Mycosphere 14(1): 1254–1339 (2023) www.mycosphere.org ISSN 2077 7019

Article

Doi 10.5943/mycosphere/14/1/14

Lasiodiplodia: Generic revision by providing molecular markers, geographical distribution and haplotype diversity

Rathnayaka AR[1,2,3], Chethana KWT[1,2], Manawasinghe IS[4], Wijesinghe SN[1,2], de Silva NI[5,6], Tennakoon DS[5,6], Phillips AJL[7], Liu JK[8], Jones EBG[9], Wang Y[10*], and Hyde KD[2,4,5,6,11*]

[1]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[2]School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand
[3]Department of Plant Medicine, National Chiayi University, 300 Syuefu Road, Chiayi City 60004, Taiwan, P.R. China
[4]Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, P.R. China
[5]Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
[6]Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
[7]Faculdade de Ciências, Biosystems and Integrative Sciences Institute (BioISI), Universidade de Lisboa, Campo Grande, 1749-016 Lisbon, Portugal
[8]School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, 11731, P.R. China
[9]Department of Botany and Microbiology, College of Science, King Saud University, P.O Box 2455, Riyadh 11451, Kingdom of Saudi Arabia
[10]Department of Plant Pathology, Agriculture College, Guizhou University, Guiyang, Guizhou Province, 550025, P.R. China
[11]Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan, P.R. China

Rathnayaka AR, Chethana KWT, Manawasinghe IS, Wijesinghe SN, de Silva NI, Tennakoon DS, Phillips AJL, Liu JK, Jones EBG, Wang Y, Hyde KD 2023 – *Lasiodiplodia*: Generic revision by providing molecular markers, geographical distribution and haplotype diversity. Mycosphere 14(1), 1254–1339, Doi 10.5943/mycosphere/14/1/14

Abstract

Lasiodiplodia (*Botryosphaeriaceae*, *Botryosphaeriales*) has a global distribution and occurs on a wide range of monocotyledonous, dicotyledonous, and gymnospermous hosts. Most *Lasiodiplodia* species are pathogens that cause various diseases, such as stem cankers, stem and branch gummosis, shoot blight, and fruit rot. In addition, *Lasiodiplodia* species occur as endophytes and saprobes. This study presents one of the most reliable molecular markers for *Lasiodiplodia*. The combination of four loci, the internal transcribed spacer region (ITS), the partial translation elongation factor 1-α gene (*tef*1-α), beta-tubulin *(tub2*), and RNA polymerase II second largest subunit (*rpb2*), provided a more reliable resolution for this genus at the species level. Geographical studies showed that *Lasiodiplodia* species are distributed in tropical and temperate regions, but not in the polar regions. Among its species, *L. theobromae* has a worldwide distribution on a wide range of hosts, including economically important crops. Combining the morphology and molecular phylogeny is necessary for accurate taxonomic identification of *Lasiodiplodia* species and is being used in this study. Multigene phylogenetic analyses were performed based on maximum likelihood and Bayesian inference analyses using combined ITS,

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Submitted 3 April 2023, Accepted 8 June 2023, Published 6 September 2023
Corresponding Author: Kevin D. Hyde – e-mail – kdhyde3@gmail.com,
Yong Wang – e-mail – yongwangbis@aliyun.com

*tef*1-α, *tub2*, and *rpb*2 sequence data. In addition, the main morphological characteristics of holotype specimens of *Lasiodiplodia* species are provided. The current study introduced 25 new host and geographical records of saprobic *Lasiodiplodia* species from Taiwan province, China and Thailand. Based on the herbarium study, two *Lasiodiplodia* species, *L. avicenniarum* and *L. krabiensis* are synonymized under *L. brasiliensis*. Our analyses revelaed that *Lasiodiplodia theobromae* as the most common species in this genus, which occurs in a wide range of hosts in tropical and subtropical regions. The present study has led to the expansion of the taxonomic framework of *Lasiodiplodia* by revealing new host and geographical records. Furthermore, the haplotype networks generated using ITS, *tef*1-α, *tub2*, and *rpb2* sequence data for 520 isolates of *L. theobromae* from 44 host families and 35 countries display that none of the *L. theobromae* isolates grouped according to their host family or country, suggesting that *L. theobromae* is a less genetically diverse, globally distributed species.

Keywords – *Botryosphaeriaceae* – *Lasiodiplodia theobromae* – new geographical records – new host records

Introduction

Lasiodiplodia was introduced by Clendenin (1896) and is typified by *L. tubericola*, which is currently accepted as *L. theobromae* (Liu et al. 2012). This genus belongs to the *Botryosphaeriaceae* in *Botryosphaeriales* (Liu et al. 2012, Hongsanan et al. 2020, Wijayawardene et al. 2022). Both sexual and asexual morphs have been recorded for this genus (Dissanayake et al. 2016). The sexual morph of *Lasiodiplodia* species is characterized by globose to subglobose ascomata, often ostiolate and uniloculate, and clavate, stipitate asci with hyaline to dark brown, aseptate ascospores (Phillips et al. 2013, 2019, Trakunyingcharoen et al. 2015, Tennakoon et al. 2016). The asexual morph is characterized by stromatic, immersed or superficial, globose, uni- or multiloculate conidiomata with a central, single, papillate ostiole. Conidiophores are usually reduced to conidiogenous cells; if present, they are characterized by hyaline, cylindrical, sometimes septate, and rarely branched conidiophores arising from the inner layer. Conidiogenous cells are hyaline, cylindrical to conical in shape, holoblastic, and smooth, arising from the inner wall of conidiomata (Phillips et al. 2013, Rangel-Montoya et al. 2021). *Lasiodiplodia* species have subglobose or oval, smooth, thick-walled conidia that are initially hyaline and become dark brown and striated when mature (Phillips et al. 2013, 2019).

Morphological characters of the ascospores and conidia have been used to differentiate the genera and families in *Botryosphaeriaceae* (Phillips et al. 2008, 2019). *Lasiodiplodia* is distinguished from other *Botryosphaeriaceae* genera by having pigmented, 1-septate conidia with longitudinal striations and pycnidial paraphyses (Phillips et al. 2013, 2019, Dou et al. 2017a). Phylogenetically, *Lasiodiplodia* is closely related to *Diplodia* and *Neodeightonia* (Dissanayake et al. 2016). However, morphologically, the striated conidia of *Lasiodiplodia* distinguish the genus from *Diplodia*, while its paraphyses differentiate it from those of *Neodeightonia*, which also has striate conidia (Phillips et al. 2013, Jayawardena et al. 2019). Molecular clock analyses performed by Rathnayaka et al. (2023) also show that *Lasiodiplodia* separated from other genera in *Botryosphaeriaceae*.

Similar cultural and conidial characters lead to inaccurate identification among *Lasiodiplodia* species (Slippers et al. 2004, Abdollahzadeh et al. 2010). Therefore, phylogeny has been vital for distinguishing species in *Lasiodiplodia* since 2004 (Abdollahzadeh et al. 2010, El-Ganainy et al. 2022). Zhang et al. (2021) synonymized many *Lasiodiplodia* species based on the phylogenetic analyses; for example, *L. hyalina* and *L. swieteniae* were synonymized under *L. thailandica* with 100% similarities in their ITS sequence data. Even though El-Ganainy et al. (2022) accepted 48 species based on morpho-molecular data, there are 86 *Lasiodiplodia* records available in the Index Fungorum (2023). Therefore, studies are required on *Lasiodiplodia* species using both morphological, phylogenetics and phylogenomics, and suitable molecular markers must be established for this genus (Liu et al. 2012, Slippers et al. 2013, El-Ganainy et al. 2022).

Lasiodiplodia species have a cosmopolitan distribution in tropical and subtropical regions and become more abundant in temperate regions (Slippers et al. 2007, Jayawardena et al. 2019). They mainly occur on a wide range of monocotyledonous, dicotyledonous, and gymnosperm hosts (Slippers et al. 2007, Alves et al. 2008, Hyde et al. 2020a). Therefore, studying the global abundance and richness of *Lasiodiplodia* species is vital for understanding the geographical distribution of fungal taxa (Hyde et al. 2020a). Furthermore, additional taxonomic and ecological research is required due to the cosmopolitan distribution of *Lasiodiplodia* species in diverse hosts.

Members of *Lasiodiplodia* exhibit different lifestyles, such as endophytes (Slippers et al. 2007, Chen et al. 2015a), pathogens, (Abdollahzadeh et al. 2010, Dissanayake et al. 2015, de Silva et al. 2019) and saprobes (Liu et al. 2012, de Silva et al. 2019). *Lasiodiplodia* includes pathogens that cause fruit or root rots, cankers, stem blight, and dieback on economically important crops, such as cashew, coconut, mango, and mulberry (Slippers & Wingfield 2007, Phillips et al. 2013, Rodríguez-Gálvez et al. 2017, Gnanesh et al. 2022) leading to crop losses (Gnanesh et al. 2022). In addition, *Lasiodiplodia* species are associated with grapevine diseases, such as cankers and diebacks, which result in stunted growth, wedge-shaped discolourations in the vascular tissues and mortality (Amponsah et al. 2011, Úrbez-Torres 2011, Úrbez-Torres et al. 2012). *Lasiodiplodia crassispora*, *L. mediterranea*, *L. missouriana*, *L. theobromae*, *L. pseudotheobromae*, *L. parva*, and *L. viticola* are reported to associate with the grapevine dieback worldwide (Úrbez-Torres 2011, Correia et al. 2013, Pitt et al. 2013, Yan et al. 2013, Linaldeddu et al. 2015). Therefore, investigating the host-fungal interactions in *Lasiodiplodia* species is essential.

Fungal pathogens like *L. theobromae* show high genetic diversity owing to their short generation time and large population size, which facilitates adaptations to environmental stress and wide distribution (Alberts et al. 2002, Lindahl & Grace 2015). The use of sequence data in diversity studies identifies genetic variations among isolates within a population (Manawasinghe et al. 2019). This knowledge can be used for sustainable breeding and designing management strategies against fungicide-resistant strains (Manawasinghe et al. 2019, Rêgo et al. 2019).

Objectives of the current study include evaluating the most reliable gene combination for species delimitation in *Lasiodiplodia* and determining genetic structures between globally distributed *L. theobromae* isolates using sequence data from four genes (ITS, *tef*1-α, *tub2*, and *rpb2*). This study presents 25 new host and geographical records of *Lasiodiplodia* species based on morpho-molecular analyses. In addition, morphological illustrations and multi-gene phylogenetic analyses with maximum likelihood (ML) and Bayesian inference (BI) analyses are provided.

Materials & Methods

Determination of molecular markers for *Lasiodiplodia*

Sequences of *Lasiodiplodia* strains were retrieved from GenBank (http://www.ncbi.nlm.nih.gov). Sequences from each locus (SSU, LSU, ITS, *tef*1-α, *tub2*, and *rpb2*) were aligned individually using MAFFT 6.864b (Katoh et al. 2019) and trimmed using trimAl v1.2 software (Capella-Gutiérrez et al. 2009). Maximum likelihood (ML) and Bayesian inference (BI) approaches were performed for single-gene and multi-gene datasets. In addition, different gene combinations were tried to select the most reliable markers for *Lasiodiplodia*. The best-fit models for BI and ML analyses were determined using MrModeltest v. 2.2 (Nylander 2004) under the AIC (Akaike Information Criterion) implemented in PAUP v. 4.0b10. The GTR+G model was the best for both ML and BI analyses for all gene regions.

Maximum Likelihood (ML) analysis was performed using IQ-Tree with bootstrap support obtained from 1,000 pseudoreplicates (Nguyen et al. 2015, Chernomor et al. 2016). MrBayes v. 3.2.6 was used for BI analyses (Ronquist et al. 2012) with GTR+G as the evolutionary model with 10,000,000 generations. The trees were sampled at every 100th generation, resulting in 10,000 trees. The first 10% of trees were discarded as the burn-in phase, while the remaining 90% were used to calculate the posterior probabilities (PP) in the majority rule consensus tree. The final phylogenetic tree was visualised with FigTree v1.4.0 program (Rambaut 2012) and reorganised with Microsoft PowerPoint (2010).

Geographical distribution patterns

The shapefile of world countries boundaries (*.shp) was downloaded from the site (http://tapiquen-sig.jimdo.com) in the WGS84 coordinate system. The data was based on shapes from the Environmental Systems Research Institute (ESRI). The geocodes of the countries that *Lasiodiplodia* taxa reported were confirmed with GoogleEarthPro version 7.3.3 (the data providers were: Image Landsat/Copernicus, Data SIO, NOAA, US. Navy, NGA, GEBCO, US Dept. of State Geographer, https://www.google.com/earth/). The global abundance and number of *Lasiodiplodia* species were mapped using QGIS version 3.20.3 (QGIS Geographic Information System, Open-Source Geospatial Foundation Project. http://qgis.org/). The previously reported *Lasiodiplodia* species were tabulated in Table 1 to illustrate the species abundances and richness (Farr & Rossman 2022).

Table 1 *Lasiodiplodia* species abundance and richness in each country.

Country	Species abundance	Species richness
Alaska	1	1
Algeria	3	2
Argentina	3	1
Australia	79	14
Bangladesh	1	1
Benin	4	4
Bolivia	2	1
Botswana	1	1
Brazil	173	18
Brunei	1	1
California	14	3
Cameroon	8	5
Chile	2	1
China	85	14
Colombia	4	2
Congo	2	2
Cook Islands	6	1
Costa Rica	3	2
Cuba	57	1
Dominican Republic	1	1
Ecuador	3	2
Egypt	9	3
Ethiopia	1	1
Fiji	18	1
Florida	13	1
France	1	1
Georgia	1	1
Germany	1	1
Guinea-Bissau (West Africa)	5	3
Haiti	1	1
Hawaii	5	1
Honduras	1	1
Hong Kong	6	1
India	43	3
Indonesia	2	2
Iran	24	7
Iraq	2	1

Table 1 Continued.

Country	Species abundance	Species richness
Italy	16	8
Japan	13	1
Korea	4	2
Laos	11	10
Madagascar	7	7
Malaysia	12	5
Mexico	32	8
Missouri	2	1
Mozambique	4	4
Myanmar	15	1
Namibia	8	4
Netherlands	3	1
Nicaragua	1	1
Nigeria	2	1
Niue	2	1
North Carolina	1	1
Oman	10	2
Pakistan	4	3
Panama	4	1
Papua New Guinea	2	1
Peru	10	5
Philippines	12	1
Portugal	1	1
Puerto Rico	14	6
Samoa	10	1
Senegal	5	5
Seychelles	1	1
Singapore	2	1
South Africa	51	11
Spain	6	2
Sri Lanka	14	3
Suriname	1	1
Switzerland	2	1
Taiwan province, China	8	2
Tanzania	2	2
Texas	1	1
Thailand	57	14
Togo	1	1
Tonga	3	1
Tunisia	5	2
Turkey	9	4
Uganda	5	1
United Arab Emirates	2	1
United States	14	5
Uruguay	3	2
Uzbekistan	1	1
Venezuela	111	4
Viet Nam	3	1
Virginia	1	1
West Indies	34	1
Western Australia	7	2
Zaire	3	1
Zimbabwe	1	1

Taxonomy & phylogeny

Specimen collections, morphological studies, and isolations

Fresh fungal materials were collected from Taiwan province, China and Thailand. The specimens were taken to the laboratory in zip-lock plastic bags. The samples were examined following the methods described by Senanayake et al. (2020). Morphological characters were examined using a LEICA EZ4 stereomicroscope (Leica Microsystems Company, Germany) and AXIOSKOP 2 PLUS compound microscope (Carl Zeiss Microscopy Company, Germany) and photographed with a Canon 550D digital camera fitted to the microscope. Measurements were made with ZEN2 (blue edition) software and calculated with the Tarosoft (R) Image Frame Work program. Photoplates and images were processed using Adobe Photoshop CS3 Extended version 10.0 software (Adobe Systems, USA).

Single spore isolations followed the methodology described in Senanayake et al. (2020) on potato dextrose agar (PDA). Herbarium specimens were deposited in the Mae Fah Luang University Herbarium (MFLU), Chiang Rai, Thailand. In addition, living cultures were deposited at the Mae Fah Luang University Culture Collection (MFLUCC) and the National Chiayi University Culture Collection, Taiwan, China (NCYUCC). Species identifications in this study followed the polyphasic approaches as guided in Chethana et al. (2021).

DNA extraction, PCR amplifications and sequencing

Genomic DNA was extracted from mycelium (50–100 mg) using the E.Z.N.A Fungal DNA Mini Kit- D3390-02 (Omega Bio-Tek, USA), following the manufacturer's instructions. Extracted DNA was stored at 4 °C for a short period and -20 °C for long-term storage. The DNA sequences were obtained from four gene regions, ITS, *tef*1-α, *tub2*, and *rpb2*. The polymerase chain reactions (PCR) for ITS, *tef*1-α, *tub2*, and *rpb2* were performed using ITS4/ ITS5 (White et al. 1990), EF1-728F/ EF1-986F (Carbone & Kohn 1999), Bt2a/ Bt2b (Glass & Donaldson 1995), and fRPB2-5f/fRPB2-7cR (Liu et al. 1999), respectively. Polymerase chain reactions (PCR) were carried out as described in Rathnayaka et al. (2022) for the above four gene regions. Amplification reactions were performed in 25µl of total reaction volume that contained 9.5 µl of sterilized water, 12.5 µl of 2×Power TaqPCR MasterMix (Tri-I Biotech, Taipei, Taiwan, China), 1 µl of each forward and reverse primers, and 1 µl of DNA template. PCR products were visualised on 1.5% agarose gels containing Safeview DNA stain (GeneMark, Taipei, Taiwan, China) and sequenced at Tri-I Biotech, Taipei, Taiwan, Biogenomed Co. Ltd., Thailand and SinoGenoMaxSanger sequencing laboratory (Beijing, China). Newly generated nucleotide sequences were deposited in GenBank (Table 2).

Phylogenetic analyses

The quality of the sequence chromatograms was checked using BioEdit v 7.0.9.0 (Hall 1999), and forward and reverse sequences were combined using Lasergene SeqMan Pro v.7. Newly generated sequences of LSU, ITS, *tef*1-α, *tub2*, and *rpb2* were first subjected for BLASTn searches -in NCBI to identify the closest matches in the GenBank. Then, closely related sequences of *Lasiodiplodia* were downloaded from GenBank based on BLAST results and relevant publications (Wu et al. 2021) (Table 2). Each locus (ITS, *tef*1-α, *tub2*, and *rpb2*) was aligned in MAFFT 6.864b (Katoh et al. 2019) and trimmed using trimAl v1.2 software (Capella-Gutiérrez et al. 2009). Finally, single and combined gene alignments were analysed individually using ML and BI. MrModeltest v. 2.2 has been used to select evolutionary models independently for each locus under the AIC (Akaike Information Criterion) implemented in PAUP v. 4.0b1 for BI and ML analyses (Nylander 2004) under the AIC (Akaike Information Criterion) implemented in PAUP v. 4.0b10. For all gene regions in both BI and ML analyses, the GTR+G model was selected as the best model.

RAxML-HPC2 on XSEDE (v. 8.2.10) (Stamatakis 2014) in the CIPRES Science Gateway (Miller et al. 2010) was used for the ML analyses. The nonparametric bootstrap iterations were run for 1,000 replications with the GTR+G substitution model. MrBayes v. 3.2.6 (Ronquist et al. 2012) was used for the BI analysis. The Markov Chain Monte Carlo (MCMC) algorithm of six chains was initiated for 1,000,000 generations, sampling at every 100th generation, resulting in 10,000 trees. The first 1,000 trees were discarded as the burn-in phase, while the remaining 9,000 trees were used to calculate the posterior probabilities (PP) in the majority rule consensus tree. Phylograms were visualised with the FigTree v1.4.0 program (Rambaut 2012) and reorganised in Microsoft PowerPoint (2010).

Table 2 Taxa used in the phylogenetic analysis and their GenBank accession numbers.

Species	**Strain no.**	**Host**	**Location**	**GenBank accession numbers**			
				ITS	***tef*1-α**	***tub2***	***rpb2***
Lasiodiplodia acaciae	CBS 136434*	*Acacia* sp.	Indonesia	MT587421	MT592133	MT592613	MT592307
L. aquilariae	CGMCC 3.18471*	*Aquilaria crassna*	Laos	KY783442	KY848600	N/A	KY848562
L. avicenniae	CMW 41467*	*Avicennia marina*	South Africa	KP860835	KP860680	KP860758	KU587878
L. avicenniae	CBS 139670 = CMW 41467	*Avicennia marina*	South Africa	KU587957	KU587947	KU587868	KU587880
L. brasiliensis	CMM 4015*	*Mangifera indica*	Brazil	JX464063	JX464049	N/A	N/A
L. brasiliensis	CMM 4469	*Anacardium occidentale*	Brazil	KT325574	KT325580	N/A	N/A
L. brasiliensis (Syn: *L. avicenniarum*)	MFLUCC 17-2591*	*Avicennia marina*	Thailand	MK347777	MK340867	N/A	N/A
L. brasiliensis (Syn: *L. krabiensis*)	MFLUCC 17-2617*	*Bruguiera* sp.	Thailand	MN047093	MN077070	N/A	N/A
L. bruguierae	CMW 41470*	*Bruguiera gymnorrhiza*	South Africa	KP860832	KP860677	KP860755	KU587875
L. bruguierae	CMW 42480	*Bruguiera gymnorrhiza*	South Africa	KP860834	KP860679	KP860757	KU587876
L. chiangraiensis	MFLUCC 21-0003*	Unknown host	Thailand	MW760854	MW815630	MW815628	N/A
L. chiangraiensis	GZCC 21-0003	Unknown host	Thailand	MW760853	MW815629	MW815627	N/A
L. chonburiensis	MFLUCC 16-0376*	*Pandanus* sp.	Thailand	MH275066	MH412773	MH412742	N/A
L. cinnamomi	CFCC 51997*	*Cinnamomum camphora*	China	MG866028	MH236799	MH236797	MH236801
L. cinnamomi	CFCC 51998	*Cinnamomum camphora*	China	MG866029	MH236800	MH236798	MH236802
L. citricola	**MFLU22-0279**	*Dracaena fragrans*	Thailand	OQ123583	N/A	N/A	N/A
L. citricola	**MFLU22-0280**	*Areca catechu*	Thailand	OQ123584	N/A	OQ509081	N/A
L. citricola	CBS 124707*	*Citrus* sp.	Iran	GU945354	GU945340	KU887505	KU696351
L. citricola	CBS 124706	*Citrus* sp.	Iran	GU945353	GU945339	KU887504	KU696350
L. crassispora	CBS 118741*	*Santalum album*	Australia	DQ103550	DQ103557	KU887506	KU696353
L. crassispora	CMW 13488	*Eucalyptus urophylla*	Venezuela	DQ103552	DQ103559	KU887507	KU696352
L. crassispora	CBS 121770	*Acacia mellifera*	Namibia	EU101307	EU101352	KU887527	KU696378
L. crassispora	**NCYUCC 19-0391**	*Garcinia subelliptica*	Taiwan province, China	OQ123585	OQ509116	N/A	N/A
L. euphorbiaceicola	CMM 3609*	*Jatropha curcas*	Brazil	KF234543	KF226689	KF254926	N/A
L. euphorbiaceicola	CMW 33268	*Adansonia* sp.	Senegal	KU887131	KU887008	KU887430	KU887367

Table 2 Continued.

Species	**Strain no.**	**Host**	**Location**	**GenBank accession numbers**			
				ITS	***tef*1-α**	***tub2***	***rpb2***
L. gilanensis	IRAN1523C*	*Citrus* sp.	Iran	GU945351	GU945342	KU887511	KP872462
L. gilanensis	IRAN1501C	*Citrus* sp.	Iran	GU945352	GU945341	KU887510	KP872463
L. gilanensis	CBS 128311	*Vitis vinifera*	USA	HQ288225	HQ288267	HQ288304	N/A
L. gonubiensis	CMW 14077*	*Syzygium cordatum*	South Africa	AY639595	DQ103566	DQ458860	N/A
L. gonubiensis	CMW 14078	*Syzygium cordatum*	South Africa	AY639594	DQ103567	EU673126	N/A
L. gravistriata	CMM 4564*	*Anacardium humile*	Brazil	KT250949	KT250950	N/A	N/A
L. gravistriata	CMM 4565	*Anacardium humile*	Brazil	KT250947	KT266812	N/A	N/A
L. hormozganensis	IRAN1500C*	*Olea* sp.	Iran	GU945355	GU945343	KU887515	KP872466
L. hormozganensis	IRAN1498C	*Mangifera indica*	Iran	GU945356	GU945344	KU887514	KP872467
L. iranensis	IRAN1520C*	*Salvadora persica*	Iran	GU945348	GU945336	KU887516	KP872468
L. iranensis	IRAN1502C	*Juglans* sp.	Iran	GU945347	GU945335	KU887517	KP872469
L. iranensis	CMM 3610	*Jatropha curcas*	Brazil	KF234544	KF226690	KF254927	N/A
L. laeliocattleyae	CBS 130992*	*Mangifera indica*	Egypt	NR_120002	KU507454	KU887508	KU696354
L. laeliocattleyae	BOT 29	*Mangifera indica*	Egypt	JN814401	JN814428	N/A	N/A
L. lignicola	CBS 134112*	Dead wood	Thailand	JX646797	KU887003	KT852958	KU696364
L. lignicola	CGMCC 3.18061*	Woody branch	China	NR_152983	KX499927	KX500002	KX499965
L. macrospora	CMM 3833*	*Jatropha curcas*	Brazil	NR_147349	KF226718	KF254941	N/A
L. mahajangana	CMW 27801*	*Terminalia catappa*	Madagascar	NR_147325	FJ900641	FJ900630	N/A
L. mahajangana	IBL366	*Terminalia catappa*	Madagascar	FJ900596	FJ900642	FJ900631	N/A
L. mahajangana	CMM 1325	*Citrus sinensis*	Brazil	KT154760	KT008006	KT154767	N/A
L. mahajangana	CBS 137785	*Quercus ilex*	Tunisia	KJ638317	KJ638336	KU887509	KU696355
L. mahajangana	**KUMCC 20-0066**	*Desmos chinensis*	Thailand	OQ123586	OQ509113	OQ509082	N/A
L. margaritacea	CBS 122519*	*Adansonia gibbosa*	Australia	KT852959	EU144065	KU887520	KU696367
L. mediterranea	CBS 137783*	*Quercus ilex*	Italy	KJ638312	KJ638331	KU887521	KU696368
L. mediterranea	CBS 137784	*Vitis vinifera*	Italy	KJ638311	KJ638330	KU887522	KU696369
L. microcondia	CGMCC 3.18485 *	*Aquilaria crassna*	Laos	KY783441	KY848614	N/A	KY848561
L. parva	CBS 456.78*	Cassava-field soil	Colombia	EF622083	EF622063	KU887523	KP872477
L. parva	CBS 494.78	Cassava-field soil	Colombia	EF622084	EF622064	EU673114	KU696373
L. plurivora	STE-U 5803*	*Prunus salicina*	South Africa	EF445362	EF445395	KP872421	KP872479
L. plurivora	STE-U 4583	*Vitis vinifera*	South Africa	AY343482	EF445396	KU887525	KU696375
L. pontae	CMM 1277*	*Spondias purpurea*	Brazil	KT151794	KT151791	KT151797	N/A
L. pseudotheobromae	CBS 116459*	*Gmelina arborea*	Costa Rica	EF622077	EF622057	EU673111	KU696376
L. pseudotheobromae	CBS 116460	*Acacia mangium*	Costa Rica	EF622078	EF622058	KU198428	N/A
L. pseudotheobromae	**MFLU22-0283**	*Panicum* sp.	Thailand	OQ123587	OQ509114	OQ509083	N/A
L. pseudotheobromae	**MFLU22-0284**	*Calamus* sp.	Thailand	OQ123588	OQ509115	OQ509084	N/A

Table 2 Continued.

Species	**Strain no.**	**Host**	**Location**	**GenBank accession numbers**			
				ITS	***tef*1-α**	***tub2***	***rpb2***
L. rubropurpurea	WAC 12535*	*Eucalyptus grandis*	Australia	DQ103553	DQ103571	EU673136	KP872485
L. rubropurpurea	WAC 12536	*Eucalyptus grandis*	Australia	DQ103554	DQ103572	KU887530	KP872486
L. subglobosa	CMM3872*	*Jatropha curcas*	Brazil	KF234558	KF226721	KF254942	N/A
L. subglobosa	CMM 4046	*Jatropha curcas*	Brazil	KF234560	KF226723	KF254944	N/A
L. syzygii	MFLUCC 19-0257*	*Syzygium samarangense*	Thailand	MT990531	MW016943	MW014331	N/A
L. thailandica	CPC 22795	*Mangifera indica*	Thailand	KJ193637	KJ193681	N/A	N/A
L. thailandica	CPC:22755	*Phyllanthus acidus*	Thailand	KM006433	KM006464	N/A	N/A
L. thailandica	CGMCC 3.17975*	*Acacia confusa*	China	NR_152982	KX499917	KX499992	KX499955
L. thailandica	MFLUCC 18-0244*	*Swietenia mahagoni*	Thailand	MK347789	MK340870	MK412877	N/A
L. thailandica	**MFLU22-0293**	*Musa* sp.	Thailand	OQ123597	N/A	OQ509090	N/A
L. thailandica	**MFLU22-0294**	*Hevea brasiliensis*	Thailand	OQ123598	OQ509098	N/A	N/A
L. thailandica	**MFLU22-0295**	*Holmskioldia* sp.	Thailand	OQ123599	OQ509099	N/A	N/A
L. thailandica	**MFLU22-0296**	*Macaranga peltate*	Thailand	OQ123600	N/A	N/A	N/A
L. thailandica	**MFLU22-0297**	*Delonix regia*	Thailand	OQ123601	OQ509100	OQ509091	N/A
L. thailandica	**MFLU22-0298**	*Wodyetia bifurcata*	Thailand	OQ123602	OQ509102	OQ509092	N/A
L. thailandica	**MFLU22-0299**	*Cocos nucifera*	Thailand	OQ123603	N/A	OQ509093	N/A
L. thailandica	**MFLU22-0300**	*Tectona grandis*	Thailand	OQ123604	N/A	OQ509094	N/A
L. thailandica	**NCYUCC 19-0399**	*Cerasus* sp.	Taiwan province, China	OQ123605	N/A	OQ509095	N/A
L. thailandica	**MFLUCC 21-0188**	*Magnolia lilifera*	Thailand	OQ123607	OQ509103	OQ509097	N/A
L. theobromae	CBS 164.96*	Fruit along coral reef coast	Papua New Guinea	NR_111174	AY640258	KU887532	KU696383
L. theobromae	CBS 111530	*Leucospermum* sp.	USA	EF622074	EF622054	KU887531	KU696382
L. theobromae	**MFLU22-0285**	*Areca catechu*	Thailand	OQ123589	OQ509104	N/A	OQ509077
L. theobromae	**MFLU22-0286**	*Dracaena aletriformis*	Thailand	OQ123590	OQ509105	OQ509085	N/A
L. theobromae	**MFLU22-0287**	*Quercus* sp.	Thailand	OQ123591	OQ509106	OQ509086	N/A
L. theobromae	**MFLU22-0288**	*Bidens pilosa*	Thailand	OQ123592	OQ509107	N/A	OQ509078
L. theobromae	**NCYUCC 19-0392**	*Ficus benguetensis*	Taiwan province, China	OQ123606	OQ509112	OQ509096	N/A
L. theobromae	**MFLU22-0289**	*Calamus* sp.	Thailand	OQ123593	OQ509108	OQ509087	N/A
L. theobromae	**MFLU22-0290**	*Artocarpus heterophyllus*	Thailand	OQ123594	OQ509109	OQ509088	OQ509080

Table 2 Continued.

Species	Strain no.	Host	Location	GenBank accession numbers			
				ITS	***tef*1-α**	***tub2***	***rpb2***
L. theobromae	**MFLU22-0291**	*Paulownia tomentosa*	Thailand	OQ123595	OQ509110	N/A	OQ509079
L. theobromae	**NCYUCC 19-0420**	*Bidens alba*	Taiwan province, China	OQ123596	OQ509111	OQ509089	N/A
L. tropica	CGMCC 3.18477*	*Aquilaria crassna*	Laos	KY783454	KY848616	KY848540	KY848574
L. venezuelensis	WAC12539*	*Acacia mangium*	Venezuela	DQ103547	DQ103568	KU887533	KP872490
L. venezuelensis	WAC12540	*Acacia mangium*	Venezuela	DQ103548	DQ103569	KU887534	KP872491
L. viticola	CBS 128313*	*Vitis vinifera*	USA	HQ288227	HQ288269	HQ288306	KU696385
L. viticola	UCD 2604MO	*Vitis vinifera*	USA	HQ288228	HQ288270	HQ288307	KP872493
L. vitis	CBS: 124060*	*Vitis vinifera*	Italy	KX464148	KX464642	KX464917	KX463994
Diplodia mutila	CMW7060*	*Vitis vinifera*	Portugal	NR_144906	MZ073947	MZ073931	N/A
D. seriata	CBS 112555*	*Vitis vinifera*	Portugal	AY259094	AY573220	DQ458856	KX463962

*Type strains; newly generated sequences in this study are in bold.

BOT: A. M. Ismail, Plant Pathology Research Institute, Egypt; CBS: Centraalbueau voor Schimmelcultures, Utrecht, The Netherlands; CFCC: China Forestry Culture Collection Center, Beijing, China; CGMCC: China General Microbiological Culture Collection Center; CMM: Culture Collection of Phytopathogenic Fungi ‘Prof. Maria Menezes’ (CMM) at the Universidade Federal Rural de Pernambuco (Recife, Pernambuco); CMW: Tree Pathology Co-operative Program, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; CPC: Culture collection of Pedro Crous; CGMCC: China General Microbiological Culture Collection Center; GZCC: Guizhou Academy of Agricultural Sciences Culture Collection, Guizhou, China; IBL: Personal culture collection, I.B.L. Coutinho; IRAN: Iranian Fungal Culture Collection, Iranian Research Institute of Plant Protection, Iran; KUMCC: Kunming Institute of Botany Culture Collection, China; MFLU: Mae Fah Luang University Herbarium, Chiang Rai, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NCYUCC: National Chiayi University Culture Collection, Chiayi, Taiwan, China; STE-U: Culture collection of the Department of Plant Pathology, University of Stellenbosch, South Africa; UCD: University of California, Davis, Plant Pathology Department Culture Collection; WAC: Department of Agriculture, Western Australia Plant Pathogen Collection, South Perth, Western Australia. ITS: internal transcribed spacer regions; *tef*1-α: translation elongation factor 1-alpha gene; *tub2*: beta-tubulin gene; *rpb2*: DNA-directed RNA polymerase II second largest subunit.

Haplotype assignment and constructing networks

The sequences of *L. theobromae* were downloaded from GenBank (Table 3). Each locus (ITS, *tef*1-α, *tub2*, and *rpb2*) was aligned individually with MAFFT 6.864b (Katoh et al. 2019) and trimmed in trimAl v1.2 (Capella-Gutiérrez et al. 2009). The number of haplotypes and haplotype diversity (Hd) for each locus (ITS, *tef*1-α, *tub2*, and *rpb2*), was determined in DnaSP v. 6 (Rozas et al. 2017), as well as for the combined dataset of the ITS and *tef*1-α. The Roehl Data file (.rdf) was generated using the following parameters: Sites with gaps/missing: not considered and Invariable sites: removed. The NETWORK 10.2.0.0 was used to construct Median-joining haplotype networks for single and combined datasets (Bandelt et al. 1999, http://www.fluxus-engineering.com/sharenet.htm).

Table 3 Sequences of *Lasiodiplodia theobromae* strains downloaded from GenBank for the haplotype network analyses

Host	Country	Strain no.	ITS	*tef*1-*α*	*tub*2	*rpb2*
Acacia karroo	South Africa	CMW38120	KC769935	KC769843	KC769887	N/A
Acacia karroo	South Africa	CMW38121	KC769936	KC769844	KC769888	N/A
Acacia karroo	South Africa	CMW38122	KC769937	KC769845	KC769889	N/A
Acacia karroo	South Africa	HSYF04	KC769935	KC769843	KC769887	N/A
Acacia karroo	South Africa	HY-3	KC769936	KC769844	KC769888	N/A
Acacia karroo	South Africa	HY-4	KC769937	KC769845	KC769889	N/A
Acacia mangium	Venezuela	A10	JX545093	JX545113	JX545133	N/A
Acacia mangium	Venezuela	A13	JX545094	JX545114	JX545134	N/A
Acacia mangium	Venezuela	CMW13501	KY473072	KY473020	KY472963	KY472889
Acacia mangium	Indonesia	CMW23003	EU588629	EU588609	KY472918	KY472846
Acacia mangium	Indonesia	CMW23008	EU588630	EU588610	KY472919	KY472847
Acacia mangium	Indonesia	CMW23018	EU588633	EU588613	KY472920	KY472848
Acacia mangium	Indonesia	CMW23031	EU588631	EU588611	KY472921	KY472849
Acacia mangium	Indonesia	CMW23073	EU588632	EU588612	KY472922	KY472850
Acacia mangium	Venezuela	D043	KY473072	KY473020	KY472963	KY472889
Acacia mangium	Indonesia	GX-5-5A	EU588629	EU588609	KY472918	KY472846
Acacia mangium	Indonesia	GZHS-2017-010	EU588630	EU588610	KY472919	KY472847
Acacia mangium	Indonesia	GZHS-2017-011	EU588633	EU588613	KY472920	KY472848
Acacia mangium	Indonesia	GZHS-2017-012	EU588631	EU588611	KY472921	KY472849
Acacia mangium	Indonesia	GZHS-2017-013	EU588632	EU588612	KY472922	KY472850
Actinidia deliciosa	China	Mht-5	JQ658976	JQ658977	JQ658978	N/A
Adansonia digitata	Nigeria	CMW33290	KY473027	KY472970	KY472896	KU887372
Adansonia digitata	Cameroon	CMW36127	KY473029	KY472977	KY472907	KU887410
Adansonia digitata	Nigeria	HNWZS03	KY473027	KY472970	KY472896	KU887372
Adansonia digitata	Cameroon	HSYF03	KY473029	KY472977	KY472907	KU887410
Albizia falcataria	China	No18	KJ676657	KJ676656	KJ676655	N/A
Anacardium occidentale	Brazil	CMM4499	KT325578	KT325587	N/A	N/A
Anacardium occidentale	Brazil	CMM4508	KT325576	KT325588	N/A	N/A
Anacardium occidentale	Brazil	CMM4513	KT325577	KT325589	N/A	N/A
Anacardium occidentale	West Africa-Guinea-Bissau	CMW24702	MN952990	MN952201	MN952205	N/A
Anacardium occidentale	Brazil	CMW54204	KT247468	KT247470	KT247476	N/A
Anacardium occidentale	Brazil	CMW54217	KT247469	KT247471	KT247477	N/A
Anacardium occidentale	Brazil	CSM_34	KT325578	KT325587	N/A	N/A
Anacardium occidentale	Brazil	CSM_36	KT325576	KT325588	N/A	N/A
Anacardium occidentale	Brazil	CSM_53	KT325577	KT325589	N/A	N/A
Ananas comosus	China	CMW32549	MK398306	MK593149	MK419015	N/A
Ananas comosus	China	CMW32571	MK398310	MK593153	MK419019	N/A
Ananas comosus	China	CMW32603	MK398301	MK593144	MK419010	N/A
Ananas comosus	China	CMW32604	MK398298	MK593142	MK419008	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Ananas comosus	China	CMW32606	MK398308	MK593151	MK419017	N/A
Ananas comosus	China	CMW32651	MK398305	MK593148	MK419014	N/A
Ananas comosus	China	CMW32666	MK398299	MK593143	MK419009	N/A
Ananas comosus	China	CMW33290	MK398304	MK593147	MK419013	N/A
Ananas comosus	China	CMW33658	MK358287	MK593141	MK419007	N/A
Ananas comosus	China	CMW33957	MK398312	MK593155	MK419021	N/A
Ananas comosus	China	CMW36127	MK398307	MK593150	MK419016	N/A
Ananas comosus	China	CMW38120	MK358286	MK593140	MK419006	N/A
Ananas comosus	China	CMW38121	MK398302	MK593145	N/A	N/A
Ananas comosus	China	CMW38122	MK398311	MK593154	MK419020	N/A
Ananas comosus	China	CMW40630	MK398303	MK593146	MK419012	N/A
Ananas comosus	China	CMW40635	MK398309	MK593152	MK419018	N/A
Annona muricata	Brazil	CDA1169	KY994618	KX528559	N/A	N/A
Annona muricata	Brazil	CDA1212	KY994617	KX528558	N/A	N/A
Annona squamosa	Brazil	CDA1211	KY994616	KX528557	N/A	N/A
Annona squamosa	China	CMW40636	MW625913	MW625914	MW625915	N/A
Annona squamosa	China	CMW41360	MW625916	MW625917	MW625918	N/A
Annona squamosa	China	CMW42341	MW876481	MW876482	MW876483	N/A
Annona squamosa	China	CMW4694	MW876484	MW876485	MW876486	N/A
Artocarpus heterophyllus	Thailand	MFLU22-0290	OQ123594	OQ509109	OQ509088	OQ509080
Auricularia auricular	China	A1	KC442315	KC442318	KC442317	N/A
Barringtonia racemosa	South Africa	CMW41360	KP860841	KP860686	KP860764	KU587888
Barringtonia racemosa	South Africa	CMW42341	KP860843	KU587945	KU587866	KU587890
Barringtonia racemosa	South Africa	IBL404	KP860841	KP860686	KP860764	KU587888
Barringtonia racemosa	South Africa	IBL405	KP860843	KU587945	KU587866	KU587890
Bidens alba	Taiwan province, China	NCYUCC 19-0420	OQ123596	OQ509111	OQ509089	N/A
Bidens pilosa	Thailand	MFLU22-0288	OQ123592	OQ509107	N/A	OQ509078
Calamus sp.	Thailand	MFLU22-0289	OQ123593	OQ509108	OQ509087	N/A
Camellia oleifera	China	YCLas1	KF811055	KJ639048	KJ639047	N/A
Camellia sinensis	China	CMW26630	MG932788	MG932789	MG932791	N/A
Camellia sinensis	China	CMW28308	MH454027	MH454032	N/A	N/A
Camellia sinensis	China	CMW28312	MH454028	MH454033	N/A	N/A
Camellia sinensis	China	CMW28547	MH454029	MH454034	N/A	N/A
Camellia sinensis	China	CMW28548	MH454030	MH454035	N/A	N/A
Camellia sinensis	China	CMW28550	MH454031	MH454036	N/A	N/A
Camellia sinensis	China	CPLt	KX505288	KX580759	N/A	N/A
Camellia sinensis	China	CRI-LP2	KX505289	KX580760	N/A	N/A
Camellia sinensis	China	CRM-B101	KX505290	KX580761	N/A	N/A
Camellia sinensis	China	CRM-B31	KX505291	KX580762	N/A	N/A
Capparis flexuosa	Brazil	CF/UENF429	KY655195	KY223712	N/A	N/A
Carica papaya	Mexico	BOM230	KR001856	KT075154	N/A	N/A
Carica papaya	Mexico	BOS104	KR001857	KT075158	N/A	N/A
Carica papaya	Mexico	BOT112	KT075139	KT075155	N/A	N/A
Carica papaya	Brazil	CMM2168	KC484817	KC481572	N/A	N/A
Carica papaya	Brazil	CMM2179	KC484787	KC481569	KX120051	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Carica papaya	Brazil	CMM2183	KC484824	KC481573	N/A	N/A
Carica papaya	Brazil	CMM2190	KC484780	KC481518	N/A	N/A
Carica papaya	Brazil	CMM2193	KC484826	KC481550	N/A	N/A
Carica papaya	Brazil	CMM2208	KC484776	KC481575	N/A	N/A
Carica papaya	Brazil	CMM2209	KC484784	KC481578	N/A	N/A
Carica papaya	Brazil	CMM2210	KC484783	KC481577	N/A	N/A
Carica papaya	Brazil	CMM2231	KC484775	KC481515	N/A	N/A
Carica papaya	Brazil	CMM2232	KC484785	KC481521	N/A	N/A
Carica papaya	Brazil	CMM2235	KC484779	KC481517	N/A	N/A
Carica papaya	Brazil	CMM2237	KC484819	KC481547	N/A	N/A
Carica papaya	Brazil	CMM2238	KC484771	KC481512	N/A	N/A
Carica papaya	Brazil	CMM2239	KC484786	KC481522	N/A	N/A
Carica papaya	Brazil	CMM2241	KC484790	KC481571	KX120055	N/A
Carica papaya	Brazil	CMM2261	KC484789	KC481579	N/A	N/A
Carica papaya	Brazil	CMM2262	KC484822	KC481581	N/A	N/A
Carica papaya	Brazil	CMM2265	KC484772	KC481574	N/A	N/A
Carica papaya	Brazil	CMM2267	KC484777	KC481576	N/A	N/A
Carica papaya	Brazil	CMM2268	KC484818	KC481580	N/A	N/A
Carica papaya	Brazil	CMM2269	KC484821	KC481585	N/A	N/A
Carica papaya	Brazil	CMM2276	KC484820	KC481548	N/A	N/A
Carica papaya	Brazil	CMM2278	KC484781	KC481519	N/A	N/A
Carica papaya	Brazil	CMM2280	KC484773	KC481513	N/A	N/A
Carica papaya	Brazil	CMM2282	KC484827	KC481551	N/A	N/A
Carica papaya	Brazil	CMM2294	KC484828	KC481552	N/A	N/A
Carica papaya	Brazil	CMM2295	KC484774	KC481514	N/A	N/A
Carica papaya	Brazil	CMM2297	KC484823	KC481582	N/A	N/A
Carica papaya	Brazil	CMM2303	KC484816	KC481546	N/A	N/A
Carica papaya	Brazil	CMM2306	KC484788	KC481570	KX120059	N/A
Carica papaya	Brazil	CMM2310	KC484782	KC481520	N/A	N/A
Carica papaya	Brazil	CMM2327	KC484778	KC481516	N/A	N/A
Carica papaya	Brazil	CMM2328	KC484825	KC481549	N/A	N/A
Carica papaya	Mexico	LAM118	KT075141	KT075156	N/A	N/A
Carica papaya	Mexico	LAM200	KX355576	KT075157	N/A	N/A
Casuarina cunninghamian	Uganda	DAR82930	DQ103534	DQ103564	KY472959	KY472884
Casuarina cunninghamiana	Uganda	CMW18420	DQ103534	DQ103564	KY472959	KY472884
Casuarina cunninghamiana	Uganda	CMW32245	KY473068	KY473016	KY472960	KY472885
Casuarina cunninghamiana	Uganda	CMW32246	KY473069	KY473017	KY472961	KY472886
Casuarina cunninghamiana	Uganda	HNDA03	KY473068	KY473016	KY472960	KY472885
Casuarina cunninghamiana	Uganda	HNDF01	KY473069	KY473017	KY472961	KY472886
Citrus latifolia	Mexico	UACH 263	MH277691	MH286528	MH279908	N/A
Citrus latifolia	Mexico	UACH 264	MH277692	MH286534	MH279909	N/A
Citrus latifolia	Mexico	UACH 272	MH277693	MH286533	MH279915	N/A
Citrus latifolia	Mexico	UACH 273	MH277694	MH286526	MH279907	N/A
Citrus latifolia	Mexico	UACH 280	MH277695	MH286527	MH279910	N/A
Citrus latifolia	Mexico	UACH 284	MH277696	MH286532	MH279914	N/A
Citrus latifolia	Mexico	UACH 285	MH277697	MH286531	MH279913	N/A
Citrus latifolia	Mexico	UACH 287	MH277698	MH286530	MH279912	N/A
Citrus latifolia	Mexico	UACH 288	MH277699	MH286529	MH279911	N/A
Citrus limon	Chile	1932	KX925548	MG019403	MG029366	N/A
Citrus limon	Chile	930	KX925546	MG019401	MG029365	N/A
Citrus limon	Chile	1931	KX925547	N/A	N/A	N/A
Citrus reticulata	Chile	1933	KX925549	MG019404	MG029368	N/A
Citrus tangerina	Puerto Rico	12	MK282712	MK294130	MK294092	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-*α***	***tub*2**	***rpb2***
Citrus tangerina	Puerto Rico	313	MK282713	MK294131	MK294093	N/A
Cocos nucifera	Unknown	CBS306.58	EF622071	EF622051	N/A	MT592334
Cocos nucifera	Brazil	CDA 425	KP244697	KP308475	KP308531	N/A
Cocos nucifera	Brazil	CDA 444	KP244699	KP308477	KP308532	N/A
Cocos nucifera	Brazil	CDA 450	KP244688	KP308478	KP308533	N/A
Cocos nucifera	Brazil	CDA 467	KP244702	KP308473	KP308536	N/A
Cocos nucifera	Brazil	CDA 469	KP244691	KP308466	KP308537	N/A
Cocos nucifera	Brazil	CDA 472	KP244692	KP308467	KP308538	N/A
Cocos nucifera	Brazil	CF/UENF419	KY655198	KY223719	N/A	N/A
Cocos nucifera	Brazil	CF/UENF420	KY655199	KY223720	N/A	N/A
Cocos nucifera	Brazil	CF/UENF421	KY655200	KY223708	N/A	N/A
Cocos nucifera	Brazil	CF/UENF428	KY655194	KY223711	N/A	N/A
Cocos nucifera	Brazil	CF/UENF430	KY655203	KY223713	N/A	N/A
Cocos nucifera	Brazil	CF/UENF431	KY655204	KY223714	N/A	N/A
Cocos nucifera	Brazil	CF/UENF432	KY655205	KY223715	N/A	N/A
Cocos nucifera	Brazil	CF/UENF435	KY655208	KY223716	N/A	N/A
Cocos nucifera	Brazil	CF/UENF437	KY655210	KY223718	N/A	N/A
Cocos nucifera	Brazil	COAD 1788	KP244698	KP308476	KP308528	N/A
Cocos nucifera	Brazil	COAD 1789	KP244700	KP308474	KP308529	N/A
Cocos nucifera	Brazil	COAD 1790	KP244703	KP308468	KP308530	N/A
Cocos nucifera	Brazil	COUFAL0102	MK792506	MK792505	N/A	N/A
Cocos nucifera	Brazil	COUFAL0103	MK792507	MK792504	N/A	N/A
Cocos nucifera	Brazil	JZB313002	KP244698	KP308476	KP308528	N/A
Cocos nucifera	Brazil	JZB313003	KP244700	KP308474	KP308529	N/A
Cocos nucifera	Brazil	JZB313004	KP244703	KP308468	KP308530	N/A
Cocos nucifera	Brazil	K286	MK792506	MK792505	N/A	N/A
Cocos nucifera	Brazil	K8	MK792507	MK792504	N/A	N/A
Cocos nucifera	Brazil	UFRPE CFS 007	MG870585	MF991281	MG870605	MG870615
Cocos nucifera	China	ZWLT 481	MK051003	MK051099	MK051097	N/A
Cocos nucifera	China	ZWLT 482	MK051004	MK051100	MK051098	N/A
Cocos nucifera fruit	Suriname	CBS:142.52	KX464143	KX464637	N/A	KX463991
Cocos sp.	Unknown	CJA279	GU973873	GU973865	N/A	N/A
Corchorus olitorius	India	CJMR140	MF480346	MF522203	N/A	N/A
Corchorus olitorius	India	CJMR148	MF480345	MF522204	N/A	N/A
Corymbia flavescens	Australia	MUCC716	GU199374	GU199398	N/A	N/A
Cucumis melo	Thailand	SDBR-CMU351	MN093981	MN114216	MN114215	N/A
Cunninghamia lanceolata	China	CERC 2957	KX278037	KX278142	KX278246	MF410190
Cunninghamia lanceolata	China	CERC 2958	KX278038	KX278143	KX278247	MF410191
Derris elliptica	Indonesia	CBS:141.49	KX464142	KX464636	KX464911	N/A
Dimocarpus longan	Puerto Rico	120	MK282711	MK294129	MK294091	N/A
Dimocarpus longan	China	CERC 3485	KX278042	KX278147	KX278251	MF410195
Dimocarpus longan	China	CERC 3486	KX278043	KX278148	KX278252	MF410196
Dimocarpus longan	China	CERC 3487	KX278044	KX278149	KX278253	MF410197
Dimocarpus longan	China	CERC 3491	KX278045	KX278150	KX278254	MF410198
Dimocarpus longan	China	CERC 3493	KX278046	KX278151	KX278255	MF410199

Table 3 Continued.

Host	Country	Strain no.	ITS	*tef*1-α	*tub*2	*rpb2*
Dimocarpus longan	USA	PHLO10	KC964547	KC964554	KC964550	N/A
Dimocarpus longan	USA	PHLO9	KC964546	KC964553	KC964549	N/A
Eucalyptus camaldulensis	Thailand	CMW15680	KY473066	KY473014	KY472957	KY472881
Eucalyptus camaldulensis	Thailand	DAR82913	KY473066	KY473014	KY472957	KY472881
Eucalyptus grandis	Indonesia	CMW22881	KY473036	KY472984	KY472917	KY472845
Eucalyptus grandis	Indonesia	FXPZ	KY473036	KY472984	KY472917	KY472845
Eucalyptus sp.	China	CMW24701	HQ332193	HQ332209	KY472908	KY472838
Eucalyptus sp.	China	CMW24702	HQ332194	HQ332210	KY472909	KY472839
Eucalyptus sp.	China	CMW33957	KY473030	KY472978	KY472910	N/A
Eucalyptus sp.	Indonesia	CMW54158	MT934407	MT920436	N/A	N/A
Eucalyptus sp.	Indonesia	CMW54160	MT934409	MT920438	N/A	MT920463
Eucalyptus sp.	Indonesia	CMW54175	MT934422	MT920448	N/A	N/A
Eucalyptus sp.	Indonesia	CMW54180	MT934424	MT920450	N/A	MT920471
Eucalyptus sp.	Indonesia	CMW54204	MT934429	MT920454	N/A	N/A
Eucalyptus sp.	Indonesia	CMW54217	MT934430	MT920455	N/A	N/A
Eucalyptus sp.	China	GZHS-2017-014	HQ332193	HQ332209	KY472908	KY472838
Eucalyptus sp.	China	GZHS-2017-015	HQ332194	HQ332210	KY472909	KY472839
Eucalyptus sp.	China	HSYF02	KY473030	KY472978	KY472910	N/A
Eucalyptus sp.	Indonesia	IRAN1499C	MT934407	MT920436	N/A	N/A
Eucalyptus sp.	Indonesia	IRNBS54	MT934409	MT920438	N/A	MT920463
Eucalyptus sp.	Indonesia	IRNBS56a	MT934422	MT920448	N/A	N/A
Eucalyptus sp.	Indonesia	IRNBS73	MT934424	MT920450	N/A	MT920471
Eucalyptus sp.	Indonesia	IRNKB210	MT934429	MT920454	N/A	N/A
Eucalyptus sp.	Indonesia	IRNKB244	MT934430	MT920455	N/A	N/A
Eucalyptus sp.	Indonesia	R3238	MT934432	MT920457	N/A	N/A
Eucalyptus sp.	Indonesia	R4128	MT934433	MT920458	N/A	N/A
Eucalyptus sp.	Indonesia	R5232	MT934434	MT920459	N/A	N/A
Eucalyptus sp.	Indonesia	R633	MT934435	MT920460	N/A	N/A
Eucalyptus urophylla	China	CERC1983	KP822979	KP822997	KP823012	N/A
Eucalyptus urophylla	China	CERC1985	KP822980	KP822998	KP823013	N/A
Eucalyptus urophylla	China	CERC1988	KP822981	KP822999	KP823014	N/A
Eucalyptus urophylla	China	CERC1989	KP822982	KP823000	KP823015	N/A
Eucalyptus urophylla	China	CERC1991	KP822983	KP823001	KP823016	N/A
Eucalyptus urophylla	China	CERC1996	KP822984	KP823002	KP823017	N/A
Eucalyptus urophylla	China	CERC2049	KP822985	KP823003	KP823018	N/A
Eucalyptus urophylla	Venezuela	CMW13490	KY473071	KY473019	KY472962	KY472888
Eucalyptus urophylla	Venezuela	CSM_54	KY473071	KY473019	KY472962	KY472888
Eucalyptus urophylla × *Eucalyptus grandis*	China	CERC 2264	KX278034	KX278139	KX278243	MF410187

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 2275	KX278035	KX278140	KX278244	MF410188
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 2934	KX278036	KX278141	KX278245	MF410189
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 2963	KX278039	KX278144	KX278248	MF410192
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3418	KX278040	KX278145	KX278249	MF410193
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3420	KX278031	KX278136	KX278240	MF410184
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3422	KX278041	KX278146	KX278250	MF410194
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3424	KX278032	KX278137	KX278241	MF410185
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3514	KX278048	KX278153	KX278257	MF410201
Eucalyptus urophylla × Eucalyptus grandis	China	CERC 3516	KX278049	KX278154	KX278258	MF410202
Euphorbia ingens	South Africa	CMW26616	KY473051	KY472999	KY472941	KY472867
Euphorbia ingens	South Africa	CMW26630	KY473052	KY473000	KY472942	KY472868
Euphorbia ingens	South Africa	HBB2	KY473051	KY472999	KY472941	KY472867
Euphorbia ingens	South Africa	HBB3	KY473052	KY473000	KY472942	KY472868
Excoecaria agallocha	China	CMW23018	MN860003	MN887512	N/A	N/A
Ficus carica	Japan	CMW23031	LC386385	LC386386	N/A	N/A
Fragaria × ananassa	Korea	LT120701	KX506787	KX506781	N/A	N/A
Fragaria × ananassa	Korea	LT120702	KX506786	KX506782	N/A	N/A
Fragaria × ananassa	Korea	LT120901	KX506788	KX506784	N/A	N/A
Fragaria × ananassa	Korea	LT120907	KX506785	KX506783	N/A	N/A
Fraxinus americana	China	BL04	MK813944	MK850548	N/A	N/A
Fraxinus americana	China	BL09	MK813945	MK850549	N/A	N/A
Fraxinus americana	China	BL12	MK813946	MK850550	N/A	N/A
Fraxinus americana	China	BL16	MK813947	MK850551	N/A	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Fraxinus Americana	China	BL20	MK813948	MK850552	N/A	N/A
Fraxinus americana	China	BL-20	MK041217	MK041218	N/A	N/A
Fraxinus americana	China	BL23	MK813949	MK850553	N/A	N/A
Fraxinus americana	China	BL26	MK813950	MK850554	N/A	N/A
Fraxinus americana	China	BL29	MK813951	MK850555	N/A	N/A
Fraxinus americana	China	BL34	MK813952	MK850556	N/A	N/A
Fraxinus americana	China	BL41	MK813953	MK850557	N/A	N/A
fruit along coral reef coast	Papua New Guinea	CBS 164.96	NR_111174	AY640258	EU673110	KU696383
Hevea brasiliensis	China	CMW32544	KT947466	KU925617	KU925616	N/A
Hibiscus mutabilis	China	MFR	KY814766	MG882078	N/A	N/A
Hibiscus rosa-sinensis	Unknown	ZJ1	MN904749	MT755638	MT741488	N/A
Hylocereus undatus	Bangladesh	BU-DLa 01	LC468780	LC468784	LC468782	N/A
Hylocereus undatus	Bangladesh	BU-DLa 02	LC468781	LC468785	LC468783	N/A
Ipomoea batatas	China	CMM4513	KU870366	KU870368	KU870370	N/A
Ipomoea batatas	China	ZJ	KJ866153	N/A	KJ866154	N/A
Jatropha curcas	Brazil	22	KF553895	KF553896	N/A	N/A
Jatropha curcas	Brazil	CMM3612	KF234546	KF226692	KF254929	N/A
Jatropha curcas	Brazil	CMM3647	KF234548	KF226704	KF254932	N/A
Jatropha curcas	Brazil	CMM3654	KF234555	KF226716	KF254939	N/A
Jatropha curcas	Brazil	CMM3831	KF234556	KF226717	KF254940	N/A
Jatropha curcas	Unknown	taxon:45133	MN561032	MN561033	N/A	N/A
Kadsura coccinea	China	CMW28556	MW045412	MW065559	MW065555	N/A
Kadsura coccinea	China	CMW28570	MW045413	MW065560	MW065556	N/A
Kadsura coccinea	China	CMW28571	MW045414	MW065561	MW065557	N/A
Kadsura coccinea	China	CMW28575	MW045415	MW065562	MW065558	N/A
Litchi chinensis	China	CMW25212	MN540675	MN539209	MN539179	N/A
Lysiphyllum cunninghami	Australia	MUCC715	GU199373	GU199397	N/A	N/A
Malus domestica branch	Chile	Bot-2017-LT13	MW560110	MW591895	MW574068	N/A
Malus domestica branch	Chile	Bot-2017-LT6	MW560108	MW591893	MW574066	N/A
Malus domestica branch	Chile	Bot-2017-LT8	MW560109	MW591894	MW574067	N/A
Malus domestica branch	Chile	Bot-2018-LT42	MW560111	MW591896	MW574069	N/A
Malus domestica branch	Chile	Bot-2018-LT45	MW560112	MW591897	MW574070	N/A
Malus domestica branch	Chile	Bot-2018-LT66	MW560113	MW591898	MW574071	N/A
Mangifera indica	Malaysia	ASWL245	MK530066	MK562438	MK573987	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Mangifera indica	Taiwan province, China	B838	GQ502456	GQ980001	GU056852	N/A
Mangifera indica	Taiwan province, China	B852	GQ502457	GQ980002	GU056851	N/A
Mangifera indica	Taiwan province, China	B886	GQ502452	GQ980005	GU056847	N/A
Mangifera indica	Taiwan province, China	B902	GQ502459	GQ980004	GU056849	N/A
Mangifera indica	Taiwan province, China	B918	GQ502458	GQ980003	GU056850	N/A
Mangifera indica	Taiwan province, China	B961	GQ502453	GQ979999	GU056845	N/A
Mangifera indica	Taiwan province, China	B965	GQ502454	GQ980000	GU056854	N/A
Mangifera indica	Egypt	BOT23	JN814400	JN814427	N/A	N/A
Mangifera indica	Egypt	BOT4	JN814395	JN814422	N/A	N/A
Mangifera indica	Egypt	BOT6	JN814399	JN814426	N/A	N/A
Mangifera indica	Egypt	BOT7	JN814396	JN814423	N/A	N/A
Mangifera indica	Malaysia	BPCA357	MK530075	MK562441	MK573991	N/A
Mangifera indica	Malaysia	BPPCA103	MK530009	MH447074	MK573990	N/A
Mangifera indica	Malaysia	BPPCA107	MK530011	MH447076	N/A	N/A
Mangifera indica	Malaysia	BPPCA108	MK530012	MH447077	N/A	N/A
Mangifera indica	Malaysia	BPPCA259	MK530068	MK562444	MK573995	N/A
Mangifera indica	Brazil	CMM1476	JX464083	JX464057	N/A	N/A
Mangifera indica	Brazil	CMM1481	JX464095	JX464021	N/A	N/A
Mangifera indica	Brazil	CMM1517	JX464060	JX464054	N/A	N/A
Mangifera indica	Brazil	CMM4019	JX464096	JX464026	N/A	N/A
Mangifera indica	Brazil	CMM4021	JX464064	JX464047	N/A	N/A
Mangifera indica	Brazil	CMM4033	JX464081	JX464032	N/A	N/A
Mangifera indica	Brazil	CMM4039	JX464065	JX464041	N/A	N/A
Mangifera indica	Brazil	CMM4041	KC184891	JX464042	N/A	N/A
Mangifera indica	Brazil	CMM4042	JX464070	JX464017	N/A	N/A
Mangifera indica	Brazil	CMM4043	JX464087	JX464056	N/A	N/A
Mangifera indica	Brazil	CMM4046	JX464091	JX464027	N/A	N/A
Mangifera indica	Brazil	CMM4047	JX464082	JX464025	N/A	N/A
Mangifera indica	Brazil	CMM4048	JX464093	JX464048	N/A	N/A
Mangifera indica	Brazil	CMM4050	JX464062	JX464024	N/A	N/A
Mangifera indica	Oman	CMW20506	KY473037	KY472985	KY472924	KY472852
Mangifera indica	South Africa	CMW25212	KU997392	KU997128	KU997566	N/A
Mangifera indica	South Africa	CMW33658	KY473065	KY473013	KY472956	N/A
Mangifera indica	Malaysia	CMW23003	MK529999	MK562451	MK574000	N/A
Mangifera indica	Malaysia	CMW23008	MK530004	MK562453	MK574003	N/A
Mangifera indica	Iran	COAD 1788	GU973869	GU973861	N/A	N/A
Mangifera indica	Iran	COAD 1789	GU973870	GU973862	N/A	N/A
Mangifera indica	Puerto Rico	CRM-B40	KC631660	KC631656	KC631652	N/A
Mangifera indica	Puerto Rico	CSM_22	KC631659	KC631655	KC631651	N/A
Mangifera indica	Brazil	CSM_33	JX464062	JX464024	N/A	N/A
Mangifera indica	Oman	DPWL2	KY473037	KY472985	KY472924	KY472852
Mangifera indica	South Africa	HBB1	KU997392	KU997128	KU997566	N/A
Mangifera indica	South Africa	HSYF01	KY473065	KY473013	KY472956	N/A
Mangifera indica	China	L1	KR260791	KR260808	KR260820	N/A
Mangifera indica	China	L10	KR260800	KR260817	KR260829	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Mangifera indica	China	L3	KR260793	KR260810	KR260822	N/A
Mangifera indica	China	L4	KR260794	KR260811	KR260823	N/A
Mangifera indica	China	L5	KR260795	KR260812	KR260824	N/A
Mangifera indica	China	L6	KR260799	KR260816	KR260828	N/A
Mangifera indica	China	L7	KR260797	KR260814	KR260826	N/A
Mangifera indica	Peru	LACIC2	KU507462	KU507429	N/A	N/A
Mangifera indica	Peru	LACIN1	KU507463	KU507430	N/A	N/A
Mangifera indica	Peru	LACIN2	KU507464	KU507431	N/A	N/A
Mangifera indica	Peru	LACIN3	KU507465	KU507432	N/A	N/A
Mangifera indica	Peru	LACIS1	KU507458	KU507425	N/A	N/A
Mangifera indica	Peru	LACIS2	KU507459	KU507426	N/A	N/A
Mangifera indica	Peru	LACIS3	KU507460	KU507427	N/A	N/A
Mangifera indica	Peru	LAHUAL1	KU507481	KU507448	N/A	N/A
Mangifera indica	Peru	LAHUAL2	KU507482	KU507449	N/A	N/A
Mangifera indica	Peru	LAHUAL3	KU507483	KU507450	N/A	N/A
Mangifera indica	Peru	LAMAL1	KU507455	KU507422	N/A	N/A
Mangifera indica	Peru	LAMAL2	KU507456	KU507423	N/A	N/A
Mangifera indica	Peru	LAMAL3	KU507457	KU507424	N/A	N/A
Mangifera indica	Peru	LAMAT1	KU507470	KU507437	N/A	N/A
Mangifera indica	Peru	LAMAT2	KU507471	KU507438	N/A	N/A
Mangifera indica	Peru	LAMAT3	KU507472	KU507439	N/A	N/A
Mangifera indica	Peru	LAREP2	KU507485	KU507452	N/A	N/A
Mangifera indica	Peru	LAREP3	KU507486	KU507453	N/A	N/A
Mangifera indica	Peru	LASID1	KU507478	KU507445	N/A	N/A
Mangifera indica	Peru	LASID2	KU507479	KU507446	N/A	N/A
Mangifera indica	Peru	LASOM1	KU507475	KU507442	N/A	N/A
Mangifera indica	Peru	LASOM3	KU507477	KU507444	N/A	N/A
Mangifera indica	Peru	LAVIN1	KU507466	KU507433	N/A	N/A
Mangifera indica	Peru	LAVIN2	KU507467	KU507434	N/A	N/A
Mangifera indica	Peru	LAVIN3	KU507468	KU507435	N/A	N/A
Mangifera indica	Peru	LAYAP2	KU507474	KU507441	N/A	N/A
Mangifera indica	Japan	Mif	AB686039	AB699591	N/A	N/A
Mangifera indica	Malaysia	PBBG179	MK530048	MK562457	MK574006	N/A
Mangifera indica	Malaysia	PBBG195	MK530054	MK562458	MK574008	N/A
Mangifera indica	Malaysia	PHM350	MK530073	MK562459	MK574009	N/A
Mangifera indica	Malaysia	PWL353	MK530074	MK562460	MK574010	N/A
Mangifera indica	Japan	Tof	AB693968	AB699592	N/A	N/A
Manilkara zapota	Thailand	B0281	KM006442	KM006473	N/A	N/A
Morus alba	China	CERC3820	KR340470	KR816837	KR816843	N/A
Morus alba	China	CMW30103	MK696042	MK697025	N/A	N/A
Morus alba	China	CMW30104	MK696043	MK697026	N/A	N/A
Morus alba	China	CMW31861	MK696044	MK697027	N/A	N/A
Morus alba	China	CMW31867	MK696047	MK697030	N/A	N/A
Morus alba	China	CMW32245	MK696048	MK697031	N/A	N/A
Morus alba	China	CMW32246	MK696045	MK697028	N/A	N/A
Morus alba	China	CMW32536	MK696046	MK697029	N/A	N/A
Morus alba	China	CMW4696	MK696026	MK697009	N/A	N/A
Morus alba	China	CMW54158	MK696025	MK697008	N/A	N/A
Morus alba	China	CMW54160	MK696027	MK697010	N/A	N/A
Morus alba	China	CMW54175	MK696024	MK697007	N/A	N/A
Morus alba	China	CMW54180	MK696028	MK697011	N/A	N/A
Morus alba	China	LL-71	MK696017	MK697000	N/A	N/A
Morus alba	China	LL-74	MK696014	MK696997	N/A	N/A
Morus alba	China	LL-79	MK696012	MK696995	N/A	N/A
Morus alba	China	LR-73	MK696040	MK697023	N/A	N/A
Morus alba	China	LR-79	MK696041	MK697024	N/A	N/A
Morus alba	China	LR-83	MK696038	MK697021	N/A	N/A
Morus alba	China	LX-3	MK696007	MK696990	N/A	N/A
Morus alba	China	LX-4	MK696005	MK696988	N/A	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Morus alba	China	LX-5	MK696009	MK696992	N/A	N/A
Morus alba	China	LX-6	MK696006	MK696989	N/A	N/A
Morus alba	China	LX-79	N/A	MK460232	N/A	N/A
Morus alba	China	NH-1	MK696029	MK697012	N/A	N/A
Morus alba	China	NH-2	MK696037	MK697020	N/A	N/A
Morus alba	China	NH-21	MK696031	MK697014	N/A	N/A
Morus alba	China	NH-24	MK696030	MK697013	N/A	N/A
Morus alba	China	NH-26	MK696032	MK697015	N/A	N/A
Morus alba	China	NH-3	MK696036	MK697019	N/A	N/A
Morus alba	China	NH-8	MK696033	MK697016	N/A	N/A
Morus alba	China	WM-28	MK696021	MK697004	N/A	N/A
Morus alba	China	WM-29	MK696023	MK697006	N/A	N/A
Morus alba	China	WM-30	MK696020	MK697003	N/A	N/A
Morus alba	China	WM-33	MK696019	MK697002	N/A	N/A
Morus alba	China	WM-35	MK696022	MK697005	N/A	N/A
Morus alba root	Unknown	XY14	HG917933	N/A	N/A	N/A
Musa sapientum	Unknown	CBS287.47	EF622069	EF622049	N/A	N/A
Musa sapientum fruit	Unknown	CBS:287.47	KX464145	KX464639	KX464914	N/A
Mustard Crop soil	India	AP2_F5	MT462580	N/A	N/A	N/A
Nopalea cochenillifera	Brazil	CMM2462	KY569623	KY569612	N/A	N/A
Passiflora edulis	China	PaP-1	MN831964	MN840489	MN840492	N/A
Passiflora edulis	China	PaP-2	MN831965	MN840490	MN840493	N/A
Passiflora edulis	China	PaP-3	MN831966	MN840491	MN840494	N/A
Passiflora edulis	China	PaS-1	MN646259	MN692921	MN692933	N/A
Passiflora edulis	China	PaS-2	MN646260	MN692922	MN692934	N/A
Passiflora edulis	China	PaS-3	MN646261	MN692923	MN692935	N/A
Passiflora edulis	Taiwan province, China	Un-140	MG814039	MN114119	N/A	N/A
Passiflora edulis	China	ZW49-1	MT644473	MT649210	MT649212	N/A
Passiflora edulis	China	ZW50-1	MT644474	MT649211	MT649213	N/A
Passiflora edulis	China	BXG-1	MT012833	MT561047	N/A	N/A
Persea americana	Australia	BRIP66332	MH183315	N/A	N/A	N/A
phaeohyphomycotic cyst	Canada	CBS339.90	EF622072	EF622052	N/A	N/A
Phaeohyphomycotic cyst of patient	Canada	CBS:339.90	KX464147	KX464641	KX464916	N/A
Philodendron bipinnatifidum	China	GUCC9239	MH644066	MH644064	MH644062	N/A
Phoenix hanceana	China	CERC 2024	KX278030	KX278135	KX278239	MF410183
Pines seed	Unknown	C333	MK635058	N/A	N/A	N/A
Pinus caribaea	Australia	BRIP62872	MH057186	MH102249	N/A	N/A
Pinus elliottii	South Africa	CMW32536	KY473055	KY473003	KY472946	KY472872
Pinus elliottii	South Africa	CMW32544	KY473056	KY473004	KY472947	KY472873
Pinus elliottii	South Africa	CMW32549	KY473057	KY473005	KY472948	KY472874
Pinus elliottii	South Africa	CMW32571	KY473058	KY473006	KY472949	KY472875
Pinus elliottii	South Africa	CMW32603	KY473059	KY473007	KY472950	KY472876
Pinus elliottii	South Africa	CMW32604	KY473060	KY473008	KY472951	KY472877
Pinus elliottii	South Africa	CMW32606	KY473061	KY473009	KY472952	KY472878
Pinus elliottii	South Africa	CMW32651	KY473062	KY473010	KY472953	KY472879
Pinus elliottii	South Africa	CMW32666	KY473063	KY473011	KY472954	N/A
Pinus elliottii	South Africa	HNDZ01	KY473055	KY473003	KY472946	KY472872
Pinus elliottii	South Africa	HNHK01	KY473056	KY473004	KY472947	KY472873
Pinus elliottii	South Africa	HNLD004	KY473057	KY473005	KY472948	KY472874

Table 3 Continued.

Host	Country	Strain no.	ITS	*tef*1-α	*tub*2	*rpb2*
Pinus elliottii	South Africa	HNLG04	KY473058	KY473006	KY472949	KY472875
Pinus elliottii	South Africa	HNQH02	KY473059	KY473007	KY472950	KY472876
Pinus elliottii	South Africa	HNQZ003	KY473060	KY473008	KY472951	KY472877
Pinus elliottii	South Africa	HNSY02	KY473061	KY473009	KY472952	KY472878
Pinus elliottii	South Africa	HNTC03	KY473062	KY473010	KY472953	KY472879
Pinus elliottii	South Africa	HNWN02	KY473063	KY473011	KY472954	N/A
Pinus elliottii var. *elliottii* x *Pinus caribaea* var. *hondurensis*	Mexico	CMM4050	MT103322	MT162470	MT212400	N/A
Pinus elliottii var. *elliottii* x *Pinus caribaea* var. *hondurensis*	Mexico	CMM4499	MT103324	MT162472	MT212402	N/A
Pogostemon cablin	China	A541	KX462997	N/A	N/A	N/A
Prunus amygdalus x *P. persica*	Turkey	NeR3-AMis	KF494367	N/A	KF515964	N/A
Prunus dulcis	Iran	COAD 1790	MN634042	MN633996	N/A	N/A
Prunus dulcis	Iran	COUFAL0102	MN634043	MN633997	N/A	N/A
Prunus dulcis	Iran	COUFAL0103	MN634044	MN633998	N/A	N/A
Prunus dulcis	Iran	CP/VPC-2	MN634045	MN633999	N/A	N/A
Prunus dulcis	Iran	CP/VPC-4	MN634046	MN634000	N/A	N/A
Psidium guajava	Malaysia	Ma	MF801620	N/A	N/A	N/A
Psidium guajava	Malaysia	P8	MW380429	MW387154	N/A	N/A
Psidium guajava	Nigeria	PGS5	MK491768	N/A	N/A	N/A
Pyrenula parvinuclea	Sri Lanka	AT/L5/E1	KY969640	N/A	N/A	N/A
Pyrus pyrifolia	China	ZHn411	KC960899	KC961038	KC960992	N/A
Ricinus communis	Brazil	CCMF-CNPA0554	MH485394	MH491477	N/A	N/A
Ricinus communis	Brazil	CCMF-CNPA0585	MH485395	MH491478	N/A	N/A
Ricinus communis	China	RiB-1	MN759432	MN719125	MN719128	N/A
Ricinus communis	China	RiB-2	MN759433	MN719126	MN719129	N/A
Roccella montagnei	Sri Lanka	N_L9_E1	KY992570	N/A	N/A	N/A
Rosa rugosa	China	CERC3821	KR816832	KR816838	KR816844	N/A
Rosa rugosa	China	CERC3822	KR816833	KR816839	KR816845	N/A
Rosa rugosa	China	CERC3823	KR816834	KR816840	KR816846	N/A
Rosa rugosa	China	CERC3824	KR816835	KR816841	KR816847	N/A
Rubus sp.	Mexico	CMW13490	MK584613	MK681713	N/A	N/A
Rubus sp.	Mexico	CMW13501	MK584592	MK681692	N/A	N/A
Rubus sp.	Mexico	CMW15680	MK584597	N/A	N/A	N/A
Sansevieria trifasciata	Malaysia	CE7	MF580791	MF580813	N/A	N/A
Scaevola taccada	Unknown	YXD-34	MN626457	N/A	N/A	N/A
Schizolobium parahyba	Ecuador	CMW22926	KY473032	KY472980	KY472912	KY472841
Schizolobium parahyba	Ecuador	CMW4694	KY473033	KY472981	KY472913	N/A
Schizolobium parahyba	Ecuador	CMW4696	KY473034	KY472982	KY472915	KY472842
Schizolobium parahyba	Ecuador	CMW9273	KY473035	KY472983	KY472916	KY472844

Table 3 Continued.

Host	Country	Strain no.	ITS	*tef*1-α	*tub*2	*rpb2*
Schizolobium parahyba	Ecuador	GBLZ16BO-003	KY473032	KY472980	KY472912	KY472841
Schizolobium parahyba	Ecuador	IRAN1233C	KY473033	KY472981	KY472913	N/A
Schizolobium parahyba	Ecuador	IRAN1496C	KY473034	KY472982	KY472915	KY472842
Schizolobium parahyba	Ecuador	JZB313001	KY473035	KY472983	KY472916	KY472844
Schizolobium parahyba var. *amazonicum*	South Africa	CMW22924	KF886709	KF886732	KY472911	KY472840
Schizolobium parahyba var. *amazonicum*	South Africa	G78	KF886709	KF886732	KY472911	KY472840
Solanum melongena	Brazil	URM7678	MG808269	MG813266	N/A	N/A
Solanum melongena	Brazil	URM7679	MG808270	MG813267	N/A	N/A
Syagrus romanzoffiana	USA	PLM-758A	MG321240	MG309748	N/A	N/A
Syagrus romanzoffiana	USA	PLM-789A	MG321241	MG309749	N/A	N/A
Syzygium cordatum	Zambia	CMW30103	FJ747640	FJ871114	N/A	N/A
Syzygium cordatum	Zambia	CMW30104	FJ747641	FJ871115	N/A	N/A
Syzygium cordatum	Zambia	HNBS01	FJ747640	FJ871114	N/A	N/A
Syzygium cordatum	Zambia	HNBT04	FJ747641	FJ871115	N/A	N/A
Syzygium cordatum	South Africa	MTU53	KY052943	N/A	KY000125	N/A
Syzygium nervosum	Australia	CMW40635	KY473024	KY472967	KY472893	N/A
Syzygium nervosum	Australia	CMW40636	KY473025	KY472968	KY472894	KY472826
Syzygium nervosum	Australia	HY-6	KY473024	KY472967	KY472893	N/A
Syzygium nervosum	Australia	HY-8	KY473025	KY472968	KY472894	KY472826
Syzygium samarangense	China	CMW23073	KC511597	N/A	N/A	N/A
Syzygium sp.	Thailand	B0451	KM006454	KM006485	N/A	N/A
Syzygium sp.	Australia	CMW40630	KY473023	KY472966	KY472892	KY472825
Syzygium sp.	Australia	HY-5	KY473023	KY472966	KY472892	KY472825
Syzygium wilsonii	Australia	BRIP58866	MH057181	MH102244	N/A	N/A
Tectona grandis	Thailand	MFLUCC11-0414	KM396891	KM409629	KM510349	N/A
Terminalia ivorensis	Cameroon	CMW28308	GQ469927	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	CMW28312	GQ469928	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	CMW28556	GQ469931	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	CMW28570	GQ469923	GQ469896	KY472903	KY472834
Terminalia ivorensis	Cameroon	CMW28571	GQ469924	GQ469897	KY472904	KY472835

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Terminalia ivorensis	Cameroon	CMW28575	GQ469926	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	CMW28626	GQ469934	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	HBB4	GQ469927	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	HBQJZ01S	GQ469928	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	HL-56	GQ469931	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	HL-57	GQ469923	GQ469896	KY472903	KY472834
Terminalia ivorensis	Cameroon	HL-61	GQ469924	GQ469897	KY472904	KY472835
Terminalia ivorensis	Cameroon	HL-62	GQ469926	N/A	N/A	N/A
Terminalia ivorensis	Cameroon	HN74	GQ469934	N/A	N/A	N/A
Terminalia mantaly	Cameroon	CMW28547	GQ469919	KY472972	KY472900	KY472831
Terminalia mantaly	Cameroon	CMW28548	GQ469920	KY472973	KY472901	KY472832
Terminalia mantaly	Cameroon	CMW28550	N/A	KY472974	KY472902	KY472833
Terminalia mantaly	Cameroon	HL-51	GQ469919	KY472972	KY472900	KY472831
Terminalia mantaly	Cameroon	HL-52	GQ469920	KY472973	KY472901	KY472832
Terminalia mantaly	Cameroon	HL-53	N/A	KY472974	KY472902	KY472833
Theobroma cacao	Peru	CMW31861	KY473048	KY472996	KY472935	N/A
Theobroma cacao	Peru	CMW31867	KY473049	KY472997	KY472936	KY472862
Theobroma cacao	Venezuela	CMW18420	MF436023	MF436011	MF436005	N/A
Theobroma cacao	Venezuela	CMW20506	MF436024	MF436012	MF436004	N/A
Theobroma cacao	Venezuela	CMW20542	MF436025	MF436013	MF436003	N/A
Theobroma cacao	Venezuela	CMW20543	MF436026	MF436014	MF436002	N/A
Theobroma cacao	Venezuela	CMW20560	MF436027	MF436015	MF436001	N/A
Theobroma cacao	Venezuela	CMW20573	MF436028	MF436016	MF436000	N/A
Theobroma cacao	Venezuela	CMW22881	KU377488	N/A	N/A	N/A
Theobroma cacao	Peru	HNCJ02	KY473048	KY472996	KY472935	N/A
Theobroma cacao	Peru	HNCM02	KY473049	KY472997	KY472936	KY472862
Theobroma cacao	USA	Miami_1	MH412989	N/A	N/A	N/A
Tomato field soil	India	AP3_12	MT462573	N/A	N/A	N/A
Torreya grandis	China	XF01	MG367174	MG367169	MG367179	N/A
Torreya grandis	China	XF02	MG367175	MG367170	MG367180	N/A
Torreya grandis	China	XF04	MG367176	MG367171	MG367181	N/A
Torreya grandis	China	XF06	MG367177	MG367172	MG367182	N/A
Unknown	Taiwan province, China	B2715	MH789983	N/A	N/A	N/A
Unknown	Unknown	c12_st	MK571611	N/A	N/A	N/A
Unknown	Thailand	C443B	MK347792	N/A	N/A	N/A
Unknown	Unknown	CBS111530	EF622074	EF622054	N/A	KU696382
Unknown	Unknown	CBS175.26	EF622067	EF622047	N/A	N/A
Unknown	Iran	CJA198	GU973871	GU973863	N/A	N/A
Unknown	Oman	CMW20542	KY473042	KY472990	KY472929	N/A
Unknown	Oman	CMW20543	KY473043	KY472991	KY472930	KY472857
Unknown	Oman	CMW20560	KY473045	KY472993	KY472932	KY472859
Unknown	Oman	CMW20573	KY473046	KY472994	KY472933	KY472860

Table 3 Continued.

Host	Country	Strain no.	ITS	*tef*1-α	*tub*2	*rpb2*
Unknown	Unknown	CMM4508	MF111089	N/A	N/A	N/A
Unknown	Iran	CMW9273	GU973868	GU973860	N/A	N/A
Unknown	Oman	DPWL45	KY473042	KY472990	KY472929	N/A
Unknown	Oman	ELS4	KY473043	KY472991	KY472930	KY472857
Unknown	Oman	FigA1	KY473045	KY472993	KY472932	KY472859
Unknown	Oman	FJAT-9860	KY473046	KY472994	KY472933	KY472860
Unknown	China	SWFU000066	MK834672	N/A	N/A	N/A
Unknown	India	VBE	EU852567	N/A	N/A	N/A
Vaccinium sect. *Cyanococcus*	USA	WFF92	GQ845095	GQ850467	N/A	N/A
Vaccinium corymbosum	Peru	LAK12	MK860751	MN000335	N/A	N/A
Vaccinium corymbosum	Peru	LAK19	MK860752	MN000336	N/A	N/A
Vaccinium corymbosum	Peru	LAK20	MK860753	MN000337	N/A	N/A
Vaccinium corymbosum	Peru	LAK8	MK860750	MN000334	N/A	N/A
Vaccinium corymbosum	Peru	LCH8	MK860741	MN000327	N/A	N/A
Vaccinium corymbosum	Peru	LPS1	MK860742	MN000328	N/A	N/A
Vaccinium corymbosum	Peru	LPS14	MK860748	MN000333	N/A	N/A
Vaccinium corymbosum	Peru	LPS2	MK860743	MN000329	N/A	N/A
Vaccinium corymbosum	Peru	LPS5	MK860744	MN000330	N/A	N/A
Vaccinium corymbosum	Peru	LPS7	MK860745	MN000331	N/A	N/A
Vaccinium corymbosum	Peru	LPS9	MK860746	MN000332	N/A	N/A
Vaccinium corymbosum	Czech Republic	MEND-F-00168	MN983134	MN989915	N/A	N/A
Vaccinium corymbosum	Peru	PPS6	MK860754	MN000338	N/A	N/A
Vaccinium spp.	Australia	CMW22924	MH160441	MH252420	N/A	MH215507
Vaccinium spp.	Australia	CMW22926	MH160442	MH252421	N/A	MH215508
Vitis vinifera	Italy	B159	KM675760	KM822731	N/A	N/A
Vitis vinifera	Italy	B202	KM675761	KM822732	N/A	N/A
Vitis vinifera	Italy	B215	KM675762	KM822733	N/A	N/A
Vitis vinifera	Italy	B342	KM675763	KM822734	N/A	N/A
Vitis vinifera	Italy	B85	KM675759	KM822730	N/A	N/A
Vitis vinifera	Brazil	CMM 0270	MH263663	MH265111	N/A	N/A
Vitis vinifera	Brazil	CMM 0307	KJ450879	KJ417879	N/A	N/A
Vitis vinifera	Brazil	CMM 0310	KJ450880	KJ417880	N/A	N/A
Vitis vinifera	Brazil	CMM 0348	MH263662	MH265112	N/A	N/A
Vitis vinifera	Brazil	CMM 0384	KJ450876	KJ417876	N/A	N/A
Vitis vinifera	Brazil	CMM 0434	MH263660	MH265113	N/A	N/A
Vitis vinifera	Brazil	CMM 0451	MH263661	MH265114	N/A	N/A
Vitis vinifera	Brazil	CMM 0455	KJ450878	KJ417878	N/A	N/A
Vitis vinifera	Brazil	CMM 0494	MH263658	MH265115	N/A	N/A
Vitis vinifera	Brazil	CMM 0820	KJ450877	KJ417877	N/A	N/A
Vitis vinifera	Brazil	CMM 0911	MH263659	MH265116	N/A	N/A
Vitis vinifera	Brazil	CMM 1032	MG954333	MG979502	MG979531	N/A
Vitis vinifera	China	CMW24701	KR232666	KR232660	KR232674	N/A
Vitis vinifera	China	CMW26616	JX275780	JX462288	JX462262	N/A
Vitis vinifera	China	CMW28626	JX275787	JX462291	JX462265	N/A
Vitis vinifera	Turkey	MH31Trs	MK817055	MK875269	N/A	N/A

Table 3 Continued.

Host	**Country**	**Strain no.**	**ITS**	***tef*1-α**	***tub*2**	***rpb2***
Vitis vinifera	China	SHYAG	JX275794	JX462302	JX462276	N/A
Vitis vinifera	Unknown	STE-U 4583	AY343482	N/A	N/A	N/A
Vitis vinifera	China	TJXHS1S1	JX275790	JX462304	JX462278	N/A
Vitis vinifera	USA	UCD2479TX	FJ790838	N/A	N/A	N/A
Vitis vinifera	USA	UCR-LT4	MZ150352	N/A	N/A	N/A
Vitis vinifera	Australia	W200	HQ392714	N/A	N/A	N/A
Vitis vinifera cv. Chardonnay	Australia	MW643	KC825336	N/A	N/A	N/A
Vitis vinifera cv. Red Globe	Peru	LA-SJ1	KM401976	KM401973	N/A	N/A
Vitis vinifera cv. Red Globe	Peru	LA-SOL1	KM401974	KM401971	N/A	N/A
Vitis vinifera cv. Red Globe	Peru	LA-SV1	KM401975	KM401972	N/A	N/A
Zea mays	China	ML	KT445902	KT985635	N/A	N/A
Zehneria scabra	Kenya	MR14	MW509854	N/A	N/A	N/A

Results

Most reliable molecular markers for *Lasiodiplodia*: ITS + *tef*1-α + *tub2* + *rpb2*

Sequences of ex-type isolates of *Lasiodiplodia* species were downloaded from GenBank for these analyses. Several possible multi-gene (SSU, LSU, ITS, *tef*1-α, *tub2*, and *rpb2*) combinations were performed from based on combinations like SSU + LSU + ITS + *tef*1-α + *tub2* + *rpb2*, ITS + LSU + *tef*1-α + *tub2* + *rpb2*, ITS + LSU + *tef*1-α + *tub2*, ITS + *tef*1-α + *tub2* +*rpb2*, and ITS + *tef*1-α + *tub2*. Among these combinations, ITS + *tef*1-α + *tub2* + *rpb2* was selected as the most reliable marker to delimit *Lasiodiplodia* species accurately. The combined ITS, *tef*1-α, *tub2*, and *rpb2* dataset included 663 taxa with *Diplodia seriata* (CBS 112555) as the outgroup taxon. The final alignment comprised 1676 characters, including gaps (ITS = 462, *tef*1-α = 315, *tub2* = 409, *rpb2* = 490). Both ML and BI analyses produced trees with similar topologies. The best-scoring ML tree with a final likelihood value of -10427.902671 is presented in Fig. 1. The data matrix included 671 distinct alignment patterns, with 43% undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.213335, C = 0.291513, G = 0.260302, T = 0.234851; substitution rates AC = 0.934397, AG = 3.042049, AT = 0.843511, CG = 0.894644, CT = 4.313786, GT = 1.0; gamma distribution shape parameter α = 0.231485. From the 10,001 trees that resulted from the 1,000,000 runs of the BI analysis, the first 1,000 trees representing the burn-in phase were discarded, while the remaining 9,001 trees were used to calculate posterior probabilities in the majority rule consensus tree. Running the BI analysis for 10,000,000 generations, the average standard deviation of split frequencies resulted in 0.01.

The phylogenetic tree generated by ML analysis based on the combined ITS, *tef*1-α, *tub2*, and *rpb2* sequences included 43 *Lasiodiplodia* species. However, some were synonymized based on the phylogenetic analyses of Zhang et al. (2021), and we also noted these synonymisations in our analysis (Fig. 1). Therefore, in our current analysis, we included 31 *Lasiodiplodia* species (Fig. 1). The combined dataset resulted in 31 well-supported clades representing each known *Lasiodiplodia* species. The majority of the strains were included in three large clades, which consist of *L. theobromae* (149 strains), *L. mahajangana* (122 strains), and *L. pseudotheobromae* (95 strains) with moderate bootstrap supports of 72% ML/0.75 posterior probability (PP), 62% ML/0.70 PP and 60% ML/0.60, respectively. More variabilities can be observed among *L. theobromae* strains. Forty-five strains of *L. iraniensis* formed a separate clade with moderate supports of 77% ML and 0.80 PP. Approximately 30 strains from each *L. brasiliensis* (33), *L. crassispora* (30), *L. euphorbiaceicola* (33), *L. gonubiensis* (27), and *L. hormozganensis* (31) formed six distinct clades with moderate to high bootstrap supports (Fig. 1).

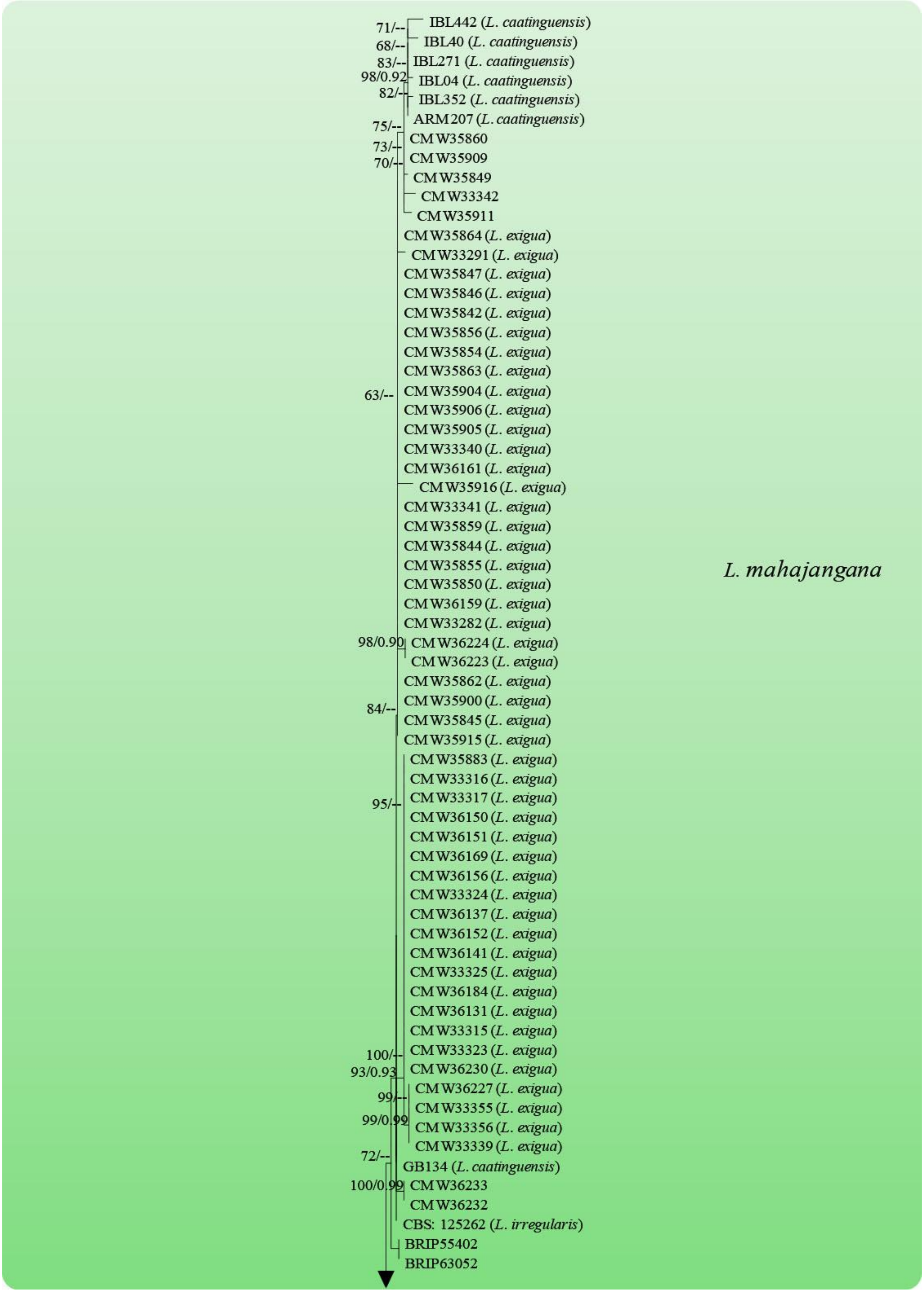


Figure 1 – Phylogenetic tree of *Lasiodiplodia* generated from ML analysis of the combined dataset of ITS, *tef*1-α, *tub2*, and *rpb2*. The tree is rooted to *Diplodia seriata* (CBS 112555). Bootstrap support values for ML ≥ 60 % and Bayesian posterior probabilities (PP) ≥ 0.90 are noted at the nodes. Ex-type strains are in bold and the species are delimited with coloured blocks. Strain numbers and possible synonyms of the species are shown. Possible synonyms done in this study are in red.

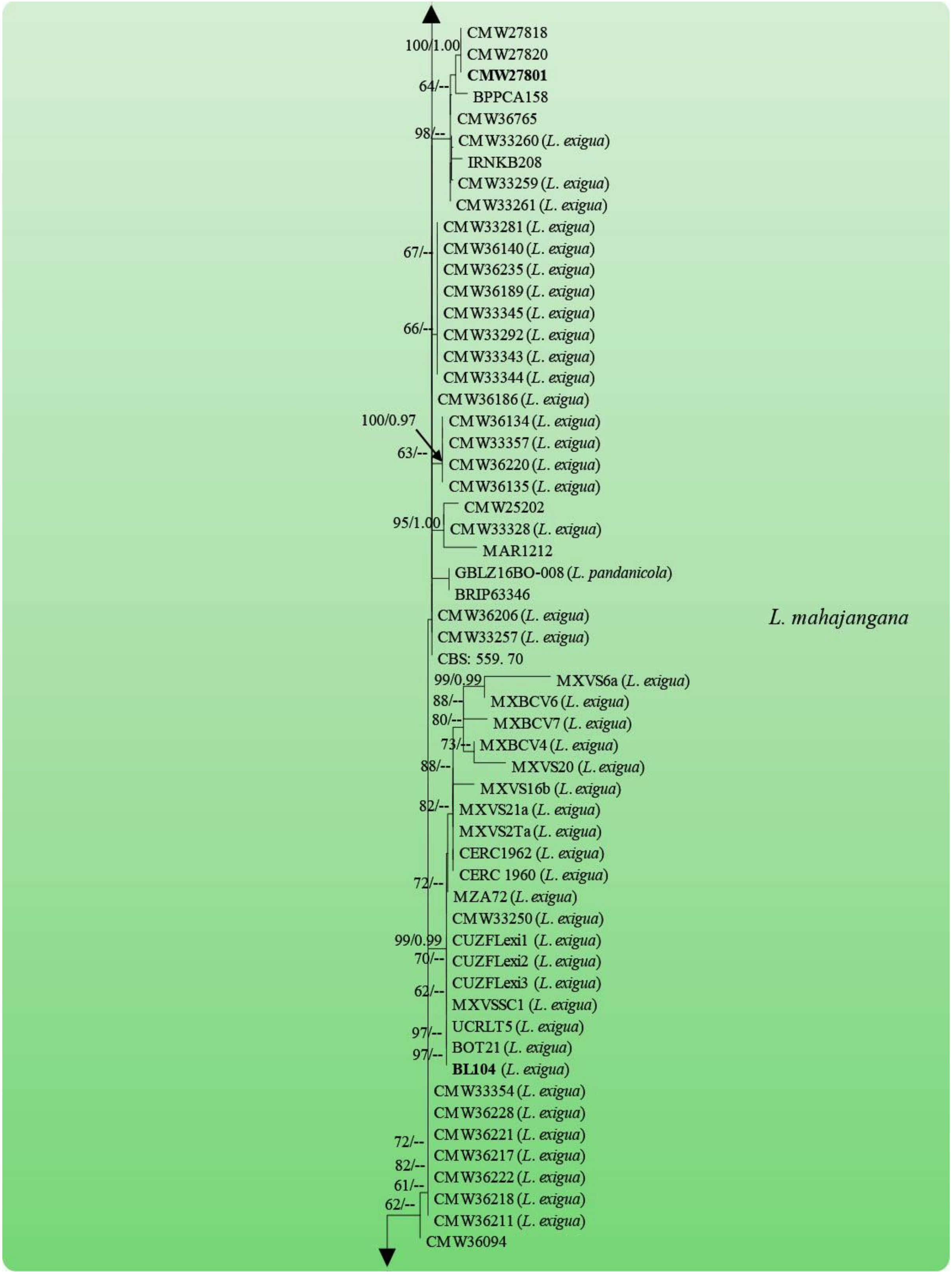
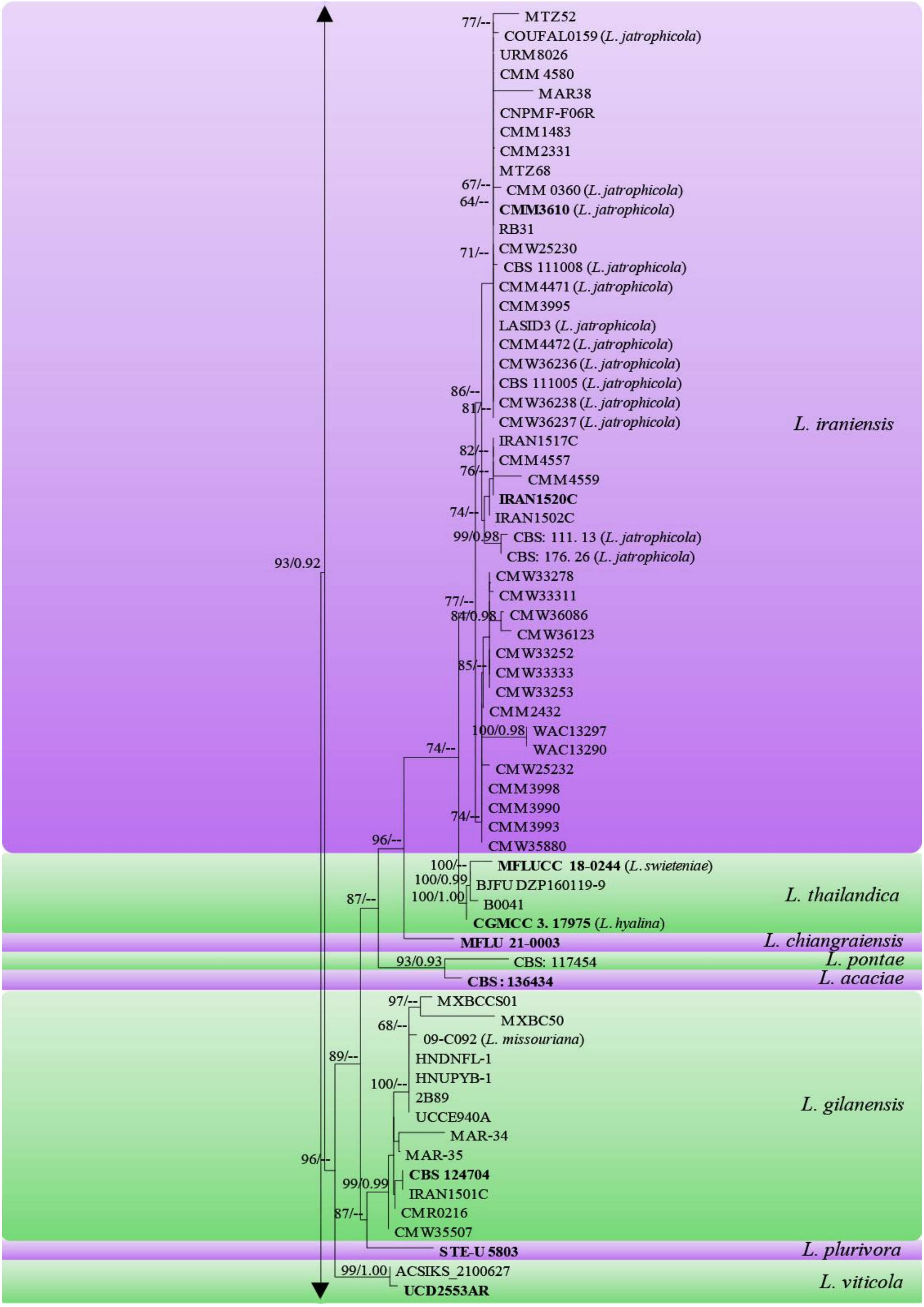


Figure 1 – Continued.

Cosmopolitan distribution patterns of *Lasiodiplodia* species

The number of individual organisms of a given species in an ecological community is known as species abundance. It quantifies the population size or the number of individuals belonging to each species within a particular habitat or ecosystem (Evans & Ochiaga 2014). Species abundance provides valuable information about the relative dominance or rarity of different species within a community. It helps ecologists understand the distribution patterns, population dynamics, and ecological roles of various species in an ecosystem (Verberk 2011).



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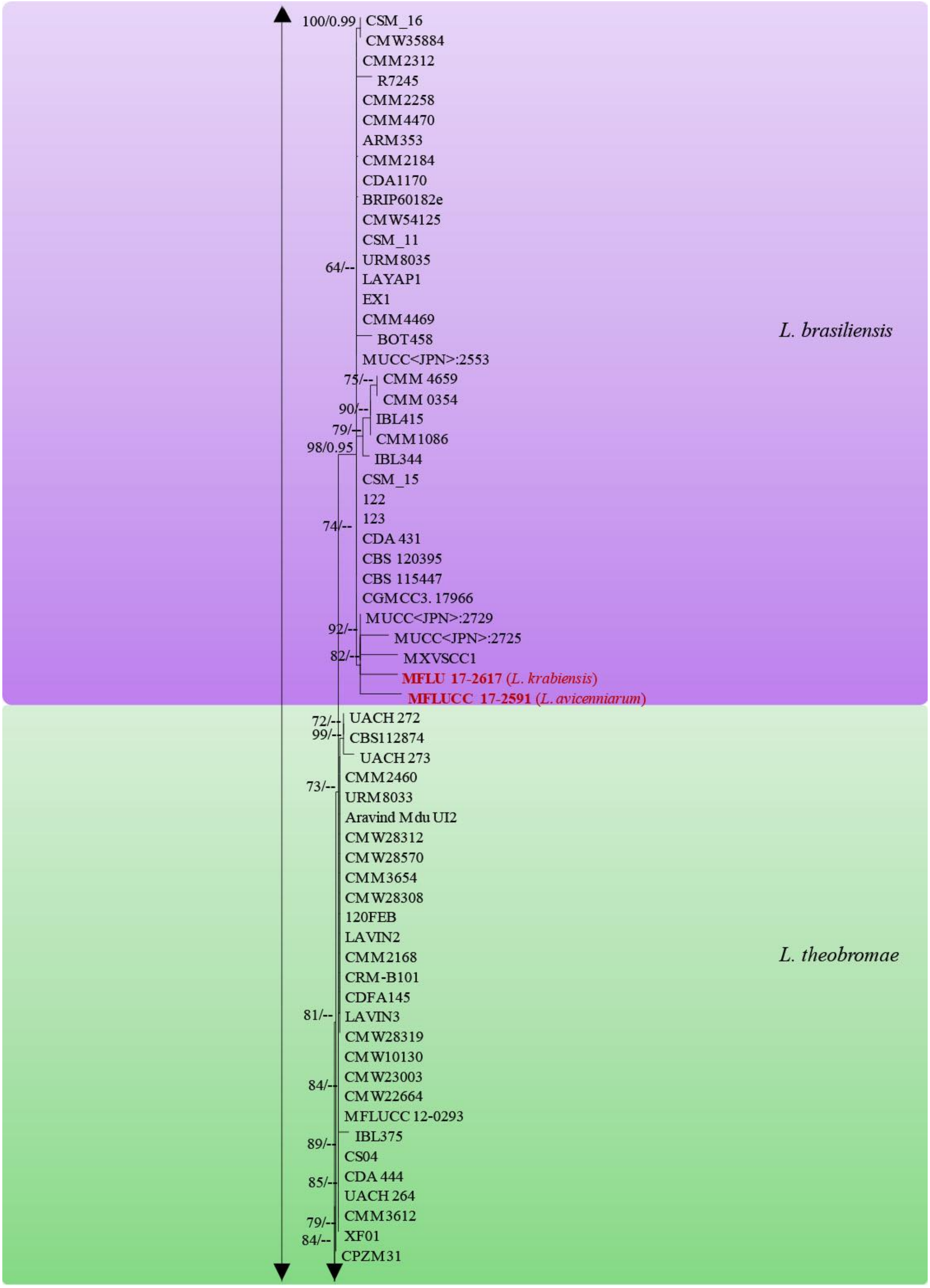


Figure 1 – Continued.

Species richness refers to the count of species in a particular area or habitat. It provides broader information about the species in that specific location (Kiester 2013). Species diversity encompasses species richness, as well as species abundance and the distribution of those species within the ecosystem (Kiester 2013).

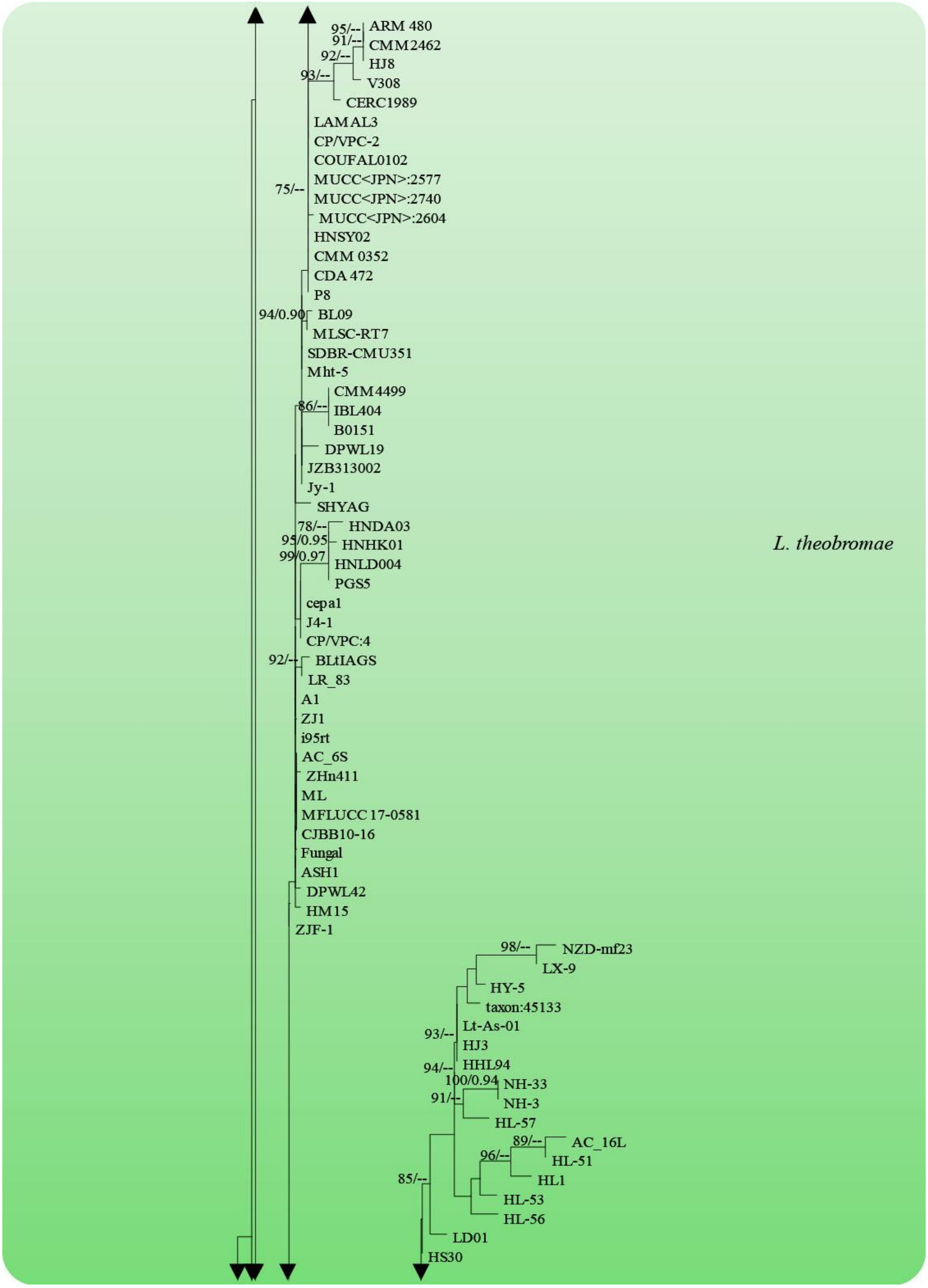


Figure 1 – Continued.

MacArthur & Wilson (1967) developed the theory of island biogeography, which proposes that species richness in a community result from an equilibrium between immigration and extinction processes. High levels of immigration increase species richness, while high levels of extinction result in decreased species richness (Brown et al. 2007). According to their theory, the island is used as a model, and the distances from the mainland affect immigration rates, with closer islands having higher rates of immigration. Also, island size influences extinction rates, as smaller islands have higher extinction rates due to their small population sizes (Brown et al. 2007). Intermediate levels of disturbance from competitors maximize species diversity and species richness. Because it reduces species abundances of dominant species, allowing other species to establish without causing significant species loss (Brown et al. 2007).

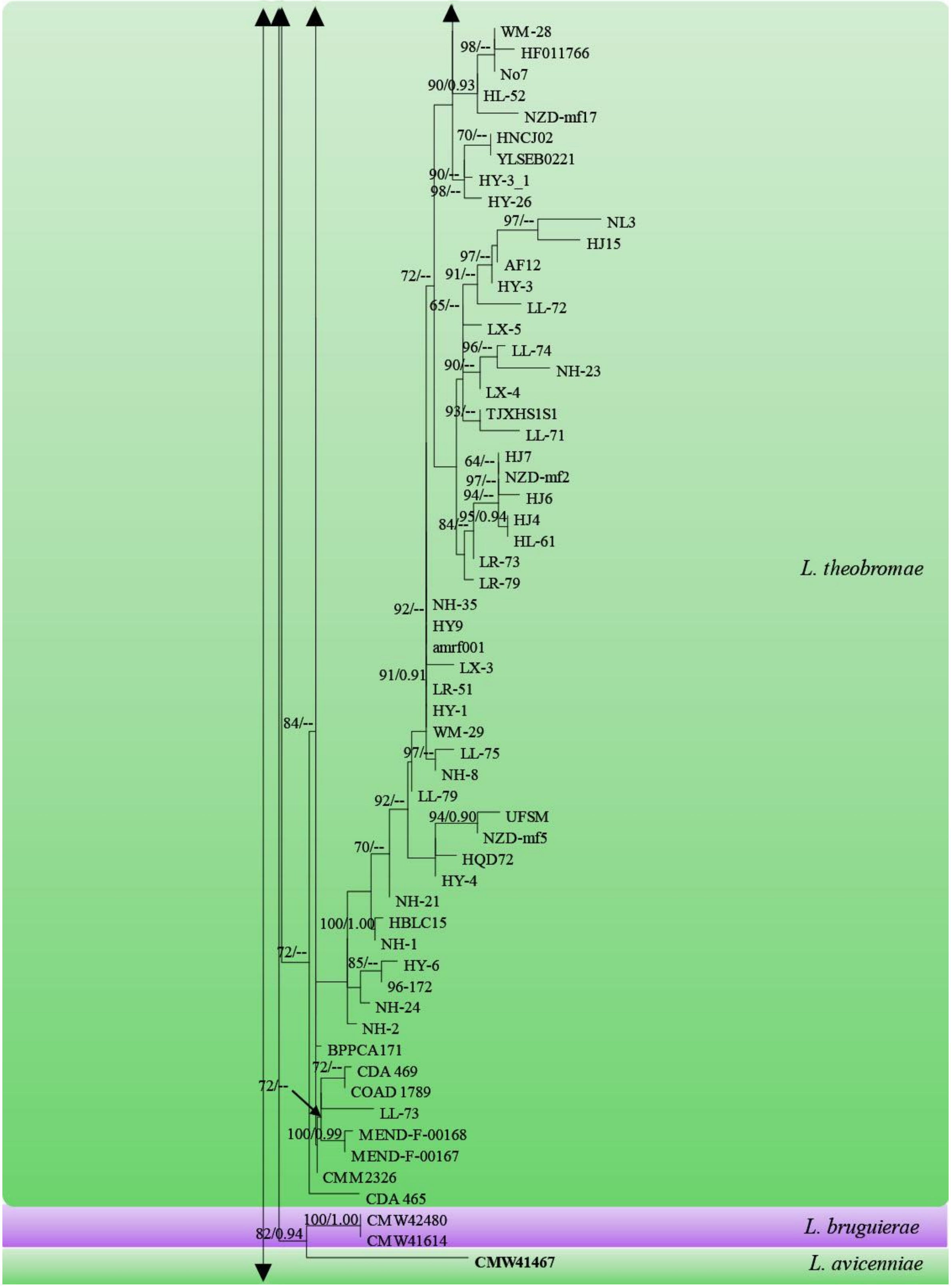
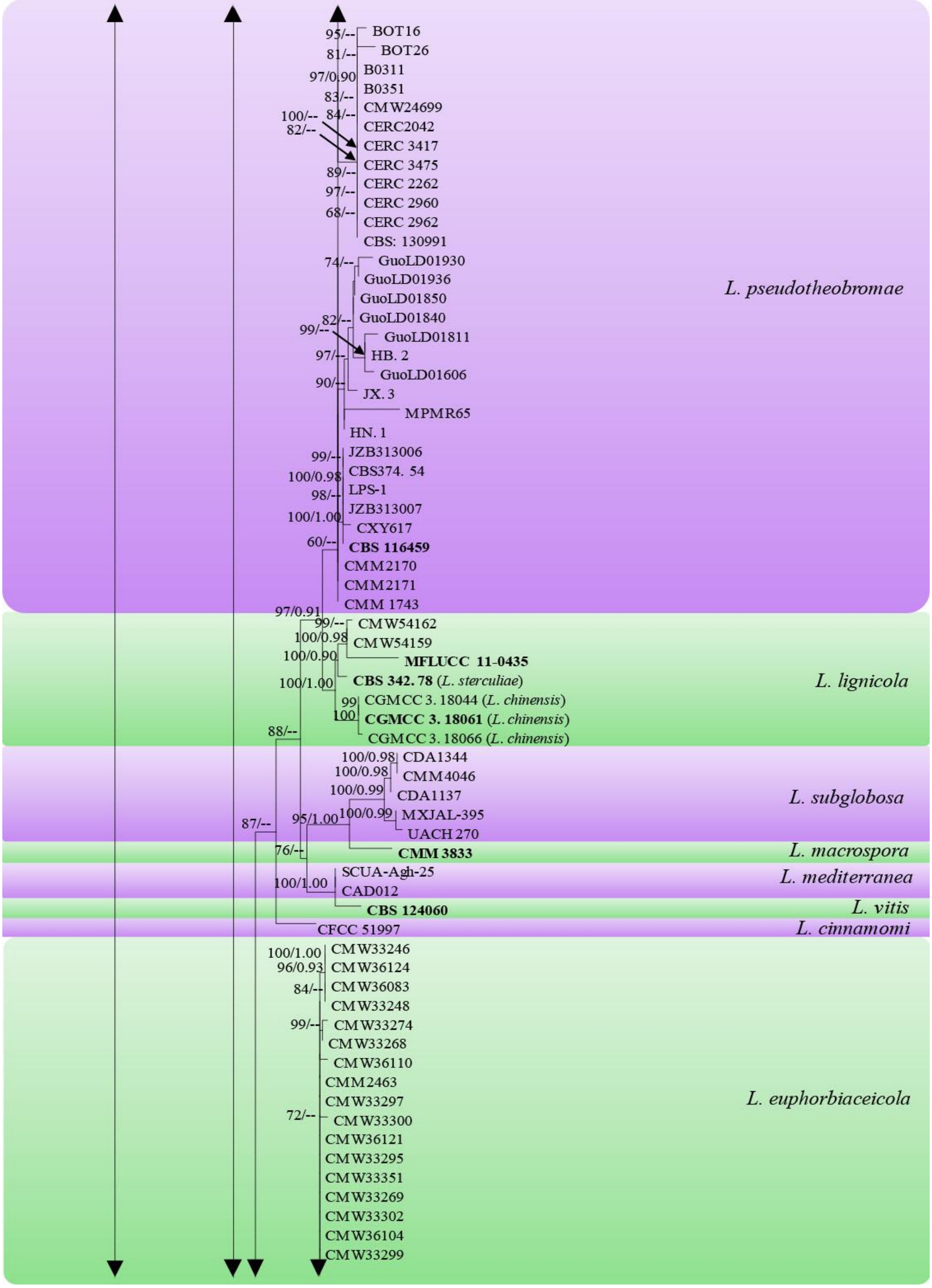


Figure 1 – Continued.

Figure 1 – Continued.

The global abundance and richness of *Lasiodiplodia* species are shown in Figs 2, 3, respectively. According to the Proportional symbol map for the global abundances of *Lasiodiplodia* spp. (Fig. 2), a greater diffusion of *Lasiodiplodia* species is evident in all tropical and subtropical regions, as well as temperate regions except the polar regions, similar to the previous study by Burgess et al. (2019). However, unlike previous studies, we provided a global distribution map for

Lasiodiplodia species. More than 50 abundances of *Lasiodiplodia* species have been recorded in Australia (79), Brazil (173), China (85), Cuba (57), South Africa (51), Thailand (55) and Venezuela (111) (Table 1).



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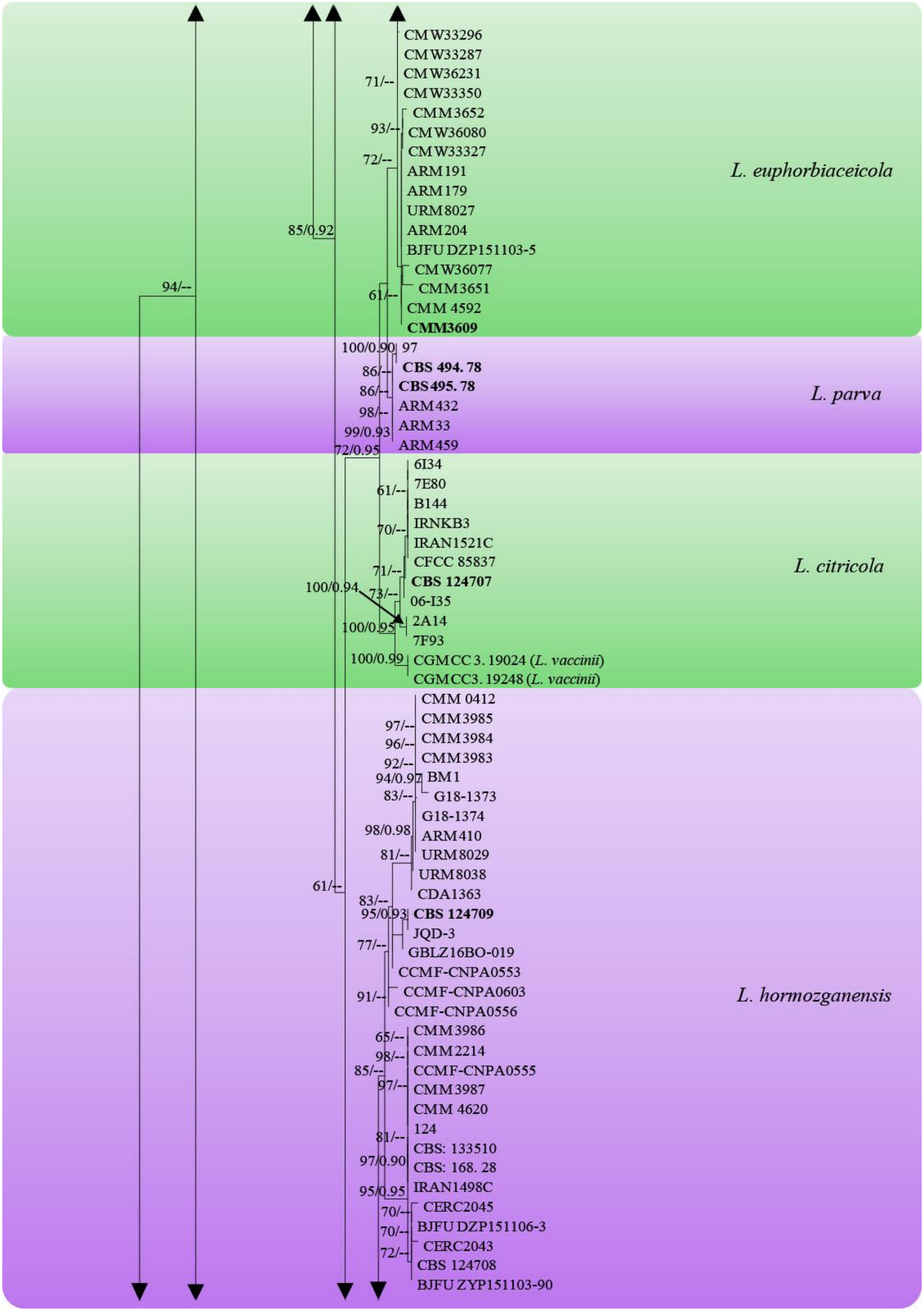
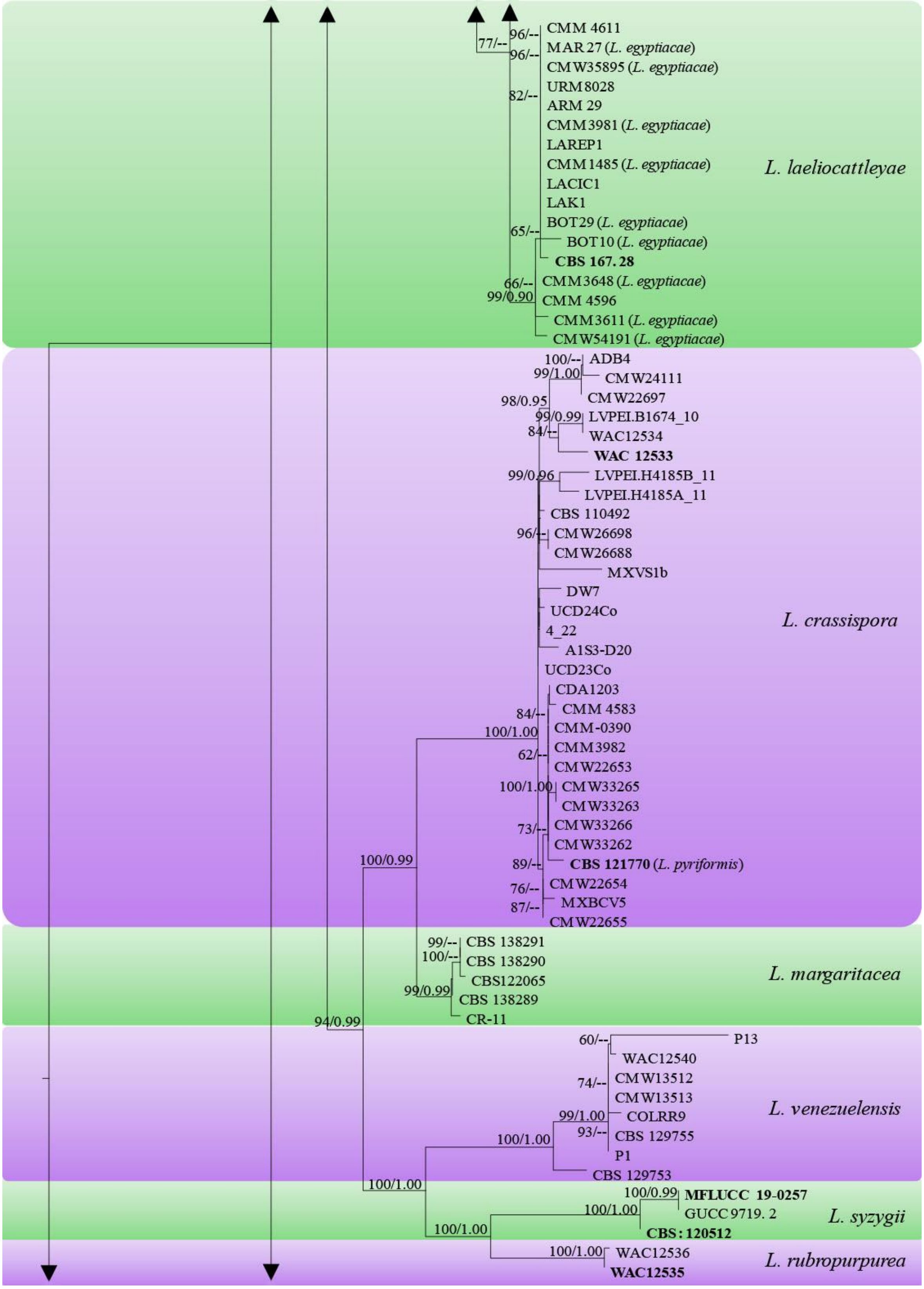


Figure 1 – Continued.

In a proportional symbol map that illustrates the global species richness of *Lasiodiplodia*, 1–5, 6–10, and 11–15 species richness are represented by blue, red and green, respectively. Yellow indicates more than 15 *Lasiodiplodia* species richness. According to the map, Australia (14), Brazil

(18), China (14), South Africa (11) and Thailand (14) recorded more than 10 *Lasiodiplodia* species. This may be due to the different levels of sampling and studies conducted across countries. *Lasiodiplodia theobromae* is the predominant species distributed globally in tropical and subtropical regions, and *L. pseudotheobromae* is the second most prevalent species (Fig. 3) (Table 1).



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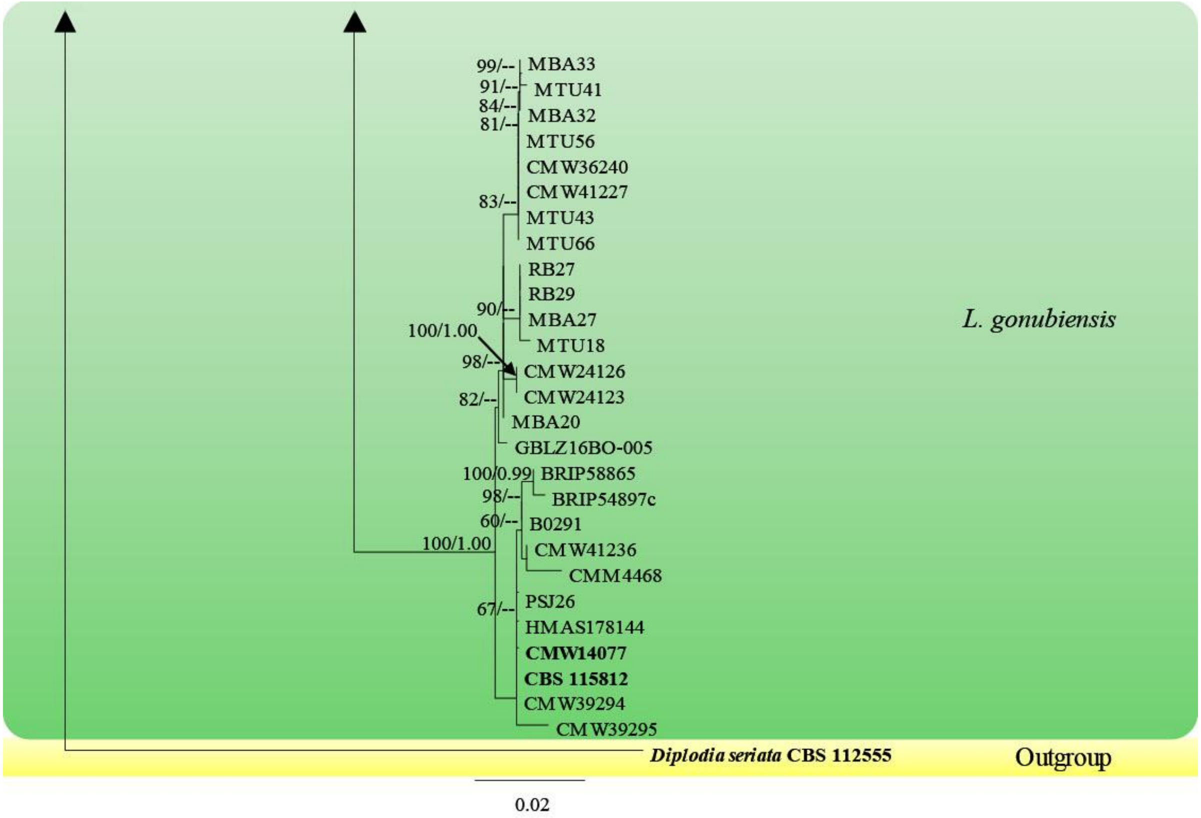

Figure 1 – Continued.

These two maps of the global abundance and richness of *Lasiodiplodia* species were prepared mainly based on previous studies (Farr & Rossman 2022). These maps show Brazil has the most abundant *Lasiodiplodia* species and high species richness. The reason may be that most *Lasiodiplodia* species studies were conducted in Brazil (Farr & Rossman 2022). Even though Thailand has less species abundance (55), it has a high species richness (14).

Fungal-host relations between *Lasiodiplodia* species and host families

The clustered heat map (double dendrogram) illustrates the density of *Lasiodiplodia* species on different host families (Fig. 4). *Lasiodiplodia* species are on the X-axis, and host families are on the Y-axis. The data matrix contains records for each *Lasiodiplodia* species and their host families. Both rows and columns were determined by performing hierarchical cluster analyses. The color gradient of cells is proportional to the number of records of each *Lasiodiplodia* species within the host family. The color range corresponds to 1–65 with two-by-two increment levels, and white represents zero records. According to the heat map, most *Lasiodiplodia* species are in the range 1–19 records. Most have one or two records, as shown in greenish-blue.

Lasiodiplodia theobromae has been reported on almost all host families except for *Dennstaedtiaceae*, *Phyllanthaceae*, *Podocarpaceae*, *Rhizophoraceae*, and *Salvadoraceae* (Fig. 4). *Lasiodiplodia theobromae* has a worldwide distribution with low host specificity (Santos et al. 2017). Hence, *L. theobromae* is recorded on a broader range of host families than other *Lasiodiplodia* species. Most of the *L. theobromae* records are on *Anacardiaceae* (59) (blue) and *Fabaceae* (65) (red) (Fig. 4). In our study, *L. theobromae* was recorded from economically important crops, such as *Anacardium occidentale*, *Carica papaya*, *Cocos nucifera*, *Mangifera indica*, and *Morus alba* or forest plants, *i.e.*, *Acacia mangium* and *Eucalyptus* sp. (Table 3). Other than *L. theobromae*, *L. brasiliensis*, *L. iraniensis*, *L. mahajangana*, and *L. pseudotheobromae* are recorded on many different host families (Farr & Rossman 2022). Some *Lasiodiplodia* species are recorded at one time on one host family, such as *L. acacia* on *Fabaceae*, *L. avicenniarum* on *Acanthaceae*, and *L. bruguierae* on *Rhizophoraceae*.

Based on the heatmap (Fig. 4), *Lasiodiplodia* species richness was highest in *Anacardiaceae, Malvaceae*, *Myrtaceae*, and *Vitaceae,* which includes economically important crops, such as *Anacardium* (cashew), *Eucalyptus* sp., Grapevines, Mango, *Pistacia* (pistachio), and *Syzygium* sp. (Java Apple, Water berry) (Wen 2007, Govaerts et al. 2008, Coutinho et al. 2017).

Lasiodiplodia species comprise important endophytic fungi from different host plants (Slippers & Wingfield 2007). Salvatore et al. (2020) mentioned several *Lasiodiplodia* species recorded as endophytes, such as *L. endophytica*, *L. gonubiensis*, *L. pseudotheobromae*, *L. thailandica*, and *L. venezuelensis*. Their study included 189 plant species from 60 families, which host *L. theobromae* in their endophytic life mode (Salvatore et al. 2020).

Lasiodiplodia species exhibit a wide range of associations, as they are not limited to latent endophytic infections in asymptomatic plants but are also known to be associated with various symptoms observed on diverse hosts, such as stem-end rot, fruit rot, decline, cankers, and dieback (El-Ganainy et al. 2022). Salvatore et al. (2020) also reported *Lasiodiplodia theobromae* as a pathogen. Furthermore, several studies suggest that pathogenic *L. theobromae* are capable of surviving and spreading as an endophytic plant associate (Gnanesh et al. 2022).

Taxonomy & Phylogeny

Phylogenetic analyses

The phylogenetic tree presented in Fig. 5 consisted of ex-type strains and an additional one or two strains of each *Lasiodiplodia* species. Here, we mentioned the host and the location of each *Lasiodiplodia* strain. Even though we used the same loci (ITS, *tef*1-α, *tub2*, and *rpb2*) to construct the phylogenetic trees in Figs 1, 5, the tree topologies are slightly different due to the differences in the sequence alignment and the taxon sampling.

The combined ITS, *tef*1-α, *tub2*, and *rpb2* dataset included 96 taxa with *Diplodia seriata* (CBS 112555) and *Diplodia mutila* (CMW 7060) as the outgroup taxa. The final alignment consisted of 1720 characters, including gaps (ITS = 544, *tef*1-α = 300, *tub2* = 390, and *rpb2* = 486). Both ML and BI analyses exhibit similar tree topologies. The best-scoring RAxML tree with a final likelihood value of -6305.360377 is presented (Fig. 5). The combined dataset included 476 distinct alignment patterns, with 24.75% undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.21947, C = 0.292027, G = 0.263398, T = 0.225106; substitution rates AC = 1.103383, AG = 4.658225, AT = 1.603723, CG = 1.172535, CT = 7.634387, GT = 1.0; gamma distribution shape parameter α = 0.205009. After running the BI analysis for 1,000,000 generations, 10,001 trees were produced. The first 1,000 trees were discarded, representing the burn-in phase, and the remaining were used to calculate posterior probabilities in the majority rule consensus tree. The 0.01 average standard deviation of split frequencies was achieved after 1,000,000 generations.

The phylogenetic tree generated by ML analysis revealed that our *Lasiodiplodia* collections were grouped into six major clades (Group A–F). Among them, most isolates (ten isolates) were grouped with *L. thailandica* (CPC 22795, CPC 22755, CGMCC 3.17975, and MFLUCC 18-0244) with moderate 60% ML bootstrap support and 0.75 posterior probability as shown in Group A (Fig. 5). Another, nine clustered within the clade containing *L. theobromae* (CBS 164.96 and CBS 111530) (Group C), with 82% ML bootstrap support and 0.85 posterior probability. Additional two *L. citricola* isolates grouped with the ex-type and other strain of *L. citricola* (CBS 116459 and CBS 116460) with 100% ML bootstrap and 0.90 posterior probability (Group D, Fig. 5). Another two isolates grouped with *L. pseudotheobromae* (CBS 124707 and CBS 124706) with 69% ML bootstrap support and 0.65 posterior probability (Group E, Fig. 5). In Group B, one of our isolates clustered to *L. mahajangana* (CBS 137785, CMW 27818, CMW 27801, and IBL366) with moderate 72% ML bootstrap support and 0.97 posterior probability. Our *L. crassispora* isolate (NCYUCC 19-0391) clustered with the ex-type and other strains of *L. crassispora* (CBS 118741, CBS 121770, and CMW13488) with 100% ML bootstrap support and 1.00 posterior probability in Group F (Fig. 5).

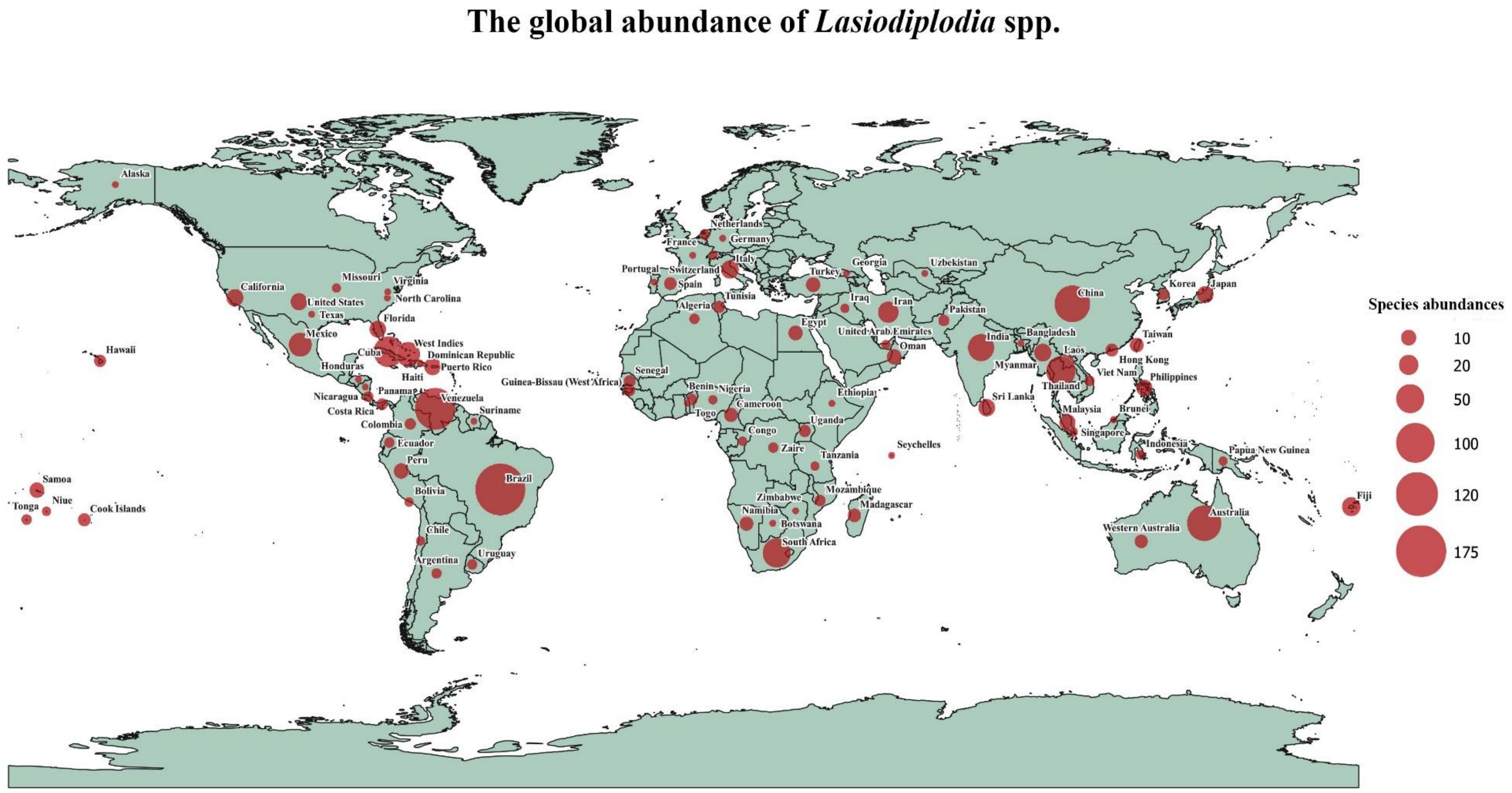

Figure 2 – Proportional symbol map for the global abundances of *Lasiodiplodia* spp.

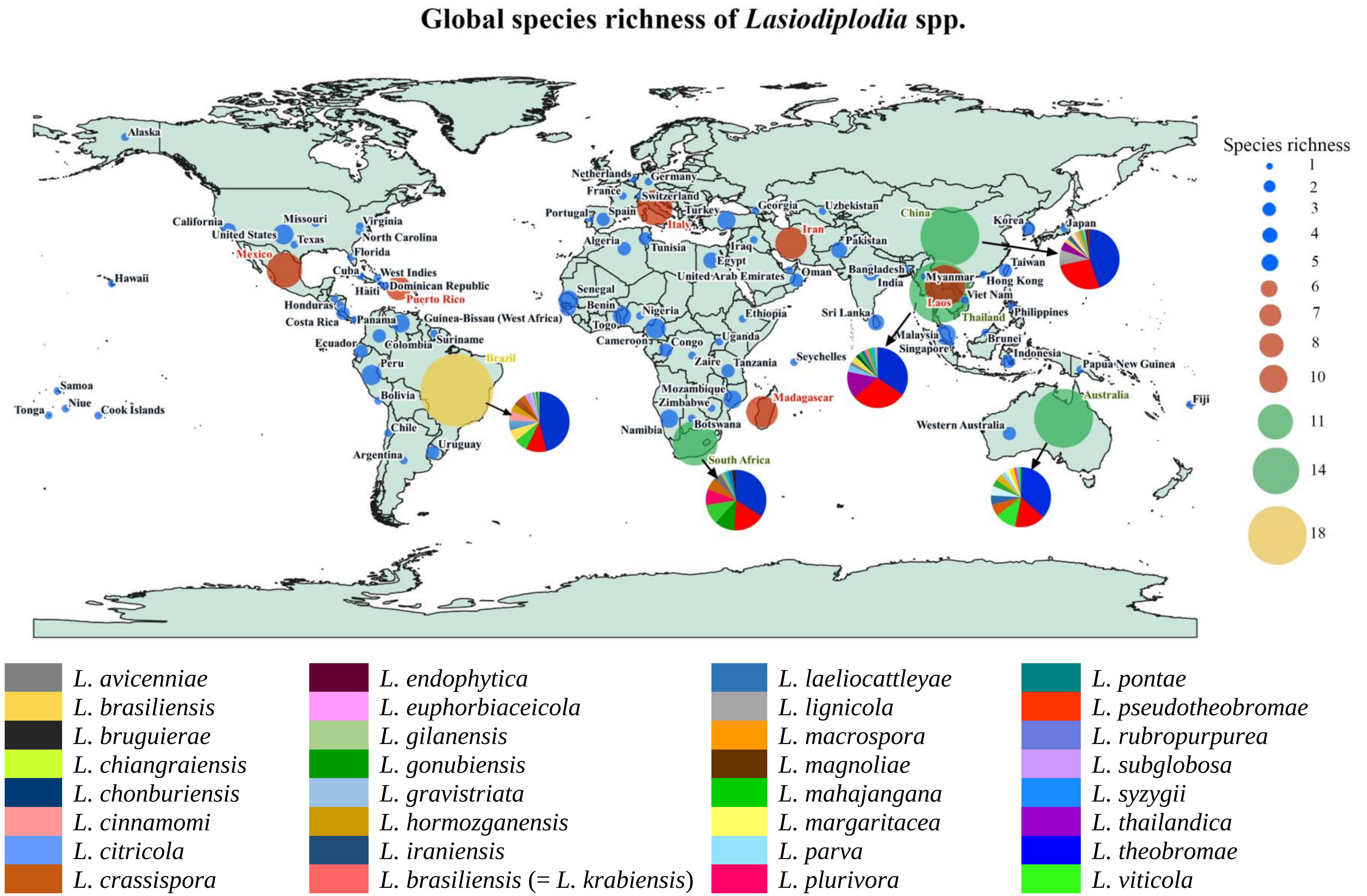

Figure 3 – Proportional symbol map for the global species richness of *Lasiodiplodia* spp. Species richness is represented by Pie charts.

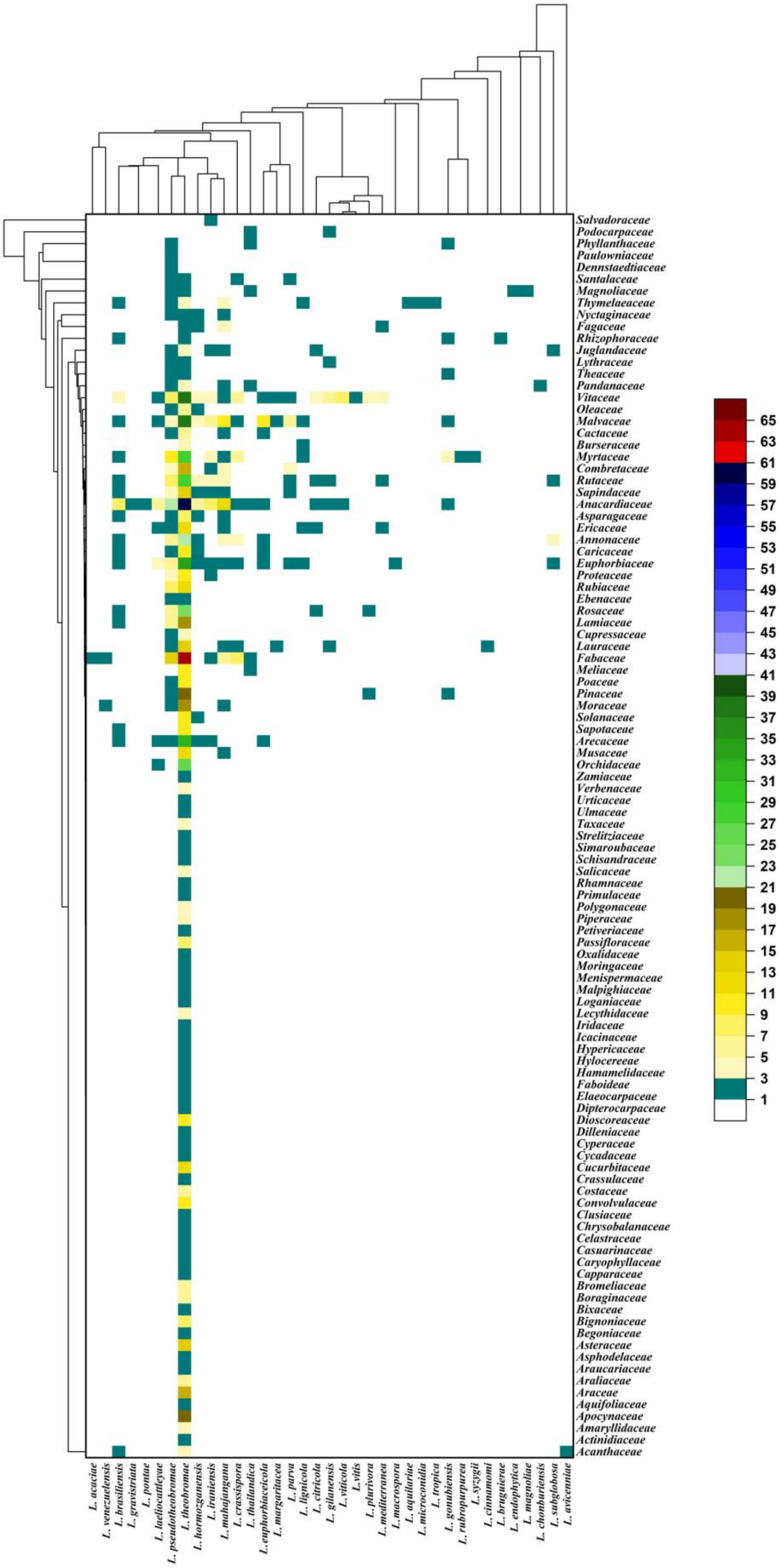

Figure 4 – Heatmap for the reported *Lasiodiplodia* species on different hosts families. The color scale from 0 to 65 indicates the number of *Lasiodiplodia* records on different hosts, where 0 indicates total absence.

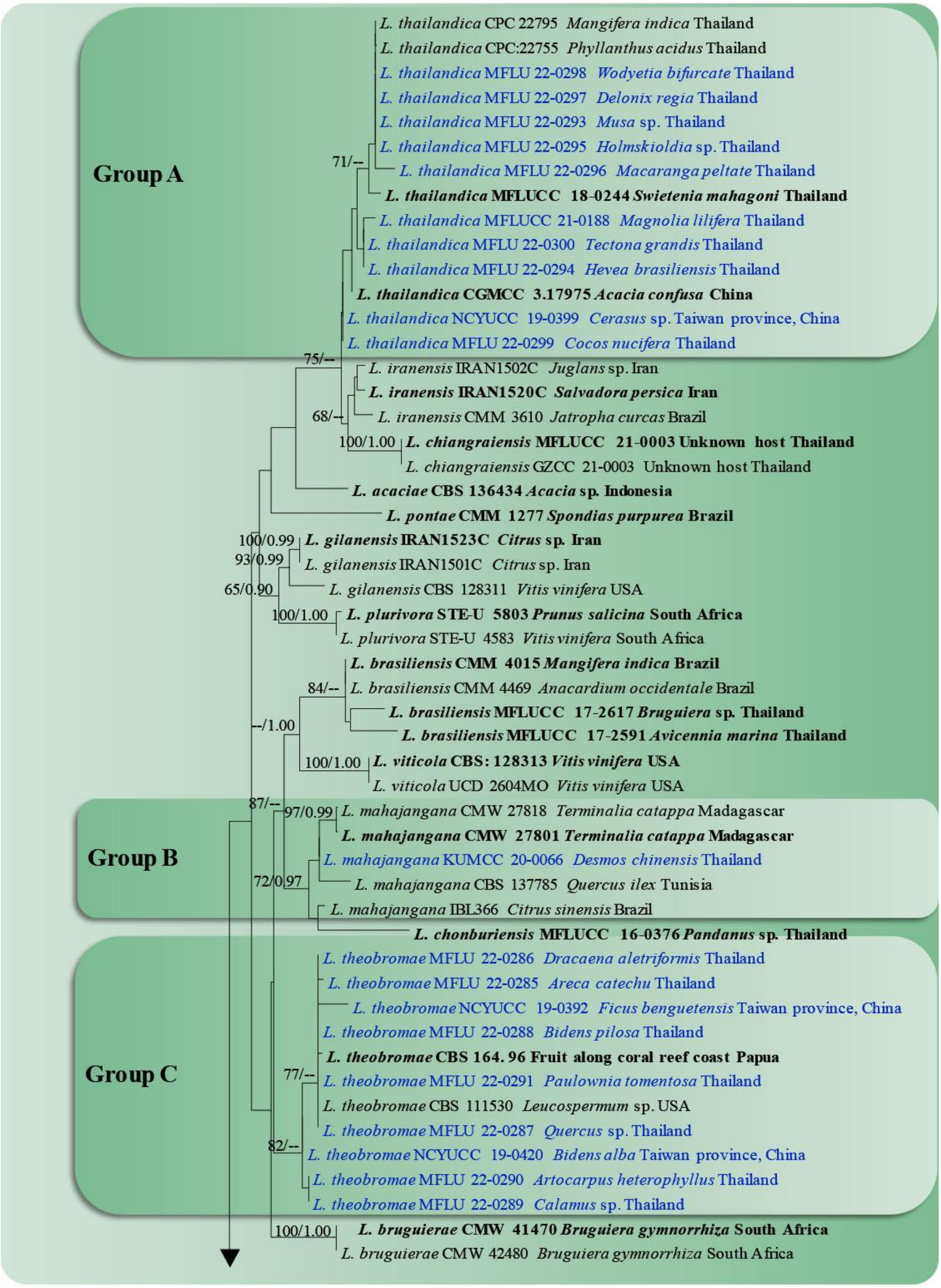

Figure 5 – Phylogenetic tree generated from ML analysis based on combined dataset of ITS, *tef*1-α, *tub2*, and *rpb2*. The tree is rooted to *Diplodia seriata* (CBS 112555) and *Diplodia mutila* (CMW 7060). Bootstrap support values for ML ≥ 65% and Bayesian posterior probabilities (PP) ≥ 0.90 are noted at the nodes. Strain numbers, hosts and locations are noted after the species names. Strains isolated in this study are represented as blue and type strains are in bold.

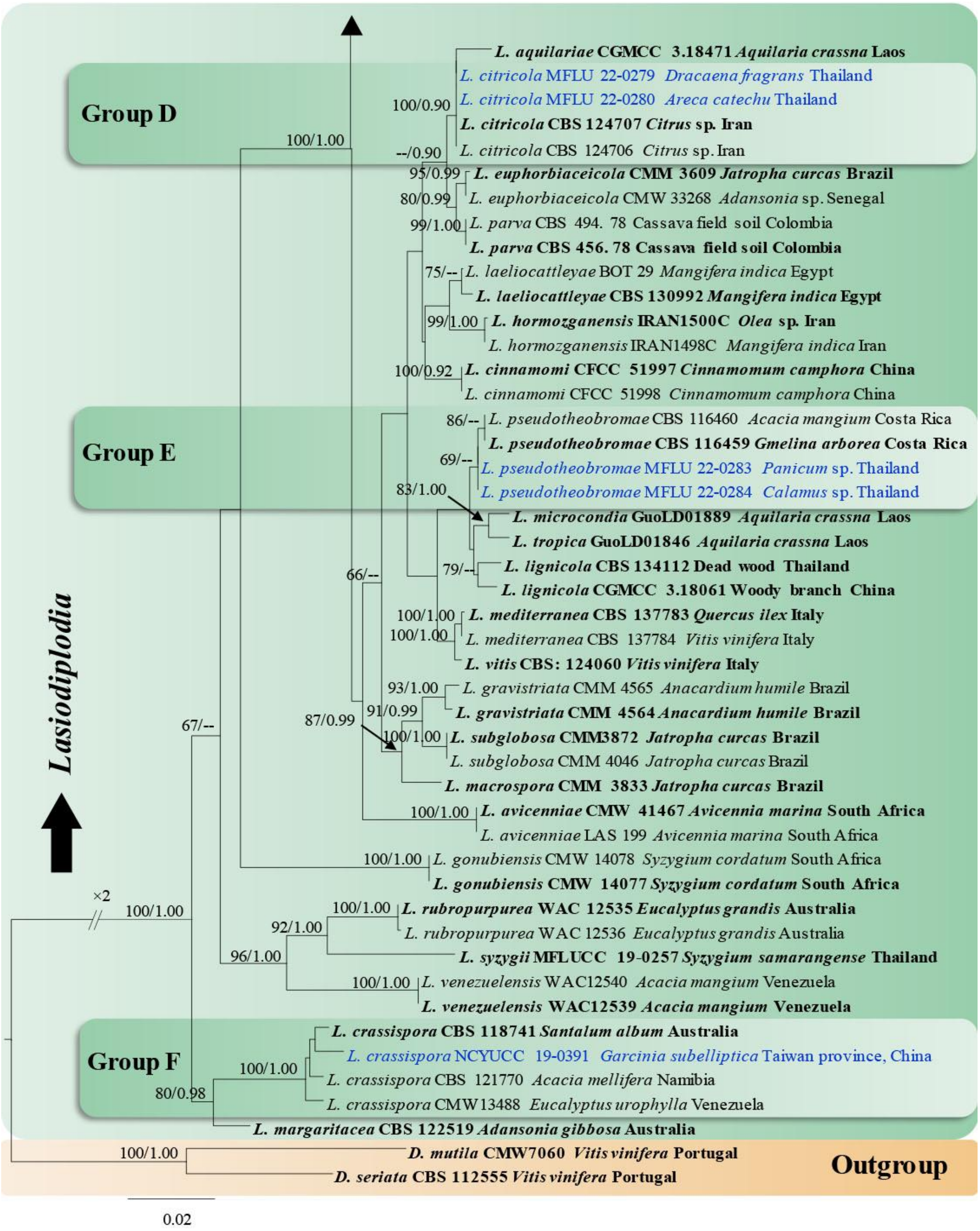

Figure 5 – Continued.

Taxonomy

Lasiodiplodia citricola Abdollahz., Javadi & A.J.L. Phillips, Persoonia 25: 4 (2010)

Figs 6, 7

Index Fungorum number: IF 516777; Facesoffungi number: FoF 09503

Saprobic on dead leaf of *Dracaena fragrans* and dead seed of *Areca catechu*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 175–305 µm high × 120–215 µm diam. (x̄ = 215 × 165 µm, n = 10) pycnidial, solitary, semi-immersed, uniloculate, globose to subglobose, appear as black dots. *Peridium* 15–40 µm wide, composed of 3–5 layers, outer layer thick-walled, consists of dark brown cells of *textura angularis*, inner layer thin-walled, consists of hyaline cells of *textura angularis*. *Paraphyses* 1.5–3 µm wide, up to 65 µm long, hyaline, cylindrical, aseptate, not branched. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 4–16 µm high × 3–6 µm diam. (x̄ = 10 × 4 µm, n = 20) lining the pycnidial cavity, holoblastic, annellidic, hyaline, cylindrical. *Conidia* 15–30 µm high × 12–25 µm diam. (x̄ = 25 × 15 µm, n = 50, L/W = 1.6) obovate to ovoid, straight, usually wider in middle, rounded at both ends, hyaline, aseptate, thick-walled, guttulate.

Culture characteristics – Conidia germinating on PDA within 6 hours. Germ tubes produced at one side of the conidium. Colonies on PDA fast growing, reaching 4–6 cm diam. after 4 days at 25 °C, circular, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, grey-black in both upper and lower sides.

Material examined – Thailand, Chiang Rai, on dead leaf of *D. fragrans* (*Asparagaceae*), 24 June 2020, Digvi Bundhun (MFLU 22-0279, new host and geographical record); *ibid*, Nang Lae village, on dead seed of *A. catechu* (*Arecaceae*), 26 July 2020, Achala Rathnayaka (MFLU 22-0280, new host record), living culture MFLUCC 23-0019.

Known hosts and distribution – *Citrus latifolia* in Mexico (Bautista-Cruz et al. 2019), *Citrus* sp. in Iran (Abdollahzadeh et al. 2010), *Juglans regia* in California and Iran (Chen et al. 2013a, Sohrabi et al. 2020), *Pistacia vera* and *Prunus persica* in California (Chen et al. 2013b, Chen et al. 2014), *Vitis vinifera* in Australia and Italy (Carlucci et al. 2015, Burgess et al. 2019), *Areca catechu* and *Dracaena fragrans* in Thailand (this study).

Notes – *Lasiodiplodia citricola* was reported from different host substrates, such as the dead leaves and seeds of *D. fragrans* and *A. catechu* respectively (in Figs 6, 7). Based on multi-gene phylogenetic analyses, our collections (MFLU 22-0279 and MFLU 22-0280) clustered with other strains of *L. citricola* (CBS 124706 and CBS 124707) (Fig. 5). Morphologically, our collections show similar characteristics to the holotype, such as globose and uniloculate conidiomata, hyaline, aseptate, granular conidia with similar size (L/M = 1.6) (Abdollahzadeh et al. 2010). However, in the holotype, conidia are pigmented, verruculose, and 1-septate with longitudinal striations, unlike our collections (Abdollahzadeh et al. 2010). According to morpho-molecular analyses, we present our collections as new host records of *L. citricola* from *A. catechu* and *D. fragrans* and a new geographical record from Thailand.

Lasiodiplodia crassispora T.I. Burgess & P.A. Barber, Mycologia 98(3): 425 (2006)

Fig. 8

Index Fungorum number: IF 500235; Facesoffungi number: FoF 06624

Saprobic on twigs of *Garcinia subelliptica*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 22–31 µm high × 30–42 µm diam. (x̄ = 25 × 38 µm, n = 10), pycnidial, solitary, immersed, becoming erumpent at maturity, formed uni loculate stromata, coriaceous, subglobose. *Peridium* 3–10 µm diam. composed of thin-walled, sub-globose, brown cells of *textura angularis*, inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 3.6–5.3 µm × 1–2.1 µm (x̄ = 5 × 1.3 µm, n = 15), lining the pycnidial cavity, holoblastic, hyaline, cylindrical, discrete, determinate, smooth walled. *Conidia* 10–12 µm × 6–8µm (x̄ = 11.3 × 7.5 µm, n = 30), oblong to ovoid, straight, rounded at both ends, cylindrical, hyaline, aseptate, thick-walled.

Culture characteristics – Conidia germinating on PDA within 6 hours. Germ tubes produced at one side of the conidium. Colonies on PDA fast growing, reaching 5–6 cm diam. after 5 days at 25 °C, circular, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, grey-black in upper side and black in lower side.

Material examined – China, Taiwan province, Chiayi, Chiayi Arboretum, living on a dead twig of *G. subelliptica* (*Clusiaceae*), 16 August 2019, Achala Rathnayaka, (MFLU 22-0281, new host and geographical record), living culture NCYUCC 19-0391.

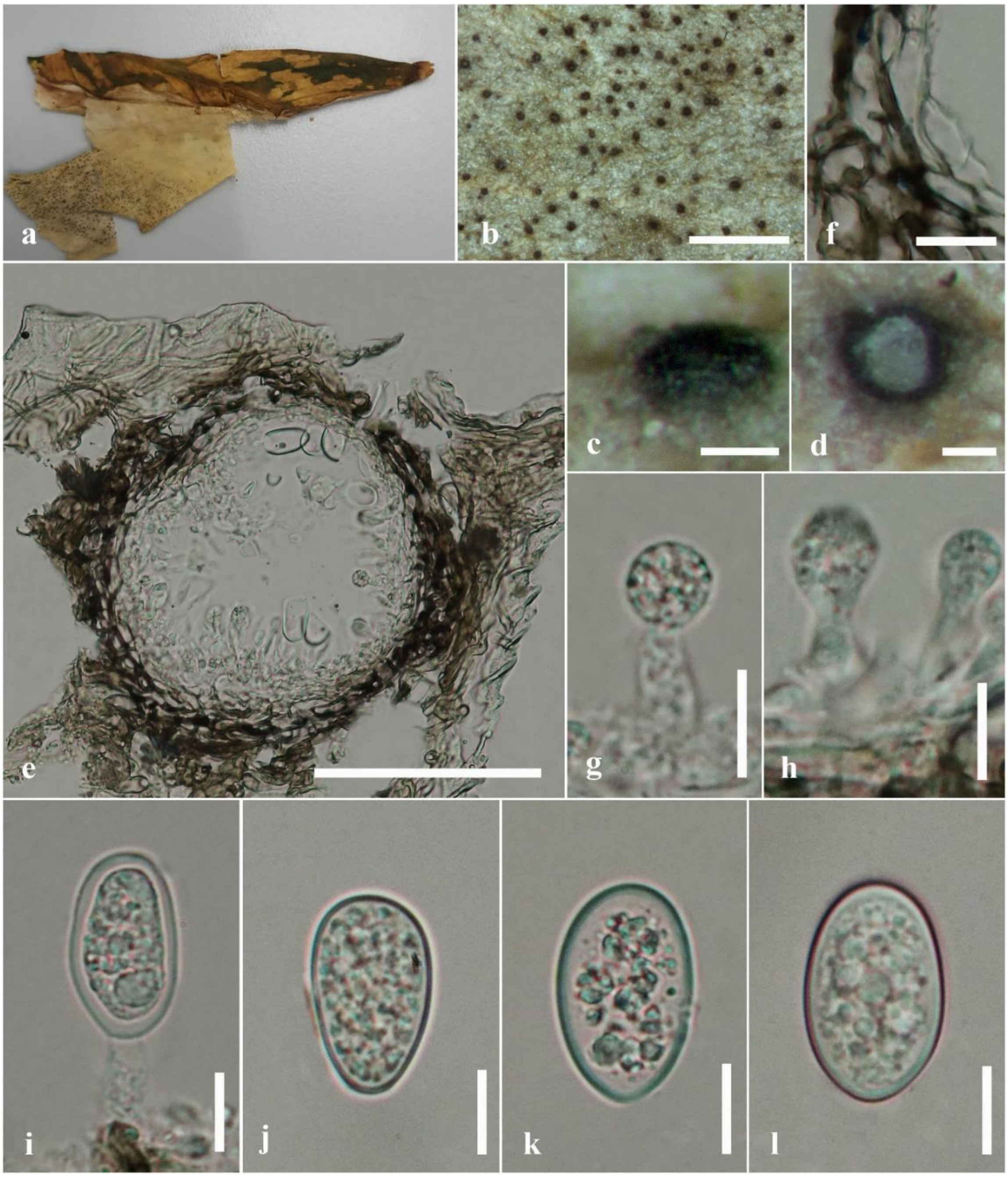

Figure 6 – *Lasiodiplodia citricola* on *D. fragrans* (MFLU 22-0279). a Dead leaf. b, c Appearance of conidiomata on host surface. d, e Section through conidioma. f Section through the peridium. g–i Conidiogenous cells. j–l Conidia. Scale bars: b = 500 µm, c–e = 100 µm, f–l = 10 µm.

Known hosts and distribution – *Adansonia digitata* in Senegal (Cruywagen et al. 2017), *Annona leptopetala*, *A. muricata*, *A. squamosa*, *Mangifera indica* in Brazil (Marques et al. 2013, Machado et al. 2019), *Cinnamomum zeylanicum* in Sri Lanka (Adikaram & Yakandawala 2020), *Corymbia flavescens*, *Corymbia* sp., *Syzygium album* in Australia (Burgess et al. 2006, Sakalidis et al. 2011, Burgess et al. 2019), *Syzygium cordatum* in South Africa (Phillips et al. 2008), *Eucalyptus urophylla* in Uruguay and Venezuela (Burgess et al. 2006, Pérez et al. 2010), *Pterocarpus angolensis* in Africa, Australia and South Africa (Mehl et al. 2011, Coutinho et al. 2017, Custódio et al. 2018), *Sclerocarya birrea* subsp. caffra in South Africa (Mehl et al. 2017), *Vitis vinifera* in Brazil, California, Mexico, South Africa and United States (Urbez-Torres et al. 2010, Van Niekerk et al. 2010, Urbez-Torres 2011, Correia et al. 2013, Rangel-Montoya et al. 2021), *G. subelliptica* in Taiwan province, China (this study).

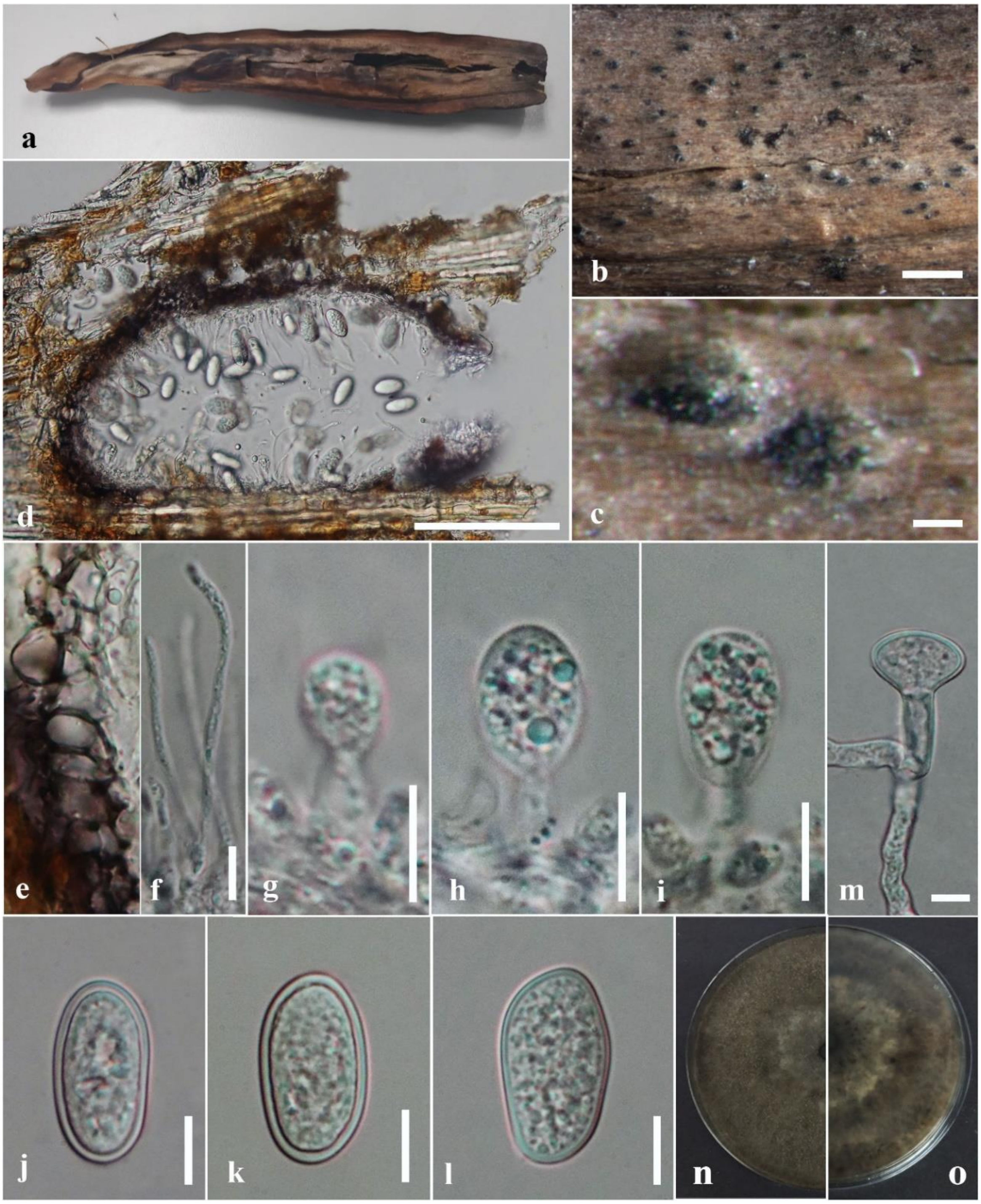

Figure 7 – *Lasiodiplodia citricola* on *A. catechu* (MFLU 22-0280). a Dead seed. b, c Appearance of conidiomata on host surface. d Section through conidioma. e Section through the peridium. f Paraphyses. g–i Conidiogenous cells. j–l Conidia. m Germinating conidium n, o Colony on PDA (n upper, o lower). Scale bars: b = 500 µm, c = 200 µm, d = 100 µm, e–m = 10 µm.

Notes – Morphologically, our collection (NCYUCC 19-0391) is similar to the holotype of *Lasiodiplodia crassispora* (MURU 407) collected from the canker of *Santalum album* in Western. Australia (Burgess et al. 2006). However, the size of conidia in the holotype (x̄ = 28.8 × 16.0, l/w = 1.8) is larger than our collection (x̄ = 11.3 × 7.5 µm, l/w = 1.5) (Burgess et al. 2006). Also, conidia before germination are pigmented in the holotype with one septum at maturity and vertical striations were observed at maturation, which could not be observed in our collections (Burgess et al. 2006). According to multi-gene phylogeny (ITS, *tef*1-α, *tub2*, and *rpb2*), our strain (NCYUCC 19-0391) clustered with other strains of *L. crassispora* (CBS 118741, CBS 121770, and CMW

13488) with relatively high bootstrap support (100% ML/1.00 pp) (Fig. 5). Based on morph-molecular analyses, we introduce our collection as a new host record of *L. crassispora* from *G. subelliptica* and a new geographical record from Taiwan province, China

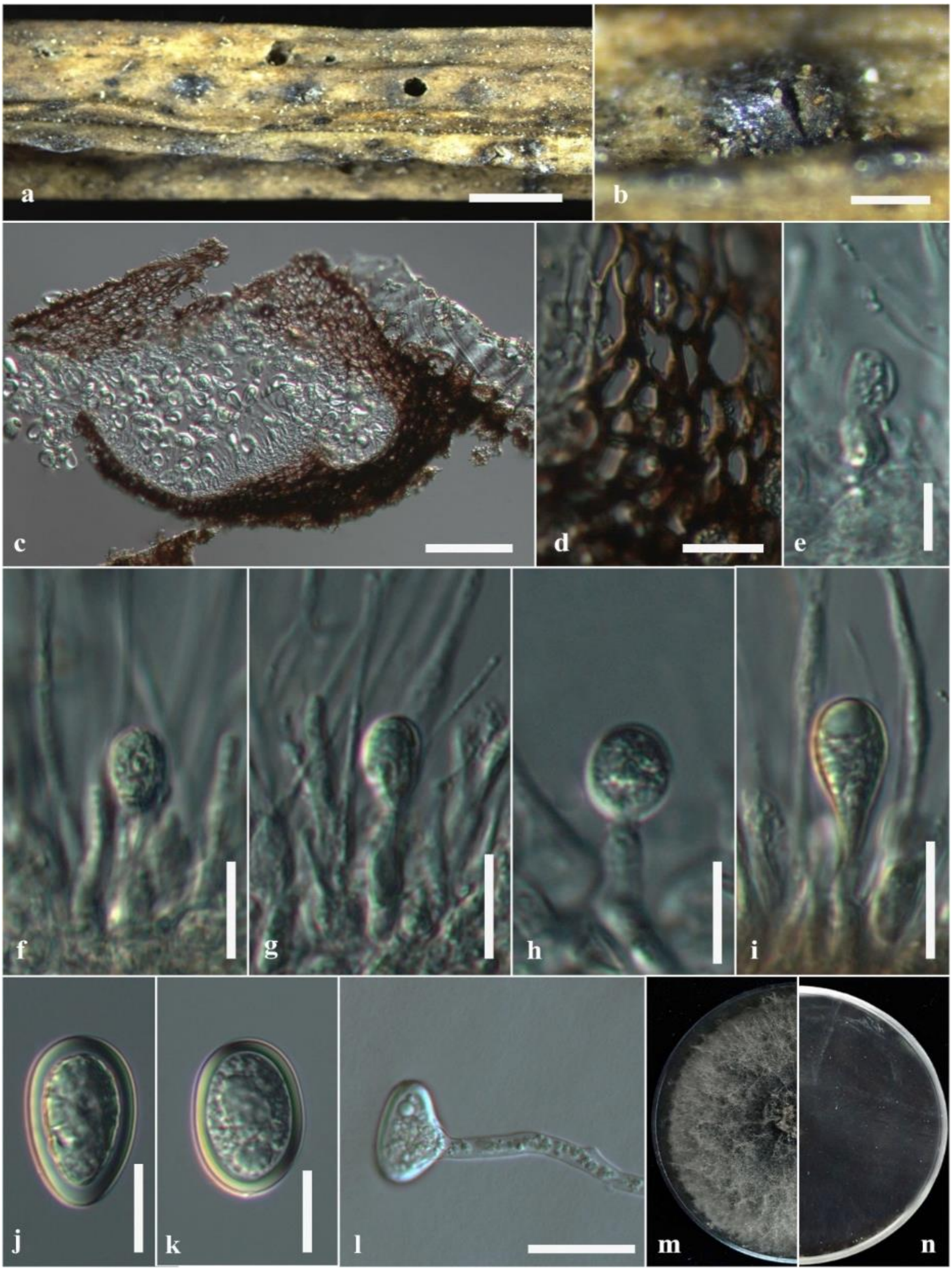

Figure 8 – *Lasiodiplodia crassispora* on dead twig of *G. subelliptica* (MFLU 22-0281). a Conidiomata on host substrate. b Close up of a conidioma erumpent through the host surface. c Cross section of conidioma. d Section through the peridium. e–i Immature conidia attached to conidiogenous cells. j, k Immature to mature conidia. l Germinating conidium. m, n Colony on PDA (m upper, n lower). Scale bars: a = 200 µm, b = 100 µm, c, d = 10 µm, e–k = 5 µm, l = 20 µm.

Lasiodiplodia mahajangana Begoude, Jol. Roux & Slippers, in Begoude et al. Mycol. Progr. 9(1): 110 (2010) Fig. 9

Index Fungorum number: IF 514012, Faces of Fungi number: FoF 14045

Saprobic on dead twigs of *Desmos chinensis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 200–260 µm high × 170–230 µm diam. (x̄ = 230×200 µm, n = 10), pycnidial, solitary, scattered, immersed to semi-immersed, uni-locular, brown, globose to subglobose, with a central ostiole. *Peridium* 26–40 µm wide, composed of light brown cells of *textura angularis*. *Paraphyses* up to 30 µm long, 2–3 µm wide, hyaline, cylindrical, aseptate, rounded at apex, unbranched. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–10 × 3–4 µm (x̄ = 9 × 3.5 µm, n = 10), holoblastic, discrete, hyaline, cylindrical to subcylindrical, smooth-walled. *Conidia* 15–20 × 6–9 µm (x̄ = 17 × 7 µm, n = 30), hyaline, subglobose to subcylindrical, with granular content, both ends rounded, wall <2 µm thick.

Culture characteristics – Colonies on PDA reaching 70 mm diameter after 5 days at 25 °C, olivaceous-grey colonies from above, circular, entire margined, fluffy appearance with abundant aerial mycelia and olivaceous-brown reverse.

Material examined – Thailand, Chiang Rai province, dead twigs attached to *D. chinensis* (Annonaceae), 8 March 2019, N. I. de Silva, DC4 (HKAS 107090, new host record), living culture KUMCC 20-0066.

Known hosts and distribution – *Acacia synchronicia*, *Annona reticulata*, *Crotalaria medicaginea*, *Ficus opposita*, *Musa* sp., and *Persea americana* in Australia (Burgess et al. 2019, Tan et al. 2019), *Adansonia digitata* in Australia, Namibia and South Africa (Jami et al. 2017, Burgess et al. 2019), *Euphorbia ingens*, *Mangifera indica* and *Sclerocarya birrea* subsp. *caffra* in South Africa (Jami et al. 2017), *Juglans regia* in Iran (Sohrabi et al. 2020), *Terminalia catappa* in Madagascar (Begoude et al. 2010), *D. chinensis* in Thailand (this study).

Notes – Our fungal collection (KUMCC 20-0066) clustered with other strains of *L. mahajangana* (CMW 27818, CMW 27801, and CBS 137785) with moderate 59% ML bootstrap support and 0.6 posterior probability based on the multi-gene phylogenic analyses (Fig. 5). Morphologically, our strain is similar to the *L. mahajangana* holotype (PREM 60288) collected from healthy branches of *Terminalia catappa* in Madagascar (Begoude et al. 2010) in having uniloculate conidiomata and hyaline, cylindrical, aseptate, unbranched paraphyses with rounded tips (Begoude et al. 2010). However, the conidial width is larger in the holotype (11.5 µm) than in our strain (7 µm) (Begoude et al. 2010). In the holotype, conidia become pigmented and one-septate after release, and vertical striations can be observed at maturity (Begoude et al. 2010). Nevertheless, in our collection, we could not observe these conidial characters. Based on morpho-molecular data analysis, we conclude that our new collection is a new host record of *L. mahajangana* on *D. chinensis* and a new geographical record from Thailand.

Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous, Fungal Diversity 28: 8 (2008) Figs 10, 11

Index Fungorum number: IF 510941; Facesoffungi number: FoF 00166

Saprobic on dead twigs of *Panicum* sp. and dead leaf of *Calamus* sp. Sexual morph: See Tennakoon et al. (2016). Asexual morph: Coelomycetous. *Conidiomata* 150–240 µm high × 205–280 µm diam. (x̄ = 190 × 245 µm, n = 15), pycnidial, solitary, immersed or semi-immersed, becoming erumpent at maturity, uniloculate, globose to subglobose, black. *Peridium* 15–55 µm wide, composed of 7–10 layers, outer layer thick-walled, consists of dark brown cells of *textura angularis,* inner layer thin-walled, consists of light brown cells of *textura angularis*. *Paraphyses* 1.5–4.5 µm wide, up to 50 µm long, hyaline, cylindrical, aseptate, not branched, rounded at the apex. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 5–12 µm × 3–6 µm (x̄ = 9 × 4 µm, n = 30), lining the pycnidial cavity, holoblastic, annellidic, hyaline, smooth, cylindrical. *Conidia* 15–30 µm × 9 – 16 µm (x̄ = 20 × 12 µm, n = 50, L/W= 1.6), oblong to ovoid, straight, rounded in both ends, cylindrical, hyaline, aseptate, thick-walled, guttulate, rarely become one septate, dark brown with age, with longitudinal striations.

Culture characteristics – Conidia germinating on PDA within 6 hours. Germ tubes produced at one side of the conidium. Colonies on PDA fast-growing, reaching 5–6.5 cm diam. after 6 days at 25 °C, circular, medium dense, flat or effuse, slightly raised, fluffy to somewhat fluffy, black in both upper and lower sides.

Material examined – Thailand, Trat province (Southern Thailand), on dead twigs of *Panicum* sp. (*Poaceae*), 09 September 2020, Rashika Sajith (MFLU 22-0283, new host record); *ibid*., Chiang Rai, Nang Lae village, on dead leaf of *Calamus* sp. (*Arecaceae*), 10 June 2020, Achala Rathnayaka (MFLU 22-0284, new host record), living culture MFLUCC 23-0020.

Known hosts and distribution – *Lasiodiplodia pseudotheobromae* has a cosmopolitan distribution and different host species (Farr & Rossman 2022).

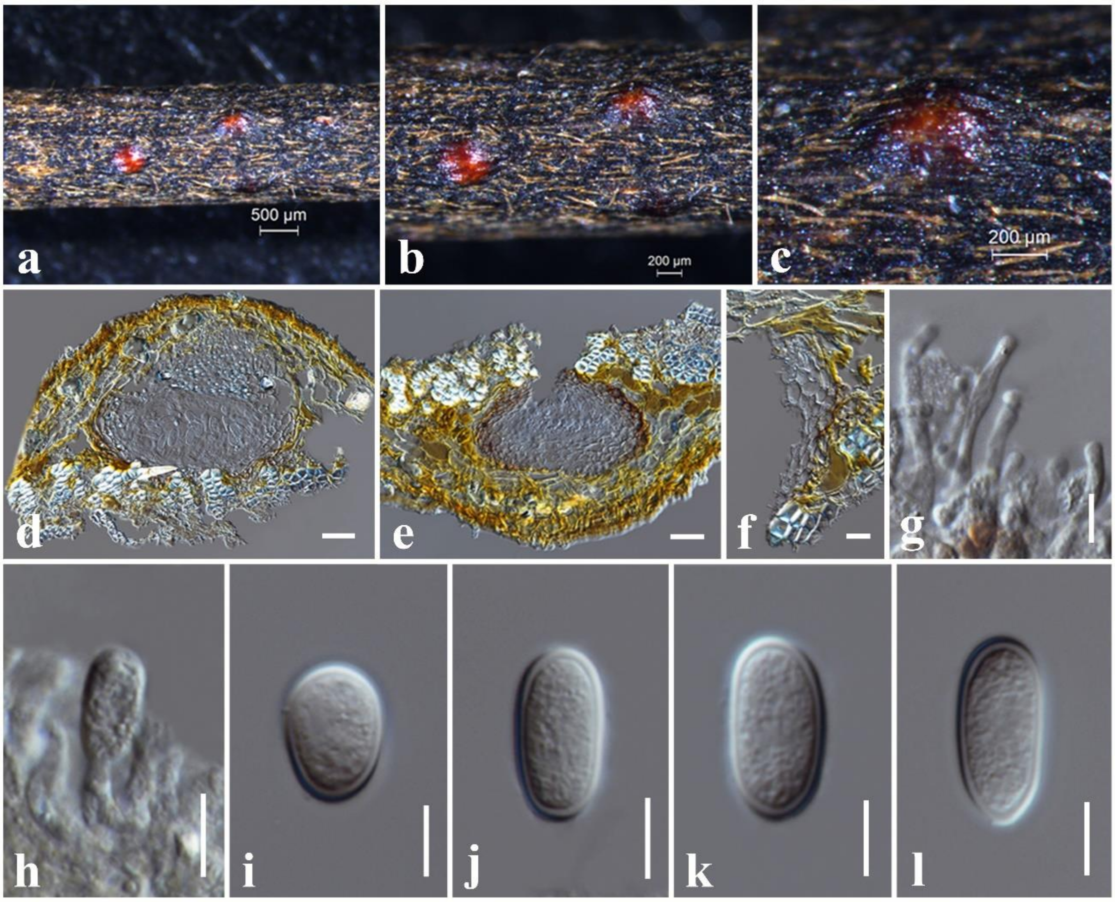

Figure 9 – *Lasiodiplodia mahajanagana* on *D. chinensis* (HKAS 107090). a–c Appearance of conidiomata on the substrate. d, e Sections through the conidioma. f Section through the peridium. g Paraphyses. h Conidiogenous cells. i–l Conidia. Scale bars: a, b = 500 µm, c = 200 µm, d, e = 50 µm, f–l = 10 µm.

Notes – Morphologically, new fungal collections (MFLU 22-0283 and MFLU 22-0284) reported on different host substrates (dead twigs and dead leaf) are similar to *L. pseudotheobromae* holotype (CBS-H 19916) collected from *Gmelina arborea* in Costa Rica (Alves et al. 2008). Both holotype and our strains have uniloculate, immersed conidiomata that become erumpent at maturity, with hyaline, aseptate conidia becoming one septate, dark brown with age, with longitudinal striations (Alves et al. 2008). However, conidial size is comparatively smaller in our strains ($\bar{x}$ = 20 × 12 µm) than in the holotype ($\bar{x}$ = 28 ± 2.5 × 16 ± 1.2 µm) (Alves et al. 2008). Based on phylogenetic analyses, our collections (MFLU 22-0283 and MFLU 22-0284) clustered with other strains of *L. pseudotheobromae* (CBS 116459 and CBS 116460) (Fig. 5). Based on the morpho-molecular evidence, we identified our new collections as new host records of *L. pseudotheobromae* on *Calamus* sp. and *Panicum* sp. in Thailand.

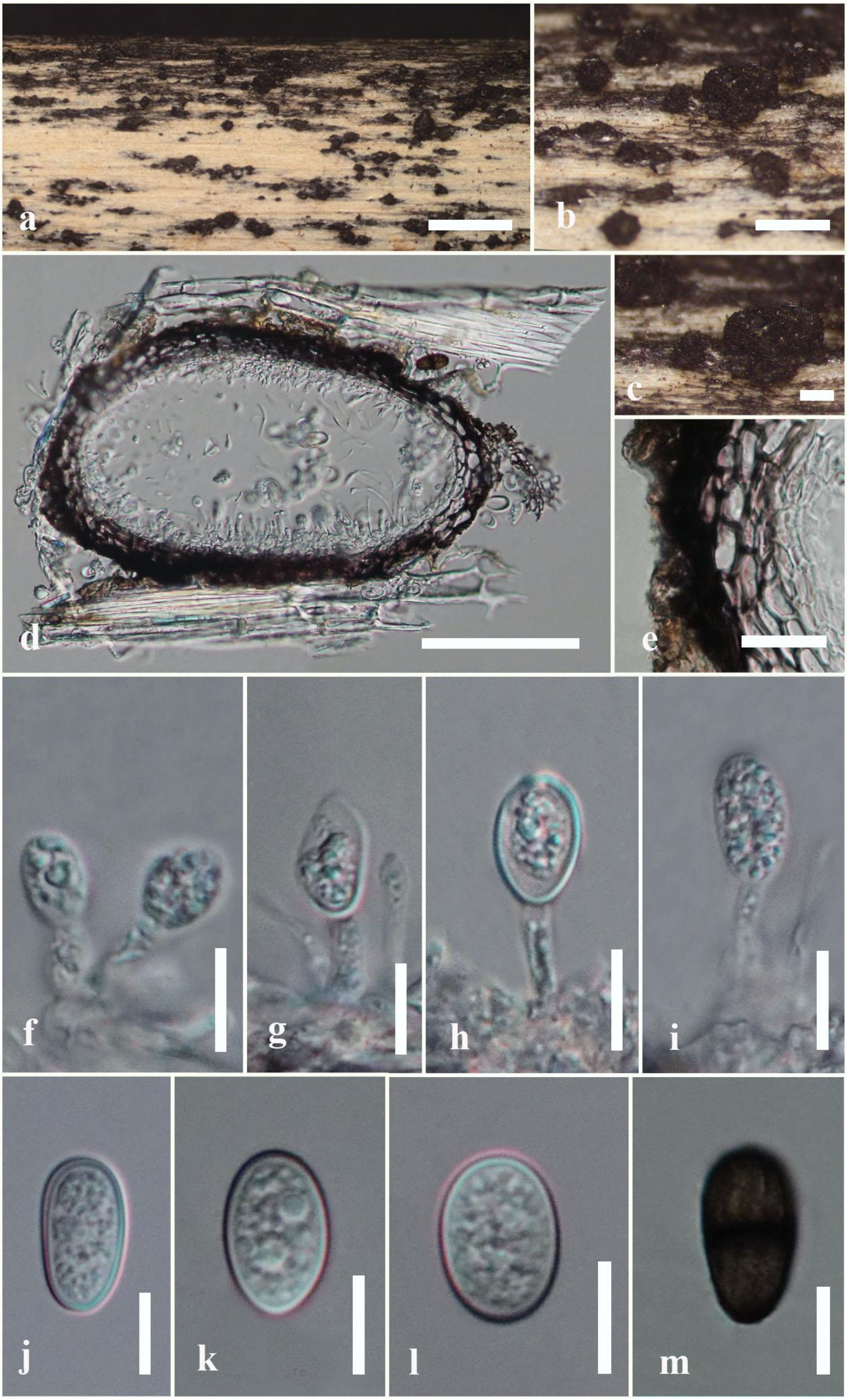

Figure 10 – *Lasiodiplodia pseudotheobromae* on *Panicum* sp. (MFLU 22-0283). a–c Appearance of conidiomata on the host surface. d A section through the conidioma. e A section through the

peridium. f–i Conidiogenous cells. j–m Conidia. Scale bars: a = 2 mm, b = 500 µm, c = 200 µm, d = 100 µm, e = 20 µm, f–m = 10 µm.

Figure 11 – *Lasiodiplodia pseudotheobromae* on *Calamus* sp. (MFLU 22-0284). a Dead leaf. b–c Appearance of conidiomata on the host surface. d, e A section through conidioma. f A section through the peridium. g Paraphyses. h–j Conidiogenous cells. k–n Conidia. o, p Colony on PDA (o upper, p lower). Scale bars: b = 1 mm, c, d = 200 µm, e = 100 µm, g–n = 10 µm.

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)

Figs 12–16

Index Fungorum number: IF 188476; Facesoffungi number: FoF 00167

Saprobic on dead twigs, leaves, seed pod and fruit of several hosts. Sexual morph: See Phillips et al. (2013). Asexual morph: Coelomycetous. *Conidiomata* 130–300 µm high × 100–260 µm diam. (x̄ = 195 × 150 µm, n = 20), pycnidial, solitary or aggregated, scattered, immersed, becoming erumpent at maturity, uniloculate, globose to subglobose, black. *Peridium* 15–50 µm wide, composed of 3–6 layers, outer layer thick-walled, consists of dark brown cells of *textura angularis* to *textura globulosa*, inner layer thin-walled, consists of light brown cells of *textura angularis* to *textura globulosa*. *Paraphyses* 1.5–3 µm wide, up to 65 µm long, hyaline, cylindrical, aseptate, not branched. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 5–16 µm × 2–8 µm (x̄ = 9 × 4 µm, n = 20), lining the pycnidial cavity, holoblastic, annellidic, hyaline, cylindrical, discrete or occasionally integrated. *Conidia* 20–30 µm × 11– 17 µm (x̄ = 25 × 14 µm, n = 50, L/W= 1.8), oblong to ovoid, straight, rounded at both ends, cylindrical, hyaline, aseptate, thick-walled, guttulate, rarely become brown and 1-septate with age.

Culture characteristics – Conidia germinating on PDA within 6 hours. Germ tubes produced at one side of the conidium. Colonies on PDA fast growing, reaching 4–6 cm diam. after 5 days at 25 ^{o}C, circular, medium dense, flat or effuse, slightly raised, cottony to fairly fluffy with sparse aspects, white in initial stage and later become black in both upper and lower sides.

Material examined – Thailand, Chiang Rai, Doi Ob Park, on dead leaf of *A. catechu* (*Arecaceae*), 01 August 2020, Achala Rathnayaka (MFLU 22-0285, new host record); *ibid*., Nang Lae village, on dead twigs of *Dracaena aletriformis* (*Asparagaceae*), 20 May 2021, Achala Rathnayaka (MFLU 22-0286, new host record); *ibid*., on dead twig of *Bidens pilosa*, 29 November 2020, Achala Rathnayaka (MFLU22-0288, new host record); *ibid*., on dead twigs of *Calamus* sp. (*Arecaceae*), 10 June 2020, Achala Rathnayaka (MFLU 22-0289, new host record); *ibid*., on dead twigs of *Artocarpus heterophyllus* (*Moraceae*), 26 July 2020, Achala Rathnayaka (MFLU 22-0290, new host record); *ibid*., dead seed pod of *Paulownia tomentosa* (*Paulowniaceae*), 19 April 2021, Achala Rathnayaka (MFLU22-0291, new host record); *ibid*., Chiang Mai, Mushroom Research Centre, on dead fruit of *Quercus* sp. (*Fagaceae*), 07 July 2021, Nuwanthika Wijesinghe (MFLU 22-0287, new host record); China, Taiwan province, Chiayi, Fanlu Township area, Dahu forest, Ali Shan Mountain, dead leaves of *Ficus benguetensis* (*Moraceae*), 22 July 2019, D. S. Tennakoon, (NCYU19-0402, new host record),living culture NCYUCC19-0392; *ibid*., Fenghuang Mountain, dead twigs of *Bidens alba* (*Asteraceae*), 17 September 2019, Achala Rathnayaka, (MFLU 22-0292, new host record), living culture NCYUCC 19-0420.

Known hosts and distribution – *Lasiodiplodia theobromae* has a cosmopolitan distribution and on different host species (Farr & Rossman 2022).

Notes – *Lasiodiplodia theobromae* were collected from different host substrates, such as dead twigs, leaves, seed pods and fruits (Figs 12–16). The holotype of *L. theobromae* (Basionym: *Botryodiplodia theobromae*) was described from *Theobroma cacao* in Ecuador (Phillips et al. 2013). Since the morphology of the holotype specimen is difficult to find, we compared the morphology of the neotype (MBT176098) with our fungal collections. Morphologically, our collections (MFLU 22-0285, MFLU 22-0286, MFLU 22-0287, MFLU22-0288, NCYUCC 19-0392, MFLU 22-0289, MFLU 22-0290, MFLU 22-0291, and NCYUCC 19-0420) are similar to *L. theobromae* neotype (MBT176098) collected from an unidentified fruit on a coral reef coast in Papua New Guinea, in having aggregated, erumpent, uniloculate conidiomata and similar size hyaline, aseptate conidia (x̄ ± S.D. = 26.2 ± 2.6 × 14.2 ± 1.2 µm, L/W ratio = 1.9 vs. x̄ = 25 × 14 µm, n = 50, L/W = 1.8) that become 1-septate, dark brown with age (Phillips et al. 2013). However, conidia in neotype have a striated appearance, which our collections could not observe (Phillips et al. 2013). In the phylogenetic analyses, our collections clustered with the ex-neotype strain (CBS 164. 96) and other strain (CBS 111530) of *L. theobromae* (Fig. 5). Based on the morpho-molecular analyses, we conclude that our new collections are new host records of *L. theobromae* from Taiwan province, China and Thailand.

Figure 12 – *Lasiodiplodia theobromae* on *A. catechu* (MFLU 22-0285). a Dead leaf. b–d Appearance of conidiomata on host surface. e Section through the conidiomata. f Section through the peridium. g–j Conidiogenous cells. k–o Conidia. Scale bars: b = 500 µm, c, d = 200 µm, e = 100 µm, f–j, l–o = 10 µm, k = 20 µm.

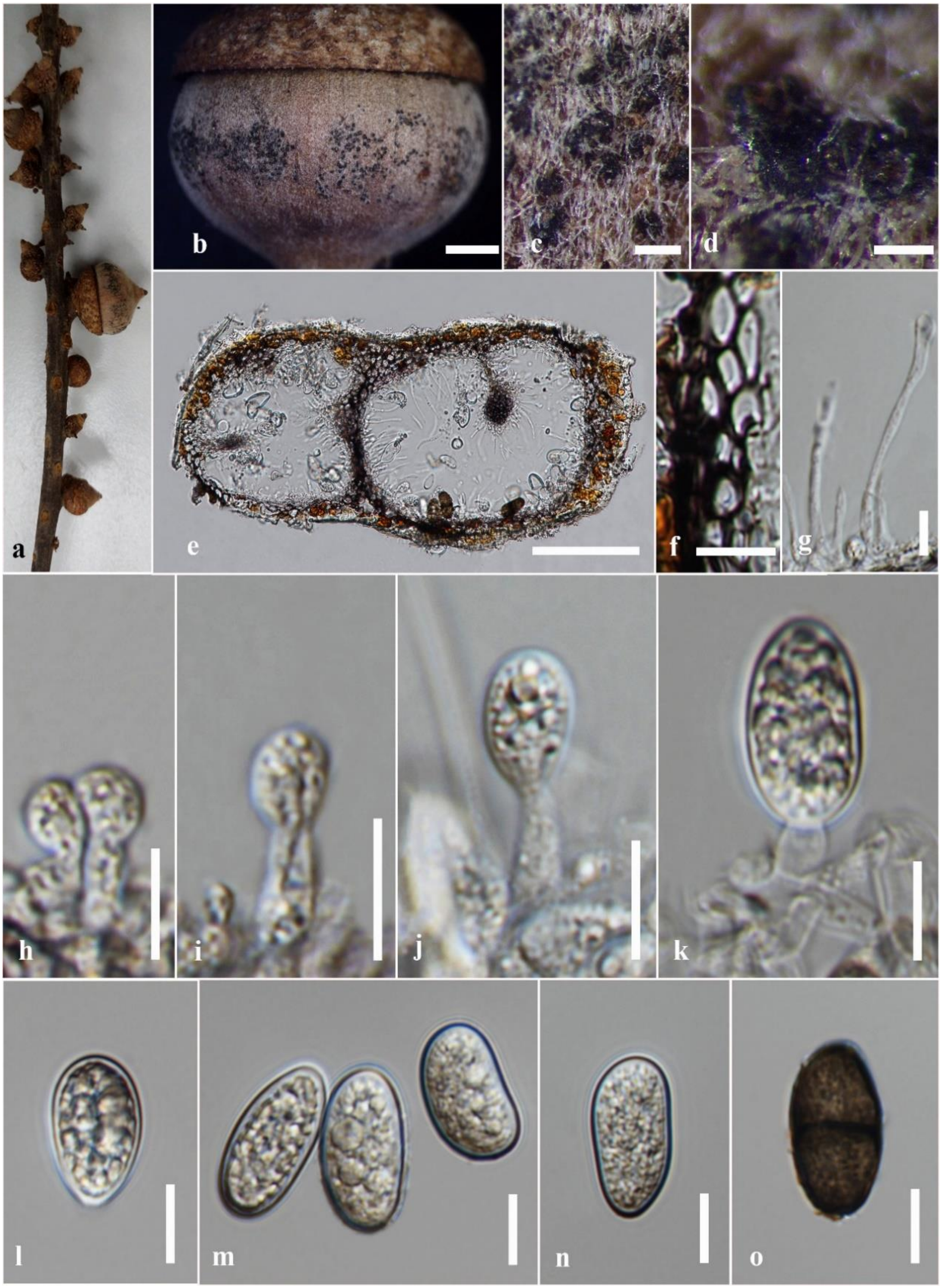

Figure 13 – *Lasiodiplodia theobromae* on *Quercus* sp. (MFLU 22-0287) a Dead fruit. b–d Appearance of conidiomata on host surface. e Section through conidioma. f Section through the peridium. g Paraphyses h–k Conidiogenous cells. l–o Conidia. Scale bars: b = 2 mm, c = 200 µm, d = 100 µm, e = 50 µm, f = 5 µm, g–o = 10 µm.

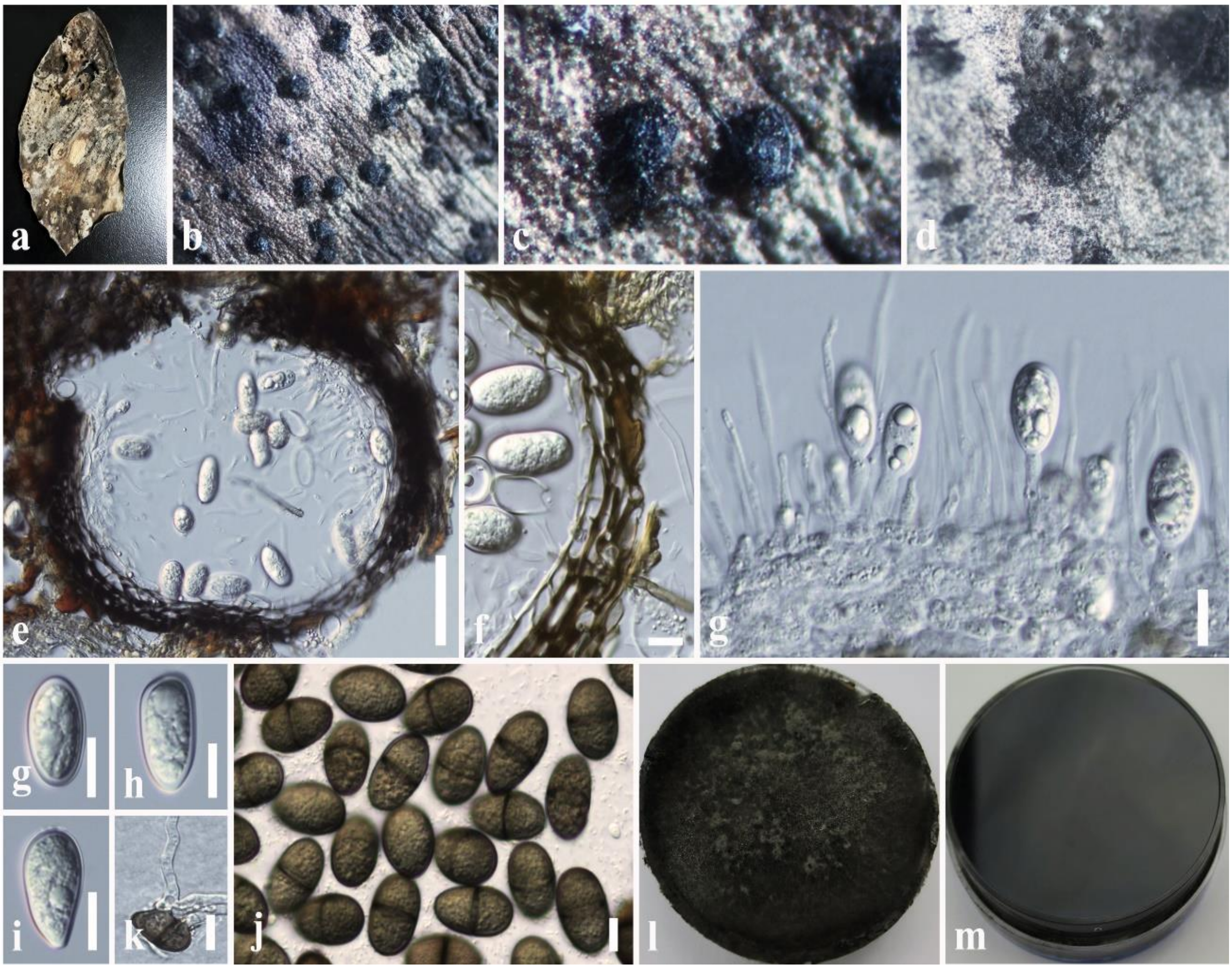

Figure 14 – *Lasiodiplodia theobromae* on *F. benguetensis* (NCYU 19-0402). a Specimen. b, c. Appearance of conidiomata on host. d Close-up of conidioma. e Section of the conidioma. f Conidioma wall. g Conidiogenous cells with developing conidia. g–i Immature conidia. j Mature conidia. k Germinated conidium. l, m. Colony on PDA (l upper, m lower). Scale bars: e = 100 µm, f = 10 µm, g–k = 10 µm.

Lasiodiplodia thailandica Trakun., L. Lombard & Crous, in Trakunyingcharoen et al. Persoonia 34: 95 (2014) Figs 17–21

Index Fungorum number: IF 810169; Facesoffungi number: FoF 09333

Saprobic on dead twigs, branches, leaves, seed pod and fruit of several hosts. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 90–250 µm high × 150–350 µm diam. (x̄ = 175 × 255 µm, n = 20), pycnidial, solitary or aggregated, immersed, becoming erumpent at maturity, globose to subglobose, uniloculate, black, ostiolate. *Ostiole* 25–35 µm width., central, papillate. *Peridium* 20–90 µm wide, composed of 4–10 layers, outer layer thick-walled, consists of dark brown cells of *textura angularis*, inner layer thin-walled, consists of light brown cells of *textura angularis* to *textura prismatica*. *Paraphyses* 1–4.5 µm wide, up to 60 µm long, hyaline, cylindrical, aseptate, unbranched or rarely branched. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 5–15 µm × 2–8 µm (x̄ = 9 × 4.5 µm, n = 30), lining the pycnidial cavity, holoblastic, annellidic, hyaline, cylindrical. *Conidia* 20–30 µm × 11–18 µm (x̄ = 26 × 14 µm, n = 50, L/W = 1.85), oblong to ovoid or cylindrical, straight, rounded in both ends, hyaline, aseptate, thick-walled, guttulate, becoming 1-septate, longitudinal striations with age.

Culture characteristics – Conidia germinating on PDA within 6 hours. Germ tubes produced at one side of the conidium. Colonies on PDA fast-growing, reaching 5–6 cm diam. after 5 days at 25 ºC, circular, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, grey-black on the upper side and black in the lower side.

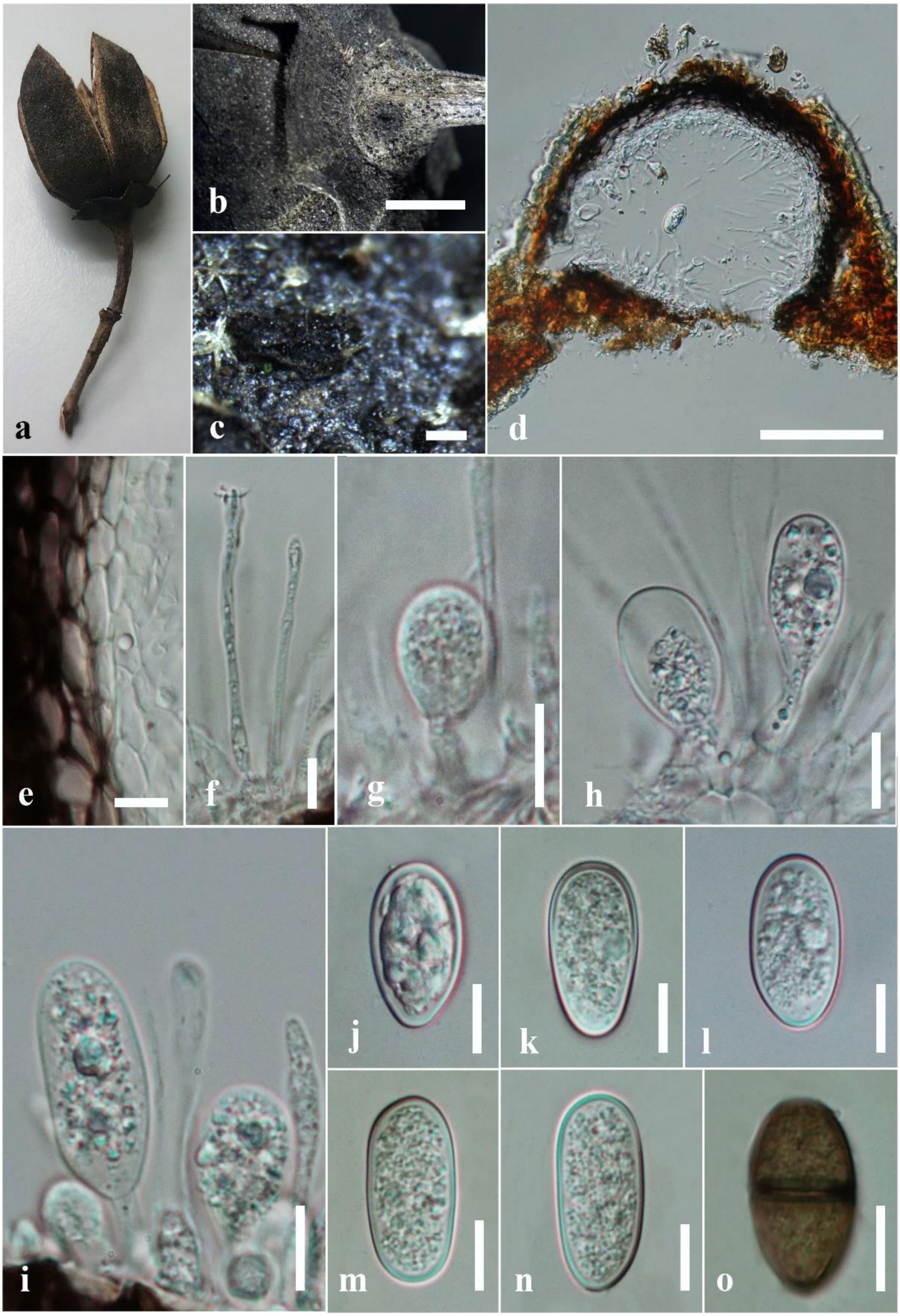

Figure 15 – *Lasiodiplodia theobromae* on *P. tomentosa* (MFLU 22-0291). a Dry seed pot. b, c Appearance of conidiomata on the host surface. d Section through the conidioma. e Section through the peridium. f Paraphyses. g–i Conidiogenous cells. j−o Conidia. Scale bars: b = 5 mm, c = 200 μm, d = 100 μm, e–o = 10 μm.

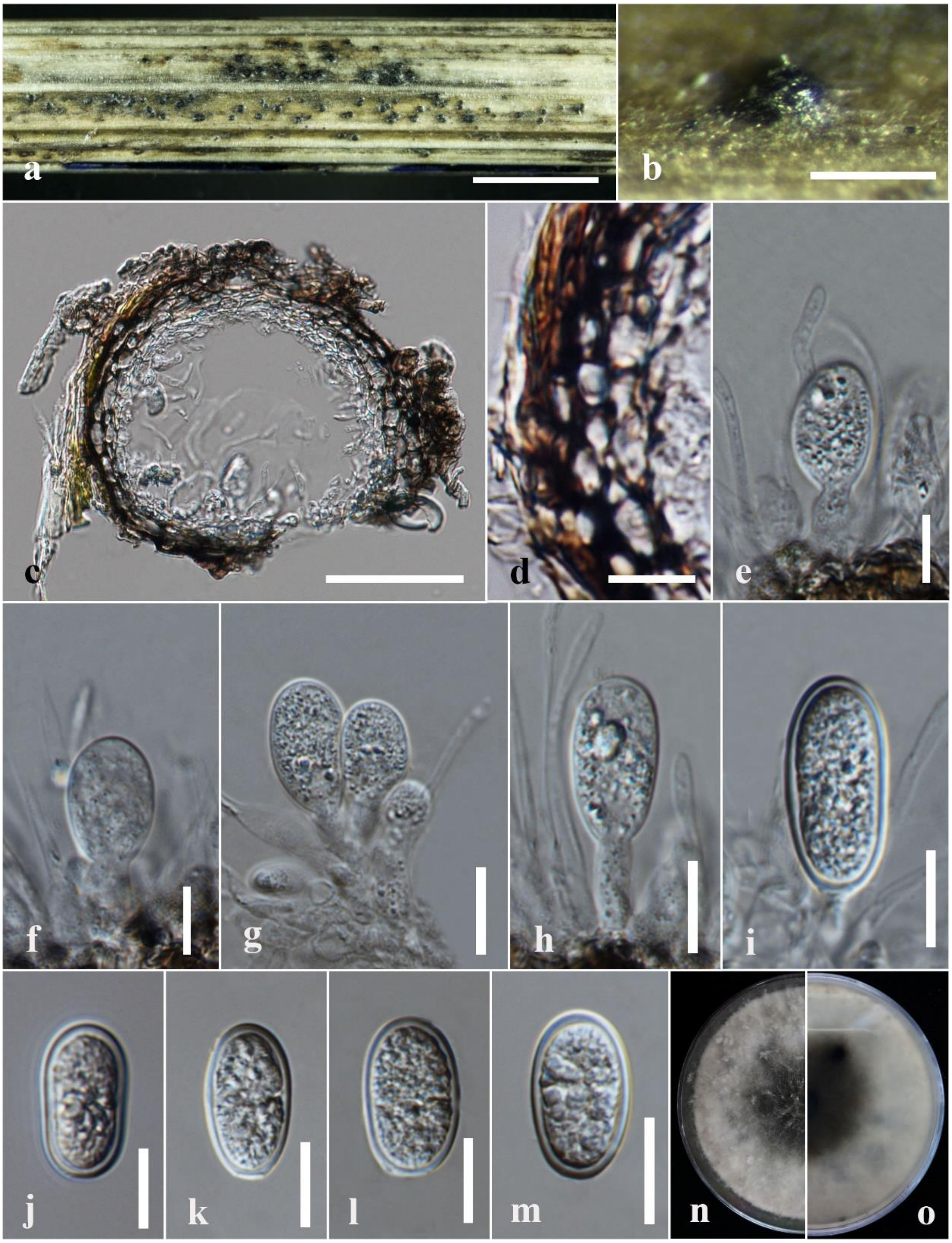

Figure 16 – *Lasiodiplodia theobromae* on *B. alba* (MFLU 22-0292). a, b Appearance of conidiomata on host surface. c Section through the conidioma. d Section through the peridium. e–i Conidiogenous cells. j–m Conidia. n, o Colony on PDA (n upper, o lower). Scale bars: a = 1 mm, b = 100 µm, c = 50 µm, e, d–m = 10 µm.

Material examined – Thailand, Chiang Rai province, on a dead leaf of *Musa* sp. (*Musaceae*), 06 July 2020, Achala Rathnayaka (MFLU 22-0293, new host record); *ibid*., dead twigs attached to *Magnolia lilifera* (*Magnoliaceae*), 11 February 2019, N. I. de Silva, NI324 (MFLU 21-0225, HKAS 107084, new host record), living culture, MFLUCC 21-0188, KUMCC 20-0054. *ibid*., Nang

Lae village, on dead twigs of *Hevea brasiliensis* (*Euphorbiaceae*), 18 May 2022, Achala Rathnayaka (MFLU 22-0294, new host record); ibid., on dead leaf of *Cocos nucifera* (*Arecaceae*), 20 March 2021, Achala Rathnayaka (MFLU 22-0299, new host record); *ibid*., on dead twigs of *Tectona grandis* (*Lamiaceae*), 19 April 2021, Achala Rathnayaka (MFLU 22-0300, new host record); *ibid*., Doi Ob park, on dead twigs of *Holmskioldia* sp. (*Lamiaceae*), 14 May 2022, Achala Rathnayaka (MFLU 22-0295, new host record); *ibid*., on dead seed pod of *Delonix regia* (*Fabaceae*), 06 September 2020, Achala Rathnayaka (MFLU 22-0297, new host record); *ibid.*, near Rajabhat University, on dead fruit of *Wodyetia bifurcata* (*Arecaceae*), 20 February 2021, Achala Rathnayaka (MFLU 22-0298, new host record); *ibid*., Chiang Mai, near Mae Tang Watershed Research station, on dead twigs of *Macaranga peltate* (*Euphorbiaceae*), 07 July 2021, Achala Rathnayaka, (MFLU 22-0296, new host record); China, Taiwan province, Ali Mountain, on dead branches of *Cerasus* sp. (*Rosaceae*), 16 August 2019, Achala Rathnayaka (MFLU 22-0301, new host and geographical record), living culture NCYUCC 19-0399

Known hosts and distribution – *Mangifera indica* and *Phyllanthus acidus* in Thailand (Trakunyingcharoen et al. 2015), *Albizia chinensis* and *Podocarpus macrophyllus* in China (Dou et al. 2017a), *Cerasus* sp. in Taiwan province, China (this study), *C. nucifera, D. regia*, *H. brasiliensis*, *Holmskioldia* sp., *M. peltate, M. lilifera*, *Musa* sp., *T. grandis* and *W. bifurcata* in Thailand (this study).

Notes – Our fungal collections of *L. thailandica* from different host substrates, such as dead twigs, branches, leaves, seed pods and fruits are shown in Figs 17–21. Based on multi-gene phylogenetic analyses, our fungal collections (MFLU 22-0293, MFLU 22-0294, MFLU 22-0295, MFLU 22-0296, MFLU 22-0297, MFLU 22-0298, MFLU 22-0299, MFLU 22-0300, MFLUCC 21-0188, and NCYUCC 19-0399) clustered with the ex-type strain (CBS 138760) and other authentic strains (CBS 138653, CGMCC 3.17975 and MFLUCC 18-0244) of *L. thailandica* (Fig. 5). Morphologically, our strains show similar characteristics to the holotype (CBS-H 21933) collected from healthy twigs of *Mangifera indica* in Thailand (Trakunyingcharoen et al. 2015). Both collections have black, solitary or aggregated, globose, uniloculate conidiomata and hyaline, septate paraphyses (Trakunyingcharoen et al. 2015). However, the size of the conidia of our new collections (20 – 30 µm high × 11 – 18 µm diam) is slightly different from the ex-type strain ((20–) 22–25(–26) × (12–)13–15(–16) µm) (Trakunyingcharoen et al. 2015). Based on the morpho-molecular analyses, we identified our fungal collections as new host records of *L. thailandica* from Taiwan province, China and Thailand, and the first geographical record from Taiwan province, China.

Possible synonyms of *Lasiodiplodia*

During our study, we synonymized *L. avicenniarum* and *L. krabiensis* into *L. brasiliensis*. To support this taxonomic revision, we re-examined herbarium specimens of *L. avicenniarum* and *L. krabiensis* and provide illustrations of morphological features (Figs 22, 23).

Lasiodiplodia brasiliensis M.S.B. Netto et al., Fungal Diversity 67: 134 (2014)

Figs 22, 23

Index Fungorum number: IF812566; Facesoffungi number: FoF 14085

= *Lasiodiplodia avicenniarum* Jayasiri et al., Mycosphere 10(1): 139 (2019)

= *Lasiodiplodia krabiensis* Dayar. et al., Mycosphere 11(1): 75 (2020)

Saprobic on fruit of *Avicennia marina* and submerged wood of *Bruguiera* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 660–720 µm high × 320–390 µm diam. ($\bar{x}$ = 690 × 350 µm, n = 10), pycnidial, solitary or aggregated, immersed to semi-immersed, becoming erumpent at maturity, globose to subglobose, uni- or multi-loculate stromata, black, ostiolate. *Ostiole* 60–65 µm width., central, papillate. *Peridium* 25–70 µm wide, composed of several layers, outer layer thick-walled, consists of dark brown cells of *textura angularis*, inner layer thin-walled, consists of light brown cells of *textura angularis*. *Paraphyses* 1–4 µm wide, up to 100 µm long, hyaline, cylindrical, aseptate, unbranched. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 7–14 µm × 3–7 µm (x̄ = 10 × 4.5 µm, n = 30), lining the pycnidial cavity, holoblastic, annellidic, hyaline, cylindrical. *Conidia* 20–25 µm × 10–14 µm (x̄ = 22 × 12 µm, n = 50, L/W = 1.83), subglobose to oval or ellipsoidal, straight, aseptate, hyaline, becoming 1-septate and dark brown, guttulate.

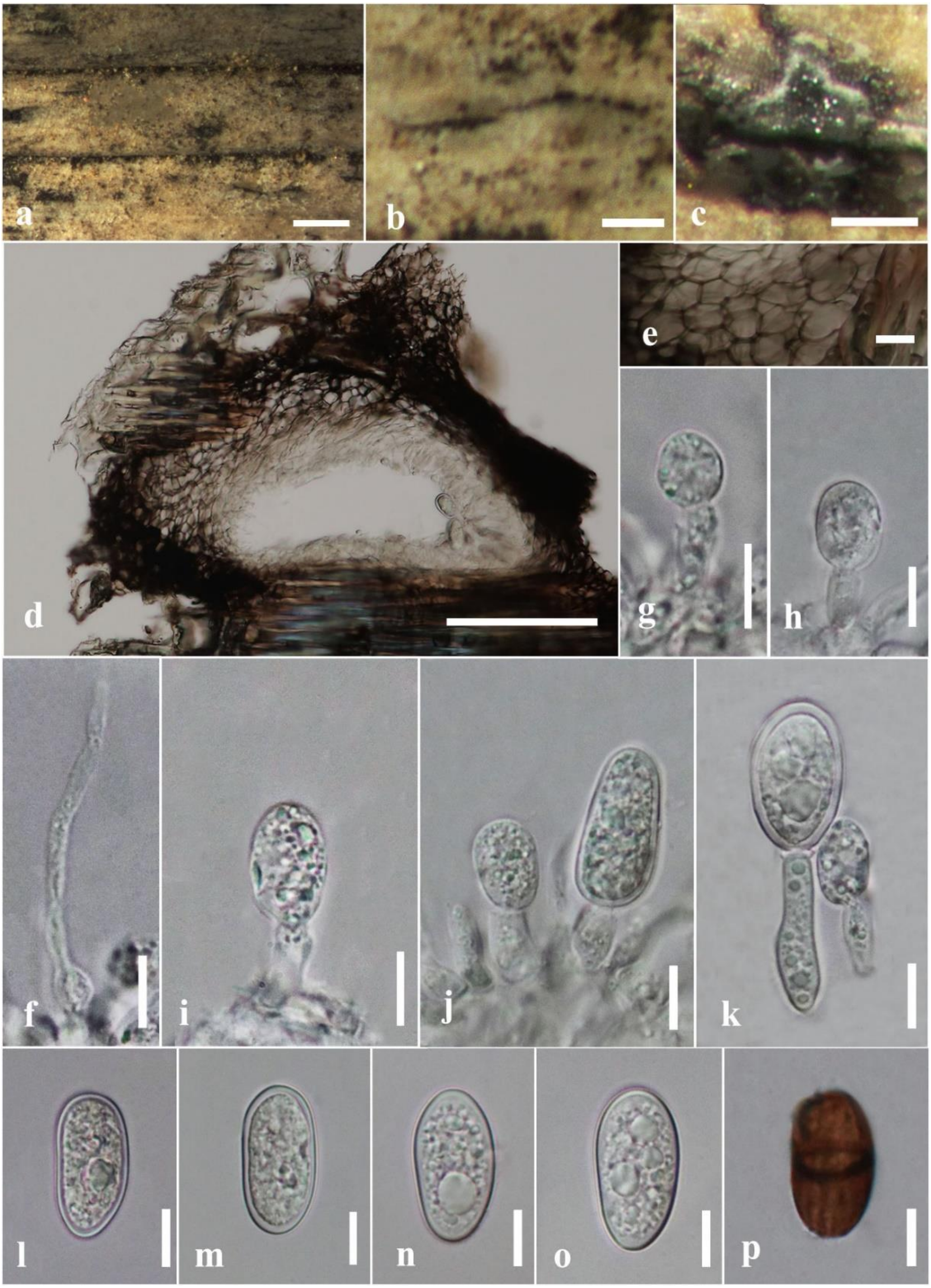

Figure 17 – *Lasiodiplodia thailandica* on *Musa* sp. (MFLU 22-0293). a–c Appearance of conidiomata on the host surface. d Section through the conidioma. e Section through the peridium.

f Paraphyses. g–k Conidiogenous cells. l–p Conidia. Scale bars: a = 1 mm, b–d = 100 µm, e–p = 10 µm.

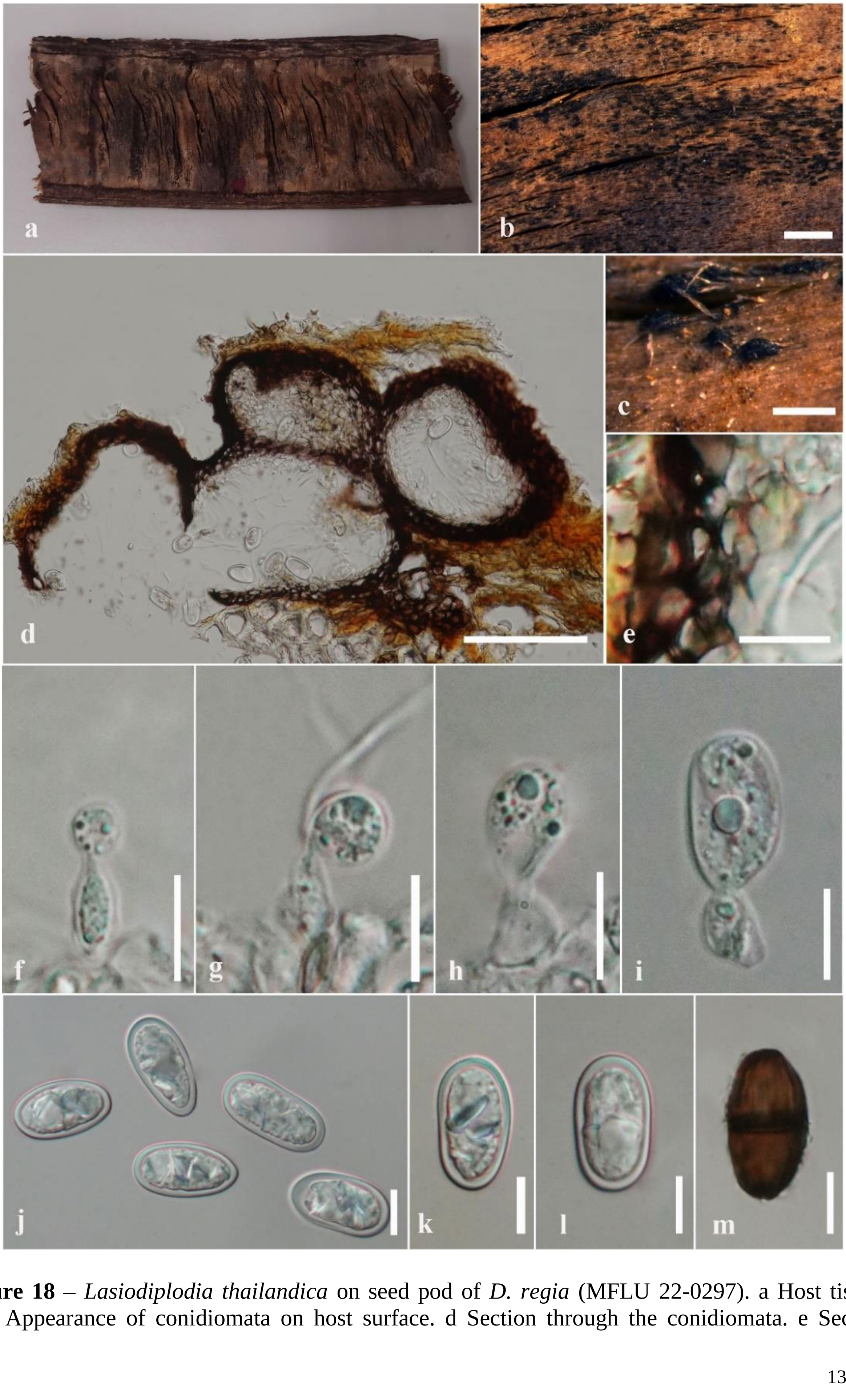

Figure 18 – *Lasiodiplodia thailandica* on seed pod of *D. regia* (MFLU 22-0297). a Host tissue. b, c Appearance of conidiomata on host surface. d Section through the conidiomata. e Section

through the peridium. f–i Conidiogenous cells. j–m Conidia. Scale bars: b = 2 mm, c = 500 μm, d = 100 μm, e–m = 10 μm.

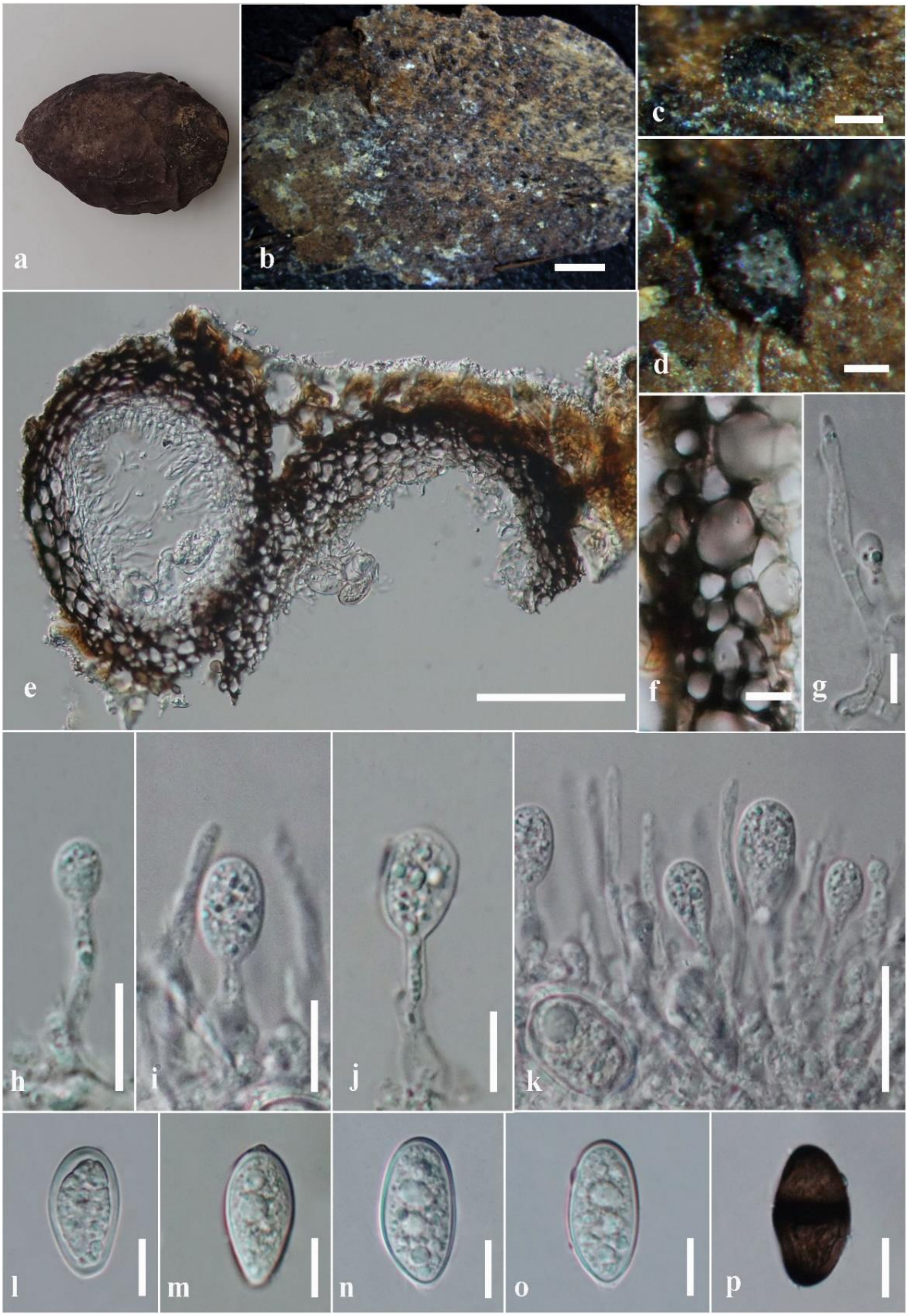

Figure 19 – *Lasiodiplodia thailandica* on fruit of *W. bifurcate* (MFLU 22-0298). a A dead fruit. b–d Appearance of conidiomata on host surface. e Section through the conidiomata. f Section

through the peridium. g Paraphyses. h–k Conidiogenous cells. l–p Conidia. Scale bars: b = 2 mm, c–e = 100 µm, f–j, l–p = 10 µm, k = 20 µm.

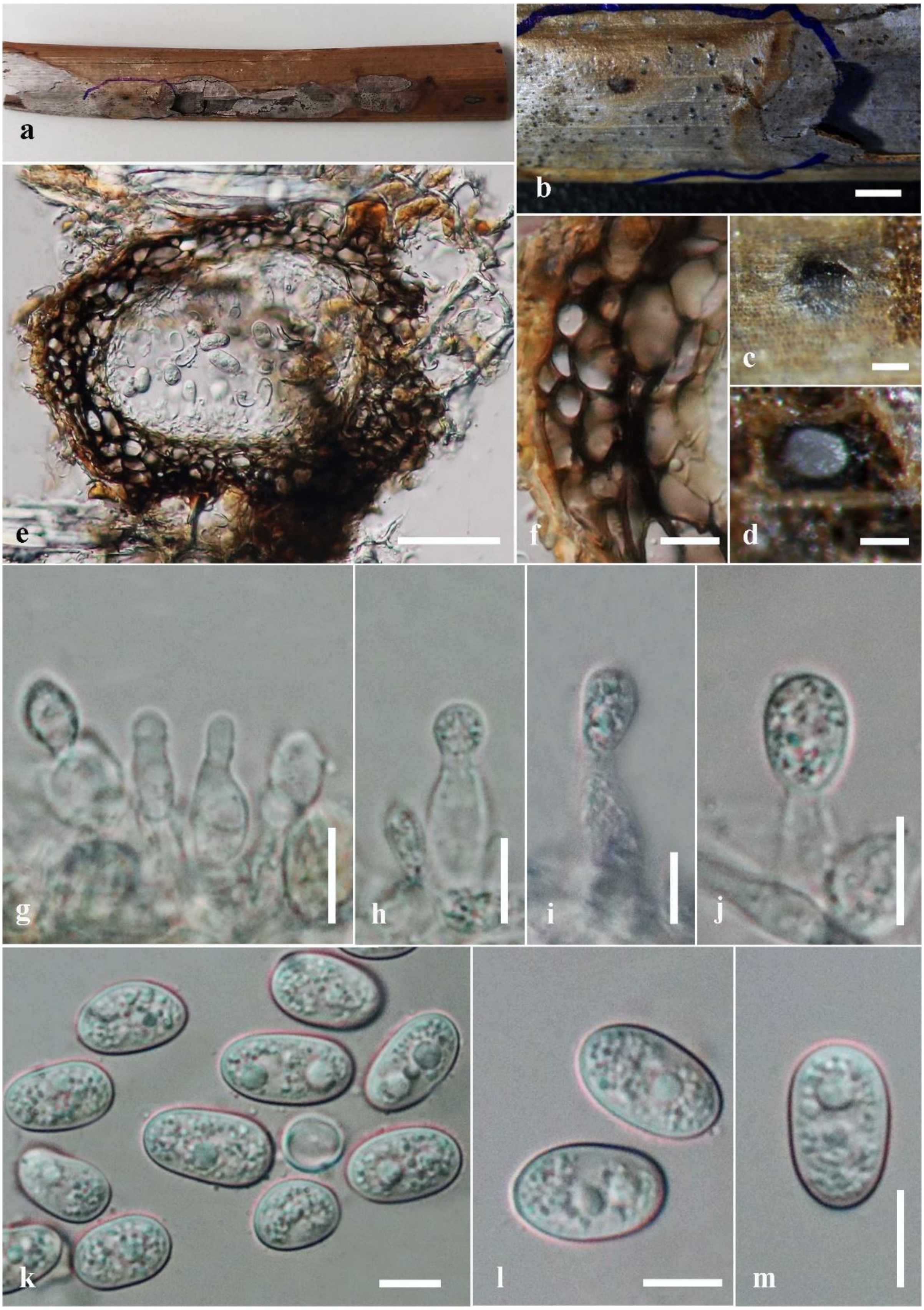

Figure 20 – *Lasiodiplodia thailandica* on fruit of *Cocos nucifera* (MFLU 22-0299). a Host. b–d Appearance of conidiomata on host surface. e Section through the conidioma. f Section

through the peridium. g–j Conidiogenous cells. k–m Conidia. Scale bars: b = 2 mm, c = 200 µm, d = 100 µm, e = 50 µm, f–m = 10 µm.

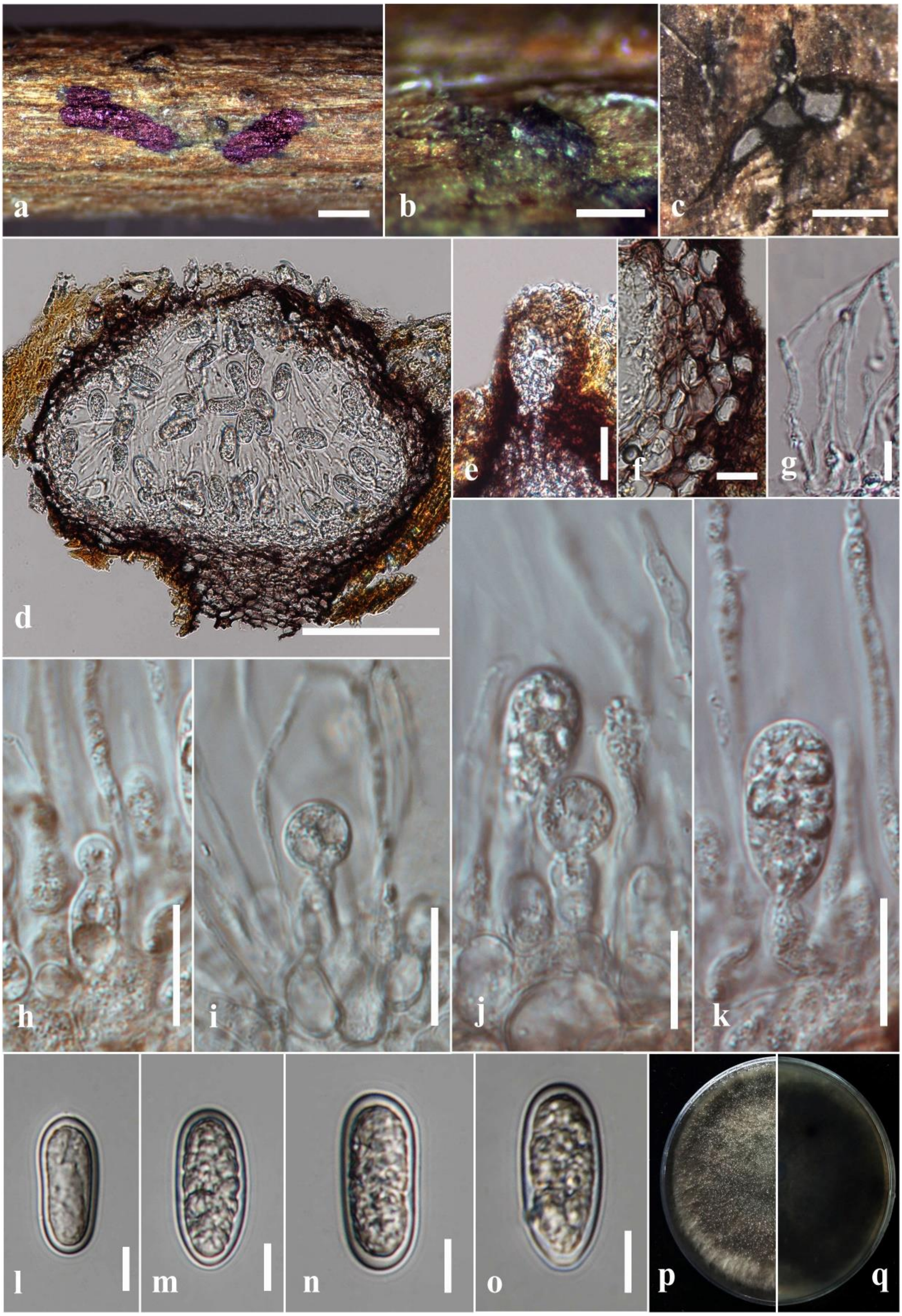

Figure 21 – *Lasiodiplodia thailandica* on *Cerasus* sp. (MFLU 22-0301). a–c Conidiomata on host surface. d Cross section through the conidioma. e Ostiole. f Section through the peridium.

g Paraphyses. h–k Conidiogenous cells. l–o Conidia. p, q Colony on PDA (n surface, q reverse). Scale bars: a = 500 µm, b, c = 200 µm, d = 100 µm, e, f = 20 µm, g–o = 10 µm.

Material examined – Thailand, Krabi province, Mueang Krabi District, on decaying fruit pericarp of *Avicennia marina* (*Acanthaceae*), 30 August 2017, S.C. Jayasiri, (MFLU 18– 2173, holotype), ex-type living culture MFLUCC17–2591; *ibid*, Phang Nga, on decaying submerged wood of *Bruguiera* sp. (*Rhizophoraceae*), 30 August 2017, M.C. Dayarathne, (MFLU 17-2617, holotype), ex-type living culture MFLUCC 17-2480.

Known hosts and distribution – *Lasiodiplodia brasiliensis* has a cosmopolitan distribution and on different host species (Farr & Rossman 2022), such as, *Adansonia madagascariensis* in Madagascar (Cruywagen et al. 2017), *Aquilaria crassna* in Laos (Wang et al. 2019), *Carica papaya*, *Citrullus lanatus*, *Cocos nucifera*, *Malus domestica*, *Mangifera indica*, *Manilkara zapota*, *Musa* sp., *Spondias purpurea*, and *Vitis vinifera* in Brazil (Netto et al. 2014, Rosado et al. 2016, Correia et al. 2016, Coutinho et al. 2017, Martins et al. 2018, Santos et al. 2022, 2023), *Dimocarpus longan* in Puerto Rico (Serrato-Diaz et al. 2020), *Mangifera indica* in Puerto Rico (Serrato-Diaz et al. 2020), *Persea americana* in Spain (Hernández et al. 2023), *Psychotria tutcheri* in Hong Kong, China (Zhang et al. 2021), *Theobroma cacao* in Cameroon (Zhang et al. 2021), *Vitis vinifera* in Mexico, and USA (Rangel-Montoya et al. 2021).

Notes – *Lasiodiplodia avicenniarum* and *L. krabiensis* are reduced to synonymy with *L. brasiliensis* according to our morphological and phylogenetic analyses (Figs 1, 22, 23). The sequences of the ex-type culture of *Lasiodiplodia brasiliensis* have the following nucleotide similarities (without gaps) with the ITS and *tef*1-α sequences of the ex-type of *L. avicenniarum* and *L. krabiensis*: 464/472 (98.3%) and 472/472 (100%) for ITS, and 314/315 (99.6%) and 274/280 (97.8%) for *tef*1-α, respectively. *Lasiodiplodia avicenniarum* and *L. krabiensis* were collected from Krabi province in Thailand from decaying fruit pericarp of *Avicennia marina* and decaying submerged wood of *Bruguiera* sp., respectively, while *L. brasiliensis* was collected in Pernambuco, Brazil from the stems of *Mangifera indica* (Netto et al. 2014, Jayasiri et al. 2019, Dayarathne et al. 2020). These three *Lasiodiplodia* species are recorded from their asexual morph. When examine the morphological characters, they have aseptate paraphyses (Netto et al. 2014, Jayasiri et al. 2019, Dayarathne et al. 2020). The conidia of *L. krabiensis* are hyaline throughout their life cycle, while the conidia of *L. avicenniarum* and *L. brasiliensis* become brown and 1-septate (Netto et al. 2014, Jayasiri et al. 2019, Dayarathne et al. 2020). However, *L. brasiliensis* conidia become verruculose and have longitudinal striations, which is not observed in *L. avicenniarum* (Netto et al. 2014, Jayasiri et al. 2019). These morphological differences between *L. avicenniarum*, *L. brasiliensis*, and *L. krabiensis* may be a result of their adaptation to different environmental conditions and hosts. Additionally, size of the conidia is similar in *L. brasiliensis* ($\bar{x}$ = 26.01 ± 1. 36 × 14.64 ± 1.16, L/W = 1.8) and *L. krabiensis* ($\bar{x}$ = 22×12, L/W = 1.83) (Netto et al. 2014, Dayarathne et al. 2020). However, after examining the herbarium material of *L. avicenniarum*, we observed a slightly different conidia length of 22 µm compared to the previously reported value of 28 µm by Jayasiri et al. (2019). Based on the examination of the herbarium material, the size of the conidia of *L. avicenniarum* ($\bar{x}$ = 22×12, L/W = 1.83) is similar to *L. brasiliensis* and *L. krabiensis*. Therefore, based on this morpho-molecular evidence, we conclude that *L. avicenniarum* and *L. krabiensis* are synonyms of *L. brasiliensis*.

The holotype morphology of *Lasiodiplodia* species

The main morphological characters of the holotype specimens of *Lasiodiplodia* species are shown in Table 4. Almost all of the species have been introduced from their asexual morphs. However, few have sexual and asexual morphs, such as *L. chinensis*, *L. gonubiensis*, *L. lignicola*, *L. pseudotheobromae*, and *L. theobromae* (Phillips et al. 2013, Trakunyingcharoen et al. 2015, Tennakoon et al. 2016, Dou et al. 2017b). Phylogenetic data, together with morphological characters, such as conidial morphology, especially the size of the conidia, and paraphyses morphology, can be used to distinguish *Lasiodiplodia* species (Phillips et al. 2013, El-Ganainy et al. 2022).

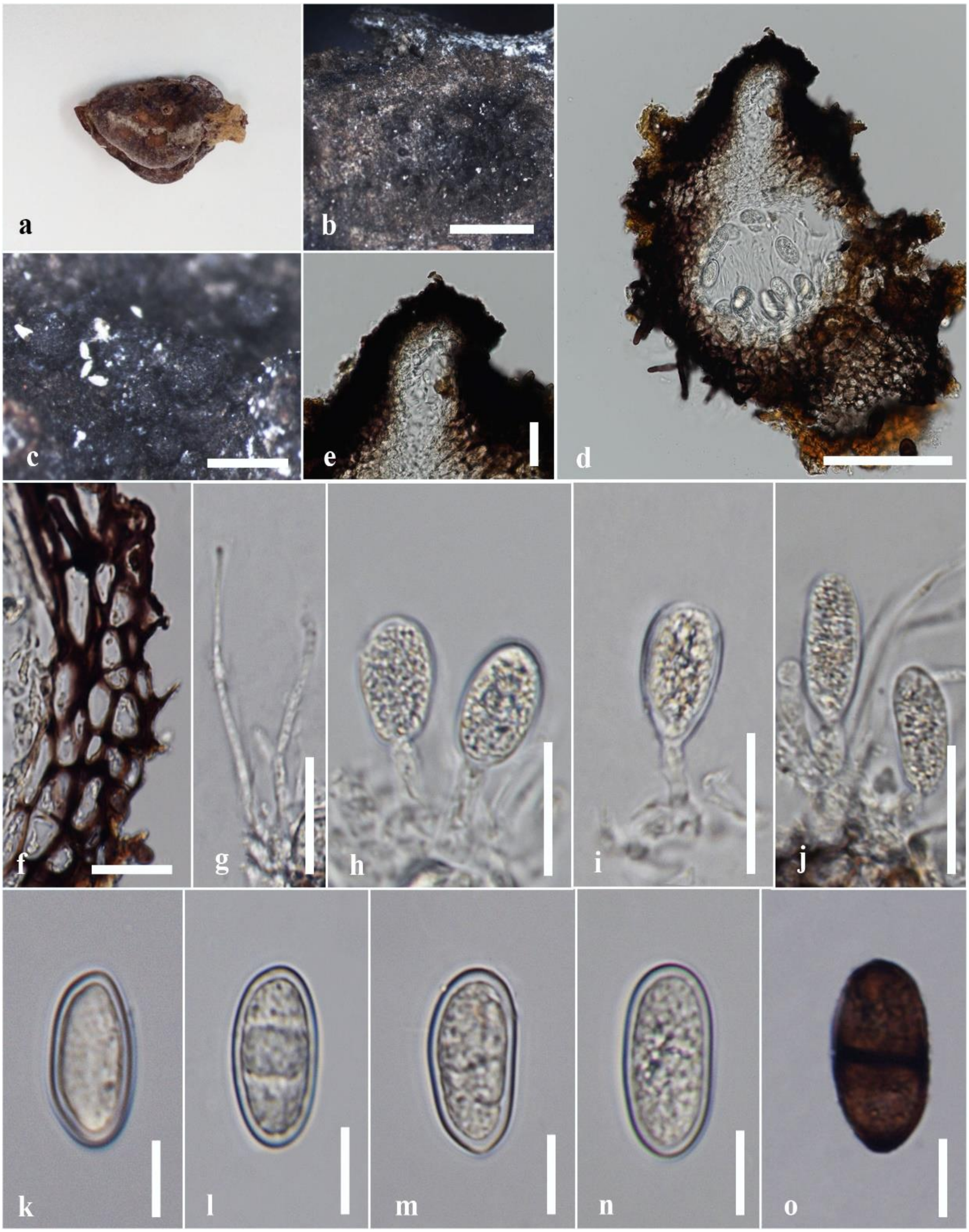

Figure 22 – *Lasiodiplodia brasiliensis* (= *Lasiodiplodia avicenniarum*) on *Avicennia marina* (MFLU 18–2173, holotype). a Dead Fruit. b, c Appearance of conidiomata on host surface. d Section through the conidioma. e Ostiole. f Section through the peridium. g Paraphyses. h–j Conidiogenous cells. k–o Conidia. Scale bars: b = 2 mm, c = 500 µm, d = 100 µm, e–j = 10 µm, k–o = 10 µm.

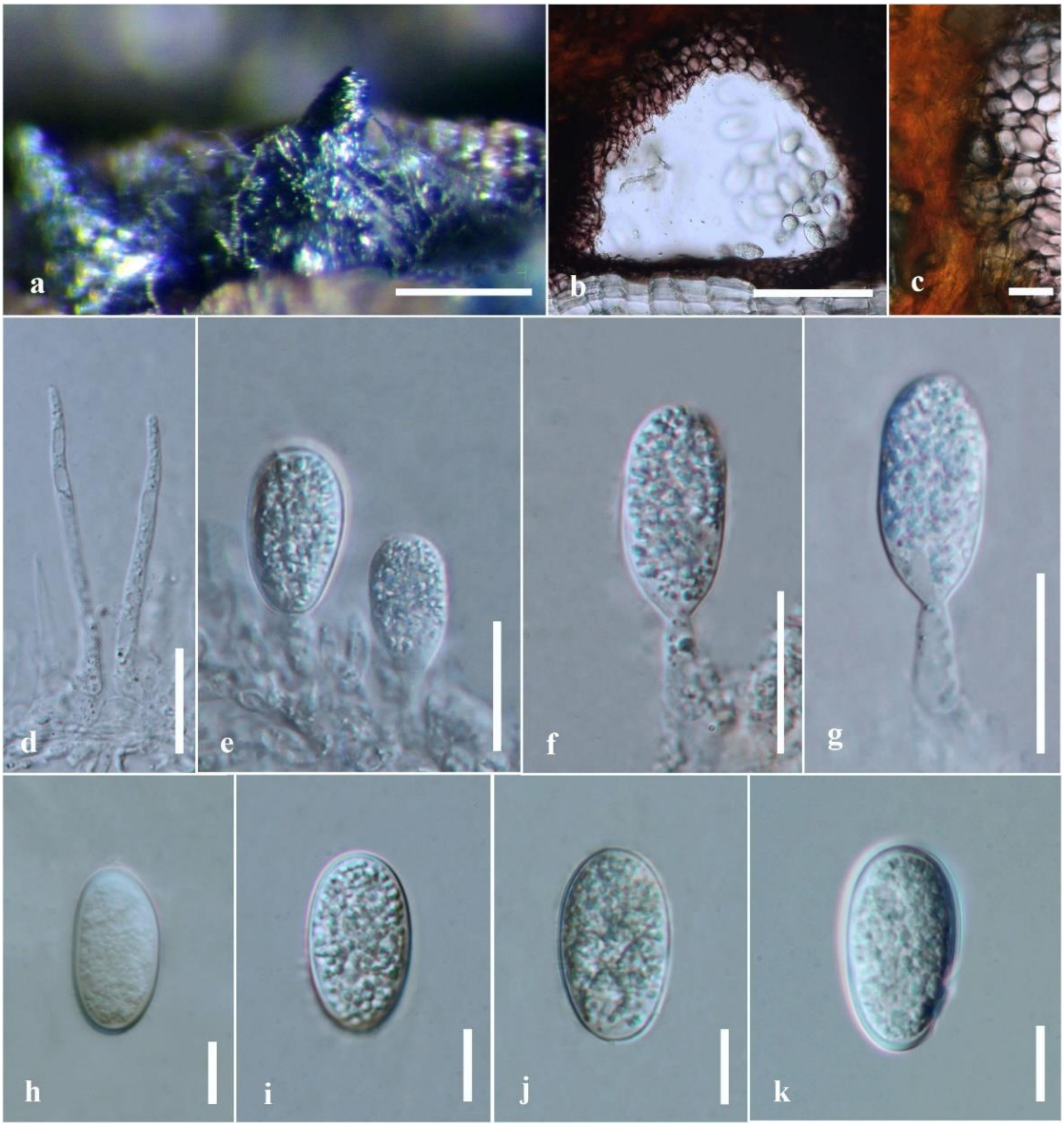

Figure 23 – *Lasiodiplodia brasiliensis* (= *Lasiodiplodia krabiensis*) on *Bruguiera* sp. (MFLU 17-2617, holotype) a Conidiomata on the host surface. b Section through the conidioma. c Section through the peridium. d Paraphyses. e–g Conidiogenous cells. h−k Conidia. Scale bars: a = 200 µm; b = 50 µm, c–g = 20 µm, h–k = 10 µm.

Haplotype assessment and networks of *L. theobromae*

The haplotype diversity and haplotype networks for *L. theobromae* were performed using single data sets of ITS, *tef*1-α, *tub2*, *rpb2*, and combined ITS and *tef*1-α dataset. The ITS dataset consisted of 520 isolates and 453 sites (excluding sites with gaps / missing data = 396). The ITS dataset yielded 14 haplotypes, and haplotype diversity (Hd) is = 0.0717 (Fig. 22a). The *tef*1-α dataset included 520 isolates with 299 sites (excluding sites with gaps / missing data = 161) and yielded six haplotypes and haplotype diversity of 0.3872 (Fig. 24b). The *tub2* dataset included 350 isolates with 434 sites (excluding sites with gaps / missing data = 63) and yielded only two haplotypes (Hd = 0.0057). The *rpb2* dataset consisted of 91 isolates and 530 sites (excluding sites with gaps / missing data = 518) and yielded a single haplotype (Hd = 0.0217). It was impossible to generate haplotype networks from the *tub2* and *rpb2* datasets due to the low number of haplotypes.

Therefore, the haplotype network was created from ITS and *tef*1-α combined dataset. The combined dataset consisted of 520 isolates with 752 sites (excluding sites with gaps / missing data = 554) and yielded 19 haplotypes (Hd = 0.4217) (Fig. 24c). The different host families and countries from which *L. theobromae* isolates were reported are shown in Figs 24, 25, respectively.

Based on the haplotype analyses, *L. theobromae* did not show a clear grouping of isolates based on their host families or the countries in which they were reported. There was no clear grouping of isolates based on region of origin. Analyses of the ITS dataset showed that one haplotype was most common (Figs 24a, 25a). The *tef*1-α dataset and the combined dataset of ITS and *tef*1-α showed that two closely related haplotypes were most common (Figs 24b, c, 25b, c). These two haplotypes were only separated by a single mutation and were included isolates from different host families and countries. The *rpb2* and *tub2* datasets were not further analysed as they resulted in only one and two haplotypes, respectively. The haplotype 1 (H1) from ITS, *tef*1-α, and combined dataset of ITS and *tef*1-α represented four host families, namely *Anacardiaceae*, *Caricaceae*, *Moraceae* and *Myrtaceae*, where *L. theobromae* was most commonly reported. Except for these four host families, the haplotype 2 (H2) in *tef*1-α, and combined dataset of ITS and *tef*1-α represented isolates from *Arecaceae* (Fig. 24).

The H1 haplotype from ITS locus represented *L. theobromae* isolates from Brazil, China, and Peru, similar to H1 from the *tef*1-α, and ITS and *tef*1-α combined dataset (Fig. 25). In addition to Brazil and China, isolates from Indonesia and Venezuela were included in the H2 haplotype from the *tef*1-α, and ITS and *tef*1-α combined dataset, respectively (Figs 24b, c, 25b, c). Only the ITS dataset produced one unique haplotype among isolates from host families (H10) and countries (H12). The combined dataset of ITS and *tef*1-α also had one unique haplotype from host families (H12) and countries (H16). From the *tef*1-α loci, no unique haplotype was detected (Figs 24, 25). Previous studies reported that sample size does not directly affect the genetic diversity (Wang et al. 2006, Santos et al. 2017). Mehl et al. (2017) used 255 isolates of *L. theobromae* for their haplotype network, while the current study used 520 isolates of *L. theobromae*. However, both studies reported the similar results for genetic diversity and haplotype network for *L. theobromae*.

Discussion

Molecular markers

Recent phylogenetic studies have revealed many *Botryosphaeriales* species, indicating that using only morphological data for species identification in this order is becoming more complex (Zhang et al. 2021). Therefore, phylogenetic analyses are required to identify cryptic species. (Pavlic et al. 2009, Sakalidis et al. 2011). For example, *Neofusicoccum parvum*/*N. ribis* species complex consists of ten closely related cryptic species that could not be distinguished based on morphological characters (Pavlic et al. 2009, Sakalidis et al. 2013, Slippers et al. 2017). In this regard, Phillips et al. (2013) suggested using at least two loci, ITS and *tef*1-α, to distinguish species in *Botryosphaeriaceae*. In a subsequent study, *tub2*, *rpb2*, and *calmodulin* (*cmdA*) proved to be useful to separate cryptic species in this family (Li et al. 2018). Species in *Botryosphaeria*, *Diplodia*, *Dothiorella*, and *Pseudofusicoccum* can be separated using ITS, *tef*1-α, and *tub2*, while species in *Lasiodiplodia*, *Neofusicoccum*, *Neoscytalidium*, *Phaeobotryon*, and *Saccharata* used ITS, LSU, *tef*1-α, *tub2*, and *rpb2* (Zhang et al. 2021).

Our preliminary analyses used LSU and SSU sequence data combined with other loci to generate the phylogenetic tree for *Lasiodiplodia*. However, when we used LSU in our combined dataset, some species, such as *L. brasiliensis*, *L. theobromae*, *L. pseudotheobromae* and *L. viticola*, did not resolve well. Furthermore, there are few SSU sequences for *Lasiodiplodia* species compared with other gene regions (around 3% – 19/663); therefore, we excluded LSU and SSU gene regions from our final analyses. According to our study, combining four gene regions, ITS, *tef*1-α, *tub2*, and *rpb2*, provides a reliable resolution for species-level identification in *Lasiodiplodia*, similar to Zhang et al. (2021). Qiao et al. (2022) also accepted this combination as the most widely used gene combination to identify *Lasiodiplodia* species accurately.

Table 4 Main morphological characters of the holotypes of *Lasiodiplodia* spp.

Species	Host	Location	Conidiomata	Paraphyses		Conidiogenous cell (µm)	Conidia			References
			Size (high × width)	Size (µm)	Septation and branching		Size (µm)	Mean (µm)	L/W	
L. acaciae	*Acacia* sp.	Indonesia	350 × 370 µm	up to 69 × 2–5	initially aseptate, becoming 1–6-septate when mature, rarely branched	(9–)11–17.5(–22) × (2.5–)3.5–5(–6)	(21.5–)25–29.5(–31) × (11–)12 –14(–15)	27.3 × 12.9	2.1	Zhang et al. (2021)
L. acerina	*Acer truncatum*	China	up to 2525 µm in diam.	39.4 ×3	aseptate, unbranched	–	(21.64-)21.97–30.83(-30.96) × (10.61-)11.48–15.87(-16.72)	26.9 × 13.5	2.0	Qiao et al. (2022)
L. americana	*Pistacia vera*	Arizona, USA.	536 × 446 µm (av. = 196 × 180 µm)	up to 90 × 2–3.5	1–3-septate, sometimes branched	10–18 × 3–5	(14.0–)17.5–20.5(–24.5) × (10.5–)11.5–13.0(–15.0)	19.3 × 12.3	1.57	Chen et al. (2015b)
L. aquilariae	*Aquilaria crassna*	LAOS	up to 550 µm diam.	up to 100 × 3	initially aseptate, becoming 1-septate when mature, unbranched	16 × 3	(23–) 25–28 (–29) × 12–16	26.9 × 14.1	1.8	Wang et al. (2019)
L. avicenniae	*Avicennia marina*	South Africa	(238–)317–485 (–560) µm	up to 170 × 2–4	septate	(6–)9–11(–15) × (3–)3.5–4.2(– 6)	(19–) 24–26(-30) × (9–)12–12.5(–15)	–	–	Osorio et al. (2016)
L. brasiliensis (as *'brasiliense'*)	*Mangifera indica*	Brazil	–	–	aseptate	–	22.7 – 29.2 × 11.7 – 17.0	26.01 ± 1.36 × 14.64 ± 1.16	1.8	Netto et al. (2014)
L. brasiliensis (Syn. *L. avicenniarum*)	*Avicennia marina*	Thailand	180–220 × 160–180 µm (av. = 213 × 174) µm	2–3	aseptate, unbranched	15–18 × 5–8	26–32 × 11–14	28 × 12	2.3	Jayasiri et al. (2019)
L. brasiliensis (Syn.*L. krabiensis*)	*Bruguiera* sp.	Thailand	680–740 × 300–360 µm (av. = 718 × 326.5 µm)	20–51 width	aseptate	10–14 × 3–5.3	24–26.8 × 13.2–16.6	25 × 14	1.78	Dayarathne et al. (2020)
L. bruguierae	*Bruguiera gymnorrhiza*	South Africa	(352–) 382–622 (–754) µm	not observed	—	(13)11–21(–23) × (2.7–)3–5	522 (19–) 25–26(–32) × (11–)12–13(–15)	–	–	Osorio et al. (2016)

Table 4 Continued.

Species	Host	Location	Conidiomata	Paraphyses		Conidiogenous cell (µm)	Conidia			References
			Size (high × width)	Size (µm)	Septation and branching		Size (µm)	Mean (µm)	L/W	
L. chiangraiensis	unidentified host	Thailand	160–190 × 170–190 µm	2–5	aseptate, unbranched	7–11 × 3.5–5	(21–)22–27(–30) × (12–)13–15(–17)	25 × 14	1.78	Wu et al. (2021)
L. chonburiensis	*Pandanus* sp.	Thailand	210–250 × 270–300 µm (av. = 236 × 287 µm)	—	—	9–13 × 3–5	15–30 × 10–15	23 × 12	1.9	Tibpromma et al. (2018)
L. cinnamomi	*Cinnamomum camphora*	China	—	≤106 × 3–4	aseptate, sometimes branched	10.4–13.6 × 2.4–6.3	(17.5–)18.7–21.1 (–22.4) × (11.5–)12.7–14.1(–15.5)	19.9 ± 1.2 × 13.4 ± 0.7	1.5 ± 0.1	Jiang et al. (2018)
L. citricola	*Citrus* sp.	Iran	to 2 mm diam.	up to 125 × 3–4	initially aseptate, becoming 1–5-septate, occasionally branched	11–16 × 3–5	(20–)22–27(–31) × (10.9–)12–17(–19)	24.5 ± 0.2 × 15.4 ± 1.8	1.6 ± 0.2	Abdollahzadeh et al. (2010)
L. citricola (syn. *L. vaccinii*)	*Vaccinium corymbosum*	China	770 – 1,330 µm in diam.	≤ 88 × 2–5	initially aseptate, becoming 1–6-septate, rarely branched	(9–)11–17(–18) × 3–5(–6)	(18 –) 21 – 27 (– 31) × (11 –) 12 – 14 (– 16)	23.3 × 12.8	1.8	Zhao et al. (2019)
L. clavispora	*Vaccinium uliginosum*	China	up to 570 µm diam.	up to 100 × 3	aseptate, unbranched	(9.5–) 11–18 (–19) × 2.5–5	(28–) 29–36 (–38) × 12–15	31.7 × 13.8	2.3	Wang et al. (2021)
L. cotini	*Cotinus coggygria*	China	up to 415 µm diam.	up to 41.9 × 2.6	aseptate, unbranched		(19.38-)20−27 (-28.81) × (12.51-)13.61−16.55(-16.62)	24.28 × 15.4	1.58	Qiao et al. (2022)
L. crassispora	*Santalum album*	Australia	0.5–1 mm diam.	(21)30–62(66) × 2–3.5(4)	1- septate	(6)8–16(19) × 3–7	27–30(–33) × 14–17	28.8 × 16.0	1.8	Burgess et al. (2006)
L. crassispora (syn. *L. pyriformis*)	*Acacia mellifera*	Namibia	up to 695 µm diam.	(27–)28.5–33.5 × 1.5–2	aseptate	(7–)9–16 × (2.5–) 3–6.5	(19–)21.5–25 (–28) × (13.5–) 15.5–19.5 (–21.5)	23.3 × 17.6	1.3	Slippers et al. (2014)
L. endophytica	*Magnolia candolii*	China	No morphological characters							

Table 4 Continued.

Species	**Host**	**Location**	**Conidiomata**	**Paraphyses**		**Conidiogenous cell (µm)**	**Conidia**			**References**
			Size (high × width)	**Size (µm)**	**Septation and branching**		**Size (µm)**	**Mean (µm)**	**L/W**	
L. euphorbiaceicola	*Jatropha curcas*	Brazil	–	up to 76 × 2−4	1- septate, occasionally branched	5−15 × 3− 4	15−23×9−12	–	–	Machado et al. (2014)
L. fici	*Ficus altissima*	China	up to 3100 µm diam	–	septate, unbranched	20–30 × 10–15	15–30 × 10–12	22 × 11	2.0	Xia et al. (2022)
**L. fiori*	–	–	–	–	–	–	24–26 × 12–15	–	–	Abdollahzadeh et al. (2010)
L. fujianensis	*Vaccinium uliginosum*	China	up to 1.3 mm in diam.	up to 95 × 3	aseptate, unbranched	(11–) 12–18.5 (–20) × (3–) 4–8 (–8.5)	(22–) 23–29 (–30) × (12–) 13–15 (–16)	26.2 × 14.5	1.8	Wang et al. (2021)
L. gilanensis	unknown woody plant	Iran	up to 940 µm diam.	up to 95 × 2–4	initially aseptate, becoming 1–3-septate, rarely branched	11–18 3–5	(25.2–)28–35 (–38.8) × (14.4–)15–18 (–19)	31 ± 2.4 × 16.6 ± 1	1.9 ± 0.2	Abdollahzadeh et al. (2010)
L. gilanensis (syn. *L. missouriana*)	*Vitis labrusca* x *Vitis vinifera* hybrid	USA, Arkansas	up to 320 µm wide	up to 55 × 2–3	aseptate, unbranched	–	(16.1–)17.4–19.6 (–21) × (8.1–)8.9–10.6(–11.8)	8.5×9.8	1.89 ± 0.3	Úrbez-Torres et al. (2012)
L. gonubiensis	*Syzygium cordatum*	South Africa	up to 460 µm diam.	(14−)26.5−47(−65) × (1.5−)2–2.5(−3)	aseptate	(6.5−)10−15(−18) × (1−)2−4(−4.5)	(28−)32−36(−39) × (14−)16−18.5 (−21)	33.8 × 17.3	1.9	Pavlic et al. (2004)
L. gravistriata	*Anacardium humile*	Brazil	—	—	aseptate	9−14 × 3−5	24.5-28.5 x 10.5-16	26.2 x 13.8	1.89	Netto et al. (2017)
L. guilinensis	*Citrus sinensis* cv. Valencia	China	up to 2 mm diam.	up to 75 × 2–5	septate, unbranched	8–54 × 3–9	(23–)28–31 (–33.5) × (13.5–) 15–16.5(–17)	29.6 × 15.7	1.9	Xiao et al. (2021)
L. henanica	*Vaccinium uliginosum*	China	up to 520 µm in diam.	up to 105 × 4	initially aseptate, becoming 1–3-septate, unbranched	(8–) 9–16 × 3–5 (–7)	(14–) 19–26 (–27) × 10–13 (–15)	22.1 × 12.0	1.86	Wang et al. (2021)
L. hormozganensis	*Olea* sp.	Iran	up to 950 µm diam.	up to 83 × 2–4	initially aseptate, becoming 1–7-septate, rarely branched	9–15 × 3–5	(15.3–)18–24(–25.2) × 11–14	21.5 ± 1.9 × 12.5 ± 0.8	1.7 ± 0.2	Abdollahzadeh et al. (2010)

Table 4 Continued.

Species	Host	Location	Conidiomata	Paraphyses		Conidiogenous cell (µm)	Conidia			References
			Size (high × width)	Size (µm)	Septation and branching		Size (µm)	Mean (µm)	L/W	
L. huangyanensis	*Citrus reticulata* cv. Succosa	China	up to 1.5 mm diam.	up to 82 × 3–4	1- septate, unbranched	8–35 × 3.5–7	(21–)28–32.5 (–34) × (13–) 14–16(–17)	30.1 × 15	2.0	Xiao et al. (2021)
L. indica	angiospermous tree	India	up to 1 mm diam.	up to 120 × 1.5-3.5	1–2-septate, occasionally branched	8.5-15(17.5) × 1.5-3.5(4)	20-38 × 11-20.5	–	–	Prasher & Singh (2014)
L. iraniensis	*Salvadora persica*	Iran	up to 980 µm diam.	up to 127 × 2–4	initially aseptate, becoming 1–6-septate, rarely branched	9–16 × 3–5	(15.3–)17–23 (–29.7) × 11–14	20.7 ± 2 × 13 ± 0.9	1.6 ± 0.2	Abdollahzadeh et al. (2010)
L. iraniensis (syn. *L. jatrophicola*)	*Jatropha curcas*	Brazil	–	up to 70 × 3	septate, occasionally branched	7−15 × 2−5	22−26×14−17	–	–	Machado et al. (2014)
L. laeliocattleyae	cultivated orchid *Laeliocattleya*	Italy	–	up to 95 × 2–3	aseptate	11–14 × 3–4	(18–)22.8(−27.4) × (11.7–)14.6 (−17.2)	22.8 ± 1.4 × 14.6 ± 1.1	1.6	Rodríguez-Gálvez et al. (2017)
L. laeliocattleyae (syn. *L. egyptiacae*)	*Mangifera indica*	Egypt	–	up to 57 × 2–3	aseptate	5–11 × 3– 5	(17–)20–24(−27) × (11–)11–12(−13)	22±2 × 12 ± 1	2.0	Ismail et al. (2012)
L. lignicola	unknown host	Thailand	–	up to 15	aseptate	10– 15 × 2.5–3.5	(15–)16–17.5 × (8–)8.5–10.5(–11)	–	1.7	Phillips et al. (2013)
L. lignicola (syn. *L. chinensis*)	unknown woody	China	210–320 µm diam.	up to 99 × 3–7	initially aseptate, becoming 9-septate, unbranched	(8–)10–15(–18) × 4–6(–7)	(18–)19–25 × 12–14	21.9 × 12.6	1.75	Dou et al. (2017b)
L. lignicola (syn. *L. sterculiae*)	*Sterculia oblonga*	Germany	up to 300 µm diam.	not observed		7–12 × 2.5–3.5	(12–)14–16 (–17) × (8–)10–11(–12)	–	–	Yang et al. (2016)
L. lignicola (syn. *L. tenuiconidia*)	*Aquilaria crassna*	Laos	up to 650 µm diam.	up to 110 × 3	initially aseptate, becoming 1–2-septate, unbranched	10–12 × 3–4	(18–) 19–24 (–26) × (11–) 12–16 (–17)	22.3 × 14.7	1.5	Wang et al. (2019)
L. linhaiensis	*Citrus unshiu*	China	up to 950 µm diam.	up to 80 × 2–6	1-septate, unbranched	7.5–22.5 × 3–5.5	(24.5–)27–30 (–32) × (12.5–13.5–15(–16)	28.5 × 14.2	2.0	Xiao et al. (2021)

Table 4 Continued.

Species	**Host**	**Location**	**Conidiomata**	**Paraphyses**		**Conidiogenous cell (µm)**	**Conidia**			**References**
			Size (high × width)	**Size (µm)**	**Septation and branching**		**Size (µm)**	**Mean (µm)**	**L/W**	
L. lodoiceae	*Lodoicea maldivica*	Mexico	2 mm × 1.5 mm	up to 60–75 × 2–3	unbranched	6–10 × 3–8	16.7–19.5 × 8.4–9.5	18.1 × 8.9	2.0	Douanla-Meli & Scharnhorst (2021)
L. macrospora	*Jatropha curcas*	Brazil	–	up to 105 × 3−4	septate, unbranched	8−20 × 2.5−4	28−35 × 15−17	–	–	Machado et al. (2014)
L. magnoliae	*Magnolia candolii*	China	200–250 × 180–200 µm	up to 60–70 × 2–4	septate	2.5−4 width	(24–)25–27(–30) × 11–15	–	–	de Silva et al. (2019)
L. mahajangana	*Terminalia catappa.*	Madagascar	up to 300 µm diam.	(27.5)33.5 – 52.5(66) × (2)2.5 – 3.5(5)	aseptate, unbranched	(10)10.5 – 18(26) × (3)3.5 – 5.5(6)	(13.5)15.5 – 19 (21.5) × (10)11.5 – 13(14)	17.5×11.5	1.4	Begoude et al. (2010)
L. mahajangana (syn. *L. caatinguensis*)	*Citrus sinensis*	Brazil	–	31.1–60.2 × 2.1–5.0	branched	7.2–14.6 × 2.2–5.8	13–20.2 × 10.1–12.5	18.15 × 11.78 ± 1.38 ± 0.59	1.54	Coutinho et al. (2017)
L. mahajangana (syn. *L. curvata*)	*Aquilaria crassna*	Laos	up to 850 µm diam.	50–160 × 1–2	unbranched	7–9 × 3–4	(18–) 20–24(– 25) × 12–15	23.6 × 13.8	1.7	Wang et al. (2019)
L. mahajangana (syn. *L. exigua*)	*Retama raetam*	Tunisia (USA)	–	80.1±19 × 2.9±0.5	mostly septate	15.6±3.2 × 4.2±1	(19.6–) 21.8 (−24.3) × (10.8–) 12.3(−13.3)	21.8±1.1×12.3±0.5	1.8±0.1	Linaldeddu et al. (2015)
L. mahajangana (syn. *L. irregularis*)	*Aquilaria crassna*	Laos	up to 400 µm diam.	up to 80 × 2–3	initially aseptate, becoming 1-septate, unbranched	15 × 2–3	(20–) 22–29 (–30) × (12–) 13 (–15)	24.8 × 13. 6	1.8	Wang et al. (2019)
L. mahajangana (syn. *L. macroconidia*)	*Aquilaria crassna*	Laos	up to 280–300 µm diam.	up to 45 × 1– 2	aseptate, branched	20 × 4	(26–) 28–34 (–36) × 13–16	29.5 × 14.6	2.0	Wang et al. (2019)
L. mahajangana (syn. *L. pandanicola*)	*Pandanus* sp.	Thailand	185–210 × 187–240 µm (av. = 198 × 211 µm)	–	–	4–6.5 × 5–7	14–38 × 9–22	27 × 14	1.92	Tibpromma et al. (2018)
L. margaritacea	*Adansonia gibbosa*	Western Australia	up to 520 µm diam.	(19–)28–46(–54) × (1.5–)2–2.5(–3)	1–2-septate	(6–) 10–11(–19.5) × (2–) 3–4 (–4.5)	(12–)14–17(–19) × (10–)11–12(–12.5)	15.3 × 11.4	1.3	Pavlic et al. (2008)
L. marypalme	*Carica papaya*	Brazil	–	–	aseptate	–	19.1– 28.5 × 10–15.3	21.2 ± 3.2 × 11.4 ± 1.6	–	Netto et al. (2014)

Table 4 Continued.

Species	**Host**	**Location**	**Conidiomata**	**Paraphyses**		**Conidiogenous cell (µm)**	**Conidia**			**References**
			Size (high × width)	**Size (µm)**	**Septation and branching**		**Size (µm)**	**Mean (µm)**	**L/W**	
L. mediterranea	*Quercus ilex*	Italy	–	87±19.9 × 2.7±0.6	Septate, sometimes branched	13.6±2.2 × 3.7±1	(26.3–) 30.6 (−37) × (13.5–)16.1 (−18)	30.6± 2.8 ×16.1±0.9	1.9± 0.2	Linaldeddu et al. (2015)
L.mexicanense	*Chamaedorea seifrizii*	Mexico	No morphological characters							Douanla-Meli & Scharnhorst (2021)
L. microcondia	*Aquilaria crassna*	Laos	up to 500 µm diam.	90 × 3	branched	5 × 2	(18–) 19–22 (–23) × 10–15	20.8 × 13.2	1.5	Wang et al. (2019)
L. mitidjana	*Citrus sinensis*	*Algeria*	–	–	initially aseptate, becoming septate	–	(22.6–) 27.7 (−31.9) × (13.5–) 16.7(−19.6)	27.7 ± 1.9 × 16.7 ± 1.1	1.7	Berraf-Tebbal et al. (2020)
L. nanpingensis	*Vaccinium uliginosum*	China	up to 640 µm diam.	up to 102 × 3.5	aseptate, branched	9–16 (–19) × 3–6 (–7)	(20–) 21–26 (–28) × 13–16 (–17)	23.9×14.8	1.6	Wang et al. (2021)
L. newvalleyensis	*Phoenix dactylifera*	Egypt	–	14.9–44.5 × 1.9–3.7	aseptate	4.6–10.5 × 3.2–5	17.2–26.7 × 10.5–13.3	22 ± 1.8 × 11.7 ± 0.7	1.8	El-Ganainy et al. (2022)
L. paraphysaria	*Azadirachta indica*	Pakistan	–	–	–	–	30–32 × 15–16	–	–	Abbas et al. (2012)
L. paraphysoides	*Vaccinium uliginosum*	China	up to 1.8 mm diam.	up to 125 × 7	initially aseptate, becoming 1–2-septate, branched	(8–) 10–16 (–18) × 3–7	(20–) 21–25 (–30) × (10–) 12–15(–17)	23.0 × 13.7	1.69	Wang et al. (2021)
L. parva	cassava field soil	Colombia	–	up 105 × 3–4	septate		(15.5–)16–23.5(–24.5) × (10–) 10.5–13(-14.5)	20.2 ± 1.9 × 11.5 ± 0.8	1.8 ± 0.1	Alves et al. (2008)
L. plurivora	*Prunus salicina*	South Africa	up to 400 µm wide	up to 130 × 2–5	2–7 celled, sometimes branched	8–13 × 4–7	(22–)26.5–32.5 (–35) × (13–)14.5–17(– 18.5)	29.6 ± 2.9 × 15.6 ± 1.2	1.9	Damm et al. (2007)
L. ponkanicola	*Citrus reticulata* cv. Ponkan	China	up to 1 mm diam.	up to 87 × 2–5	septate, unbranched	8.5–40 × 2.5–9	(16–)23.5–27.5(–28.5) × (11) –13–14.5(–15.5)	25.4 × 13.7	1.9	Xiao et al. (2021)
L. pontae	*Spondias purpurea*	Brazil	–	19.2–46.3 × 2.4–3.1	branched	5.8–15.7 × 3.1–5.4	16.4–26.46 × 9.6–15	21 ± 1.8 × 12.1 ± 0.9	1.74	Coutinho et al. (2017)
L. pseudotheobromae	*Gmelina arborea*	Costa Rica	–	up 58 × 3–4	mostly aseptate, sometimes branched	–	(22.5–)23.5–32(–33) × (13.5–)14–18(–20)	28 ± 2.5 × 16 ± 1.2	1.7 ± 0.2	Alves et al. (2008)

Table 4 Continued.

Species	Host	Location	Conidiomata	Paraphyses		Conidiogenous cell (µm)	Conidia			References
			Size (high × width)	**Size (µm)**	**Septation and branching**		**Size (µm)**	**Mean (µm)**	**L/W**	
L. riauensis	Asymptomatic twig	Indonesia	–	26–43 (34.2 ± 6.98) × 2.5–5 (3.5±1.51)	septate, unbranched	9–16 (11.5 ±1.89) × 2.5–5 (3.3 ± 0.51)	26.5–33 × 11–14	29.4 ± 1.54 × 12.6 ±0.38	2.33	Jami et al. (2022)
**L. ricini*	*Ricinus communis*	Malta	–	25–35 × 2	1-septate	–	16–19 × 10–11	–	–	Machado et al. (2014)
L. rubropurpurea	*Eucalyptus grandis*	Australia	0.5–1.5 mm diam.	(30)32–52(58) × 1.5–3.5	aseptate	7–13(15) × 3–5	24–33 × 13–17	28.2 × 14.6	1.9	Burgess et al. (2006)
L. subglobosa	*Jatropha curcas*	Brazil	–	up to 41 × 2−3	aseptate, unbranched	8− 18 × 3 −4.5	16−23× 11−17	–	–	Machado et al. (2014)
L. syzygii	*Syzygium samarangense*	Thailand	up to 2 mm diam.	–	aseptate	10–14.5 × 3–4	(27–)30–32(–36) × (13–)15–17 (–20)	31.3 × 16.4	1.9	Meng et al. (2021)
L. thailandica	*Mangifera indica*	Thailand	310–330 × 300–370 µm	25–51 × 1–1.5	1–3-septate	8–9 × 2–4	(20–)22–25 (–26) × (12–) 13–15(–16)	–	–	Trakunyingcharoen et al. (2015)
L. thailandica (syn. *L. hyalina*)	*Acacia confusa*	China	255–500 µm diam.	24–82 × 3–7	initially aseptate, becoming 1–7-septate, sometimes branched or connected to the ladder shaped or H form	(8–)9–18(–20) × 4–7	(19–)20–27 (–28) × 12–16	24 × 13.6	1.77	Dou et al. (2017b)
L. thailandica (syn. *L. swieteniae*)	*Swietenia* sp.	Thailand	310–330 × 300–370 µm (av. = 315 × 345 µm)	2–3 width	aseptate	11–13 × 7–8.5	24–32 × 11–14	30 × 13	2.3	Jayasiri et al. (2019)
L. theobromae	*Theobroma cacao*	Ecuador	–	up to 55 × 3–4	1–3-septate, occasionally branched	–	(19–)21.5–31.5 (–32.5) × (12–)13–17 (–18.5)	26.2–27× 14–14.4	1.9	Phillips et al. (2013)

Table 4 Continued.

Species	Host	Location	Conidiomata	Paraphyses		Conidiogenous cell (µm)	Conidia			References
			Size (high × width)	Size (µm)	Septation and branching		Size (µm)	Mean (µm)	L/W	
L. theobromae (syn. *L. laosensis*)	*Aquilaria crassna*	Laos	up to 270 µm diam.	up to 74 × 4	initially aseptate, becoming 1-septate, unbranched	133–6	(23–) 24–28 (–30) × (13–) 14–15 (–17)	25.8 × 14.9	1.7	Wang et al. (2019)
L. tropica	*Aquilaria crassna*	Laos	up to 500 µm diam	up to 60 × 3–4	initially aseptate, becoming 1–2-septate, unbranched	8–12 × 3–4	(17–) 18–24 (–25) × (12–) 13–14 (–15)	21.2 × 12.4	1.7	Wang et al. (2019)
**L. undulata*	–	–	–	89–90 × 1.5	–	–	20–32.×. 13.5–19.2	–	–	Abdollahzadeh et al. (2010)
L. venezuelensis	*Acacia mangium*	Venezuela	0.5–1 mm diam.	(12)16–41(45) × (1.5)2–5	1–2- septate	(5)7–14 (15) × 3–4.5(5)	26–33 × 12–15	28.4 × 13.5	2.1	Burgess et al. (2006)
L. viticola	Vignoles	USA, Arkansas	up to 900 µm wide	up to 60 × 2–3	aseptate, unbranched		(16.8–)18.2–20.5(–22.9) × (7.9–)8.8–10.1(–10.7)	19.5×9.5	2.05± 0.2	Úrbez-Torres et al. (2012)
L. vitis	*Vitis vinifera*	Italy	up to 400 µm diam.	up to 60 × 2–3	aseptate, unbranched	5–15 × 5–8	(25–)26–28 (–32) × (12–)15–16(–17)	–	–	Yang et al. (2016)

Geographical distribution

The proportional symbol maps in Figs 2, 3 indicate a widespread distribution of *Lasiodiplodia* species in tropical and subtropical regions, followed by temperate areas (except for polar regions). The climate influences the behavioural changes of fungi that live in symbiosis or mutualism with other organisms (Félix et al. 2016). The increase in temperature caused by climate change can cause stress to pathogenic fungal species, which can affect their interactions with their hosts and potentially increase their virulence (Lindner et al. 2010, Félix et al. 2019). Furthermore, changes in environmental conditions can cause fungal species to change their biogeographical distribution ranges (MacDonald et al. 2008). For example, *Lasiodiplodia theobromae* causes plant diseases in tropical and subtropical regions (Alves et al. 2008, Phillips et al. 2013) and is able to grow in a wide range of temperatures from 9 to 39 ^{o}C but the optimal temperature for this species is between 27 and 33 ^{o}C. Therefore *L. theobromae* can increase their growth rate in high temperatures (D'souza & Ramesh 2002). Our maps illustrate that the occurrence of this widely distributed species is mainly limited to regions within 40^{o} north and south of the equator similar to other studies (Félix et al. 2016). Furthermore, *Lasiodiplodia theobromae* is a latent pathogen which initially occur as an endophyte and becomes a pathogen when plants are under stress (Jami et al. 2013, Chethana et al. 2016).

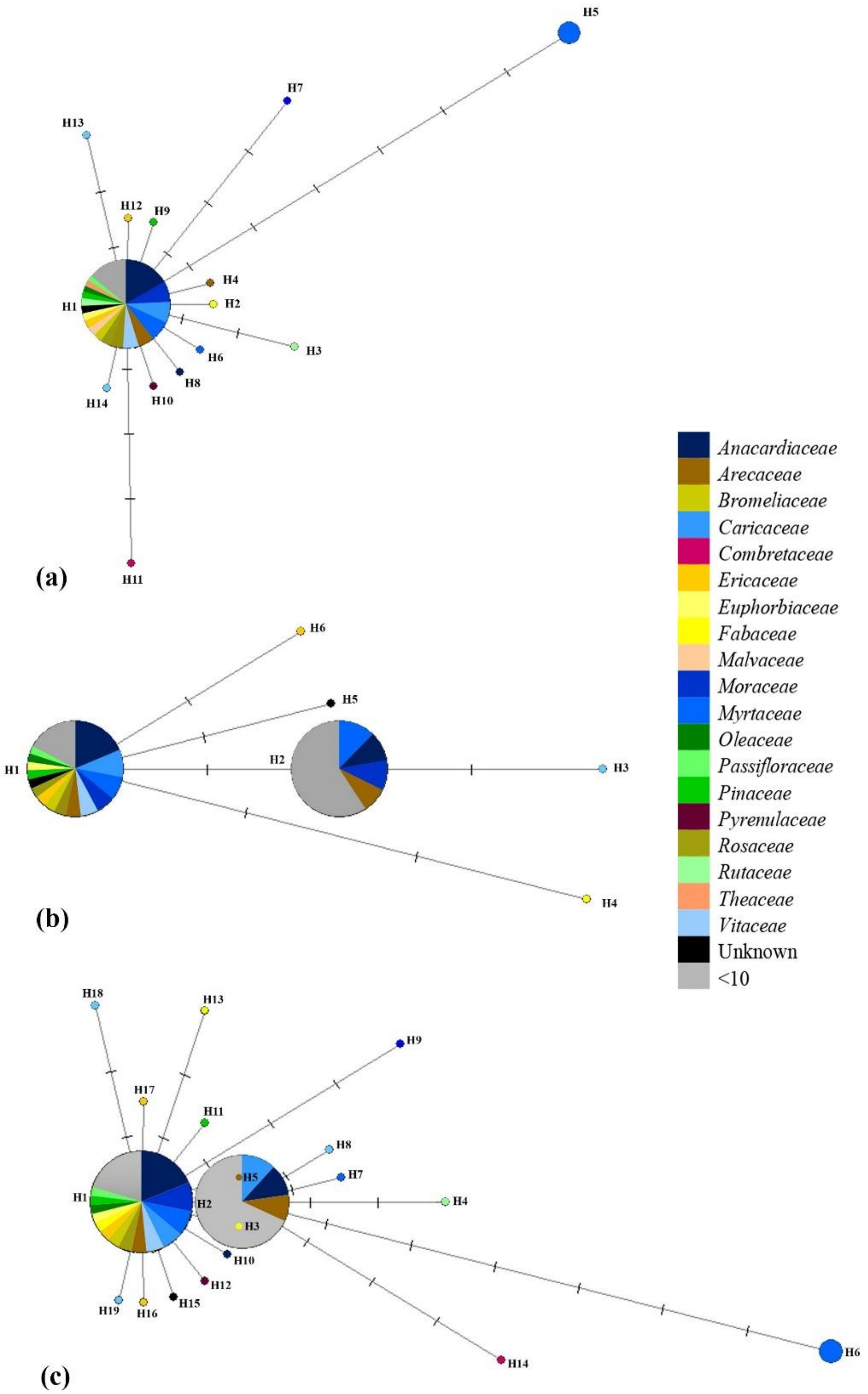

Figure 24 – Haplotype networks generated for the (a) ITS (b) *tef*1-α (c) ITS and *tef*1-α combined dataset. Circle sizes are proportional to haplotype frequency. Colours represent the different host families where *L*. *theobromae* isolates were reported. H1- H19 represent the haplotypes. The figure legend shows the host families in which *L*. *theobromae* isolates were reported.

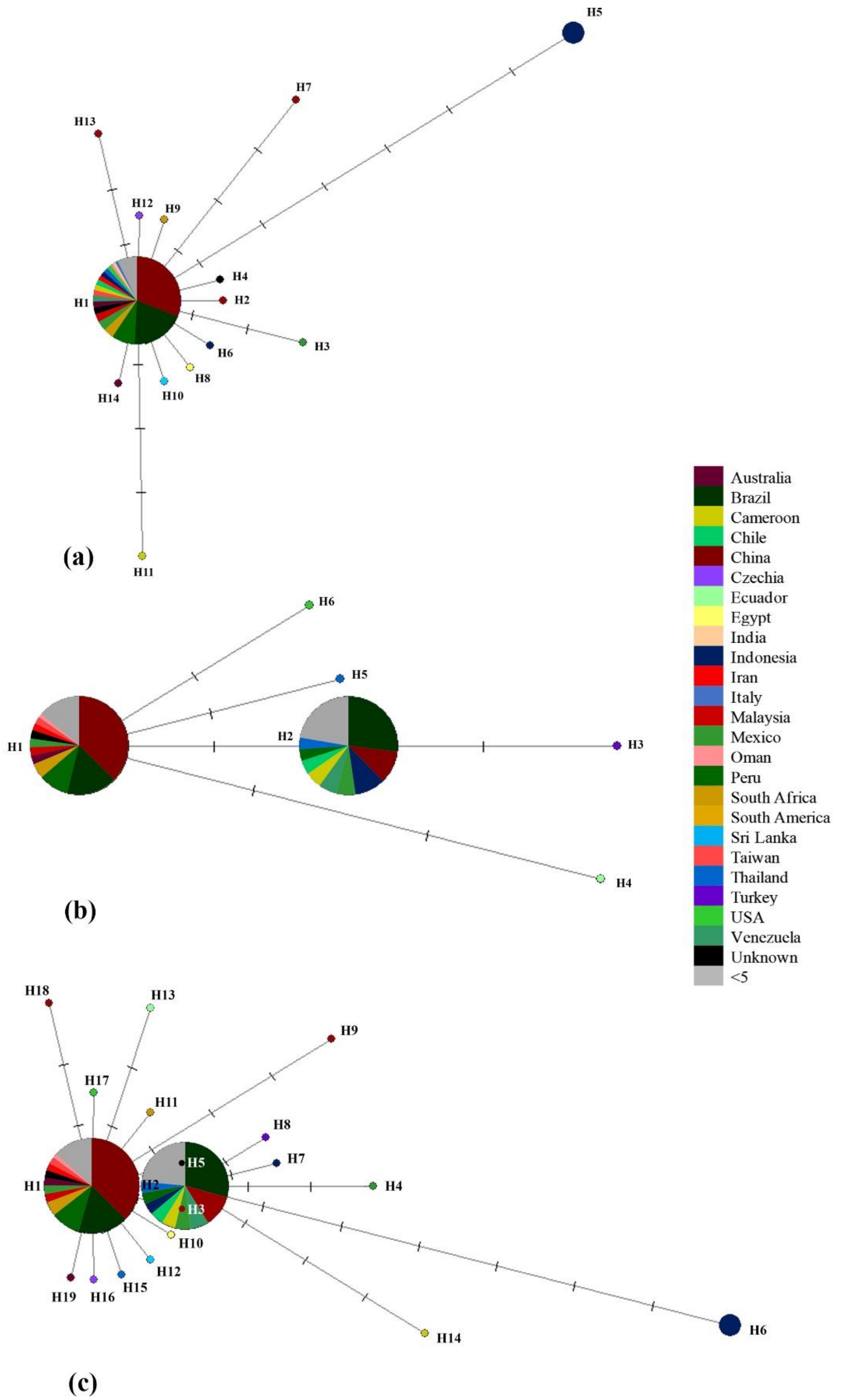

Figure 25 – Haplotype networks generated for the (a) ITS (b) *tef*1-α (c) ITS and *tef*1-α combined dataset. Circle sizes are proportional to haplotype frequency. Colours represent the different countries that *L*. *theobromae* isolates were reported. H1- H19 represents the haplotypes. The figure legend shows the countries where *L*. *theobromae* isolates were reported.

According to Úrbez-Torres (2011) and Yan et al. (2017), larger lesions caused by *L. theobromae* were observed in grapevines when the plants were grown at a temperature of 35 ^{o}C. Also, Félix et al. (2016) suggest that the pathogenicity of *L. theobromae* increases at high temperatures, especially at 37 ^{o}C, by producing more biomass and extracellular enzymes. Based on these findings, we can suggest that pathogenic *Lasiodiploia* species may have a higher growth rate in high-temperature regions. This situation is alarming for the cultivators as with temperature increase worldwide, *Lasiodiplodia theobromae* can pose a risk for many economically and ecologically important plants.

Haplotype assignment and networks of *L. theobromae*

The haplotype diversity and networks for *L. theobromae* were generated using four loci (ITS, *tef*1-α, *tub2*, and *rpb2*) and ITS, *tef*1-α combined dataset. The dataset consisted of 520 isolates from 44 host families and 35 countries (Table 3). The calculated haplotype diversity of *L. theobromae* was less than 0.5 (Hd<0.5), suggesting that *L. theobromae* have low levels of genetic diversity. Previous studies mentioned that *L. theobromae* primarily reproduce asexually, contributing to low genetic diversity (Mohali et al. 2005, Marsberg et al. 2017). Furthermore, this fungus has a low host specificity, enabling the fungus to colonize different hosts in a given area; this may be one of the reasons for little genetic variations among the geographic locations (Marsberg et al. 2017). Furthermore, Mehl et al. (2017) mentioned that *L. theobromae* is globally distributed with low host-specificity, less genetic diversity, and did not show grouping patterns based on regions, which was also confirmed by our results.

In addition to *L. theobromae*, *Botryosphaeria dothidea* and *Neofusicoccum parvum* also show similar global diversity distributions and lack of phylogeographic structure (Sakalidis et al. 2013, Marsberg et al. 2017). Manawasinghe et al. (2018) revealed high genetic diversity of the *B. dothidea* populations collected from Chinese grapevines. Pavlic-Zupanc et al. (2015) observed high genetic diversity in the *N. parvum* population isolated from *Syzygium cordatum*.

The genetic structures of *L. theobromae* from different countries and hosts have been analysed in previous studies. Mohali et al. (2005) found low levels of genotypic diversity in the *L. theobromae* collection from *Pinus caribaea* var. *hondurensis*, *Eucalyptus urophylla*, and *Acacia mangium* in Venezuela, whereas high levels of genetic diversity in the *L. theobromae* collection from *Pyrus* sp. in India discovered by Shah et al. (2011). Begoude et al. (2012) reported that *L. theobromae* collected from *Theobroma cacao* and *Terminalia* spp. in Cameroon have high to moderate levels of genetic diversity. A recent study by Rêgo et al. (2019) showed low genetic diversity among *L. theobromae* collected from Brazil. The current study observed the same based on haplotype analyses. Rêgo et al. (2019) mentioned that these variable results occurred due to the inherent characteristics of the different countries and hosts used in different studies.

Diversity of *Lasiodiplodia*, are there any more species?

The number of species within a fungal taxon differs depending on the criteria used to identify them (Chethana et al. 2021). Most mycologists used morphological characters with phylogenetic data to identify fungal species (Hyde et al. 2020b). The phylogenetic species concept, which relies on molecular techniques, has become the dominant approach for species delineation in fungal taxonomy, providing a more accurate and reliable means for identifying and classifying fungal species (Chethana et al. 2021, Manawasinghe et al. 2021). The polyphasic approach, combining morphological and phylogenetic data, has been used commonly to distinguish *Lasiodiplodia* species (Phillips et al. 2013, El-Ganainy et al. 2022). To date, 37 species are accepted under *Lasiodiplodia* (Wijayawardene et al. 2022), while the Index Fungorum (2023) lists 86 epithets.

Hyde et al. (2014) mentioned that the genera belonging to *Botryosphaeriaceae* are commonly associated with plant diseases and are asexual. Within these genera, genetic variation mainly occurs due to mutations (Hyde et al. 2014). *Lasiodiplodia* species are opportunistic pathogens that develop diseases when the host becomes stressed due to environmental conditions (Xia et al. 2022). However, identifying specific traits that contribute to the fungal pathogenesis of opportunistic pathogens becomes more difficult as they can occur in saprobic, endophytic or parasitic nutritional modes (Gilbert et al. 2015, Manawasinghe et al. 2021). Manawasinghe et al. (2021) provided some recommendations for identifying and establishing beyond species-level rankings for phytopathogenic fungi. Therefore, it is important to follow these recommendations when introducing new species in pathogenic *Lasiodiplodia* species.

Most *Lasiodiplodia* research has been conducted on pathogenic isolates (Úrbez-Torres et al. 2008, Rodríguez-Gálvez et al. 2017, Gnanesh et al. 2022) than those of endophytic and saprobic (Rathnayaka et al. 2023). As a result, the fungal diversity of *Lasiodiplodia* might be underestimated. In recent years, studies have shown that exploring understudied habitats has led to the discovery of numerous new species (Hyde et al. 2018). In addition, terrestrial habitats have been well-studied for *Lasiodiplodia,* increasing the number of species in this genus (Table 4). However, freshwater and marine habitats have received less attention (Dayarathne et al. 2020, Calabon et al. 2022). Therefore, research on freshwater and marine habitats may lead to identifying a significant number of new species in this genus.

Based on our study's results, *Lasiodiplodia* species found in Australia, Brazil, China, Laos, Mexico, South Africa, and Thailand have received relatively more attention than other countries (Fig. 3). Consequently, there is a higher potential to discover the novel *Lasiodiplodia* species in countries with less focus. Furthermore, by expanding the investigation into underexplored regions, we can understand the distribution, diversity, and ecological significance of *Lasiodiplodia* species worldwide. Based on the factors discussed above, it is reasonable to predict that the actual diversity of *Lasiodiplodia* may be significantly higher than the currently recorded number of species. Therefore, it is crucial that we continue to investigate the underexplored regions and habitats to understand the diversity of *Lasiodiplodia* and its impact on our ecosystems.

Conclusions

In this study, we revisited *Lasiodiplodia* by providing most suitable molecular markers, geographical distributions, a fungal-host relationship, and new host and geographic records of *Lasiodiplodia* species. Additionally, haplotype diversity and haplotype networks for *L. theobromae* are provided. The study provided important insights into the taxonomy, diversity, and distribution of *Lasiodiplodia* species, with several key findings: 1). The combination of ITS + *tef*1-α + *tub2* + *rpb2* markers is the most reliable combination for identifying *Lasiodiplodia* species. 2). *Lasiodiplodia* species are commonly recorded in tropical and temperate regions but not in polar regions. *Lasiodiplodia theobromae* is the predominant species distributed globally, followed by *L. pseudotheobromae*. *Lasioiplodia brasiliensis*, *L. iraniensis*, *L. mahajangana*, *L. pseudotheobromae,* and *L. theobromae* are recorded on a diverse range of host families. 3). In taxonomic analyses, we provided four new host records (two new geographical records) from Taiwan province, China and 21 new host records (one new geographical record) from Thailand for *Lasiodiplodia* species. 4). Based on phylogenetic analyses and herbarium studies, *L. avicenniarum* and *L. krabiensis* were synonymized into *L. brasiliensis*. 5). Haplotype diversity and haplotype networks showed that *L. theobromae* is a globally distributed species with low genetic diversity. Overall, this study provides valuable insights into the diversity, distribution and taxonomy of *Lasiodiplodia* species.

Acknowledgements

Achala Rathnayaka offers her profound gratitude to the Thesis or Dissertation Writing Grant, reference no Oh 7702(6)/125, The Center of Excellence in Fungal Research (CEFR) scholarship, Thailand Science Research and Innovation (TSRI) grant 'Macrofungi diversity research from the Lancang-Mekong Watershed and Surrounding areas' (grant no. DBG6280009) and Mae Fah Luang University for the financial support and acknowledge Prof. R. J. U. Jayalal, A. J. Gajanayake, D.S. Marasinghe, A.D. Madagammana, Rashika Sajith, Digvi Bundhun for their valuable suggestions and kind support. Kevin D. Hyde would like to thank the National Research Council of Thailand (NRCT) grant "Total fungal diversity in a given forest area with implications towards species numbers, chemical diversity and biotechnology” (grant no. N42A650547). Alan JL Phillips acknowledges the support from UIDB/04046/2020 and UIDP/04046/2020 Centre grants from FCT, Portugal (to BioISI). Yong Wang would like to thank the National Natural Science Foundation of China (No. 31972222, 31560489), Program of Introducing Talents of Discipline to Universities of China (111 Program, D20023), Talent Project of Guizhou Science and Technology Cooperation Platform ([2017]5788-5, [2019]5641 and [2020]5001), Guizhou Science, Technology Department International Cooperation Basic project ([2018]5806).

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