypa* and proposed eight new combinations, viz., *P. alsophila*, *P. arecae*, *P. comosa*, *P. curvispora*, *P. gliricidiae*, *P. kochiana*, *P. scoparia* and *P. obesa*. *Peroneutypa* is characterized by solitary to gregarious, immersed to erumpent, dark brown to black stromata with long prominent necks, unitunicate, apically rounded to truncate, cylindrical or clavate asci and subhyaline to pale yellowish, elongate-allantoid, curved, guttulate, aseptate ascospores (Carmarán et al., 2006; Senwanna et al., 2017; Shang et al., 2017; Dissanayake et al., 2024). There are 73 epithets in Index Fungorum (2025, June), which are mainly sexual morphs and rarely reported asexual morph taxa (Shang et al., 2018; Du et al., 2022).

Peroneutypa rosae N. Wu & Jian K. Liu, sp. nov. Figure 3.131

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS ML149

Saprobic on dead branches of *Rosa roxburghii*. Sexual morph: *Stromata* solitary to gregarious, immersed, becoming raised to erumpent by a long ostiolar canal, dark

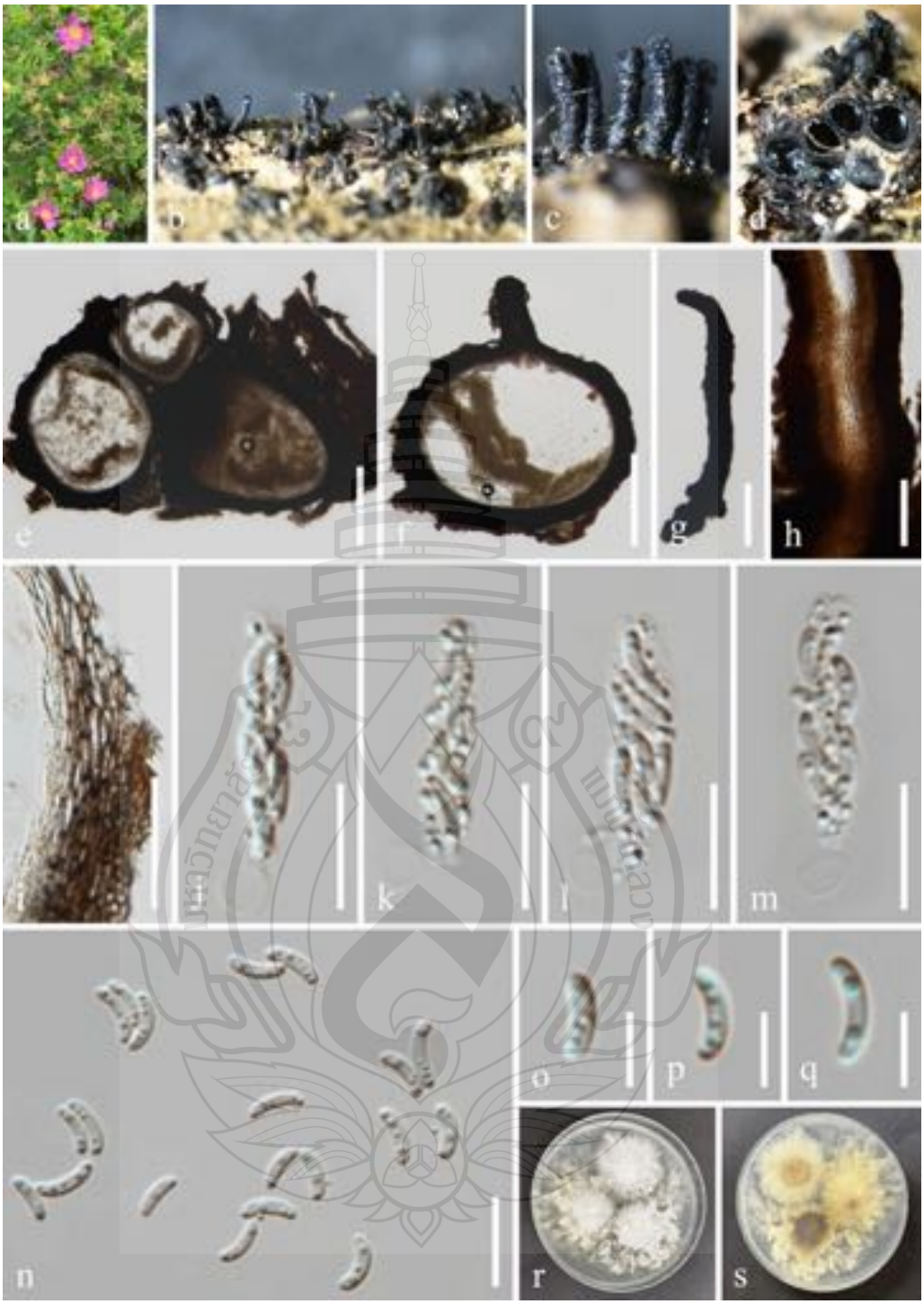
brown to black, multi-ascoma, circular to irregular in shape, arranged in longitudinally, with conspicuous, clustered, roundish to cylindrical prominent ostioles in the centre. *Ascomata* 580–785 μm wide, 610–677 μm high, perithecial, immersed in stroma, dark brown to black, pyriform or subglobose, glabrous, coriaceous or carbonaceous, individual ostioles with long necks. *Ostiolar canals* 1370–1730 μm long, 88–130 μm wide, cylindrical, sulcate, at the apex curved, periphysate. *Peridium* 65–90 μm wide, composed of thick-walled, dark brown cells of *textura angularis* on the exterior, gradually merging with light brown to hyaline cells of *textura prismatica* in inner layers. *Hamathecium* not observed. *Asci* 19.5–24 × 5–6.5 μm ($\bar{x}$ = 21.5 × 5.5 μm; n = 20), 8-spored, unitunicate, cylindrical or clavate, sessile, apically rounded to truncate. *Ascospores* 7–8.5 × 1.5–2 μm ($\bar{x}$ = 7.5 × 1.7 μm; n = 30), irregularly arranged or crowded, subhyaline to pale yellowish, elongate-allantoid, aseptate, usually slightly curved, guttulate, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tubes produced from one or both ends. Colonies on PDA medium reaching 40 mm diam. after two weeks at 25°C in dark, circular to irregular, dense, flat or effuse, slightly raised, with edge fimbriate, first white, becoming ash-gray on the surface after one week and finally pale brown after two weeks.

Material examined – CHINA, Guizhou Province, Zunyi City, Bozhou District, Tuanxi Town, Ximashui Village, elevation 990.6 m, 27°27′36″ N, 107°4′12″ E, on dead branches of *Rosa roxburghii*, 2 February 2023, N. Wu, ML149 (HKAS XX, holotype); ex-type living culture CGMCC XX.

Notes – In the phylogenetic analysis, *Peroneutypa rosae* grouped with *P. mackenziei* (MFLUCC 16-0072) with a good support (Figure 3.130). *Peroneutypa rosae* resembles *P. mackenziei* with solitary to gregarious, dark brown to black stromata, immersed to semi-immersed ascomata with individual ostioles with long necks, unitunicate, cylindrical or clavate asci, and elongate-allantoid, aseptate, curved, guttulate, subhyaline to pale yellowish ascospores (Shang et al., 2017). Nevertheless,

P. *rosae* differs from the latter in that its ascomata are larger (610–677 × 580–785 µm vs. 375–555 × 260–450 µm), its ostiolar canals are longer (1370–1730 µm × 88–130 vs. 105–420 × 80–120µm) and its asci are wider (19.5–24 × 5–6.5 µm vs. 14.5–21.5 × 3–5 µm). Comparisons of the ITS and LSU sequences of *P. rosae* (UESTCC ML149) and *P*. *mackenziei* (MFLUCC 16-0072) revealed 98.05% (554/565 bp) and 99.50% (799/803 bp) sequence similarities, respectively. Although the molecular data shows high similarity, I recognize *P*. *rosae* as a new species based on their morphological differences.



Note a Host: *Rosa roxburghii.* b, c Appearance of stromata on substrate. d Cross-section through stroma. e, f Vertical sections of stroma. g, h Ostiolar canal. i Peridium. j–m Asci. n–q Ascospores. r, s Colony on PDA, above (s), below (r). Scale bars: e–f = 300 µm; h, i = 50 µm; j–n = 10 µm; o–p = 5 µm.

Figure 3.131 *Peroneutypa rosae* (HKAS ML149, holotype)

Xylariaceae Tul. & C. Tul.

Type genus – *Xylaria* Hill ex Schrank

Notes – Xylariaceae is a large family in Xylariales, typically comprising saprobic, pathogenic or endophytic fungi on plants (Maharachchikumbura et al., 2015, 2016; Zhang et al., 2024a). Forty-two genera were accepted in Xylariaceae (Hyde et al., 2024), which are characterized by small to medium-sized ascomata, unitunicate, cylindrical asci, with or without an iodinepositive ascus apical ring, and hyaline to olive-greenish or brown, guttulate, oblong-ellipsoidal ascospores with hyaline dwarf cells or a straight germ slit or pores, sometimes covered with a thin mucilaginous sheath; the asexual morphs are geniculosporium-like, nodulisporium-like, or libertella-like (Rogers, 2000; Daranagama et al., 2018, Samarakoon et al., 2022; Zhang et al., 2024a).

Occultitheca J.D. Rogers & Y.M. Ju, Sydowia 55(2): 359 (2003)

Type species – *Occultitheca costaricensis* J.D. Rogers & Y.M. Ju

Notes – *Occultitheca* was established by Rogers and Ju (2003) in the family Xylariaceae, order Xylariales, with *O. costaricensis* as the type species, which was collected in Costa Rica. Using DNA sequence data, Samarakoon et al. (2022) described the second species, *O. rosae*, and confirmed the systematic placement of the genus in Xylariaceae. Lately, Tian et al. (2024a) introduced another new species, *O. ananasi*, to the genus based on morphological characters and molecular data. Species in the genus were reported as saprobes from terrestrial habitat in China and Costa Rica. *Occultitheca* is characterized by immersed, subglobose to pyriform, unilocular ascomata, unitunicate, cylindrical asci with a wedge-shaped, J+ subapical ring, and uniseriate, hyaline to olive-greenish or brown, guttulate, oblong-ellipsoidal ascospores with hyaline dwarf cells and a straight germ slit, sometimes covered with a thin mucilaginous sheath (Rogers & Ju, 2003; Samarakoon et al., 2022; Tian et al., 2024a; Sun et al., 2025). Additionally, the large distance between the uppermost ascospore and the ascus apex is a distinguishing characteristic of the genus (Rogers & Ju, 2003; Samarakoon et al., 2022).

Occultitheca rosae Samarak., Jian K. Liu & K.D. Hyde, Fungal Diversity 112: 72 (2022) Figure 3.132

Index Fungorum number: IF558741; Facesoffungi number: FoFxx

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 290–371 μm wide, 300–390 μm high, mostly solitary, occasionally gregarious, immersed, slightly erumpent, visible as blackened, raised areas, dark brown to black domes on the host surface, subglobose to pyriform, unilocular, glabrous, coriaceous to carbonaceous, short papillate, ostiolate. *Ostiole* 50–60 μm wide, 100–112 μm high, single, short-cylindrical, central, periphysate. *Peridium* 23–32 μm wide at the side, composed of brown cells of *textura angularis*, outer layer brown and thicker, inner layer hyaline. *Paraphyses* 4–5 μm wide, hypha-like, septate, constricted at the septa, guttulate, numerous between asci and embedded in a gelatinous matrix. *Asci* 135–155 × 12–15 μm ($\bar{x}$ = 143 × 14 μm; n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, apically rounded, with a distinct wedge-shaped, subapical ring. *Ascospores* 15.6–20.5 × 7–9 μm ($\bar{x}$ = 18.3 × 8 μm; n = 30), obliquely uniseriate, oblong-ellipsoidal, with a slightly acute apex, and a blunt base, straight, smooth-walled, aseptate, hyaline to olive-greenish or brown, with a small, hyaline, rounded, basal cell, 1.7–2.6 μm ($\bar{x}$ = 2.2 μm; n = 25), guttulate and surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h. Colonies on PDA medium reaching 18–20 mm diam. after two weeks at 25°C in dark, circular, ring-like, dense, velvety, white.

Materials examined – CHINA, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village, elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *Rosa sterilis*, 1 February 2023, N. Wu, ML06 (HUEST XX), living culture UESTCC XX; *ibid.*, Dafang County, Wenge Town, Anqing Village, elevation 1496 m, 27°8′60″ N, 105°25′48″ E, on dead branches of *R. roxburghii*, 2 February 2023, N. Wu, ML154 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* and *R. sterilis* (present study); *Rosa* sp. (Samarakoon et al., 2022); *Rubus* sp. (Sun et al., 2025).

Known geographical distribution – China.

Notes – *Occultitheca rosae*, as the name implies, is a species collected from a dead branch of *Rosa* sp. in China (Samarakoon et al., 2022). My collection morphologically fits well with *O. rosae*, and by the dimensions of asci (135–155 × 12–15 μm vs. 90–140 × 11–13 μm) and ascospores (15.6–20.5 × 7–9 μm vs. 16.5–20 × 6.5–8 μm) are also comparable with the type (Samarakoon et al., 2022). However, a straight germ slit along the entire spore length was described in the type specimen of *O. rosae*, but not observed in my specimens. Based on further molecular evidence (Figure 3.133), I identify my specimens as *O. rosae* and extend its host range to *Rosa roxburghii* and *R. sterilis*.



Note a Host: *Rosa sterilis*. b, c Appearance of ascomata on host surface. d, e Vertical sections of ascomata. f Peridium. g Pseudoparaphyses. h, i Asci. j Apex of the ascus. k–n Ascospores. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: e = 150 μm; f = 40 μm; g, o = 20 μm; h, i = 40 μm; j–n = 10 μm.

Figure 3.132 *Occultitheca rosae* (HUEST ML06, new host record)

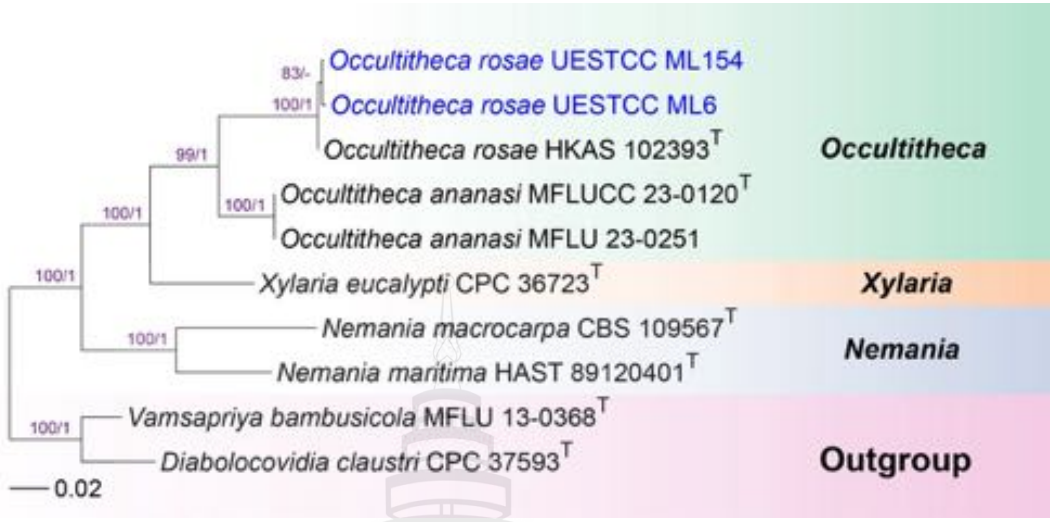


Figure 3.133 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1α* sequence data of *Occultitheca*

Figure 3.133 The tree is rooted with *Diabolocovidia claustri* (CPC 37593) and *Vamsapriya bambusicola* (MFLU 13-0368). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

3.3 Discussion

3.3.1 Comparison of Isolated Saprobic Fungal Species on *Rosa roxburghii* and *R. sterilis*

Both *Rosa roxburghii* and *R. sterilis* were found to support diverse assemblages of isolated saprobic fungi. To explore whether the two hosts harbor similar fungal communities, we systematically compared the saprobic fungi isolated from their dead twigs and branches. Of the total species identified, 21 species were shared between the two hosts (Figure 3.134), indicating that although each host supports a distinct fungal

assemblage, there are also several fungi capable of colonizing both hosts. These overlapping species include generalists such as *Botryosphaeria dothidea*, *Diplodia mutila* and *Neovaginatispora fuckelii*, which have been frequently reported from a wide range of plant hosts (Hyde et al., 2016; Tennakoon et al., 2018; Li et al., 2023b; Zhang et al., 2021c, 2024a). In comparison, Phukhamsakda et al. (2020) studied microfungi associated with *Clematis* (Ranunculaceae) and identified 73 taxa. Among these, only two species, *Dendryphion europaeum* and *Parathyridaria clematidis*, were recorded from multiple *Clematis* species, including *C. serratifolia*, *C. virginiana*, *C. vitalba* and C. *viticella*. This indicates that the overlap observed in *Rosa* is relatively higher, likely due to the hosts' closer relatedness and similar habitats.

Nevertheless, significant differences exist in the overall isolated fungal diversity of the two hosts. A total of 98 fungal species were isolated from dead twigs and branches of *Rosa roxburghii*, of which 37 were described as new species and 61 represented new host records. In contrast, 35 species were isolated from *R. sterilis*, including nine new species and 26 new host records. Excluding the shared species, there were 77 unique isolated saprobic fungi on *R. roxburghii*, but only 14 on *R. sterilis*. In addition, the fungi isolated from *R. roxburghii* showed greater phylogenetic diversity, covering several important saprobic groups such as Botryosphaeriales and Pleosporales; by comparison, the unique taxa of *R. sterilis* were fewer and concentrated in a limited number of genera. We presume that the higher fungal diversity on *R. roxburghii* is mainly related to its broader sampling range. In this study, 172 samples of *R. roxburghii* were collected from 19 localities in Guizhou, Sichuan, and Yunnan Provinces, whereas *R. sterilis* was collected in only three regions of Guizhou Province (Anshun, Qianxinan, and Bijie cities), and this difference may have led to the lower fungal diversity on *R. sterilis*. Overall, our study together with previous results emphasize the important status of *Rosa* species in fungal diversity research, and provide valuable opportunities for discovering numerous novel fungal taxa and host records.

3.3.2 Comparison of Fungi Associated with *Rosa* Hosts, the Native Tree (*Tectona grandis*), and the Invasive Weed (*Chromolaena odorata*)

Major differences in fungal communities have been observed among different *Rosa* hosts in different studies. Wanasinghe et al. (2018) carried out a comprehensive study on Rosaceae and reported 131 taxa belonging to 28 families, including 41 new species and 54 new host records. At the host genus level, a comparison of the species from the Rosaceae from Wanasinghe et al. (2018) and ours revealed only three shared species: *Diplodia seriata* (isolated from *Rosa sterilis*), and *Lasiodiplodia theobromae* and *Paraphaeosphaeria michotii* (from *R. roxburghii*). All three were previously reported from *Rosa canina* (Wanasinghe et al., 2018). This limited overlap of isolated taxa indicates that although congeners can share a few cosmopolitan species, each *Rosa* host tends to maintain a distinct mycobiota, consistent with patterns reported for other plant-associated fungi (Dong et al., 2021; Thambugala et al., 2017; Nizamani et al., 2023; Sun et al., 2025; Zhang et al., 2025). In contrast, 21 fungal species were shared between *R. roxburghii* and *R. sterilis* in our collections (Figure 3.134). This suggests that closely related hosts with overlapping distribution areas and similar habitats may promote higher community overlap, even if each host maintains a distinct assemblage.

To interpret our results in a broader ecological and biogeographical context, we compared the saprobic fungi on *Rosa roxburghii* and *R. sterilis* with those reported from both native and invasive plants in Asia. On *Tectona grandis* (teak), a native tree species in northern Thailand, 28 fungal species were reported (Doilom et al., 2017). Although *R. roxburghii* and *R. sterilis* were collected in China and *T. grandis* in Thailand, all represent important native hosts within their respective regions. Only *Lasiodiplodia theobromae* overlapped with our collections from *R. roxburghii*, and this species is a well-known cosmopolitan taxon occurring on a wide range of hosts. The almost complete lack of overlap between these host systems suggests that host identity and habitat exert a strong influence on fungal community composition, while

geographical and environmental differences may further contribute to the observed divergence (Du et al., 2025; Sun et al., 2025; Zhang et al., 2025).

When compared with the fungi associated with the invasive plant *Chromolaena odorata*, the overlap was also extremely low, with only two shared species: *Acrocalymma medicaginis* and *Muyocopron lithocarpi*. Both species have been reported from multiple hosts in China and Thailand and are regarded as widespread taxa with broad host and geographic ranges. In addition, Mapook et al. (2020) established the new genus *Chromolaenicola* to accommodate four new species and one new combination based on isolates obtained from *Chromolaena odorata*. Although no *Chromolaenicola* species overlapped between our study and theirs, we discovered one new species, *C. rosae*, and two new host records (*C. clematidis* and *C. sapindi*) from *Rosa roxburghii*. This indicates that *Chromolaenicola* is not restricted to *Chromolaena* but may possess a broader ecological amplitude and host adaptation potential. It also reinforces the idea that cross-host overlap is often driven by a few cosmopolitan species, whereas most taxa exhibit distinct host or habitat preferences.

Taken together, there is nearly zero overlap with the native host (*Tectona grandis*), the extremely low overlap with the invasive host (*Chromolaena odorata*), and the limited overlap within the genus *Rosa.* A few cosmopolitan taxa (e.g., *Lasiodiplodia theobromae*, *Acrocalymma medicaginis* and *Muyocopron lithocarpi*) are shared across hosts. In contrast, most taxa are strongly shaped by host identity and environmental conditions, resulting in distinct host-associated fungal communities. Meanwhile, the large number of novel taxa and new host records discovered from *Rosa* further emphasizes that systematic, host-targeted sampling is an effective approach for uncovering fungal diversity and delineating its boundaries, which could be useful for further studies on the ecological and potential biotechnological significance of fungal species.

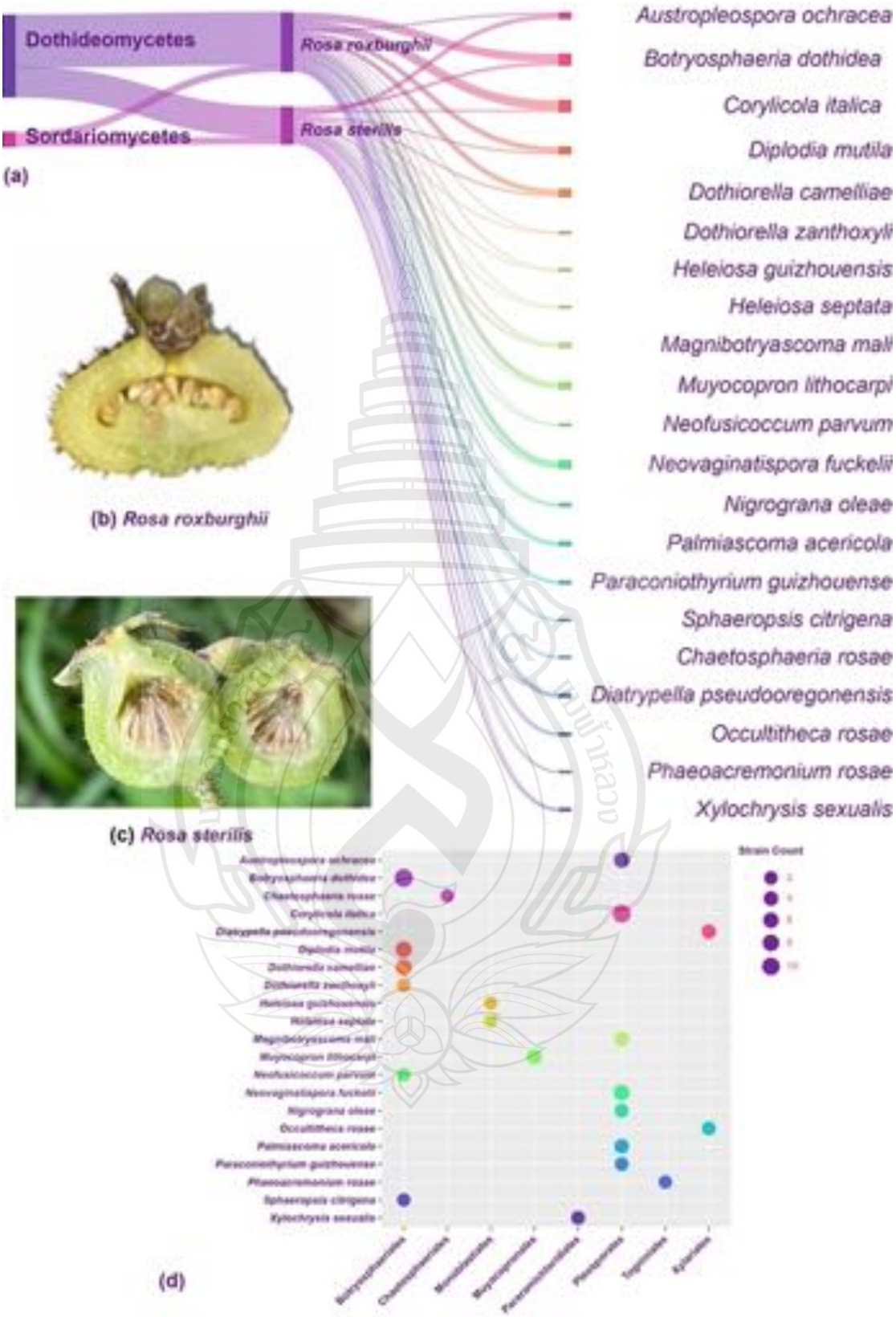


Figure 3.134 Comparative analysis of fungal taxa shared by *Rosa roxburghii* and *R. sterilis*

Figure 3.134 (a) Sankey diagram illustrating the distribution of 21 saprobic fungal species co-occurring on both *R. roxburghii* and *R. sterilis*, grouped by fungal class. (b) Longitudinal section of the fruit of *R. roxburghii* (seeded). (c) Longitudinal section of the fruit of *R. sterilis* (seedless). (d) Dot plot showing the number of isolates (strain count) for each of the 21 shared fungal species across different orders. The size of the circles corresponds to the number of isolates per species.

3.3.3 Sources and Spread of Fungi in *Rosa roxburghii* and *R. sterilis*

Among all the species identified from *R. roxburghii* and *R. sterilis*, most were introduced as new host records for China, while only 28 species had been recorded on other hosts from other countries, viz., *Acrocalymma hyalinum*, *A. medicaginis*, *Aplosporella javeedii*, *Biappendiculispora japonica*, *Botryosphaeria dothidea*, *Chromolaenicola clematidis*, *Corylicola italica*, *Diplodia mutila*, *D. pseudoseriata*, *D. seriata*, *Dothiorella citricola*, *Flabellascoma pistaciae*, *Lasiodiplodia theobromae*, *Leptoparies magnoliae*, *Magnibotryascoma mali*, *Muyocopron lithocarpi*, *Neovaginatispora fuckelii*, *Nigrograna thymi*, *Paraconiothyrium brasiliense*, *P. fuckelii*, *Paraphaeosphaeria michotii*, *Phaeoacremonium argentinense*, *Pha. chiangmaiense*, *Phaeoisaria clematidis*, *Phragmocephala atra*, *Pseudodinemasporium fabiforme*, *Sphaeropsis citrigena* and *Xylochrysis lucida*. The remaining 84 species were described as new taxa or reported as new host records in China. *Rosa roxburghii* and *R. sterilis* are widely distributed across natural or semi-natural habitats in southwestern China. These environments harbor rich plant diversity, which provides favorable conditions for fungal transmission among different plant hosts (Du et al., 2025; Sun et al., 2025; Zhang et al., 2025). Unlike invasive plants that commonly acquire their associated fungi via co-introduction or host-jumping, such as the fungi on *Chromolaena odorata* in Thailand, native plants such as *R. roxburghii* and *R. sterilis* mainly form communities through host-jumping. Therefore, the fungi associated with them are more likely to have originated locally and gradually co-evolved with their

hosts through long-term ecological interactions (Mapook et al., 2020a; Zhang et al., 2025).

It is particularly worth noting that *Rosa sterilis* has scarcely been investigated for fungal associations in the past, and most of the taxa recorded in this study represent new host records (Shi et al., 2022). This indicates that the fungal community associated with this host remains largely undocumented. Broader investigations are needed to clarify the true fungal diversity and community assembly mechanisms of this host. Additionally, plant propagation methods may influence fungal dispersal. In agricultural contexts, *R. roxburghii* and *R. sterilis* are commonly propagated vegetatively via stem cuttings, layering, or grafting. These practices may unintentionally facilitate the spread of certain endophytic or seed-transmitted fungi across different geographical regions. In this study, *Austropleospora ochracea*, *Botryosphaeria dothidea*, *Corylicola italica*, *Diatrypella pseudooregonensis, Diplodia mutila*, *Magnibotryascoma mali*, *Muyocopron lithocarpi*, *Neovaginatispora fuckelii*, *Nigrograna oleae*, *N. thymi*, *Palmiascoma acericola*, *Pseudoneodictyosporium rosae* and *Xylochrysis sexualis* were found on both *R. roxburghii* or *R. sterilis* across multiple geographic locations, suggesting the possibility that these species were dispersed through the movement of plant material during cultivation. However, in the absence of supporting population genetic data, it remains unclear whether these widespread fungi colonized via local host-jumping or were co-dispersed with their host plants (Zhou & Hyde, 2001; McTaggart et al., 2016).

In summary, the fungal communities associated with *R. roxburghii* and *R. sterilis* may have multiple origins, while some may be native symbionts that co-evolved with their hosts, others may be widespread environmental species or endophytes that jumped from other hosts and subsequently adapted to new ecological niches. Future studies that integrate ecological and taxonomic approaches, especially genomic and functional analyses, will be crucial for unraveling the origins, evolutionary processes, and ecological functions of these fungal communities.

3.3.4 Genus-level Fungal Diversity Across Sampling Locations

To further explore the geographic patterns of fungal distribution, we analyzed the genus-level diversity of isolates across the eleven sampling locations (Figure 3.135). Species of the genera *Austropleospora*, *Botryosphaeria*, *Diplodia*, *Heleiosa*, *Muyocopron*, *Neovaginatispora*, and *Nigrograna* were collected across multiple localities in Guizhou, Sichuan, and Yunnan Provinces, indicating their broad ecological adaptability and low host-specificity, and suggesting that these genera may represent core components of the fungal communities associated with *Rosa* species. In contrast, species of genera including *Allocryptovalsa*, *Anteaglonium*, *Aplosporella*, *Brunneofusispora*, *Chaetosphaeria*, *Cylindrotrichum*, *Cytospora*, *Dendryphion*, *Discosia*, *Distoseptispora*, *Floricola*, *Fusivaginella*, *Kalmusia*, *Leucaenicola*, *Melomastia*, *Montagnula*, *Neohysterium*, *Neoloculosulcatispora*, *Neomassaria*, *Neooccultibambusa*, *Occultitheca*, *Oleaginea*, *Parasulcatispora*, *Parathyridaria*, *Peroneutypa*, *Phaeoisaria*, *Phragmocephala*, *Phyllosticta*, *Pseudocoleophomopsis*, *Pseudodinemasporium*, *Pseudolentistoma*, *Stilbochaeta*, and *Virosphaerella* were collected from only a single collection site. Previous studies have shown that many fungi display clear geographic constraints, often linked to specific hosts or environments (Taylor et al., 2006). Therefore, the contrasting patterns observed here suggest a dual community structure. On one hand, core genera that are widespread and ecologically flexible, and on the other hand, regionally restricted or rare taxa that enhance overall diversity and reflect the influence of local ecological and geographic factors (Peay et al., 2016). Additionally, Anshun, Bijie and Liupanshui cities in Guizhou Province contributed the highest number of fungal genera and strains, which may be attributed to the intensive sampling effort in these regions. Our findings underscore the importance of comprehensive regional surveys in revealing the full extent of fungal biodiversity associated with *Rosa* and other hosts to enable a valuable basis for future biodiversity conservation and taxonomic studies.

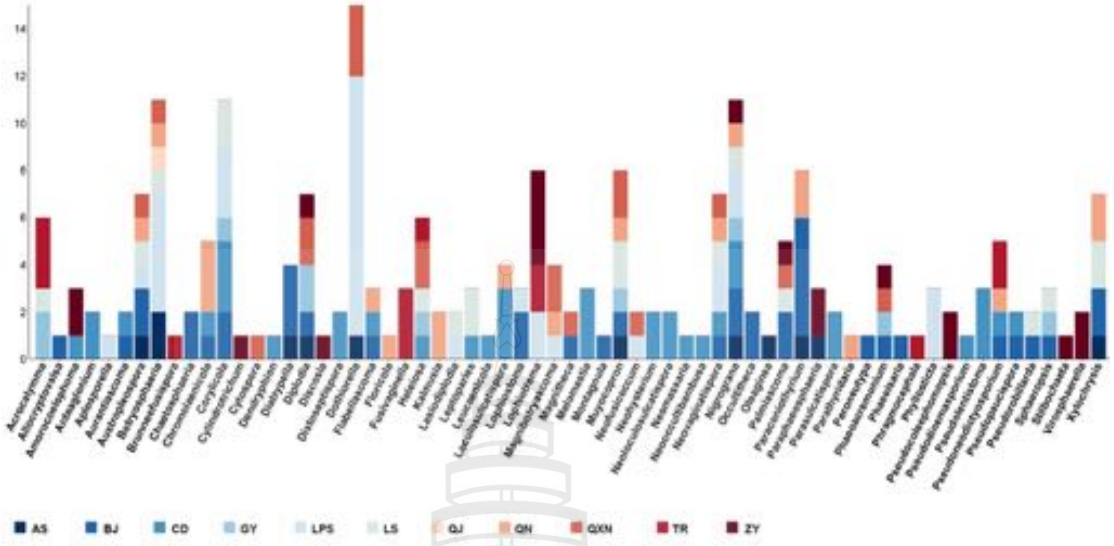


Figure 3.135 Distribution of fungal genera isolated from *Rosa roxburghii* and *R. sterilis*

Figure 3.135 across 11 sampling regions in southwestern China. Each bar represents the total number of strains belonging to each genus, color-coded by region: AS = Anshun city, BJ = Bijie city, CD = Chengdu city, GY = Guiyang city, LPS = Liupanshui city, LS = Leshan city (Sichuan province), QJ = Qujing city (Yunnan province), QN = Qiannan Buyi and Miao Autonomous Prefecture, QXN = Qianxinan Buyi and Miao Autonomous Prefecture, TR = Tongren city, ZY = Zunyi city. The height of each colored segment reflects the number of isolates from the corresponding region.

3.3.5 Checklist of Fungi Associated with *Rosa roxburghii* and *R. sterilis*

To systematically gather information on diversity of species associated with *Rosa roxburghii* and *R. sterilis*, we compiled a comprehensive checklist based on the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2020) and relevant published literature. This study fills a critical gap in our knowledge of fungal assemblages on these two hosts. Previous studies have reported 184 fungal species associated with *R. roxburghii* and *R. sterilis*, which belong to three phyla, eight classes, 22 orders, 56 families, and 90 genera (Table 3.2). With the

inclusion of our new data, the number of fungi associated with the two hosts is now 297 species, which belong to three phyla, eight classes, 30 orders, 81 families, and 145 genera. Notably, except for *Neopestalotiopsis clavispora*, which had previously been reported as a pathogen on *R. sterilis* (Shi et al., 2022), all other fungi associated with *R. sterilis* are recorded here for the first time. This highlights the lack of prior systematic investigations on the fungal community associated with *R. sterilis*. Consequently, instead of preparing two independent checklists, we integrated the records into a single dataset, which can later be separated once studies on *R. sterilis* become more extensive. This checklist provides detailed information on their taxonomic positions, hosts, ecological lifestyles and distributions.

At the phylum level, these fungi are predominantly distributed in Ascomycota, which accounts for 93.94% (279/297) of the total, followed by Basidiomycota (5.72%, 17/297), while Mucoromycota is represented by only one species. Among Ascomycota, Sordariomycetes is the most abundant (135 species, 45%), followed by Dothideomycetes (125 species, 42%), while Eurotiomycetes and Leotiomycetes contain a small number of species, and two other classes are represented by only one species each. A circular barplot illustrates fungal distribution across different classes within the three phyla (Figure 3.136). At the order level, Pleosporales is the dominant group, comprising 24 families and 92 species (31% of the total), followed by Hypocreales with five families and 45 species (15%) (3.137a). At the family level, Botryosphaeriaceae is the dominant group with eight genera, while Didymosphaeriaceae, Lophiostomataceae, and Nectriaceae each include seven genera (Figure 3.137b). Interestingly, 57 families are represented by only one genus. At the genus level, *Fusarium* is the most numerous (21 species), followed by *Diaporthe* (11 species), while 86 genera contain only one species (Figure 3.137c).

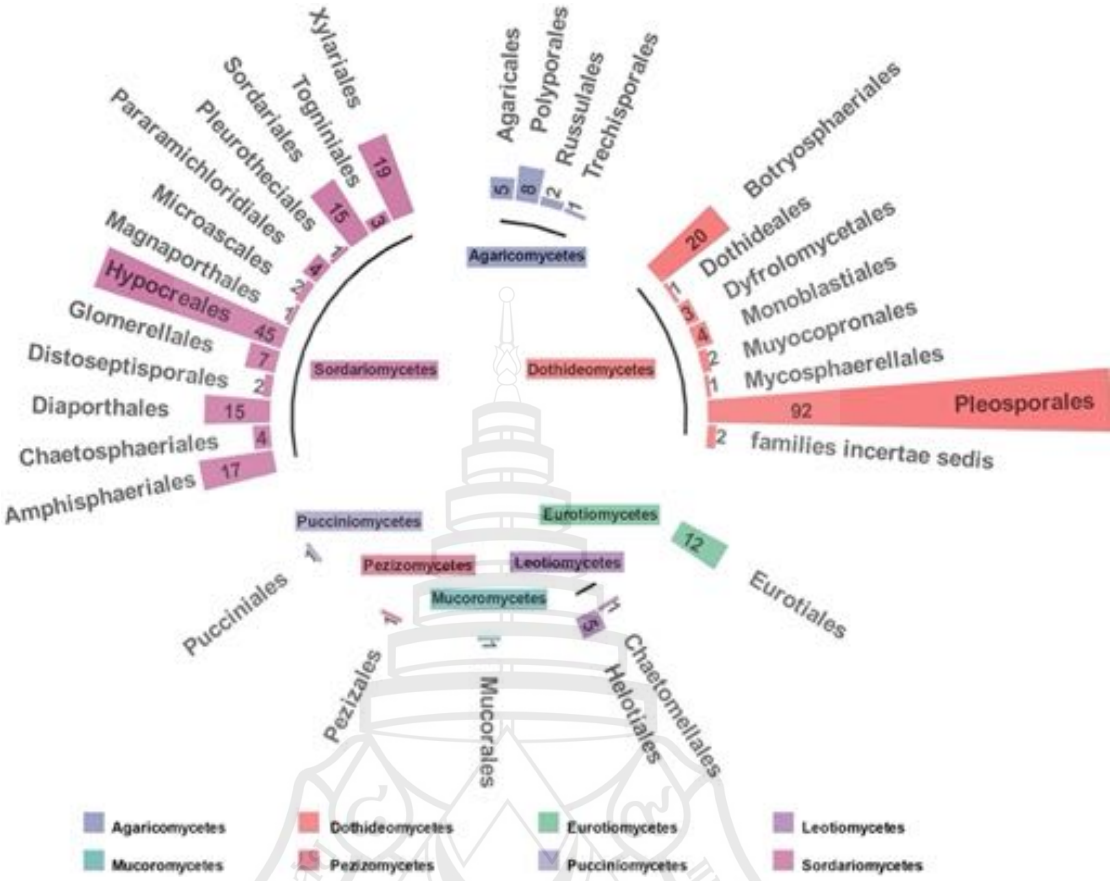
Previous literature has documented endophytic, epiphytic, and pathogenic fungi associated with *Rosa roxburghii* (Xu et al., 2007; Li et al., 2021; Liu et al., 2021; Zhang et al., 2021a, 2021b, 2022, 2024,2023b; Shi et al., 2022; An et al., 2024; Jia et al., 2024;

Hu et al., 2025; Sun et al., 2022, 2025). In contrast, the present study focused on saprobic fungi isolated from dead tissues of *R. roxburghii* and *R. sterilis*. Some saprobes isolated from dead branches might have originated from pre-existing endophytes that shifted to a saprobic lifestyle in response to host senescence or changing environmental conditions (Fisher & Petrini, 1992; Langer et al., 2021; Zhang et al., 2021a, b, 2022, 2023b, 2024; Bhunjun et al., 2024). Consequently, we found only five overlapping species, *Botryosphaeria dothidea*, *Neofusicoccum parvum*, *Phyllosticta capitalensis*, *Paraconiothyrium brasiliense*, and *Neovaginatispora fuckelii*, which were previously reported as endophytes, epiphytes or pathogens (Liu et al., 2021; Zhang et al., 2022; Hu et al., 2025). Among these, *B. dothidea*, *Neofusicoccum parvum*, and *Neovaginatispora fuckelii* were recovered from both *R. roxburghii* and *R. sterilis*.

With regards to lifestyle, saprobic and endophytic fungi exhibited nearly equal species numbers (Figure 3.138). Endophytes and epiphytes were recorded exclusively on *Rosa roxburghii*, while all fungi isolated from *R. sterilis* were saprobes. Among the 297 species in the checklist, 138 had previously been reported as endophytes (46%), 51 as epiphytes (17%), 13 as pathogens (4.4%), and 113 as saprobes, of which 112 were obtained in this study (Wu et al., 2024). Some taxa exhibit different lifestyles (Figure 3.138). For example, eight species had been reported both as endophytes and epiphytes on *R. roxburghii*, three species as endophytes and pathogens, and *Didymella segeticola* as both an epiphyte and pathogen (Table 3.1). Notably, *Neofusicoccum parvum*, *Paraconiothyrium brasiliense*, and *Phyllosticta capitalensis* were previously reported as endophytes but recorded as saprobes in this study. *Neovaginatispora fuckelii* was previously reported as an epiphyte but here as a saprobe. *Botryosphaeria dothidea* had been reported as both an endophyte and pathogen but was here identified as a saprobe. These lifestyle overlaps indicate that many fungi can switch ecological roles depending on host condition or environment. Considering the relatively low number of fungi recorded from *R. sterilis*, the apparent host-specificity patterns observed here are more likely attributable to uneven sampling effort rather than true host restriction. Future

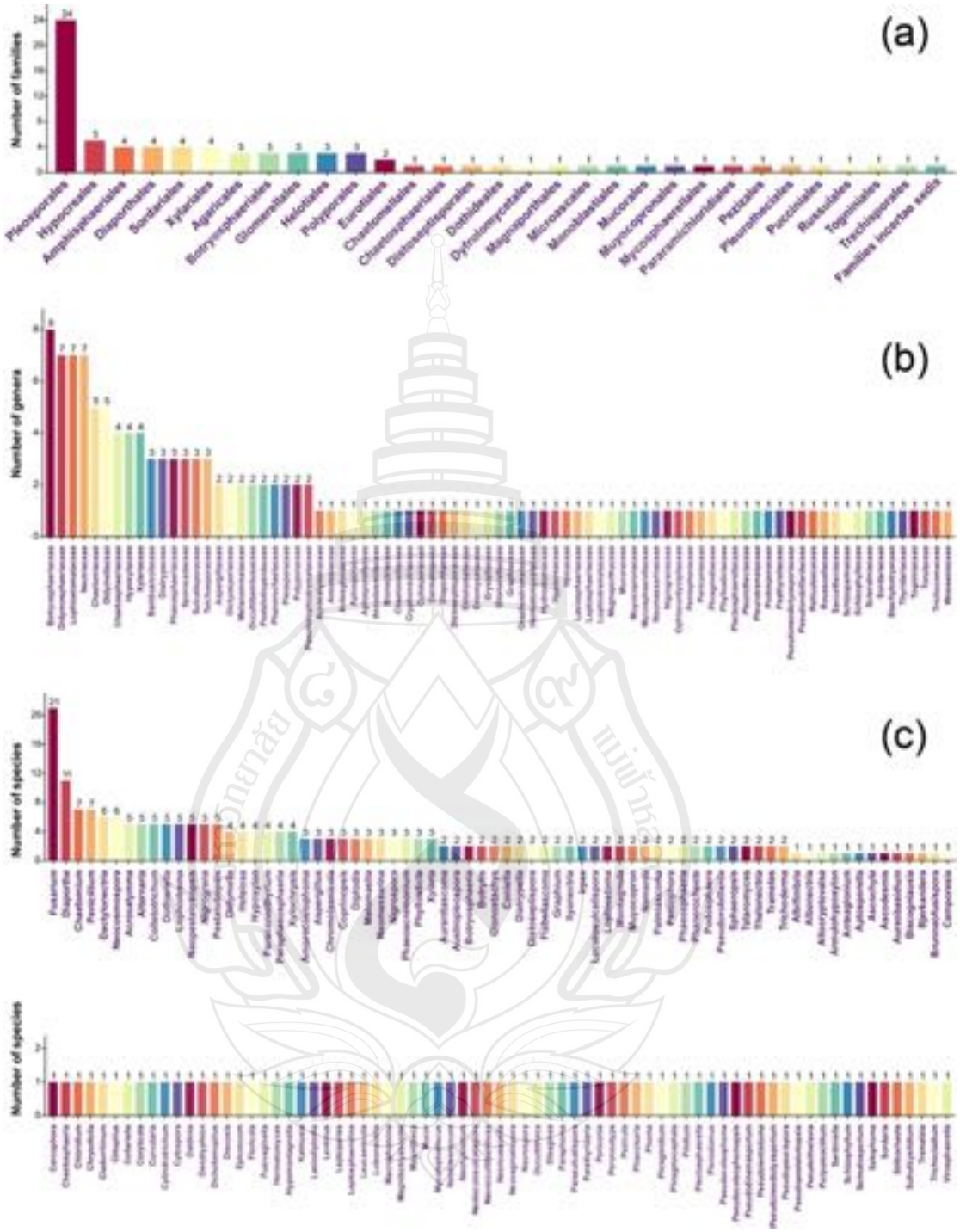
studies should prioritize broader and more balanced sampling of *R. sterilis* to better evaluate its fungal diversity and host association patterns (Hyde et al., 2024). The checklist presented here not only integrates existing records but also significantly expands the known fungal diversity of *R. sterilis*, thereby providing an essential foundation for ecological, taxonomic, and applied studies on *Rosa* associated fungi.

Despite the increasing economic importance of *Rosa roxburghii*, no dedicated platform or database currently exists to document its associated fungal taxa. Establishing a curated, *Rosa* specific fungal database would provide a critical resource for integrating data from fungal taxonomy, plant pathology, ecology, and agroecosystem management. Such a platform could facilitate the early detection of potential fungal pathogens, track host fungus associations, and support the conservation of microbial diversity. Moreover, it would promote the sustainable utilization of fungal resources in the expanding *Rosa* industry. In the future, the integration of high throughput sequencing, functional annotation, and AI assisted taxonomy could enable dynamic updates, species delimitation, and predictive modeling. Establishing such a system would foster interdisciplinary collaboration and provide an accessible digital framework for researchers, growers, and policymakers.



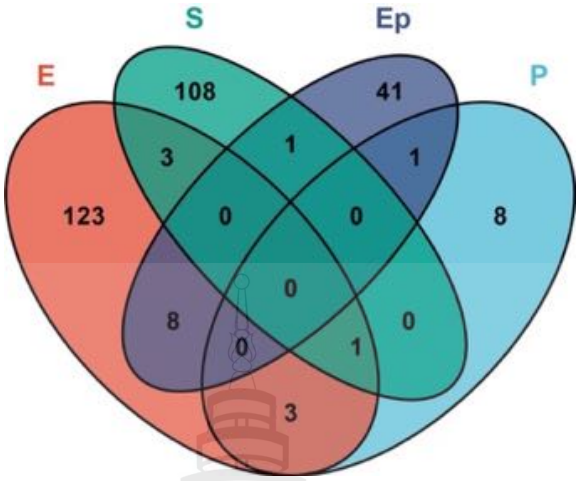
Note Different colors indicate fungal classes, and numbers represent the number of species within each order.

Figure 3.136 Circular barplot illustrating the hierarchical distribution of fungi across classes and orders in this study



Note (a) Numbers of families in each order. (b) Numbers of genera in each family. (c) Numbers of species in each genus.

Figure 3.137 Bar charts showing the taxonomic distribution of fungi recorded in this study across different taxonomic levels



Note (E), saprobes (S), epiphytes (Ep), and pathogens (P). Numbers within the diagram indicate the number of taxa unique to or shared among the respective group.

Figure 3.138 Venn diagram showing the distribution of fungal taxa across four trophic modes endophytes

Table 3.1 List of fungal taxa with overlapping lifestyles

Overlapping lifestyle (s)	Number of taxa	Fungal taxa	References
Endophytic, Pathogenic and Saprobic	1	*Botryosphaeria dothidea*	Liu et al. (2021), Hu et al. (2025), This study
Endophytic and Epiphytic	8	*Alternaria alternata*	Liu et al. (2021)
		Annulohypoxylon stygium	Liu et al. (2021)
		Aspergillus sydowii	Liu et al. (2021), Zhang et al. (2022)
		Coniella quercicola	Liu et al. (2021), Zhang et al. (2024)
		Fusarium oxysporum	Zhang et al. (2021a), Liu et al. (2021)
		Pestalotiopsis vismiae	Liu et al. (2021)
		Phanerochaete concrescens	Liu et al. (2021)
		Trametes hirsuta	Liu et al. (2021)
Endophytic and Pathogenic	3	*Colletotrichum fructicola*	Zhang et al. (2021a), Li et al. (2022), Luo et al. (2023)
		Diaporthe eres	Zhang et al. (2021a), Jia et al. (2024)
		Neopestalotiopsis saprophytica	Zhang et al. (2021a), Zheng et al. (2025)
Endophytic and Saprobic	3	*Neofusicoccum parvum*	Liu et al. (2021), Zhang et al. (2022), This study
		Paraconiothyrium brasiliense	Zhang et al. (2022), This study
		Phyllosticta capitalensis	Liu et al. (2021), Zhang et al. (2022), This study
Epiphytic and Pathogenic	1	*Didymella segeticola*	Liu et al. (2021), An et al. (2024)
Epiphytic and Saprobic	1	*Neovaginatispora fuckelii*	Liu et al. (2021), This study

Table 3.2 Checklist of fungi associated with *Rosa roxburghii* and *R. sterilis*

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
Ascomycota, Dothideomycetes, Botryosphaeriales, Aplosporellaceae	*Aplosporella* (1)	*Aplosporella javeedii*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Botryosphaeriales, Botryosphaeriaceae	*Botryosphaeria* (2)	*Botryosphaeria dothidea*	*R. roxburghii*; *R. sterilis*	E or P or S	China	Liu et al. (2021), Hu et al. (2025), This study
		B. wangensis	*R. roxburghii*	E	China	Zhang et al. (2022)
	Diplodia (3)	*Diplodia mutila*	*R. roxburghii*; *R. sterilis*	S	China	This study
		D. pseudoseriata	*R. roxburghii*	S	China	This study
		D. seriata	*R. sterilis*	S	China	This study
	Dothiorella (5)	*Dothiorella acericola*	*R. roxburghii*	S	China	This study
		D. camelliae	*R. roxburghii*; *R. sterilis*	S	China	This study
		D. citricola	*R. roxburghii*	S	China	This study
		D. sarmentorum	*R. roxburghii*	S	China	This study
		D. zanthoxyli	*R. roxburghii*; *R. sterilis*	S	China	This study
	Lasiodiplodia (1)	*Lasiodiplodia theobromae*	*R. roxburghii*	S	China	This study
	Macrophomina (1)	*Macrophomina phaseolina*	*R. roxburghii*	E	China	Zhang et al. (2022)
	Neofusicoccum (1)	*Neofusicoccum parvum*	*R. roxburghii*; *R. sterilis*	E or S	China	Liu et al. (2021), Zhang et al. (2022), This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Sardiniella (1)	*Sardiniella celtidis*	*R. roxburghii*	Ep	China	Liu et al. (2021)
	Sphaeropsis (2)	*Sphaeropsis citrigena*	*R. roxburghii*; *R. sterilis*	S	China	This study
		S. linhaiensis	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Botryosphaeriales, Phyllostictaceae	*Phyllosticta* (3)	*Phyllosticta capitalensis*	*R. roxburghii*	E or S	China	Liu et al. (2021), Zhang et al. (2022), This study
		P. rosae	*R. roxburghii*	S	China	This study
		P. telopeae	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Dothideomycetes, Dothideales, Saccotheciaceae	*Aureobasidium* (1)	*Aureobasidium microstictum*	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Dothideomycetes, Dyfrolomycetales, Pleurotremataceae	*Melomastia* (3)	*Melomastia diqingensis*	*R. roxburghii*	S	China	This study
		M. puerensis	*R. roxburghii*	S	China	This study
		M. sichuanensis	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Monoblastiales, Eriomycetaceae	*Heleiosa* (4)	*Heleiosa ellipsoidispora*	*R. roxburghii*	S	China	This study
		H. guizhouensis	*R. roxburghii*; *R. sterilis*	S	China	This study
		H. rosae	*R. roxburghii*	S	China	This study
		H. septata	*R. roxburghii*; *R. sterilis*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
Ascomycota, Dothideomycetes, Muyocopronales, Muyocopronaceae	*Muyocopron* (2)	*Muyocopron lithocarpi*	*R. roxburghii*; *R. sterilis*	S	China	This study
		M. rosae	*R. sterilis*	S	China	This study
Ascomycota, Dothideomycetes, Mycosphaerellales, Mycosphaerellaceae	*Virosphaerella* (1)	*Virosphaerella rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Acrocalymmaceae	*Acrocalymma* (5)	*Acrocalymma hyalinum*	*R. roxburghii*	S	China	This study
		A. medicaginis	*R. roxburghii*	S	China	This study
		A. rosae	*R. roxburghii*	S	China	This study
		A. rosicola	*R. roxburghii*	S	China	This study
		Acrocalymma sp.	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Amorosiaceae	*Amorocoelophoma* (3)	*Amorocoelophoma guizhouensis*	*R. roxburghii*	S	China	This study
		A. rosae	*R. roxburghii*	S	China	This study
		A. sichuanensis	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Anteagloniaceae	*Anteaglonium* (1)	*Anteaglonium rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Bambusicolaceae	*Corylicola* (1)	*Corylicola italica*	*R. roxburghii*; *R. sterilis*	S	China	This study
	Leucaenicola (1)	*Leucaenicola rosae*	*R. roxburghii*	S	China	This study
	Palmiascoma (2)	*Palmiascoma acericola*	*R. roxburghii*; *R. sterilis*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		P. qujingense	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Dictyosporiaceae	*Neohysterium* (1)	*Neohysterium rosae*	*R. roxburghii*	S	China	This study
	Pseudocoleophoma (1)	*Pseudocoleophoma rosae*	*R. roxburghii*	S	China	Wu et al. (2024)
Ascomycota, Dothideomycetes, Pleosporales, Didymellaceae	*Ascochyta* (1)	*Ascochyta medicaginicola*	*R. roxburghii*	Ep	China	Liu et al. (2021)
	Epicoccum (1)	*Epicoccum latusicollum*	*R. roxburghii*	E	China	Zhang et al. (2022)
	Didymella (4)	*Didymella bellidis*	*R. roxburghii*	E	China	Liu et al. (2021)
		D. pomorum	*R. roxburghii*	Ep	China	Liu et al. (2021)
		D. segeticola	*R. roxburghii*	Ep or P	China	Liu et al. (2021), An et al. (2024)
		D. sinensis	*R. roxburghii*	E	China	Liu et al. (2021)
	Leptosphaerulina (1)	*Leptosphaerulina australis*	*R. roxburghii*	Ep	China	Liu et al. (2021)
	Phoma (1)	*Phoma* sp.	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Didymosphaeriaceae	*Austropleospora* (2)	*Austropleospora keteleeriae*	*R. roxburghii*	S	China	This study
		A. ochracea	*R. roxburghii*; *R. sterilis*	S	China	This study
	Chromolaenicola (3)	*Chromolaenicola clematidis*	*R. roxburghii*	S	China	This study
		C. rosae	*R. roxburghii*	S	China	This study
		C. sapindi	*R. roxburghii*	S	China	This study
	Kalmusia (1)	*Kalmusia rosae*	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Montagnula (2)	*Montagnula chromolaenicola*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		M. verniciae	*R. sterilis*	S	China	This study
	Paraconiothyrium (4)	*Paraconiothyrium brasiliense*	*R. roxburghii*	E or S	China	Zhang et al. (2022), This study
		P. fuckelii	*R. sterilis*	S	China	This study
		P. guizhouense	*R. roxburghii*; *R. sterilis*	S	China	This study
		P. rosicola	*R. sterilis*	S	China	This study
	Paraphaeosphaeria (4)	*Paraphaeosphaeria camelliae*	*R. roxburghii*	S	China	This study
		P. neglecta	*R. roxburghii*	p	China	Sun et al. (2025)
		P. michotii	*R. roxburghii*	S	China	This study
		P. verruculosa	*R. roxburghii*	S	China	This study
	Tremateia (1)	*Tremateia guiyangensis*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Hermatomycetaceae	*Hermatomyces* (1)	*Hermatomyces pandanicola*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Leptosphaeriaceae	*Plenodomus* (1)	*Plenodomus sinensis*	*R. roxburghii*	E	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Lophiostomataceae	*Biappendiculispora* (1)	*Biappendiculispora japonica*	*R. sterilis*	S	China	This study
	Flabellascoma (2)	*Flabellascoma fusiforme*	*R. roxburghii*	S	China	This study
		F. pistaciae	*R. sterilis*	S	China	This study
	Leptoparies (1)	*Leptoparies magnoliae*	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Neovaginatispora (1)	*Neovaginatispora fuckelii*	*R. roxburghii*; *R. sterilis*	Ep or S	China	Liu et al. (2021), This study
	Oleaginea (1)	*Oleaginea sichuanensis*	*R. sterilis*	S	China	This study
	Pseudolentistoma (1)	*Pseudolentistoma rosae*	*R. roxburghii*	S	China	This study
	Pseudolophiostoma (1)	*Pseudolophiostoma rosae*	*R. roxburghii*	S	China	This study
	Pseudopaucispora (1)	*Pseudopaucispora rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Lophiotremataceae	*Lophiotrema* (5)	*Lophiotrema hydei*	*R. roxburghii*	S	China	This study
		L. karsti	*R. roxburghii*	S	China	This study
		L. rosae	*R. roxburghii*	S	China	This study
		L. rosicola	*R. roxburghii*	S	China	This study
		L. rubusiicola	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Melanommataceae	*Magnitheca* (1)	*Magnitheca* rosae	*R. sterilis*	S	China	This study
	Phragmocephala (1)	*Phragmocephala atra*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Neomassarinaceae	*Neomassarina* (3)	*Neomassarina chromolaenae*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		N. formosana	*R. roxburghii*	S	China	This study
		N. thailandica	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Nigrograna ceae	*Nigrograna* (5)	*Nigrograna camelliae*	*R. roxburghii*	S	China	This study
		N. oleae	*R. roxburghii*; *R. sterilis*	S	China	This study
		N. rosae	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		N. thymi	*R. roxburghii*	S	China	This study
		N. triseptata	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Occultibambusaceae	*Brunneofusispora* (1)	*Brunneofusispora rosae*	*R. roxburghii*	S	China	This study
	Neoocculitibambusa (1)	*Neoocculitibambusa kaiyangensis*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Periconiaceae	*Periconia* (1)	*Periconia byssoides*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Dothideomycetes, Pleosporales, Phaeosphaeriaceae	*Paraphoma* (1)	*Paraphoma vinacea*	*R. roxburghii*	E	China	Zhang et al. (2022)
	Phaeosphaeria (2)	*Phaeosphaeria oryzae*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. eriobotryae	*R. roxburghii*	Ep	China	Liu et al. (2021)
	Setophoma (1)	*Setophoma terrestris*	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Dothideomycetes, Pleosporales, Pleosporaceae	*Alternaria* (5)	*Alternaria alternata*	*R. roxburghii*	E or Ep	China	Liu et al. (2021)
		A. daucifolii	*R. roxburghii*	E	China	Zhang et al. (2022)
		A. longipes	*R. roxburghii*	E	China	Zhang et al. (2022)
		A. solani	*R. roxburghii*	E	China	Liu et al. (2021)
		A. tenuissima	*R. roxburghii*	E	China	Liu et al. (2021), Zhang et al. (2022)
	Curvularia (1)	*Curvularia kusanoi*	*R. roxburghii*	Ep	China	Liu et al., (2021)
Ascomycota, Dothideomycetes, Pleosporales, Pseudolophiotremataceae	*Fusivaginella* (1)	*Fusivaginella rosae*	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Pseudocoleophomopsis (1)	*Pseudocoleophomopsis rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Roussoellaceae	*Neoroussoella* (1)	*Neoroussoella* sp.	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Dothideomycetes, Pleosporales, Sulcatisporaceae	*Loculosulcatispora* (2)	*Loculosulcatispora hongheensis*	*R. roxburghii*	S	China	This study
		L. paeoniae	*R. roxburghii*	S	China	This study
	Neoloculosulcatispora (1)	*Neoloculosulcatispora rosae*	*R. roxburghii*	S	China	This study
	Parasulcatispora (1)	*Parasulcatispora rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Teichosporaceae	*Aurantiascoma* (2)	*Aurantiascoma minimum*	*R. roxburghii*	S	China	This study
		A. rosae	*R. sterilis*	S	China	This study
	Floricola (1)	*Floricola rosae*	*R. roxburghii*	S	China	This study
	Magnibotryascoma (1)	*Magnibotryascoma mali*	*R. roxburghii*; *R. sterilis*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Thyridariaceae	*Parathyridaria* (1)	*Parathyridaria rosicola*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, Pleosporales, Torulaceae	*Dendryphion* (1)	*Dendryphion verrucosum*	*R. roxburghii*	S	China	This study
Ascomycota, Dothideomycetes, families *incertae sedis*, Pseudorobillardaceae	*Pseudorobillarda* (2)	*Pseudorobillarda camelliae-sinensis*	*R. roxburghii*	S	China	This study
		P. rosae	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
Ascomycota, Eurotiomycetes, Eurotiales, Aspergillaceae	*Aspergillus* (3)	*Aspergillus fumigatus*	*R. roxburghii*	E	China	Zhang et al. (2022)
		A. sydowii	*R. roxburghii*	Ep or E	China	Liu et al. (2021), Zhang et al. (2022)
		A. uvarum	*R. roxburghii*	E	China	Zhang et al. (2022)
	Penicillium (7)	*Penicillium crustosum*	*R. roxburghii*	E	China	Zhang et al. (2022)
		P. ochrochloron	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. ortum	*R. roxburghii*	E	China	Liu et al. (2021)
		P. oxalicum	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. rotoruae	*R. roxburghii*	E	China	Zhang et al. (2022)
		P. steckii	*R. roxburghii*	E	China	Zhang et al. (2022)
		P. victoriae	*R. roxburghii*	P	China	Hu et al. (2024)
Ascomycota, Eurotiomycetes, Eurotiales, Trichocomaceae	*Talaromyces* (2)	*Talaromyces rosorhiza*	*R. roxburghii*	E	China	Zhang et al. (2021b)
		T. verruculosus	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Leotiomycetes, Chaetomellales, Chaetomellaceae	*Pilidium* (1)	*Pilidium lythri*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Leotiomycetes, Helotiales, Dermateaceae	*Pezicula* (1)	*Pezicula radicicola*	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Leotiomycetes, Helotiales, Erysiphaceae	*Podosphaera* (2)	*Podosphaera pannosa*	*R. roxburghii*	P	China	Xu et al. (2007)
		Podosphaera sp.	*R. roxburghii*	P	China	Li et al. (2021)
Ascomycota, Leotiomycetes, Helotiales, Sclerotiniaceae	*Botrytis* (2)	*Botrytis elliptica*	*R. roxburghii*	E	China	Zhang et al. (2022)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		Botrytis sp.	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Pezizomycetes, Pezizales, Ascodesmidaceae	*Ascodesmis* (1)	*Ascodesmis rosicola*	*R. roxburghii*	E	China	Zhang et al. (2021b; 2022)
Ascomycota, Sordariomycetes, Amphisphaeriales, Apiosporaceae	*Nigrospora* (3)	*Nigrospora falsivesicularis*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		N. musae	*R. roxburghii*	E	China	Zhang et al. (2021a)
		N. oryzae	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Amphisphaeriales, Pestalotiopsidaceae	*Pestalotiopsis* (5)	*Pestalotiopsis biciliata*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. cocculi	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. microspora	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. trachycarpicola	*R. roxburghii*	E	China	Zhang et al. (2021a)
		P. vismiae	*R. roxburghii*	E or Ep	China	Liu et al. (2021)
	Pseudopestalotiopsis (1)	*Pseudopestalotiopsis theae*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Sordariomycetes, Amphisphaeriales, Pseudoneodictyosporiaceae	*Pseudoneodictyosporium* (1)	*Pseudoneodictyosporium rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Sordariomycetes, Amphisphaeriales, Sporocadaceae	*Discosia* (1)	*Discosia castaneae*	*R. roxburghii*	S	China	This study
	Neopestalotiopsis (5)	*Neopestalotiopsis brasiliensis*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		N. caulicola	*R. roxburghii*	E	China	Zhang et al. (2024)
		N. clavispora	*R. sterilis*	P	China	Shi et al. (2022)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		N. fructicola	*R. roxburghii*	E	China	Zhang et al. (2024)
		N. saprophytica	*R. roxburghii*	E or P	China	Zhang et al. (2021a), Zheng et al. (2025)
	Seimatosporium (1)	*Seimatosporium endophyticum*	*R. roxburghii*	E	China	Zhang et al. (2024)
Ascomycota, Sordariomycetes, Chaetosphaeriales, Chaetosphaeriaceae	*Chaetosphaeria* (1)	*Chaetosphaeria rosae*	*R. roxburghii*; *R. sterilis*	S	China	This study
	Chloridium (1)	*Chloridium aseptatum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Pseudodinemasporium (1)	*Pseudodinemasporium fabiforme*	*R. roxburghii*	S	China	This study
	Stilbochaeta (1)	*Stilbochaeta sinensis*	*R. roxburghii*	S	China	This study
Ascomycota, Sordariomycetes, Diaporthales, Cryphonectriaceae	*Chrysofolia* (1)	*Chrysofolia fructicola*	*R. roxburghii*	E	China	Zhang et al. (2024)
Ascomycota, Sordariomycetes, Diaporthales, Schizoparmaceae	*Coniella* (2)	*Coniella cili*	*R. roxburghii*	E	China	Zhang et al. (2024)
		C. quercicola	*R. roxburghii*	E or Ep	China	Liu et al. (2021), Zhang et al. (2024)
Ascomycota, Sordariomycetes, Diaporthales, Cytosporaceae	*Cytospora* (1)	*Cytospora rosae*	*R. sterilis*	S	China	This study
Ascomycota, Sordariomycetes, Diaporthales, Diaporthaceae	*Diaporthe* (11)	*Diaporthe arctii*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. arecae	*R. roxburghii*	E	China	Zhang et al. (2021a)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		D. eres	*R. roxburghii*	E or P	China	Zhang et al. (2021a), Jia et al. (2024)
		D. ganjae	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. juniperivora	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. leucospermi	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. oncostoma	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. phoenicicola	*R. roxburghii*	P	China	Chen et al. (2025)
		D. sclerotioides	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. sojae	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. stewartii	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Sordariomycetes, Distoseptisporales, Distoseptisporaceae	*Distoseptispora* (2)	*Distoseptispora alangii*	*R. roxburghii*	S	China	This study
		D. sinensis	*R. roxburghii*	S	China	This study
Ascomycota, Sordariomycetes, Glomerellales, Glomerellaceae	*Colletotrichum* (5)	*Colletotrichum aenigma*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. citri	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. fructicola	*R. roxburghii*	E or P	China	Zhang et al. (2021a), Li et al. (2022), Luo et al. (2023)
		C. gloeosporioides	*R. roxburghii*	E	China	Zhang et al. (2021a), Liu et al. (2021)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		C. karsti	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Glomerellales, Plectosphaerellaceae	*Plectosphaerella* (1)	*Plectosphaerella humicola*	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Glomerellales, Reticulascaceae	*Cylindrotrichum* (1)	*Cylindrotrichum rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Sordariomycetes, Hypocreales, Bionectriaceae	*Clonostachys* (2)	*Clonostachys rhizophaga*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. rosea	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Hypocreales, Hypocreaceae	*Trichoderma* (2)	*Trichoderma hamatum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		T. virens	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Hypocreales, Nectriaceae	*Albonectria* (1)	*Albonectria guizhouensis*	*R. roxburghii*	E	China	Zhang et al. (2023b)
	Dactylonectria (6)	*Dactylonectria alcacerensis*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. macrodidyma	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. novozelandica	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. pauciseptata	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. riojana	*R. roxburghii*	E	China	Zhang et al. (2021a)
		D. valentina	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Fusarium (21)	*Fusarium acuminatum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		F. annulatum	*R. roxburghii*	P	China	Wang et al. (2024)
		F. arbusti	*R. roxburghii*	E	China	Zhang et al. (2023b)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		F. avenaceum	*R. roxburghii*	E	China	Zhang et al. (2021a, 2023b)
		F. caulendophyticum	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. caulicola	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. cili	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. cugenangense	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. fujikuroi	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. graminearum	*R. roxburghii*	E	China	Zhang et al. (2021a)
		F. lateritium	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. meridionale	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. nirenbergiae	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. oxysporum	*R. roxburghii*	E or Ep	China	Zhang et al. (2021a), Liu et al. (2021)
		F. proliferatum	*R. roxburghii*	E	China	Zhang et al. (2021a)
		F. qiannanense	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. radicigenum	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. rosae-roxburghii	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. rosendophyticum	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. rosiradicicola	*R. roxburghii*	E	China	Zhang et al. (2023b)
		F. solani	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Ilyonectria (2)	*Ilyonectria radicigena*	*R. roxburghii*	E	China	Zhang et al. (2024)
		I. robusta	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Luteonectria (1)	*Luteonectria nematophila*	*R. roxburghii*	E	China	Zhang et al. (2021a, 2023b)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Neocosmospora (6)	*Neocosmospora falciformis*	*R. roxburghii*	E	China	Zhang et al. (2023b)
		N. ipomoeae	*R. roxburghii*	E	China	Zhang et al. (2023b)
		N. lichenicola	*R. roxburghii*	E	China	Zhang et al. (2021a, 2023b)
		N. liupanshuiensis	*R. roxburghii*	E	China	Zhang et al. (2023b)
		N. pisi	*R. roxburghii*	E	China	Zhang et al. (2023b)
		N. solani	*R. roxburghii*	E	China	Zhang et al. (2023b)
	Thelonectria (2)	*Thelonectria blackeriella*	*R. roxburghii*	E	China	Zhang et al. (2021a, 2023b)
		Thelonectria sp.	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Hypocreales, Ophiocordycipitaceae	*Purpureocillium* (1)	*Purpureocillium lilacinum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Hypocreales, Stachybotryaceae	*Albifimbria* (1)	*Albifimbria verrucaria*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Sordariomycetes, Magnaporthales, Magnaporthaceae	*Mycoleptodiscus* (1)	*Mycoleptodiscus terrestris*	*R. roxburghii*	E	China	Zhang et al. (2022)
Ascomycota, Sordariomycetes, Microascales, Graphiaceae	*Graphium* (2)	*Graphium basitruncatum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		G. euwallaceae	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Pararamichloridiales, Woswasiaceae	*Xylochrysis* (4)	*Xylochrysis asexualis*	*R. roxburghii*	S	China	This study
		X. lucida	*R. roxburghii*	S	China	This study

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		X. rosae	*R. roxburghii*	S	China	This study
		X. sexualis	*R. roxburghii*; *R. sterilis*	S	China	This study
Ascomycota, Sordariomycetes, Pleurotheciales, Pleurotheciaceae	*Phaeoisaria* (1)	*Phaeoisaria clematidis*	*R. sterilis*	S	China	This study
Ascomycota, Sordariomycetes, Sordariales, Chaetomiaceae	*Chaetomium* (7)	*Chaetomium globosum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. novozelandicum	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. rectangulare	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. rosifloricola	*R. roxburghii*	E	China	Zhang et al. (2024)
		C. rosiradicicola	*R. roxburghii*	E	China	Zhang et al. (2024)
		C. subaffine	*R. roxburghii*	E	China	Zhang et al. (2021a)
		C. tenue	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Collariella (1)	*Collariella carteri*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Dichotomopilus (1)	*Dichotomopilus variostiolatus*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Pseudothielavia (1)	*Pseudothielavia arxii*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Trichocladium (1)	*Trichocladium* sp.	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Sordariales, Lasiosphaeriaceae	*Cercophora* (1)	*Cercophora* sp.	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Sordariales, Podosporaceae	*Cladorrhinum* (1)	*Cladorrhinum coprophilum*	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Sordariales, Sordariaceae	*Neurospora* (1)	*Neurospora* sp.	*R. roxburghii*	E	China	Zhang et al. (2021a)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
	Sordaria (1)	*Sordaria sibutii*	*R. roxburghii*	E	China	Zhang et al. (2021a)
Ascomycota, Sordariomycetes, Togniniales, Togniniaceae	*Phaeoacremonium* (3)	*Phaeoacremonium argentinense*	*R. roxburghii*	S	China	This study
		P. chiangmaiense	*R. sterilis*	S	China	This study
		P. rosae	*R. roxburghii*; *R. sterilis*	S	China	This study
Ascomycota, Sordariomycetes, Xylariales, Diatrypaceae	*Allocryptovalsa* (1)	*Allocryptovalsa xishuangbanica*	*R. sterilis*	S	China	This study
	Diatrypella (2)	*Diatrypella pseudooregonensis*	*R. roxburghii*; *R. sterilis*	S	China	This study
		D. vulgaris	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Peroneutypa (1)	*Peroneutypa rosae*	*R. roxburghii*	S	China	This study
Ascomycota, Sordariomycetes, Xylariales, Graphostromataceae	*Biscogniauxia* (1)	*Biscogniauxia petrensis*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Ascomycota, Sordariomycetes, Xylariales, Hypoxylaceae	*Annulohypoxylon* (1)	*Annulohypoxylon stygium*	*R. roxburghii*	E or Ep	China	Liu et al. (2021)
	Daldinia (1)	*Daldinia eschscholtzii*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Hypomontagnella (1)	*Hypomontagnella monticulosa*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Hypoxylon (4)	*Hypoxylon florendophyticum*	*R. roxburghii*	E	China	Zhang et al. (2024)
		H. perforatum	*R. roxburghii*	Ep	China	Liu et al. (2021)
		H. pulicicidum	*R. roxburghii*	E	China	Zhang et al. (2024)
		H. rosicaulendophyticum	*R. roxburghii*	E	China	Zhang et al. (2024)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
Ascomycota, Sordariomycetes, Xylariales, Xylariaceae	*Camporesia* (1)	*Camporesia sambuci*	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Nemania (2)	*Nemania diffusa*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		N. primolutea	*R. roxburghii*	E	China	Zhang et al. (2021a)
	Occultitheca (1)	*Occultitheca rosae*	*R. roxburghii*; *R. sterilis*	S	China	This study
	Xylaria (3)	*Xylaria allantoidea*	*R. roxburghii*	E	China	Zhang et al. (2021a)
		X. brevipes	*R. roxburghii*	E	China	Zhang et al. (2021a)
		Xylaria sp.	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae	*Clitopilus* (1)	*Clitopilus* sp.	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Agaricales, Psathyrellaceae	*Coprinopsis* (3)	*Coprinopsis cinerea*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		C. velatopruinatus	*R. roxburghii*	Ep	China	Liu et al. (2021)
		C. xanthothrix	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Agaricales, Schizophyllaceae	*Schizophyllum* (1)	*Schizophyllum commune*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Polyporales, Irpicaceae	*Irpex* (2)	*Irpex lacteus*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		I. latemarginatus	*R. roxburghii*	E	China	Zhang et al. (2022)
Basidiomycota, Agaricomycetes, Polyporales, Phanerochaetaceae	*Bjerkandera* (1)	*Bjerkandera adusta*	*R. roxburghii*	E	China	Zhang et al. (2022)
	Phanerochaete (2)	*Phanerochaete concrescens*	*R. roxburghii*	E or Ep	China	Liu et al. (2021)

Table 3.2 (continued)

Phylum, Class, Order, Family	Genus (species number)	Species	Host	Life mode	Distribution	References
		P. sordida	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Polyporales, Polyporaceae	*Lentinus* (1)	*Lentinus arcularius*	*R. roxburghii*	Ep	China	Liu et al. (2021)
	Trametes (2)	*Trametes hirsuta*	*R. roxburghii*	E or Ep	China	Liu et al. (2021)
		T. versicolor	*R. roxburghii*	E	China	Zhang et al. (2022)
Basidiomycota, Agaricomycetes, Russulales, Peniophoraceae	*Peniophora* (2)	*Peniophora bicornis*	*R. roxburghii*	Ep	China	Liu et al. (2021)
		P. crassitunicata	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Agaricomycetes, Trechisporales, Hydnodontaceae	*Subulicystidium* (1)	*Subulicystidium longisporum*	*R. roxburghii*	Ep	China	Liu et al. (2021)
Basidiomycota, Pucciniomycetes, Pucciniales, Phragmidiaceae	*Phragmidium* (1)	*Phragmidium rosae-roxburghii*	*R. roxburghii*	P	China	Sun et al. (2022)
Mucoromycota, Mucoromycetes, Mucorales, Mucoraceae	*Mucor* (1)	*Mucor fragilis*	*R. roxburghii*	Ep	China	Liu et al. (2021)

Note The current name is used according to Index Fungorum (2025), and the classification follows Hyde et al. (2024). Genera and species are listed in alphabetical order. The number of species in each genus is given in parentheses after the genus name. For example, *Botryosphaeria* (2) denotes two species of *Botryosphaeria*.

The mode of life is given as (E) endophyte, (Ep) epiphytes, (P) pathogen and (S) saprotroph.

CHAPTER 4

BIODIVERSITY, TAXONOMY AND PHYLOGENY OF BOTRYOSPHARIALES

4.1 Introduction

The order Botryosphaeriales (Dothideomycetes) was established by Schoch et al. (2006), including a single family Botryosphaeriaceae. A recent comprehensive study by Phillips et al. (2019) accepted six families, viz. Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae, and Saccharataceae are in this order based on morphological and phylogenetic analysis. Members of Botryosphaeriales have worldwide distribution on many different host plants (Wulandari et al., 2009; Liu et al., 2012; Dissanayake et al., 2016; Wang et al., 2019; Senwanna et al., 2021; De Silva et al., 2022) and occur as endophytes, pathogens, and saprobes. As opportunistic pathogens, they are of considerable importance to agriculture, horticulture, and forestry (Chethana et al., 2016; Manawasinghe et al., 2016) while causing severe diseases of economically important crops and plants, leading to huge economic losses (Slippers et al., 2007; Mehl et al., 2017).

The family Botryosphaeriaceae was introduced by Theissen and Sydow (1918) with three genera, *Botryosphaeria* (type genus), *Dibotryon* and *Phaeobotryon*. In recent years, genera in this family have been subjected to continuous revisions (Arx & Müller, 1954, 1975, Barr, 1987, Crous et al., 2006, Liu et al., 2012, Phillips et al., 2013, 2019, Dissanayake et al., 2016, Wijayawardene et al., 2020). The subsequent study by Hongsanan et al. (2020) based on morphology and phylogeny, accepted 22 genera in Botryosphaeriaceae, consisting of more than 170 species. Among all the families within Botryosphaeriales, Botryosphaeriaceae is the largest with a broad host range. Fungi in

this family are well-known as plant endophytes, saprobes and pathogens, causing ulceration, dieback and stem-end rot of plants or fruits, e.g., *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia* and *Neofusicoccum* (Smith et al., 1996; Phillips et al., 2006, 2013; Slippers & Wingfield, 2007; Liu et al., 2012; Li et al., 2014; Dissanayake et al., 2016; Zhang et al., 2021). The sexual morphs of Botryosphaeriacea*e* are characterized by solitary or clustered ascostromata, often with two-layers of dark brown to hyaline cells; 8-spored, short-stipitate, clavate asci and hyaline or pigmented, aseptate or septate, ellipsoid or ovoid ascospores, and its asexual morphs are coelomycetous, characterized by ovoid, hyaline or brown, aseptate, one- or multi-septate conidia, and conidiophores mostly reduced to conidiogenous cells (Denman et al., 2000; Crous et al., 2006; Phillips et al., 2006, 2013, 2019; Liu et al., 2012; Slippers et al., 2013).

Phyllostictaceae was proposed by Fries (1849) and accepted by Hawksworth and David (1989). Seaver (1922) used Phyllostictales and Phyllostictaceae for *Phyllosticta*. After that, Schoch et al. (2006) suggested that *Phyllosticta* belongs to Botryosphaeriaceae and this was accepted by Crous et al. (2006) and Liu et al. (2012) who noted that *Phyllosticta* is distinct from other genera in Botryosphaeriaceae. Therefore, Wikee et al. (2013) suggested Phyllostictaceae as a distinct family in Botryosphaeriales and Slippers et al. (2013) formally re-instated the family and the type genus is *Phyllosticta*. Phyllostictaceae has uniloculate ascostromata and mucilage sheath ascospores, and most species have wide host ranges as foliicolous, pathogenic, endophytic or saprobic in the family.

During recent investigations of Botryosphaeriales diversity in China and Thailand, several isolates resembling members of Botryosphaeriaceae were obtained from decaying woody hosts. Morphological comparisons combined with multi-gene phylogenetic analyses (ITS, LSU, *tef1-α*, *tub2*) confirmed their taxonomic placement and revealed a high diversity of species across different hosts and regions. In this study, I introduce seven novel species, namely *Dothiorella ovata*, *D. rosacearum*, *D. septata*,

Lasiodiplodia chiangraiensis, *L. delonicis*, *Neodeightonia septata*, and *Phyllosticta rosae*, together with numerous new host records of previously known species such as *Botryosphaeria dothidea*, *Diplodia seriata*, *Lasiodiplodia theobromae*, and *Neofusicoccum parvum*. Notably, most of these taxa were collected from *Rosa roxburghii* and *R. sterilis*, highlighting these hosts as reservoirs of fungal diversity within Botryosphaeriales. Additionally, this study extended the taxonomic framework of Botryosphaeriaceae by discovering new species, new host records, and new geographical records in China and Thailand.

4.2 Results

Ascomycota Caval.-Sm.

Dothideomycetes O.E. Erikss. & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Aplosporellaceae Slippers, Boissin & Crous

Type genus – *Aplosporella* Speg.

Notes – Based on the phylogeny inferred from SSU-LSU-ITS-*tef1α*-*tub2*-mtSSU sequences, Slippers et al. (2013) established the family Aplosporellaceae to accommodate *Aplosporella* and synonymized *Bagnisiella* under the type genus (Ekanayaka et al., 2016; Phillips et al., 2019). Subsequently, Sharma et al. (2017) introduced *Alanomyces* into this family, which currently comprises two species, *A. indicus* (Sharma et al., 2017) and *A. manoharacharyi* (Rana et al., 2024). Members of this family are characterized by immersed to semi-immersed, erumpent to superficial, unilocular or multilocular ascomata, bitunicate, short pedicellate, cylindric-clavate asci with hyaline, aseptate, thick-walled, ellipsoid to ovate ascospores. The asexual morph is coelomycetous, having multiloculate conidiomata, holoblastic, smooth, cylindrical

conidiogenous cells with hyaline to brown, aseptate to septate, ellipsoidal to subcylindrical conidia (Ekanayaka et al., 2016; Rana et al., 2024; Du et al., 2025).

Aplosporella Speg., Anal. Soc. cient. argent. 10(4): 157 (1880)

Type species – *Aplosporella chlorostroma* Speg.

Notes – *Aplosporella* was initially placed in the family Botryosphaeriaceae, but was later treated as a member of Aplosporellaceae based on morphological characteristics and multi-gene phylogenetic analyses (Damm et al., 2007a; Slippers et al., 2013; Lin et al., 2023a). To date, more than 300 epithets are listed in Index Fungorum (2025, June), but only a few have molecular data (Hyde et al., 2024).

Aplosporella javeedii Jami, Gryzenh., Slippers & M.J. Wingf., Fungal Biology 118(2): 174 (2013) Figure 4.1

Index Fungorum number: IF803637; Facesoffungi number: FoF07383

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 260–330 μm wide, 240–280 μm high, solitary to gregarious, dark brown to black, immersed to superficial or erumpent through bark, pulvinate to subconical, coriaceous, mostly multi-locular, occasionally unilocular, glabrous, with locules 144–180 μm diam., 240–280 μm high, ovoid to subglobose, thick-walled, ostiolate. *Ostiole* single, central. *Conidiomatal wall* 30–35 μm wide, carbonaceous and brittle when dry, composed of dark brown, thick-walled cells of *textura angularis* in the outer layers, and pale brown to hyaline, thin-walled cells in the inner layers. *Hamathecium* 2–3.5 μm wide, cylindrical to filiform, aseptate, branching paraphyses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–15 × 3.5–7 μm ($\bar{x}$ = 11.5 × 5.5 μm; n = 30), hyaline, holoblastic, oblong to ampuliform, and arising from the inner layers of conidiomata. *Conidia* 22.5–29 × 8.5–14 μm ($\bar{x}$ = 24.5 × 11 μm; n = 30), hyaline when immature, becoming brown to dark brown when mature, aseptate, ellipsoid or oval to reniform, truncate at base, rounded at apex, straight or slightly curved, thick-walled.

Culture characteristics – Conidia germinated on PDA medium within 12 h. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25°C in dark, circular, white in first few days, becoming pale gray from the center after two weeks, and finally black after three weeks, felt-like, flattened, surface smooth; in reverse, olive-green to black.

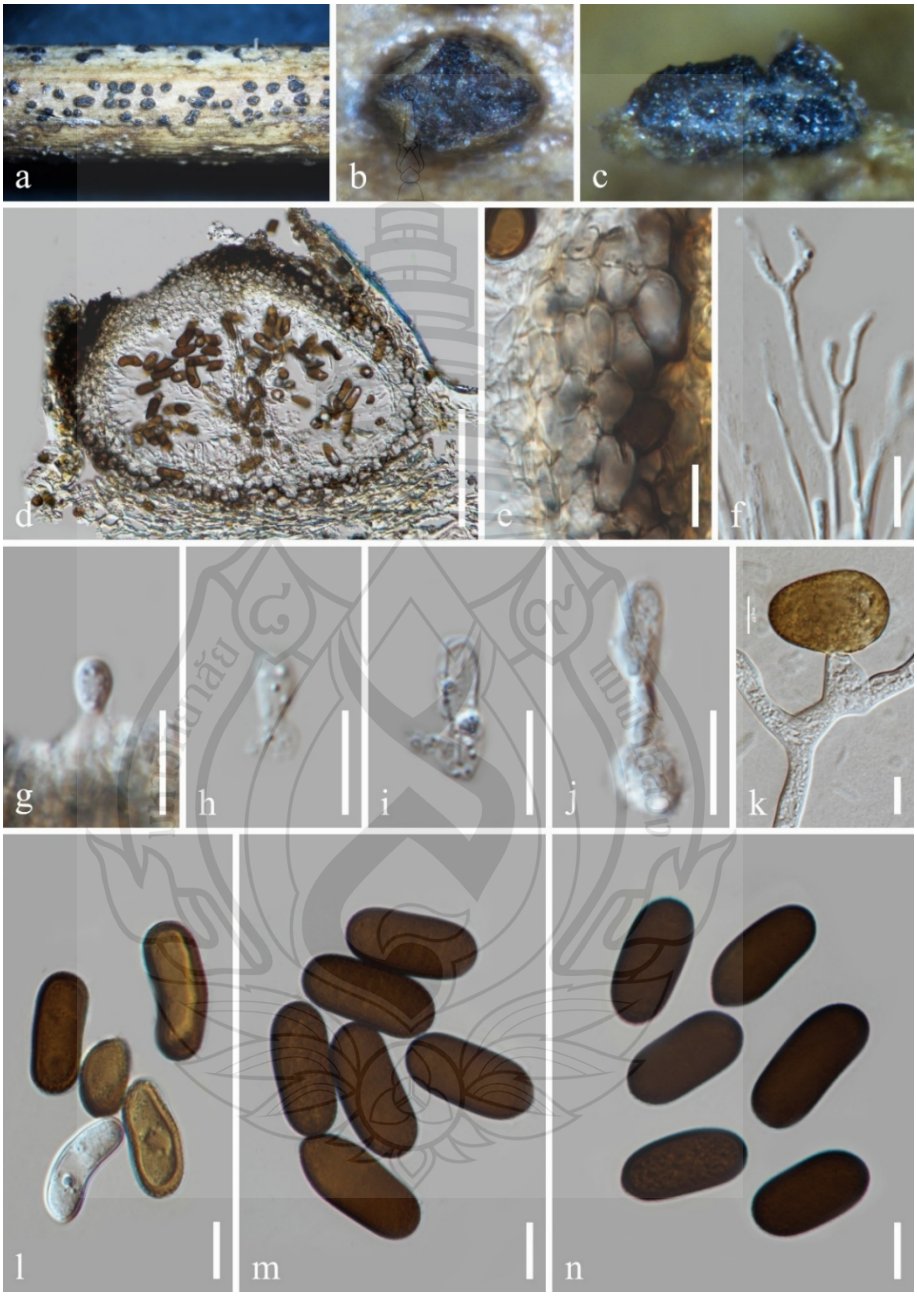
Material examined – CHINA, Guizhou Province, Liupanshui City, Panzhou, Huopu Town, on branches of *Rosa roxburghii* Tratt., 28 September 2021, N. Wu, CL43 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer buergerianum*, *Chaenomeles sinensis*, *Juglans regia* and *Sophora japonica* (Dou et al., 2017b), *Albizia julibrissin*, *Broussonetia papyrifera*, *Gleditsia sinensis*, *Juniperus chinensis* and *Styphnolobium japonicum* (Fan et al., 2015c), *Amorpha fruticosa*, *Celastrus orbiculatus*, *Prunus* sp. and *Populus* sp. (Pan et al., 2019), *Celtis africana* and *Searsia lancea* (Jami et al., 2013), *Euonymus japonicus*, *Populus alba* var. *pyramidalis*, *P. canadensis* and *P. beijingensis* (Lin et al., 2023a), *Orychophragmus violaceus* (Gao et al., 2020), *Rosa roxburghii* (present study), *Rhus typhina* and *Ziziphus jujube* (Zhu et al., 2018).

Known geographical distribution – China, South Africa

Notes – *Aplosporella javeedii* has a broad host range but has not been reported outside China and South Africa. This species was first introduced by Jami et al. (2013) as an endophyte isolated from healthy branches of *Celtis africana* and *Searsia lancea* in South Africa. Subsequently, Fan et al. (2015c) and Zhu et al. (2018) isolated *A. javeedii*, associated with canker disease or dieback on *Albizia julibrissin*, *Broussonetia papyrifera*, *Gleditsia sinensis*, *Juniperus chinensis*, *Styphnolobium japonicum* and *Ziziphus jujuba*. Additionally, Gao et al. (2020) reported that when *this species* was grown on solid rice medium, it produced six polyketides. My collection matches well with *A. javeedii* in morphology but has larger conidia than the holotype (Jami et al., 2013). The phylogenetic analysis revealed my collection clustered together with *A. javeedii* (CFCC 50054 and

CFCC 52435) with a strong support (Figure 4.2). Thus, my collection is identified as *A. javeedii* based on morphology and molecular evidence. This study extends the known host records of this species to *Rosa roxburghii* in China.



Note a–c Conidiomata on natural substrate. d Vertical section of conidiomata. e Conidiomatal wall. f Hamathecium. g–j Conidiogenous cells and developing conidia. k Germinating conidium. l–n Conidia. Scale bars: d = 100 μm; e–n = 10 μm.

Figure 4.1 *Aplosporella javeedii* (HUEST CL43, new host record)

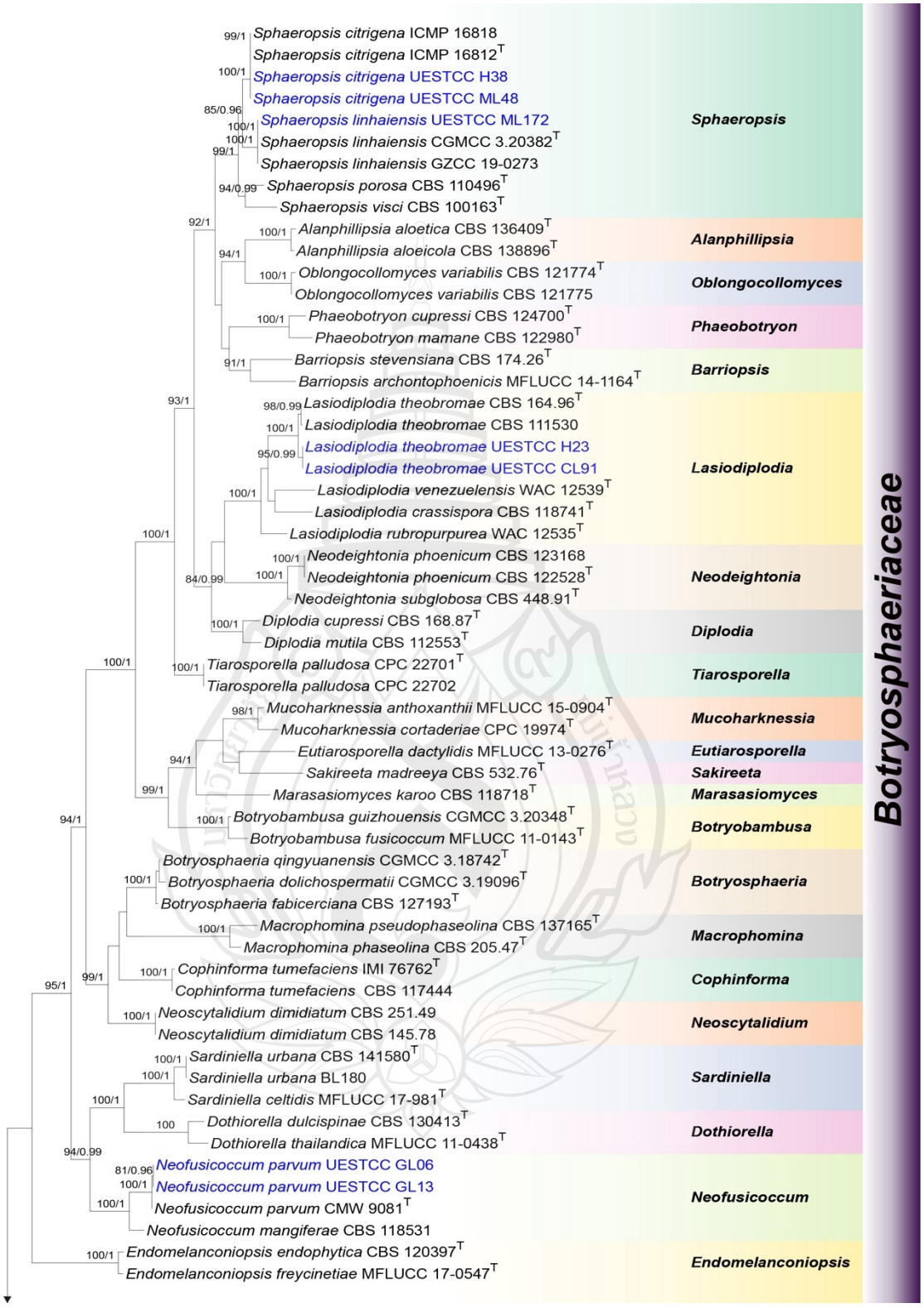


Figure 4.2 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1α* sequence data of Botryosphaeriales

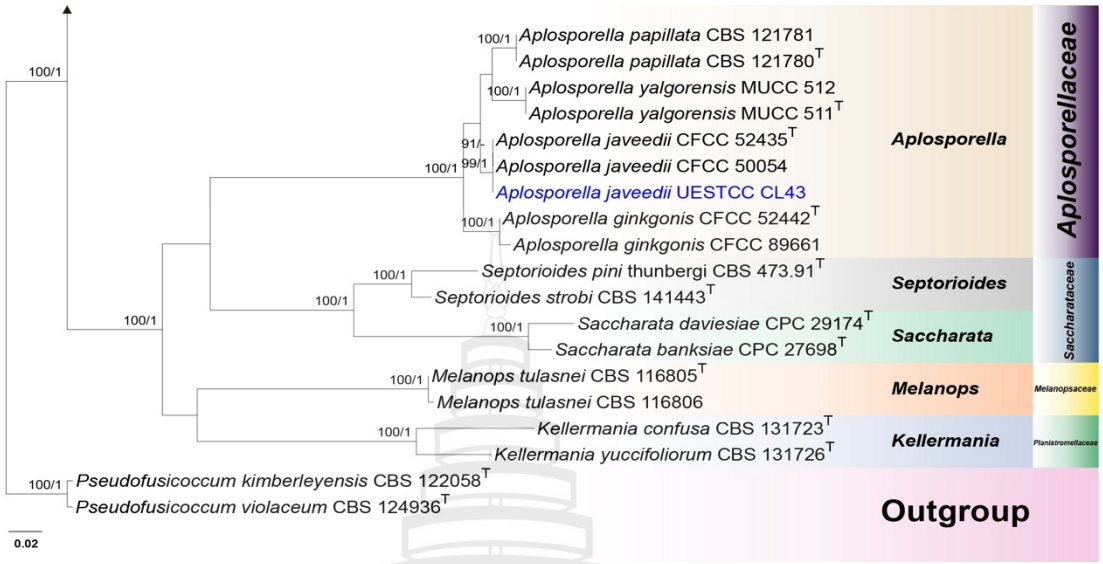


Figure 4.2 (continued)

Figure 4.2 The tree is rooted with *Pseudofusicoccum kimberleyensis* (CBS 122058) and *Pse. violaceum* (CBS 124936). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number

Botryosphaeriaceae Theiss. & Syd. [as 'Botryosphaeriacae']

Type genus – *Botryosphaeria* Ces. & De Not.

Notes – Botryosphaeriaceae is the largest family within Botryosphaeriales and currently comprises 22 genera (Hyde et al., 2024). Members of this family are well-known as saprobes, pathogens and endophytes, causing ulceration, dieback and stem-end rot of plants or fruits, e.g., *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia* and *Neofusicoccum* (Smith et al., 1996; Phillips et al., 2006, 2013; Slippers & Wingfield, 2007; Liu et al., 2012; Zhang et al., 2021c). The sexual morphs of Botryosphaeriaceae are characterized by solitary to gregarious ascostromata, 8-spored, short-stipitate,

clavate asci and hyaline or pigmented, aseptate or septate, ellipsoid or ovoid ascospores, and its asexual morphs are coelomycetous, characterized by ovoid, hyaline or brown, aseptate, one- or multi-septate conidia, and conidiophores mostly reduced to conidiogenous cells (Denman et al., 2000; Crous et al., 2006; Phillips et al., 2006, 2013, 2019; Slippers et al., 2013; Du et al., 2025).

Botryosphaeria Ces. and De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 211 (1863)

Type species – *Botryosphaeria dothidea* (Moug.) Ces. & De Not.

Notes – *Botryosphaeria* was introduced by Cesati and De Notaris (1863), with *B. dothidea* as the type species. *Botryosphaeria* species are commonly found as saprobes, plant pathogens and endophytes with a broad host range in terrestrial habitats (Crous et al., 2006; Liu et al., 2012; Phillips et al., 2013, 2019; Hattori et al., 2021). Over 300 epithets are listed in Index Fungorum (2025, June), however, only a limited number of species are currently accepted and have available sequence data, namely, *B. agaves*, *B. corticis*, *B. dolichospermatii*, *B. dothidea*, *B. fabicerciana*, *B. fujianensis*, *B. guttulata*, *B. kuwatsukai*, *B. osmanthi*, *B. puerensis*, *B. qingyuanensis*, *B. ramose*, *B. salicicola*, *B. scharifii* and *B. tenuispora* (Phillips et al., 2013; Zhang et al., 2021c; Sun et al., 2022; Hyde et al., 2024). Members of this genus are characterized by immersed to semi-immersed, unilocular or multilocular ascomata with an ostiolate with papilla, trabeculate, branched pseudoparaphyses, short-pedicellate asci with an ocular chamber and oval to fusiform, hyaline, uniseptate ascospores; dark brown to black, immersed to partly erumpent, ostiolate conidiomata, conidiophores reduced to holoblastic, subcylindrical to doliiform conidiogenous cells with narrowly fusiform, hyaline, aseptate conidia (Liu et al., 2012; Dissanayake et al., 2021a; Sun et al., 2022).

Botryosphaeria dothidea (Moug.) Ces. & De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 212 (1863) Figure 4.3; Figure 4.4

Index Fungorum number: IF8183247; Facesoffungi number: FoF03512

Saprobic on dead branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 115–215 µm wide, 100–220 µm high, solitary to gregarious or confluent, dark brown to black, initially immersed, becoming erumpent through bark fissures, pyriform to subglobose, mostly multi-locular, occasionally unilocular, glabrous, with locules 50–67 µm diam., 100–210 µm high, thick-walled, short papillate, ostiolate. *Ostiole* 70–80 µm wide, 70–80 µm high, cylindrical to subcylindrical, straight or curved, centrally or laterally located, the region between the perithecial necks were occupied by hyaline pseudoparenchymatous tissue. *Peridium* 25–30 µm wide, carbonaceous and brittle when dry, composed of dark brown, thick-walled cells of *textura angularis* in the outer layers, and pale brown to hyaline, thin-walled cells in the inner layers. *Hamathecium* 3–4.5 µm wide, branched, trabeculate, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 80–95 × 16–21 µm ($\bar{x}$ = 89 × 19 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with a small ocular chamber. *Ascospores* 20–26 × 7.5–12 µm ($\bar{x}$ = 23 × 9.6 µm; n = 30), crowded or irregularly arranged, hyaline, aseptate, fusoid to ovoid, sometimes with tapered ends giving a spindle shaped appearance, widest in the middle to upper third, smooth with granular contents. Asexual morph: Coelomycetous. *Conidiomata* 174–200 µm wide, 106–145 µm high, solitary to gregarious or confluent, dark brown to black, semi-immersed to superficial, pyriform to subglobose, unilocular or multilocular, glabrous, coriaceous, thick-walled, papillate, ostiolate. *Ostiole* 30–53 µm wide, 41–52 µm high, single, central. *Conidiomatal wall* 20–25 µm wide, composed of dark brown to brown cells of *textura angularis* in outer several layers, gradually merging with hyaline cells in inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–16 × 4–5 µm ($\bar{x}$ = 13.5 × 4.5 µm; n = 30), hyaline, phialidic, cylindrical to doliiform, smooth-walled, and arising from the inner layers of conidiomata. *Conidia* 20.5–27 × 6.3–8.5 µm ($\bar{x}$ = 23 × 7.5 µm;

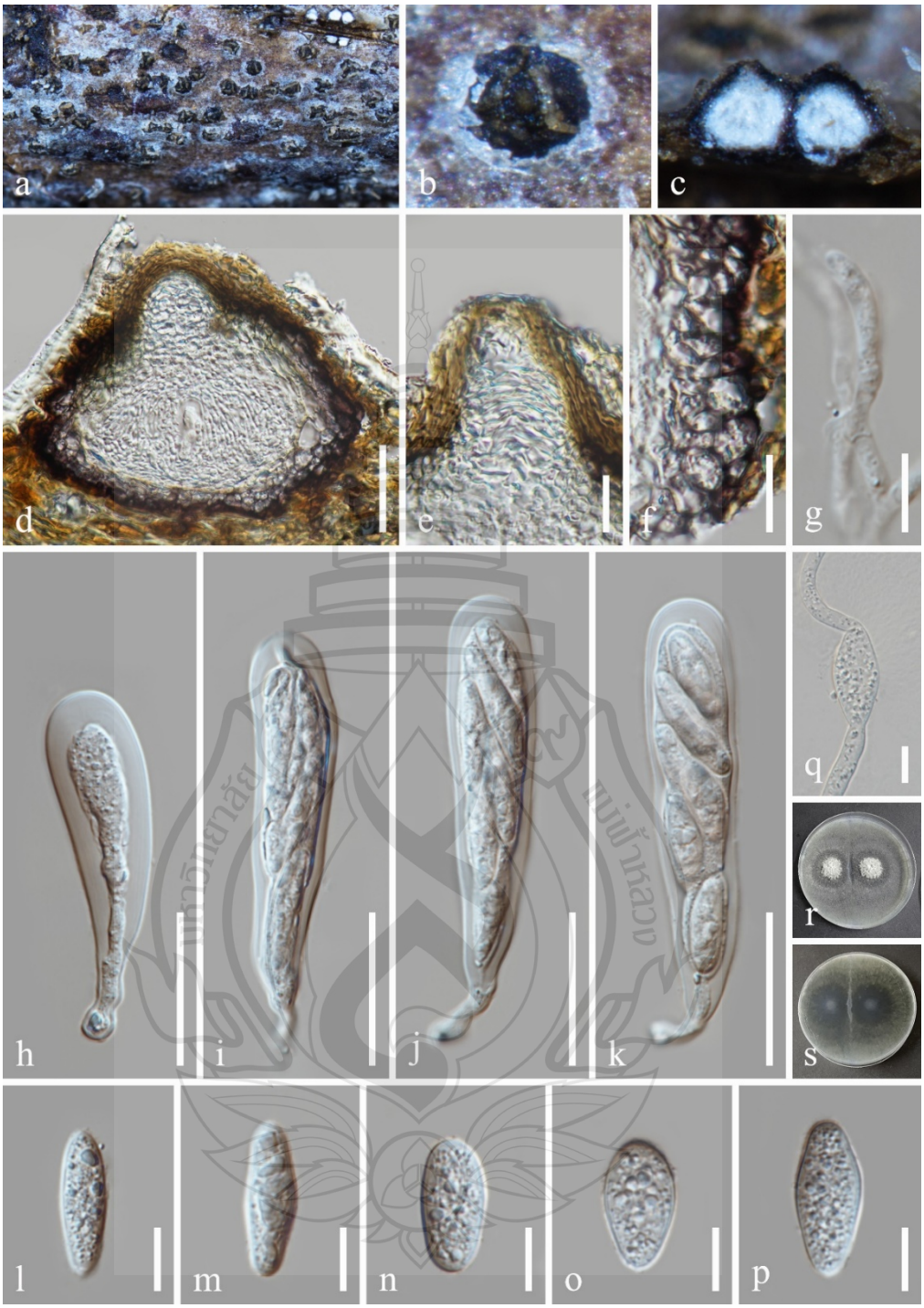
n = 30), hyaline, aseptate, narrowly fusiform, or irregularly fusiform, straight or slightly curved, base subtruncate to bluntly rounded, smooth with granular contents.

Culture characteristics – Ascospores and conidia germinated on PDA medium within 12 h and germ tubes produced from one or both ends. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25℃ in dark, circular, initially white, becoming ash-gray on the surface after one week and finally black after two weeks, felt-like.

Materials examined – CHINA, Guizhou Province, Anshun City, Maguan Town, Gaoyang Village, elevation 1,350 m, 26°12′40″ N, 105°46′37″ E, on branches of *Rosa roxburghii* Tratt., 3 July 2022, N. Wu, GL158 (HUEST XX), living culture UESTCC XX; *ibid.*, Puding County, Baiyan Town, Huangmao Village, elevation 1,410 m, 26°17′19″ N, 105°50′48″ E, on dead branches of *R. sterilis* S. D. Shi, 3 July 2022, N. Wu, GL108 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″N, 104°37′28″ E, on branches of *R. roxburghii*, 9 July 2022, N. Wu, GL124 (HUEST XX), living culture UESTCC XX; *ibid.*, GL147 (HUEST XX), living culture UESTCC XX; *ibid.*, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL29 (HUEST XX), living culture UESTCC XX; *ibid.*, CL42 (HUEST XX), living culture UESTCC XX; *ibid.*, CL92 (HUEST XX), living culture UESTCC XX; *ibid.*, Qiannan Autonomous Prefecture, Longli County, elevation 1,119 m, 26°25′48″ N, 106°54′36″ E, on dead branches of *R. roxburghii*, 4 February 2023, N. Wu, ML179 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL49 (HUEST XX), living culture UESTCC XX; *ibid.*, Yunnan Province, Qujing City, Haidai Town, Yangchang Village, elevation 1,740 m, 26°3′55″ N, 104°20′22″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL04 (HUEST XX), living culture UESTCC XX; *ibid.*, Sichuan Province, Leshan City,

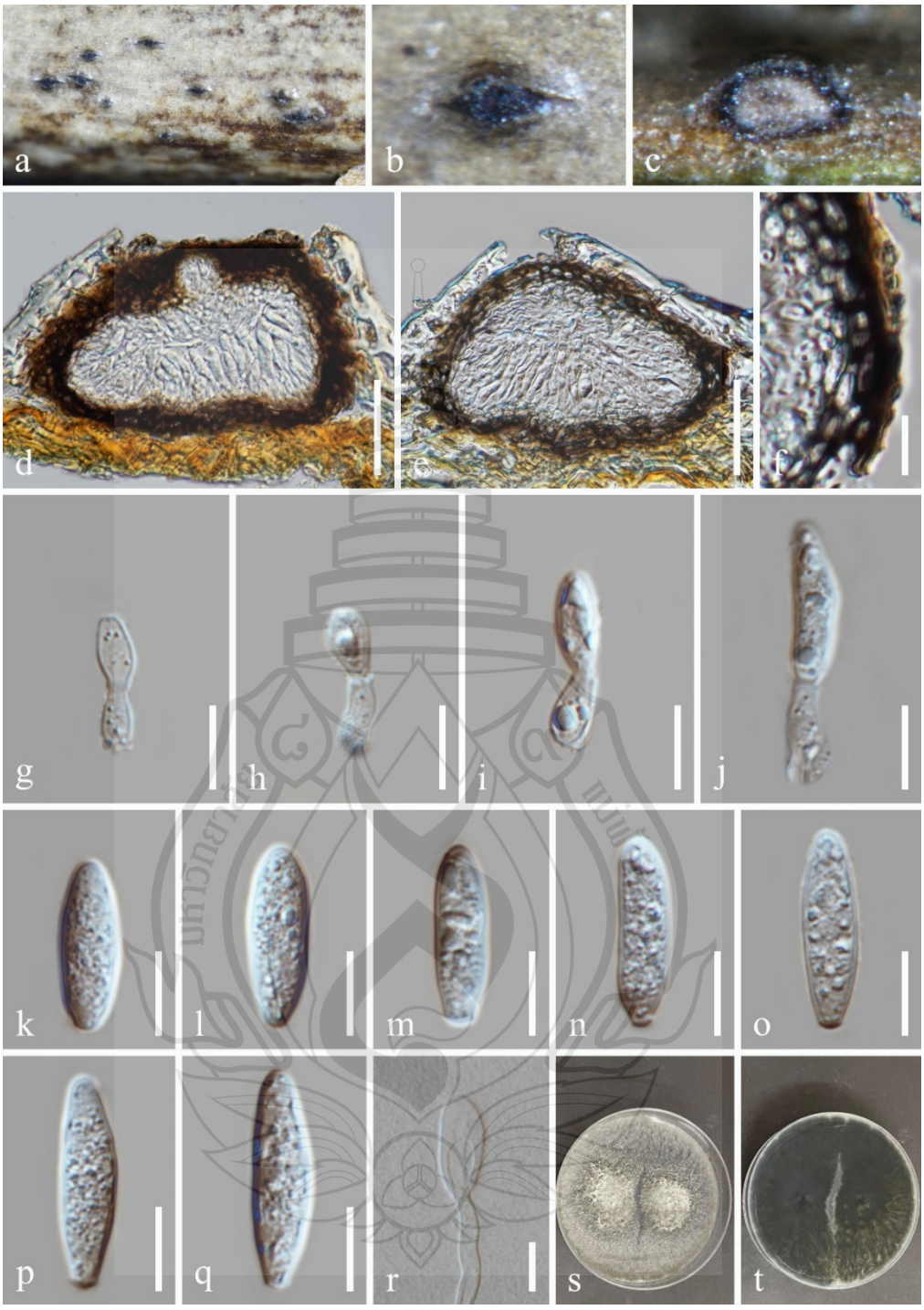
Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R*. *roxburghii*, 30 October 2021, N. Wu, H14 (HUEST XX), living culture UESTCC XX.

Notes – Multi-gene phylogenetic analysis showed that my eight isolates clustered together with several strains of *Botryosphaeria dothidea* (Figure 4.5). Morphologically, both the sexual and asexual forms of my collections are most similar to those of *B*. *dothidea*, with no significant differences (Cesati & De Notaris, 1863; Zhang et al., 2021c; Du et al., 2025). Therefore, I identified the newly collected taxa as *B*. *dothidea* based on the recommendations of Jeewon and Hyde (2016). This study represents the first report of *B*. *dothidea* on *Rosa roxburghii* and *R*. *sterilis* from Guizhou, Sichuan, and Yunnan Provinces in China.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–p Ascospores. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 50 µm; e, f = 20 µm; h–k = 30 µm; g, l–q = 10 µm.

Figure 4.3 *Botryosphaeria dothidea* (HUEST GL158; sexual morph, new host record)



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k–q Conidia. r Germinating conidium. s, t Colony on PDA, above (s), below (t). Scale bars: d, e = 50 μm; f–r = 10 μm.

Figure 4.4 *Botryosphaeria dothidea* (HUEST GL124; asexual morph, new host record)

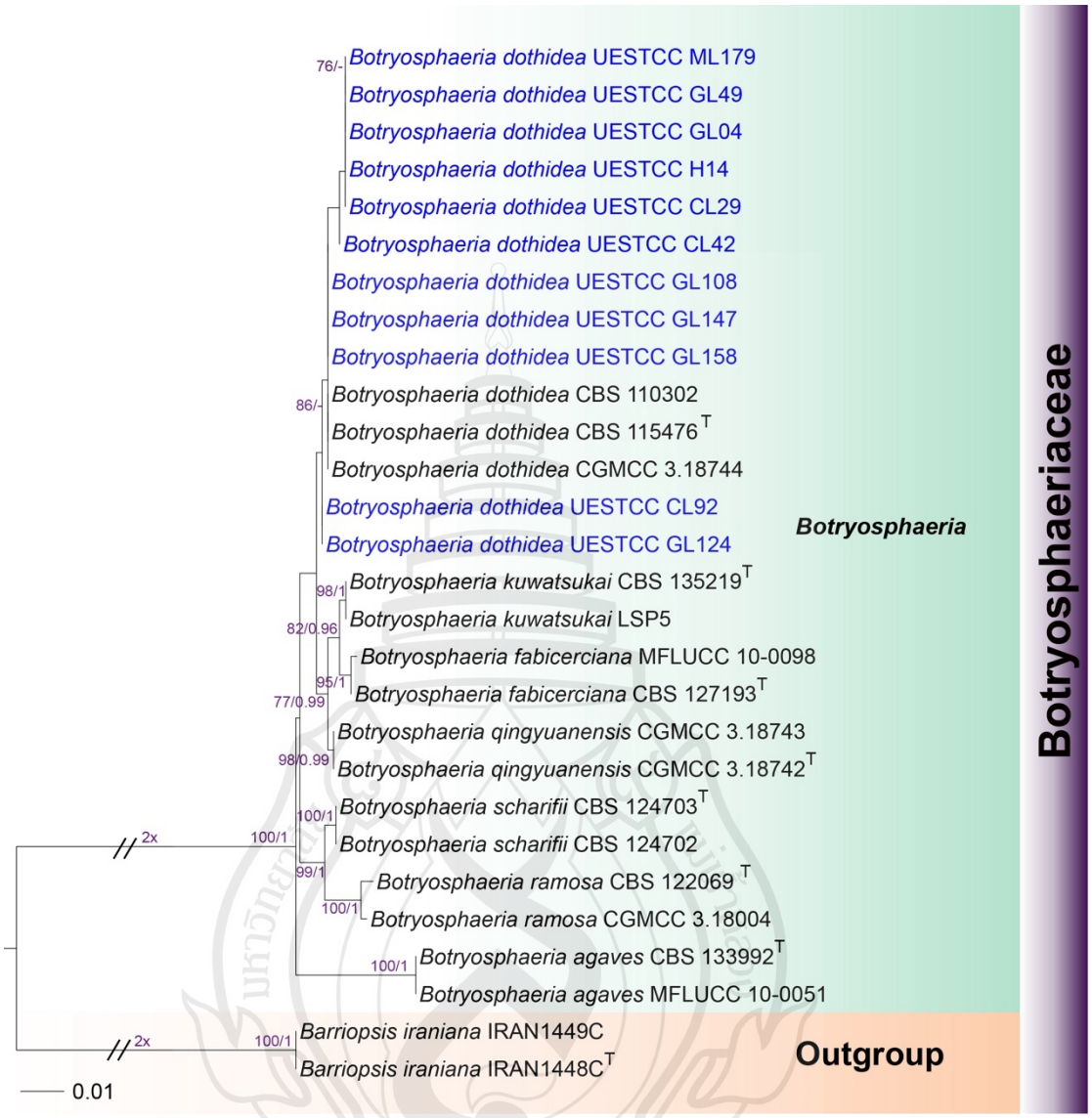


Figure 4.5 Phylogram generated from maximum likelihood (ML) analysis based on combined ITS and *tef1α* sequence data of *Botryosphaeria*

Figure 4.5 The tree is rooted with *Barriopsis iraniana* (IRAN1448C and IRAN1449C). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "^{T}" after the strain number.

Botryosphaeria fujianensis Z.P. Dou, W. He & Y. Zhang bis, Mycosystema 40(3): 482 (2021) Figure 4.6

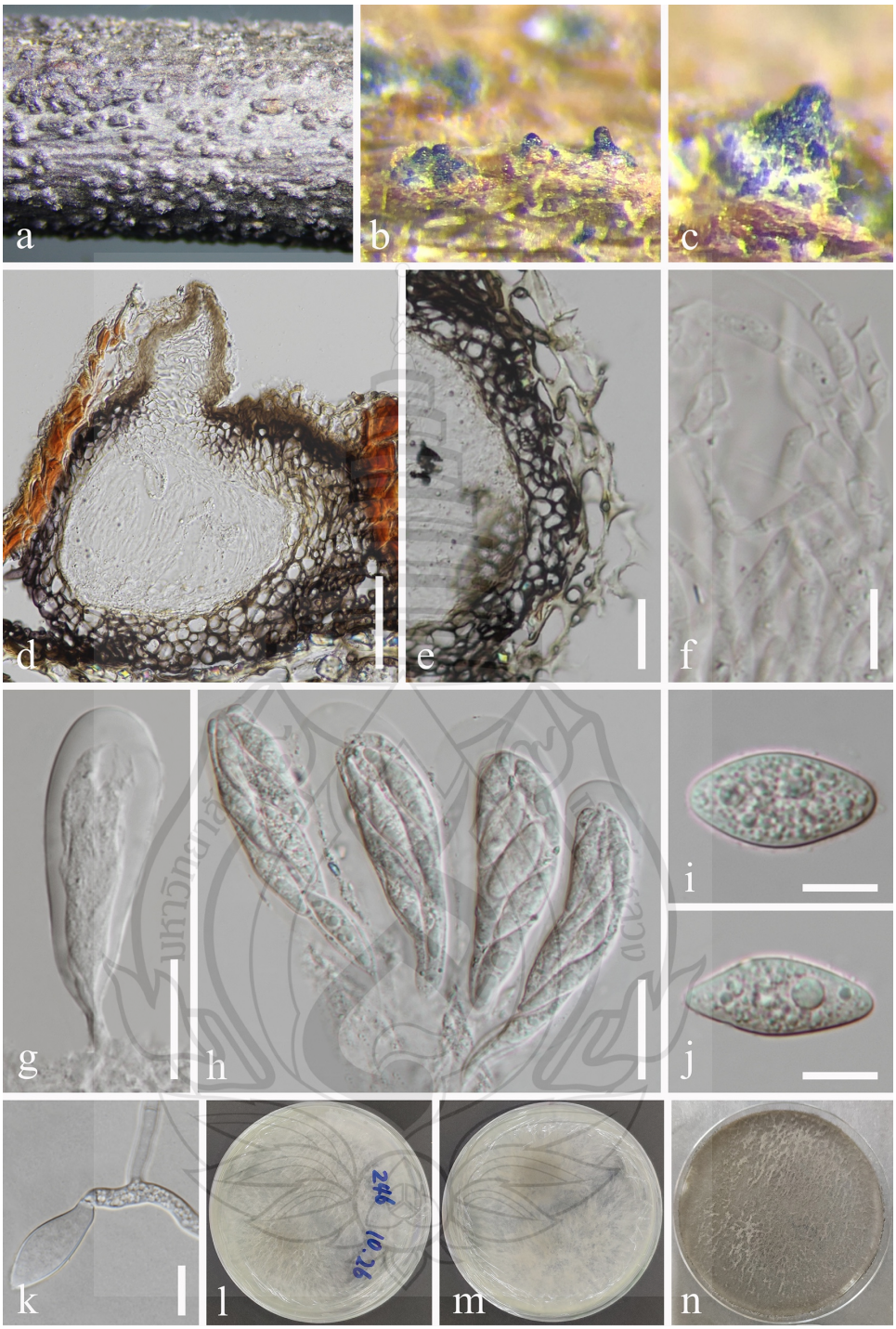
Index Fungorum number: IF826938

Saprobic on twigs of Tectona grandis L.F. Sexual morph: *Ascomata* 140–216 × 178–278 μm ($\bar{x}$ = 182 × 211 μm, n = 20), well-developed, bursting through the bark, generally emerged from the host surface, scattered or gregarious, black, subglobose to obpyriform. *Peridium* 16–56 μm wide, composed of five strata; an outer stratum has black, thick-walled cells, and the middle and inner layers have black, thin-walled cells. *Hamathecium* comprising up to 3–5 μm wide, dense, cellular pseudoparaphyses, anastomosing above and between the asci. *Asci* 76–125 × 20–33 μm (n = 20), bitunicate, eight-spored, broadly clavate, apically rounded and with a visible ocular chamber. *Ascospores* 20–27 × 7–11 μm ($\bar{x}$ = 24 × 10 μm, n = 50), initially rhomboid, hyaline, aseptate, elliptical to ovoid, thick-walled, smooth at maturity, apiculus at either end. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 12 h. Colonies are fast growing on PDA, reaching 60 mm diam. after 7 d at 20–25°C. Circular, white in first few days, becoming pale grey from the center after two weeks, and finally black after three weeks, felt-like, flattened, surface smooth.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Pa Pae, 19◦06′32.6″ N, 98◦44′21.1″ E, on dead twigs of Tectona grandis (Lamiaceae), 8 August 2019, Na Wu, YW246 (MFLU 23-0012), living culture MFLUCC 23-0041.

Notes – The phylogenetic results (Figure 4.7) showed that my newly obtained isolate clustered together with *Botryosphaeria fujianensis*, and I identified it as *B. fujianensis*. There was only the asexual morph provided when Chu et al. (2021) described this species, and I illustrate the sexual morph of *B. fujianensis* and reported it as the new record from Thailand in this study.



Note a–c Ascomata on host substrate. d Vertical section of ascomata. e Structure of the peridium. f Pseudoparaphyses. g, h Asci. i, j Ascospores. k Germinated ascospore. l–n Colonies on PDA, above (l, n) and below (m). Scale bars: d = 50 µm, e = 5 µm, f–j = 10 µm, k = 50 µm.

Figure 4.6 *Botryosphaeria fujianensis* (MFLU 23-0012, new host record)

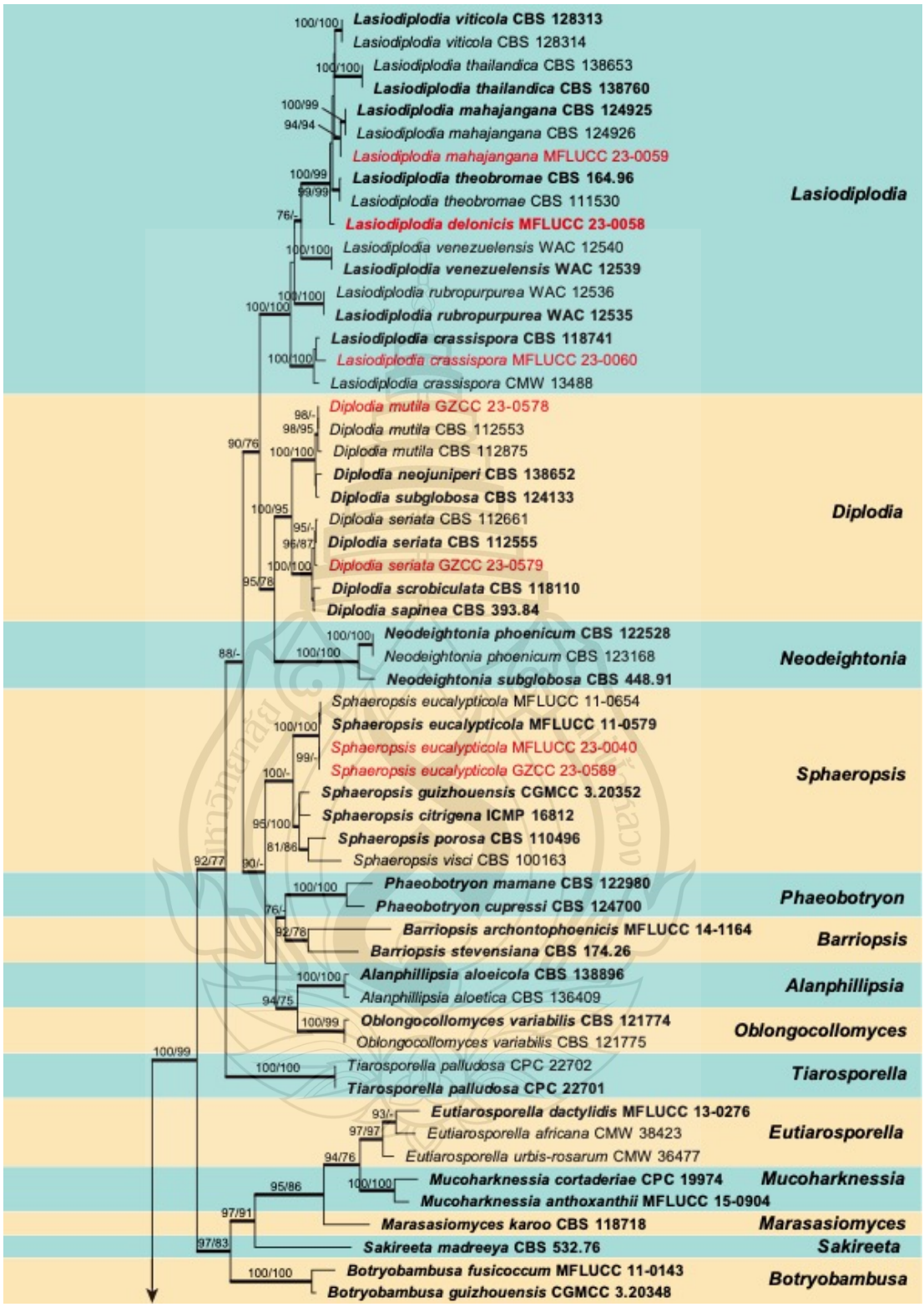


Figure 4.7 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined ITS, LSU, *tef1α* and *tub2* se-quence data for selected closely related genera within the family Botryosphaeriaceae

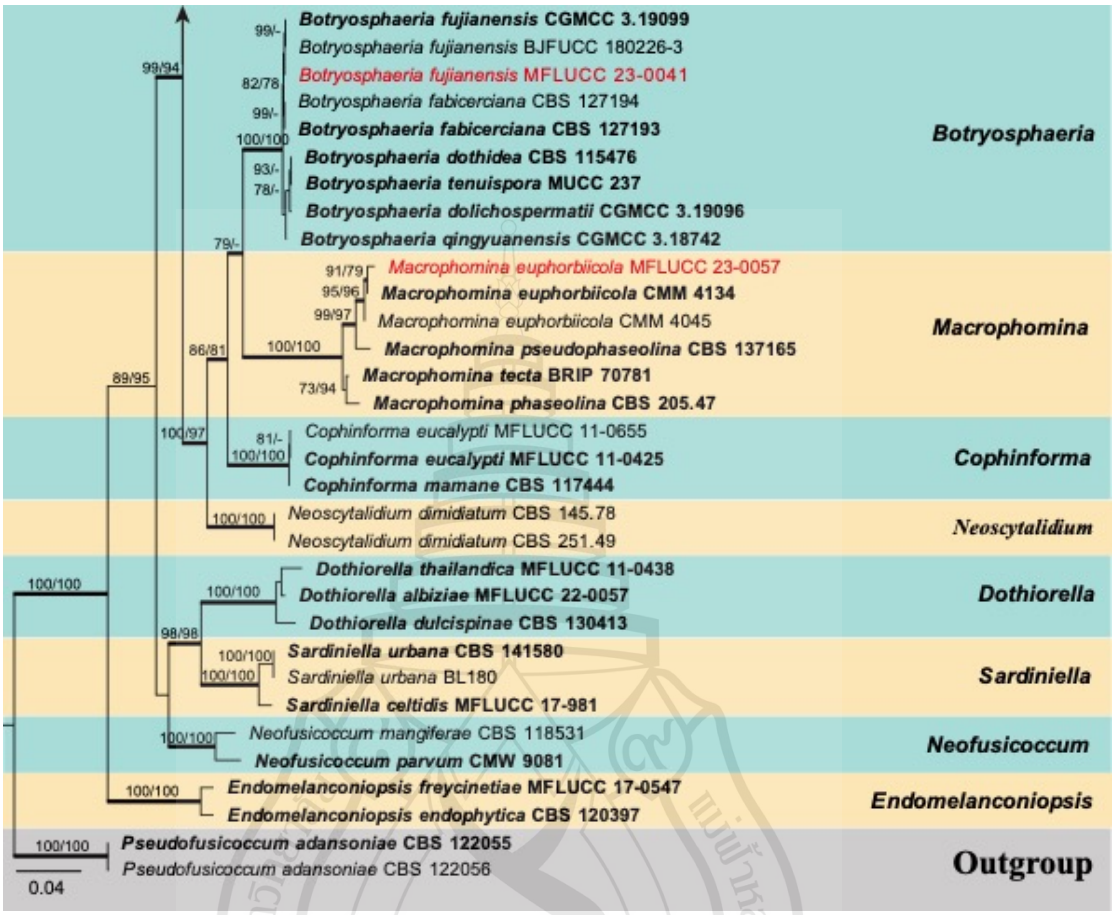


Figure 4.7 (continued)

Figure 4.7 The newly generated isolates of this study are in red. The tree is rooted with two isolates of *Pseudofusicoccum adansoniae* (CBS 122055, CBS 122056). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75% are given near the nodes. Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are denoted in thickened branches. The strain numbers are given after the species names, and ex-type strains are indicated in bold.

Diplodia Fr., Annls Sci. Nat., Bot., sér. 2 1: 302 (1834)

Type species – *Diplodia mutila* (Fr.) Fr.

Notes – *Diplodia* was established by Montagne (1834) with *D. mutila* as the type species. Members of this genus mainly occur on woody hosts, causing rots, cankers, shoot and tip blights (Crous et al., 2006; Slippers & Wingfield, 2007; Linaldeddu et al., 2014; Giambra et al., 2016). *Diplodia* is a large genus with 1269 epithets currently listed in Index Fungorum (2025, June). However, based on morphology coupled with phylogenetic analyses, 36 species have been accepted and uploaded to the Botryosphaeriales website (https:// botryosphaeriales.org/) (Zhang et al., 2021c; Wu et al., 2021b; Li et al., 2023a; Zhou et al., 2025). *Diplodia* species produce two types of conidia, one type is consistently hyaline and aseptate, while the other is initially hyaline and aseptate, becoming pale brown and either aseptate or septate when mature. (Li et al., 2023a; Du et al., 2025). *Diplodia* is morphologically similar to *Lasiodiplodia*, *Neodeightonia* and *Sphaeropsis*, but can be distinguished by the conidial striation and the absence of paraphyses (Phillips et al., 2013; Wu et al., 2023; Du et al., 2025).

Diplodia mutila (Fr.) Mont., Ann. Sci. nat., sér. 2, 1: 302 (1834) Figure 4.8

Index Fungorum number: IF201741; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis* (Rosaceae). Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 180–316 µm wide, 225–300 µm high, solitary to gregarious, semi-immersed to superficial, visible as black dots on host substrate, pycnidial, pyriform to globose or subglobose, mostly unilocular, occasionally multi-locular, coriaceous or carbonaceous, glabrous, short papillate, ostiolate. *Ostiole* 60–95 µm wide, 65–90 µm high, single, central. *Conidiomatal wall* 30–35 µm wide, composed of dark brown to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9–13 × 3–5 µm ($\bar{x}$ = 10.5 × 4 µm; n = 30), hyaline, cylindrical, discrete, smooth-walled, slightly swollen at the base, forming a single conidium at the tip. *Conidia* 27–33.5 × 12–15 µm

($\bar{x}$ = 29 × 13.5 μm; n = 30), hyaline, aseptate, externally smooth, internally verruculose, thick-walled, oblong to ovoid, or irregularly ovoid, straight or slightly curved, both ends broadly rounded.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25℃ in dark; circular, felt-like, dense, aerial, flat to slightly raised, dull green to dark and the margin creamy white.

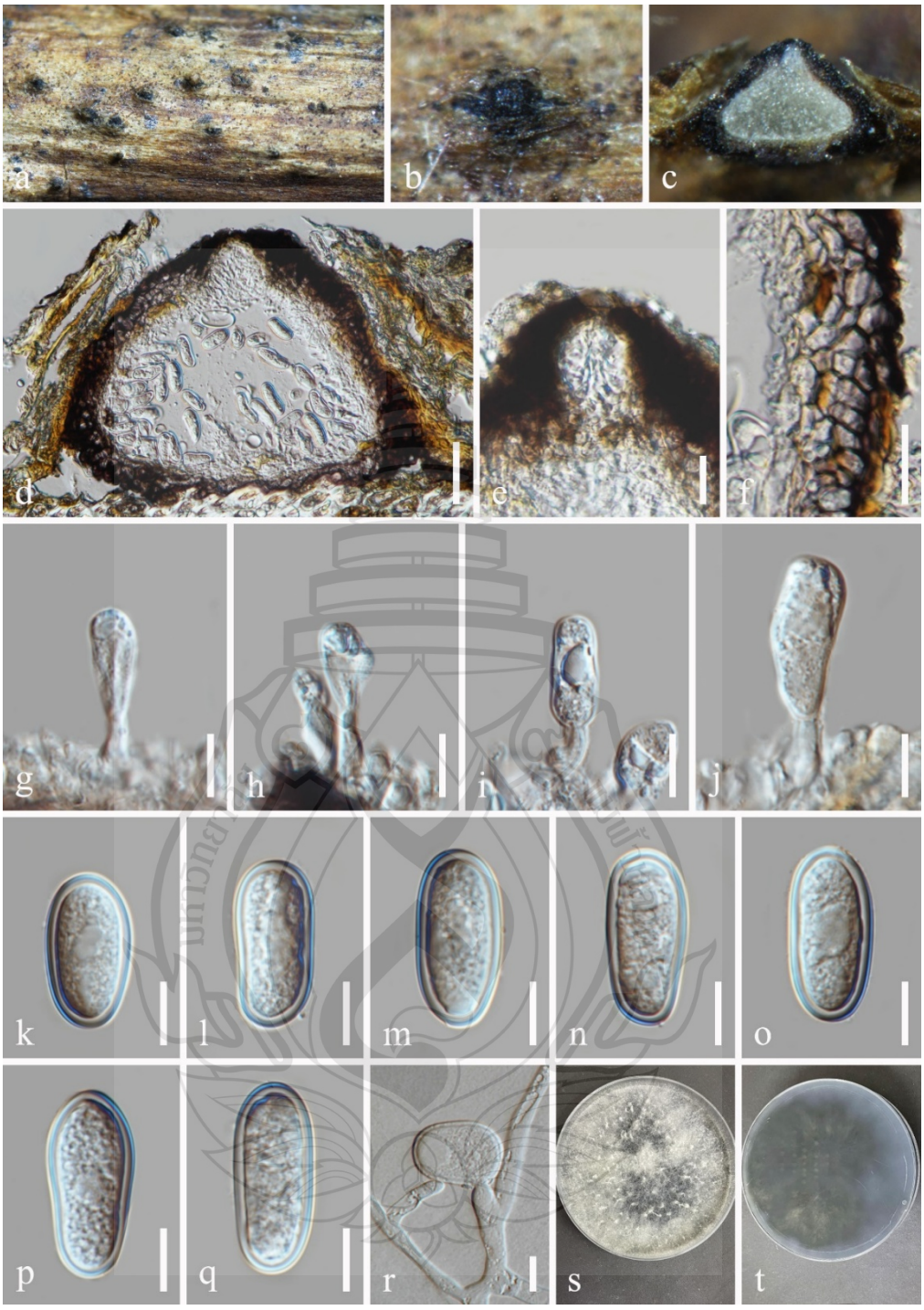
Materials examined – CHINA, Guizhou Province, Zunyi City, Suiyang County, Taibai Town, Fuyu Village, elevation 1,279.6 m, 28°23′24″ N, 107°2′24″ E, on branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML98 (HUEST XX), living culture UESTCC XX; *ibid*., 0 City, Qixingguan District, Salaxi Town, Longfeng Village, elevation 1,869 m, 27°13′22″ N, 105°3′7″ E, on dead branches of *R. roxburghii*,1 February 2023, N. Wu, ML142 (HUEST XX), living culture UESTCC XX; *ibid*., Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *R. roxburghii*, 6 February 2023, N. Wu, ML173 (HUEST XX), living culture UESTCC XX; *ibid*., W8 (HUEST XX), living culture UESTCC XX; *ibid*., Anshun City, Maguan Town, Gaoyang Village, elevation 1,350 m, 26°12′40″ N, 105°46′37″ E, on branches of *R. roxburghii*, 3 July 2022, N. Wu, GL156 (HUEST XX), living culture UESTCC XX; *ibid*., Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis* S. D. Shi, 3 July 2022, N. Wu, GL40 (HUEST XX), living culture UESTCC XX; *ibid*., GL24 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia oleifera*, *Olea europaea* and *Vernicia fordii* (Li et al., 2023a), *Chamaecyparis lawsoniana*, *Fraxinus excelsior*, *Populus alba* and *Taxus baccata* (Alves et al., 2013, 2014), *Forsythia suspensa* (Du et al., 2025), *Fraxinus ornus*, *Magnolia grandiflora*, *Populus brabantica*, *Prunus salicina* and *Pyrus* sp. (Zhang et al.,

2021c), *Phoenix dactylifera* (Phillips et al., 2008), *Prunus persica* (Wu et al., 2023), *Rosa roxburghii* and *R. sterilis* (present study), *Vitis vinifera* (Alves et al., 2004, 2014).

Known geographical distribution – China, England, Germany, Italy, Netherlands, Portugal, South Africa, USA.

Notes – Phylogenetic analysis revealed that the newly collected isolates (UESTCC ML98, UESTCC ML142, UESTCC ML173, UESTCC GL156 and UESTCC GL40) formed a distinct clade closely related to *Diplodia mutila* (Figure 4.9). Based on morphological characteristics and phylogenetic evidence, I identified these isolates as *D. mutila*. The type species of the genus, *D. mutila* is a well-known and most frequently reported species, associated with more than 60 hosts (Batista et al., 2021; Zhang et al., 2021c; Li et al., 2023a; Wu et al., 2023; Du et al., 2025). In the present study, *D. mutila* was collected from Anshun, Bijie, Guiyang, Zunyi Cities and the Qiannan Buyi and Miao Autonomous Prefecture in Guizhou Province, indicating that this species is widely distributed in the region and exhibits strong ecological adaptability. To my knowledge, this is the first report of *D. mutila* isolated from *Rosa roxburghii* and *R. sterilis*.



Note a, b Conidiomata on natural substrate. c, d Vertical sections of conidiomata. e Ostiole. f Conidiomatal wall. g–j Conidiogenous cells and developing conidia. k–q Conidia. r Germinating conidium. s, t Colony on PDA, above (s), below (t). Scale bars: d = 50 μm; e, f = 20 μm; g–r = 10 μm.

Figure 4.8 *Diplodia mutila* (HUEST ML98, new host record)

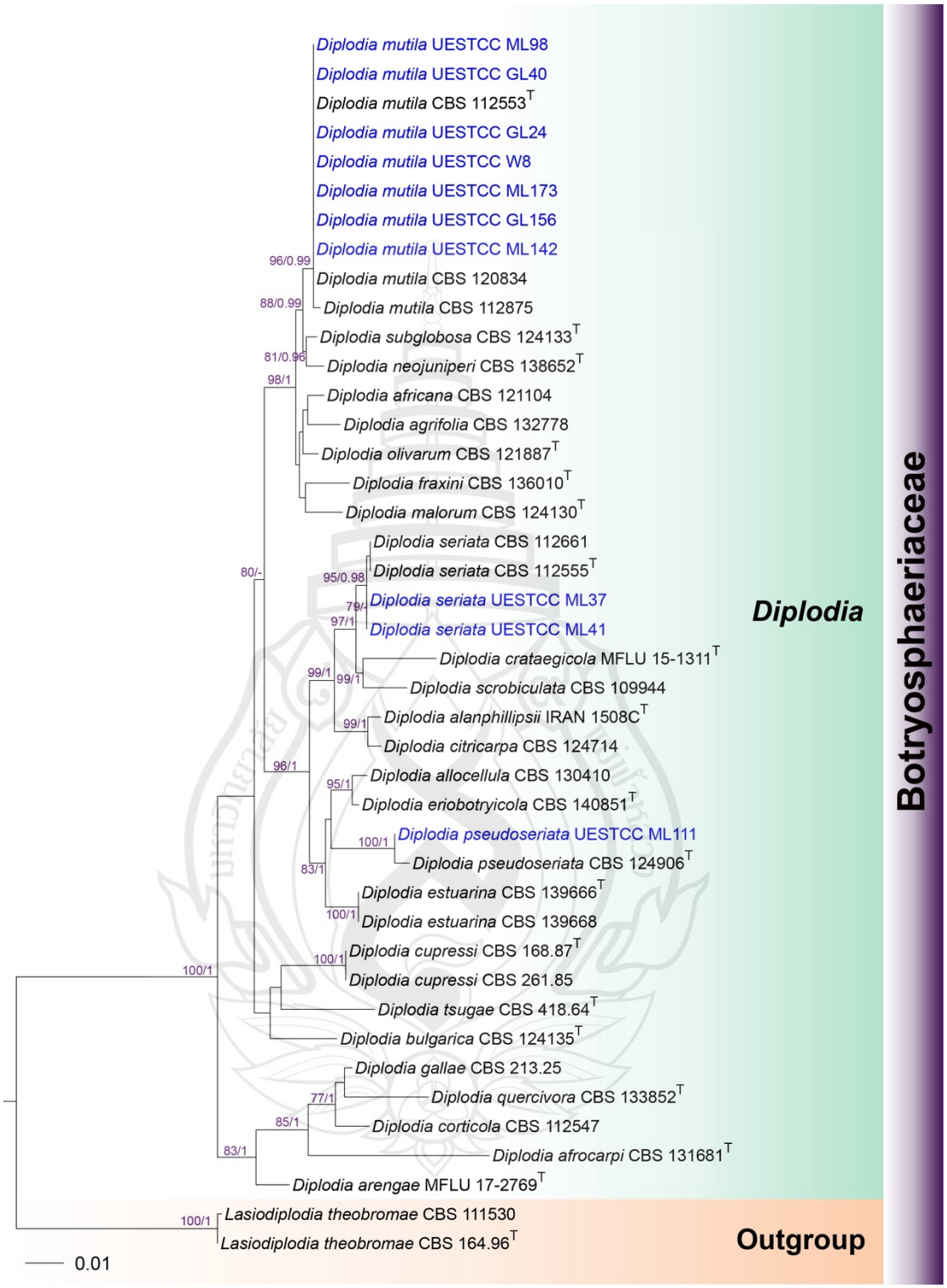


Figure 4.9 Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1α* and *tub2* sequence data of *Diplodia*

Figure 4.9 The tree is rooted with *Lasiodiplodia theobromae* (CBS 164.96 and CBS 111530). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Diplodia pseudoseriata C.A. Pérez, Blanchette, Slippers & M.J. Wingf., Fungal Diversity 41(1): 63 (2009) Figure 4.10

Index Fungorum number: IF513545; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 165–200 µm wide, 111–190 µm high, mostly solitary, occasionally gregarious, semi-immersed to superficial, visible as black dots on host substrate, pycnidial, globose to subglobose, unilocular, coriaceous or carbonaceous, glabrous, short papillate, ostiolate. *Ostiole* 30–50 µm wide, 45–50 µm high, single, subcylindrical, centric or eccentric. *Conidiomatal wall* 15–23 µm wide, composed of brown, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–13 × 3–7.5 µm ($\bar{x}$ = 10 × 5 µm; n = 30), hyaline, holoblastic, cylindrical, determinate, smooth-walled, slightly swollen at the base, forming a single conidium at the tip. *Conidia* 22–26.5 × 10.5–13.5 µm ($\bar{x}$ = 24 × 12 µm; n = 30), initially hyaline becoming dark brown, aseptate, thick-walled, wall externally smooth, roughened on the inner surface, obovoid to ellipsoid, both ends broadly rounded, straight or slightly curved.

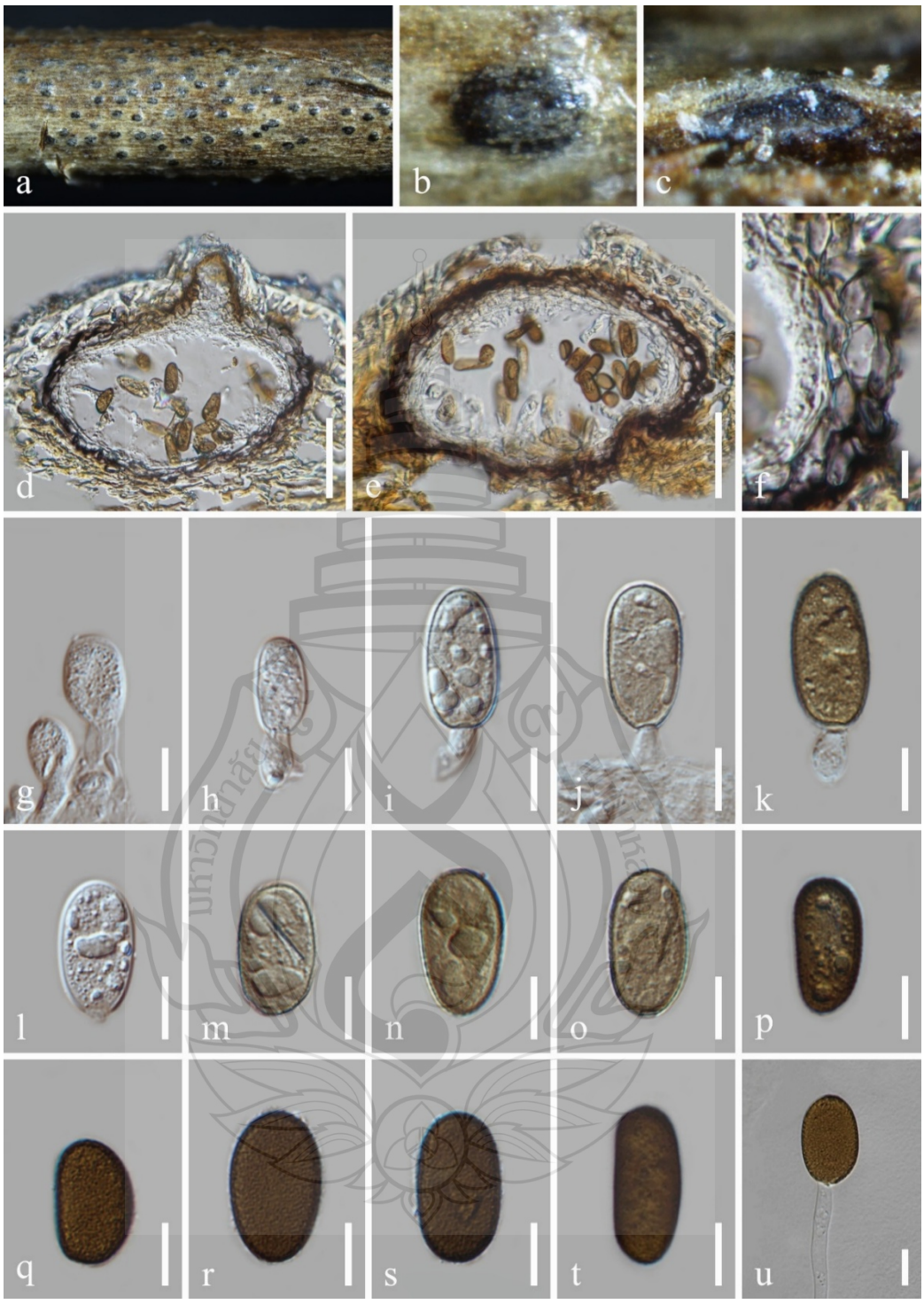
Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25°C in dark, circular, velvety, dense, aerial, flat to slightly raised, initially white and later turning dull green to dark from the surrounding of the colony; in reverse, dark gray with an entire margin.

Material examined – CHINA, Guizhou Province, Tongren City, Dejiang County, Fengxiangxi Town, Xisha Village, elevation 636 m, 28°5′24″ N, 108°18′36″ E, on decaying branches of *Rosa roxburghii*, 3 February 2023, N. Wu, ML111 (HUEST XX), living culture UESTCC XX.

Hosts – *Acca sellowiana*, *Blepharocalyx salicifolius*, *Eugenia involucrata*, *E. uniflora*, *Hexachlamys edulis*, *Myrceugenia euosma*, *Myrcianthes cisplatensis* and *Myrciaria tenella* (Pérez et al., 2010), *Acer truncatum* (Li et al., 2023a), *Eriobotrya japonica*, *Pistacia lentiscus*, *Platanus* sp. and *Pterocarpus angolensis* (Zhang et al., 2021c), *Nandina domestica* (Du et al., 2025), *Rosa roxburghii* (present study).

Known geographical distribution – China, Italy, South Africa, Spain, Uruguay.

Notes – Pérez et al. (2010) introduced *Diplodia pseudoseriata* from an asymptomatic twig of *Blepharocalyx salicifolius* in Uruguay. The asexual morph of *Di. pseudoseriata* was initially formed in culture on sterilized pine needles, but its sexual morph is unclear. Zhang et al. (2021c) synonymized *Di. alatafructa*, *Di. insularis* and *Di. pseudoplatani* under *Di. pseudoseriata* based on their high sequence similarities. Recently, Li et al. (2023a) introduced *Di. acerigena* (on decaying branches of *Acer truncatum*) from China, which was represented by both sexual and asexual morphs, with pycnidia produced on the mycelium in PDA. However, Du et al. (2025) synonymized *Di. acerigena* under *Di. pseudoseriata* based on morpho-molecular evidence, thus confirming the sexual morph of this species. My collection fits the morphology of *Di. pseudoseriata*, although the conidia are slightly smaller (22–26.5 × 10.5–13.5 μm vs. 23–30.5 × 10–14 μm) (Pérez et al., 2010). The ITS, *tef1α* and *tub2* sequences of my collection showed 99.25% (528/532 bp), 99.25% (528/532 bp) and 98.09% (411/419 bp) similarities with the holotype of *Di. pseudoseriata* (CBS 124906), respectively. I therefore identify my collection as *Di. pseudoseriata* and report it as a new host record of this species from *Rosa roxburghii* in China. The phylogenetic placement of my collection is shown in Figure 4.9.



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–k Conidiogenous cells and developing conidia. l–t Conidia. u Germinating conidium. Scale bars: d, e = 50 µm; f–u = 10 µm.

Figure 4. 10 *Diplodia pseudoseriata* (HUEST ML111, new host record)

Diplodia seriata De Not., Mém. R. Accad. Sci. Torino, Ser. 2 7: 26 (1845) Figure 4.11

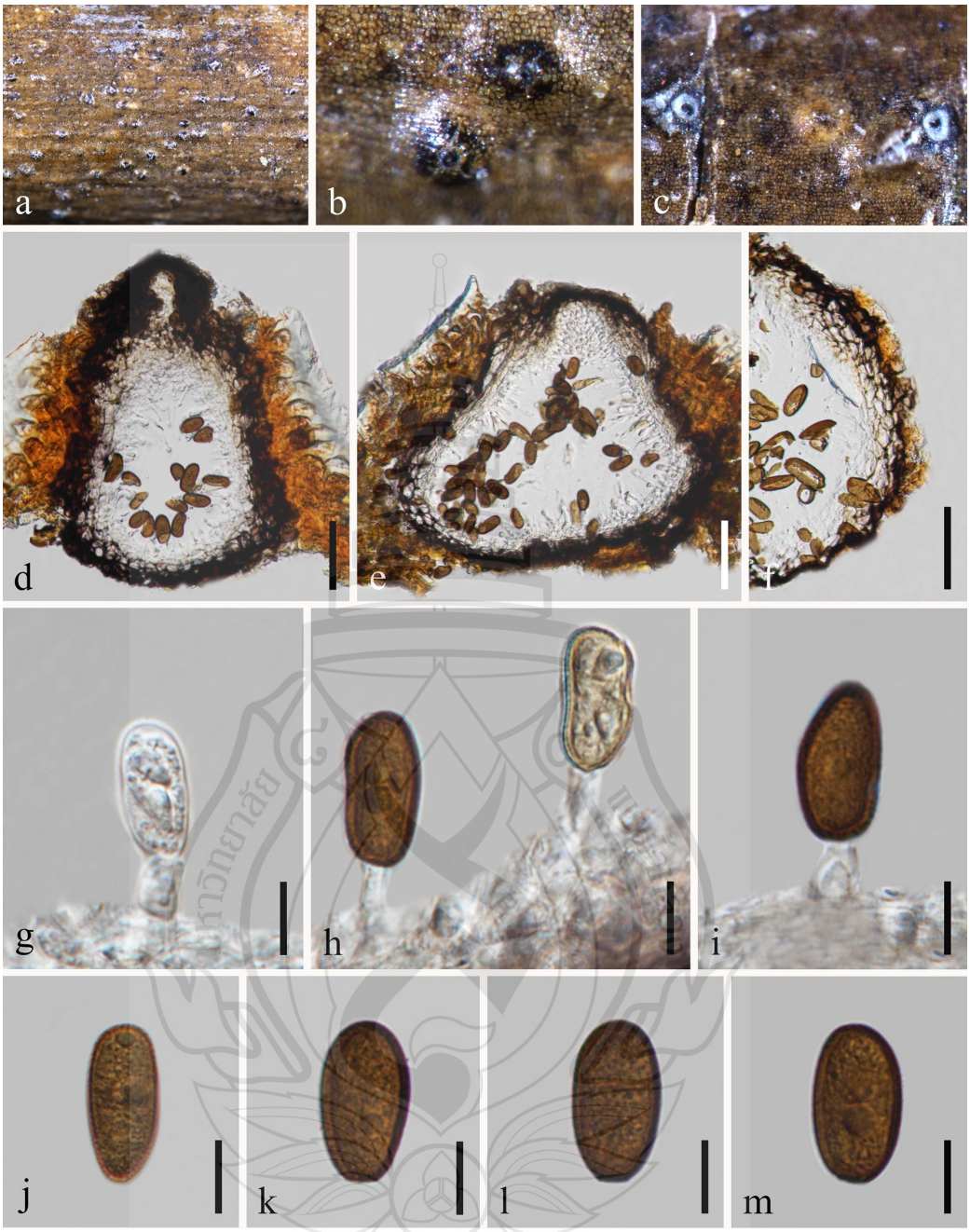
Index Fungorum number: IF180468

Saprobic on dead twigs of *Wisteria sinensis* L. Sexual morph: Not observed. Asexual morph: *Conidiomata* 138–245 × 206–240 µm ($\bar{x}$ = 175 × 228 µm, n = 20), semi- immersed or immersed in the substrate, dark brown to black, solitary, pyriform, initially in-traepidermal, visible as black dots on the host when mature, thick-walled, glabrous, centrally ostiolate. *Ostiole* 16–30 µm diam., centrally located, short papillate. *Peridium* up to 12–30 µm wide, 3–5 layers, consisting of brown and small-celled textura angularis, becoming hyaline towards the inner region. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–13 × 3–5 µm ($\bar{x}$ = 8 × 4 µm, n = 20), hyaline, cylindrical, discrete, smooth-walled, slightly swollen at the base, forming a single conidium at the tip. *Conidia* 18–27 × 9–13 µm ($\bar{x}$ = 22 × 11 µm, n = 50), brown, aseptate, externally smooth, internally verruculose, subcylindrical to ellipsoid, moderately thick-walled, ends rounded, often with a truncate base.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies are fast growing at 20–25°C, becoming ash-grey on the surface after 7 days, and finally black after two weeks, velvety and floccose, dense, convex with papillate surface, aerial.

Material examined – China, Sichuan Province, Chengdu City, High Tech West Zone, Xi Yuan Avenue, University of Electronic Science and Technology of China campus, 30°45'9"N, 103°55'31"E, on dead twigs of *Wisteria sinensis* L., 22 November 2020, H.Z. Du, YW297 (GZAAS 23-0583), living culture GZCC 23-0579.

Notes – The sexual morph of *Diplodia seriata* is linked to *Botryosphaeria obtusa* Shoe-maker (1964). I identified my isolate as *Di. seriata* based on morphology and phylogeny. This is the first record of *Di. seriata* found on *Wisteria sinensis* in China.



Note a–c Conidiomata on host substrate. d, e Vertical section of conidiomata. f Section of peridium. g–i Conidiogenous cells and developing conidia. j–m Conidia. Scale bars: d–f = 20 µm, g–m = 10 µm.

Figure 4.11 *Diplodia seriata* (GZAAS 23-0583, new host record)

Dothiorella Sacc., Michelia 2(no. 6): 5 (1880)

Type species – *Dothiorella pyrenophora* Berk. ex Sacc.

Notes – *Dothiorella* was introduced by Saccardo (1880) with *D. pyrenophora* as the type species. Crous and Palm (1999) regarded *Dothiorella* as a synonym of *Diplodia*, but Phillips et al. (2005) later resurrected the genus *Dothiorella*. Species of *Dothiorella* are common plant pathogens, endophytes, and saprobes with a worldwide distribution. Over 420 morphological species related to *Dothiorella* are listed in Index Fungorum (2025, June), but only 43 species have molecular data. Members of this genus are characterized by semi-immersed to superficial, unilocular or multilocular ascomata with an ostiolate papilla, trabeculate, branched pseudoparaphyses, short-pedicellate asci with an ocular chamber and hyaline, aseptate, fusiform ascospores, becoming brown, 1-septate, ellipsoidal to obovoid or oblong when mature, and its asexual morphs are coelomycetous, characterized by dark brown to black, immersed to semi-immersed, unilocular or multilocular, ostiolate conidiomata, conidiophores reduced to holoblastic, subcylindrical conidiogenous cells with ovoid, initially hyaline and aseptate, becoming brown and 1-septate when mature (Zhang et al., 2021c; Wu et al., 2023; Du et al., 2025). *Dothiorella* is morphologically similar to *Diplodia* however can be distinguished by the morphology of its conidia, which are brown and 1-septate in their early development (Phillips et al., 2013).

Dothiorella acericola Phookamsak, Tennakoon & K.D. Hyde, Fungal Diversity 95: 78 (2019) Figure 4.12

Index Fungorum number: IF556178; Facesoffungi number: FoF05711

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 220–315 µm wide, 185–210 µm high, mostly solitary, occasionally gregarious, dark brown to black, immersed to partly erumpent, oval or globose to subglobose, unilocular or multilocular, with locule 130–160 µm diam., 185–200 µm high, glabrous, coriaceous, short papillate,

inconspicuous ostiolate. *Ostiole* single, central. *Conidiomatal wall* 25–30 μm wide, composed of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–12 × 4–7 μm ($\bar{x}$ = 9.3 × 5 μm; n = 30), hyaline, cylindrical, sometimes slightly curved, phialidic, hyaline, thick and smooth-walled. *Conidia* 19–25 × 8–12 μm ($\bar{x}$ = 21.5 × 10.5 μm; n = 30), ovoid, rounded at both ends, guttulate, initially hyaline and aseptate, becoming brown to dark brown and 1-septate at maturity, occasionally slightly constricted at septum, straight or slightly curved, smooth-walled.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium fast-growing and reaching 80 mm diam. after one week at 25°C in dark, circular or irregular, cottony, velvety, whitened in the first few days, the outside area becoming yellowish gray after one week, after two weeks becoming black, felt-like, sparse, aerial; in reverse, olive-green to black.

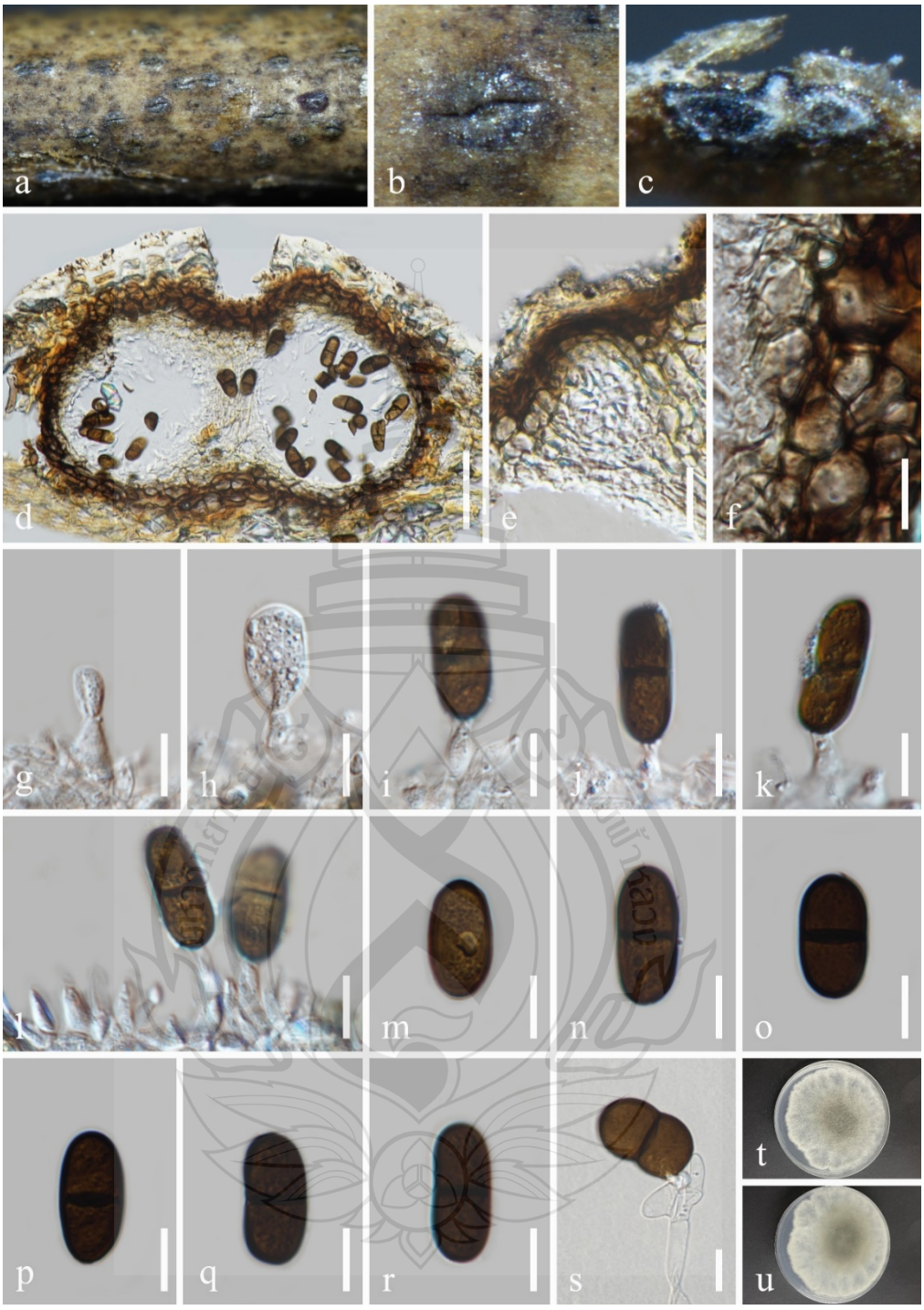
Materials examined – CHINA, Guizhou Province, Anshun City, Maguan Town, Gaoyang Village, elevation 1,350 m, 26°12′40″ N, 105°46′37″ E, on branches of *Rosa roxburghii*, 3 July 2022, N. Wu, GL160 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL58 (HUEST XX), living culture UESTCC XX; *ibid.*, GL80 (HUEST XX), living culture UESTCC XX.

Hosts – *Acer palmatum*, *Euonymus japonicus*, *Koelreuteria paniculata* and *Ziziphus jujuba* (Phookamsak et al., 2019; Pan et al., 2021, 2023; Lin et al., 2023b), *Cercis chinensis*, *Paeonia suffruticosa* and *Stachyurus chinensis* (Du et al., 2025), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – Phookamsak et al. (2019) introduced *Dothiorella acericola* (on dried twigs of *Acer palmatum*) from China, which was represented by its asexual morph. This

species has so far only been found in China and has been reported as a saprobe and pathogen on a wide range of hosts (Pan et al., 2021; Du et al., 2025). My new collection (UESTCC GL160, UESTCC CL58 and UESTCC GL80) is placed within *Dothiorella* and clustered with *Do*. *acericola* (Figure 4.13). Additionally, my collection matches well with the holotype of *Do*. *acericola* by morphology (Phookamsak et al., 2019). Based on morphological and phylogenetic evidence, my collection is identified as *Do*. *acericola* and reported as a new host record on *Rosa roxburghii.*



Note a, b Conidiomata on natural substrate. c, d Vertical sections of conidiomata. e Ostiole. f Conidiomatal wall. g–l Conidiogenous cells and developing conidia. m–r Conidia. s Germinating conidium. t, u Colony on PDA, above (t), below (u). Scale bars: d = 50 µm; e = 20 µm; f–s = 10 µm.

Figure 4.12 *Dothiorella acericola* (HUEST GL160, new host record)

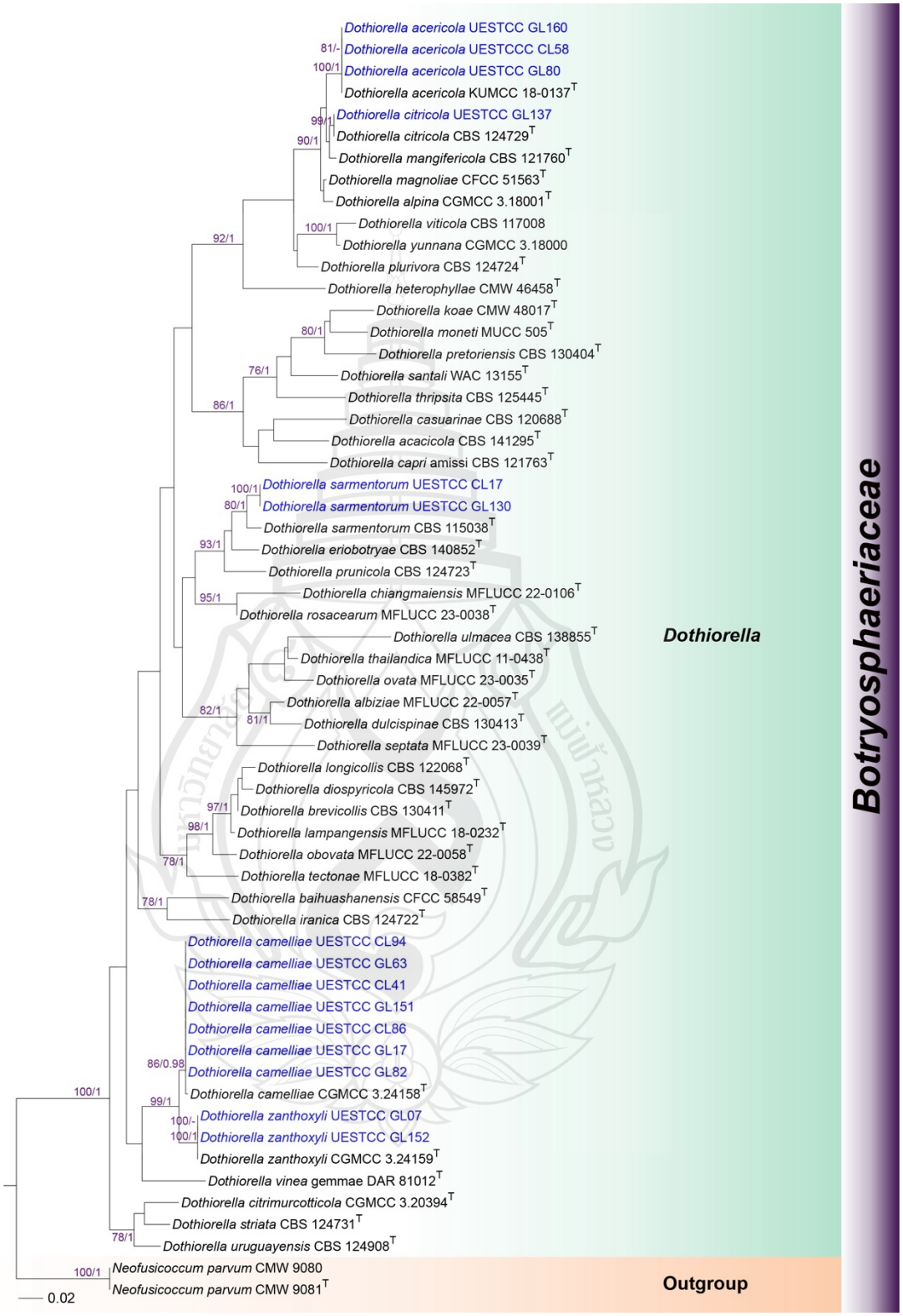


Figure 4.13 Phylogram generated from maximum likelihood analysis based on combined ITS and *tef1α* sequence data of *Dothiorella*

Figure 4.13 The tree is rooted with *Neofusicoccum parvum* (CMW 9080 and CMW 9081). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Dothiorella camelliae L.W. Li & Jian K. Liu, MycoKeys 97: 94 (2023) Figure 4.14

Index Fungorum number: IF847167; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 280–370 µm wide, 160–320 µm high, solitary to gregarious or confluent, dark brown to black, immersed to superficial or erumpent through bark, subglobose, mostly multi-locular, occasionally unilocular, glabrous, with locule 185–200 µm diam., 165–320 µm high, ovoid to subglobose, thick-walled, ostiolate. *Ostiole* 70–80 µm wide, 80–105 µm high, well-developed, subcylindrical, single to each locule, straight or curved, central or laterally located. *Peridium* 55–65 µm wide, composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* 4–5 µm wide, composed of dense, filamentous, rarely branched, septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 95–125 × 25–29 µm ($\bar{x}$ = 107 × 26 µm; n = 20), 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 22–26 × 10.5–12 µm ($\bar{x}$ = 24 × 11 µm; n = 30), irregularly arranged or crowded, oblong, ovate to sub-clavate, initially hyaline and aseptate, becoming brown to dark brown and 0–1-septate at maturity, slightly constricted at the septum, straight or slightly curved, upper cell slightly longer than lower cell, slightly acute at both ends, smooth-walled, with granular contents. **Asexual morph:** Undetermined.

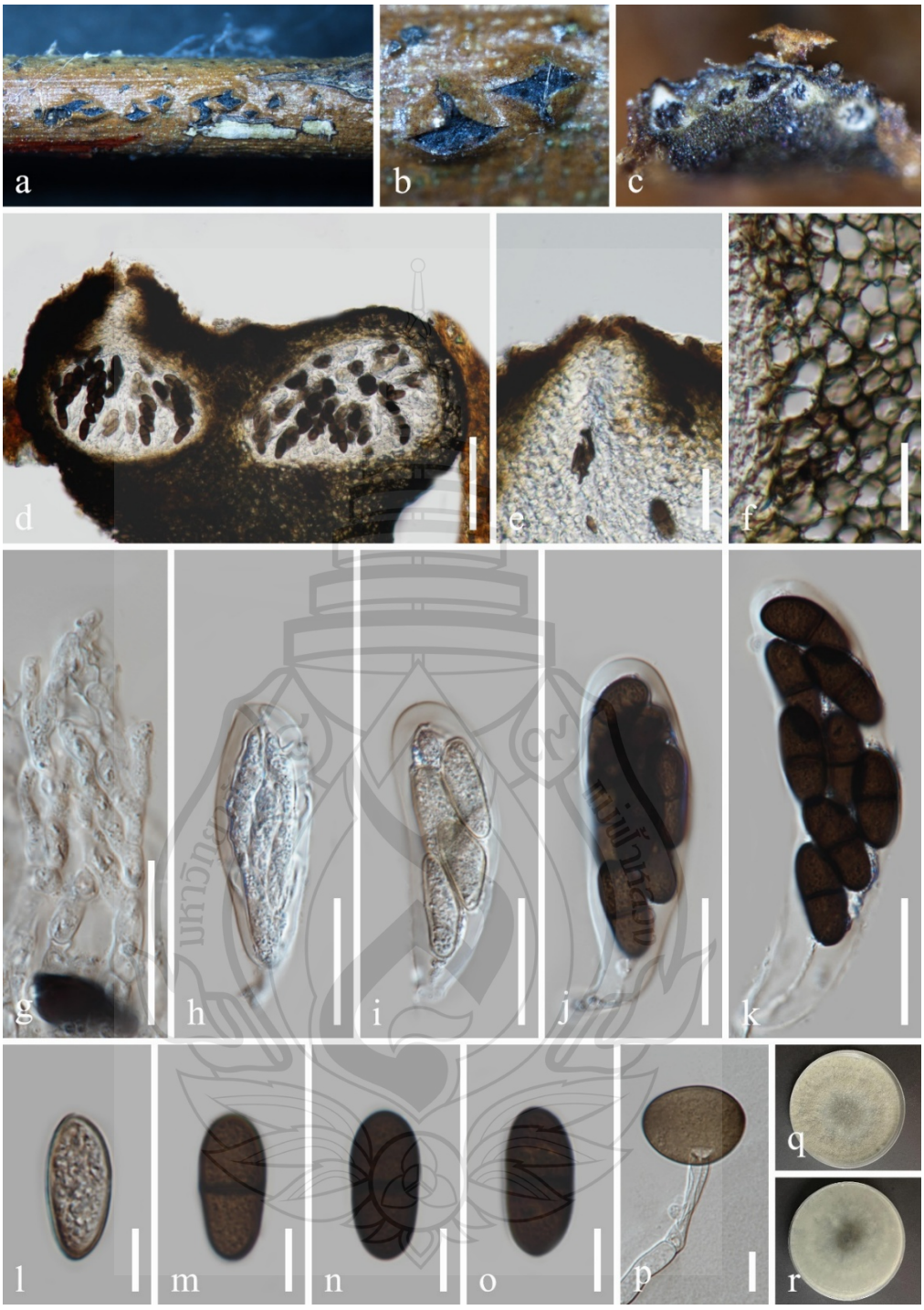
Culture characteristics – Ascospores germinated on PDA medium within 12 h. Colonies on PDA medium fast-growing and reaching 70 mm diam. after one week at 25°C in dark, circular, velvety, grayish green mycelium; in reverse, dark green to black with an entire margin.

Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *Rosa roxburghii*, 9 July 2022, N. Wu, GL151 (HUEST XX), living culture UESTCC XX; *ibid.*, GL82 (HUEST XX), living culture UESTCC XX; *ibid.*, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL41 (HUEST XX), living culture UESTCC XX; *ibid.*, CL86 (HUEST XX), living culture UESTCC XX; *ibid.*, CL94 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *R. sterilis*, 3 July 2022, N. Wu, GL17 (HUEST XX), living culture UESTCC XX; *ibid.*, GL63 (HUEST XX), living culture UESTCC XX.

Hosts – *Camellia oleifera* and *Paeonia suffruticosa* (Li et al., 2023a), *Rosa roxburghii* and *R. sterilis* (present study).

Known geographical distribution – China.

Notes – *Dothiorella camelliae* was introduced by Li et al. (2023a) based on its sexual morph, which was collected from two woody oil plants. In the phylogenetic analysis (Figure 4.13), my three strains (UESTCC GL151, UESTCC CL41 and UESTCC GL17) clustered with *Do. camelliae* (CGMCC 3.24158). Morphologically, my collection is similar to *Do. camelliae* in having multilocular or unilocular, globose to subglobose ascomata, bitunicate, clavate asci with hyaline to dark brown, (0–)1-septate, oblong to ovate or sub-clavate ascospores. I therefore recognize my collection as *Do. camelliae*. To my knowledge, this is the first report of *Do. camelliae* on *Rosa roxburghii* and *R. sterilis* in China.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: d = 100 µm; e–k = 30 µm; l–p = 10 µm.

Figure 4.14 *Dothiorella camelliae* (HUEST GL151, new host record)

Dothiorella citricola (A.J.L. Phillips & Abdollahz.) Tao Yang & Crous, Fungal Biology 121(4): 335 (2016) Figure 4.15

Index Fungorum number: IF817674; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 320–380 μm wide, 230–350 μm high, solitary to gregarious or confluent, dark brown to black, initially immersed, becoming erumpent through bark fissures, subglobose, mostly unilocular, occasionally multi-locular, coriaceous, glabrous, thick-walled, ostiolate. *Ostiole* 95–120 μm wide, 110–150 μm high, central or laterally located, long, subcylindrical, single. *Conidiomatal wall* 35–50 μm wide, composed of dark brown to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–10 × 3.5–6 μm ($\bar{x}$ = 9 × 4.8 μm; n = 30), hyaline, cylindrical to lageniform, discrete or integrated, holoblastic, indeterminate, thin-walled, smooth. *Conidia* 23–26 × 10–12 μm ($\bar{x}$ = 25 × 11.5 μm; n = 30), oblong to subcylindrical, ends truncate, initially hyaline and aseptate, becoming brown to dark brown and 0–1-septate at maturity, not constricted at the septum, straight or slightly curved, smooth-walled, with finely verruculose contents.

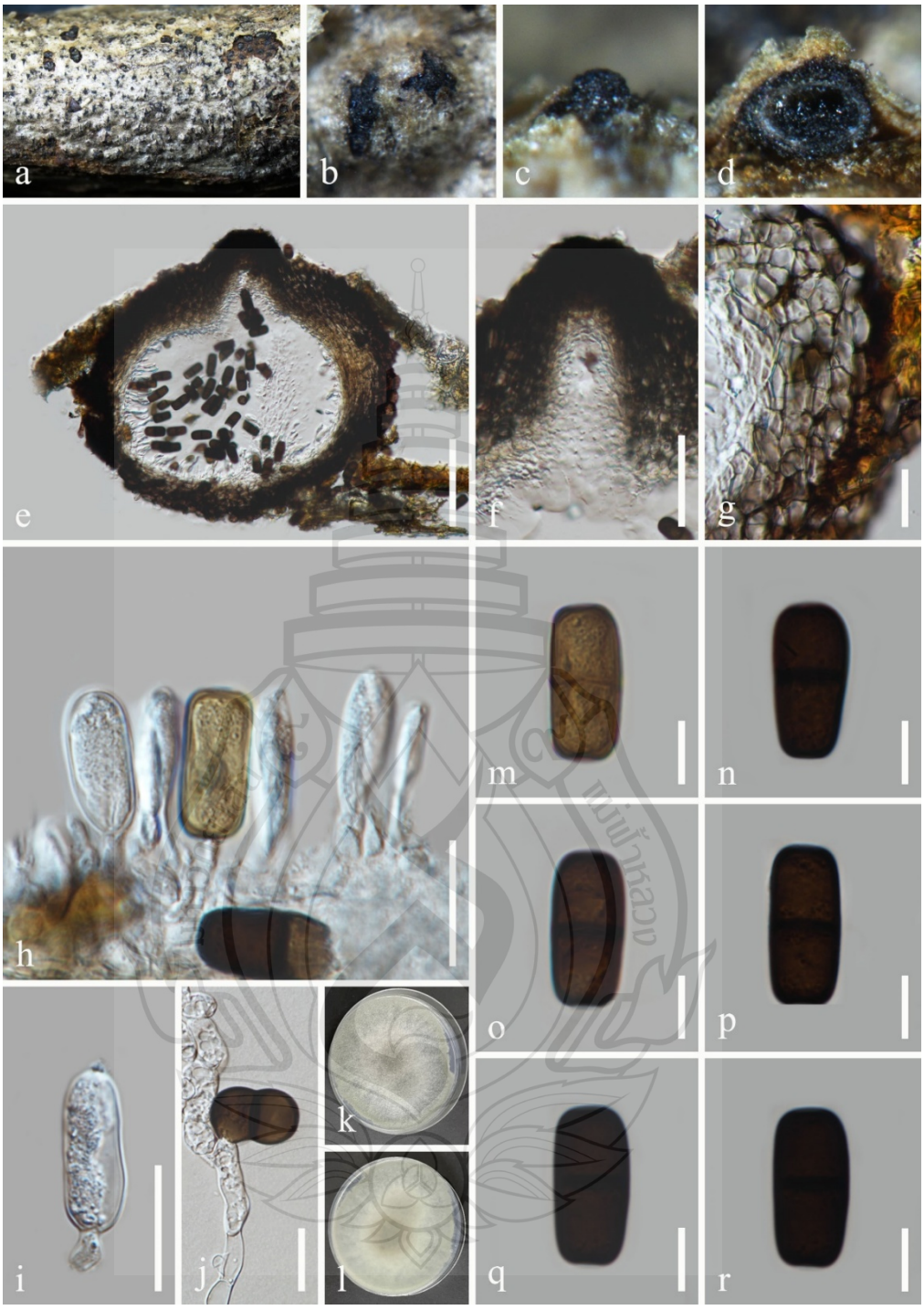
Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium fast-growing and reaching 80 mm diam. after one week at 25°C in dark, circular, cottony, dense, aerial, smoke-gray, in reverse, pale brown to greenish olivaceous.

Material examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *Rosa roxburghii*, 9 July 2022, N. Wu, GL137 (HUEST XX), living culture UESTCC XX.

Hosts – *Acacia karroo* and *Citrus sinensis* (Abdollahzadeh et al., 2014; Yang et al., 2017; Zhang et al., 2021c), *Rosa roxburghii* (present study).

Known geographical distribution – China, New Zealand, South Africa.

Notes – *Dothiorella citricola* was previously introduced as *Spencermartinsia citricola* by Abdollahzadeh et al. (2014), based on a specimen collected from *Citrus sinensis* in New Zealand. Its taxonomic placement was later updated by Yang et al. (2017), who transferred it to *Dothiorella* based on phylogenetic evidence. Based on a BLAST search on NCBI GenBank, the ITS sequence of my collection shows 99.61% identity to *Dothiorella citricola* (CBS 124729). Phylogenetic analysis revealed that my collection clustered with the strains of *Do*. *citricola* (CBS 124728 and CBS 124729) (Figure 4.13). Additionally, the morphology of my collection fits well with the holotype of *Do*. *citricola* (Abdollahzadeh et al., 2014). Therefore, I recognize my collection as *Do*. *citricola*, representing the first record of this species on *Rosa roxburghii* in China.



Note a–c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Ostiole. g Conidiomatal wall. h, i Conidiogenous cells and developing conidia. j Germinating conidium. k, l Colony on PDA, above (k), below (l). m–r Conidia. Scale bars: e = 100 µm; f = 50 µm; g–j = 20 µm; m–r = 10 µm.

Figure 4.15 *Dothiorella citricola* (HUEST GL137, new host record)

Dothiorella ovata N. Wu, Dissan. & Jian K. Liu, sp. nov. Figure 4.16

Index Fungorum number: IF900578; Facesoffungi number: FoF14258

Etymology – In reference to the ovoid conidia.

Holotype – MFLU 23-0009

Saprobic on a dead wood. Sexual morph: Not observed. Asexual morph: *Conidiomata* 119–173 × 160–273 μm ($\bar{x}$ = 141 × 204 μm, *n* = 20), semi-immersed or immersed in the substrate, emerging through the epidermis when mature, globose to subglobose, pyriform, dark brown, unilocular, solitary, glabrous, ostiolate. *Ostiole* 22–26 μm diam., single, cir- cular, papillate, centrally located. *Peridium* up to 16–38 μm wide, comprising host and fungal tissues, thick-walled, dark brown to hyaline cells of *textura angularis*. Paraphyses absent. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 4–11 × 3–4 μm ($\bar{x}$ = 7 × 4 μm, *n* = 20), hyaline, phialidic, cylindrical, straight or curved, smooth-walled. *Conidia* 20–26 × 9–11 μm ($\bar{x}$ = 22 × 10 μm, *n* = 50), hyaline, aseptate, ovoid, rounded at both ends or sometimes with truncate bases, becoming pigmented brown and one septate at maturation, constricted in the middle, smooth-walled, without longitudinal striations or mucilaginous sheath.

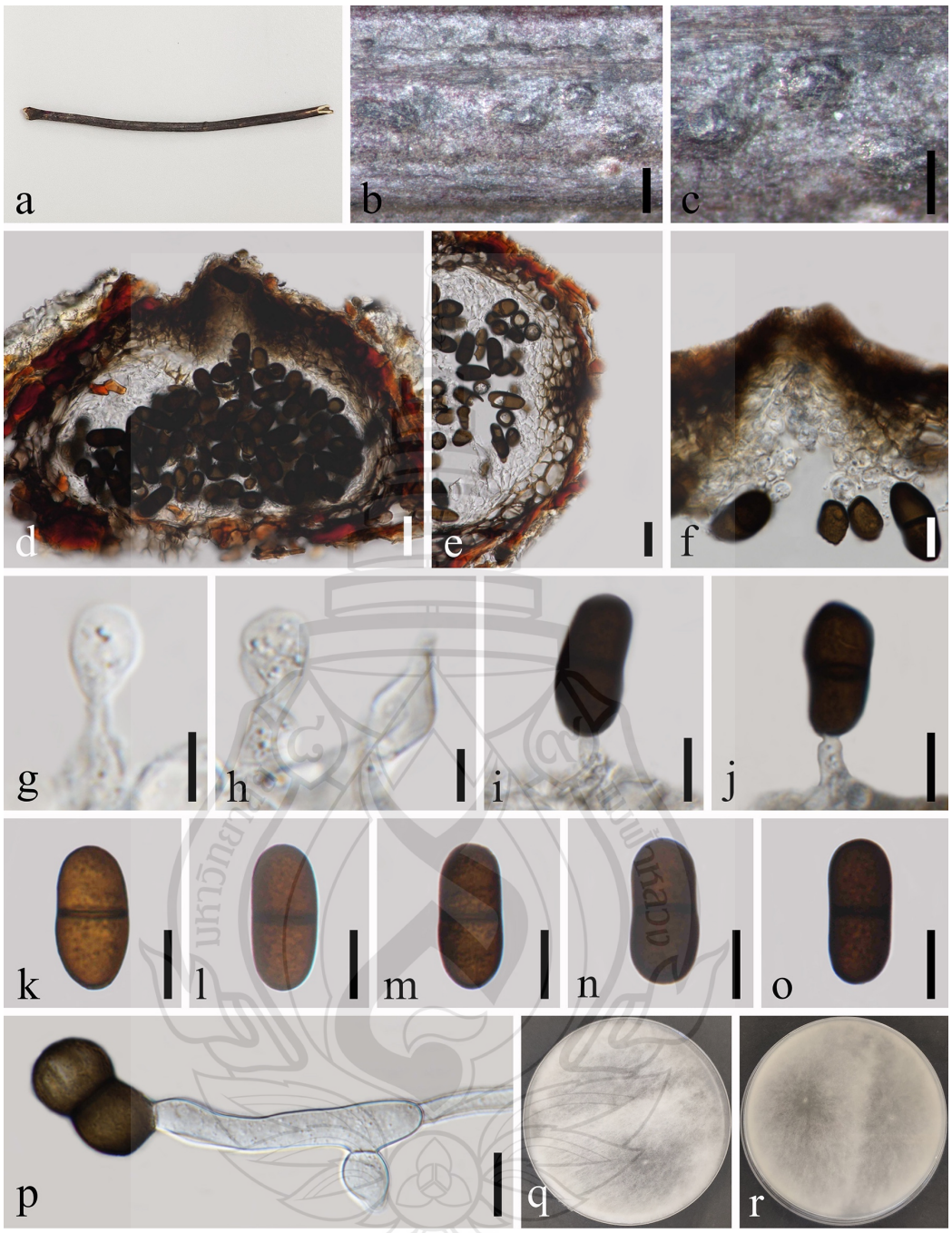
Culture characteristics – Conidia germinating on PDA within 12 h. Colonies are fast growing on PDA, reaching 90 mm diam. after 5–6 days at 20–23°C. Sparse, aerial, filamentous, white in first few days, after 2 weeks, becoming black.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Cho Lae, on an unidentified dead wood, 6 August 2019, Na Wu, YW177 (MFLU 23-0009, holotype); ex-type living culture MFLUCC 23-0035; *ibid*., 7 August 2019, Na Wu, YW231 (MFLU 23-0010, paratype), living culture MFLUCC 23-0036.

Notes – *Dothiorella ovata* is nested in between *Do. albiziae*, *Do. septata* and *Do. thailandica* but can be recognized as a distinct lineage (Figure 4.7). Morphologically, *Do. ovata* is similar to *Do. septata* and *Do. albiziae*, which in having oblong to ovoid, hyaline conidia becoming brown and one septate at maturation.

However, *Do. ovata* differs from *Do. septata* and *Do. albiziae* by its slightly constricted septum and the larger conidia. In addition, a comparison of *tef1α* sequences data of *Do. ovata* and *Do. albiziae* showed that there are 14 bp (base pair) differences (of 252 bp including the gaps), while *Do. ovata* and *Do. thailandica* showed 18 bp differences (of 302 bp including the gaps). Therefore, I introduce *Do. ovata* as a new species.





Note a–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Ostiolar region with periphyses. g–j Conidiogenous cells and developing conidia. k–o Conidia. p Germinated conidium. q, r Colonies on PDA, above (q) and below (r). Scale bars: b, c = 50 µm, d, e = 20 µm, f = 10 µm, g, h = 5 µm, i–p = 10 µm.

Figure 4.16 *Dothiorella ovata* (MFLU 23-0009, holotype)

Dothiorella rosacearum N. Wu, Dissan. & Jian K. Liu, sp. nov. Figure 4.17

Index Fungorum number: IF900579; Facesoffungi number: FoF14259

Etymology – Referring to the host family Rosaceae on which the type specimen was collected.

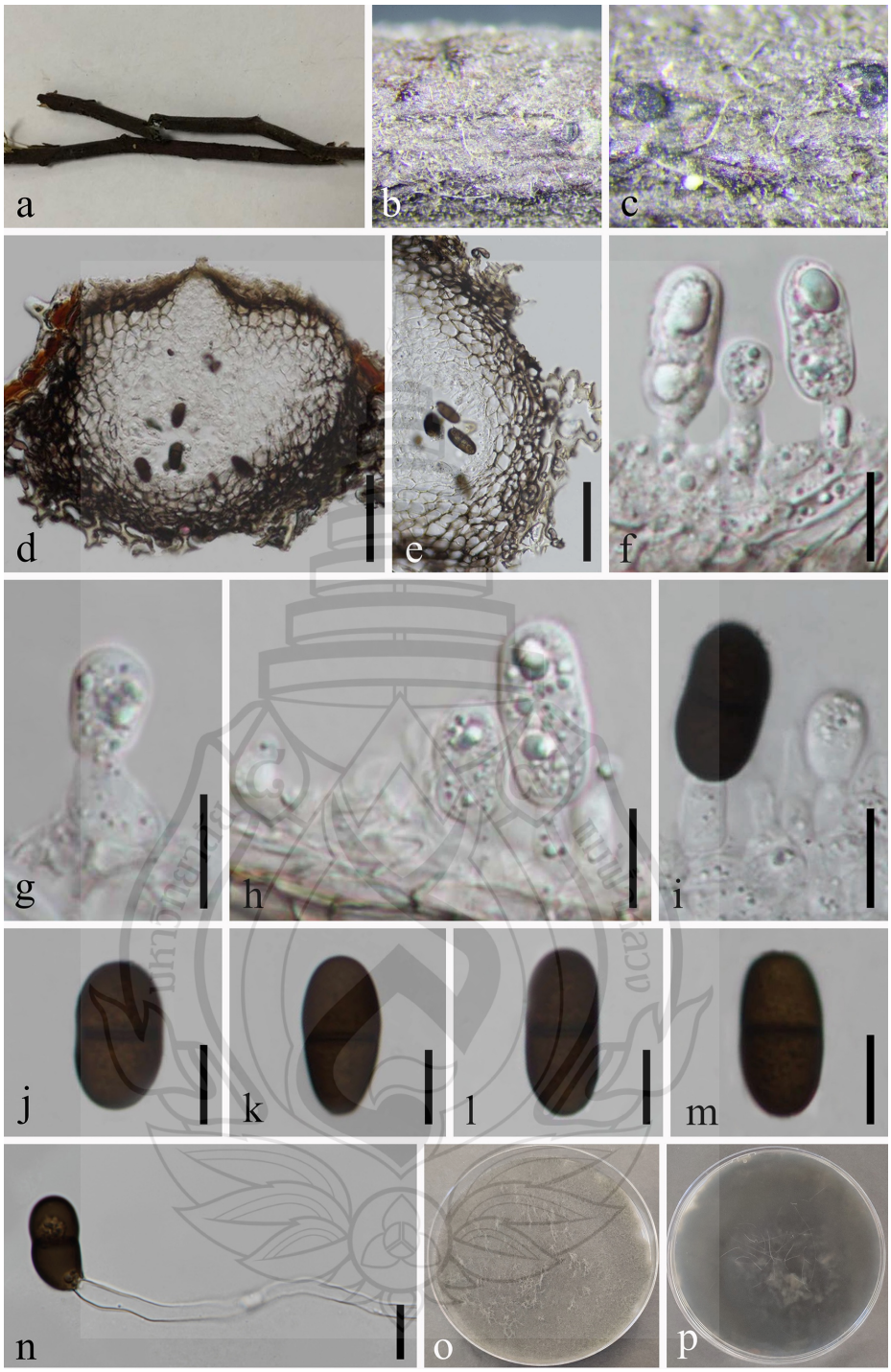
Holotype – MFLU 23-0014

Saprobic on dead twigs of *Amygdalus* sp. (Rosaceae). Sexual morph: Not observed. Asexual morph: *Conidiomata* 153–234 × 222–336 μm ($\bar{x}$ = 187 × 270 μm, n = 20), immersed, scattered, dark brown to black, globose or subglobose, solitary, initially intraepidermal, visible as black dots on the host when mature, thick-walled, glabrous. *Ostiole* 30–32 μm diam., single, straight, sometimes bent, centrally located. *Peridium* up to 31–45 μm wide, comprising host and fungal tissues, dark brown to black, 5–10 cell layers of *textura angularis*, becoming thin-walled and hyaline towards the inner region. *Paraphyses* absent. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 4–9 × 3–5 μm ($\bar{x}$ = 7 × 4 μm, n = 20), hyaline, aseptate, contents granular, cylindrical to ellipsoidal, smooth-walled, unbranched or occasionally branched, with swollen bases. *Conidia* 17–21 × 7–10 μm ($\bar{x}$ = 18 × 8 μm, n = 50), hyaline, aseptate, contents granular, smooth, thin-walled, oval, straight, rounded at the apex, or sometimes with truncate bases, becoming brown and septate when aged, without longitudinal striations or mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies are fast growing on PDA, reaching 90 mm diam. after 5–6 days at 20–23°C. Sparse, aerial, filamentous, becoming dark brown to black after 2 weeks.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Pa Pae, on dead twigs of *Amygdalus* sp. (*Rosaceae*), 8 August 2019, Na Wu, YW255 (MFLU 23-0014, holotype); ex-type living culture MFLUCC 23-0038; *ibid.*, on an unidentified decaying wood, 7 August 2019, Na Wu, YW253 (MFLU 23-0013, paratype), living culture MFLUCC 23-0037.

Notes – The phylogenetic result (Figure 4.7) showed that two isolates of *Dothiorella rosacearum* constitute a distinct lineage but claded closer to *Do. brevicollis*, *Do. diospyricola*, *Do. lampangensis*, *Do. longicollis*, *Do. obovata* and *Do. tectonae*. A comparison of ITS sequences data between *Do. rosacearum* and *Do. tectonae* showed that there are 19 bp of 539 base pairs differences (including the gaps). In addition, the shortly raised irregular striations can be found on the conidia of *Do. tectonae*, while no striations were observed in *Do. rosacearum*. Therefore, *Do*. *rosacearum* is a morphologically and phylogenetically distinct species and herein introduced as a new species.



Note a–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f–i Conidiogenous cells and developing conidia. j–m Conidia. n Germinated conidium. o, p Colonies on PDA, above (o) and below (p). Scale bars: d, e = 50 μm, f–n = 10 μm.

Figure 4.17 *Dothiorella rosacearum* (MFLU 23-0014, holotype)

Dothiorella sarmentorum (Fr.) A.J.L. Phillips, A. Alves & J. Luque, Mycologia 97(2): 522 (2005) Figure 4.18

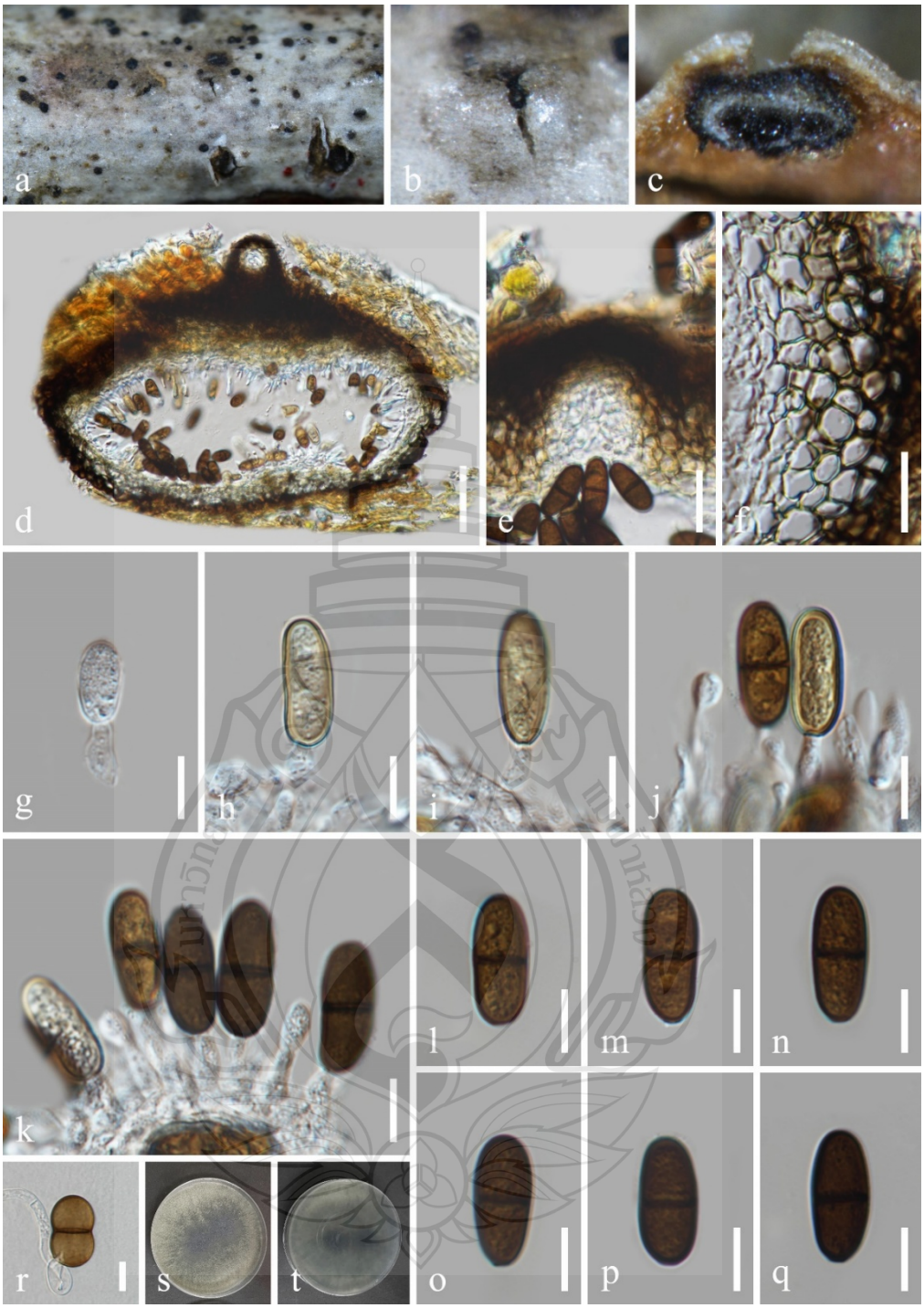
Index Fungorum number: IF501403; Facesoffungi number: FoF02148

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 225–350 μm wide, 170–245 μm high, solitary to gregarious, dark brown to black, initially immersed, becoming erumpent through bark fissures, subglobose, mostly unilocular, occasionally multi-locular, glabrous, coriaceous, thick-walled, short papillate, ostiolate. *Ostiole* 58–67 μm wide, 65–70 μm high, single, oval or circular, centric or eccentric. *Conidiomatal wall* 20–30 μm wide, composed of dark brown to brown cells of *textura angularis* in several outer layers, gradually merging with hyaline cells in inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–12 × 3–5 μm ($\bar{x}$ = 9 × 3.7 μm; n = 30), hyaline, cylindrical to doliiform, determinate, smooth-walled. *Conidia* 20–23 × 8.5–10 μm ($\bar{x}$ = 21.5 × 9.5 μm; n = 30), ellipsoid to obovoid, rounded at apex, truncate at base, initially hyaline to pale brown and aseptate, becoming brown to dark brown and 1-septate at maturity, occasionally slightly constricted at the septum, straight or slightly curved, smooth-walled, with finely verruculose contents.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium fast-growing and reaching 70 mm diam. after one week at 25℃ in dark, circular, effuse, velvety, mycelium initially white, becoming black in the center, grayish green towards the margin; in reverse, dark green to black with an entire margin.

Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *Rosa roxburghii*, 9 July 2022, N. Wu, GL130 (HUEST XX), living culture UESTCC XX; *ibid.*, Huopu Town, on branches of *R. roxburghii*, 28 September 2021, N. Wu, CL17 (HUEST XX), living culture UESTCC XX.

Notes – Phillips et al. (2005) introduced *Dothiorella sarmentorum* with both asexual and sexual morphs. My collection matches with the original diagnosis of *Do*. *sarmentorum* (Phillips et al., 2005). In the phylogenetic analysis (Figure 4.7), my isolates (UESTCC GL130 and UESTCC CL17) clustered as sister taxa to the type material of *Do*. *sarmentorum* (CBS 115038). Thus, I identified my isolates as *Do*. *sarmentorum* based on morphology and phylogeny. This is the first record of *Do*. *sarmentorum* found on *Rosa roxburghii* in China.



Note a, b Conidiomata on natural substrate. c, d Vertical sections of conidiomata. e Ostiole. f Conidiomatal wall. g–k Conidiogenous cells and developing conidia. l–q Conidia. r Germinating conidium. s, t Colony on PDA, above (s), below (t). Scale bars: d = 50 μm; e, f = 20 μm; g–r = 10 μm.

Figure 4.18 *Dothiorella sarmentorum* (HUEST GL130, new host record)

Dothiorella septata N. Wu, Dissan. & Jian K. Liu, sp. nov. Figure 4.19

Index Fungorum number: IF900580; Facesoffungi number: FoF14260

Etymology – The epithet "*septata*" refers to the septum observed in mature conidia.

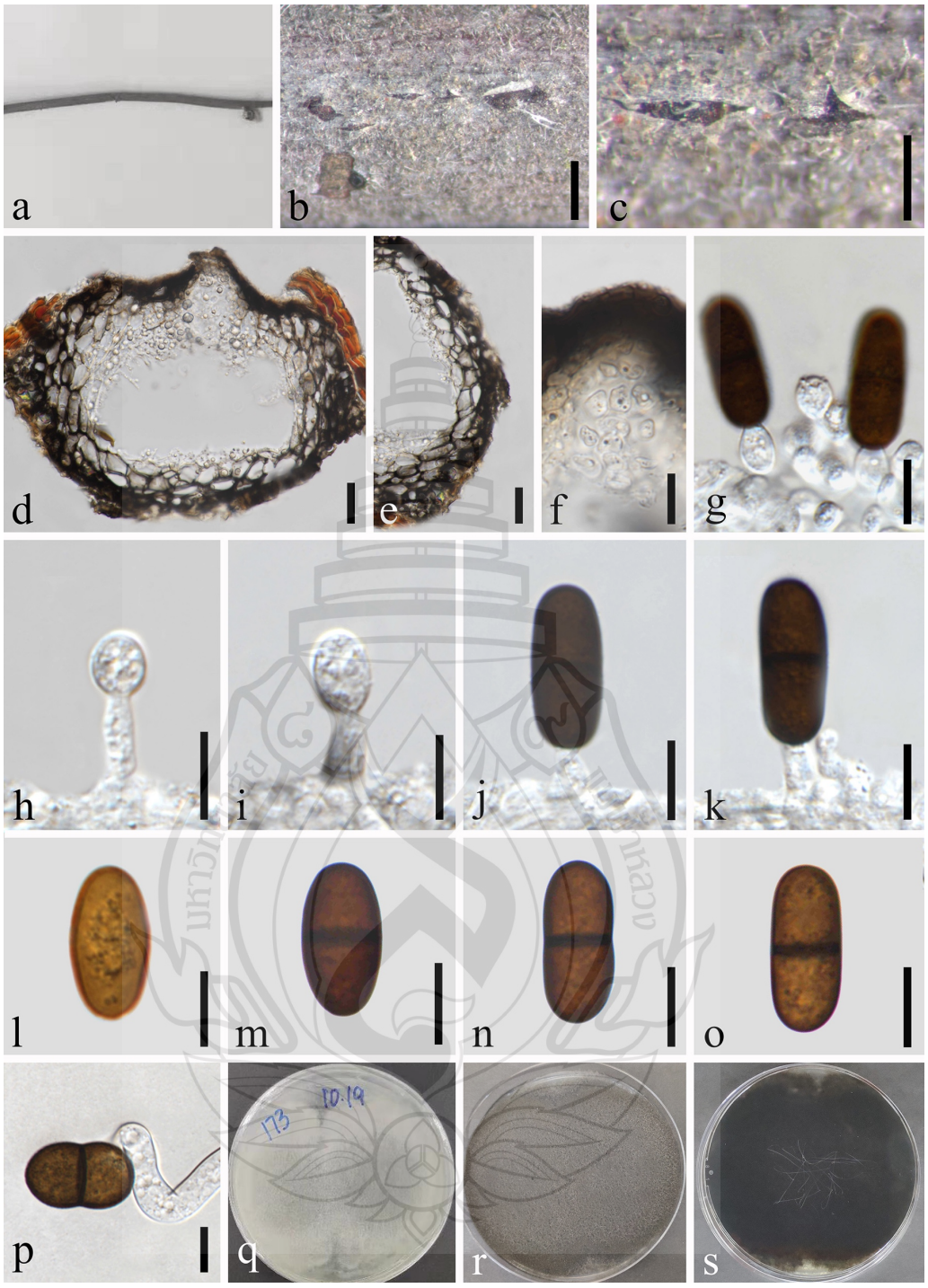
Holotype – MFLU 23-0007

Saprobic on an unidentified dead wood. Sexual morph: Not observed. Asexual morph: *Conidiomata* 114–139 × 150–198 µm ($\bar{x}$ = 126 × 172 µm, n = 20), pyriform or subglobose, immersing through the host epidermis, unilocular, glabrous, thick-walled, ostiolate. *Ostiole* 19–25 µm diam., single, straight, centrally located. *Peridium* up to 16–303 µm wide, with outer 3–5 layers of brown cells of *textura angularis* and inner 1–2 layers of hyaline cells of *textura angularis*. *Paraphyses* absent. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 2–5 µm ($\bar{x}$ = 7 × 3 µm, n = 20), hyaline, phialidic, subcylindrical, smooth-walled. *Conidia* 19–21 × 8–10 µm ($\bar{x}$ *x* = 21 × 9 µm, n = 50), oblong to ovoid with a broadly rounded apex, initially hyaline to yellowish and aseptate, becoming brown to dark brown and one septate at maturation, slightly constricted at the septum, smooth-walled, without a mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies are fast growing on PDA, reaching 90 mm diam. after 5–6 days. Sparse, aerial, filamentous, smooth with a crenate edge, white in first few days, becoming grey after one week, and after 2 weeks, becoming black.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Sop Poeng, on an unidentified dead wood, 9 August 2019, Na Wu, YW173 (MFLU 23-0007, holotype); ex-type living culture MFLUCC 23-0039; *ibid*., on a decaying wood in a mountain, 7 August 2019, Na Wu, YW217 (GZAAS 23-0587, paratype), living culture GZCC 23-0583; *ibid.*, YW228 (GZAAS 23-0588, paratype), living culture GZCC 23-0584.

Notes – The phylogenetic results (Figure 4.7) showed that my isolates clustered with *Do. ovata* and formed a sister group. A comparison of ITS and *tef1α* nucleotides shows that *Do. septata* is significantly different from its sister species, *Do. ovata* by 7/569 bp (1.2%) in ITS and 13/303 bp (4.3%) in *tef1α*. In the phylogenetic analysis, these two species formed two distinct clades in *Dothiorella*. Morphologically, there are several differences in conidial morphology between these two species. Considering the morpho-molecular data, I introduced *Do. septata* as a new species.



Note a–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Ostiolar region with periphyses. g–k Conidiogenous cells and developing conidia. l–o Conidia. p Germinated conidium. q–s Colonies on PDA, above (q) and below (r, s). Scale bars: b = 50 µm, c, d = 20 µm, e–p = 10 µm.

Figure 4.19 *Dothiorella septata* (MFLU 23-0007, holotype)

Dothiorella zanthoxyli W. L. Li & Jian K. Liu, MycoKeys 97: 98 (2023) Figure 4.20

Index Fungorum number: IF847168; Facesoffungi number: FoFX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 187–305 μm wide, 190–210 μm high, solitary to gregarious or confluent, dark brown to black, immersed to superficial or erumpent through bark, visible as black dots on the host, subglobose to pyriform, unilocular or multilocular, glabrous, coriaceous to carbonaceous, thick- and smooth-walled, papillate, ostiolate. *Ostiole* 45–55 μm wide, 50–67 μm high, single, cylindrical to subcylindrical, straight or curved, central or laterally located. *Peridium* 35–50 μm wide, composed of few layers of hyaline to dark brown cells of *textura angularis*. *Hamathecium* 4–5 μm wide, composed of dense, filamentous, rarely branched, septate, constricted at the septum, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 90–105 × 23.5–31 μm ($\bar{x}$ = 95 × 28 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 22–27 × 11–14 μm ($\bar{x}$ = 25 × 12 μm; n = 30), irregularly arranged or crowded, fusiform to oblong, initially hyaline and aseptate, becoming brown to dark brown and 1-septate at maturity, slightly constricted at the septum, straight or slightly curved, smooth-walled, with finely verruculose contents. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h. Colonies on PDA medium fast-growing and reaching 60 mm diam. after one week at 25°C in dark, circular, velvety to woolly, grayish green; in reverse, pale brown to black.

Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Jichangping Town, Songhe Township, elevation 1,800 m, 26°3′7″ N, 104°35′36″ E, on branches of *Rosa roxburghii*, 10 July 2022, N. Wu, GL152 (HUEST XX), living culture UESTCC XX; *ibid.*, Qianxinan Autonomous Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead

branches of *R*. *sterilis*, 3 July 2022, N. Wu, GL07 (HUEST XX), living culture UESTCC XX.

Hosts – *Rosa roxburghii* and *R*. *sterilis* (present study), *Zanthoxylum bungeanum* (Li et al., 2023a).

Known geographical distribution – China.

Notes – My collection matches well with the holotype of *Dothiorella zanthoxyli* in morphology (Li et al., 2023a), though the dimension of asci is larger and with slightly broader ascospores. Molecular data strongly support the identification of my collection as *Do*. *zanthoxyli* (Figure 4.13). I report *Rosa roxburghii* and *R*. *sterilis* as new host records for *Do*. *zanthoxyli* in this study.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Germinating ascospore. q, r Colony on PDA, above (q), below (r). Scale bars: d = 100 µm; e–j = 30 µm; k–p = 10 µm.

Figure 4.20 *Dothiorella zanthoxyli* (HUEST GL152, new host record)

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

Type species – *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl.

Notes – *Lasiodiplodia* was formally established by Clendenin (1896) with *L. tubericola* Ellis and Everhart (= *L. theobromae*; Liu et al., 2012) as the type species. Members of this genus mainly occur on various woody hosts in tropical and subtropical regions, causing fruit and root rots, cankers, stem blight or dieback and sap staining (Punithalingam, 1980; Slippers & Wingfield, 2007; Ismail et al., 2012; Marques et al., 2013; Phillips et al., 2013; Dissanayake et al., 2016; Zhao et al., 2019). *Lasiodiplodia* is morphologically similar to *Diplodia* and *Neodeightonia* but can be distinguished by its striate conidia and the presence of paraphyses, which are unique to *Lasiodiplodia* in the asexual morph (Phillips et al., 2013; Wu et al., 2021a, 2023; Sun et al., 2025).

Lasiodiplodia chiangraiensis N. Wu, A.J. Dissanayake & Jian K. Liu sp. nov. Figure 4.21

Index Fungorum number: MB839203; Facesoffungi number: FoF09518

Etymology – Named after Chiang Rai Province in Thailand, where the fungus was collected.

Holotype – MFLU 21-0003.

Saprobic on the bark of an unidentified host, forming conspicuous, black spots on the host surface. Sexual morph: not observed. Asexual morph: *Conidiomata* 170–190 µm diam., 160–190 µm high, semi-immersed or immersed in the substrate, solitary, gregarious or confluent, globose to subglobose, short neck, dark brown. *Peridium* up to 21–35 µm wide, consisting of brown, small cells of textura angularis, becoming thin-walled and hyaline towards the inner region. *Ostiole* 30–70 µm diam., centrally located, papillate. *Paraphyses* 2–5 µm wide, hyaline, cylindrical, aseptate, not branched, rounded at apex. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 7–11 µm long, 3.5–5 µm wide, hyaline, cylindrical. *Conidia* (21–)22–27(–30) × (12–)13–15(–17) µm ($\bar{x}$ = 25 × 14 µm, n = 30), subglobose to oval, rounded at the apex,

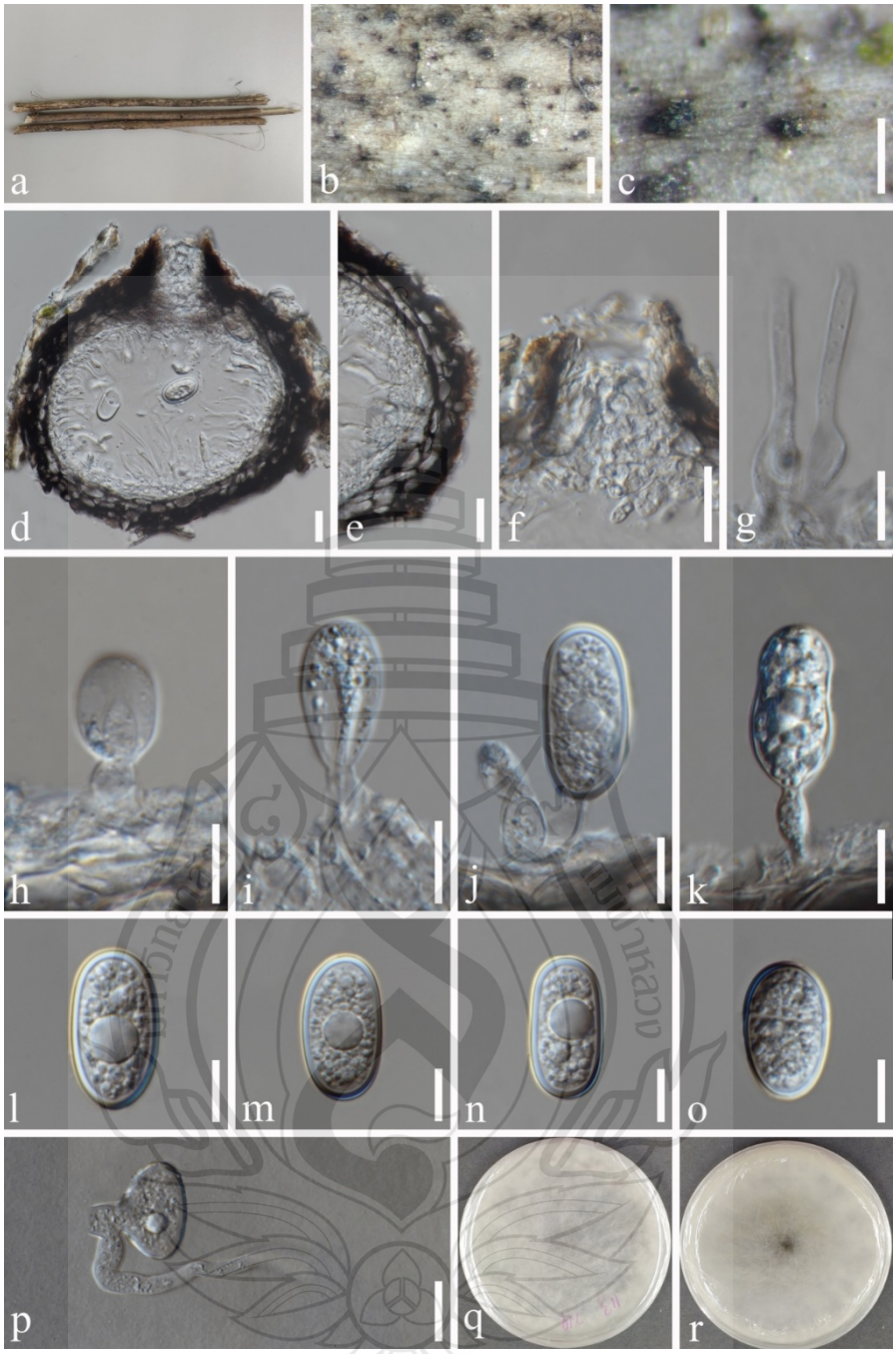
frequently constricted in the middle, hyaline, aseptate or one-septate, guttulate, without longitudinal striations or mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching 90 mm diam. after 4–5 days at 20–23°C, circular, white during the first few days, sparse, aerial, surface smooth with crenate edge, filamentous, after 2 weeks becoming black.

Material examined – THAILAND. Chiang Rai: Amphoe Mueang, Tambon Nang Lae, Mae Fah Luang University, Botanical Garden, on unidentified dead wood, 17 July 2019, Na Wu, YW113 (MFLU 21-0003, holotype; GZAAS 21-0003, isotype), ex-type living culture MFLUCC 21-0003; ibid., on decaying wood, 12 December 2019, Na Wu, YW401 (GZAAS 21-0014), living culture GZCC 21-0003.

Known distribution – Chiang Rai, Thailand.

Notes – *Lasiodiplodia chiangraiensis* is phylogenetically closely related to *L. iranensis* but formed a distinct linage (Figure 4.22), and can be recognized as a new species. Morphologically, these species can be distinguished from the dimensions of their conidia. In addition, conidia of *L. chiangraiensis* are hyaline without longitudinal striations, while those of *L. iraniensis* become dark brown with age. In terms of the nucleotides comparison, *L. chiangraiensis* (MFLUCC 21-0003) and *L. iraniensis* (CBS 124710, ex-type) differed in one base pair (bp) in ITS region, seven in *tef1α* region and two in *tub2*.



Note a–c Conidiomata on host surface. d Section through conidiomata. e Peridium. f Ostiolar region with periphyses. g Paraphyses. h–k Conidia developing on conidiogenous cells. l–o Hyaline, aseptate conidia. p Germinating conidium. q, r Colonies after 7 days on PDA (q from above, r from below). Scale bars: b = 500 µm, c = 200 µm, d–e = 10 µm, f = 20 µm, g–p = 10 µm.

Figure 4.21 *Lasiodiplodia chiangraiensis* (MFLU 21-0003, holotype)

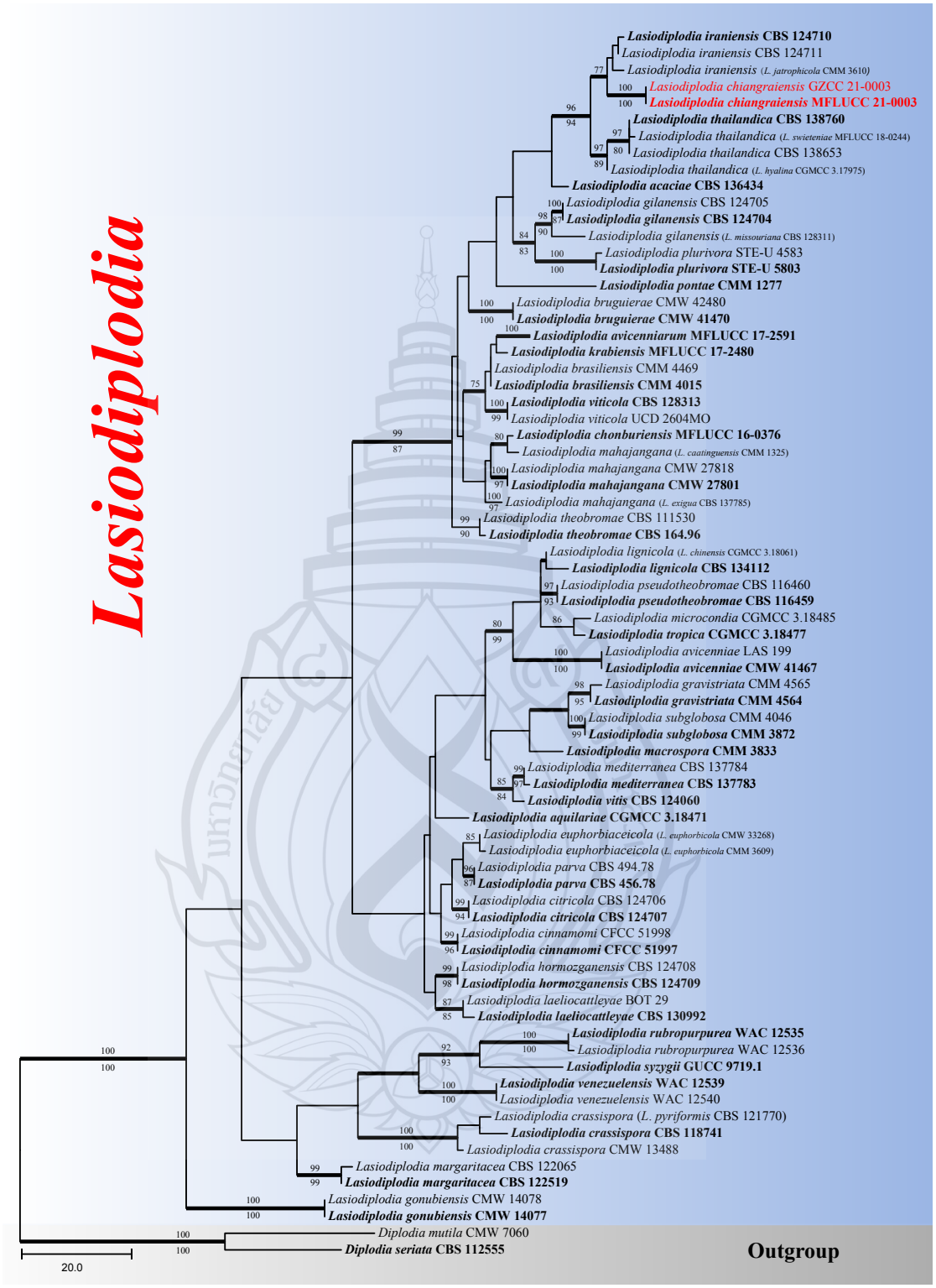


Figure 4.22 Phylogenetic tree generated from maximum parsimony (MP) analysis based on combined ITS, *tef1α* and *tub2* sequence data of *Lasiodiplodia*

Figure 4.22 The tree is rooted to *Diplodia mutila* (CMW 7060) and *D. seriata* (CBS 112555). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are thickened. The new isolates are indicated in red and ex-type strains are in bold. The scale bar shows 20 changes

Lasiodiplodia crassispora T.I. Burgess & P.A. Barber, Mycologia 98(3): 425 (2006) Figure 4.23

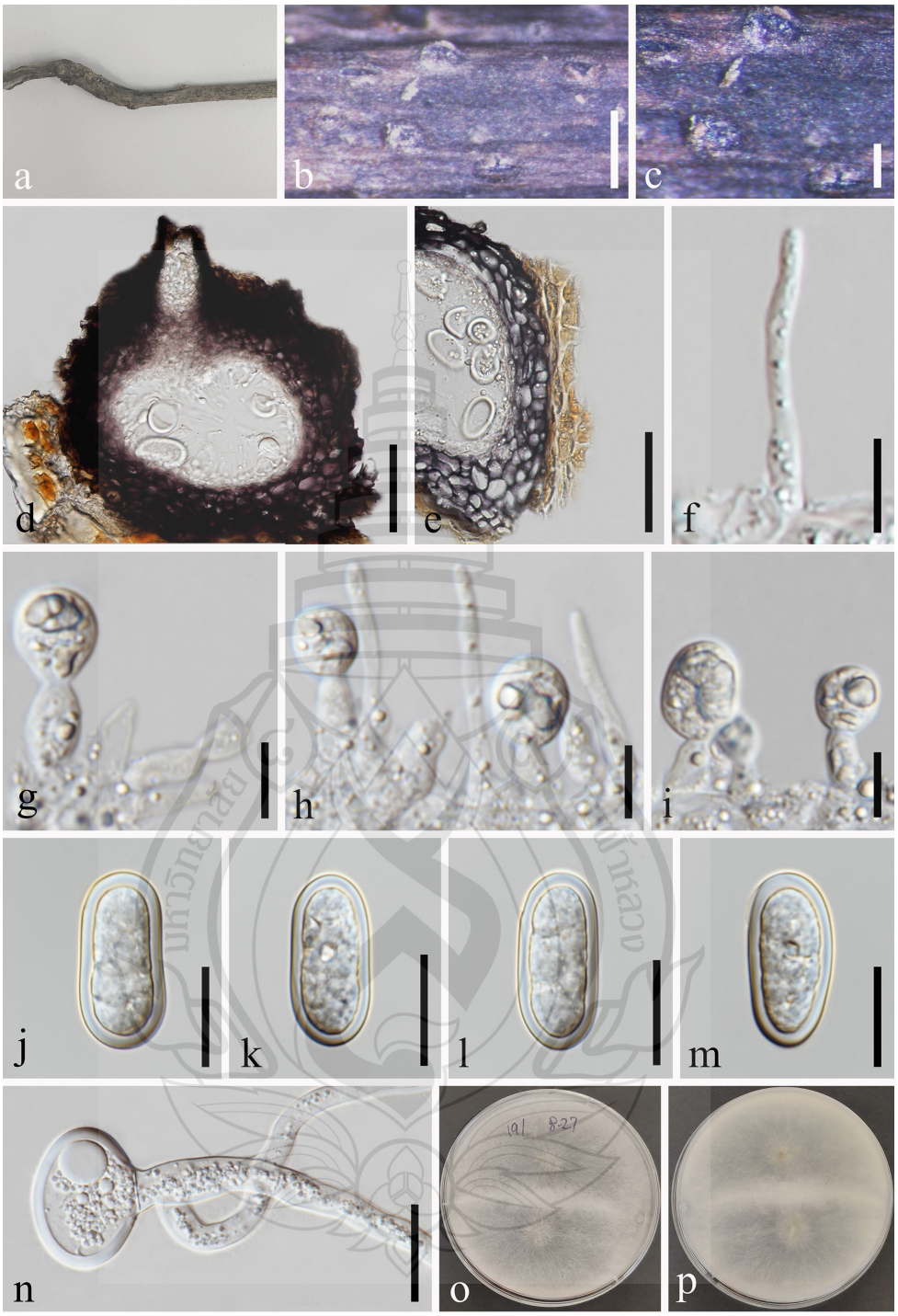
Index Fungorum number: IF500235

Saprobic on an unidentified dead wood. Sexual morph: Not observed. Asexual morph: *Conidiomata* 151–191 × 178–202 µm ($\bar{x}$ = 171 × 188 µm, n = 20), semi-immersed or immersed in the substrate, solitary, gregarious or confluent, globose to subglobose, centrally ostiolate. *Ostiole* 21–33 µm diam., centrally located, papillate. *Peridium* up to 19–46 µm wide, consisting of black and small-celled *textura angularis*. *Paraphyses* 2–3 µm wide, hyaline, cylindrical, aseptate, not branched, rounded at apex. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 7–12 ×4–7 µm ($\bar{x}$ = 9 × 5 µm, n = 20), hyaline, cylindrical. *Conidia* 27–33 × 14–17 µm ($\bar{x}$ = 30 × 16 µm, n = 50), hyaline, aseptate, ellipsoid to ovoid, thick-walled, without longitudinal striations or mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies are fast growing on PDA, becoming ash-grey on the surface after 7 days, the reverse is pale grey to grey, and finally black after two weeks, felt-like, sparse, aerial, surface smooth with a crenate edge, filamentous.

Material examined – Thailand, Chiang Mai, Amphoe Mae Taeng, Tambon Cho Lae, on an unidentified dead wood, 6 August 2019, Na Wu, YW191 (MFLU 23-0011), living culture MFLUCC 23-0060.

Notes – The morphology of my collection obtained from decaying woody is similar to the original description of *Lasiodiplodia crassispora*. In the multi-gene phylogenetic analysis, my new collection clustered with the ex-type strain of *L. crassispora* (CBS 118741) with strong bootstrap support, and I identified it as *L. crassispora*.



Note a–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Paraphyses. g–i Conidiogenous cells and developing conidia. j–m Conidia. n Germinated conidium. o, p Colonies on PDA, above (o) and below (p). Scale bars: b = 500 µm, c = 200 µm, d, e = 50 µm, f–i = 10 µm, j–n = 20 µm.

Figure 4.23 *Lasiodiplodia crassispora* (MFLU 23-0011, new host record)

Lasiodiplodia delonicis N. Wu, Dissan. & Jian K. Liu, sp. nov. Figure 4.24

Index Fungorum number: IF900581; Facesoffungi number: FoF14261

Etymology: Referring to the host genus on which the fungus was collected, *Delonix regia* (*Fabaceae*).

Holotype: MFLU 23-0005

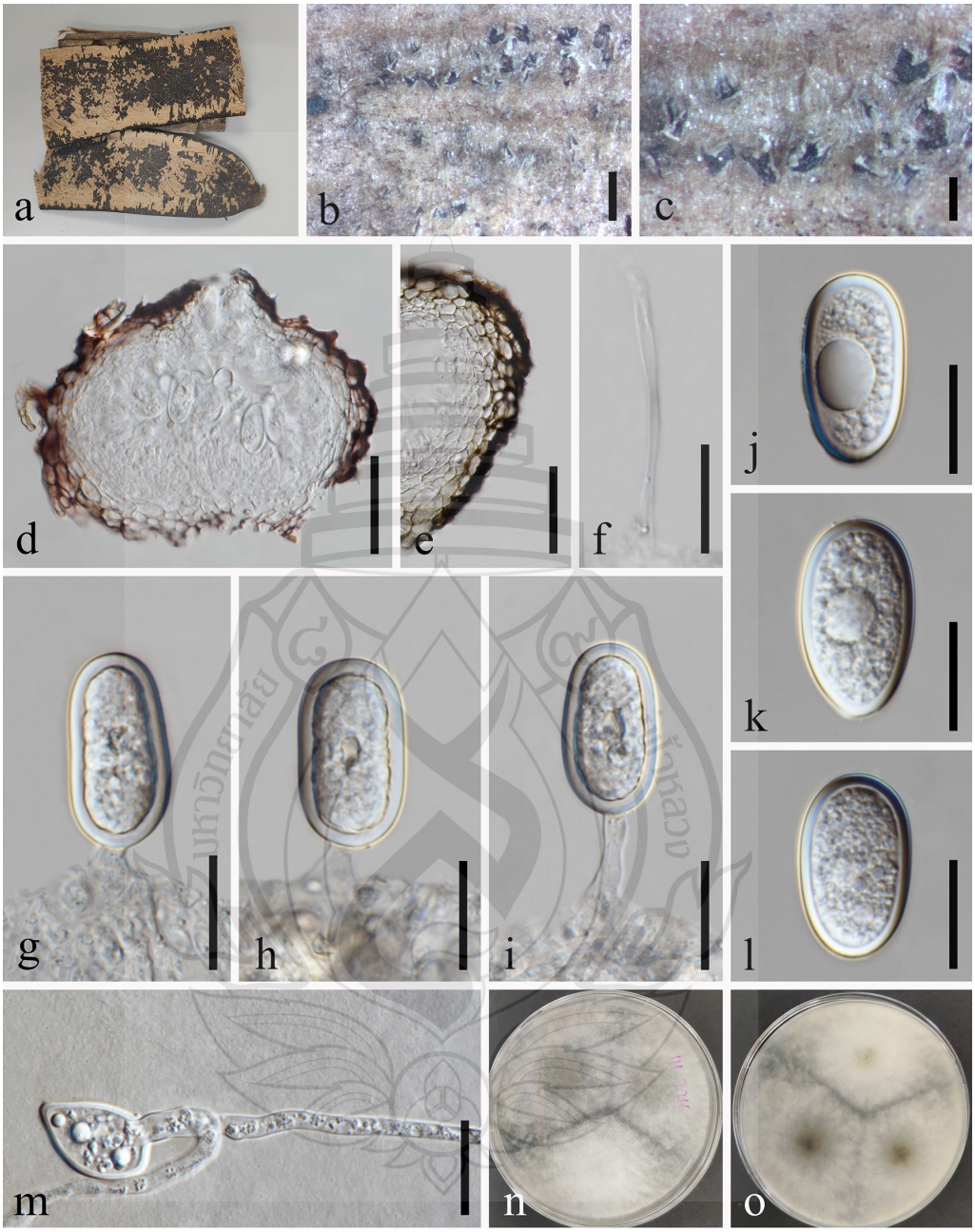
Saprobic on a fallen pod of *Delonix regia* L. Sexual morph: Not observed. Asexual morph: *Conidiomata* 110–180 × 124–171 μm ($\bar{x}$ = 139 × 151 μm, n = 20), pyriform, immersed to semi-immersed, solitary, black, ostiolate. *Ostiole* 20–31 μm diam., central, cylindrical to subcylindrical. *Peridium* up to 18–35 μm wide, with outer 3–4 layers of brown cells of *textura angularis* and inner 1–2 layers of hyaline cells of *textura angularis*. *Paraphyses* 2–3 μm wide, hyaline, cylindrical, aseptate, not branched. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 4–16 × 4–6 μm ($\bar{x}$ = 8 × 5 μm, n = 20), hyaline, cylindrical, sometimes slightly curved. *Conidia* 26–38 × 13–29 μm ($\bar{x}$ = 32 × 17 μm, n = 50), ellipsoid to ovoid, hyaline, aseptate, thick-walled with granular content, occasionally truncate at base, without longitudinal striations or mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies are fast growing on PDA, reaching 90 mm diam. after 5 days at 20–25°C, becoming ash-grey on the surface after one week, with the reverse side of the colonies pale grey to grey, and finally black after two weeks, felt-like, sparse, aerial, surface smooth with crenate edge, filamentous.

Material examined – Thailand, Chiang Rai Province, Amphoe Mueang, Tambon Nang Lae, on a fallen pod of *Delonix regia*, 17 July 2019, Na Wu, YW111 (MFLU 23-0005, holotype); ex-type living culture MFLUCC 23-0058.

Notes – The phylogenetic tree based on ITS, LSU, *tef1α*, and *tub2* sequence data showed that the new species *Lasiodiplodia delonicis* (Figure 4.2) is supported by an absolute bootstrap support (ML/MP/BI = 100/100/1.0). Morphologically, *L. delonicis* is

distinct from other *Lasiodiplodia* species by its thicker conidial wall and larger conidia. Additionally, conidia of *L. delonicis* are hyaline throughout the life cycle.



Note a Specimen. b–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Paraphyses. g–i Conidiogenous cells and developing conidia. j–l Conidia. m Germinated conidium. n, o Colonies on PDA, above (n) and below (o). Scale bars: b = 50 µm, c = 20 µm, d, e = 50 µm, f–m = 20 µm.

Figure 4.24 *Lasiodiplodia delonicis* (MFLU 23-0005, holotype)

Lasiodiplodia mahajangana Begoude, Jol. Roux & Slippers, Mycol. Progr. 9(1): 110 (2010) Figure 4.25

Index Fungorum number: IF514012

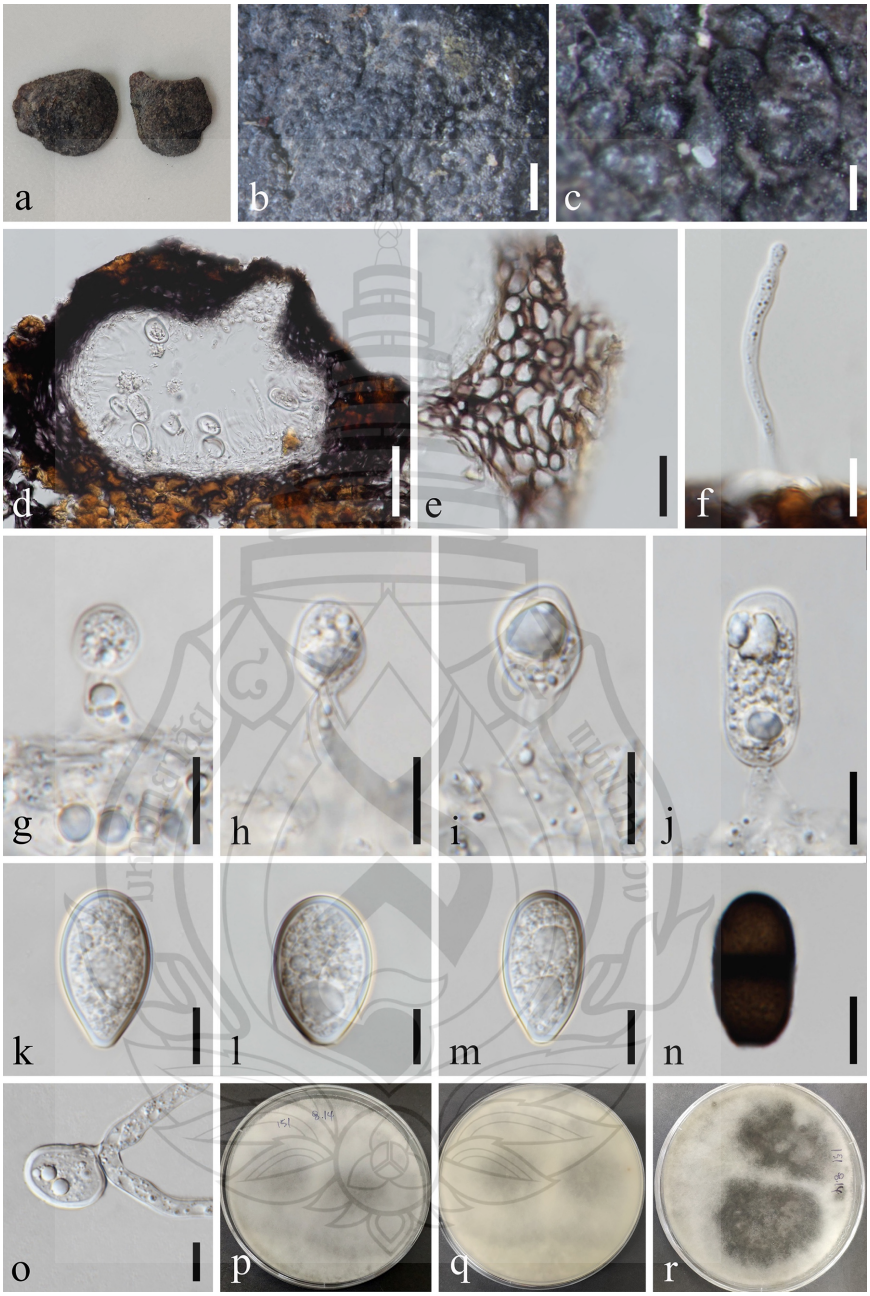
Saprobic on dead seeds of *Dipterocarpus retusus* L. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 127–164 × 133–192 µm ($\bar{x}$ = 148 × 160 µm, n = 20), solitary or compound, superficial or immersed, unilocular or multilocular, globose to subglobose, thick-walled, glabrous, ostiolate. *Ostiole* 26–33 µm diam., single, long, cylindrical to subcylindrical, eccentric. *Peridium* up to 14–23 µm wide, consisting of brown and small-celled *textura angularis*. *Paraphyses* 2–4 µm wide, hyaline, cylindrical, aseptate, not branched, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–13 ×4–5 µm ($\bar{x}$ = 8 × 5 µm, n = 20), hyaline, cylindrical, proliferating percurrently to form a periclinal thickening. Conidia 24–31 × 14–18 µm ($\bar{x}$ = 27 × 16 µm, n = 50), initially aseptate, hyaline, ellipsoid to ovoid, thick-walled with granular content, rounded at apex, occasionally truncate at the base, one-septate at maturation, without longitudinal striations or mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies are fast growing on PDA at 20–25°C, becoming ash-grey on the surface after 7 days, with the reverse side of the colonies pale grey to grey, and finally black after two weeks, felt-like, sparse, aerial, surface smooth with crenate edge, filamentous.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Cho Lae, 19°08'01.3"N, 99°00'29.4"E, on dead seeds of Dipterocarpus retusus L., 10 Aug 2019, Na Wu, YW151 (MFLU 23-0006), living culture MFLUCC 23-0059.

Notes – In the phylogenetic tree, an isolate obtained in this study (MFLUCC 23-0059) grouped with *Lasiodiplodia mahajangana* (Figure 4.2) (ML/MP/BI = 94/95/1.0). My sample is morphologically similar to L. mahajangana as of the report by Begoude et al., (2010), having hyaline, aseptate, ellipsoid to ovoid, thick-walled conidia, which

becomes one-septate after maturation. I identified my collection as *L. mahajangana* based on morphology and phylogeny.



Note a–c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Paraphyses. g–j Conidiogenous cells and developing conidia. k–n Conidia. o Germinated conidium. p–r Colonies on PDA, above (p, r) and below (q). Scale bars: b = 100 µm, c = 20 µm, d = 50 µm, e = 20 µm, f–o = 10 µm.

Figure 4.25 *Lasiodiplodia mahajangana* (MFLU 23-0006, new host record)

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909) Figure 4.26

Index Fungorum number: IF188476; Facesoffungi number: FoF00167

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 212–250 μm wide, 140–180 μm high, solitary to gregarious, dark, immersed to superficial or erumpent through bark, subglobose or pyriform to irregular, unilocular, glabrous, coriaceous, papillate, ostiolate. *Ostiole* 50–60 μm wide, 70–80 μm high, single, short, rounded, excentric. *Conidiomatal wall* 18–25 μm wide, composed of brown thickened cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–12.5 × 4.5–8 μm ($\bar{x}$ = 10.5 × 6 μm; n = 30), hyaline, cylindrical to doliiform, determinate, smooth-walled. *Conidia* 23–29 × 13.5–15.5 μm ($\bar{x}$ = 26 × 14.5 μm; n = 30), hyaline, ellipsoid to oval with rounded to obtuse ends, straight or slightly curved, aseptate, granulate, smooth-walled.

Culture characteristics – Conidia germinated on PDA medium within 12 h and germ tube produced from one end. Colonies on PDA medium fast-growing and reaching 80 mm diam. after one week at 25℃ in dark, circular, cottony, white during the first few days, sparse, aerial, filamentous, after 2 weeks becoming black.

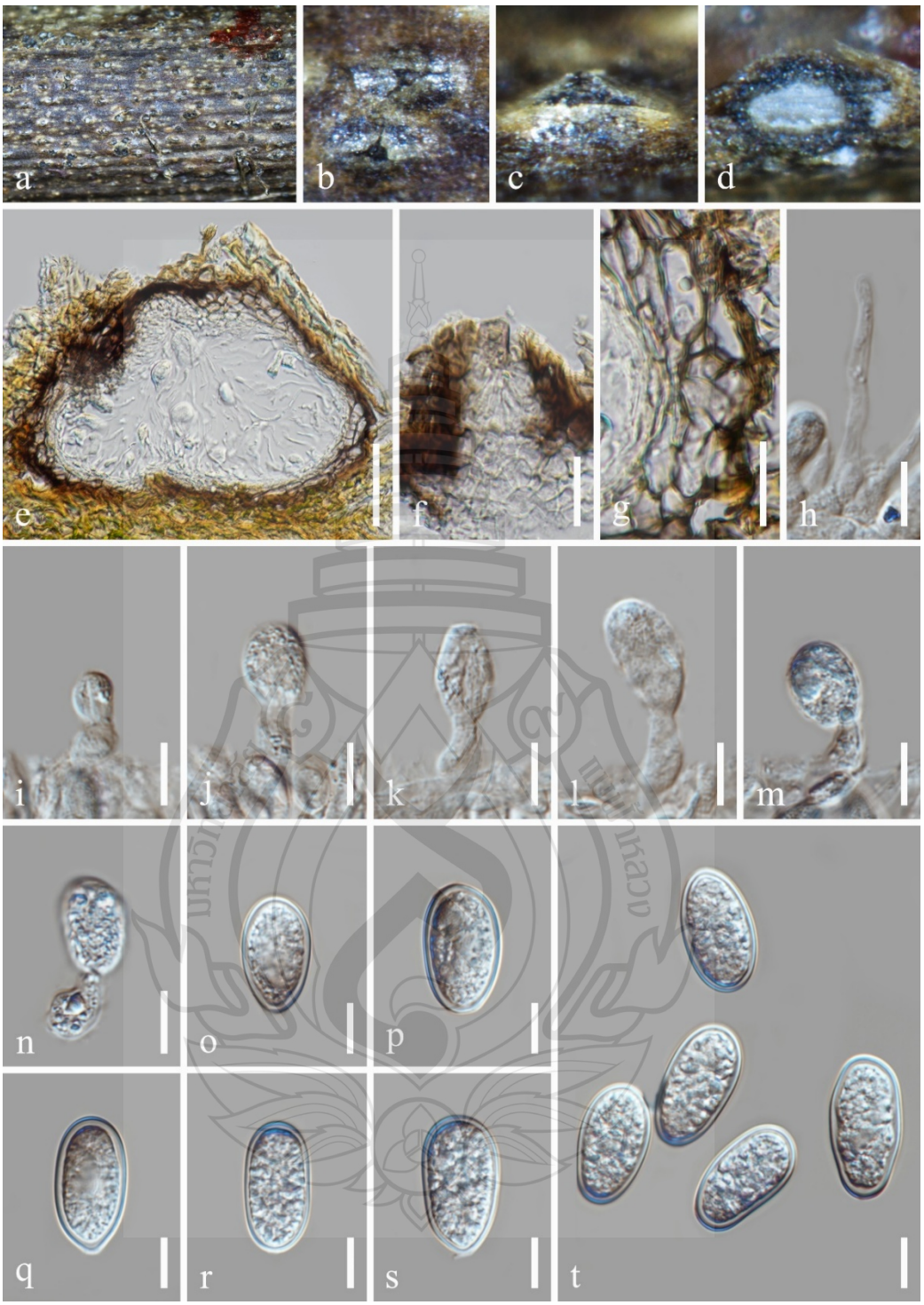
Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Huopu Town, on branches of *Rosa roxburghii*, 28 September 2021, N. Wu, CL91 (HUEST XX), living culture UESTCC XX; *ibid.*, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *R. roxburghii*, 30 October 2021, N. Wu, H23 (HUEST XX), living culture UESTCC XX.

Hosts – *Acacia crassipa* and *Dillenia suffruticosa* (Zhang et al., 2021c); *Amomum villosum*, *Angelica dahurica*, *Bletilla striata*, *Dracaena fragrans*, *Polygonatum cyrtonema*, *Uncaria rhynchophylla* and *Wikstroemia indica* (Du et al.,

2025); *Aquilaria crassna* (Wang et al., 2019); *Eucalyptus* sp. (Liu et al., 2012); *Persea americana*, *Pinus* sp., *Vitex doniana* and *Vitis vinifera* (Alves et al., 2008); *Rosa roxburghii* (present study).

Known geographical distribution – Argentina, China, Indonesia, Laos, Mexico, South Africa, Tanzania, Thailand, Uganda and USA.

Notes – *Lasiodiplodia theobromae*, which was originally described as *Botryodiplodia tubericola* (Ellis & Everh.) Petr., Ann. Mycol. (1923) was designed as the type species of *Lasiodiplodia* by Phillips et al. (2013), based on a specimen collected from *Theobroma cacao* in Ecuador. In the phylogenetic tree, two isolates obtained in this study (UESTCC CL91 and UESTCC H23) clustered with *L. theobromae* (CBS 164.96 and CBS 111530) (Figure 4.2). Based on morphological and phylogenetic evidence, I identified these isolates as *L. theobromae*.



Note a–c Conidiomata on natural substrate. d, e Vertical sections of conidiomata. f Ostiole. g Conidiomatal wall. h Paraphyses. i–n Conidiogenous cells and developing conidia. o–t Conidia. Scale bars: e = 50 µm; f, g = 20 µm; h–t = 10 µm.

Figure 4.26 *Lasiodiplodia theobromae* (HUEST CL91, new host record)

Macrophomina euphorbiicola A.R. Machado, D.J. Soares & O.L. Pereira, Eur. J. Pl. Path. 153(1): 96 (2018) Figure 4.27

Index Fungorum number: IF815562

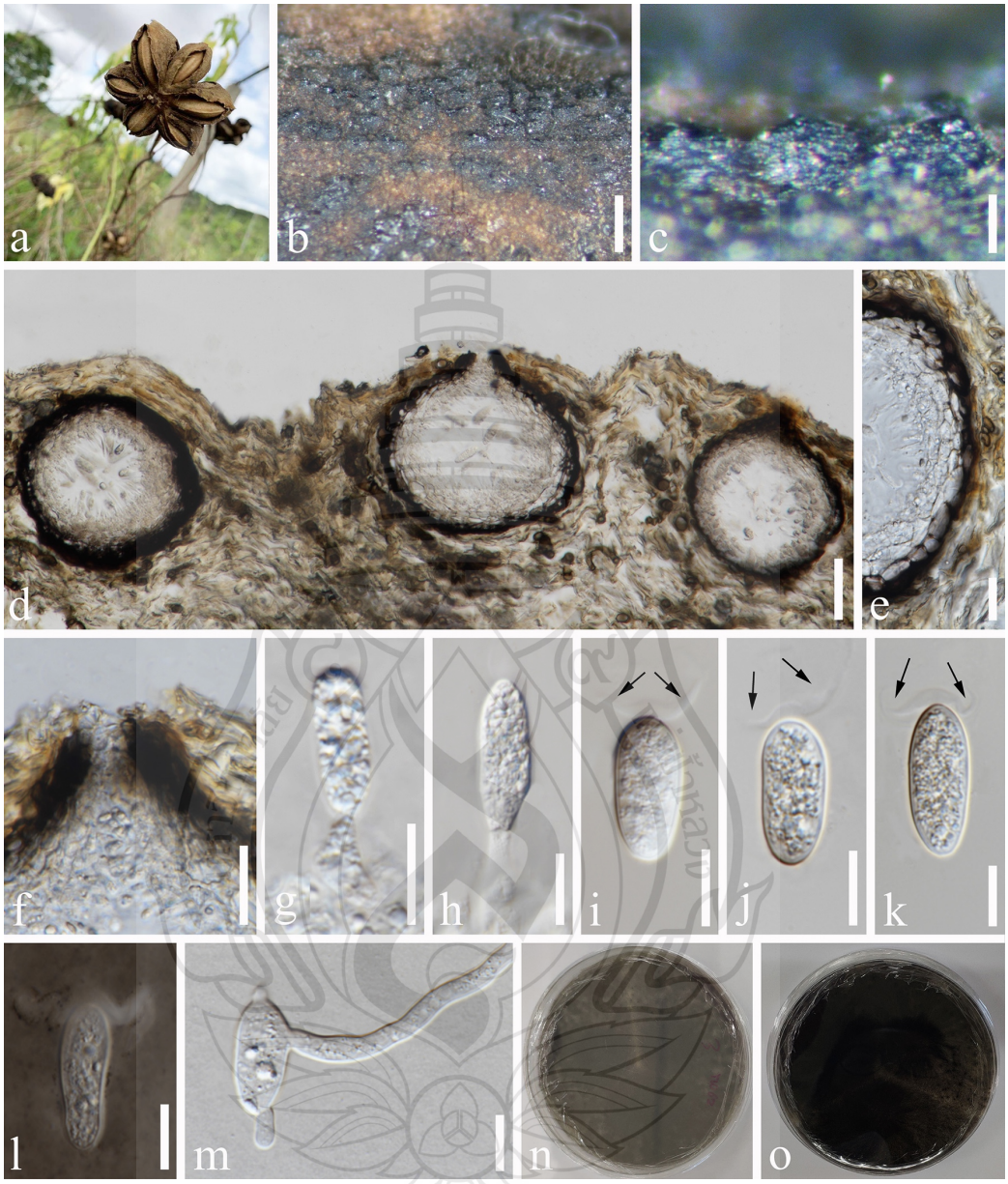
Saprobic on dead seeds of *Plukenetia volubilis* L. Sexual morph: Not observed. Asexual morph: *Conidiomata* 116–172 × 130–161 µm ($\bar{x}$ = 137 × 149 µm, n = 20), circular, dark brown to black, solitary or gregarious, immersed through the epidermis, visible as black dots or papilla on the host, glabrous. *Peridium* up to 11–24 µm wide, composed of dark brown to black thick-walled *textura angularis*, becoming thin-walled and hyaline towards the inner region. *Ostiole* 12–32 µm diam., cylindrical, short, straight, centrally or laterally located. *Paraphyses* absent. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells. *Conidiogenous cells* 6–14 × 2–5 µm ($\bar{x}$ = 9 × 3 µm, n = 20), terminal, hyaline, cylindrical to ellipsoidal, smooth-walled. *Conidia* 22–26 × 8–11 µm ($\bar{x}$ = 23 × 9 µm, n = 50), hyaline, oblong to cylindrical, with rounded apex, and narrow, straight, frequently constricted in the middle, aseptate, contents granular, thick- and smooth-walled, bearing octagonal beardshaped appendages, or widely flared or irregular, undulate, mucoid apical appendage, basal appendages absent.

Culture characteristics – Conidia germinating on PDA within 12 h with germ tubes produced from the middle or each end. Colonies are fast growing on PDA, reaching 90 mm diam. after 5–6 days. Sparse, aerial, filamentous, after 2 weeks, becoming dark brown to black.

Material examined – Thailand, Chiang Rai Province, Thoeng, Tambon Nang Lae, Rai Ruen Rom Organic Farm, on dead seeds of *Plukenetia volubilis* L., 11 June 2019, Na Wu, YW62 (MFLU 23-0004), living culture MFLUCC 23-0057.

Notes – *Macrophomina euphorbiicola* was introduced by Machado et al. (2018). Due to the previous cultures failing to sporulate, comparison with the type species was not possible. The phylogenetic analysis showed that my isolate was nested within

M. euphorbiicola and claded closer to *M. pseudophaseolina* (Figure 4.7). I, thus, identify the new collection as *M. euphorbiicola.*



Note a Specimen. b, c Conidiomata on host substrate. d Vertical section of conidiomata. e Section of peridium. f Ostiole. g, h Conidiogenous cells and developing conidia. i–l Conidia bearing apical appendages. m Germinated conidium. n, o Colonies on PDA, above (n) and below (o). Scale bars: (b) = 50 µm, (c–e) = 20 µm, (f–m) = 10 µm.

Figure 4.27 *Macrophomina euphorbiicola* (MFLU 23-0004, new host record)

Neodeightonia C. Booth, Mycol. Pap. 119: 17 (1970) [1969]

Type species – *Neodeightonia subglobosa* C. Booth

Notes – Punithalingam (1969) established the genus *Neodeightonia* with *N. subglobosa* Booth as the type. However, Arx and Müller (1975) transferred *N. subglobosa* to *Botryosphaeria*. Phillips et al. (2008) discussed the synonymy of *Neodeightonia* and lectotypified it as a genus distinct from *Botryosphaeria* based on morphology and molecular phylogeny. Ten species are currently accepted in *Neodeightonia* (Xiao et al., 2021, Zhang et al., 2021, Wijayawardene et al., 2022). The sexual morph of *Neodeightonia* is characterized by clavate to cylindrical-clavate asci and hyaline, aseptate, oval to broadly ellipsoidal ascospores surrounded by a mucilaginous sheath, while the asexual morph is characterized by ellipsoidal to obovoid, longitudinally striated conidia which are initially hyaline and become brown or dark brown and one- or multi-septate at maturity with smooth to finely roughened walls (Phillips et al., 2008, 2013; Liu et al., 2010, 2012, Adamčík et al., 2015, Konta et al., 2016a, Dai et al., 2017, Jayasiri et al., 2019, Xiong et al., 2021).

Neodeightonia septata N. Wu, A.J. Dissanayake & Jian K. Liu, sp. nov. Figure 4.28

Index Fungorum number: IF 844409, Facesoffungi number: FoF010671

Etymology – The specific epithet “septata” refers to the septum observed in mature conidia.

Holotype – MFLU 22-0003

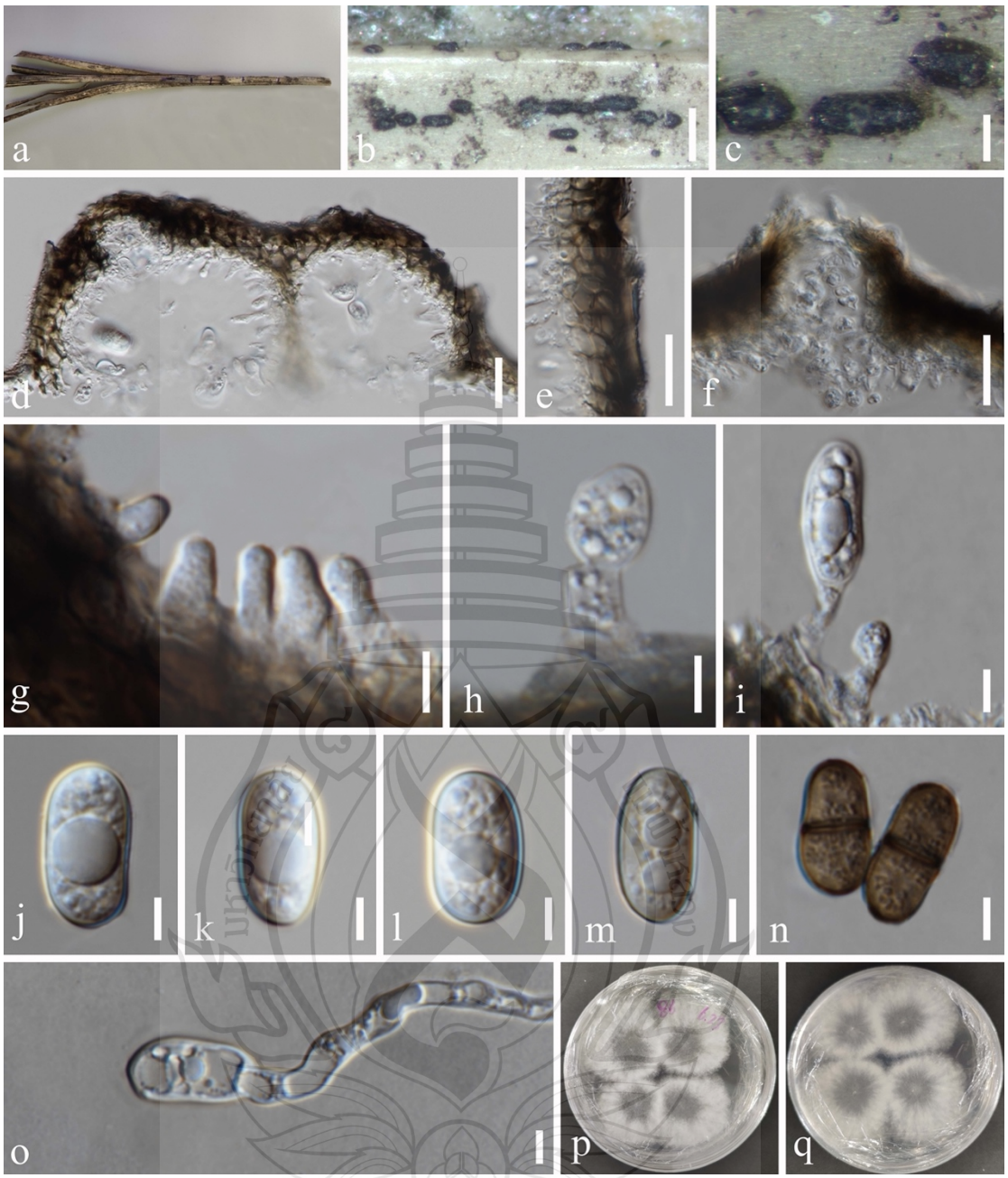
Saprobic on a dead culm of palm, as raised black spots on the host surface. Sexual morph: not observed. Asexual morph: *Conidiomata* 80–135 µm diam., 50–105 µm high (n = 20), superficial or semi-immersed in the substrate, unilocular to multilocular, solitary or aggregated, cylindrical or subglobose, dark brown to black. *Peridium* up to 10–21 µm wide, composed of dark brown, thick-walled, *textura angularis* cells, becoming thin-walled and hyaline towards the inner region. *Ostiole* 25–

30 µm diam., cylindrical, straight or curved, centrally or laterally located. *Paraphyses* absent. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–8 µm long, 3–5 µm wide (n = 20), cylindrical, hyaline, straight to curved, smooth-walled. *Conidia* (13.5–)15–19(–21) × (6–)8–9(–12) µm ($\bar{x}$ = 17 × 9 µm, n = 50), ellipsoidal to obovoid, rounded at the apex, frequently constricted in the middle, initially hyaline, aseptate, guttulate, without mucilaginous sheath, becoming pale to dark brown when mature, granulate, forming a septum.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching 90 mm diam. after 4–5 days at 20–23°C, circular, white during the first few days, sparse, aerial, surface smooth with crenate edge, filamentous, after 2 weeks becoming dark brown to black.

Material examined – THAILAND. Chiang Rai: Thoeng, Tambon Nang Lae, Rai Ruen Rom Organic Farm, 19°39’30.2’’N, 100°09’26.4’’E, on a dead palm culm, 11 June 2019, Na Wu, YW86 (MFLU 22-0003, holotype), ex-type living culture MFLUCC 22-0004; *ibid.,* (GZAAS 22-0068, isotype), living culture GZCC 22-0067.

Notes – The phylogenetic result showed that the two isolates of *Neodeightonia septata* clustered together and formed a distinct lineage with absolute bootstrap support (Figure 4.29). It is phylogenetically close to *N. rattanica* and *N. rattanicola* but is represented as a distinct species. In addition, *N. septata* is morphologically distinguished from the above- mentioned species by having 1-septate conidia, while no septum was observed in *N. rattanica* nor in *N. rattanicola*.



Note a Substrate with conidiomata. b, c Appearance of black conidiomata on palm culm. d Vertical section of conidiomata. e Section of peridium. f Ostiolar region. g–i Conidiogenous cells and developing conidia. j–m Hyaline, aseptate immature conidia. n Brown, 1-septate mature conidia. o Germinating conidium. p, q Colonies after 7 days on PDA (p from above, q from below). Scale bars: b = 50 μm, c = 10 μm, d–f = 20 μm, g–o = 5 μm.

Figure 4.28 *Neodeightonia septata* (MFLU 22-0003, holotype)

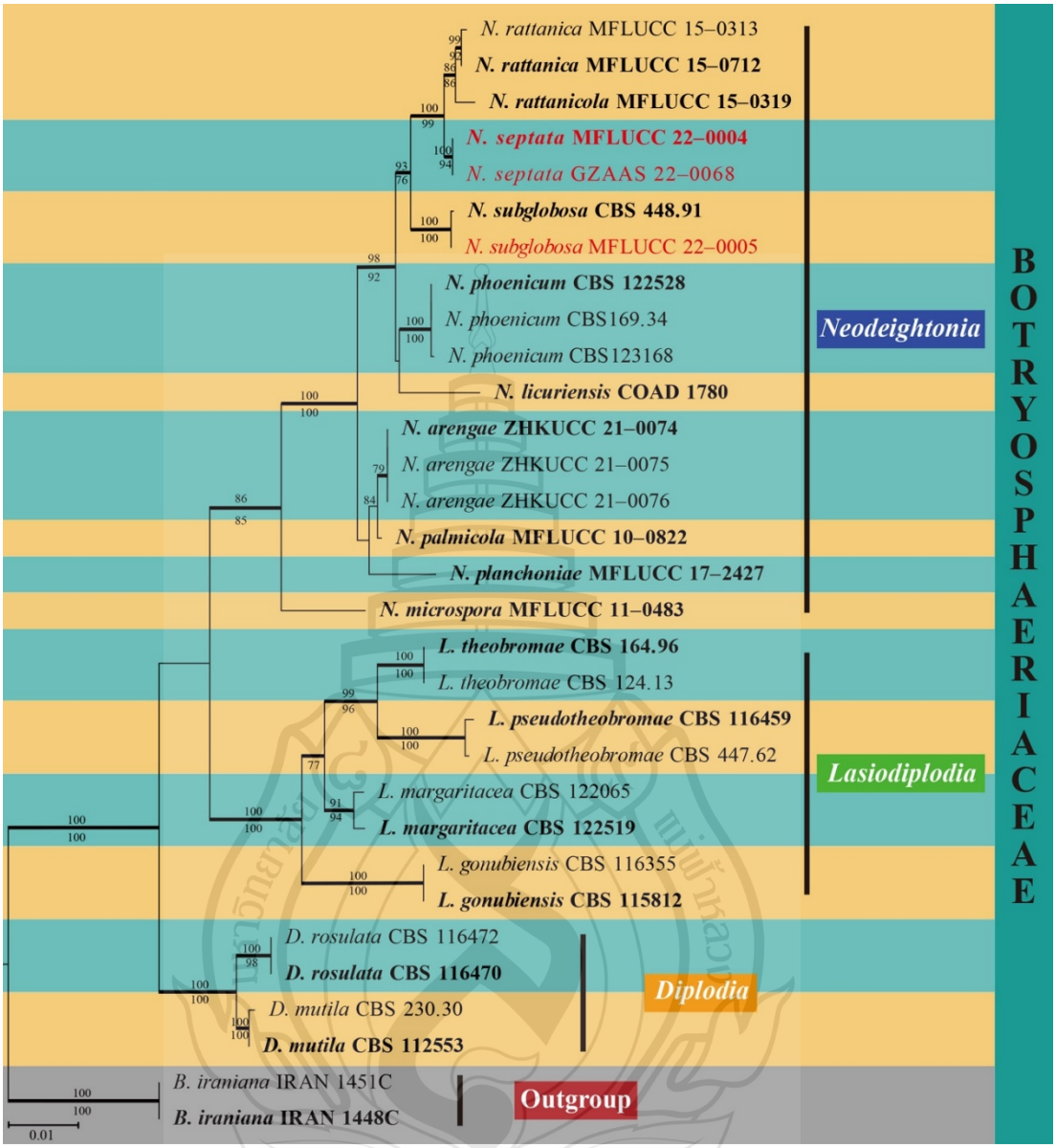


Figure 4.29 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined ITS, LSU, SSU and *tef1α* sequence data for all accepted species of *Neodeightonia* and closely related genera within the family *Botryosphaeriaceae*

Figure 4.29 The tree is rooted with two isolates of *Barriopsis iraniana* (IRAN 1448C, IRAN 1451C). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75% are placed above and below the branches,

respectively. Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are denoted in thickened branches. The strain numbers are given after the species names, and ex-type strains are indicated in bold. The newly generated isolates are in red.

Neodeightonia subglobosa C. Booth, in Punithalingam, Mycol. Pap. 119: 19 (1970) [1969] Figure 4.30

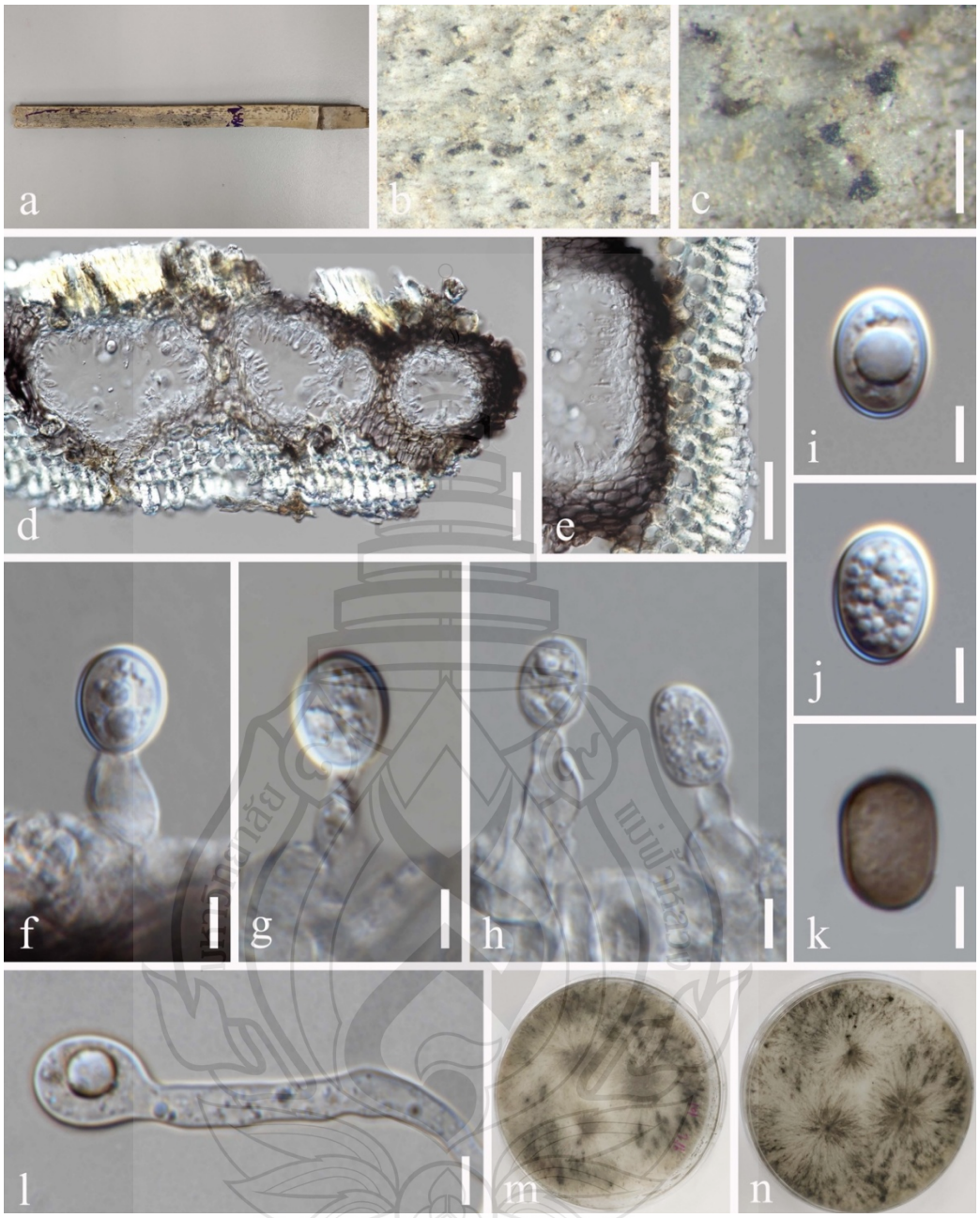
Index Fungorum number: IF318601, Facesoffungi number: FoF01966

Saprobic on a dead culm of bamboo, forming conspicuous, black spots on the host surface. Sexual morph: not observed. Asexual morph: *Conidiomata* 95–185 µm diam., 60–170 µm high (n = 20), semi-immersed or immersed in the substrate, uni-locular to multilocular, solitary or aggregated, globose or subglobose to obpyriform, dark brown to black. *Peridium* up to 10–38 µm wide, consisting of brown, small cells of *textura angularis*, becoming thin-walled and hyaline towards the inner region. *Ostiole* 17–20 µm diam., centrally located, occasionally observed. *Paraphyses* absent. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–20 µm long, 3–5 µm wide (n = 20), subcylindrical, hyaline. *Conidia* (10–)11–12(–13) × (6–)8–9(–12) µm ($\bar{x}$ = 12 × 9 µm, n = 50), subglobose to oval, rounded at the apex, initially hyaline, aseptate, granulate, without longitudinal striations or mucilaginous sheath, becoming brown when mature.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching 90 mm diam. after 4–5 days at 20–23°C, circular, white during the first few days, sparse, aerial, smooth surface with crenate edge, filamentous, after 2 weeks becoming black.

Material examined – THAILAND. Chiang Rai: Amphoe Mueang, Tambon Nang Lae, Mae Fah Luang University garden, 20°02’22.7’’N, 99°53’38.1’’E, on a dead bamboo culm, 17 July 2019, Na Wu, YW101 (MFLU 22-0004), living culture MFLUCC 22-0005.

Notes – *Neodeightonia subglobosa*, the type species of the genus *Neodeightonia*, was originally collected from *Bambusa arundinacea* in Africa (Punithalingam 1969). Liu et al. (2012) and Dai et al. (2017) found the sexual morph of *N. subglobosa* from *Bambusa* sp. in Thailand. The phylogenetic result showed that my strain (MFLUCC 22-0005) clustered with the ex-type strain of *N. subglobosa* (CBS 448.91) with the absolute bootstrap support (100% ML, 100% MP and 100% BYPP) and I identify it as this species (Figure 4.29). This is the first time that its asexual morph was observed from a natural substrate, as previous studies reported it only from sporulation of the culture.



Note a Substrate with conidiomata. b, c Appearance of black conidiomata on bamboo culm. d Vertical section of conidiomataum. e Section of peridium. f–h Conidiogenous cells and developing conidia. i, j Hyaline, aseptate immature conidia. k Brown, aseptate mature conidium. l Germinating conidium. m, n Colonies after 7 days on PDA (m from above, n from below). Scale bars: b = 50 µm, c = 20 µm, d–e = 50 µm, f–l = 5 µm.

Figure 4.30 *Neodeightonia subglobosa* (MFLU 22-0004, new host record)

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

Type species – *Neofusicoccum parvum* (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips

Notes – Crous et al. (2006) established the genus *Neofusicoccum* to accommodate species previously classified under *Fusicoccum*, including *N. andinum*, *N. arbuti*, *N. australe*, *N. eucalypticola*, *N. eucalyptorum*, *N. luteum*, *N. macroclavatum*, *N. mangiferae*, *N. parvum*, *N. protearum*, *N. ribis*, *N. viticlavatum* and *N. vitifusiforme.* Zhang et al. (2021c) re-evaluated *Neofusicoccum* species based on phylogeny and morphology, recognizing 36 species with several possible synonyms. Herein I isolated the type species, *N. parvum*, from *Rosa roxburghii* and *R. sterilis*, representing a new host record for this species.

Neofusicoccum parvum (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips, Stud. Mycol. 55: 248 (2006) Figure 4.31

Index Fungorum number: IF500879; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 145–260 µm wide, 170–230 µm high, solitary to gregarious, dark brown to black, initially immersed, becoming erumpent through bark fissures, globose to subglobose or irregular in shape, unilocular or multilocular, glabrous, coriaceous, short papillate, ostiolate. *Ostiole* 55–62 µm wide, 72–95 µm high, single, short-cylindrical, central. *Peridium* 20–30 µm wide, composed of dark brown to black compressed cells of *textura angularis*. *Hamathecium* 3–3.5 µm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 72–100 × 18–26 µm ($\bar{x}$ = 82.5 × 21.5 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, apically rounded with an ocular chamber. *Ascospores* 19.5–24 × 8–9.5 µm ($\bar{x}$ = 21 × 8.5 µm; n = 30), overlapping to crowded, hyaline, fusiform, with tapered ends and appearing spindle-shape, aseptate, externally smooth, internally finely verruculose. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25℃ in dark, circular, cottony, velvety, dark grayish green mycelium; in reverse, brown in the center, pale gray towards the margin.

Materials examined – CHINA, Guizhou Province, Qianxinan Prefecture, Xingren City, Baling Town, Lvyinhe Village, elevation 1,290 m, 25°29′11″ N, 105°19′21″ E, on dead branches of *Rosa sterilis*, 3 July 2022, N. Wu, GL13 (HUEST XX), living culture UESTCC XX; *ibid.*, Liupanshui City, Panzhou City, Danxia Town, Danxia Mountain, elevation 1,760 m, 25°39′46″ N, 104°37′28″ E, on branches of *R. roxburghii*, 9 July 2022, N. Wu, GL06 (HUEST XX), living culture UESTCC XX.

Notes – Pennycook and Samuels (1985) described *Botryosphaeria parvum* (*Neofusicoccum parvum*) and designated *Fusicoccum parvum* as its asexual morph. *Neofusicoccum parvum* is a widespread and highly virulent plant pathogen or saprobe reported on various plants (Chen et al., 2021; Haenzi et al., 2021; Si et al., 2023; Du et al., 2025). Zhang et al., (2021c) synonymized *N. algeriense*, *N. italicum* and *N. pandanicola* under *N. parvum*. Subsequently, Du et al. (2025) reported the collection of *N. parvum* from 23 different medicinal plants and synonymized *N. hyperici*, *N. sichuanense* and *N. yunnanense* under *N. parvum*. In the present study, my collection clustered with *N. parvum* strains (Figure 4.2), one of which was found on *Rosa roxburghii* from China, and the other on *R. sterilis.* Morphologically, my collection is identical to the original description of *N. parvum* and was identified as *N. parvum* and extend its host range to *Rosa roxburghii* and *R. sterilis.*



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g, h Asci. i–m Ascospores. n Germinating ascospore. o, p Colony on PDA, above (o), below (p). Scale bars: d = 100 µm; e, g, h = 30 µm; f, i–n = 10 µm.

Figure 4.31 *Neofusicoccum parvum* (HUEST GL13, new host record)

Sphaeropsis Sacc., Michelia 2(no. 6): 105 (1880)

Type species – *Sphaeropsis visci* (Alb. & Schwein.) Sacc.

Notes – *Sphaeropsis* was typified with *S. visci* by Saccardo (1880). *Sphaeropsis* species are distributed worldwide on a wide range of hosts. There are 633 epithets in Index Fungorum (2025, June), but only five species are currently recognized with accessible cultures (Phillips et al., 2013; Rathnayaka et al., 2022). The sexual morph is characterized by solitary to gregarious, immersed to superficial or erumpent through bark, unilocular ascomata with ostiolate papilla, the region between the perithecial necks were occupied by hyaline to brown pseudoparenchymatous tissue, trabeculate, branched pseudoparaphyses, thick endotunica, bitunicate asci and hyaline to brown, aseptate, ellipsoidal to fusiform ascospores, and its asexual morphs are coelomycetous, characterized by oval, oblong or clavate, aseptate conidia (Phillips et al., 2013; Wu et al., 2023; Du et al., 2025; Sun et al., 2025). Herein, I identified *S. citrigena* and *S. linhaiensis* from *Rosa roxburghii* and *R. sterilis*, representing new host records for these species.

Sphaeropsis eucalypticola A.J.L. Phillips, Stud. Mycol. 76: 158 (2013) Figure 4.32

Index Fungorum number: IF805464; Facesoffungi number: FoF00169

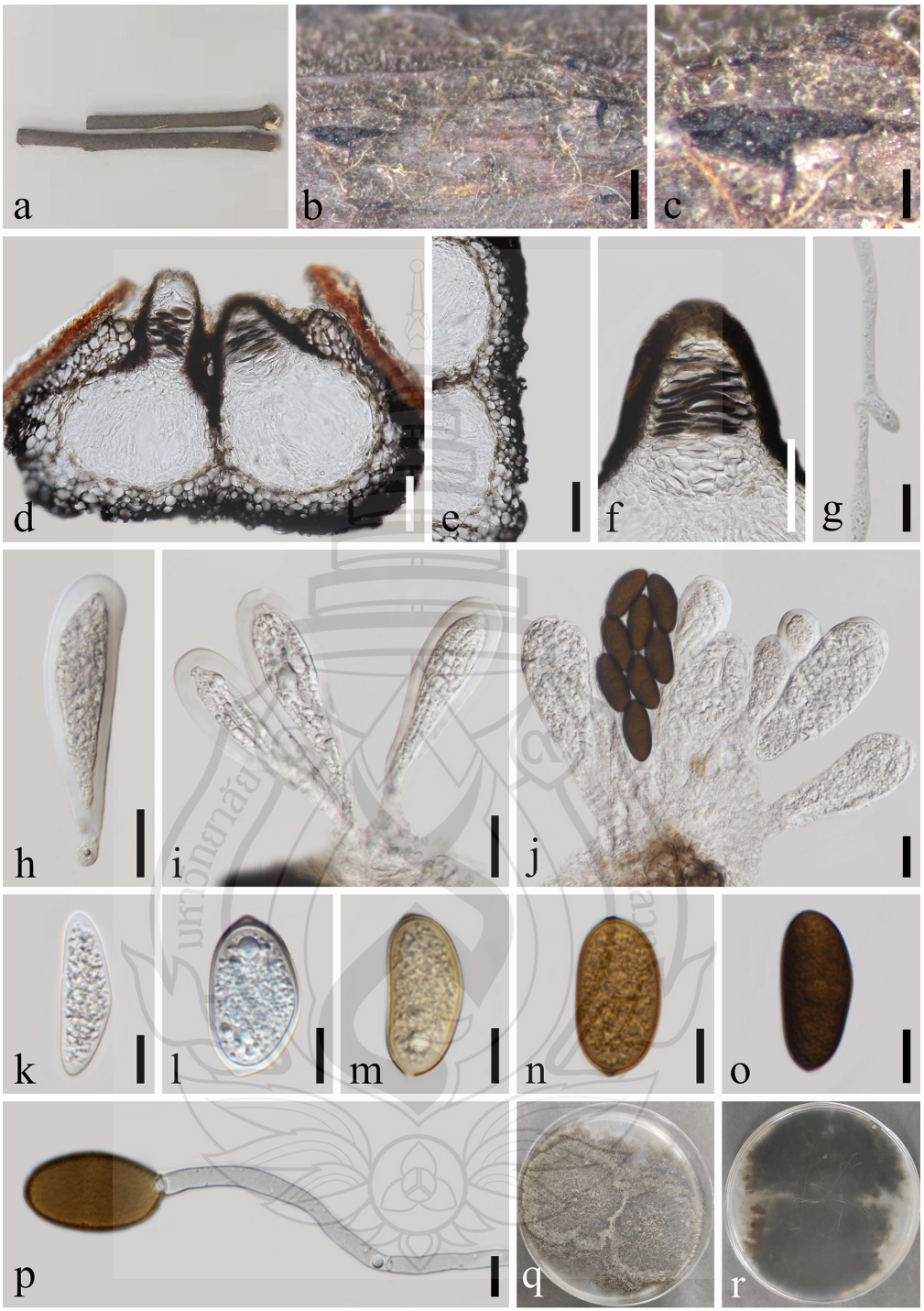
Saprobic on dead twigs of *Tectona grandis*. Sexual morph: *Ascomata* 186–257 × 345–466 μm ($\bar{x}$ = 233 × 373 μm, n = 20), well-developed, bursting through the bark, generally strongly emerged from the host surface, scattered or gregarious, black, subglobose to obpyri- form, ostiolate. *Ostiole* central, subconical to flattened and the region between the perithecial necks were occupied by black pseudoparenchymatous tissue. *Peridium* 31–59 μm wide, composed of three strata; an outer stratum is black, thick-walled cells, middle layer and inner layer, black thin-walled cells. *Hamathecium* comprising up to 2–5 μm wide, dense, cellular pseu- doparaphyses, anastomosing above and between the asci. *Asci* 86–134 × 22–36 μm ($\bar{x}$ = 113 × 30 μm, n = 20),

bitunicate, eight-spored, broadly clavate, apically rounded with a visible ocular chamber. *Ascospores* 29–34 × 15–19 µm ($\bar{x}$ = 32 × 17 µm, n = 50), initially rhomboid, hyaline, aseptate, becoming pigmented, brown to dark brown, elliptical to ovoid, thick-walled, smooth at maturity, with an apiculus at either end. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 24 h. Colonies are fast growing on PDA, reaching 60 mm diam. after 5 d. Circular, white in first few days, becoming pale grey from the center after one week, and finally black after two weeks, felt-like, sparse, aerial, surface smooth with a crenate edge, filamentous.

Material examined – Thailand, Chiang Mai Province, Amphoe Mae Taeng, Tambon Cho Lae, on dead twigs of *Tectona grandis* (*Lamiaceae*), 6 Au- gust 2019, Na Wu, YW174 (MFLU 23-0008), living culture MFLUCC 23-0040; *ibid*., 7 August 2019, Na Wu, YW213 (GZAAS 23-0589), living culture GZCC 23-0589.

Notes – The phylogenetic results (Figure 4.7) showed that my newly obtained isolate clustered together with *Sphaeropsis eucalypticola* and I identified it as *S. eucalypticola*. This is the first record of *S. eucalypticola* found on *Tectona grandis* in Thailand.



Note a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Ostiole. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Germinated ascospore. q, r Colonies on PDA, above (q) and below (r). Scale bars: b = 50 µm, c = 20 µm, d–f = 50 µm, g = 10 µm, h–j = 20 µm, k–p = 10 µm.

Figure 4.32 *Sphaeropsis eucalypticola* (MFLU 23-0008, new host record)

Sphaeropsis citrigena (A.J.L. Phillips, P.R. Johnst. & Pennycook) A.J.L. Phillips & A. Alves, Stud. Mycol. 76: 158 (2013) Figure 4.33

Index Fungorum number: IF805463; Facesoffungi number: FoFXX

Saprobic on decaying branches of *Rosa roxburghii* and *R. sterilis*. Sexual morph: *Ascomata* 305–335 μm wide, 270–290 μm high, solitary to gregarious, dark, initially immersed under host epidermis, becoming semi-immersed to erumpent, breaking through cracks in bark, uniloculate, subglobose to pyriform, coriaceous to carbonaceous, short papillate, ostiolate. *Ostiole* 90–100 μm wide, 120–135 μm high, single, straight or curved, eccentric, subconical to flattened and the region between the perithecial necks were occupied by hyaline pseudoparenchymatous tissue. *Peridium* 20–30 μm wide, composed of several layers of relatively thick-walled, dark brown to black-walled *textura angularis* cells. *Hamathecium* 3.5–5 μm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 100–160 × 36–40 μm ($\bar{x}$ = 133 × 38 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, pedicellate, apically rounded and thickened with an ocular chamber. *Ascospores* 35–40 × 16–18 μm ($\bar{x}$ = 37 × 17 μm; n = 30), irregularly arranged or crowded, hyaline to dark brown, aseptate, ellipsoidal to fusiform, usually widest in the middle, guttulate, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 12 h. Colonies on PDA medium fast-growing and reaching 90 mm diam. after two weeks at 25°C in dark, circular, velvety, flat or effuse, dense, dull green, with a creamy white margin.

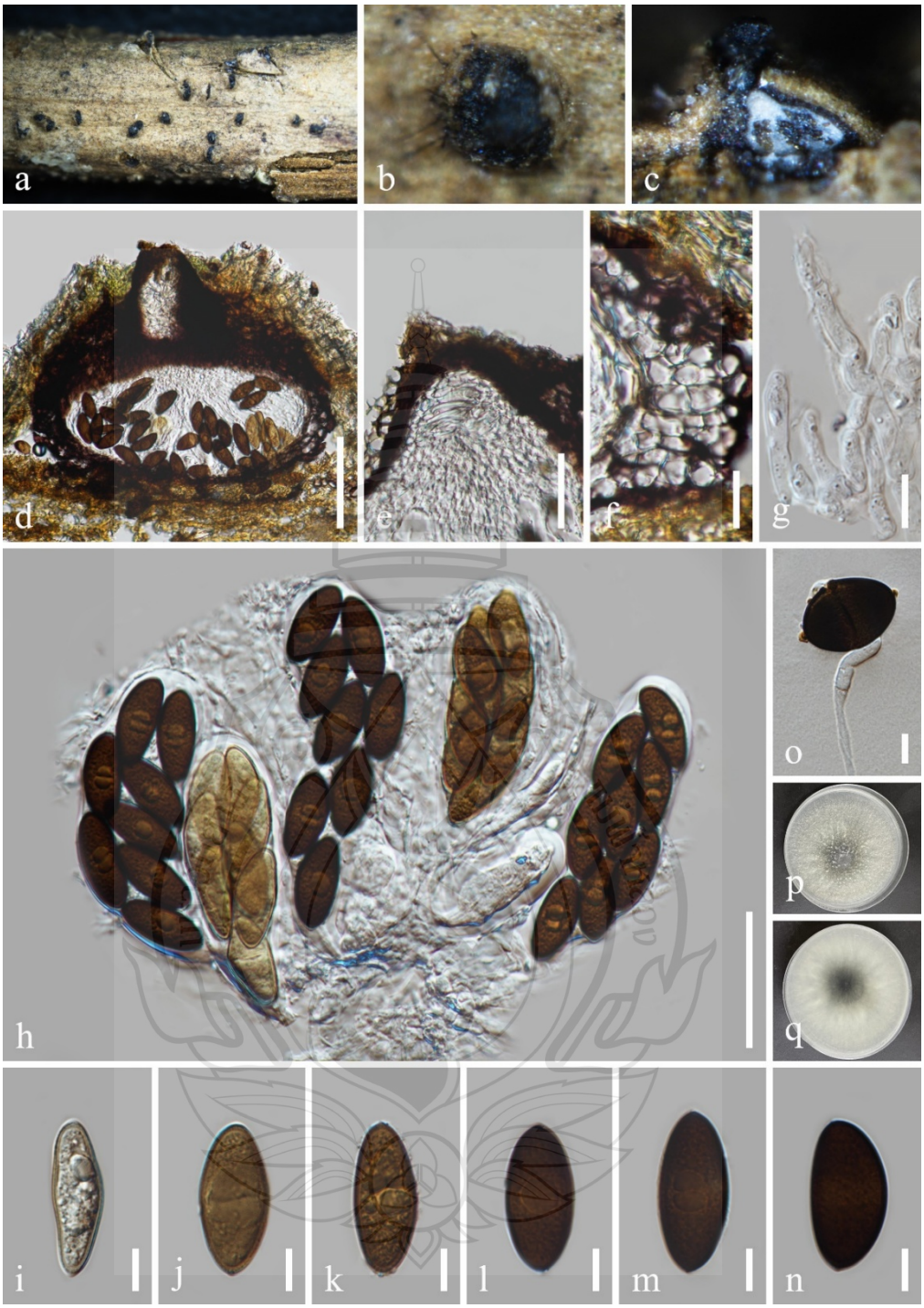
Materials examined – CHINA, Sichuan Province, Leshan City, Huangdan Town, Muchuan County, 28°49′56″ N, 103°40′40″ E, on dead branches of *Rosa roxburghii*, 30 October 2021, N. Wu, H38 (HUEST XX), living culture UESTCC XX; *ibid.*, Guizhou Province, Bijie City, Nayong County, Lezhi Town, Duichaba Village,

elevation 1,493 m, 26°50′57″ N, 105°30′54″ E, on dead branches of *R. sterilis*, 1 February 2023, N. Wu, ML48 (HUEST XX), living culture UESTCC XX

Hosts – *Acer truncatum* and *Camellia oleifera* (Li et al., 2023a), *Citrus sinensis* (Phillips et al., 2008), *Mahonia bealei* and *Stachyurus chinensis* (Du et al., 2025), *Rosa roxburghii* and *R. sterilis* (present study).

Known geographical distribution – China, New Zealand.

Notes – Phillips et al. (2008) introduced *Phaeobotryosphaeria citrigena* (on recently dead bark-covered twigs of *Citrus sinensis*) from New Zealand, which was represented by both asexual and sexual morphs. Based on the morphological comparisons and phylogenetic analysis, *P. citrigena* was later transferred to *Sphaeropsis* by Phillips et al. (2013). Li et al. (2023a) and Du et al. (2025) reported the sexual morph of *S. citrigena* collected from woody oil plants and medicinal plants, respectively. To date, the asexual morph of *S. citrigena* has not yet been found after the work by Phillips et al. (2008). In the present study, my collection (UESTCC H38 and UESTCC ML48) clustered with *S. citrigena* (ICMP 16812 and ICMP 16818) (Figure 4.2). Morphologically, my collection fits well with the holotype of *S. citrigena* in having immersed to partly erumpent ascomata, multiseptated, constricted at septa, smooth pseudoparaphyses and bitunicate, 8-spored, stipitate, thick-walled asci with hyaline to brown, ellipsoid to ovoid, biseriate ascospores. Thus, I identify my collection as *S. citrigena*, representing its first report on *Rosa roxburghii* and *R. sterilis*.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Ostiole. f Peridium. g Pseudoparaphyses. h Asci. i–n Ascospores. o Germinating ascospore. p, q Colony on PDA, above (p), below (q). Scale bars: d = 100 μm; e, h = 50 μm; f = 20 μm; g, i–o = 10 μm.

Figure 4.33 *Sphaeropsis citrigena* (HUEST H38, new host record)

Sphaeropsis linhaiensis X.E. Xiao, Crous & H.Y. Li, Persoonia 47: 131 (2021) Figure 4.34

Index Fungorum number: IF840686; Facesoffungi number: FoF11773

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 265–335 μm wide, 270–330 μm high, solitary to gregarious, dark, immersed to superficial or erumpent through bark, oval or globose to subglobose, unilocular or multilocular, glabrous, coriaceous, ostiolate. *Ostiole* 100–135 μm wide, 113–135 μm high, single, long, straight or curved, central or laterally located, cylindrical to subcylindrical and the region between the perithecial necks were occupied by hyaline to pale brown pseudoparenchymatous tissue. *Peridium* 40–60 μm wide, composed of cells of *textura angularis*, outer layer black and thicker, middle layer pale brown and thinner and inner layer brown and thicker. *Hamathecium* 3.5–6 μm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 145–153 × 29–36 μm ($\bar{x}$ = 149 × 32.5 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, short pedicellate, apically rounded with an inconspicuous ocular chamber. *Ascospores* 31.5–39 × 12–18 μm ($\bar{x}$ = 34 × 15.3 μm; n = 30), irregularly arranged or crowded, ellipsoid to ovoid, hyaline to yellowish, brown when immature, becoming fusiform, brown to dark brown at maturity, aseptate, usually widest in the middle, tapering toward narrow ends, straight or slightly curved, occasionally with a hyaline apiculus at either end. Asexual morph: Undetermined.

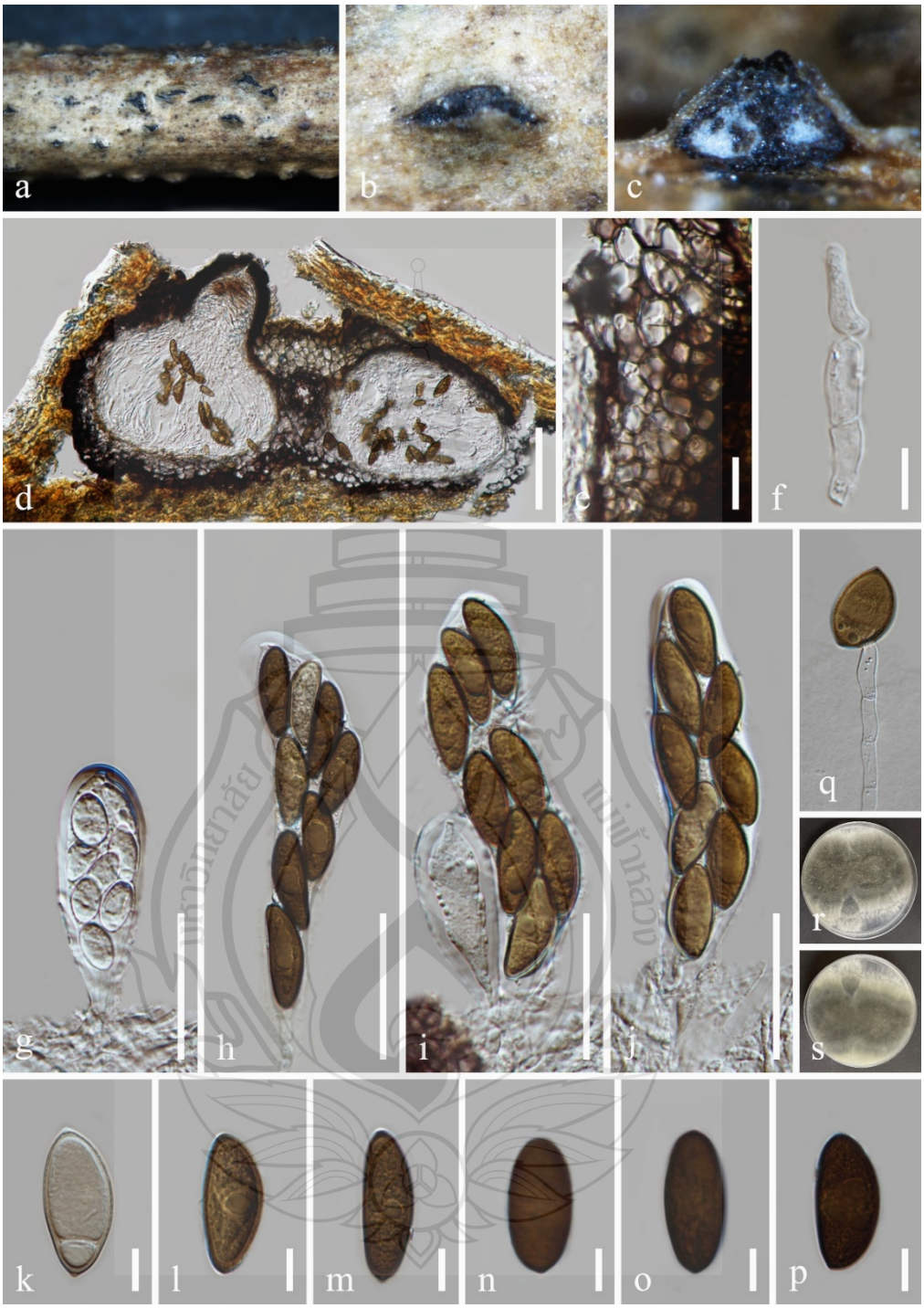
Culture characteristics – Ascospores germinated on PDA medium within 12 h and germ tube produced from the apex. Colonies on PDA medium fast-growing and reaching 50 mm diam. after two weeks at 25°C in dark, circular, velvety, dark grayish green mycelium; in reverse, dark green to white with an entire margin.

Material examined – CHINA, Guizhou Province, Guiyang City, Xifeng County, elevation 1,233 m, 27°5′24″ N, 106°45′36″ E, on decaying branches of *Rosa roxburghii*, 6 February 2023, N. Wu, ML172 (HUEST XX), living culture UESTCC XX.

Hosts – *Cinnamomum camphora* (Rathnayaka et al., 2022), *Citrus unshiu* (Xiao et al., 2021), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Sphaeropsis linhaiensis* was originally introduced based on its asexual morph, which was produced in culture (Xiao et al., 2021). Subsequently, Rathnayaka et al. (2022) discovered its sexual morph on a dead branch of *Cinnamomum camphora* and synonymized *S. guizhouensis* (Dissanayake et al., 2021a) under *S. linhaiensis*. To date, *S. linhaiensis* has only been reported in China (Guizhou Province and Zhejiang Province) as a saprobic and pathogenic fungus in terrestrial habitat. My specimen matches the description of the epitype provided by Rathnayaka et al., (2022), though its asci are slightly larger (145–153 × 29–36 μm vs. 61–120 × 23–35 μm). This study represents the first record of *S. linhaiensis* on *Rosa roxburghii* in China. The phylogenetic placement of my collection is shown in Figure 4.2.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f Pseudoparaphyses. g–j Asci. k–p Ascospores. q Germinating ascospore. r, s Colony on PDA, above (r), below (s). Scale bars: d = 100 µm; e = 20 µm; g–j = 50 µm; f, k–p = 10 µm.

Figure 4.34 *Sphaeropsis linhaiensis* (HUEST ML172, new host record)

Phyllostictaceae Fr. [as 'Phyllostictei']

Type genus – *Phyllosticta* Pers.

Notes – The family Phyllostictaceae was originally proposed as Phyllostictei by Fries (1849). Later, Seaver (1922) placed *Phyllosticta* within Phyllostictaceae, Phyllostictales and this classification was accepted by Hawksworth and David (1989). However, Schoch et al. (2006) suggested that *Phyllosticta* belongs to Botryosphaeriaceae. Subsequently, Wikee et al. (2013) recognized Phyllostictaceae as a distinct family within Botryosphaeriales, and Slippers et al. (2013) formally reinstated the family. Phyllostictaceae is a holomorphic family that accommodates two genera, *Phyllosticta* and *Pseudofusicoccum* (Phillips et al., 2019; Hongsanan et al., 2020b).

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

Type species – *Phyllosticta convallariae* Pers.

Notes – Persoon (1818) introduced the genus *Phyllosticta*, currently classified in Phyllostictaceae (Botryosphaeriales) (Phillips et al., 2019). Norphanphoun et al. (2020) reappraised *Phyllosticta* and introduced six species complexes to facilitate species delimitation, including *P. capitalensis*, *P. concentrica*, *P. cruenta*, *P. owaniana*, *P. rhodorae*, and *P. vaccinii.* To date, over 3000 *Phyllosticta* epithets are listed in Index Fungorum (2025, June), but only a few are supported with molecular data. The genus is characterized by immersed to erumpent, unilocular ascomata, bitunicate, clavate to broadly ellipsoid asci and hyaline, aseptate, ellipsoid to broadly fusoid or limoniform ascospores, with mucilaginous pads at each end; and its asexual morphs are coelomycetous, characterized by black, immersed to semi-immersed conidiomata, phialidic, cylindrical conidiogenous cells and hyaline, aseptate, ovoid to ellipsoidal conidia, surrounded by a mucilaginous sheath and bearing a single mucoid apical appendage (Liu et al., 2012; Wang et al., 2023c; Zhang et al., 2024a).

Phyllosticta capitalensis Henn., Hedwigia 48: 13 (1908) [1909] Figure 4.35

Index Fungorum number: IF168326; Facesoffungi number: FoF06888

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 125–150 µm wide, 80–105 µm high, solitary to gregarious, immersed to semi-immersed, visible as black dots on the host when mature, subglobose to pyriform, unilocular, thick-walled, glabrous, ostiolate. *Ostiole* single, central or laterally located. *Peridium* 13–25 µm wide, composed of dark brown to black compressed cells of *textura globulosa* to *textura angularis. Hamathecium* 2.5–3.5 µm wide, composed of dense, filamentous, rarely branched, remotely septate, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 53–65 × 14–19 µm ($\bar{x}$ = 59.5 × 16.3 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded with an inconspicuous ocular chamber. *Ascospores* 14.5–16.5 × 5.5–7.5 µm ($\bar{x}$ = 15.5 × 6.5 µm; n = 30), irregularly arranged or crowded, hyaline, ellipsoid to broadly fusoid, externally smooth, internally verruculose, aseptate, guttulate, with mucilaginous polar appendages at both ends; appendages cap-like, 3.3–3.9 µm wide, 2.3–3.2 µm high. Asexual morph: Undetermined.

Material examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Huopu Town, on branches of *Rosa roxburghii*, 28 September 2021, N. Wu, CL40 (HUEST XX), living culture UESTCC XX.

Hosts – *Rubus corchorifolius* (Du et al., 2025), *Rosa roxburghii* (present study).

Known geographical distribution – China.

Notes – *Phyllosticta capitalensis* is represented by both asexual and sexual morphs. The species has been recorded from more than 30 plant hosts across ten countries (Liu et al., 2012; Wikee et al., 2013; Cheng et al., 2019; Du et al., 2025). Based on a BLASTn search of my collection in NCBIs GenBank, the closest match to the ITS sequence is *P. capitalensis*: GenBank ON014497 (identities = 596/597 (99.83%), 1 gap); the closest match to the *tef1α* sequence is *P. capitalensis*: GenBank

OP893054 (identities = 213/215 (99.07%), 1 gap). Morphologically, my specimen matches the description provided by Liu et al. (2012), although its asci are slightly wider (53–65 × 14–19 μm vs. 54–60 × 11–13 μm). Therefore, I identify my collection as a sexual morph of *P. capitalensis*, which was collected from *Rosa roxburghii* in China for the first time. The phylogenetic placement of my collection is shown in Figure 4.36.



Note a, b Appearance of ascomata on host surface. c, d Vertical sections of ascomata. e Peridium. f–i Asci. j–n Ascospores. Scale bars: d, f = 50 µm; e, j–n = 10 µm; g–i = 30 µm.

Figure 4.35 *Phyllosticta capitalensis* (HUEST CL40, new host record)

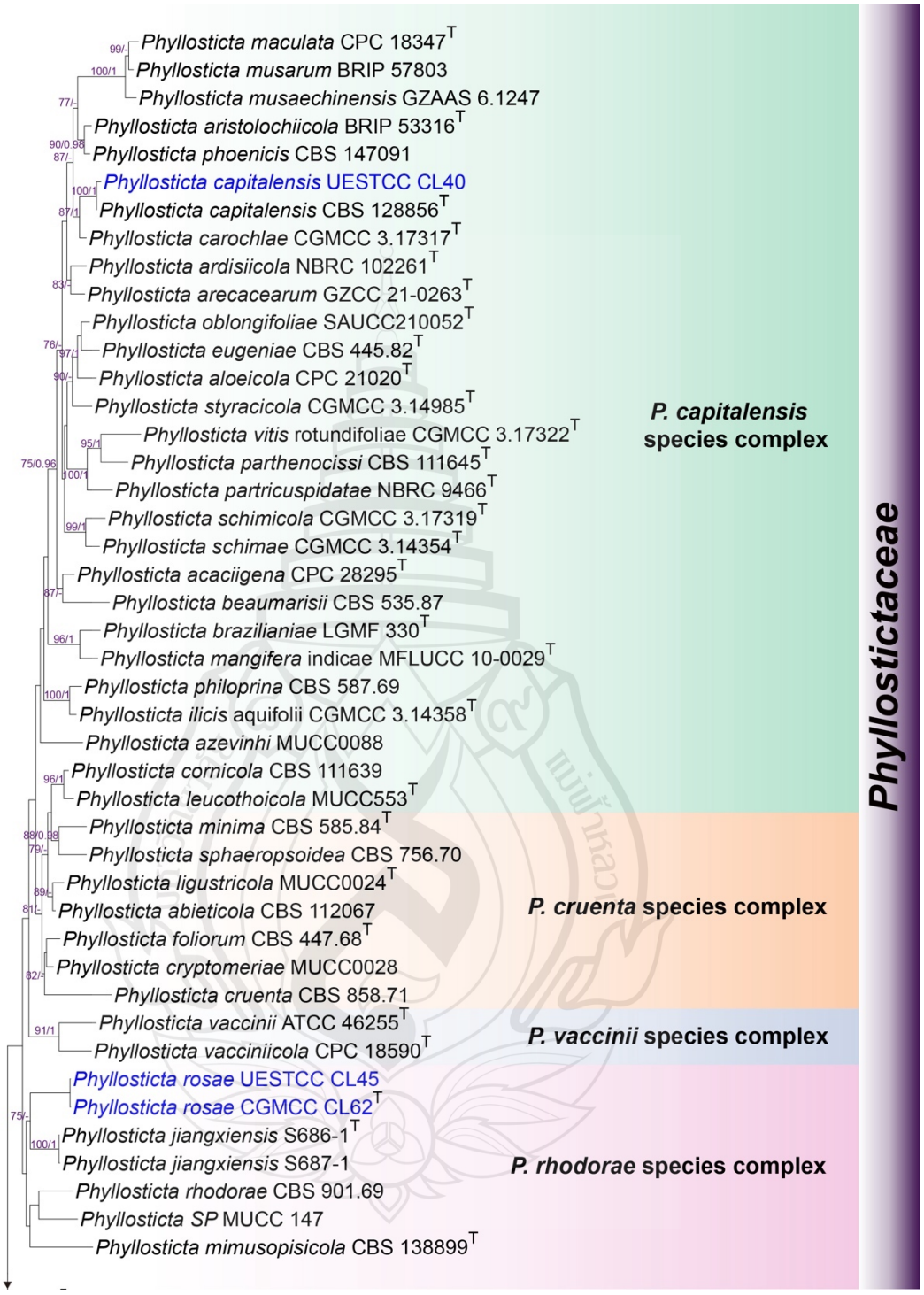


Figure 4.36 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1α*, *act*, and *gapdh* sequence data of *Phyllosticta*

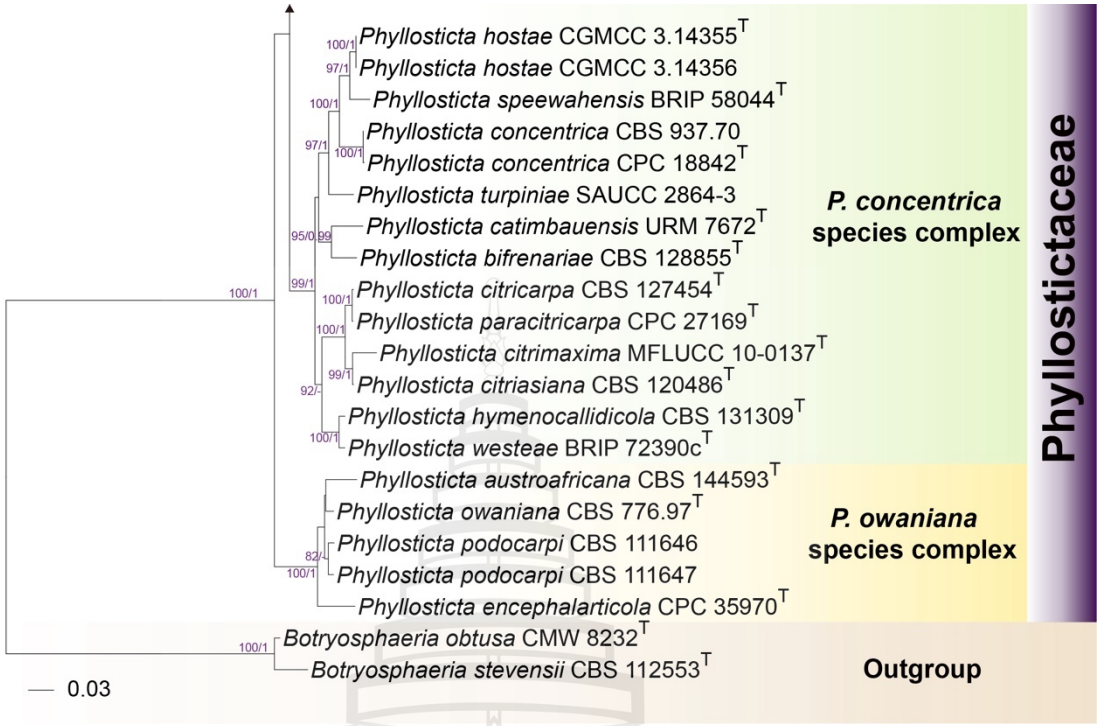


Figure 4.36 (continued)

Figure 4.36 The tree is rooted with *Botryosphaeria obtusa* (CMW 8232) and *B. stevensii* (CBS 112553). Bootstrap values for maximum likelihood (ML) equal to or greater than 75 and Bayesian posterior probabilities greater than 0.90 are indicated above the branches. Hyphen ("-") indicates a posterior probability lower than 0.90 for Bayesian. The isolates obtained in the present study are in blue and ex-type strains are indicated by superscript "T" after the strain number.

Phyllosticta rosae N. Wu & Jian K. Liu, sp. nov. Figure 4.37; Figure 4.38

Index Fungorum number: IFXX; Facesoffungi number: FoFXX

Etymology – The epithet "*rosae*" refers to the host genus, *Rosa*, from which the fungus was originally isolated.

Holotype – HKAS CL62

Saprobic on decaying branches of *Rosa roxburghii*. Sexual morph: *Ascomata* 140–150 μm wide, 110–130 μm high, solitary to gregarious, immersed to erumpent,

visible as small black dots on host surface, globose or subglobose to obpyriform, unilocular, glabrous, coriaceous, ostiolate. *Ostiole* single. *Peridium* 12–25 µm wide, composed of brown cells of *textura globulosa* to *textura angularis*. *Hamathecium* 3–4 µm wide, filamentous, rarely branched, septate, constricted at the septum, hyaline, cellular pseudoparaphyses in a gelatinous matrix. *Asci* 46–60 × 17–20 µm ($\bar{x}$ = 51.5 × 19 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 13–16.3 × 5.8–8 µm ($\bar{x}$ = 14.6 × 7 µm; n = 30), irregularly arranged or crowded, hyaline, ellipsoid to limoniform, with rounded to obtuse ends, externally smooth, internally verruculose, aseptate, guttulate, with mucilaginous polar appendages at both ends; appendages cap-like, 2.6–3.6 µm wide, 1.5–3.3 µm high. Asexual morph: Coelomycetous. *Conidiomata* 100–155 µm wide, 77–108 µm high, solitary to gregarious, immersed to erumpent, visible as small black dots on host surface, globose or subglobose to obpyriform, unilocular, glabrous, coriaceous, ostiolate. *Ostiole* 18–27 µm wide, 30–35 µm high, single, centrical. *Conidiomatal wall* 10–15 µm wide, composed of thick-walled, brown cells of *textura globulosa* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–9 × 4–8.4 µm ($\bar{x}$ = 7.7 × 5.6 µm; n = 30), hyaline, enteroblastic, cylindrical to doliiform, determinate, straight or slightly curved, smooth-walled. *Conidia* 11.5–14 × 8.2–9.5 µm ($\bar{x}$ = 12.7 × 8.9 µm; n = 30), hyaline, oval to ellipsoid, with a truncate base bearing a minute marginal frill, aseptate, guttulate, smooth-walled, surrounded in a mucoid envelope 1.5–3 µm wide at each side, bearing appendage at apex, appendage 7–10 µm long, single, unbranched.

Culture characteristics – Ascospores and conidia germinated on PDA medium within 12 h and germ tubes produced from both ends. Colonies on PDA medium fast-growing and reaching 13–15 mm diam. after two weeks at 25°C in dark, circular, velvety to woolly, grayish green; in reverse, pale brown with white entire margin.

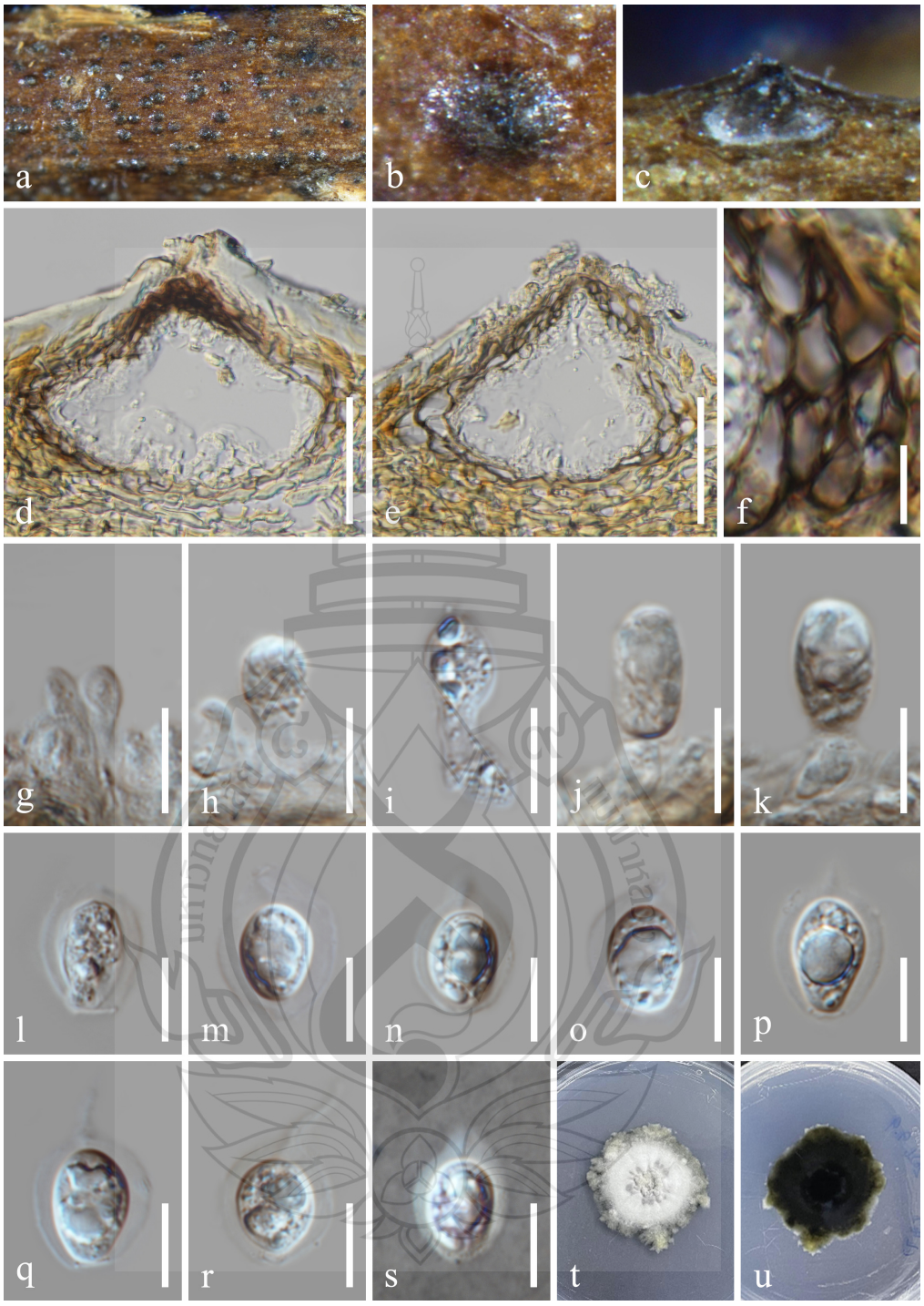
Materials examined – CHINA, Guizhou Province, Liupanshui City, Panzhou City, Huopu Town, on branches of *Rosa roxburghii*, 28 September 2021, N. Wu, CL62 (HKAS XX, **holotype**); ex-type living culture CGMCC XX; *ibid.*, CL45 (HUEST XX, paratype), living culture UESTCC XX.

Notes – I isolated both the asexual and sexual morphs of *Phyllosticta rosae* from the same substrate, *Rosa roxburghii*. Phylogenetic analysis indicates that my two isolates are identical (CGMCC CL62 and UESTCC CL45) (Figure 4.36). Moreover, these two isolates had only one nucleotide difference in ITS region and two nucleotide differences in *tef1α* region. The multi-gene phylogeny showed that *P. rosae* forms a sister clade to *P. jiangxiensis* (S686-1 and S687-1) with a moderate statistical support (Figure 4.36). *Phyllosticta jiangxiensis* was introduced as a coelomycetous fungus isolated from diseased leaves of *Camellia oleifera* (Sui et al., 2023). *Phyllosticta rosae* shares similar conidiogenous cells and conidial morphology with *P. jiangxiensis*. However, *P. rosae* has slightly longer and wider conidia than *P. jiangxiensis* (11.5–14 × 8.2–9.5 μm vs. 8–12 × 6–8 μm). Additionally, a comparison of the ITS regions reveals that *P. rosae* differs from *P. jiangxiensis* by 23 (3.8%) nucleotide differences, indicating that they can be recognized as different species (Jeewon & Hyde, 2016). Therefore, I propose *P. rosae* as a new species based on morphological characteristics and phylogenetic evidence.



Note a Host: *Rosa roxburghii*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e–g Asci. h–m Ascospores. n, o Colony on PDA, above (n), below (o). Scale bars: d = 50 µm; e–g = 20 µm; h–m = 10 µm.

Figure 4.37 *Phyllosticta rosae* (HKAS CL62, holotype; sexual morph)



Note a, b Conidiomata on natural substrate. c–e Vertical sections of conidiomata. f Conidiomatal wall. g–k Conidiogenous cells and developing conidia. l–r Conidia. s Conidium stained with Indian ink. t, u Colony on PDA, above (t), below (u). Scale bars: d, e = 50 µm; f–s = 10 µm.

Figure 4.38 *Phyllosticta rosae* (HKAS CL45, holotype; asexual morph)

4.3 Discussion

Studies on Botryosphaeriaceae focusing on morphology and phylogenetic analyses of isolates associated with different hosts have increased markedly in recent years, which has facilitated the accurate identification of taxa worldwide at the species level (Dissanayake et al., 2016; 2021, Phillips et al., 2019, Garcia et al., 2021, Xiao et al., 2021, Zhang et al., 2021, Li et al., 2023, Lin et al., 2023). In the present study, 57 Botryosphaeriaceae isolates were obtained from decaying woody hosts, including dead aerial twigs, branches, stems, bark, and seed pods, in southwestern China and northern Thailand (Figure 4.39). These isolates were identified as 25 species using a polyphasic approach that combined morphological features with molecular phylogeny. The taxa included *Botryosphaeria dothidea*, *Botryosphaeria fujianensis*, *Diplodia mutila*, *Diplodia pseudoseriata*, *Diplodia seriata*, *Dothiorella acericola*, *Dothiorella camelliae*, *Dothiorella citricola*, *Dothiorella ovata*, *Dothiorella rosacearum*, *Dothiorella sarmentorum*, *Dothiorella septata*, *Dothiorella zanthoxyli*, *Lasiodiplodia chiangraiensis*, *Lasiodiplodia crassispora*, *Lasiodiplodia delonicis*, *Lasiodiplodia mahajangana*, *Lasiodiplodia theobromae*, *Macrophomina euphorbiicola*, *Neodeightonia septata*, *Neodeightonia subglobosa*, *Neofusicoccum parvum*, *Sphaeropsis eucalypticola*, *Sphaeropsis citrigena* and *Sphaeropsis linhaiensis*. Among these, *Dothiorella ovata*, *Do. rosacearum*, *Do. septata*, *Lasiodiplodia chiangraiensis*, *L. delonicis* and *Neodeightonia septata* are introduced here as novel species, while the remaining taxa represent new host or new geographical records. All species collected in this study were saprobic on their hosts.

Macrophomina and *Sphaeropsis* are two of the least represented genera in the family Botryosphaeriaceae. Currently, five species of *Macrophomina* are validly recognized, among which *M. phaseolina* and *M. euphorbiicola* have been introduced as pathogens (Su et al., 2001, Babu et al., 2007, Sarr et al., 2014, Machado et al., 2018).

In this study, the asexual morph of *M. euphorbiicola* was collected from *Plukenetia volubilis* in northern Thailand. Previous cultures of this species failed to sporulate, and thus, no morphological description had been available (Machado et al., 2018). My study provides the first detailed morphological description and illustration of *M. euphorbiicola*, and documents a new host record from *P. volubilis* in Thailand. For *Sphaeropsis*, the type species *S. visci* was introduced by Saccardo (1880), with 633 names listed in Index Fungorum (Accessed August 2025), yet only nine species are currently recognized with available cultures (Phillips et al., 2013, Wu et al., 2021). In this study, *S. eucalypticola* was collected from *Tectona grandis* in Thailand and reported as a new host record. This species has previously been recorded from *Bauhinia purpurea* and *Eucalyptus* sp. in Thailand (Liu et al., 2012, Phookamsak et al., 2019), while *S. chromolaenicola* was identified from *Chromolaena odorata* by Mapook et al. (2020). However, most members of *Sphaeropsis* remain unrecorded in Thailand.

Two species of *Diplodia*, namely *Di. mutila* and *Di. seriata*, were recovered from Sichuan Province. My findings are consistent with Li et al. (2023), who reported these species from *Camellia oleifera* along with two additional species (*Di. acerigena* and *Di. pistaciicola*). *Diplodia* species are typically associated with woody hosts and are known to cause rots, cankers, and shoot blight (Crous et al., 2006; Slippers & Wingfield, 2007; Phillips et al., 2012; Linaldeddu et al., 2014; Giambra et al., 2016). Their frequent occurrence highlights their ecological and economic significance, as well as the need for more comprehensive surveys in woody plant ecosystems.

In the present study, *Dothiorella* was the most frequently isolated genus, with eight species obtained from dead and decaying woody hosts in China and Thailand (Figure 4.40). *Dothiorella* was originally introduced by Saccardo (1880), with *Do. pyrenophora* as the type species, and currently, 38 species are accepted in the genus (Wu et al., 2021, Li et al., 2023, Lin et al., 2023). Zhang et al. (2021) provided a systematic revision of *Dothiorella*, synonymizing 15 previously described species to

establish a more stable classification. Historically, *Dothiorella* species were rarely reported in Thailand; however, in recent years, several studies have documented their occurrence (Doilom et al., 2015; Jayasiri et al., 2019; Rathnayaka et al., 2022a, 2022b). In this study, three novel species, *Do. ovata*, *Do. rosacearum*, and *Do. septata*, are introduced based on asexual morphological features and phylogenetic evidence, which further expand the diversity of the genus.

Lasiodiplodia is one of the largest genera within Botryosphaeriaceae, and numerous species have been discovered globally in recent years, confirming its cosmopolitan distribution across diverse regions, including Algeria, Australia, Brazil, China, India, Iran, Madagascar, South Africa, Thailand, and the USA (Abdollahzadeh et al., 2010; Ismail et al., 2012; Marques et al., 2013; Machado et al., 2014; Netto et al., 2014; Linaldeddu et al., 2015; Trakunyingcharoen et al., 2015; Dou et al., 2017a; Rodríguez-Gálvez et al., 2017). The type species, *L. theobromae*, is a common and destructive pathogen causing a variety of diseases in woody plants (Punithalingam, 1980; Burgess et al., 2006; Burruano et al., 2008; Wright & Harmon, 2009; Luo et al., 2011; Fan et al., 2013; Sinha et al., 2018). Zhang et al. (2021) reevaluated the taxonomy of *Lasiodiplodia* and synonymized more than 20 species to prevent redundant introductions. At present, 42 species are accepted in the genus, including *L. chiangraiensis* and *L. delonicis* introduced in this study with full morphological and phylogenetic support. While *L. crassispora* and *L. mahajangana* are known species with broad host ranges, my report represents the first record of *L. crassispora* in Thailand and expands the distribution of *L. mahajangana* to *Dipterocarpus retusus*. The discovery of *L. delonicis* from a fallen pod of *Delonix regia* further broadens the taxonomic framework of the genus. Importantly, variation in conidial striation patterns observed between cultures and natural environments highlights the influence of ecological conditions on morphological traits, underscoring the necessity of collecting more fresh specimens to validate such observations.

Neodeightonia species are morphologically similar to *Diplodia* and *Lasiodiplodia*, particularly in their asexual morphs, which necessitates molecular data for accurate identification. Unlike the latter two genera, *Neodeightonia* lacks paraphyses, a distinguishing feature that also characterizes the novel species introduced in this study. Palms have proven to be important hosts for *Neodeightonia*, as seven of the eleven accepted species are associated with palms (Phillips et al., 2008; Liu et al., 2010; Adamčík et al., 2015; Konta et al., 2016a, b; Hyde et al., 2018; Xiong et al., 2021). In this study, *N. septata* was recovered from a palm, providing further evidence that palms represent favorable hosts for the genus. These findings suggest that additional novel *Neodeightonia* species may be discovered from palms in future surveys.

Finally, *Botryosphaeria fujianensis* was originally introduced as a pathogen causing stem canker on blueberry in Fujian Province, China (Chu et al., 2021). In the present study, it was isolated from dead twigs of *Tectona grandis* in Chiang Mai Province, Thailand, marking the first record of this species in Thailand. Given its pathogenic potential, the possibility of its occurrence on additional hosts in the region cannot be excluded.

The results of this study reinforce the view that the family Botryosphaeriaceae is highly diverse and widely distributed, with numerous novel taxa and host records continuously being discovered (Hyde et al., 2020; Senwanna et al., 2021; Manawasinghe et al., 2021; Manawasinghe et al., 2022; Sun et al., 2022). However, challenges remain in defining species boundaries, clarifying their opportunistic pathogenicity, and incorporating environmental isolates into taxonomic frameworks. As Botryosphaeriaceae includes many species that are significant threats to agricultural crops, urban trees, and natural forests (Karani et al., 2022; Wijesinghe et al., 2022; Wonglom et al., 2022), continued surveys and integrative taxonomic approaches are essential for understanding their diversity, preventing further spread, and developing effective management strategies.

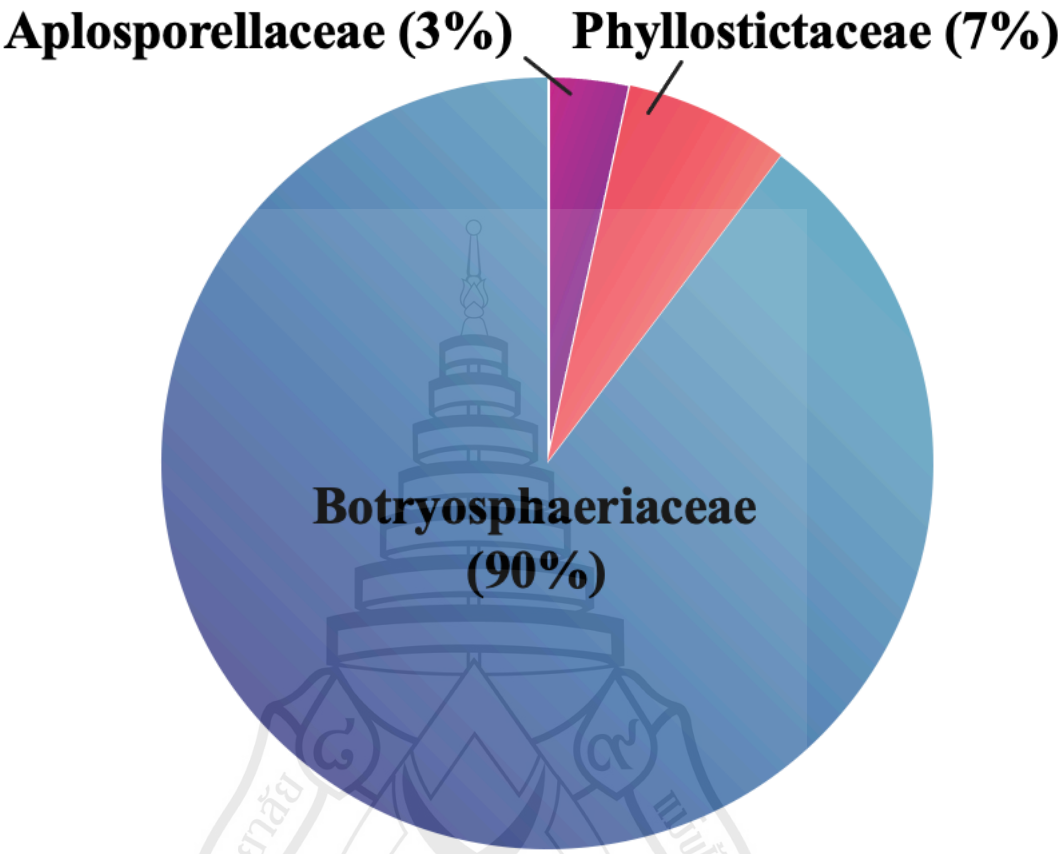
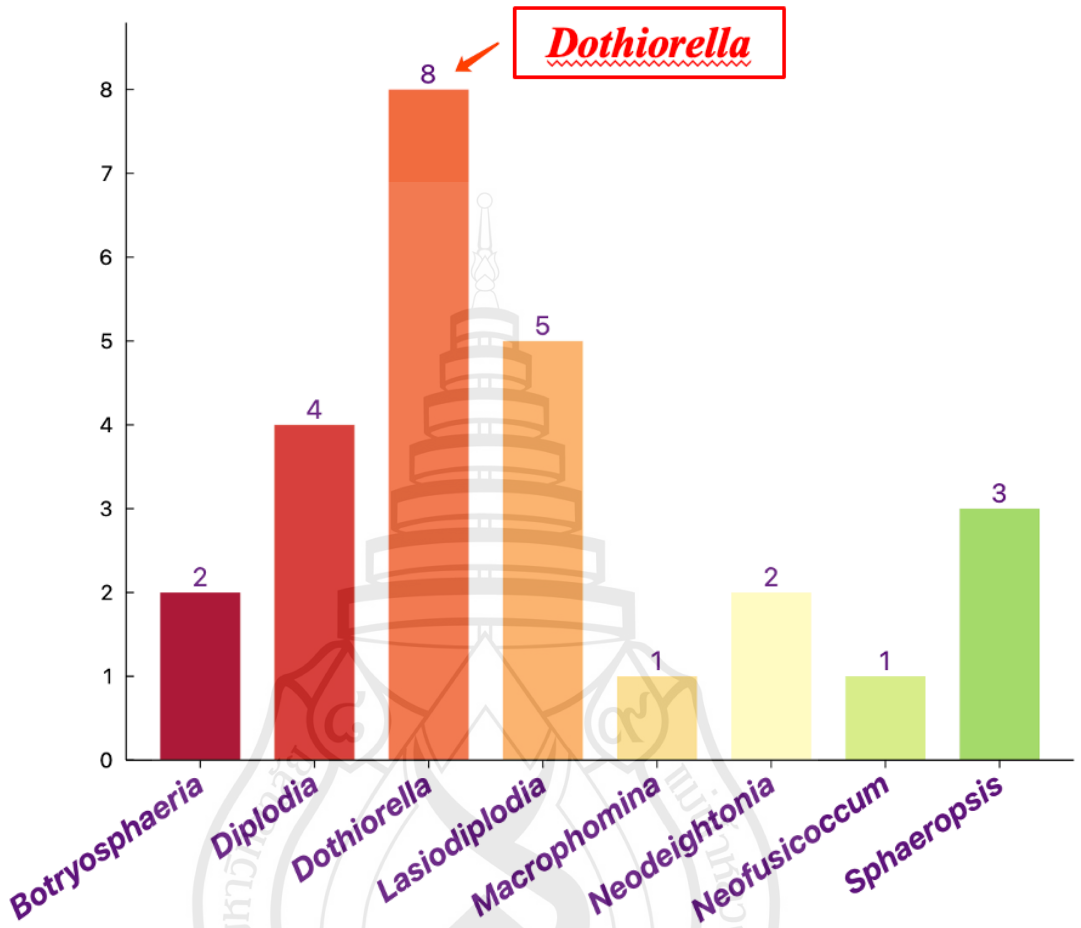


Figure 4.39 Distribution of Botryosphaeriales obtained in this study



Note The number above each bar indicates the number of species, with *Dothiorella* highlighted as the most represented genus.

Figure 4.40 Distribution of Botryosphaeriales genera isolated in this study

CHAPTER 5

TAXONOMY AND PHYLOGENY OF FUNGI FROM MEDICINAL PLANTS IN CHINA

5.1 Introduction

Medicinal plants are cultivated and utilized for their therapeutic value, with a wide variety distributed and grown worldwide (Marinelli, 2004; Dar et al., 2017; Phumthum et al., 2019; Rasool et al., 2020). They serve as vital resources for preventing and treating diseases, as their flowers, fruits, leaves, roots, or entire plants can be used directly as therapeutic agents or in the pharmaceutical industry for drug production. In particular, medicinal plants play a significant role in modern drug discovery and development, contributing to the advancement of anticancer, antibacterial, and antiviral medications (Anand et al., 2019; Ali et al., 2021; Atanasov et al., 2021; Adeleye et al., 2022; Chaachouay & Zidane, 2024). The growth, reproduction, and overall quality of medicinal herbs are influenced by numerous biotic and abiotic factors, among which microfungi are particularly important. Microfungi associated with medicinal plants include endophytes, saprobes, and pathogens, which are mainly distributed in Dothideomycetes and Sordariomycetes, with a smaller proportion in Eurotiomycetes (Bhagat et al., 2012; Niu et al., 2016; Long et al., 2019; Ma et al., 2019; Hyde et al., 2020; Tennakoon et al., 2021). These fungi not only affect plant health but also contribute significantly to ecological processes and biodiversity.

Helotiales was established by Nannfeldt (1932) to accommodate species with cupulate apothecia covered by long hairs and is the largest and most diverse order in Leotiomycetes. This order accounts for about 80% of the class Leotiomycetes, comprising 36 families, 328 genera, and more than 5,000 species, with another 144

genera as families incertae sedis (Eriksson, 2005, Ekanayaka et al., 2019, Wijayawardene et al., 2022). Members of Helotiales are ecologically diverse, including endophytes, plant pathogens and saprobes (Pöder & Scheuer, 1994, Hosoya & Otani, 1995, Monreal et al., 2000, Boddy, 2001, Grünig et al., 2002, Shoemaker et al., 2002, Johnston & Park, 2005, Wang et al., 2006).

Pleosporales is considered to be the largest and the most diverse order of the class Dothideomycetes, was introduced by Nitschke (1869), and later validated by Barr (1987). Luttrell (1975) included eight families in this order, Kirk et al. (2008) listed 23 families, Lumbsch and Huhndorf (2010) accepted 28 families, and Zhang et al. (2012) included 25 families in the phylogenetic analysis. Forty-one families were placed in Pleosporales by Hyde et al. (2013), based on the multi-gene analyses and morphological study of family types. Currently, about more than 4,700 species (Ariyawansa et al., 2018) classified in more than 400 genera and 75 families (Wijayawardene et al., 2018; Hongsanan et al., 2020b; Hyde et al., 2024). The taxonomic circumscription of Pleosporales has changed frequently in recent years due to the addition of large numbers of families, genera and species.

Pleosporalean species are characterised by pseudothecial ascomata usually with a papilla and a peridium composed of several layers of cells (Zhang et al., 2009a, 2012; Hyde et al., 2013; Jaklitsch & Voglmayr, 2016; Jaklitsch et al., 2018). Asci are bitunicate, usually fissitunicate and produced within a persistent hamathecium with or without pseudoparaphyses (Ariyawansa et al., 2013, 2014b, 2015b; Hyde et al., 2013). Ascospores are generally septate but vary in colour and shape, with or without a gelatinous sheath (Zhang et al., 2009a, 2012; Hyde et al., 2013; Jaklitsch & Voglmayr, 2016; Jaklitsch et al., 2018). Asexual morphs can be coelomycetous or hyphomycetous (Zhang et al., 2009a, b; Hyde et al., 2013; Ariyawansa et al., 2014b, 2015b; Hernández-Restrepo et al., 2017; Valenzuela-Lopez et al., 2018). Members of Pleosporales are ubiquitous, occurring in various habitats and can be recognized as epiphytes,

endophytes or parasites of living leaves or stems, hyperparasites on fungi or insects, lichenised or saprobes of dead plant stems, leaves or bark (Zhang et al., 2012; Hyde et al., 2013; Ariyawansa et al., 2014b).

In recent years, increasing attention has been paid to microfungi associated with medicinal plants, leading to the discovery of many novel species (Zhao et al., 2010; 2014; Han et al., 2012; Jafari 2018; Kumar et al., 2019; Phukhamsakda et al., 2020; Sun et al., 2022, 2023a, 2023b). During my investigations of microfungi associated with medicinal plants in China, several asexual and sexual morphs were collected, enriching the taxonomic knowledge of these fungi. Given the wide diversity and rich resources of medicinal plants (Chen et al., 2016; Rasool et al., 2020), they provide suitable habitats for exploring and documenting fungal diversity. Moreover, the discovery of new microfungi, including novel species and new records, offers essential data for the conservation and sustainable utilization of medicinal plants.

5.2 Results

Ascomycota Caval.-Sm.

Dothideomycetes O.E. Erikss. & Winka

Pleosporales Luttr. ex M.E. Barr, Prodr. Cl. Loculoasc. (Amherst): 67 (1987)

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016)

Type genus – *Dictyosporium* Corda

Notes – The family Dictyosporiaceae, which was originally proposed as Dictyosporaceae by Liu et al. (2015b), was introduced by Boonmee et al. (2016) within the order Pleosporales and class Dothideomycetes. Although Hyde et al. (2024) listed 21 genera in Dictyosporiaceae but without the inclusion of the genera *Pseudocyclothyriella* and *Neoxylochrysis* (Jiang et al., 2021b; Wu et al., 2024).

Moreover, the genus *Paradictyocheirospora* has already been synonymized with *Digitodesmium* by Tian et al. (2022).

Aquadictyospora Z.L. Luo, K.D. Hyde & Hong Y. Su, Mycosphere 8: 1590 (2017)

Type species – *Aquadictyospora lignicola* Z.L. Luo, W.L. Li, K.D. Hyde & Hong Y. Su

Notes – *Aquadictyospora* was introduced by Li et al. (2017) to accommodate the species, *A. lignicola*, collected from submerged decaying wood in China. Phukhamsakda et al. (2020) introduced the second species, *A. clematidis*, based on morphology and phylogenetic analyses. *Aqua- dictyospora* is an asexual morph genus, with no sexual morph linked to it. The genus is characterized by superficial, compact, scattered, globose or subglobose, dark brown to black conidiomata, micronematous conidiophores with monoblastic conidiogenous cells, and uniformly medium brown conidia with a broadly ovate to subglobose, hyaline cell in the lower half (Li et al., 2017; Phukhamsakda et al., 2020).

Aquadictyospora lignicola Z.L. Luo, W.L. Li, K.D. Hyde & Hong Y. Su, Mycosphere 8(10): 1591 (2017) Figure 5.1

Index Fungorum number: IF553862; Faces of Fungi number: FoF03768

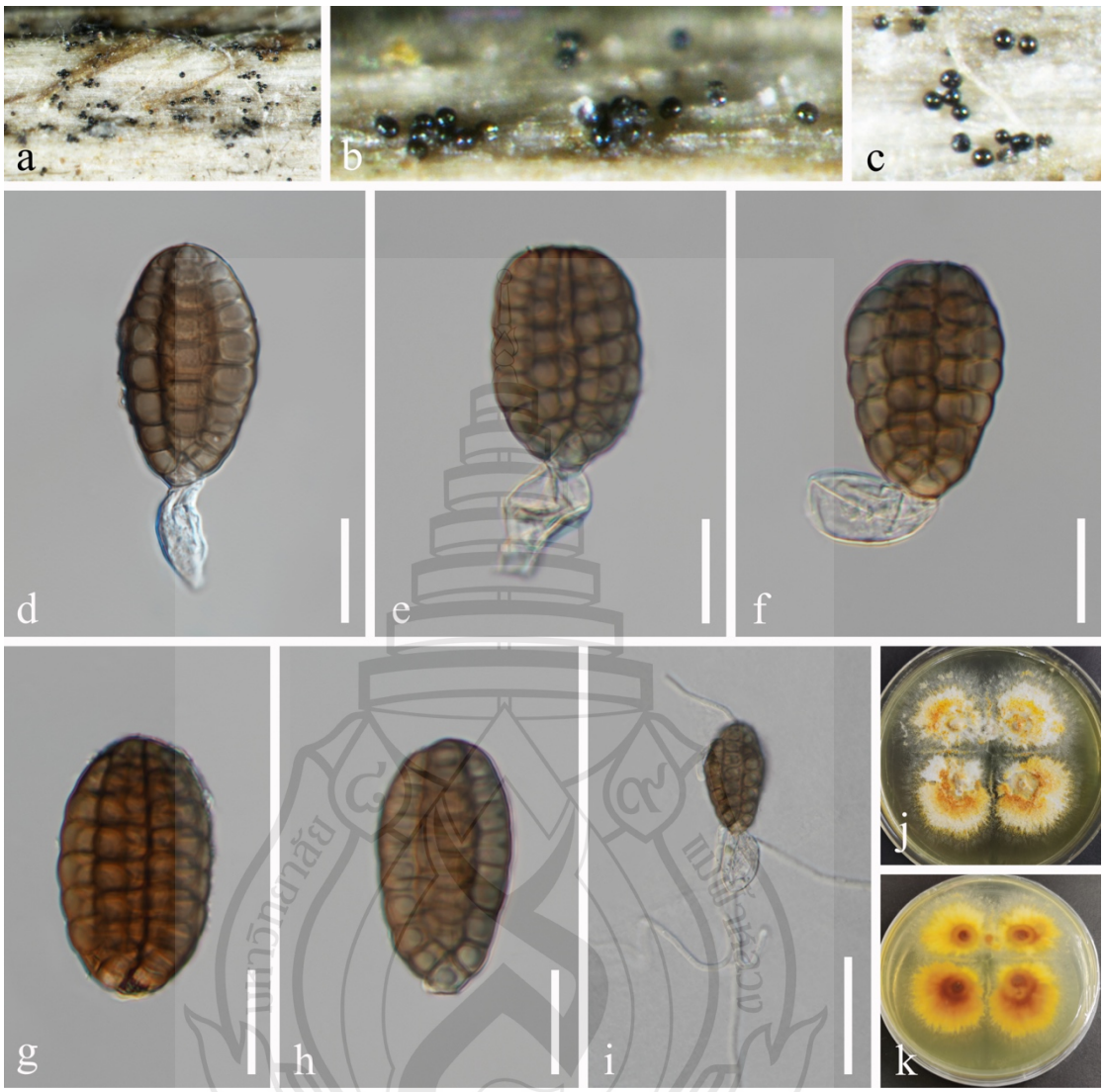
Saprobic on dead twigs of *Periploca forrestii* Schltr. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* superficial, gregarious, scattered, punctiform, sporodochial, scattered, black, velvety, glistening, orbicular. *Mycelium* mostly immersed or partly superficial, smooth, with hyaline to pale brown hyphae. *Conidiophores* mi-cronematous, cylindrical, hyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, hyaline to pale brown, smooth-walled. *Conidia* 38–52 × 19–33 µm ($\bar{x}$ = 47 × 26 µm, n = 50), solitary, acrogenous, cheiroid, smooth-walled, yellowish-brown to light brown, with a basal connecting cell,

consisting of 5–7 (mostly 6) rows of cells, euseptate, unseparated, each row with 8–9 cells, individual rows discoid, secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h. Germ tubes produced from both ends. Colonies on PDA reaching 20–30 mm diam. after 2 weeks at 25°C in natural light, circular, wrinkled, with dense white to pale yellow mycelia in the middle, sparser towards the edge; in reverse yellowish brown in the middle, pale yellow at the entire margin.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Qingcheng Mountain scenic spot, 103°28′36″ E, 30°55′9″ N, on dead twigs of medicinal plant *Periploca forrestii*, 27 March 2021, H.Z. Du, S172 (HUEST 23.0213), living culture UESTCC 23.0213.

Notes – *Aquadictyospora lignicola*, the type species of *Aquadictyospora*, was introduced by Li et al. (2017) from submerged decaying wood. In this study, an isolate was obtained from *Periploca forrestii*. My collection (HUEST 23.0213) is similar to *A. lignicola* (MFLU 17-1422) in having yellowish-brown to light brown conidia, composed of 4–7 compactly arranged rows of cells, with a basal hyaline cell. Phylogenetic analysis showed that my strain clustered with the type strain of *A. lignicola* (MFLUCC 17-1318) with ML/BI 100%/1 bootstrap support (Figure 5.2). Thus, I identified my collection as *A. lignicola* and report it as a new host record.



Note a–c Colonies on a woody substrate. d–f Conidia with partial conidiophores. g, h Conidia. i Germinated conidium. j, k Colonies on PDA, from above (j), from below (k). Scale bars: d–h = 20 µm, i = 50 µm

Figure 5.1 *Aquadictyospora lignicola* (HUEST 23.0213, new host record)

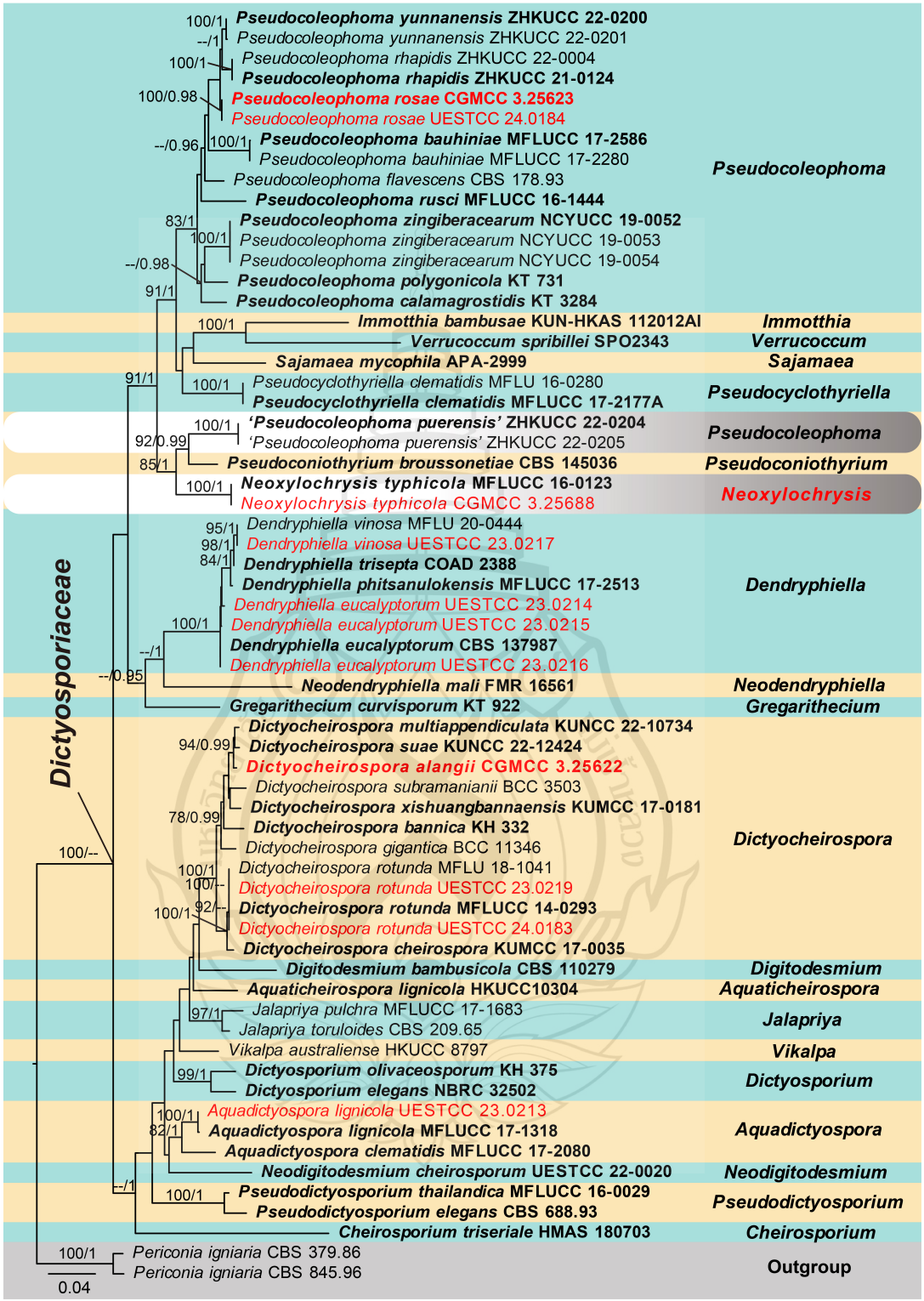


Figure 5.2 Phylogenetic tree generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU and *tef1α* sequence data of Dictyosporiaceae

Figure 5.2 The tree is rooted with *Periconia igniaria* (CBS 379.86 and CBS 845.96). The ML (≥75%) and BI (≥95%) bootstrap supports are given near the nodes, respectively. The new isolates obtained in this study are indicated in red and ex-type strains are in bold.

Dendryphiella Bubák & Ranoj., Annls mycol. 12(4): 417 (1914)

Type species – *Dendryphiella vinosa* (Berk. & M.A. Curtis) Reisinger

Notes – *Dendryphiella* was introduced by Ranojevic (1914)with the type species *D. interseminata* Bubák. This asexual genus has 20 epithets in Index Fungorum (accessed September 2024). It is characterized by macronematous, fasciculate, septate conidiophores with polytretic, verrucose conidiogenous cells enlarged at the apex, and solitary to catenate, aseptate or septate, hyaline to pale brown, thick-walled, verrucose conidia (Ranojevic 1914; Ellis 1971). It is worth noting that the mode of conidiogenous cell development of *Dendryphiella* members is tretic, while other asexual morphs in the family are blastic (Ellis, 1971; Boonmee et al., 2016; Shen et al., 2022).

Dendryphiella eucalyptorum Crous & E. Rubio, Persoonia 32: 231 (2014) Figure 5.3

Index Fungorum number: IF808918; Faces of Fungi number: FoF06712

Saprobic on dead twigs of *Sambucus javanica* Blume. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, effuse, dark brown. *Mycelium* mostly immersed, composed of smooth, septate, branched, brown hyphae. *Conidiophores* 185–300 µm long, 3–4 µm wide, macronematous, mononematous, brown, wider at the base, slightly paler at the apex, fasciculate, thick-walled, erect, straight or slightly flexuous, smooth or verruculose, septate, unbranched or sometimes branched, wider at the base. *Conidiogenous cells* 12–30 µm long, 5–7 µm wide ($\bar{x}$ = 20 × 6 µm, n = 30), polytretic, integrated, terminal and intercalary, later becoming subterminal, pro- liferating asymmetrically, clavate, brown, enlarged at the vertex. *Conidia* 12–27 × 5–7 µm ($\bar{x}$ = 21 × 6 µm, n = 50), subcylindrical,

apex obtuse, base bluntly rounded, pale brown, asep- tate or 1-septate when young, brown or dark brown, 3-septate when mature, constricted at septa, thick-walled, verruculose to verrucose.

Culture characteristics – Conidia germinated on PDA medium within 24 h. Germ tubes produced from both ends. Colonies on PDA reaching 10–15 mm diam. after two weeks, circular, cottony, with regular margins, white from above and white to pale grey from below.

Material examined – China, Sichuan Province, Chengdu City, High-tech West District, Yaobo Park, on dead twigs of medicinal plant *Sambucus javanica*, 11 August 2021, H.Z. Du, S343 (HUEST 23.0214), living culture UESTCC 23.0214; *ibid*., Leshan City, Muchuan County, Huangdan Town, on dead leaves of medicinal plant *Ophiopogon japonicus* (L. f.) Ker-Gawl., 31 October 2021, H.Z. Du, S463 (HUEST 23.0215), living culture UESTCC 23.0215; *ibid*., Yaan City, Mingshan District, Wangu Town, on dead twigs of medicinal plant *Leonurus japonicus* Houttuyn, 29 October 2021, H.Z. Du, S459 (HUEST 23.0216), living culture UESTCC 23.0216.

Notes – *Dendryphiella eucalyptorum* (CBS 137987) was collected from *Eucalyptus globulus* in Spain (2014). I identified my collections as *D. eucalyptorum* based on morphology and phylogeny, and report them as new host records from medicinal plants (*Leonurus japonicus*, *Ophiopogon japonicus* and *Sambucus javanica*).



Note a, b Host. c, d Colo-nies on a woody substrate. e, f Conidiophores. g–i Conidiogenous cells and conidia. j–p Co-nidia. q Germinated conidium. r, s Colonies on PDA, from above (r), from below (s). Scale bars: e = 100 µm, f = 50 µm, g–i = 20 µm, j–q = 10 µm.

Figure 5.3 *Dendryphiella eucalyptorum* (HUEST 23.0214, new host record)

Dendryphiella vinosa (Berk. & M.A. Curtis) Reisinger, Bull. trimest. Soc. mycol. Fr. 84(1): 27 (1968) Figure 5.4

Index Fungorum number: IF329796; Faces of Fungi number: FoF08673

Saprobic on the twigs of *Phytolacca americana* L. Sexual morph: Not observed. Asex- ual morph: Hyphomycetous. *Colonies* on natural substrate superficial, effuse, brown to dark brown. *Conidiophores* 180–230 μm long, 4–7 μm wide, macronematous, mononematous, erect, straight or slightly flexuous, smooth or verruculose, septate, unbranched or sometimes branched, wider at the base. *Conidiogenous cells* 12–28 μm long, 5–7 μm wide ($\bar{x}$ = 18 × 6 μm, n = 30), polytretic, terminal, proliferating asymmetrically, brown, verru- cose, enlarged at the vertex. *Conidia* 19–30 × 6–8 μm ($\bar{x}$ = 25 × 7 μm, n = 50), fusiform to ellipsoidal, pale brown to brown or dark brown, aseptate when young, 3-septate when mature, constricted at septa, thick-walled, smooth or occasionally verruculose.

Culture characteristics – Conidia germinated on PDA medium within 24 h. Germ tubes produced from both ends. Colonies on PDA reaching 40–50 mm diam. after two weeks at 25°C in natural light. Mycelium superficial, with regular margins, white from above, and brown to yellowish in the middle zone from below, paler toward the margins.

Material examined – China, Guizhou Province, Guiyang City, Huaxi District, on dead twigs of medicinal plant *Phytolacca americana*, 24 January 2021, H.Z. Du, S61 (HUEST 23.0217), living culture UESTCC 23.0217.

Notes – *Dendryphiella vinosa* was initially isolated from unidentified rotten leaves by Reisinger (1968). It has also been reported on decomposing leaves in Japan (2006) and *Dendrobium officinale* in China (2021). I identify my isolate as *D. vinosa* based on morphology and phylogenetic evidence. Therefore, I report *D. vinosa* from *Phytolacca americana* as a new host record in China.



Note a, b Host. c–e Colonies on a woody substrate. f, g Conidiophores. h–j Conidiogenous cells and conidia. k–p Conidia. q, r Colony on PDA, from above (q), from below (r). Scale bars: f, g = 50 µm, h–j = 20 µm, k–p = 10 µm.

Figure 5.4 *Dendryphiella vinosa* (HUEST 23.0217, new host record)

Dictyocheirospora M.J. D'souza, Boonmee & K.D. Hyde, Fungal Diversity 80: 465 (2016)

Type species – *Dictyocheirospora rotunda* M.J. D'souza, Bhat & K.D. Hyde

Notes – Boonmee et al. (2016) established *Dictyocheirospora* to accommodate three species, *D. bannica*, *D. rotunda* (type species) and *D. vinaya*, and transferred four species of *Dictyosporium* to *Dictyocheirospora*. Currently, 34 epithets of *Dictyocheirospora* are listed in Index Fungorum (accessed September 2025). *Dictyocheirospora* is similar to *Dictyosporium* except for the conidial arms, which are arranged differently (Prasher et al., 2015; Boonmee et al., 2016; Silva et al., 2016; Tennakoon et al., 2023). The sexual stage of *Dictyocheirospora* has never been reported.

Dictyocheirospora alangii H.Z. Du, N. Wu & Jian K. Liu, sp. nov. Figure 5.5

Index Fungorum number: IF902300; Faces of Fungi number: FoF16017

Etymology: The epithet '*alangii*' refers to the host genus *Alangium* from which the fungus was collected.

Holotype: HKAS 131314

Saprobic on dead twigs of *Alangium chinense* (Lour.) Harms. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate were punctiform, solitary, sporodochial, scattered, dark brown to black. *Mycelium* immersed, composed of pale brown, smooth, septate, branched hyphae. *Conidiophores* micronematous, short, branched, hyaline to pale brown. *Conidiogenous cells* 8–13 µm long, 3–6 µm wide ($\bar{x}$ = 10 × 5 µm, n = 20), holoblastic, cylindrical, integrated, terminal, pale brown, smooth, thin-walled. *Conidia* 44–60 × 17–27 µm ($\bar{x}$ = 49 × 20 µm, n = 50), solitary, cheiroid, ellipsoid to cylindrical, not complanate, pale brown to brown, consisting of 6–7 rows of cells, closely appressed, with rows cylindrical, palmately divergent, each row composed of 8–12 cells, euseptate, slightly constricted at the septa, guttulate, smooth, sometimes with 1–2 hyaline, globose to subglobose appendages which are 10–15 × 7–10 µm, and mostly attached at the central part of two outer arms.

Culture characteristics – Conidia germinated on PDA medium within 12 h. Germ tubes produced from both ends. Colonies on PDA reaching 40–50 mm diam. after one month. Mycelium superficial, with irregular margins, white from above, and yellowish in the middle zone from below, paler toward the margins.

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Xiangzhigou scenic spot, near freshwater stream, on dead twigs of medicinal plant *Alangium chinense*, 24 February 2021, H.Z. Du, S130 (HKAS 131314, holotype); ex-type living culture CGMCC 3.25622 = UESTCC 23.0218.

Notes – The phylogenetic analysis showed that *Dictyocheirospora alangii* (CGMCC 3.25622) nested within *Dictyocheirospora*, close to *Di. multiappendiculata* (KUNCC 22-10734) and *Di. suae* (KUNCC 22-12424) with good bootstrap support (94% MLBS, 0.99 PP) (Figure 5.2). *Dictyocheirospora alangii*, *Di. multiappendiculata* and *Di. suae* share similar morphology, having cheiroid, ellipsoid to cylindrical, pale brown to brown conidia with hyaline, globose to subglobose appendages. However, *Di. alangii* differs from *Di. multiappendiculata* and *Di. suae* based on the number and location of appendages. *Dictyocheirospora multiappendiculata* has 1–6 subapical appendages, *Di. suae* has 1–3 subapical appendages, and sometimes two ellipsoid appendages are closer together on the same side of the conidia or both sides, whereas *Di. alangii* has only 1–2 appendages, one on each side of the conidia, and located in the central cells of the outer cell-row rather than near the apex. Therefore, *Di. alangii* is introduced as a new species based on morphology and phylogeny.



Note a–d Colonies on a woody sub-strate. e, f Squash mount of a sporodochium. g–i Conidia with partial conidiophores. j Co-nidium. k Squashed conidium. l, m Arms of conidia. n, o Colonies on PDA, from above (n), from below (o). Scale bars: e, f = 30 µm, g–m = 20 µm.

Figure 5.5 *Dictyocheirospora alangii* (HKAS 131314, holotype)

Dictyocheirospora rotunda M.J. D'souza, Bhat & K.D. Hyde, Fungal Diversity 80: 465 (2016) Figure 5.6

Index Fungorum number: IF551581; Faces of Fungi number: FoF01262

Saprobic on dead twigs of *Euonymus japonicus* Thunb. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate scattered, scattered and dark brown. *Mycelium* composed of immersed or partly superficial, pale brown, smooth, thin-walled hyphae. *Conidiophores* micronematous, pale brown, smooth-walled. *Conidiogenous cells* holoblastic, integrated, terminal, cylindrical to subglobose, hyaline to pale brown, smooth, and thin-walled. *Conidia* 45–53 × 17–23 μm ($\bar{x}$ = 50 × 21 μm, n = 50), solitary, acrogenous, cheiroid, pale brown to brown, consisting of 5–7 rows of cells, rows digitate, cylindrical, inwardly curved at the tip, arising from a basal cell, without appendages, with each row composed of 10–12 cells, euseptate.

Culture characteristics – Conidia germinated on PDA medium within 24 h. Germ tubes produced from both ends. Colonies on PDA reaching 10–20 mm diam. after two weeks. Mycelium superficial, with regular margins, white from above, and brown to yellowish in the middle zone from below, paler toward the margins.

Material examined – China, Guizhou Province, Guiyang City, Huaxi District, on dead twigs of medicinal plant *Euonymus japonicus*, 24 January 2021, Y.R. Sun, CL30YR (HUEST 24.0200), living culture UESTCC 24.0183; *ibid*., Sichuan Province, Chengdu City, Dujiangyan City, Qingcheng Mountain scenic spot, on dead twigs of medicinal plant *Prinsepia utilis*, 27 March 2022, R.R. Liang, 123rui (HUEST 23.0219), living culture UESTCC 23.0219.

Notes – Boonmee et al. (2016) introduced *Dictyocheirospora* with *D. rotunda* as the type species from decaying wood in Thailand. The new strains (UESTCC 23.0219 and UESTCC 24.0183) were collected from *Euonymus japonicus* and *Prinsepia utilis* in China. I identified my collections as *D. rotunda* (Figure 5.2) and report them as new host records from medicinal plants.



Note a–c Colonies on a woody substrate. d Squash mount of a sporodochium. e–h Conidia with partial conidiophores. i–l Conidia. m Germinated conidium. n,o Colonies on PDA, from above (n), from below (o). Scale bars: d = 50 µm, e–l = 30 µm, m = 20 µm.

Figure 5.6 *Dictyocheirospora rotunda* (HUEST 23.0219, new host record)

Neoxylochrysis N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: IF902299; Faces of Fungi number: FoF16018

Etymology – "*Neoxylochrysis*" refers to the resemblance of its conidial morphology to the genus *Xylochrysis*.

Saprobic on *Typha latifolia*. Sexual morph: Not observed. Asexual morph: *Conidiomata* semi-immersed or immersed, visible as black shiny dots on the host, subcuticular in origin, then becoming erumpent, subglobose, brown to black, uniloculate solitary to scattered, glabrous, ostiolate. *Ostiole* single, centrally or laterally located. *Conidiomatal wall* comprising 4–5 layers, hyaline to dark brown, thick-walled cells of *textura angularis* in the upper part, becoming pale brown, thin-walled at the base. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, determinate, discrete, smooth-walled, aseptate, cylindrical to subcylindrical, or ampulliform, hyaline. *Conidia* hyaline, aseptate or 1-euseptate, without constrictions at the septum, oval or oblong to cylindrical, with rounded or obtuse ends, smooth, thin-walled, often with 2–4 small guttules in each cell, without sheath or appendages.

Type Species – *Neoxylochrysis typhicola* (Kamolhan, Banmai, Boonmee, E.B.G. Jones and K.D. Hyde) N. Wu and Jian K. Liu.

Life Mode and Known Distribution – *Neoxylochrysis* is reported as a saprobe on submerged stems of *Typha latifolia* in freshwater habitat. The genus is presently known from UK (2016).

Notes – A new monospecific genus, *Neoxylochrysis*, is introduced herein to accommo- date an asexual species in Dictyosporiaceae, typified by *N. typhicola*, based on distinct morphology and multi-locus phylogenetic analysis. *Neoxylochrysis typhicola* was previously described as *Pseudocoleophoma typhicola* by Hyde et al. (2016) from submerged stems of *Typha latifolia* in freshwater environments from UK. *Neoxylochrysis* is phylogenetically related to *Pseudoconiothyrium* in the phylogenetic tree and formed an independent clade separated from *Pseudocoleophoma*. The asexual

morph of *Neoxylochrysis* differs from the members of *Pseudocoleophoma* by having small, hyaline, oval-shaped, smooth, thin-walled, septate conidia with rounded or obtuse ends and guttules in each cell (Table 5.1). Since the sexual morph of *Neoxylochrysis* has not been discovered, it is impossible to compare the sexual morphologies of *Neoxylochrysis* with that of *Pseudocoleophoma*. Therefore, a new genus, *Neoxylochrysis*, is introduced in Dictyosporiaceae to accommodate a single coelomycetous species, *N. typhicola*.

Neoxylochrysis typhicola (Kamolhan, Banmai, Boonmee, E.B.G. Jones & K.D. Hyde) N. Wu & Jian K. Liu, comb. nov. Figure 5.7

Index Fungorum number: IF902298; Faces of Fungi number: FoF16019

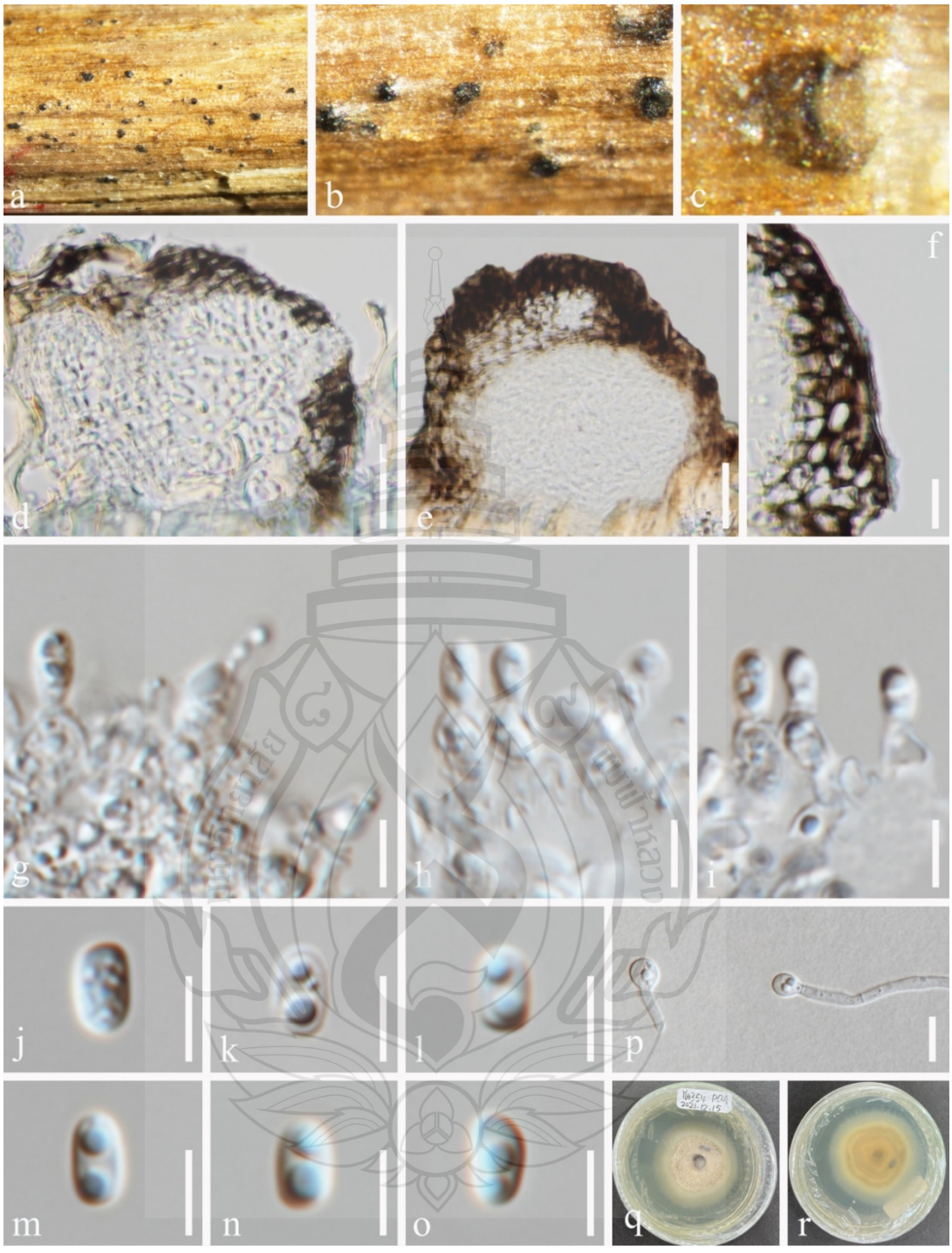
Basionym – *Pseudocoleophoma typhicola* Kamolhan, Banmai, Boonmee, E.B.G. Jones and K.D. Hyde, in Hyde et al., Fungal Diversity 80: 34 (2016) (2016)

Saprobic on host plants, such as *Rhaphiolepis indica* and *Typha latifolia*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 90–115 µm high × 130–150 µm diam. ($\bar{x}$ = 105 × 135 µm, n = 10), semi-immersed or immersed, visible as black shiny dots on the host, subcuticular in origin, then becoming erumpent, subglobose, brown to black, unilocular, glabrous, ostiolate. *Ostiole* 50–75 µm long, 70–100 µm wide, centrally or laterally located. *Conidiomatal wall* 20–25 µm wide ($\bar{x}$ = 23 µm, n = 20), comprising 4–5 layers, dark brown, thick-walled cells of textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–5.5 × 2–3 µm ($\bar{x}$ = 3.5 × 2.5 µm, n = 30), phialidic, smooth-walled, aseptate, hyaline. *Conidia* 7.5–11 × 2–3 µm ($\bar{x}$ = 10 × 2.5 µm, n = 30), hyaline, aseptate, oval, smooth, thin-walled, with 1(–2) guttules in each cell.

Culture characteristics – Conidia germinated on PDA within 12 h. Germ tubes produced from one end. Colonies on PDA reaching 30−35 mm diam. after two weeks at 25°C in natural light. Mycelium superficial, grayish white from above, pale brown at the center, and yellowish white at the margin from below.

Material examined – UK, Hampshire, Swanick Lakes, on submerged stems of Typha latifolia in freshwater habitat, 28 August 2015, E.B.G. Jones, GJ190 (MFLU 16-0966, hol-otype; HKAS 94520 isotype), ex-type living culture, MFLUCC 16-0123, KUMCC 16-0007; China, Guizhou Province, Panzhou City, Wetland Park, 104°29′14″ E, 25°39′33″ N, on dead twigs of *Rhaphiolepis indica* in terrestrial habitat, 21 July 2022, Na Wu, YW354 (HKAS 131316), living culture, CGMCC 3.25688 = UESTCC 23.0221.

Notes – In my phylogeny (Figure 5.2), *Neoxylochrysis typhicola* (CGMCC 3.25688, MFLUCC 16-0123) clustered with *Pseudocoleophoma puerensis* (ZHKUCC 22-0204, ZHKUCC 22-0205) and *Pseudoconiothyrium broussonetiae* (CBS 145036), forming an in-dependent clade in Dictyosporiaceae. This fungus was initially introduced by Hyde et al. (2016) from submerged stems of *Typha latifolia* in freshwater, based on morphology and ITS and LSU sequence data. *Neoxylochrysi typhicola* can be distinguished from the above closely related species based on ITS and LSU base pair differences from P. puerensis by 76/557 bp (13.6%) in ITS and 17/841 bp (2.0%) in LSU, and *P. broussonetiae* by 55/557 bp (9.9%) in ITS, 15/841 bp (1.8%) in LSU. *Neoxylochrysi* is similar to *Pseudoconiothyrium*, *Pseudocyclothyriella* and *Xylochrysis* in their asexual morphs. However, *Xylochrysis* belongs to Woswasiaceae, whereas *Neoxylochrysi* belongs to Dictyosporiaceae. The genus *Neoxylochrysi* differs from *Pseudoconiothyrium* and *Pseudocyclothyriella* in having conidia that are hyaline, oval or oblong to cylindrical, rounded or obtuse ends, smooth, thin-walled, often with 2–4 small guttules in each cell, aseptate or 1-euseptate, not constricted at the septum, and without a sheath or appendages (Table 5.2). The asexual morph of *P. puerensis* is undetermined and thus, the asexual morphologies of *P. puerensis* and *N. typhicola* could not be compared.



Note a–c Appearance of black conidiomata. d,e Vertical section of conidiomata. f Section of the peridium. g–i Conidiogenous cells and devel-oping conidia. j–o Conidia. p Germinated conidium. q,r Colony on PDA, from above (q), from below (r). Scale bars: d, e = 20 µm, f = 10 µm, g–o = 5 µm, p = 10 µm.

Figure 5.7 *Neoxylochrysis typhicola* (HKAS 131316)

Table 5.1 Comparison of asexual morphs in *Pseudocoleophoma*

Species	Morphology of Conidia	Conidiomata	Conidiogenous Cells	Conidia	References
P. bauhiniae		130–150 × 90–115 µm, immersed to superficial, subglobose, dark brown, multiloculate	2.5–5.5 × 2–3 µm, phialidic, hyaline, aseptate, doliiform to lageniform	7.5–11 × 2–3 µm, hyaline, oblong to ellipsoidal, aseptate, with guttules	Jayasiri et al. (2019)
P. calamagrostidis		(150–)250–500 × 220–300 µm, immersed to erumpent, depressed globose, glabrous	5–9 × 2–4 µm, hyaline, doliiform to subglobose	6–10 × 2–2.5 µm, hyaline, cylindrical, aseptate, with guttules at each end	Tanaka et al. (2015)
P. flavescens		20–140 µm diam., globose, glabrous or covered by hyphae, solitary or confluent	4–6 × 3–6 µm, globose to doliiform	4–7 × 2–3.5 µm, hyaline, ellipsoidal, aseptate, with 2 very large polar guttules	Boerema et al. (2004), Li et al. (2020)
P. polygonicola		170–250 µm diam., superficial, ampulliform, glabrous, uniloculate	7–17 × 3.5–5 µm, hyaline, aseptate, doliiform to lageniform	(9–)11.5–18(–21.5) × 3–4.5 µm, hyaline, cylindrical, aseptate	Tanaka et al. (2015)
P. rhapidis		150–225 × 225–300 µm, immersed, subglobose, black, uniloculate	7–10 × 13–17 µm, phialidic, hyaline, doliiform	20–25 × 10–15 µm, hyaline, oblong to obovoid, aseptate	Kularathnage et al. (2022)
P. rosae		100–184 × 98–215 µm, semi-immersed, solitary to gregarious, globose to subglobose, pyriform or irregular, unilocular	3–5 × 4–7 µm, phialidic, aseptate, smooth-walled, hyaline	6–9 × 2–4 µm, hyaline, aseptate, oblong to cylindrical, thin-walled, guttules concentrated at the ends	Wu et al. (2024)

Table 5.1 (continued)

Species	Morphology of Conidia	Conidiomata	Conidiogenous Cells	Conidia	References
P. rusci		130–200 × 250–330 µm, deeply immersed, globose, subglobose or ovoid, brown, glabrous, unilocular	4–9 × 3–7 µm, phialidic, enteroblastic, hyaline, doliiform, ampulliform to subcylindrical	8–14 × 3–6 µm, hyaline, cylindrical or fusiform, with a rounded apex and a slightly narrow truncate base	Li et al. (2020)
P. zingiberacearum		200–220 × 110–150 µm, immersed, multi-loculate, depressed globose, glabrous, non-ostiolate	1.5–2.5 × 1–1.5 µm, phialidic, doliiform to lageniform, hyaline, aseptate	12–14 × 2–3 µm, solitary, hyaline, aseptate, oblong to ellipsoidal, with rounded to obtuse ends, with guttules	Tennakoon et al. (2019)
Neoxylochrysis typhicola (*P. typhicola*)		60–100 × 140–150 µm, semi-erumpent, uniloculate solitary to scattered, subglobose	2–5 × 2–5 µm, enteroblastic, smooth-walled, hyaline	9–11 × 2–3 µm, hyaline, oblong to cylindrical, with rounded or obtuse ends, septate, guttulate	Hyde et al. (2016), Wu et al. (2024)

Table 5.2 Comparison of sexual morphs in *Pseudocoleophoma*

Species	Morphology of Ascospores	Ascomata	Asci	Ascospores	References
P. bauhiniae		100–120 × 125–145 µm, immersed, subglobose to obpyriform, dark brown, coriaceous	65–80 × 5–8 µm, 8-spored, clavate to cylindric-clavate, short-pedicellate with an ocular chamber	17–20 × 3.5–4.5 µm, hyaline, cylindric-fusiform, 1–3-septate, 3–4-guttulate, without appendages and sheath	Jayasiri et al. (2019)
P. calamagrostidis		160–220 × 140–200 µm, immersed, globose to depressed globose	62.5–80 × 7.5–10 µm, 8-spored, cylindrical, rounded at the apex, short-stalked	(14.5–)16–19(–21) × 3–4.5 µm, hyaline, fusiform, 1-septate, 3–4-guttulate, with an entire sheath	Tanaka et al. (2015)
P. polygonicola		280–350 × 230–310 µm, immersed to erumpent	(67–) 74–90 (–100) × 9–12.5 µm, cylindrical to clavate	(17.5–)19–23(–25) × 4–6 µm, hyaline, fusiform, 1-septate, 4–6-guttulate, surrounded by a sheath	Tanaka et al. (2015)
P. puerensis		150–300 × 170–220 µm, immersed to erumpent, brown to black, globose or subglobose	50–70 × 7–11 µm, 8-spored, cylindrical, long-stalked with club-like pedicel	10–15 × 3.5–6 µm, hyaline to brown, narrowly ellipsoid or oblong, 1–3 thick and dark eusepta, normally 4-guttulate, without a sheath	Lu et al. (2022)

Table 5.2 (continued)

Species	Morphology of Ascospores	Ascomata	Asci	Ascospores	References
P. rosae		170–220 × 170–220 µm, semi-immersed or immersed, dark brown, globose to subglobose, unilocular, glabrous, thick-walled, thickened at the apex, visible as black dots or papilla on the host	70–88 × 8–12 µm, 8-spored, cylindrical to clavate, some slightly curved, with an ocular chamber, short-stalked with club-shaped pedicel	12–21 × 3–6 µm, hyaline, smooth-walled, fusiform with acute ends, 1-septate, slightly constricted at the septum, and occasionally 2–4-guttulate when young, surrounded by a mucilaginous sheath	Wu et al. (2024)
P. yunnanensis		160–280 × 200–280 µm, semi-immersed to erumpent, dark brown to black, subglobose to obpyriform, solitary or scattered, coriaceous	65–90 × 8–11 µm, 8-spored, clavate to cylindrical, short-stalked with club-shaped pedicel	16–26 × 4–8 µm, hyaline, fusiform, 1-septate, 4-guttulate, with a distinct sheath	Lu et al. (2022)

Neomassariaceae H.A. H.A. Ariy., Jaklitsch & Voglmayr

Type genus – *Neomassaria* Mapook, Camporesi & K.D. Hyde

Notes – Neomassariaceae was established by Ariyawansa et al. (2018), with *Neomassaria* as the type genus (type species *N. fabacearum*). Morpho-phylogenetic evidence supported the acceptance of three genera in this family, *Neomassaria*, *Pigmentatineomassaria* and *Pseudoneohendersonia* (Wijesinghe et al., 2023; Yang et al., 2024). Members of Neomassariaceae are characterized by immersed to erumpent ascomata, 8-spored, bitunicate, oblong to cylindrical, pedicellate asci, and hyaline to brown, septate, ellipsoid to fusiform ascospores with or without a gelatinous sheath, and its asexual morphs are characterized by macronematous, mononematous, unbranched, brown conidiophores, and monoblastic, holoblastic, terminal, brown conidiogenous cells, and acrogenous, solitary, pale brown to brown, 4–30-septate, smooth-walled, obclavate conidia (Hyde et al., 2016; Ariyawansa et al., 2018; de Silva et al., 2022; Hu et al., 2022; Yang et al., 2022a, 2024; Wijesinghe et al., 2023; Zhang et al., 2024a; Wu et al., 2025).

Neomassaria Mapook, Camporesi & K.D. Hyde, Fungal Diversity 80: 74 (2016)

Type species – *Neomassaria fabacearum* Mapook, Camporesi & K.D. Hyde

Notes – Hyde et al. (2016) introduced the genus *Neomassaria* to accommodate a single species, *N. fabacearum*, and placed it in Massariaceae based on LSU and SSU sequence data. Subsequently, Ariyawansa et al. (2018) recognized the second *Neomassaria* species, *N. formosana*, and introduced the family Neomassariaceae to accommodate *N. fabacearum* and *N. formosana*. Currently, 13 epithets of *Neomassaria* are listed in Index Fungorum (2025, June). *Neomassaria* was known only from sexual morphs until Zhang et al. (2024a) introduced an asexual morph species, *N. thailandense*, collected from *Rhapis excelsa* in China. Wu et al. (2025) presented the first documentation of *Neomassaria* associated with *Camellia sinensis* and introduced two new asexual morph species, *N. camelliae* and *N. sichuanensis.*

Neomassaria camelliae Y.H. Lu, N. Wu, K.D. Hyde & Jian K. Liu, sp. nov. Figure 5.8

Index Fungorum Number: IF903742; Facesoffungi Number: FoF 17631

Etymology – The epithet '*camelliae*' refers to the host genus *Camellia* on which the holotype was collected.

Holotype – HKAS 131293

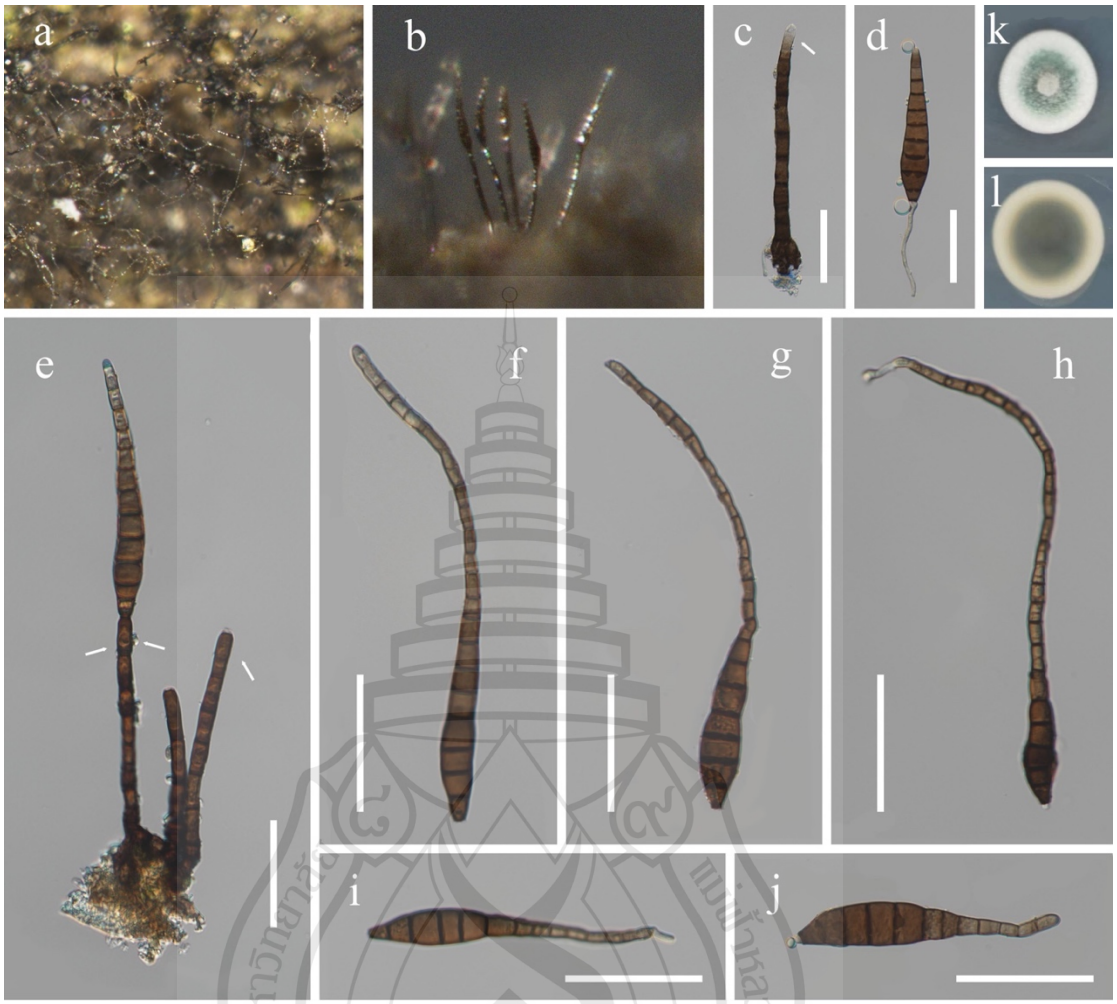
Saprobic on dead branches of *Camellia sinensis* (Theaceae) in a terrestrial habitat. Asexual morph: Hyphomycetous. *Colonies* on the substrates superficial, effuse, hairy, velvety, glistening, dark brown to dark. *Mycelium* mostly immersed, composed of septate, rough-walled, brown hyphae. *Conidiophores* 93–230 × 6–19 µm ($\bar{x}$ = 188 × 14 µm, n = 30) macronematous, mononematous, erect, solitary, straight or partly curved, cylindrical, rounded at the apex, rough-walled, 7–20-septate, unbranched, dark brown. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, cylindrical, pale brown, rounded and hyaline at the apex. *Conidia* 111–305 × 13–17 µm ($\bar{x}$ = 220 × 15 µm, n = 30), solitary, acrogenous, obclavate, rostrate, brown, paler towards the apex, 10–34-septate, smooth, thick-walled, with a long and slender apex, straight or partial curved, tapering to the apex, and with the proximal part usually verrucose. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes are produced from both ends. Colonies on PDA reaching 15 mm diam. after seven days 25°C, and about 32 mm diam. after two weeks, rough surface, with dense mycelia, dry, flat, from above light green to white, from below dark green with white mycelium of the outer ring.

Material examined – CHINA, Guizhou Province, Guiyang City, Huaxi County, 106°39'32"E, 26°30'43"N, elevation 1,150 m, on dead branches of *Camellia sinensis*, 2 February 2023, Y.X. Yu, GY37 (HKAS 131293, holotype), ex-type living culture CGMCC 3.25585; *ibid.*, Sichuan Province, Zigong City, Rongxian County, 104°22'23"

E, 29°47'11" N, elevation 570 m, on dead branches of *Camellia sinensis*, 3 November 2022, Y.H. Lu, CS01 (HUEST 23.0154, paratype), living culture UESTCC 23.0154.

Notes – In the phylogenetic analysis, two isolates of *Neomassaria camelliae* clustered closer to *N. sichuanensis* (CGMCC 3.25586 and UESTCC 23.0158) with 97% ML bootstrap and 0.99 BI statistical support (Figure 5.9). Morphologically, *N. camelliae* is a sporidesmium-like species (Liu et al., 2024) and similar to *N. sichuanensis* and *N. thailandica* in having macronematous, mononematous, brown, unbranched, septate conidiophores, monoblastic, terminal conidiogenous cells and septate, brown, obclavate conidia (Zhang et al., 2024). However, *N. camelliae* differs from *N. sichuanensis* and *N. thailandica* by its longer conidiophores (93–230 × 6–19 µm vs. 90–180 × 4–8 µm vs. 65–115 × 4.5–5 µm) and larger conidia (111–305 × 13–17 µm vs. 90–180 × 4–8 µm vs. 45–70 × 6.8–9 µm) (Zhang et al., 2024). Additionally, *N. camelliae* possesses 7–20-septate conidiophores and 10–34-septate conidia while *N. sichuanensis* possesses 9–15-septate conidiophores and 4–14-septate conidia, and *N. thailandica* possesses 3–7-septate conidiophores and 5–8-septate conidia. Furthermore, *N. camelliae* has proliferating rostrate structures with a long and slender apex. Therefore, I introduce *N. camelliae* as a new species.



Note a, b colonies on the host surface c conidiophores d germinating conidium e conidiophores with conidiogenous cells and conidia f–j conidia k, l surface and reverse colonies on PDA after 14 days of incubation at 25°C. Scale bars: c–j = 50 µm.

Figure 5.8 *Neomassaria camelliae* (HKAS 131293, holotype)

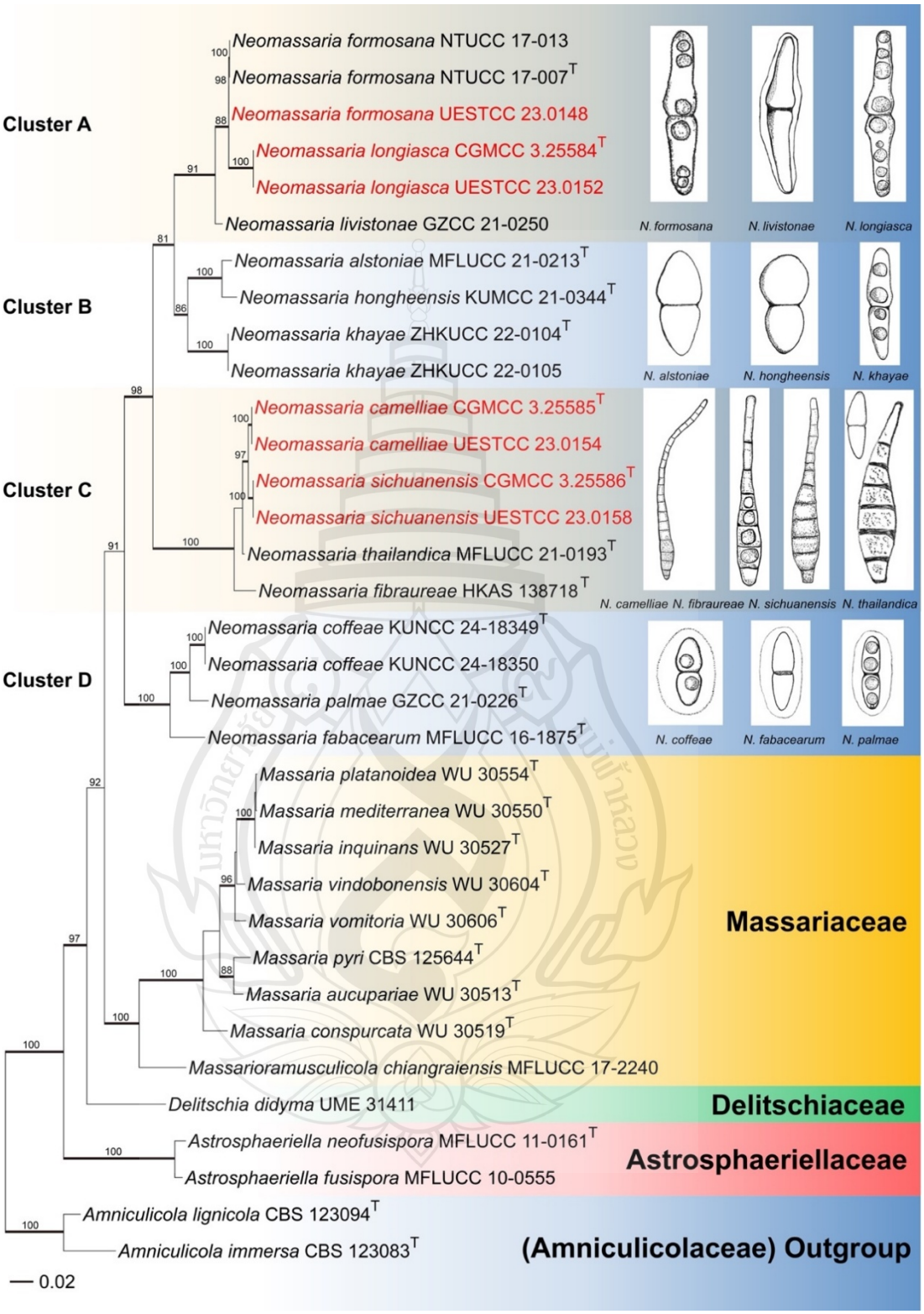


Figure 5.9 Phylogenetic tree based on the combined LSU, SSU, *tef1α* and *rpb2* sequences constructed by maximum likelihood (RAxML) of selected members of *Neomassaria*

Figure 5.9 The tree is rooted with *Amniculicola immersa* (CBS 123083) and *A*. *lignicola* (CBS 123094). Bootstrap values for maximum likelihood (ML) equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are thickened. The new isolates are indicated in red; "[T]" denotes ex-type strains. The illustrations of species in *Neomassaria* are displayed near the specific names.

Neomassaria formosana H.A. Ariyaw., Jaklitsch & Voglmayr, Cryptog. Mycol. 39(3): 368 (2018) Figure 5.10

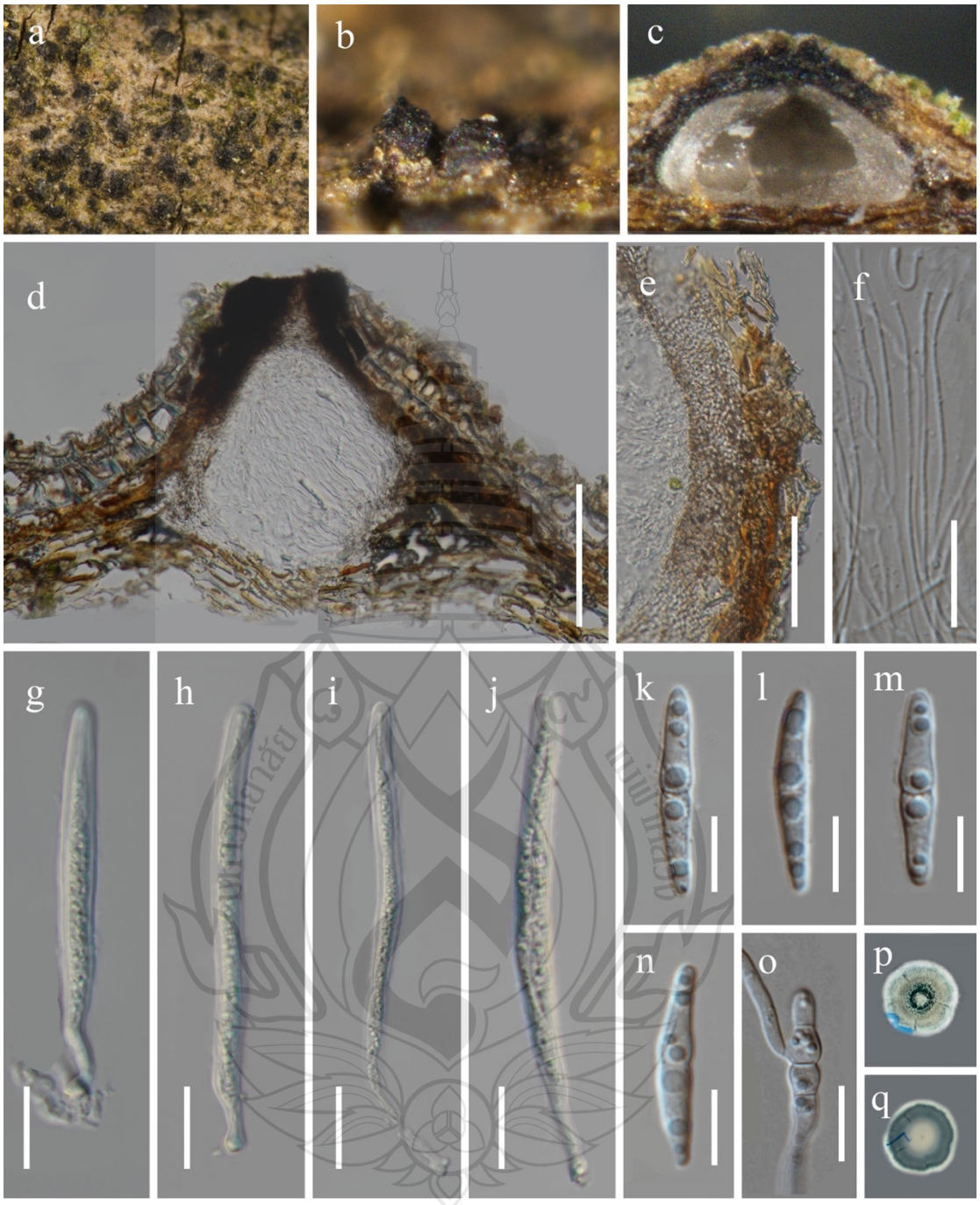
Index Fungorum Number: IF827114; Facesoffungi Number: FoF 17579

Saprobic on dead branches of *Camellia sinensis* (Theaceae) in a terrestrial habitat. Asexual morph: Undetermined. Sexual morph: *Ascomata* 130–280 µm high, 150–340 µm diam ($\bar{x}$ = 210 × 250 µm, n = 10), immersed, solitary or gregarious, globose to subglobose, black, visible as black dots on the host surface, with ostiole central. *Ostiole* 10–20 µm diam, papillate to depressed. *Peridium* 5–20 µm wide, with multi-layers, comprising hyaline to brown cells of *textura angularis*. *Hamathecium* 0.5–1.1 µm wide, composed of numerous, hyaline, filamentous, septate, branched, cellular pseudoparaphyses surrounding the numerous asci. *Asci* 70–115 × 6–10 µm ($\bar{x}$ = 95 × 8 µm, n = 30), 8-spored, bitunicate, cylindrical or clavate, pedicellate, apically rounded, with a short pedicel. *Ascospores* 15–30 × 3–5 µm ($\bar{x}$ = 24 × 4 µm, n = 30), overlapping, fusiform to ellipsoid, hyaline, straight or slightly flexuous, 1–3-septate, slightly constricted at the septa, tapering from the middle to both ends, without sheath, mature ascospores contain 2–4 distinctly refractive oil globules.

Culture characteristic – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies on PDA reaching 10 mm diam. after seven days 25°C, and about 35 mm diam. after three weeks, circular, umbonate, radially striate, with a slightly lobate edge; surface smooth, with cottony texture, green to light green or grey white, reverse dark green expanding from the center.

Material examined – CHINA, Sichuan Province, Yaan City, Mingshan County, Mengding Mountain, 103°2'23"E, 30°4'32"N, elevation 1,200 m, on dead branches of *Camellia sinensis,* 16 July 2023, Y.H. Lu MD36 (HUEST 23.0148), living culture UESTCC 23.0148.

Notes – *Neomassaria formosana* was introduced by Ariyawansa et al. (2018) from dead stems of *Rhododendron* sp. in Taiwan Province, China. My collection is extremely similar with *N. formosana* in its sexual morph. The phylogeny inferred using analysis of LSU, SSU, *tef1α* and *rpb*2 sequence data showed that my isolate (UESTCC 23.0148) clustered with *N. formosana* (NTUCC 17-007 and NTUCC 17-013) with 98% ML bootstrap and 0.99 BI posterior probability support (Figure 5.9).Therefore, I identified my collection as *N. formosana* based on morphology and phylogeny. This is the first record of *N. formosana* found on *Camellia sinensis* in China.



Note a–c ascomata on the host surface d vertical section of ascoma e peridium f hamathecium g–j asci k–n ascospores. o germinating ascospore. p, q surface and reverse colonies on PDA after 14 days of incubation at 25 °C. Scale bars: d = 100 µm, e = 50 µm,f–j = 20 µm, k–o = 10 µm.

Figure 5.10 *Neomassaria formosana* (HUEST 23.0148, new host record)

Neomassaria longiasca Y.H. Lu, N. Wu, K. D. Hyde & Jian K. Liu, sp. nov. Figure 5.11

Index Fungorum Number: IF903741; Facesoffungi Number: FoF 17632

Etymology – The epithet '*longiasca*' refers to the long asci.

Holotype – HKAS 131292

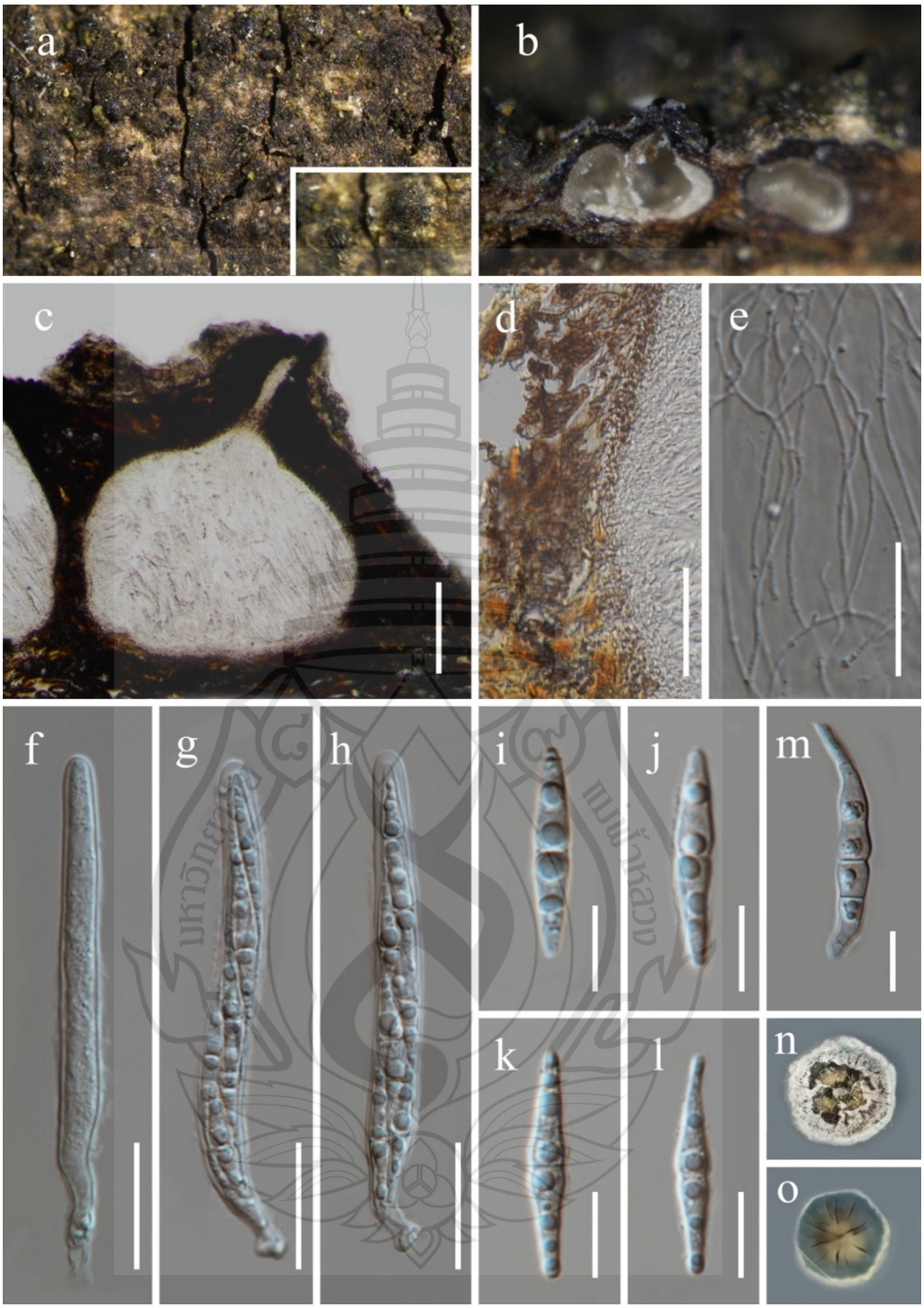
Saprobic on dead branches of *Camellia sinensis* (Theaceae) in a terrestrial habitat. Asexual morph: Undetermined. Sexual morph: *Ascomata* 240–420 μm high, 150–370 μm diam ($\bar{x}$ = 297 × 245 μm, n = 10), immersed, solitary or gregarious, globose to collabent, visible as small black spots on host surface, dark brown to black, rough walled, white interior, with ostiole central. *Ostiole* 5.5–20 μm diam. *Peridium* 6.5–15 μm wide, composed of 2–3 layers of brown cells of *textura angularis*. *Hamathecium* 0.6–1.3 μm, composed of numerous, hyaline, filamentous, branched, without septa, cellular pseudoparaphyses. *Asci* 70–125 × 6–10 μm ($\bar{x}$ = 100 × 8 μm, n = 30), 8-spored, fissitunicate, bitunicate, cylindrical or clavate, apically rounded, with a short pedicel. *Ascospores* 16–30 × 3–5 μm ($\bar{x}$ = 23 ×4 μm, n = 30) overlapping, fusiform to ellipsoid, hyaline, straight, many guttules when immature, 1-septate, without sheath, when mature, narrowly rounded to nearly acute at the ends and 4–8 distinctly refractive oil globules.

Culture characteristic – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA, reaching 5 mm diam. after seven days 25°C, and about 20 mm diam. after three weeks, circular, umbonate, radially striate, with slightly lobate edge; surface rough and broken, with liquid texture, grey white, reverse dark green expanding from the center.

Material examined – CHINA, Sichuan Province, Yaan City, Mingshan County, Mengding Mountain, 103°2'20"E, 30°4'35"N, elevation 1,250 m, on dead branches of *Camellia sinensis*, 16 July 2023, Y.H. Lu, KY03 (HKAS 131292, holotype), ex-type living culture CGMCC 3.25584; *ibid.*, Guizhou Province, Guiyang City, Huaxi County,

106°39'32"E, 26°30'43"N, elevation 1,150 m, on the branches of *Camellia sinensis*, 02 February 2023, Y.X. Yu, KY13 (HUEST 23.0152, paratype), living culture UESTCC 23.0152.

Notes – *Neomassaria longiasca* morphologically fits into the generic concept of *Neomassaria* by having immersed ascomata with ostiole, peridium comprising cells of *textura angularis*, and 8-spored, bitunicate, oblong to cylindrical, pedicellate asci, containing 1-septate, hyaline, ellipsoid to fusiform ascospores, without a mucilaginous sheath (Ariyawansa et al., 2018; Yang et al., 2022). In the phylogenetic analysis, *N. longiasca* (CGMCC 3.25584 and UESTCC 23.0152) was positioned as a sister taxon to *N. formosana* (NTUCC 17-007 and NTUCC 17-013) with 88% ML bootstrap and 1.00 BI posterior probability support (Figure 5.9). However, *N. longiasca* differs from *N. formosana* in having thin-walled (6.5–15 µm vs. 13–40 µm) and larger ascomata (240–420 × 150–370 µm vs. 100–370 × 100–200 µm). Additionally, the ascospores of *N. longiasca* are straight and slightly constricted at the septum, while in *N. formosana*, they are slightly curved and deeply constricted at the septum. Therefore, *N. longiasca* is introduced as a new species based on morphology and phylogeny.



Note a, b ascomata on the host surface c vertical section of an ascoma d peridium e hamathecium f–h asci i–l ascospores m germinating ascospore n, o surface and reverse colonies on PDA after 14 days of incubation at 25 °C. Scale bars: c = 100 µm, d = 50 µm, e–h = 20 µm, i–m = 10 µm.

Figure 5.11 *Neomassaria longiasca* (HKAS 131292, holotype)

Neomassaria sichuanensis Y.H. Lu, N. Wu, K. D. Hyde & Jian K. Liu, sp. nov. Figure 5.12

Index Fungorum Number: IF903740; Facesoffungi Number: FoF 17633

Etymology – The epithet '*sichuanensis*' refers to Sichuan Province where the fungus was collected.

Holotype – HKAS 131294

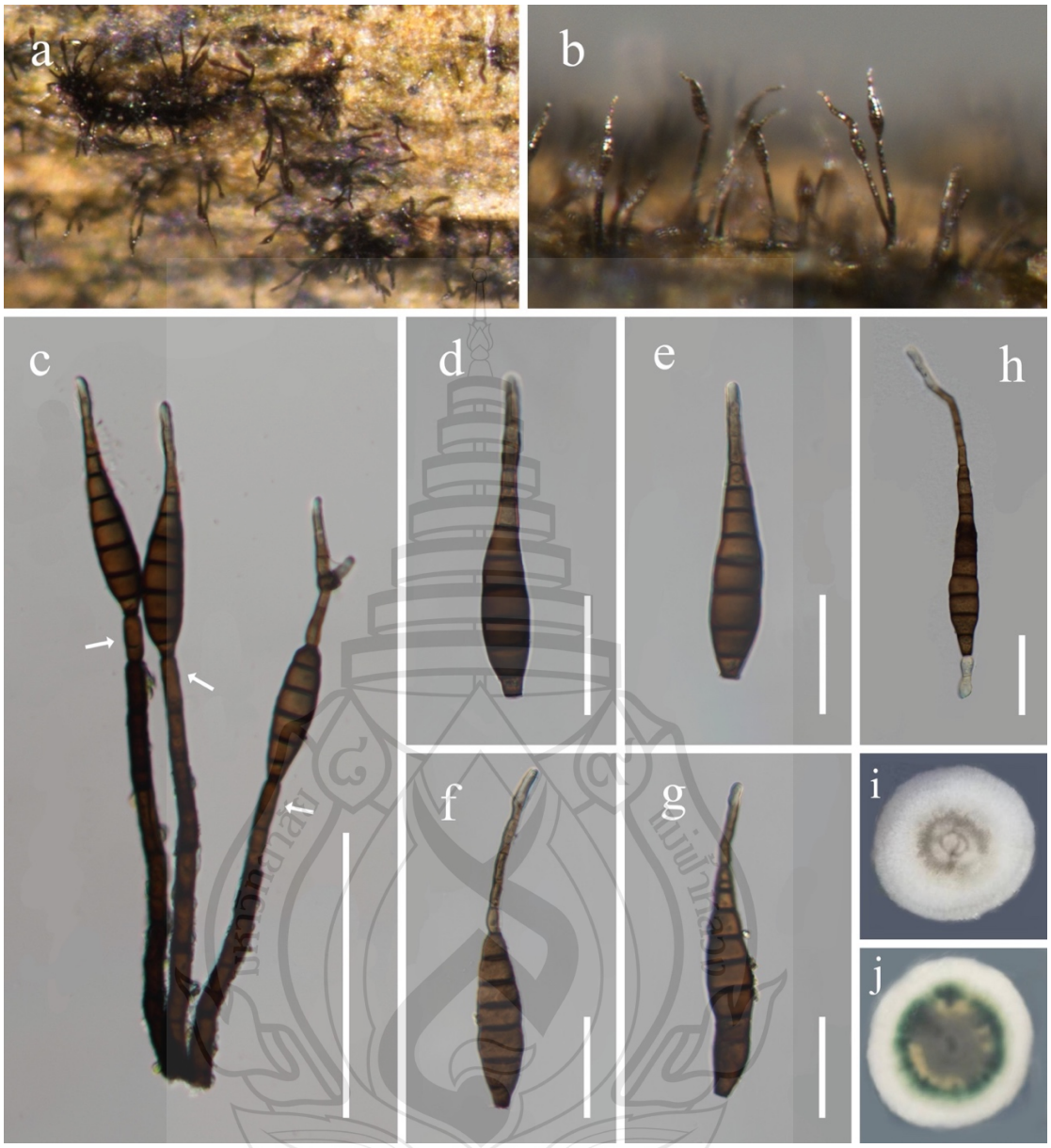
Saprobic on dead branches of *Camellia sinensis* (Theaceae) in a terrestrial habitat. Asexual morph: Hyphomycetous. *Colonies* on natural substrates superficial, effuse, dark brown, hairy, glistening, scattered or in small groups. *Mycelium* partly immersed, partly superficial, composed of septate, smooth-walled, dark brown hyphae. *Conidiophores* 90–180 × 4–8 μm ($\bar{x}$ = 120 × 6 μm, n = 30) macronematous, mononematous, solitary, erect, cylindrical, rounded at the apex, straight or flexuous, 9–15-septate, mostly unbranched, dark brown, smooth-walled. *Conidiogenous cells* monoblastic, terminal, integrated, determinate, cylindrical, pale brown, rounded and darkened at the apex. *Conidia* 70–190 × 9–20 μm ($\bar{x}$ = 105 × 14 μm, n = 30), acrogenous, obclavate, rostrate, brown or mid brown, paler towards the apex, 4–14-septate, smooth-walled, truncate and darkened at the base. Sexual morph: Undetermined.

Culture characteristic – Conidia germinated on PDA within 24 h, and germ tubes produced from both ends. Colonies growing on PDA, reaching 3 mm diam. after seven days 25℃, and about 40 mm diam. after three weeks, circular, umbonate; surface smooth, with cottony texture, grey white; reverse light green expanding from the center, white mycelium of the outer ring.

Material examined – CHINA, Sichuan Province, Leshan City, Muchuan County, Lijiashan, 103°83'30" E, 28°89'14" N, elevation 1,109 m, on dead branches of *Camellia sinensis*, 4 November 2022, Y.H. Lu, L20A (HKAS 131294, holotype); ex-holotype living culture CGMCC 3.25586); *ibid.*, Zigong City, Rongxian County, 104°22'23" E,

29°47'11" N, elevation 570 m, on dead branches of *Camellia sinensis*, 3 November 2022, Y.H. Lu, L25 (HUEST 23.0158, paratype), living culture UESTCC 23.0158.

Notes – In the phylogenetic analysis, *Neomassaria sichuanensis* (CGMCC 3.25586 and UESTCC 23.0158) grouped with *N. camelliae* (CGMCC 3.25585 and UESTCC 23.0154) and *N. thailandica* (MFLUCC 21-0193), and formed a distinct branch within *Neomassa* with 97% ML bootstrap and 0.99 BI posterior probability support (Figure 5.9). The sexual morph of *N. thailandica* was originally isolated from dead twigs of *Anomianthus dulcis* in Thailand (de Silva et al., 2022), while its asexual morph was collected from decaying rachides of *Rhapis excelsa* (Zhang et al., 2024). *Neomassaria sichuanensis* resembles the asexual morph of *N. thailandica* in morphology, possessing macronematous, mononematous, cylindrical, unbranched conidiophores and brown, rostrate, septate, obclavate conidia. However, the conidia of *N. sichuanensis* are comparatively larger (70–190 × 9–20 µm vs. 45–70 × 6.8–9 µm), smooth, aguttulate, and constricted at the septa, whereas in *N. thailandica* they are verruculose, guttulate but not constricted at the septa. Additionally, conidia of the former have 4–14 transverse septa, while the latter often reaches 5–8. I therefore treat it in *Neomassaria* as a new species *N. sichuanensis*, based on the morphological and phylogenetic evidence.



Note a, b Colonies on the host surface. c Conidiophores with conidiogenous cells and conidia. d–g Conidia h germinating conidium. i, j Surface and reverse colonies on PDA after 14 days of incubation at 25 °C. Scale bars: c = 100 µm,d–h = 40 µm.

Figure 5.12 *Neomassaria sichuanensis* (HKAS 131294, holotype)

Torulaceae Corda

Type genus – *Torula* Pers.

Notes – Torulaceae was initially established by Sturm (1829) to accommodate the type genus *Torula*, which is only known by its asexual morph. Crous et al. (2015) confirmed its familial placement within Pleosporales and accepted two genera, *Dendryphion* and *Torula*, in the family based on multilocus phylogeny and morphology (Su et al., 2016, 2018; Li et al., 2017; Boonmee et al., 2021). To date, seven genera have been accepted in Torulaceae according to the latest outline by Hyde et al. (2024). This family is 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 arranged in branched chains (Crous et al., 2014, 2015; Hyde et al., 2016; Li et al., 2016; Su et al., 2016, 2018). Members of Torulaceae are distributed worldwide, and most taxa are saprobic, found on dead or decaying wood in freshwater and terrestrial habitats (Crous et al., 2015; Su et al., 2016, 2018; Li et al., 2017; Pratibha & Prabhugaonkar, 2017; Hyde et al., 2020; Boonmee et al., 2021).

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

Type species – *Torula herbarum* (Pers.) Link

Notes – *Torula* was initially introduced by Persoon (1794) and is typified by *T. herbarum*, which was accepted within Torulaceae by Crous et al. (2015) based on multilocus phylogenetic analysis. This genus is primarily characterized by cupulate conidiogenous cells produced in branched chains, as well as subglobose, verrucose, septate conidia (Crous et al., 2015; Crane & Miller, 2016; Hyde et al., 2016; Su et al., 2018). Species of *Torula* are found on a wide range of hosts and are widely distributed in both terrestrial and freshwater habitats worldwide (Su et al., 2018; Hyde et al., 2020; Boonmee et al., 2021). In recent years, the number of species of *Torula* has gradually increased with the continuous discovery of new species and records (Li et al., 2023;

Wang et al., 2023; Dong et al., 2023; He et al., 2024; Tian et al., 2024; Zhang et al., 2024b). However, studies on species from this genus occurring on medicinal plants are limited.

Torula chinensis W.H. Tian, Y.Peng Chen & Maharachch., J. Fungi 9(2, no. 150): 4 (2023) Figure 5.13

Index Fungorum number: IF 847014

Synonym – *Torula phytolaccae* Y.X. Li, C.F. Liao & Doilom, Phytotaxa 584(1): 9 (2023)

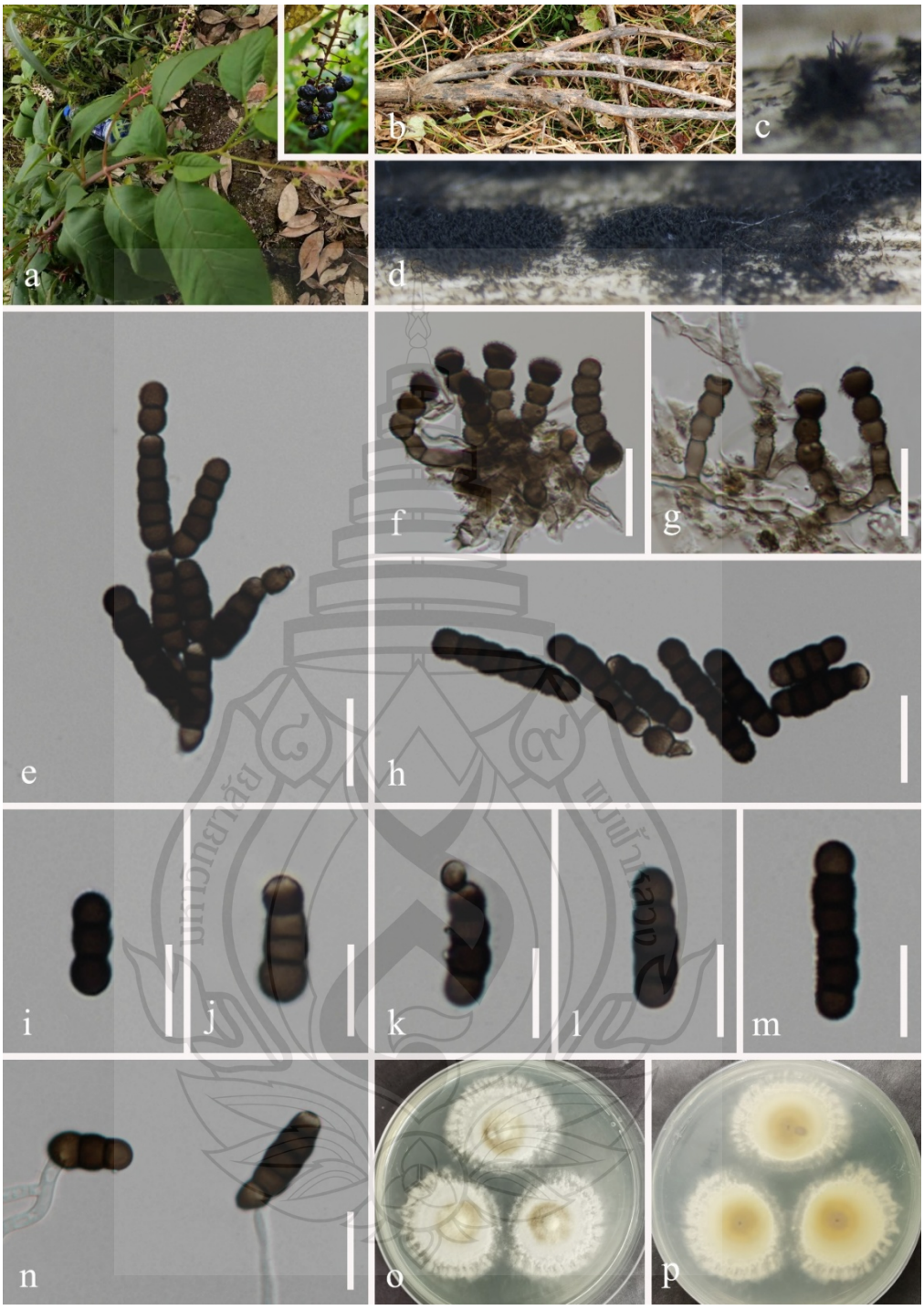
Saprobic on dead branches of *Phytolacca americana* L. (Phytolaccaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, dense, velvety, scattered, hairy, dark brown to black, dry. *Mycelium* immersed to superficial on the substrate, septate, branched, smooth to minutely verruculose, brown. *Conidiophores* 10–28 × 3–6 μm ($\bar{x}$ = 20 × 5 μm, n = 20), micronematous to semi-macronematous, mononematous, flexuous, unbranched, verruculose, thick-walled, doliiform to subcylindrical, consisting of 1–3 cells or reduced to conidiogenous cells, smooth, straight, or slightly flexuous, pale brown to brown. *Conidiogenous cells* 4–7 × 5–8 μm ($\bar{x}$ = 5 × 5.5 μm, n = 20), mono- or polyblastic, integrated, lateral to terminal, dark brown to black, verruculose, thick-walled, doliiform to cupulate. *Conidia* (16–) 22–35 (–65) × 5–9 μm ($\bar{x}$ = 29 × 7 μm, n = 30), solitary to catenate, acrogenous, simple, phragmosporous, straight or slightly curved, dark brown to black, verrucose, predominantly 3–5-septate, rounded at both ends, mostly subcylindrical, composed of subglobose cells, thick-walled, constricted at the septa, subhyaline to pale brown at the apex.

Culture characteristics – Conidia germinated on the PDA within 24 h, and germ tubes are produced from the basal cells. Colonies growing on PDA reached 30–33 mm in diam. after three weeks at 25°C in the dark. Colonies from above are medium dense, regular, white aerial mycelium slightly raised, fluffy, filiform, pale greenish-grey in the

center, white hairy at the margin; in reverse, pale yel- low at the center, off-white at the margin, the color gradually lightens from the center to the edge, without pigment produced in PDA.

Material examined – China, Guizhou Province, Guiyang City, Huaxi District, 26°30'41"N, 106°39'23"E, elevation 1,126 m, on dead branches of *Phytolacca americana* (Phytolaccaceae), 24 January 2021, Hong-Zhi Du, S62 (HUEST 24.0247), living culture UESTCC 24.0234.

Notes – *Torula chinensis* was introduced by Tian et al. (2023) from unidentified dead woody substrates and formally published on 22 January 2023. Around the same time, *T. phytolaccae* was described by Li et al. (2023) from dead stems of *Phytolacca acinosa* and published on 9 February 2023. In my phylogenetic tree (Figure 5.14), my collection (UESTCC 24.0234) and *T. phytolaccae* (ZHKUCC 22- 0107 and ZHKUCC 23-0884) clustered together with the ex-type strain (UESTCC 22.0085) of *T. chinensis*. Comparisons of nucleotides between *T. chinensis* (UESTCC 22.0085) and *T. phytolaccae* (ZHKUCC 22-0107, ex-type strain) showed 100% similarity (534/534 bp, without gaps) in ITS, 99.9% (803/804 bp, without gaps) in LSU, and 99.4% (810/815 bp, without gaps) in SSU. Additionally, my collection (UESTCC 24.0234) shows 100% similarity to *T. chinensis* in the ITS, LSU, and SSU gene regions. Therefore, following the guidelines of Jeewon and Hyde (2016), I synonymized *T. phytolaccae* under *T. chinensis*, identified my collection as *T. chinensis*, and reported it as a new host record from the medicinal plant *Phytolacca americana* in Guizhou Province, China.



Note a Host: *Phytolacca americana*. b Branches of *P. americana*. c, d Colonies on the host surface. e, h−m Conidia. g Conidiophores, conidiogenous cells, and conidia. n Germinated conidium. o, p Colonies on PDA, above (o) and below (p). Scale bars: e, f = 50 μm, g = 20 μm, h−n = 15 μm.

Figure 5.13 *Torula chinensis* (HUEST 24.0247, new host record)

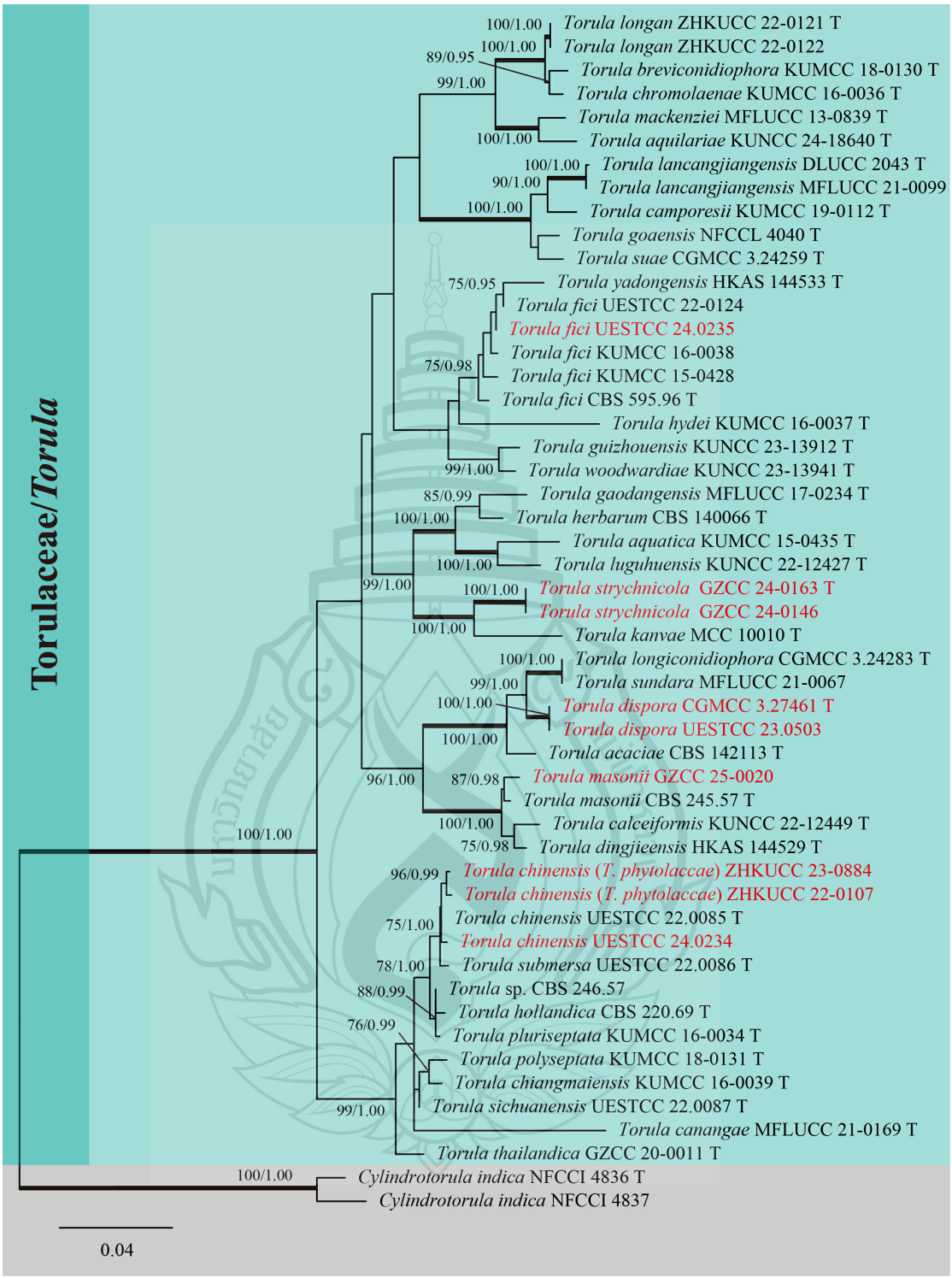


Figure 5.14 Phylogenetic tree constructed from maximum likelihood (RAxML) analysis based on the combined ITS, LSU, SSU, *tef1α*, and *rpb2* sequence data for selected members of *Torula* (Torulaceae)

Figure 5.14 The tree was rooted with *Cylindrotorula indica* (ex-type strain NFCCI 4836 and NFCCI 4837). Branch support for ML equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below branches as MLBS/BIPP. The abbreviation 'T' indicates the ex-type strain. Species names and culture collections in red are newly collected taxa and synonymized isolates.

Torula dispora H.Z. Du, N. Wu, K.D. Hyde & Jian K. Liu, sp. nov. Figure 5.15

Index Fungorum number: IF855436

Etymology – The epithet '*dispora*' refers to the host genus *Disporum* from which the fungus was originally isolated.

Holotype – HKAS 132495

Saprobic on dead twigs of *Disporum cantoniense* (Loureiro) Merrill (Liliaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, scattered, hairy, dark brown to black, dry. *Mycelium* mostly immersed, hyaline, septate, branched hyphae. *Conidiophores* 15–40 × 4–6 µm ($\bar{x}$ = 32 × 5 µm, n = 20), micronematous to semi-macronematous, subcylindrical, erect, septate, smooth, straight, or slightly flexuous, brown to dark brown. *Conidiogenous cells* 5–8 × 4–5 µm ($\bar{x}$ = 7 × 4.5 µm, n = 20), monoblastic, integrated, terminal, subglobose or spherical to coronal, brown to dark brown. *Conidia* two types; short *conidia* 16–35 × 5–9 µm ($\bar{x}$ = 27 × 7 µm, n = 30), acrogenous, phragmosporous, branched in chains with subglobose cells, dry, brown to dark brown, subhyaline at the terminal cell, 4–9-septate, constricted at septa, and the central cells larger than end cells, verrucose, easily separating, with spinulose on the substrate; long *conidia* 178–389 × 4–6 µm ($\bar{x}$ = 256 × 5 µm, n = 30), acrogenous, phragmosporous, dry, straight to flexuous, pale brown to brown, terminal cell subhyaline, 20–40-septate, constricted at septa, verrucose, easily separating, fusiform to ellipsoidal cells and uniform in size.

Culture characteristics – Conidia germinated on the PDA within 24 h, and germ tubes are produced from the basal cell. Colonies growing on PDA reached 45–48 mm in diam. after three weeks at 25°C in the dark. Colonies from above irregular, mycelium slightly raised, fluffy, filiform, white aerial hyphae at the surface, spreading from the center, and hyaline mycelium at the edge; in reverse, brown to dark-brown in the center, with grayish white at the edge, the color gradually lightens from the center to the edge.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Qingcheng Mountain scenic spot, 30°55'9"N, 103°28'36"E, elevation 1,185 m, on dead twigs of *Disporum cantoniense* (Liliaceae), 27 March 2021, H.Z. Du, S173 (HKAS 132495, holotype), ex-type living culture CGMCC 3.27461; *ibid*., S82 (HUEST 23.0504), living culture UESTCC 23.0503.

Notes – Multi-locus phylogeny (Figure 5.14) showed that *Torula dispora* (CGMCC 3.27461 and UESTCC 23.0503) clustered together with *T. longiconidiophora* (CGMCC 3.24283) and *T. sundara* (MFLUCC 21-0067) with high support (99% MLBS/1.00 BIPP), forming a distinct lineage. Morphologically, *T. dispora* (HKAS 132495, holotype) is similar to *T. longiconidiophora* and *T. sundara* in having micronematous to semi-macronematous conidiophores, terminal, subglobose or spherical to coronal conidiogenous cells, and two types of conidia (short and long) forming in chains (Jayawardena et al., 2022; Tian et al., 2023). However, *T. dispora* (HKAS 132495, holotype) can be distinguished from *T. longiconidiophora* and *T. sundara* by the spinulose characteristics on the conidial substrate (Jayawardena et al., 2022; Tian et al., 2023). In addition, *T. dispora* differs from *T. sundara* by its smaller short-type conidia (16–35 × 5–9 μm vs. 41–60 × 9–15 μm) and fewer septa in conidia (20–40 vs. up to 50) (Jayawardena et al., 2022). The nucleotide base pair comparison between *T. dispora* (CGMCC 3.27461, ex-type strain) and *T. sundara* (KUNCC 22-12399) revealed 10/509 bp (2.0%, 2 gaps) in ITS, 16/900 bp (1.8%, 4 gaps) in *tef1α*, and 24/885 bp (2.7%, without gaps) in *rpb*2 differences (He et al., 2024), while

T. dispora (CGMCC 3.27461) can be distinguished from *T. longiconidiophora* (CGMCC 3.24283, ex-type strain) by 11/519 bp (2.1%, 3 gaps) in ITS and 33/982 bp (3.3%, without gaps) in *rpb2* sequence data (Tian et al., 2023). Therefore, based on the morphological and phylogenetic evidence (Jeewon & Hyde, 2016), *T. dispora*, associated with the medicinal plant *Disporum cantoniense*, is introduced as a new species from Sichuan Province, China.



Note a Host: *Disporum cantoniense*. b Twigs of *D. cantoniense*. c, d Colonies on the host surface. e–h Conidiophores with conidia. i Conidiophores with conidiogenous cells. j–n Conidia. o, p Colonies on PDA, above (o) and below (p). Scale bars: e, f = 50 μm, g = 20 μm, h–n = 15 μm.

Figure 5.15 *Torula dispora* (HKAS 132495, holotype)

Torula fici Crous [as '*ficus*'], IMA Fungus 6 (1): 192 (2015) Figure 5.16

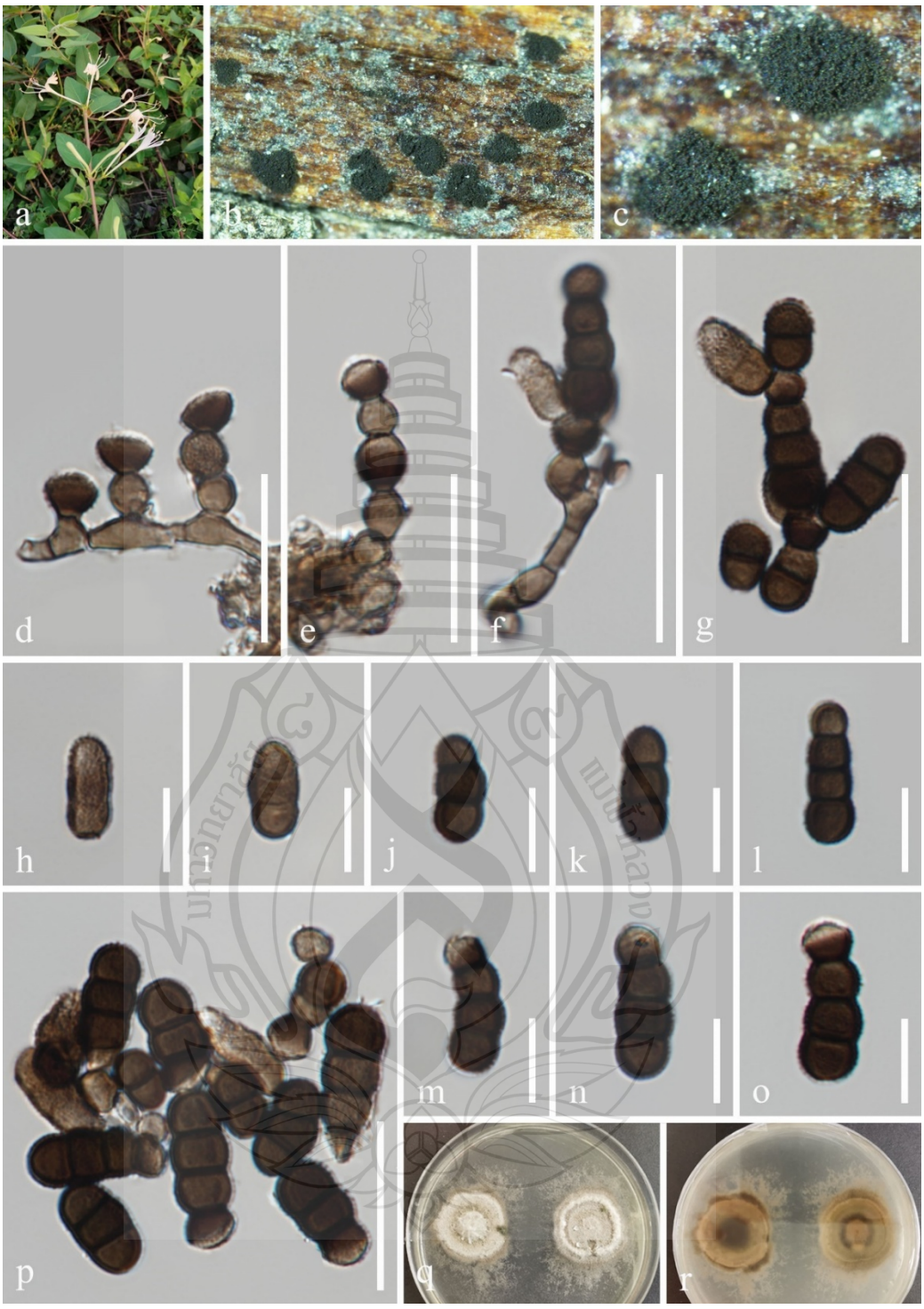
Index Fungorum number: MB 816154

Saprobic on the dead vines of *Lonicera japonica* Thunb. (Caprifoliaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, scattered, black, clustered on substrates. *Mycelium* slightly immersed, septate, branched, smooth, with pale brown hyphae. *Conidiophores* arising from prostrate hypha, 4–6 μm wide, macronematous to semi-macronematous, mononematous, solitary, erect, thick-walled, erect, straight, or slightly flexuous, without apical branches, pale brown to brown, ellipsoid to subcylindrical, smooth, septate. *Conidiogenous cells* 5.5–6.5 × 4.8–5.5 μm ($\overline{x}$ = 6 × 5 μm, n = 20), mono- to polyblastic, integrated, terminal, thick-walled, doliiform to subglobose, brown to dark brown. *Conidia* 8–19 × 5–7 μm ($\overline{x}$ = 15 × 6 μm, n = 30) phragmosporous, solitary to catenate, acrogenous, pale brown, aseptate or indistinctly septate at immature stage, becoming brown to dark brown at maturity, composed of subglobose cells, apical cell often pale brown, rounded at both ends, mostly 2–4-septate, constricted at the septa, minutely verruculose, easily separating.

Culture characteristics – Conidia germinated on the PDA within 24 h, and germ tubes are produced from the basal cell. Colonies growing on PDA reached 35–40 mm in diam. after three weeks at 25°C in the dark, mycelium partly immersed to superficial, slightly effuse, hairy, with a regular edge, pink or pale brown. Colonies from above, circular with an irregular edge, white aerial mycelium slightly raised, medium dense, fluffy, filiform, spreading from the center and hyaline mycelium at the edge; in reverse, pale brown to brown in the center, with off-white at the edge.

Material examined – CHINA, Sichuan Province, Chengdu City, Xindu District, Xinfan Street, 104°4′49″E, 30°50′51″N, elevation 549 m, on dead vines of *Lonicera japonica* (Caprifoliaceae), 22 July 2021, H.Z. Du, D10 (HUEST 24.0248), living culture UESTCC 24.0235.

Notes – *Torula fici* was introduced by Crous et al. (2015) as a hyphomycetous asexual morph species found on *Ficus religiosa* in Cuba. It is a widespread species, mostly reported in China and Thailand, and has been collected from various hosts, including *Ananas comosus*, *Chromolaena odorata*, *Cocos nucifera*, *Garcinia* sp., *Magnolia grandiflora*, *Mangifera indica*, *Musa* sp. and *Pandanus* sp. (Jayasiri et al., 2019; Jayawardena et al., 2022; Tian et al., 2024; Zhang et al., 2024). Based on the phylogenetic analysis (Figure 5.14), my collection (UESTCC 24.0235) clustered with *T. fici* (CBS 595.96, KUMCC 16-0038, KUMCC 15-0428 and UESTCC 22.0124). The morphology of my collection matches well with the type material of *T. fici*, which was characterized by doliiform to subglobose or clavate conidiogenous cells and brown or dark brown, phragmosporous, verruculose, branched chains and septate conidia (Crous et al., 2015). Therefore, I identified my new collection as *T. fici* and reported its association with the medicinal plant *Lonicera japonica* in Sichuan Province, China for the first time.



Note a Host *Lonicera japonica*. b, c Colonies on the host surface. d−f Conidiophores and conidiogenous cells. g−o Conidia. q, r Colonies on PDA, above (q) and below (r). Scale bars: d−g, p = 20 µm, h−o = 10 µm.

Figure 5.16 *Torula fici* (HUEST 24.0248, new host record)

Torula masonii P.W. Crous, IMA Fungus 6 (1): 192 (2015) Figure 5.17

Index Fungorum number: IF 812806

Saprobic on dead branches of *Gardenia jasminoides* J. Ellis (Rubiaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, scattered, hairy, velvety, dark brown to black. *Mycelium* immersed or superficial, composed of septate, branched, dark brown to black hyphae. *Conidiophores* 2–4 µm wide, macronematous to semi-macronematous, septate, erect, straight or slightly flexuous, brown to dark brown, subcylindrical to subglobose, thick-walled, with 1–2 doliiform to globose cells. *Conidiogenous cells* 6–9 × 5–8 µm ($\overline{x}$ = 7.5 × 6.5 µm, n = 20), polyblastic, terminal or intercalary, dark brown to black, doliiform to subglobose, smooth to verruculose, thick-walled. *Conidia* 20–60 × 4–9 µm ($\overline{x}$ = 36 × 6 µm, n = 30), phragmosporous, catenated, acrogenous, minutely verruculose, rounded at both ends, composed of subglobose cells, dark brown to black, 1–2 smaller cells at the apex, 3–18-septate, easily separating, slightly constricted at some septa and chiefly subcylindrical.

Culture characteristics – Conidia germinated on the PDA within 24 h, and germ tubes are produced from the basal cell. Colonies growing on PDA reached 33–35 mm in diam. after three weeks at 25℃ in the dark. Colonies from above medium dense, regular, white aerial mycelium slightly raised, fluffy, filiform. In reverse, greenish-grey in the centre, off-white ring at the margin, without pigments produced in PDA.

Material examined – CHINA, Sichuan Province, Guangyuan City, Qingquan Town, 105°58′39″E, 32°41′35″N, elevation 817 m, on dead branches of *Gardenia jasminoides* (Rubiaceae). 20 April 2021, H.Z. Du, L2092 (GZAAS 25-0020), living culture GZCC 25-0020.

Notes – Crous et al. (2015) introduced *Torula masonii*, which was collected from *Brassica* sp. in the UK. Subsequently, Li et al. (2017) and Su et al. (2018) recollected and described *T. masonii* from *Iris germanica* in Italy and submerged

decaying wood in China, respectively. In this study, multi-locus phylogenetic analysis showed that my isolate (GZCC 25-0020) clustered together with *T. masonii* ex-type (CBS 245.57) with 87% MLBS and 0.98 BIPP support (Figure 5.14). Additionally, my collection (GZAAS 25-0020) shows similar morphological characteristics to *T. masonii* (CBS H-22278). Therefore, I identified my new collection as *T. masonii*, which associated with the medicinal plant *Gardenia jasminoides* in Sichuan Province, China.



Note a Host *Gardenia jasminoides*. b, c Colonies on the host surface. d, e Colonies on PDA, above (d) and below (e). f–h Conidiophores and conidiogenous cells. i–o, q Conidia. p Germinated conidium. Scale bars: f–h = 20 μm, i–n, p = 15 μm, o, q = 10 μm.

Figure 5.17 *Torula masonii* (GZAAS 25-0020, new host record)

Torula strychnicola H.Z. Du, N. Wu, K.D. Hyde & Jian K. Liu, sp. nov. Figure 5.18

MycoBank number: MB 856185

Etymology – The epithet '*strychnicola*' refers to the host genus *Strychnos* from which the fungus was originally isolated.

Holotype – HKAS 139505

Saprobic on dead branches of medicinal plant *Strychnos nux-vomica* L. (Loganiaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, sparse, hairy, velvety, dark brown to black on the substrate. Mycelium immersed or superficial, composed of septate, branched, dark brown to black hyphae. *Conidiophores* 2–4 μm wide, macronematous to semi-macronematous, erect, septate, smooth, straight, or slightly flexuous, brown to dark brown, subcylindrical to subglobose and thick-walled, with 1–2 doliiform to globose cells. *Conidiogenous cells* 4–6 × 3–5 μm ($\overline{x}$ = 5 × 4 μm, n = 20), monoblastic, integrated, terminal, subglobose or spherical, brown to dark brown. *Conidia* (16–) 25–50 (–65) × 5–8 μm ($\overline{x}$ = 38 × 7 μm, n = 30), catenated, acrogenous, simple, phragmosporous, arranged in branched chains, dry, brown to dark brown, cylindrical, rounded at both ends, composed of globose to ellipsoidal cells, occasionally smaller at the apex (1–2 cells black at the apex), subhyaline at the terminal cell, 2–15-septate, constricted at septa, verrucose, with spinulose on the substrate.

Culture characteristics – Conidia germinated on the PDA within 24 h, and germ tubes are produced from the basal cell. Colonies growing on PDA reached 40–43 mm in diam. after two weeks at 25℃ in the dark. Colonies from above regular, white aerial mycelium slightly raised, medium dense, fluffy, filiform, velvety, pale purple; in reverse, purplish brown at the center, with greyish white at the edge, with pale brown ring between them, the color gradually lightens from the center to the margin.

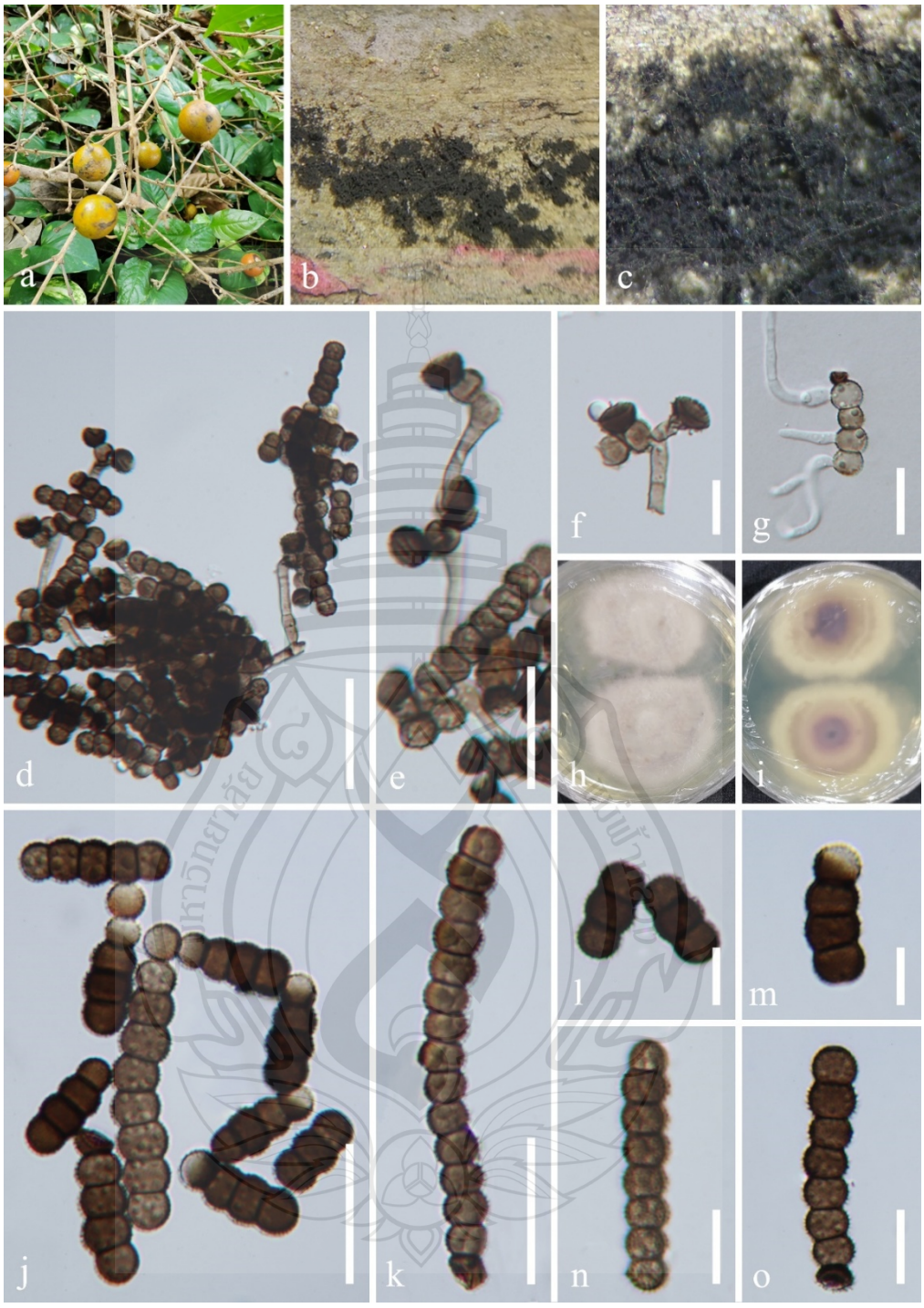
Material examined – CHINA, Hainan Province, Wuzhishan City, Shuiman River tropical rainforest scenic area in Wuzhishan, 109°34′36″E, 18°53′29″N, elevation 1,845 m, on dead branches of *Strychnos nux-vomica* (Loganiaceae), 15 August 2021, Jian Ma, WZS71.1 (HKAS 139505, holotype), ex-type living culture GZCC 24-0163; *ibid.*, WZS73 (GZAAS 23-0630, isotype), living culture GZCC 24-0146.

Notes – Multi-locus phylogeny (Figure 5.14) showed that *Torula strychnicola* (GZCC 24-0163 and GZCC 24-0146) was sister to *T. kanvae* (MCC-10010) with a strong support (100% MLBS/1.00 BIPP) and formed a distinct lineage. Morphologically, *Torula strychnicola* can be distinguished from *T. kanvae* by distinct spinulose conidia on the substrate. Based on the comparison of the septa and the conidial size, *T. strychnicola* (septa: 2–15, conidia: 25–50 × 5–8 μm) differs from *T. kanvae* by having 3–4 septa and conidia of 3–6 × 3–8 μm (Crous et al., 2024). The nucleotide base pair comparison between *T. strychnicola* (GZCC 24-0163, ex-type strain) and *T. kanvae* (MCC-10010, ex-type strain) revealed 63/529 bp (11.9%, 16 gaps) in ITS, 24/420 bp (5.7%, 6 gaps) in *tef1α*, and 144/997 bp (14.4%, 4 gaps) in *rpb2* sequence data. In addition, *Torula strychnicola* and *T. kanvae* have a close phylogenetic relationship with *T. aquatica* (KUMCC 15-0435, ex-type strain), *T. gaodangensis* (MFLUCC 17-0234, ex-type strain), *T. herbarum* (CBS 140066, ex-type strain), and *T. luguhuensis* (KUNCC 22-12427, ex-type strain) with 99% MLBS and 1.00 BIPP support (Figure 5.14), base pair differences between ex-type strain of *T. strychnicola* and these species are shown in Table 5.3 (Crous et al., 2015; Su et al., 2018; Hyde et al., 2017; Luan et al., 2023). Therefore, based on the morphological and phylogenetic evidence, I established *T. strychnicola* as a new species from Hainan Province, China.

Table 5.3 Comparisons of base pair differences between ex-type strain of *Torula strychnicola* (GZCC 24-0163) and members of adjoining clades

Species	**Strain no.**	**ITS (bp)**	**LSU (bp)**	***tef1α* (bp)**	***rpb2* (bp)**
T. aquatica	KUMCC 15-0435	43/459 (9.4%, 13 gaps)	9/826 (1.1%, 1 gap)	N/A	95/796 (11.9%, 0 gap)
T. gaodangensis	MFLUCC 17-0234	40/508 (7.7%, 12 gaps)	13/896 (1.5%, 1 gap)	N/A	N/A
T. herbarum	CBS 140066	39/508 (7.7%, 9 gaps)	12/891 (1.3%, 1 gap)	N/A	N/A
T. luguhuensis	KUNCC 22-12427	43/499 (8.6%, 15 gaps)	15/843 (1.8%, 4 gaps)	35/868 (4.0%, without gaps)	103/987 (10.4%, without gaps)

Note N/A denotes unavailable sequence in GenBank



Note a Host *Strychnos nux-vomica*. b, c Colonies on the host surface. d, e Conidiophores, conidiogenous cells with conidia. f Conidiophores with conidiogenous cells. g Germinated conidium. h, i Colonies on PDA, above (h), below (i). j–o Conidia. Scale bars: d = 30 µm, e = 20 µm, f = 10 µm, g, j, k = 20 µm, l–o = 10 µm.

Figure 5.18 *Torula strychnicola* (HKAS 139505, holotype)

Leotiomycetes O.E. Erikss. & Winka

Helotiales Nannf.

Patellariopsidaceae Karun., Camporesi & K.D. Hyde

Type genus – *Patellariopsis* Dennis

Notes – The Patellariopsidaceae was introduced by Karunarathna et al. (2020) based on morphological distinctiveness and multi-gene phylogenetic analyses to accommodate a single genus, *Patellariopsis*, with *P. clavispora* (Berk. & Broome) Dennis as the type species. The sexual morphs of Patellariopsidaceae are characterized by sessile, discoid apothecia, 8-spored, cylindric-clavate, amyloid asci with hyaline, septate, ellipsoid to fusoid ascospores, and its asexual morphs are characterized by sub-epidermal or sub-peridermal, solitary sporodochia with dark brown, lateral, acropetal, septate, eguttulate, smooth, spherical conidia (Dennis, 1974, Karunarathna et al., 2020).

Velutinus N. Wu & Jian K. Liu, gen. nov.

Index Fungorum number: MB 901518, Facesoffungi number: FoF 15233

Type species – *Velutinus sichuanensis* N. Wu & Jian K. Liu

Etymology – Referring to the texture of conidiomata such as “velvety”

Saprobic on dead branches in terrestrial habitats. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Conidiomata* sporodochial, solitary, scattered, convex, spherical, dark brown to black, glistening, velvety. *Mycelium* mostly immersed, hyaline to pale brown hyphae. *Conidiophores* hyaline, cylindrical, straight or slightly curved, smooth, septate, unbranched, constricted at septa, guttulate, covered with a sheath. *Conidiogenous cells* monoblastic, holoblastic, integrated, terminal. *Conidia* acrogenous, hyaline to pale brown, spherical or subglobose, septate, eguttulate, smooth, cheiroid, eccentric, conidium-complex, arranged in branched chains, bearing basal appendages.

Notes – Phylogenetic analyses based on ITS and LSU sequence data showed that my two collections of *Velutinus* formed an independent clade in Patellariopsidaceae

and present as a sister group to *Patellariopsis* with 100% maximum likelihood bootstrap and 1.00 Bayesian posterior probability support. *Velutinus* is morphologically similar to *Patellariopsis* and *Cheirospora* in having sporodochial, solitary conidiomata and acropetal, thick-walled, dark brown, septate, eguttulate, smooth, cheiroid conidia arranged in branched chains. However, *Velutinus* differs from *Patellariopsis* and *Cheirospora* in having convex, velvety conidiomata and septate, guttulate, unbranched conidiophores covered with a sheath, and hyaline to pale brown, ellipsoidal conidia with basal appendages. In contrast, the latter two genera have narrower conidiophores lacking gelatinous sheath and smaller conidia without basal appendage. In addition, *Cheirospora* is phylogenetically distinct from *Velutinus* as they are distributed in different families (Figure 5.20).

Velutinus sichuanensis N. Wu & Jian K. Liu, sp. nov. Figure 5.19

Index Fungorum number: IF 901519, Facesoffungi number: FoF 15234

Etymology – The epithet refers to the location where the fungus was collected, Sichuan Province, China.

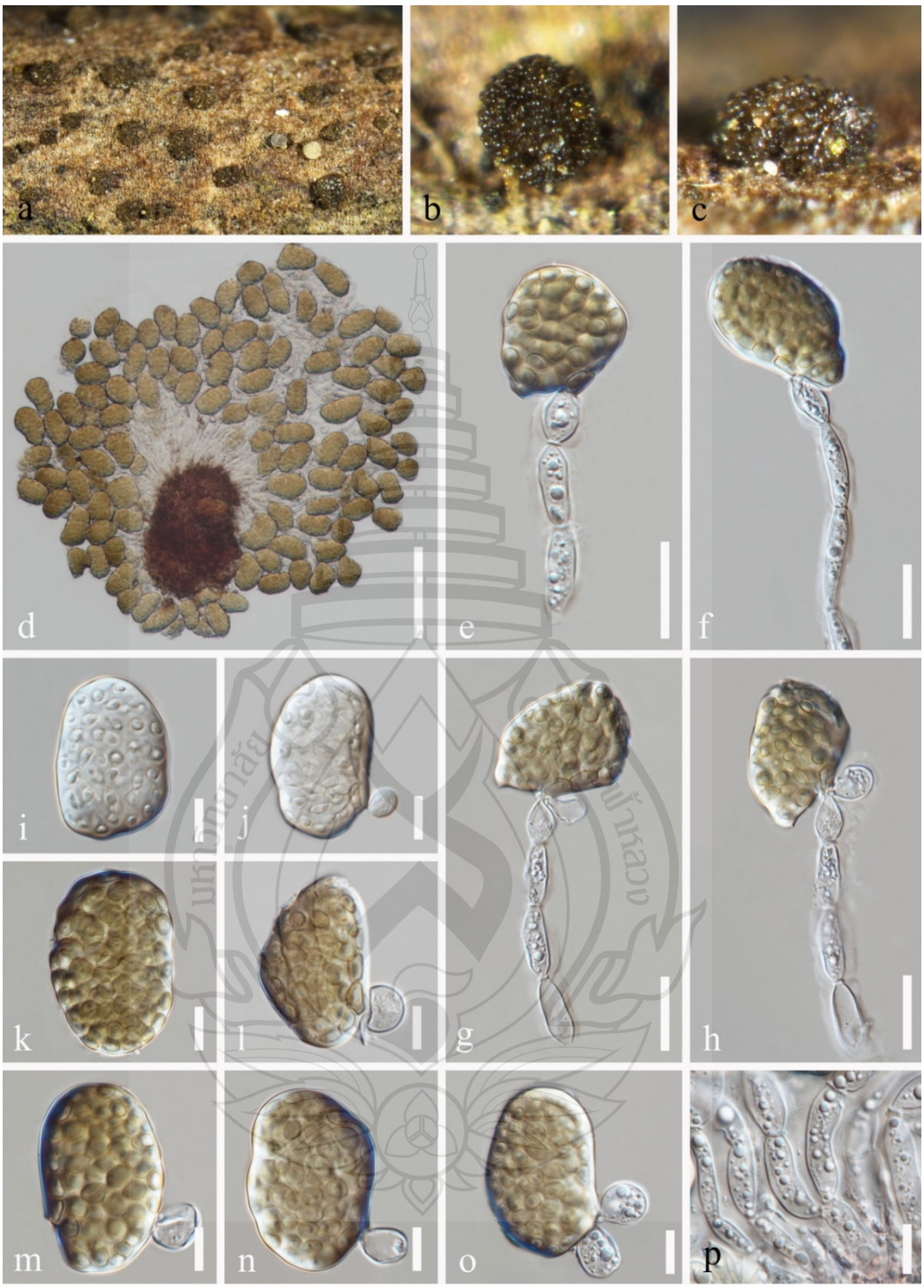
Holotype – HKAS 131317

Saprobic on dead branches of *Loropetalum chinense* (Hamamelidaceae) in terrestrial habitats. Sexual morph: Not observed. Asexual morph: *Conidiomata* 180–250 μm high, 250–360 μm diam. ($\bar{x}$ = 210 × 300 μm, n = 10), sporodochial, solitary, scattered, convex, spherical, dark brown to black, glistening, velvety. *Mycelium* mostly immersed, hyaline to pale brown hyphae. *Conidiophores* 60–120 × 7–9 μm ($\bar{x}$ = 96 × 8 μm, n = 20), hyaline, cylindrical, straight or slightly curved, 3–4-septate, smooth-walled, unbranched, constricted at septa, guttulate, covered with a 2–4 μm ($\bar{x}$ = 3.5 μm, n = 10) thick, mucilaginous sheath, sometimes reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, terminal, determinate, hyaline to pale brown. *Conidia* 25–38 × 23–30 μm ($\bar{x}$ = 33 × 25 μm, n = 50), acrogenous, hyaline when young, pale brown when mature, proliferating with several short, lateral, acropetal, branched

chains, with 1–2 hyaline, globose to subglobose basal appendages that are thin, easy to rupture and shrink, guttulate, eccentric. Primary branches give rise to secondary branches which eventually form ellipsoidal to spherical, whole conidia that are made from an infinite number of tiny, closely compact cells.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Qingcheng Mountain scenic spot, 103°28′36″E, 30°55′9″N, on dead branches of medicinal plant *Loropetalum chinense*, 27 March 2021, Na Wu, YW322 (HKAS 131317, holotype; HUEST 23.0222, isotype); *ibid*., 10 July 2022, YW385 (HUEST 23.0584).

Notes – My two collections share similar morphology and can be identified as one species, and the molecular data (ITS and LSU gene regions) also confirm this identification. Thus, the new species *Velutinus sichuanensis* is introduced to accommodate these taxa. In addition, *V. sichuanensis* resembles the asexual morph of *Patellariopsis atrovinosa* in having holoblastic conidiogenous cells and dark brown, septate, smooth conidia. However, *V. sichuanensis* differs from *P. atrovinosa* by having guttulate conidiophores covered with a thick mucilaginous sheath and hyaline to pale brown, ellipsoidal to spherical conidia with globose to subglobose appendages, while *P. atrovinosa* has branched conidiophores without sheath and dark brown, and irregularly spherical conidia without appendages (Karunarathna et al., 2020). A comparison of ITS and LSU nucleotides shows that *V. sichuanensis* is significantly different from its sister clade, *P. atrovinosa*, by having 39/459 bp differences (8.5%) in ITS and 10/843 bp differences (1.2%) in LSU.



Note a–c Colonies on woody substrate. d Squash mount of a sporodochium. e–h Conidia attached to the conidiophores. i–o Conidia. p Partial conidiophores. Scale bars: d = 100 µm, e–h = 20 µm, i–p = 10 µm.

Figure 5.19 *Velutinus sichuanensis* (HKAS 131317, holotype)

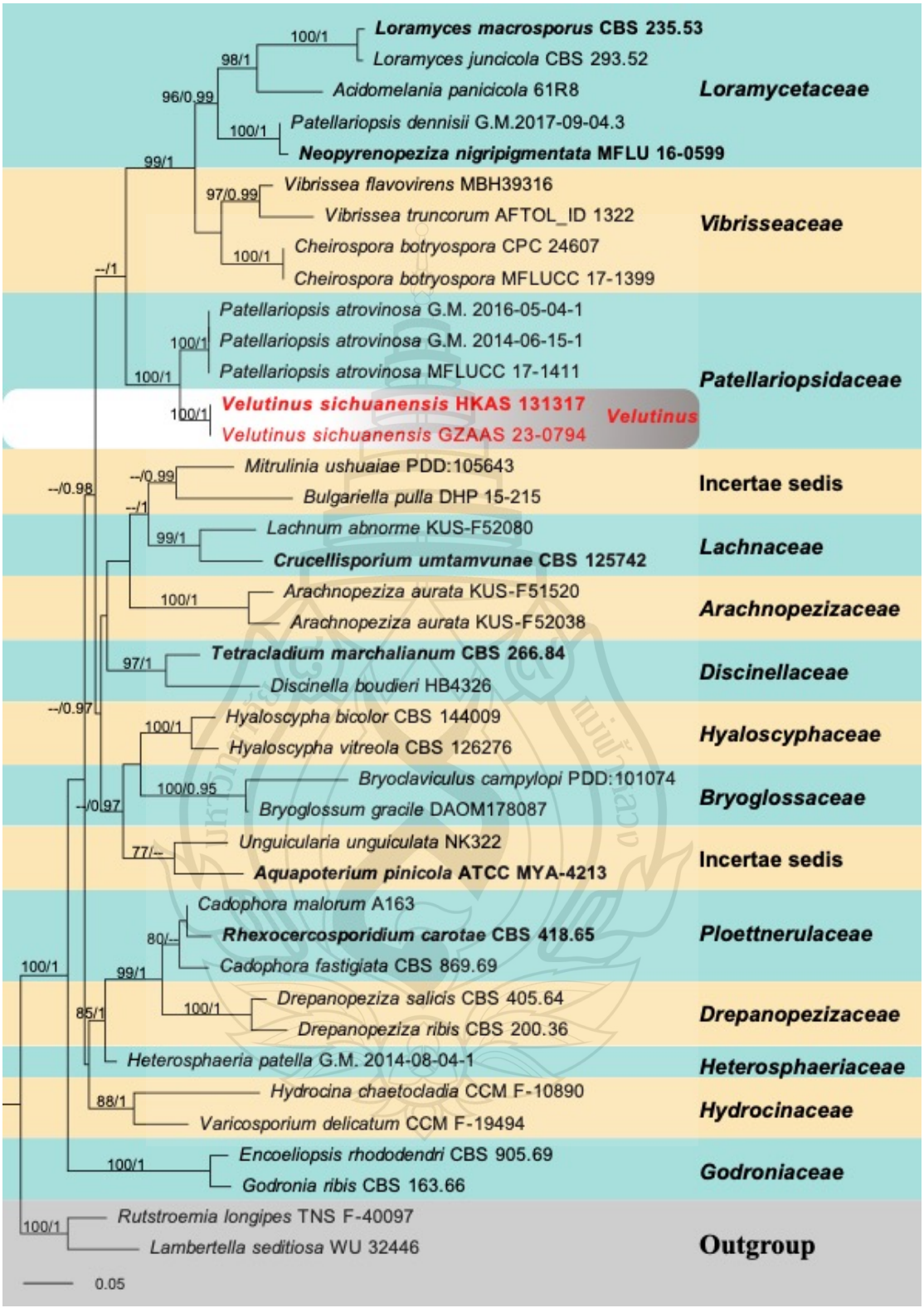


Figure 5.20 Phylogenetic tree generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of Helotiales

Figure 5.20 The tree is rooted with *Lambertella seditiosa* (WU 32446) and *Rutstroemia longipes* (TNS F-40097). The ML (≥ 75%) and BI (≥ 95%) bootstrap supports are given near the nodes, respectively. The new isolates obtained in this study are indicated in red and ex-type strains are in bold.

5.3 Discussion

This study advances the understanding of fungal diversity, taxonomy, and phylogeny associated with medicinal plants in Southwestern China, with a particular focus on members of the families Dictyosporiaceae and Neomassariaceae. Both families represent lineages that have undergone frequent taxonomic revisions and phylogenetic realignments, reflecting the complexity of their evolutionary histories (Wijayawardene et al., 2018; Karunarathna et al., 2020). By combining morphological observations with multi-locus phylogenetic analyses, my research contributes new taxa, novel records, and refined classifications, thereby enriching the overall framework of fungal diversity associated with medicinal plants.

The taxa of Dictyosporiaceae are known for their taxonomic complexity and ecological versatility, often requiring phylogenetic data to clarify their relationships. In this study, Dictyosporiaceae species were collected from ten different medicinal plants in Guizhou and Sichuan Provinces, regions characterized by subtropical climates with favorable temperature and humidity for fungal colonization. All identified taxa were saprobes, and no evidence indicated negative effects on their host plants. This finding underscores that medicinal plants provide not only abundant habitats but also diverse ecological niches for saprobic fungi, which may indirectly influence host health and ecological functioning (Zhao et al., 2010, 2014; Han et al., 2012; Sun et al., 2022, 2023a, 2023b).

My study also provides significant contributions to the taxonomy and phylogeny of *Neomassaria*. Three novel species (*N. camelliae*, *N. longiasca*, *N. sichuanensis*) and a new host record (*N. formosana*) were discovered from *Camellia sinensis*, marking the first documentation of *Neomassaria* on this important medicinal and economic plant. This expands both the diversity and host range of the genus and refines the understanding of its ecological associations (Wijesinghe et al., 2023; Yang et al., 2024; Zhang et al., 2024; Lu et al., 2025; Sun et al., 2025).

My phylogenetic analyses revealed that sexual and asexual morphs of *Neomassaria* clustered into distinct groups. Notably, asexual morph species (*N. camelliae*, *N. sichuanensis*, *N. fibraureae*, *N. thailandica*) formed a separate cluster, whereas sexual morph species were distributed across Clusters A and B. Interestingly, only a subset of species possessed mucilaginous ascospore sheaths (e.g., *N. coffeae*, *N. fabacearum*, *N. palmae*), suggesting that ascospore sheaths may represent an important but not universal trait for phylogenetic delimitation within the genus. Further collections from natural substrates are needed to determine whether this character consistently correlates with phylogenetic placement.

Furthermore, the discovery of a new genus, *Velutinus*, as the second genus in Patellariopsidaceae, alongside the previously monotypic genus *Patellariopsis*, highlights the dynamic nature of fungal classification. The establishment of *Velutinus* enriches the taxonomy of fungi on medicinal plants and expands the phylogenetic framework of Patellariopsidaceae (Karunarathna et al., 2020; Hyde et al., 2024b). These findings emphasize the importance of continued inventories of subtropical host plants in poorly studied areas, as such efforts are critical to uncovering the actual richness and ecological roles of fungi.

The findings of this study highlight the saprobic dominance of Dictyosporiaceae and Neomassariaceae taxa associated with medicinal plants. While no pathogenic interactions were recorded, these fungi are ecologically significant as decomposers and

potential contributors to nutrient cycling in subtropical ecosystems. Moreover, the consistent association of *Neomassaria* with woody medicinal plants supports the hypothesis that this genus is specialized to saprobic lifestyles on lignified substrates (Hyde et al., 2016; de Silva et al., 2022; Yang et al., 2022, 2023). From an applied perspective, documenting new species and host associations provides essential data for biodiversity conservation and sustainable utilization of medicinal plants. The rich diversity of fungi discovered here reinforces the value of medicinal plants as reservoirs of novel taxa, which may also have potential roles in biotechnology, agriculture, or pharmacology.

Overall, this study refines the taxonomy and expands the known biodiversity of Dictyosporiaceae and Neomassariaceae associated with medicinal plants in China. By integrating detailed morphological descriptions with multi-locus phylogeny, I provide a clearer understanding of evolutionary relationships, host specificity, and ecological strategies within these families. The discovery of new taxa such as *Velutinus* and novel *Neomassaria* species further underscores the importance of continued exploration of subtropical medicinal plants for uncovering fungal diversity and informing future taxonomic frameworks.

CHAPTER 6

HTTPS://BOTRYOSPHAERIALES.ORG/, AN ONLINE PLATFORM FOR UP-TO-DATE CLASSIFICATION AND ACCOUNT OF TAXA OF BOTRYOSPHAERIALES

6.1 Introduction

The order Botryosphaeriales (Dothideomycetes, Ascomycota) comprises a diverse group of fungi distributed worldwide. These fungi exhibit a range of lifestyles, including saprobes, endophytes, and pathogens on numerous plant hosts (Chethana et al., 2016; Manawasinghe et al., 2016). Many species are economically important plant pathogens that cause serious diseases in fruit crops, forest trees, and ornamental plants, while others play crucial ecological roles in nutrient cycling as saprobes or exist asymptomatically as endophytes (Kaliterna et al., 2012; C´aceres et al., 2016; Zhang et al., 2017; Abbas et al., 2018; Besoain et al., 2019).

Over the past two decades, extensive revisions based on morphology and multi-gene phylogeny have significantly reshaped the taxonomy of Botryosphaeriales, leading to the recognition of multiple families and numerous new genera (Dissanayake et al., 2016; Wijayawardene et al., 2018; Hyde et al., 2024). However, the high morphological plasticity and overlapping features among taxa continue to present challenges in their classification and identification. Moreover, the rapid accumulation of newly described taxa has outpaced the capacity of traditional monographs and checklists, which often become outdated and lack interactive tools for comparative analyses (Liu et al., 2012; Zhang et al., 2021; Hyde et al., 2024).

Although several fungal databases such as MycoBank, Index Fungorum, and Faces of Fungi provide valuable resources for taxonomy and nomenclature, these platforms are either too general or lack detailed ecological and phylogenetic information specific to Botryosphaeriales. Consequently, researchers working on this order have faced difficulties in accessing up-to-date classifications, descriptions, illustrations, and phylogenetic frameworks in a single platform.

To address this gap, this study established Botryosphaeriales.org, an online database dedicated to the taxonomy, phylogeny, and ecological information of the order. The platform was designed to consolidate scattered information, provide updated taxonomic accounts, and serve as a reference tool for researchers, students, and practitioners in agriculture, forestry, and mycology.

6.2 Results

As of the latest update, the platform includes all six currently recognized families of Botryosphaeriales, encompassing over 32 genera and more than 1,500 species worldwide (Hyde et al., 2024). Each taxon page contains standardized descriptions, high-quality illustrations, reference sequences, and links to GenBank accession numbers. In addition, the platform documents host associations with economically important plants, including *Rosa roxburghii* and *R. sterilis*, which are widely cultivated in Southwest China. Several newly described taxa from these hosts have been incorporated into the database, further expanding the known diversity and host range of Botryosphaeriales.

The Botryosphaeriales.org platform was successfully developed as a comprehensive, user-friendly online database. The website consists of several key modules:

6.2.1 Home

The homepage briefly introduces the objectives of the website and has links to highlights of information. Colour photos of Botryosphaeriales are displayed representing the key morphological features of this order (Figure 6.1). The relevant informa- tion can be accessed easily using the search box located at the right top corner (Figure 6.2). Beneath the search box, there is quick access to recent notes, recent genera and recent species. Clicking on these options opens the link in a new window (Figure 6.3).

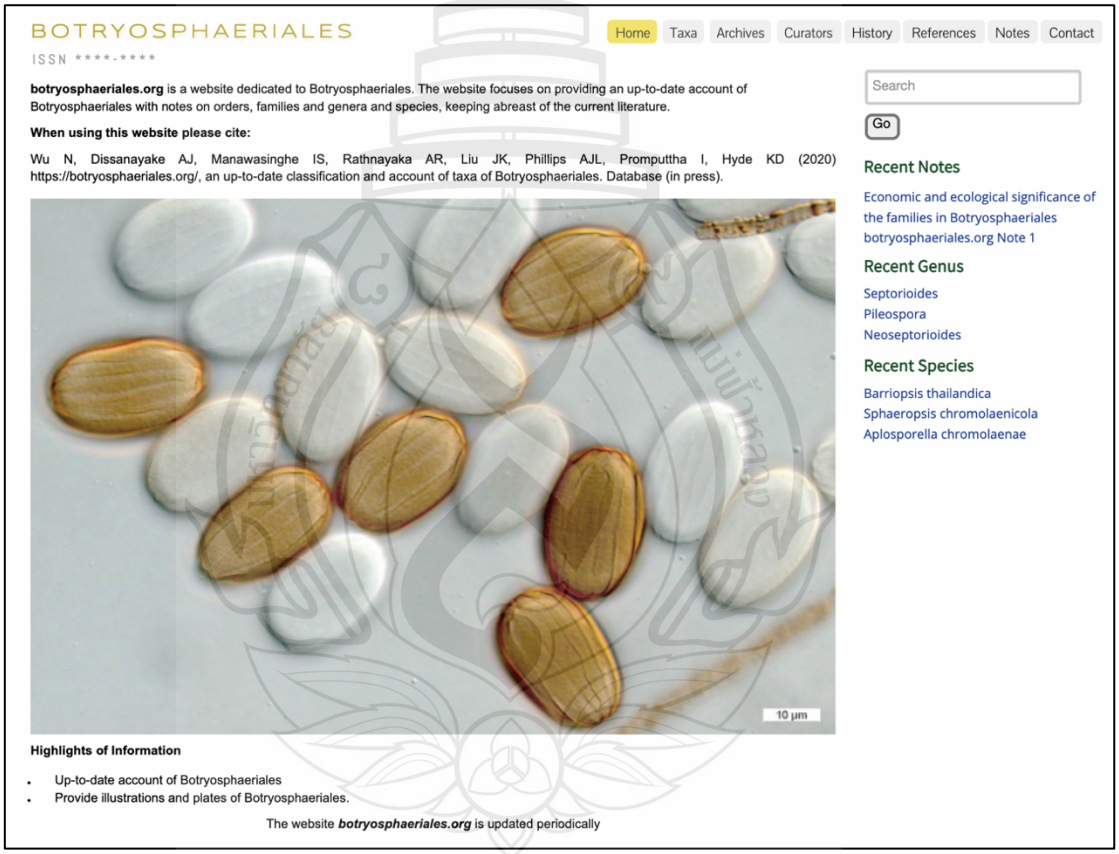


Figure 6.1 The homepage of Botryosphaeriales webpage

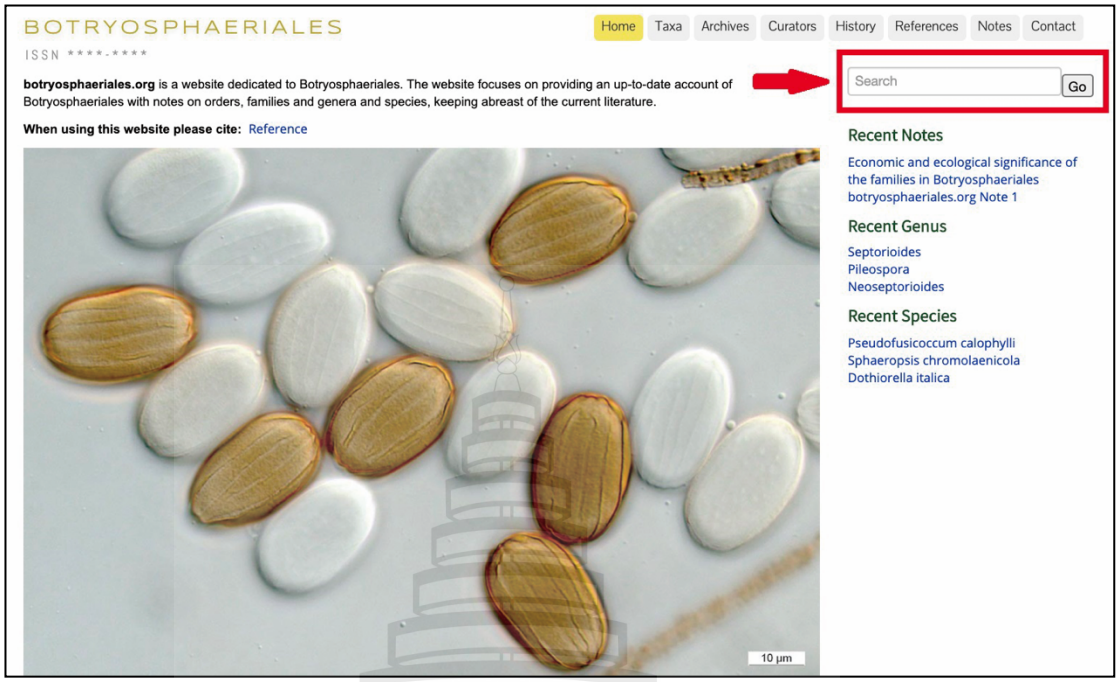


Figure 6.2 Red arrow indicates search tool to enter the taxon name

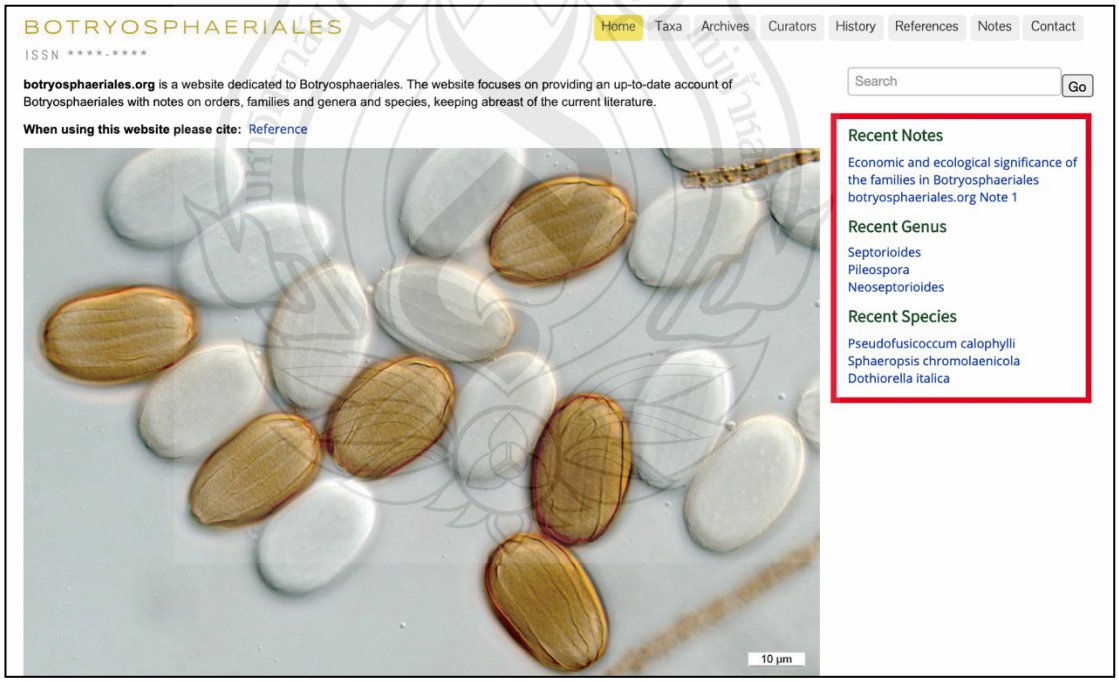


Figure 6.3 The recent notes, genus and species to enable easy access

6.2.2 Taxa

Under the ‘Taxa’ heading, the recent taxonomic classification as families, genera and species of Botryosphaeriales is provided (Figure 6.4). In addition, an updated phylogenetic tree for the order is given at the bottom. The search box at the top left corner will facilitate quick access to each entry on the website. Clicking a listed species name will direct to the full description and details in the archives section (Figure 6.5).

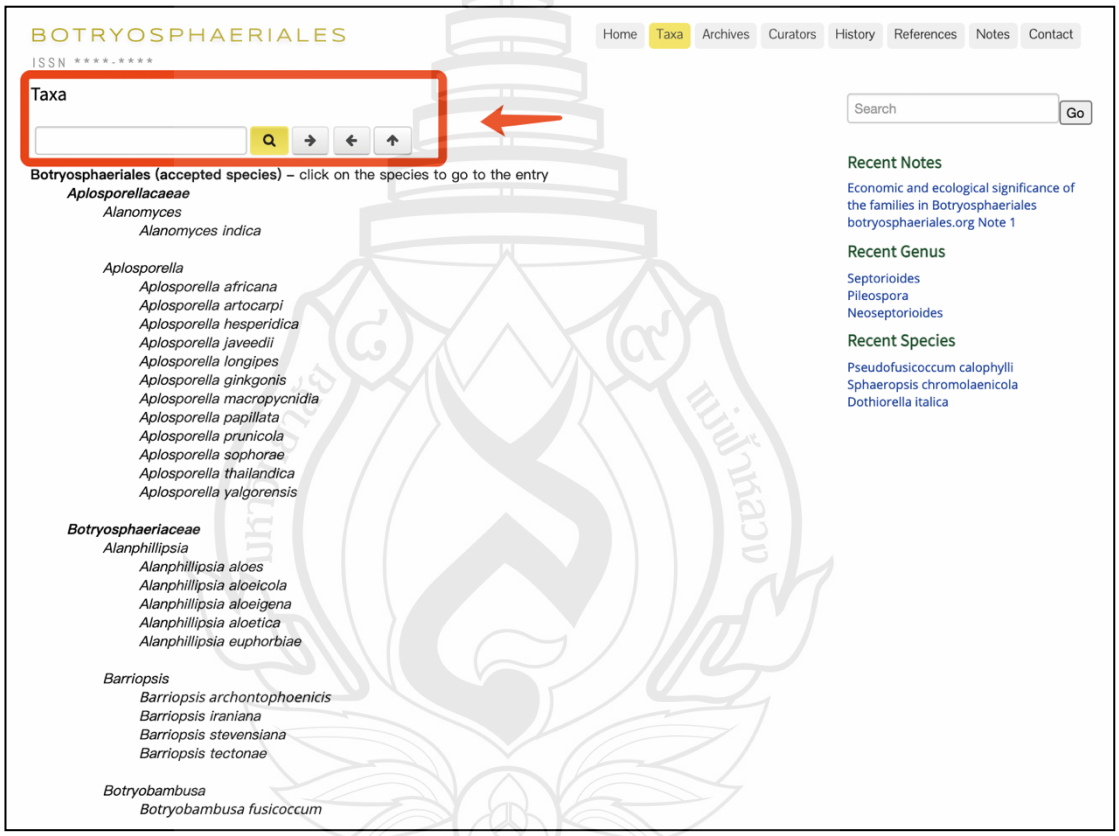


Figure 6.4 The “Taxa” view of the Botryosphaeriales webpage

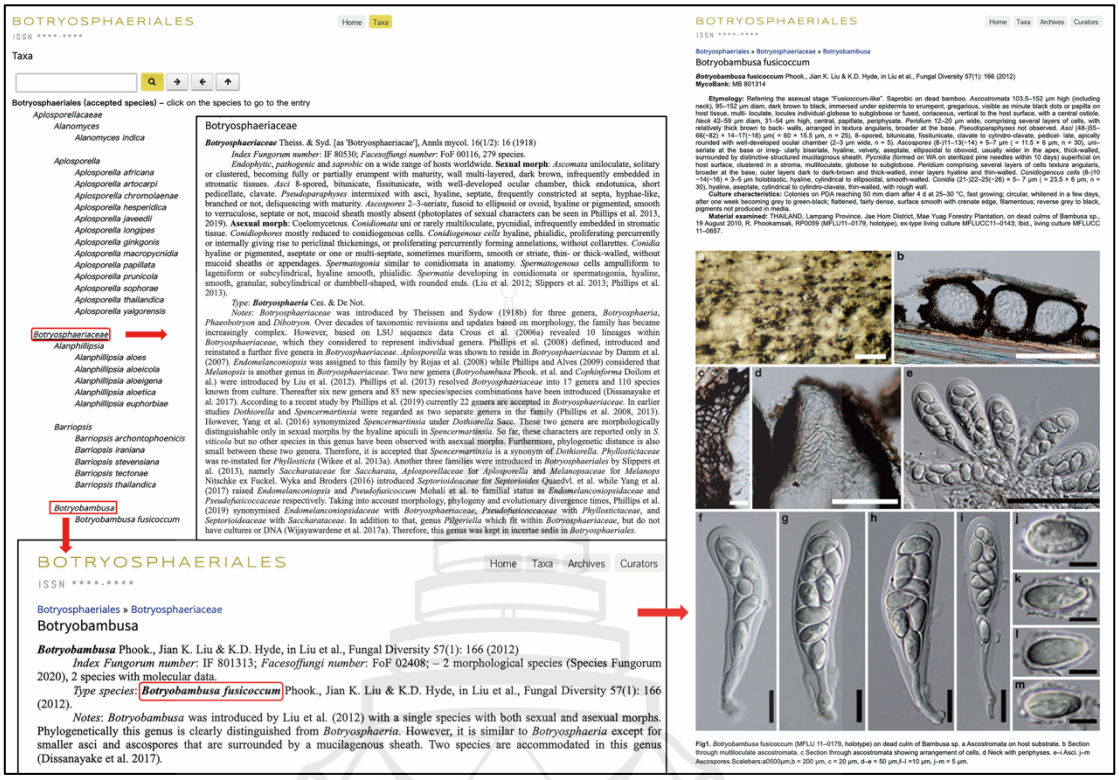


Figure 6.5 Details of the genus *Botryobambusa*

6.2.3 Archives

The 'Archives' is the main section containing all information on every entry in the website (Figure 6.6). It consists of six tabs representing each family in Botryosphaeriales. Clicking on a particular family will automatically generate a dropdown list including all the genera belonging to the particular family (Figure 6.7). This can be further expanded into genus and species levels. By clicking the link for each species will open a new window containing all information on that species (Figure 6.8).

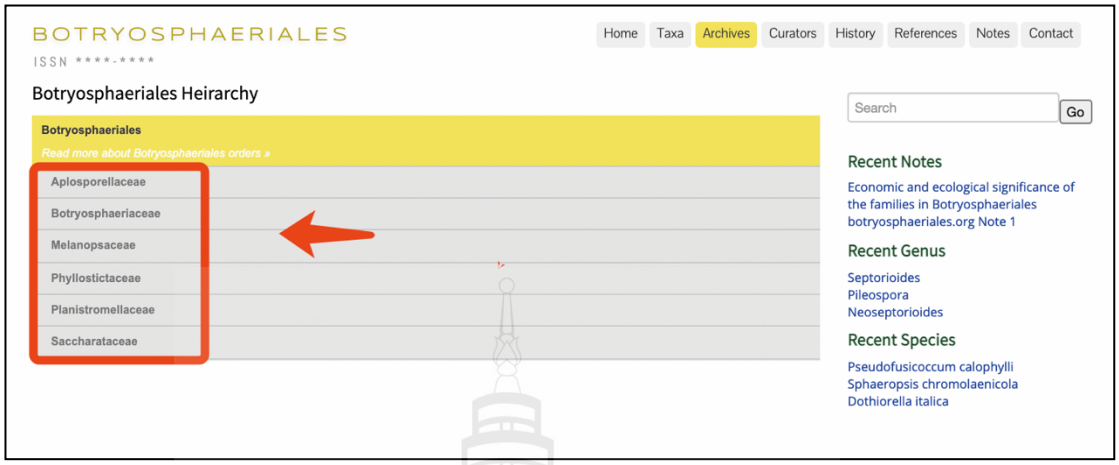


Figure 6.6 Appearance of the "Archives" section in Botryosphaeriales webpage

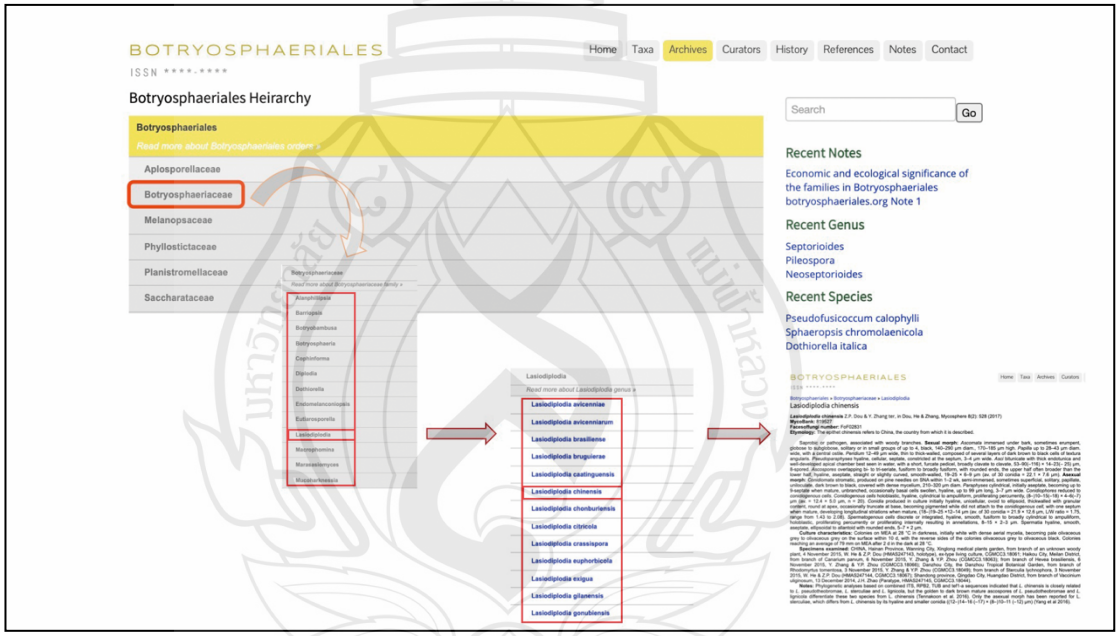


Figure 6.7 User friendly interface of the "Archives" section in Botryosphaeriales webpage

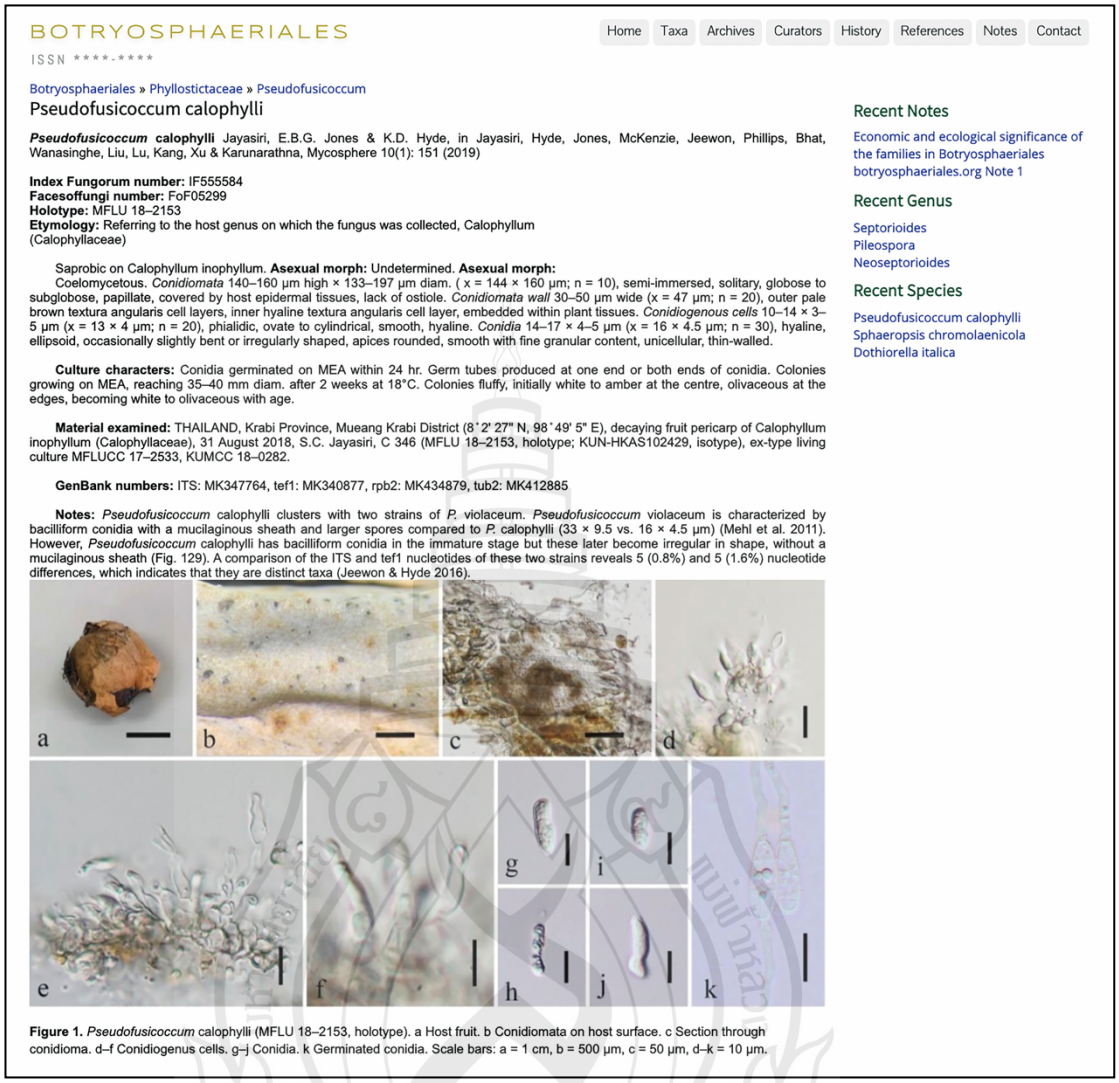


Figure 6.8 An entry with description, notes and plate (15)

6.2.4 Curators

This section provides information about the curators who handle and update the website (Figure 6.9).

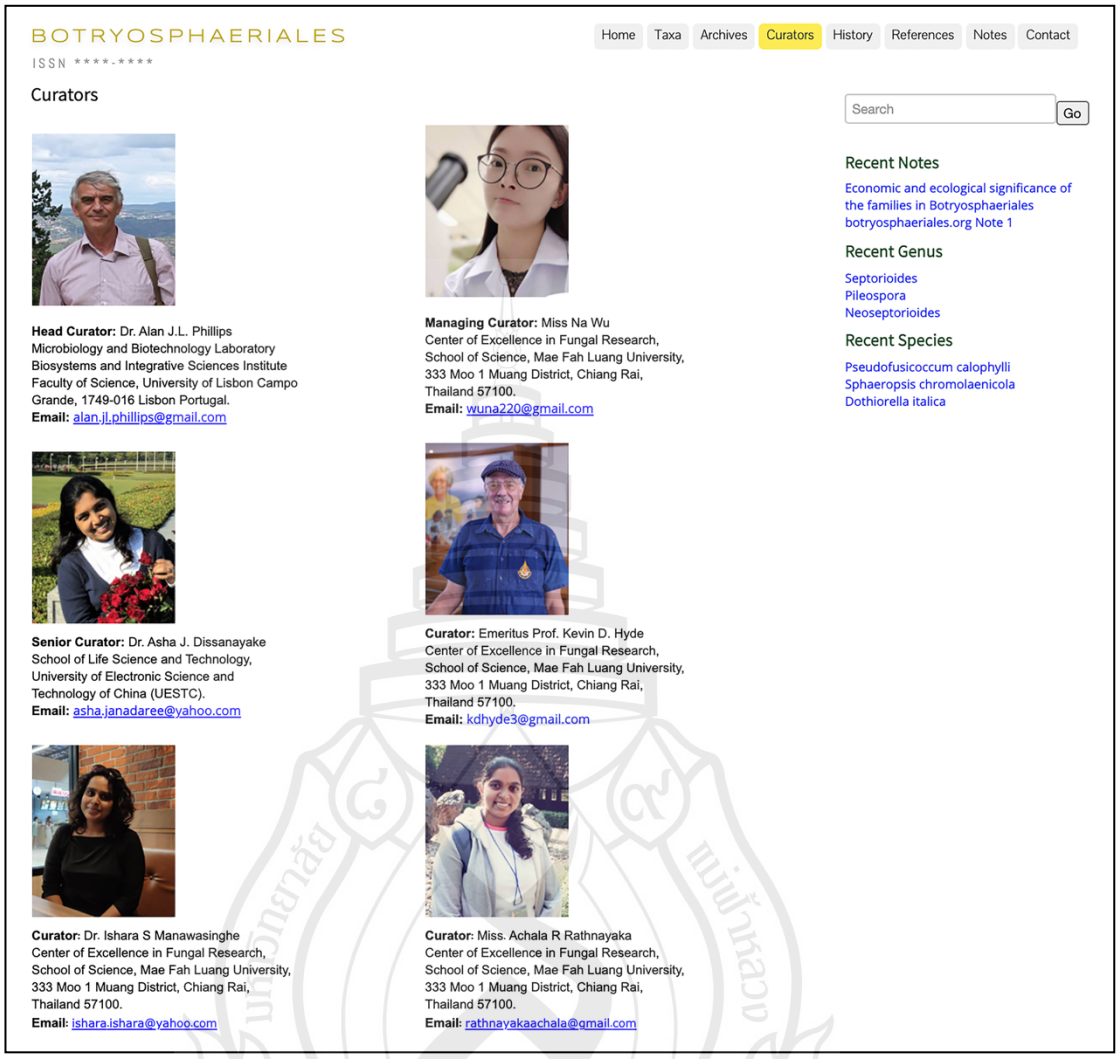


Figure 6.9 Curators of Botryosphaeriales webpage

6.2.5 History

This section provides a brief account of the classification of Botryosphaeriales.

6.2.6 References

A list of the citations used in the entries and history as well as other related information are provided under this heading.

6.2.7 Notes

Economic and ecological significance of families in Botryosphaeriales are given in this section. In addition, trends and current applications of the species of Botryosphaeriales will be added regularly to this section.

6.2.8 Contact

This section provides the contact details of the website and allows users to communicate any comments and suggestions.

6.3 Discussion

The development of Botryosphaeriales.org fills an important gap in fungal systematics by integrating taxonomy, nomenclature, morphology, and phylogeny into a single, accessible framework. This digital platform provides a reliable resource for researchers, students, and practitioners working on Botryosphaeriales and related fungal groups. Compared to static monographs, the platform can be dynamically updated, reflecting the latest taxonomic changes and discoveries (Dissanayake et al., 2016; Phillips et al., 2019; Wijayawardene et al.,, 2020; Hyde et al., 2024).

From an ecological perspective, the platform enables comparative analyses of host associations and geographic distributions, helping to elucidate patterns of host specialization, co-evolution, and biogeographic spread (Slippers & Wingfield, 2007; Mehl et al., 2017). Its inclusion of both saprobic and pathogenic species provides a basis for understanding lifestyle transitions and the ecological roles of Botryosphaeriales in natural and agricultural ecosystems.

Furthermore, by linking molecular sequence data with morphology and taxonomy, the platform contributes to more accurate species delimitation and identification. This is especially valuable for disease management in economically important hosts such as *Rosa*, *Vitis*, and *Mangifera*, where Botryosphaeriales includes

major plant pathogens (Slippers & Wingfield, 2007; Phillips et al., 2019). In the future, the integration of high-throughput sequencing and AI-assisted taxonomy into the platform could further enhance its functionality, enabling predictive modeling of host-pathogen interactions and monitoring of fungal diversity under changing environmental conditions. Thus, Botryosphaeriales.org not only supports taxonomic and phylogenetic research but also provides applied value for agriculture, forestry, and biodiversity conservation.



CHAPTER 7

CONCLUSIONS

7.1 Overall Conclusion

Rosa roxburghii and *R. sterilis* are two closely related perennial deciduous shrubs, which are also important fruit crops within Rosaceae (Zong et al., 2024). Both species originated in Guizhou Province and are currently widely cultivated across southwestern China (Liang et al., 1989; Liu et al., 2016). However, these two species differ in reproductive biology; *R. roxburghii* produces seeded fruits, whereas *R. sterilis* produces seedless fruits (Liu et al., 2016). These characteristics make the two species an ideal system for exploring host-associated fungal diversity and for evaluating host-specificity versus generalist (Hyde et al., 2020; Mapook et al., 2020a; Zhang et al., 2025). We collected 608 saprobic fungal specimens associated with *R. roxburghii* and *R. sterilis* from 22 collection sites in southwestern China. A total of 227 fungal isolates were successfully obtained and identified based on morphological examinations and phylogenetic analyses. These taxa are taxonomically distributed in two classes, Dothideomycetes and Sordariomycetes, belonging to 15 orders and 36 families. Within Dothideomycetes, six new genera, 33 new species, 56 new records, and seven new combinations were identified. Pleosporales was the dominant order, with Didymosphaeriaceae and Lophiostomataceae containing the highest number of taxa. This was followed by Botryosphaeriales, among which Botryosphaeriaceae was the most representative family (Figure 7.1). Additionally, one new family, one new genus, ten new species, and twelve new host records were identified within Sordariomycetes, with Pararamichloridiales being the dominant order. The Dothideomycetes are the most represented class reported from a broad range of hosts in numerous studies, possibly

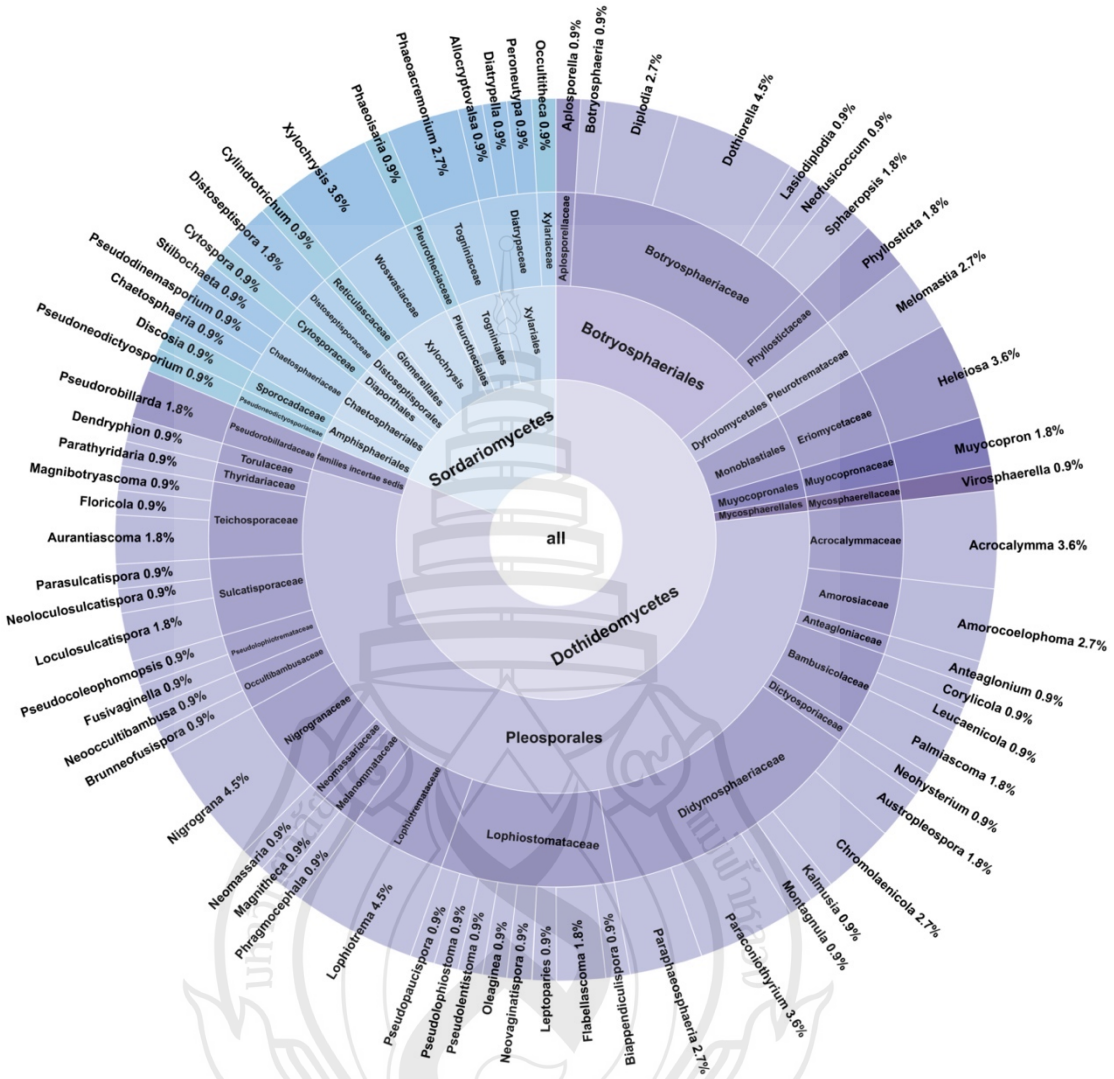
because they are the largest class in Ascomycota and accommodate diverse families and orders (Wijayawardene et al., 2018; Hyde et al., 2024).

Although numerous specimens were collected in this and previous studies, only 30–50% of them yielded germinating spores and viable cultures. The number of isolates successfully obtained from host samples was consistently limited, and this phenomenon was particularly evident in samples collected from leaf litter, dead branches, herbaceous plants, or extreme environments (Ruibal et al., 2009; Ohm et al., 2012; Murgia et al., 2018; Tennakoon et al., 2021a). The main reasons could be attributed to spore dormancy, desiccated or empty ascomata, and reduced capability of spore germination caused by unfavorable environmental factors such as temperature, humidity, and ultraviolet radiation (Gottlieb, 1950; Ayerst, 1969; Osman & Valadon, 1981; Fourtouni et al., 1998; Mitakakis et al., 2003; Dagno et al., 2011; Wenneker et al., 2013). In our study, 608 fungal specimens were collected, but only 37% (227/608) were successfully cultured. These findings are consistent with previous studies. For example, Mapook et al. (2020a) investigated 253 samples of *Chromolaena odorata* (Siam weed), of which only 88 (about 35%) yielded viable fungal isolates. These associated saprobic fungi were dominated by Dothideomycetes. Similarly, Zhang et al. (2024) collected 538 palm samples from China and Thailand, and only 248 (about 46%) fungi were successfully isolated and described Again, Dothideomycetes were the most abundant group, followed by Sordariomycetes, Lecanoromycetes, Leotiomycetes, and Orbiliomycetes (Zhang et al., 2024).This definitely indicates that better fungal estimate and assessment of global fungal number, there is a need to revise our sampling strategies and methods of isolation (Hyde et al., 2024).

This study is the first systematic investigation of saprobic fungi associated with *Rosa roxburghii* and *R. sterilis*. It is worth noting that 38% (43/112) of the isolated saprobic fungi identified are new to science, and the remaining isolated species represent new host records on *R. roxburghii* and *R. sterilis*. We found that 55.5%

(126/227) of the collections produced hyaline spores, while 44.5% (101/227) produced pigmented spores, of which 80% (81/101) were darkly pigmented and 20% (20/101) lightly pigmented. About 19% (44/227) of the saprobic taxa identified had spores with appendages or mucilaginous sheaths. Previous studies have suggested that such features may help spores withstand unfavorable conditions such as drought and ultraviolet radiation (Mapook et al., 2020a).

With the integration of morphology and multi-gene phylogeny, several linkages between sexual and asexual morphs were confirmed. Both sexual and asexual morphs were observed for *Austropleospora ochracea*, *Botryosphaeria dothidea*, *Corylicola italic*a, *Heleiosa septata*, *Palmiascoma acericola* and *Paraconiothyrium guizhouense* on *Rosa roxburghii* and *R. sterilis*. In addition, the sexual and asexual morphs of *Diplodia seriata* were found on *R. sterilis*, and those of *Phyllosticta rosae* were found on *R. roxburghii*. These findings highlight the coexistence of both sexual and asexual morphs on these hosts, which is further supported by the overall proportion of sexual and asexual isolates revealed in this study. Overall, the isolated saprobic fungi associated with *Rosa roxburghii* and *R. sterilis* in our study were mainly sexual morphs, accounting for approximately 65% (148 isolates), while 35% (79 isolates) were asexual morphs. The results also suggest that sexual reproduction may play an important role in shaping and maintaining fungal communities on these hosts (Maynard Smith, 1978; Colegrave, 2012; Wallen & Perlin, 2018; Mapook et al., 2020a). Among the asexual morphs, 91% (72/79) were coelomycetous and 7% (7/79) were hyphomycetous. The predominance of coelomycetous fungi over hyphomycetous ones may be related to their protective conidiomata, which enable better adaptation to decaying substrates (Li et al., 2020; Liu et al., 2024a).



Note Percentages indicate the proportion of species in each genus relative to the total number (n = 112)

Figure 7.1 Hierarchical pie chart showing the taxonomic distribution of fungi recognized in the present study

7.2 Research Advantages

This study represents the first systematic investigation of microfungi associated with *Rosa roxburghii* and *R. sterilis* in southwestern China. Based on detailed

morphological examinations and multi-locus phylogenetic analyses, this research introduced one new family, seven new genera, forty-six new species, seven new combinations, and seventy new host or geographical records. These results greatly enrich the taxonomic framework of several fungal lineages and contribute to a deeper understanding of fungal diversity in this region.

This study focused on saprobic fungi, providing comprehensive morphological descriptions, photographic plates, and multi-gene phylogenetic analyses. It is also the first to reveal a high diversity of saprobic *Botryosphaeriales* species from a single host (*Rosa roxburghii* or *R. sterilis*), including 57 isolates representing 16 species. The newly discovered *Botryosphaeriales* taxa fill important taxonomic and phylogenetic gaps within the order and establish a solid foundation for future studies on fungal taxonomy, genomics, and evolution.

Furthermore, this work provides the first worldwide checklist of fungi associated with *R. roxburghii* and *R. sterilis*. By integrating records from published literature, online databases, and my own collections, the checklist highlights the remarkable diversity and wide distribution of fungi linked to these hosts. This comprehensive resource not only documents underexplored fungal groups but also serves as a valuable reference for subsequent ecological, phylogenetic, and applied research.

In addition, a digital platform (https://botryosphaeriales.org) has been established to consolidate published data and provide continuous updates on the taxonomy of *Botryosphaeriales*. By integrating morphological, molecular, and ecological information, this platform enhances accessibility, facilitates global collaboration, and ensures that newly described taxa and host records are rapidly incorporated into an evolving, interactive online database.

7.3 Future Work

Building upon the results of this study, several research directions are proposed to further advance the understanding of fungal diversity, ecology, and evolution associated with *Rosa roxburghii* and *R. sterilis*.

7.3.1 Saprobic fungi: Future studies will expand field sampling across different regions and seasons to capture broader fungal diversity. This will enable the discovery of additional saprobic taxa and potentially reveal new fungal resources with ecological and biotechnological significance.

7.3.2 Endophytic fungi: Further work should explore the diversity of endophytic fungi inhabiting *Rosa* hosts. Isolates will be screened for beneficial strains with antagonistic or bioactive potential, aiming to identify candidates for natural product discovery and biological control applications.

7.3.3 Pathogenic fungi: Pathogenic fungi associated with *Rosa roxburghii* and *R. sterilis* warrant detailed investigation. Future research will focus on identifying pathogenic taxa, verifying their pathogenicity through inoculation tests, and examining the pathogenic potential of existing *Botryosphaeriales* strains.

7.3.4 Soil and rhizosphere microbiome: Comparative studies between healthy and diseased plants will be conducted to characterize the soil and rhizosphere microbiome. Identifying core microbial communities will provide insights into plant-microbe interactions and may contribute to the development of sustainable biocontrol and biofertilizer resources.

7.3.5 Genomic and functional exploration: Genomic and transcriptomic approaches will be applied to reveal the genetic diversity, adaptive evolution, and metabolic potential of fungi associated with *R. roxburghii* and *R. sterilis*. These analyses will deepen our understanding of fungal adaptation to host environments and ecological niches.

7.3.6 Digital platforms: The existing digital platform, Botryosphaeriales.org, will be continuously maintained and updated to integrate new taxonomic and phylogenetic data. A complementary database, Cilifungi.org, will be developed to integrate fungal and microbial data, relevant literature, and disease image libraries, thereby promoting open data sharing and supporting future taxonomic and applied studies.

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APPENDIX A

MEDIA

1. Malt Extract Agar (MEA) used for fungal cultivation

Agar 15 g

Peptone 0.78 g

Glycerol 2.35 g

Dextrin 2.75 g

Maltose, Technical 12.75 g

Suspend 33.6 g of malt extract agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the power and bring volume to 1000 ml. Autoclave at 121ºC for 20 minutes.

2. Potato dextrose agar (PDA) used for fungal cultivation

Potato starch (from the infusion) 4 g

Dextrose 20 g

Agar 15 g

Suspend 39 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121ºC for 20 minutes.

3. Water Agar (WA) Used for Fungal Isolation

Agar 15 g

Suspend 15 g of agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121°C for 20 minutes.

4. Indian ink used for observing gelatinous appendages of ascospores in some species

APPENDIX B

ABSTRACT OF PUBLICATIONS

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Morpho-phylogenetic evidence reveals *Lasiodiplodia chiangraiensis* sp. nov. (*Botryosphaeriaceae*) associated with woody hosts in northern Thailand

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Abstract

Lasiodiplodia species are commonly as endophytes, saprobes and pathogens in tropics and subtropics. During an investigation of *Botryosphaeriaceae* in Thailand, two *Lasiodiplodia* taxa were isolated. Morphological characteristics and phylogenetic analyses based on combined ITS, *tef* and *tub2* sequence data support the establishment of a novel species, *Lasiodiplodia chiangraiensis*, isolated from woody hosts. *Lasiodiplodia chiangraiensis* is phylogenetically close to *L. iraniensis* and *L. thailandica*, but represents a distinct lineage. The new species could be distinguished from extant *Lasiodiplodia* species by its mature conidial dimensions. A detailed description and illustration are provided, as well as an updated phylogenetic tree (ITS, *tef* and *tub2*) including all species (with available molecular data) of *Lasiodiplodia*. In addition, the accepted genera in *Botryosphaeriaceae* based on recent studies are given.

Keywords: 1 new taxon, asexual morph, multi-gene, phylogeny, taxonomy

Introduction

The family *Botryosphaeriaceae* was introduced by Theissen & Sydow (1918) with three genera, *Botryosphaeria* (type genus), *Dibotryon* and *Phaeobotryon*. In recent years, genera in this family have been subjected to continuous revisions (Arx & Müller 1954, 1975, Barr 1987, Crous *et al.* 2006, Liu *et al.* 2012, Phillips *et al.* 2013, 2019, Dissanayake *et al.* 2016, Wijayawardene *et al.* 2020). The subsequent study by Hongsanan *et al.* (2020) based on morphology and phylogeny, accepted 22 genera (TABLE 1) in *Botryosphaeriaceae*, consisting of more than 170 species. Among all the families within Botryosphaeriales, *Botryosphaeriaceae* is the largest with a broad host range. Fungi in this family are well-known as plant endophytes, saprobes and pathogens, causing ulceration, dieback and stem-end rot of plants or fruits, e.g., *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia* and *Neofusicoccum* (Smith *et al.* 1996, Phillips *et al.* 2006, 2013, Slippers & Wingfield 2007, Liu *et al.* 2012, Li *et al.* 2014, Dissanayake *et al.* 2016, Zhang *et al.* 2021). The sexual morphs of *Botryosphaeriaceae* are characterized by solitary or clustered ascostromata, often with two-layers of dark brown to hyaline cells; 8-spored, short-stipitate, clavate asci and hyaline or pigmented, aseptate or septate, ellipsoid or ovoid ascospores, and its asexual morphs are coelomycetous, characterized by ovoid, hyaline or brown, aseptate, one- or multi-septate conidia, and conidiophores mostly reduced to conidiogenous cells (Denman *et al.* 2000, Crous *et al.* 2006, Phillips *et al.* 2006, 2013, 2019, Liu *et al.* 2012, Slippers *et al.* 2013).

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https://botryosphaeriales.org/, an online platform for up-to-date classification and account of taxa of Botryosphaeriales

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Abstract

Fungi are eukaryotes that inhabit various ecosystems worldwide and have a decomposing effect that other organisms cannot replace. Fungi are divided into two main groups depending on how their sexual spores are formed, viz. Ascomycota and Basidiomycota. The members of Botryosphaeriales (Dothideomycetes, Ascomycota) are ubiquitous. They are pathogenic on a wide range of hosts, causing diverse diseases including dieback, canker, leaf spots and root rots and are also reported as saprobes and endophytes worldwide. As an important fungal group, of which most are plant pathogens, it is necessary to organize data and information on Botryosphaeriales so that scientific literature can be used effectively. For this purpose, a new website, https://botryosphaeriales.org is established to gather all published data together with updates on the present taxonomy of Botryosphaeriales. The website consists of an easy-to-operate searching system and provides an up-to-date classification together with accounts of Botryosphaeriales taxa, including colour illustrations, descriptions, notes and numbers of species in each genus, as well as their classification. Thus, readers will be able to obtain information on botryosphaerialean taxa through this platform.

Database URL: https://botryosphaeriales.org/

Introduction

Botryosphaeriales (Dothideomycetes) was established in 2006, to accommodate a single family, Botryosphaeriaceae (1). Nine families—Aplosporellaceae, Botryosphaeriaceae, Endomelanconiopsisaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae, Pseudofusicoccumaceae, Saccharataceae and Septorioideaceae—were accepted in Botryosphaeriales by Wijayawardene *et al.* (2). However, based on morpho-molecular analyses and evolutionary divergence times, the number of families accepted in Botryosphaeriales was reduced to six, namely Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae and Saccharataceae (3, 4). Endomelanconiopsisaceae and Pseudofusicoccumaceae were synonymized under Botryosphaeriaceae and Phyllostictaceae, respectively, while Septorioideaceae was synonymized under Saccharataceae (3). Members of Botryosphaeriales are found worldwide, on many different host plants (5–17). They are endophytes, pathogens and saprobes and as opportunistic pathogens, they are of considerable importance to agriculture, horticulture and forestry (18, 19). They cause severe diseases of economically important crops and plants leading to huge economic losses (20, 21). *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia*, *Neofusicoccum* and *Phyllosticta* are the major pathogenic genera in Botryosphaeriales. *Botryosphaeria dothidea*, *Diplodia seriata*, *Lasiodiplodia theobromae* and *Neofusicoccum parvum* are associated with grapevine dieback worldwide (27). *Diplodia seriata* has been reported as a pathogen on a wide range of hosts including eucalyptus, pine and stone fruits (22–26). *Phyllosticta citricarpa* and *P. citriasiana* cause freckle on banana and brown spots on pomelo, respectively (6, 9). One species can occur on several hosts in the same country, and pathogenicity of a species can vary from one region to another (19). This reflects the importance of gathering data on these fungal taxa to understand disease epidemiology.

Aplosporellaceae, Melanopsaceae and Planistromellaceae have immersed or semi-immersed multiloculate ascostromata,

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Neodeightonia septata sp. nov. and *N. subglobosa* (*Botryosphaeriaceae*) from northern Thailand

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Abstract

Neodeightonia species are mostly known from bamboo and palms. During an investigation of *Botryosphaeriaceae* species in northern Thailand, three *Neodeightonia* isolates were obtained. Morphological characteristics coupled with phylogenetic analyses based on the combined ITS, LSU, SSU and *tef* sequence data indicated that these taxa can be recognized as *Neodeightonia septata sp. nov.* (from palms) and *Neodeightonia subglobosa* (from bamboo). *Neodeightonia septata* is phylogenetically close to *N. rattanica* and *N. rattanicola* but formed a distinct lineage and differs morphologically from the latter in having 1-septate conidia. In addition, the asexual morph of *N. subglobosa* is reported for the first time from a natural substrate. Detailed descriptions, illustrations and phylogenetic trees are provided.

Keywords: 1 new taxon, asexual morph, multi-gene, phylogeny, taxonomy

Introduction

The family *Botryosphaeriaceae* was introduced by Theissen & Sydow (1918) to accommodate the genera *Botryosphaeria* (type genus), *Dibotryon* and *Phaeobotryon.* To date, twenty-two genera with more than 170 species are accepted for the family based on morphology and phylogeny (Phillips *et al*. 2019, Hongsanan *et al*. 2020, Wu *et al*. 2021, Wijayawardene *et al.* 2022). The *Botryosphaeriaceae* is composed of important plant pathogens, saprobes and endophytes (Smith *et al*. 1996, Crous *et al*. 2006, Phillips *et al*. 2006, 2013, Slippers & Wingfield 2007, Liu *et al*. 2012, Li *et al*. 2014, Dissanayake *et al*. 2016, Zhang *et al*. 2020).

Punithalingam (1969) established the genus *Neodeightonia* with *N. subglobosa* Booth as the type. However, Arx & Müller (1975) transferred *N. subglobosa* to *Botryosphaeria*. Phillips *et al*. (2008) discussed the synonymy of *Neodeightonia* and lectotypified it as a genus distinct from *Botryosphaeria* based on morphology and molecular phylogeny. Ten species are currently accepted in *Neodeightonia* (Xiao *et al*. 2021, Zhang *et al*. 2021, Wijayawardene *et al.* 2022). The sexual morph of *Neodeightonia* is characterized by clavate to cylindrical-clavate asci and hyaline, aseptate, oval to broadly ellipsoidal ascospores surrounded by a mucilaginous sheath, while the asexual morph is characterized by ellipsoidal to obovoid, longitudinally striated conidia which are initially hyaline and become brown or dark brown and one- or multi-septate at maturity with smooth to finely roughened walls (Phillips *et al*. 2008, 2013, Liu *et al*. 2010, 2012, Adamčík *et al*. 2015, Konta *et al*. 2016a, Dai *et al*. 2017, Jayasiri *et al*. 2019, Xiong *et al*. 2021).

As part of an ongoing study of Botryosphaeriales in northern Thailand, two collections from palms are described as *Neodeightonia septata sp. nov.*, while another isolate obtained from bamboo was identified as *N. subglobosa* based on morphology and molecular phylogeny. In addition, an updated phylogenetic tree of *Neodeightonia* is presented.

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Morpho-Phylogenetic Evidence Reveals Novel Species and New Records of *Botryosphaeriaceae* in China and Thailand

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Abstract: Species in the *Botryosphaeriaceae* are common plant pathogens, endophytes, and saprobes found on a variety of mainly woody hosts. *Botryosphaeriaceae* is a high-profile fungal family whose genera have been subjected to continuous revisions in recent years. Surveys conducted during 2019 and 2020 on several decaying woody hosts (from dead arial twigs, branches, stems, bark, and seed pods) in China and Thailand revealed a high diversity of *Botryosphaeriaceae* fungi. Identification of 16 *Botryosphaeriaceae* isolates was carried out based on both morphological characteristics and phylogenetic analyses of combined ITS, LSU, *tef1-α*, and *tub2* sequence data. Four novel species (*Dothiorella ovata*, *Do. rosacearum*, *Do. septata*, and *Lasiodiplodia delonicis*) and seven previously known species (*Botryosphaeria fujianensis*, *Diplodia mutila*, *Di. seriata*, *L. crassispora*, *L. mahajangana*, *Macrophomina euphorbiicola* and *Sphaeropsis eucalypticola*) were identified while new hosts and geographical records were reported. This study indicates that the fungal family *Botryosphaeriaceae* seems to be common and widespread on a broad range of hosts in China and Thailand.

Keywords: 4 new taxa; asexual morph; multi-gene; phylogeny; sexual morph; taxonomy

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1. Introduction

The order *Botryosphaeriales* (Dothideomycetes) was established by Schoch et al. [1], including a single family *Botryosphaeriaceae*. A recent comprehensive study by Phillips et al. [2] accepted six families, viz. *Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Phyllostictaceae*, *Planistromellaceae*, and *Saccharataceae* are in this order based on morphological and phylogenetic analysis. Members of *Botryosphaeriales* have worldwide distribution on many different host plants [3–8] and occur as endophytes, pathogens, and saprobes. As opportunistic pathogens, they are of considerable importance to agriculture, horticulture, and forestry [9,10] while causing severe diseases of economically important crops and plants, leading to huge economic losses [11,12].

The family *Botryosphaeriaceae* was established by Theissen and Sydow [13] to accommodate three genera, *Botryosphaeria*, *Dibotryon*, and *Phaeobotryon*, with *Botryosphaeria* as the type genus [1]. Subsequently, Kirk et al. [14] estimated 26 genera within the family *Botryosphaeriaceae*, while Liu et al. [4] reevaluated the family and recognized 29 genera. Up to date, 22 genera with more than 200 species are accepted within the family, based on morphology and molecular evidence [2,15–18].

During an investigation of *Botryosphaeriaceae* diversity in China and Thailand, a collection of 16 *Botryosphaeriaceae*-like isolates was obtained from several arial parts of the decaying woody hosts. A multi-gene phylogeny based on combined ITS, LSU, *tef1-α*, and

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Velutinus, a novel genus in Patellariopsidaceae from medicinal plants in Sichuan Province, China

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Abstract

Velutinus sichuanensis gen. et sp. nov. was collected from dead branches of the medicinal plant *Loropetalum chinense* var. *rubrum* (Hamamelidaceae) in Sichuan Province, China. The genus *Velutinus* is characterized by having cylindrical, straight or slightly curved, septate, hyaline conidiophores, holoblastic, polyblastic conidiogenous cells, and thick-walled, dark brown, septate, spherical conidia, sometimes with conspicuous appendages. Molecular phylogenetic analyses based on the combined ITS and LSU sequences data showed that *Velutinus* forms a distinct lineage in Patellariopsidaceae, Helotiales, Leotiomycetes. The new genus, *Velutinus* is introduced to accommodate *V. sichuanensis* based on morphological characteristics and multi-gene phylogenetic analyses. Detailed descriptions and illustrations of the new taxa are provided.

Key words: 2 new taxa, asexual morph, Leotiomycetes, phylogeny, taxonomy

Introduction

Medicinal plants are cultivated and utilized for their therapeutic value with a wide variety distributed and grown worldwide (Marinelli 2004, Dar *et al*. 2017, Phumthum *et al*. 2019, Rasool *et al*. 2020). Recently, the microfungi associated with medicinal plants has received a lot of attention, and many interesting fungal species have been discovered (Zhao *et al*. 2010, 2014, Han *et al*. 2012, Jafari 2018, Kumar *et al*. 2019, Phukhamsakda *et al*. 2020, Sun *et al*. 2022, 2023a, b). Microfungi on medicinal plants comprise endophytes, saprobes, and pathogens, mainly distributed across Dothideomycetes and Sordariomycetes, with a few in Eurotiomycetes (Bhagat *et al*. 2012, Niu *et al*. 2016, Long *et al*. 2019, Ma *et al*. 2019, Hyde *et al*. 2020, Tennakoon *et al*. 2021).

Helotiales was established by Nannfeldt (1932) to accommodate species with cupulate apothecia covered by long hairs and is the largest and most diverse order in Leotiomycetes. This order accounts for about 80% of the class Leotiomycetes, comprising 36 families, 328 genera, and more than 5,000 species, with another 144 genera as families *incertae sedis* (Eriksson 2005, Ekanayaka *et al*. 2019, Wijayawardene *et al*. 2022). Members of Helotiales are ecologically diverse, including endophytes, plant pathogens and saprobes (Pöder & Scheuer 1994, Hosoya & Otani 1995, Monreal *et al*. 2000, Boddy 2001, Grünig *et al*. 2002, Shoemaker *et al*. 2002, Johnston & Park 2005, Wang *et al*. 2006). The Patellariopsidaceae was introduced by Karunarathna *et al*. (2020) based on morphological distinctiveness and multi-gene phylogenetic analyses to accommodate a single genus, *Patellariopsis*, with *P. clavispora* (Berk. & Broome) Dennis as the type species. The sexual morphs of Patellariopsidaceae are characterized by sessile, discoid apothecia, 8-spored, cylindric-clavate, amyloid asci with hyaline, septate, ellipsoid to fusoid ascospores, and its asexual morphs are characterized by sub-epidermal or sub-peridermal, solitary sporodochia with dark brown, lateral, acropetal, septate, eguttulate, smooth, spherical conidia (Dennis 1974, Karunarathna *et al*. 2020).

In this study, we deal with two asexual morph taxa collected on medicinal plants from Sichuan Province, China. Based on phylogenetic and morphological studies they are identified as a new species. The novel genus, *Velutinus*, is

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Additions to Dictyosporiaceae: *Neoxylochrysis typhicola* comb. et gen. nov., Two New Species and Four New Host Records from Medicinal Plants in Southwestern China

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Abstract: Medicinal plants serve as vital resources for preventing and treating diseases, with their flowers, fruits, leaves, roots, or entire plants being utilized in the pharmaceutical industry or as direct therapeutic agents. During our investigation of microfungi associated with medicinal plants in Guizhou and Sichuan Provinces, China, several asexual and sexual fungal morphs were collected. Multi-locus phylogenetic analysis based on combined ITS, LSU, SSU and *TEF1-α* datasets revealed that these taxa are related to the family Dictyosporiaceae. Morphological characteristics, along with multi-locus phylogenetic analysis, supported the establishment of *Dictyocheirospora alangii* sp. nov. and *Pseudocoleophoma rosae* sp. nov., as well as the introduction of a novel genus *Neoxylochrysis*, which accommodates *Neoxylochrysis typhicola* comb. nov. (≡*Pseudocoleophoma typhicola*). In addition, four new host records are introduced for *Aquadictyospora lignicola* from *Periploca forrestii*, *Dendryphiella eucalyptorum* from *Leonurus japonicus*, *Ophiopogon japonicus* and *Sambucus javanica*, *D. vinosa* from *Phytolacca americana*, and *Dictyocheirospora rotunda* from *Euonymus japonicus* and *Prinsepia utilis*. Detailed descriptions, micrographs of the new taxa and a phylogenetic tree are provided.

Keywords: Dothideomycetes; multi-locus phylogeny; *Pseudocoleophoma*; taxonomy

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1. Introduction

The family Dictyosporiaceae, originally proposed as Dictyosporaceae by Liu et al. [1], was formally introduced by Boonmee et al. [2] within the order Pleosporales and class Dothideomycetes. The type genus of Dictyosporiaceae is *Dictyosporium* Corda, with *D. elegans* designated as the type species. This holomorphic family is globally distributed and consists of 20 genera. Most asexual morphs in this family are hyphomycetous, viz., *Aquadictyospora*, *Aquaticheirospora*, *Cheirosporium*, *Dendryphiella*, *Dictyocheirospora*, *Dictyopalmispora*, *Dictyosporium*, *Digitodesmium*, *Jalapriya*, *Neodendryphiella*, *Neodigitodesmium*, *Pseudodictyosporium* and *Vikalpa*, characterized by the production of cheiroid (digitate), multi-septate, palmate or dictyosporous, and pale brown to brown conidia [2–7]. A few genera, viz., *Immotthia*, *Pseudocoleophoma*, *Pseudoconiothyrium*, *Pseudocyclothyriella*, *Sajamaea* and *Verrucoccum* have coelomycetous asexual morphs [8–13]. Among these, only five genera viz., *Dictyosporium*, *Gregarithecium*, *Immotthia*, *Pseudocoleophoma* and *Verrucoccum*, are known to produce sexual morphs, which are characterized by brown to black ascomata,

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Research Article

Morpho-phylogenetic evidence reveals novel species and new records of *Torula* (Torulaceae, Pleosporales) from medicinal plants in China

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Abstract

During a saprobic fungi survey in China, five hyphomycetous fungi of *Torula* (Torulaceae, Pleosporales, Dothideomycetes) were discovered. These taxa were characterized and identified based on morphology, culture characteristics, and phylogenetic analysis of the combined ITS, LSU, SSU, *tef*1-α, and *rpb*2 sequence dataset. Consequently, two novel species, *Torula dispora* and *T. strychnicola*, are introduced based on the distinct spinulose characteristics on the conidial substrate and the size of conidia. Phylogenetic results indicated that our isolates of *T. dispora* and *T. strychnicola* each represent a distinct lineage. Additionally, three new host records of *T. chinensis*, *T. fici*, and *T. masonii* are reported. Based on morphological and phylogenetic evidence, we formally propose the synonymization of *T. phytolaccae* under *T. chinensis*. Detailed descriptions, illustrations, and informative notes are provided for all species.

Key words: Asexual morph, Dothideomycetes, multi-locus, taxonomy, two new taxa

Introduction

Medicinal plants, as a valuable resource for modern drug discovery and development—such as anticancer, antibacterial, and antiviral medications—play a significant role in human healthcare (Anand et al. 2019; Ali et al. 2021; Atanasov et al. 2021; Adeleye et al. 2022; Chaachouay and Zidane 2024). The growth and reproduction, as well as the quality, of these medicinal herbs are influenced by numerous factors. It is worth noting that microfungi are a crucial factor affecting the quality of medicinal plants, including endophytes (Keshri et al. 2021; Purushotham et al. 2021; Zhang et al. 2024a), pathogens (Niu et al. 2016; Petrasch et al. 2019),

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