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Pterula siamensis sp. nov. (Basidiomycota, Pterulaceae) and the first record of *Pterulicium xylogenum* from Thailand

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Abstract

The Pterulaceae, recognized by their coralloid and filiform basidiomes, include species with diverse ecologies. This study identifies a new species, *Pterula siamensis*, and the first record of *Pterulicium xylogenum* from Thailand. Diagnostic features of *Pterula siamensis* are its coriaceous stipe with flexuous, concolorous tips and cylindrical, sometimes capitate cystidia. It possesses unique ITS, LSU, and *rpb*2 sequences and is phylogenetically separated from other *Pterula species* with strong support from maximum likelihood bootstrap (99%) and Bayesian posterior probability (1.0) values. *Pterulicium xylogenum*, which we collected from recently cut bamboo culms and dead bamboo culms, branches, and leaves, has previously been reported as a bamboo and sugarcane pathogen. These findings contribute to a more comprehensive understanding of Pterulaceae diversity and distribution, underscoring Thailand's extensive fungal biodiversity and emphasizing the necessity for continued research on fungal taxonomy and ecology in the region.

Key words: Coralloid fungi, Molecular phylogeny, New species, Systematics, Taxonomy, Tropical Asia

Introduction

The Pterulaceae are easily recognized by their coralloid-filiform basidiomes with a dimitic hyphal structure (Corner 1970). The type genus of Pterulaceae, *Pterula*, was introduced by Fries (1825). Corner (1950, 1952a, 1952b, 1966, 1967, 1970) later conducted major and comprehensive analyses of the family's genera, formally introducing the Pterulaceae, including *Allantula* Corner (1952), *Deflexula* Corner (1950), *Dimorphocystis* Corner (1950) [= *Actiniceps* Berk. & Broome (1876)], *Parapterulicium* Corner (1952), *Pterula* and *Pterulicium* Corner (1950) as new genera and at least 45 species. The latest reclassification of the family led to the introduction of *Myrmecopterula* Leal-Dutra, Dentinger & G.W. Griff. (2020) (ant-associated species), the reintroduction of *Phaeopterula* (Henn.) Sacc. & D. Sacc. (1905) and the synonymizing of *Deflexula* with *Pterulicium*, hence limiting the family to seven genera (Leal-Dutra *et al*. 2020). *Pterulicium* is differentiated from *Pterula* by its production of resupinate, *Corticium*-like patches with downward-facing hymenium, composed solely of generative hyphae without skeletal hyphae (Corner 1950). The establishment of the genus was subsequently supported by phylogenetic studies (Leal-Dutra *et al*. 2020).

The Pterulaceae exhibit a global distribution with a propensity for diverse ecological niches. They are notably prevalent in temperate and tropical regions, demonstrating adaptation to a wide range of environmental conditions. Pterulaceae species' ecology, however, remains poorly understood, most species being identified as saprotrophs that grow on decayed wood or leaf litter. (Leal-Dutra *et al*. 2020). The nutrition mode of the Pterulaceae has also been recorded to extend beyond saprotrophism, hinting at complex interactions within ecological communities. Some species within the family have been reported to engage in symbiotic relationships with plants, and recent research has uncovered intriguing associations with fungus-farming ants (Leal-Dutra *et al*. 2020). *Pterula* cf. *tenuissima* has been recorded as

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an endophyte in healthy *Magnolia grandiflora* L. (1759) leaves (Munkacsi *et al*. 2004). *Pterulicium xylogenum* (Berk. & Broome) Corner (1950) has been documented to be responsible for bamboo culm rot disease (Harsh *et al*. 2005) and potentially also a pathogen of sugarcane (Corner 1952b). According to the most recent checklist of basidiomycetes in Thailand, seven Pterulaceae species have been recorded from the country, namely, *Pterula capillaris, P. complanata, P. laxa, P. subulate, P. verticillata, Pterulicium fasciculare*, and *Ptm. subsimplex* (Chandrasrikul *et al*. 2011).

This study contributes to the understanding of the Pterulaceae in Thailand by providing a taxonomic account of a newly discovered *Pterula* and the first record of *Pterulicium xylogenum* from Thailand. Our analysis includes morphological descriptions, ecological considerations, and molecular investigations to ascertain their taxonomic affiliation within the Pterulaceae genera.

Methods

Specimen collection and morphological analyses

We collected the samples during 2022 and 2023 in Chiang Rai Province, Northern Thailand. For each collection, photographs of fresh basidiomes were taken in the field or in the laboratory, and notes such as location, forest type, habit, habitat, and substrate were recorded (Rathnayaka *et al*. 2024). Macromorphology was described based on the fresh materials. Growth habits and structural details were noted. Descriptions include color changes when fresh and dried, surface textures, branching patterns and tiers (levels of branches), and axils (angles between branches). The dimensions of the basidiomes, including the branches, were measured in terms of height and width. Colours were coded following Kornerup & Wanscher (1978). A portion of the fresh samples was preserved in CTAB buffer for DNA extraction. Samples were dehydrated in a hot food desiccator with a temperature from 40 to 60 °C for ca. 24 hours or until specimens were thoroughly desiccated and then preserved in ziplock bags. Dried specimens were later deposited in Mae Fah Luang University Herbarium (MFLU). The micromorphology was examined from dry specimens. Thin sections were made by free hand with a razor blade using a stereomicroscope Zeiss Stemi 305, and mounted in water, 5% KOH and 1% Congo red. Microscopic structures were observed, photographed, and measured using a compound microscope Olympus BX53. The measurements of 70 basidiospores, 30 basidia, and 30 cystidia were taken collectively from all specimens using cellSens version 4 (Olympus). The notation [n,m,p] indicates that measurements were made on ‘n’ basidiospores from ‘m’ basidiomes in ‘p’ collections. The dimensions of microscopic structures are given as follows: (a–)b–c–d(−e), where c denotes the average, b represents the 5th percentile, and d signifies the 95th percentile, with the minimum and maximum values, a and e, shown in parentheses. The Q value, which is the length-to-width ratio of the spores, is also presented in this format.

DNA extraction, PCR, sequencing, and sequence analyses

We extracted the specimens’ DNA using a CTAB extraction protocol that was slightly modified from Doyle & Doyle (1990). Sequence markers that are commonly used for Pterulaceae were amplified. The Internal Transcribed Spacer (ITS) region of the nuclear rDNA cistron, including ITS1-5.8S-ITS2, was amplified by polymerase chain reaction using the primers ITS1-F (Gardes & Bruns 1993) and ITS4 (White *et al*. 1990). Part of the nuclear rDNA large subunit (LSU) was amplified using the primers LR0R and LR5 (Vilgalys & Hester 1990). The PCR cycling conditions for both gene regions were: an initial denaturation at 94 °C for 3 minutes; followed by 35 cycles of denaturation at 94 °C for 30 seconds, annealing at 52 °C for 30 seconds, and extension at 72 °C for 1 minute; and a final extension at 72 °C for 10 minutes. Parts of the DNA-dependent RNA polymerase II subunit 2 (*rpb2*) gene were also amplified using bRPB2-6F and bRPB2-7.1R primers (Matheny 2005). Chromatograms were edited and contigs assembled using SeqMan (DNAstar, Madison, WI, USA). Sequences of *Pterulaceae* specimens from this study were visually checked for quality and were blasted against the GenBank database (http://www.ncbi.nlm.nih.gov/genbank/).

Sequence alignment and phylogenetic analyses

In all, sequences of 43 specimens were retrieved from Genbank and included in the ingroup along with the newly generated sequences. Among those 43 specimens, 22 represented 15 known species, while 21 represented unidentified species. Sequences from *Phaeopterula juruensis* Henn. (1904), *Phaeopterula stipata* (Corner) Leal-Dutra, Dentinger

& G.W. Griffith (2020), and *Phaeopterula* sp. were used as the outgroup. Alignments of the sequences were conducted using MAFFT version 7 (Katoh & Standley 2013), checked and amended, when necessary, with Bioedit version 7.0.5 (Hall 2007), and poorly aligned regions were removed using TrimAl (Capella-Gutiérrez *et al*. 2009).

Maximum Likelihood (ML) was used to infer the phylogenies and node support from the three single-gene alignments separately. RAxML-HPC2 version 8.2.12 (Stamatakis 2014) with 1,000 rapid bootstraps was used for the ML analyses, via the Cipres portal (Miller *et al*. 2010). As there were no supported (BS ≥ 70%) conflicts between the three single-gene phylogenies, their alignments were concatenated with SequenceMatrix (Vaidya *et al*. 2011). The concatenated alignment was submitted to Zenodo (https://doi.org/10.5281/zenodo.14218926). For the Bayesian Inference (BI), jModeltest 2.1 (Darriba *et al*. 2012) was used to identify the optimal substitution model for each character set (LSU+5.8S, ITS1+ITS2, *rpb*2), using the corrected Akaike information criterion. The best-fit models were GTR+I+G for LSU+5.8S and *rpb*2, and GTR+G for ITS1+ITS2.

Partitioned Bayesian analysis was executed with MrBayes version 3.2.7a (Ronquist *et al*. 2012) on the Cipres portal (Miller *et al*. 2010). Two runs of six chains were performed with generations set to 10^6, and trees and parameters were sampled every 200 generations. Convergence of the two independent runs was monitored using the average standard deviation of split frequencies and ensuring that the Potential Scale Reduction Factor was close to one and the Effective Sample Size larger than 200 for each parameter. The average deviation of split frequencies was 0.006997 at the end of the analysis. Log-likelihood scores for all sampling points were checked using Tracer v 1.7.1 (Rambaut *et al*. 2018) to determine the appropriate burn-in value. Chains were considered stationary when the log likelihood values reached a plateau. A 50% majority-rule consensus tree was then built with associated posterior probabilities. Clades were deemed to be supported when displaying a maximum likelihood bootstrap proportion (MLBS) ≥ 70% and a Bayesian posterior probability (BIPP) ≥ 0.90.

TABLE 1. Species name, voucher code, country, reference, and corresponding GenBank accession numbers for each specimen used for the phylogenetic analyses. Newly generated sequences are in bold; – indicates the unavailability of sequence data.

Taxon	Voucher specimen	Country	ITS	LSU	*rpb*2	Reference
Phaeopterula juruensis	F41	Brazil	MK953304	MK953420	MK944332	Leal-Dutra *et al*. 2020
Phaeopterula sp.	F78	Brazil	MK953321	MK953428	MK944338	Leal-Dutra *et al*. 2020
Phaeopterula stipata	M15	Brazil	MK953330	MK953431	–	Leal-Dutra *et al*. 2020
Pterula multifida	KM195746	UK	MK953335	MK953399	MK944372	Leal-Dutra *et al*. 2020
Pterula siamensis	**MFLU24-0324**	**Thailand**	**PQ035117**	**PQ035123**	**PQ505628**	**This study**
***Pterula siamensis* TYPE**	**MFLU24-0323**	**Thailand**	**PQ035116**	**PQ035124**	**PQ505629**	**This study**
Pterula sp.	F42	Brazil	MK953336	MK953433	–	Leal-Dutra *et al*. 2020
Pterula sp.	F48	Brazil	–	MK953434	–	Leal-Dutra *et al*. 2020
Pterula sp.	M54	Brazil	MK953341	MK953438	–	Leal-Dutra *et al*. 2020
Pterula sp.	M71_consensus1	Brazil	MK953342	MK953439	MK944342	Leal-Dutra *et al*. 2020
Pterula sp.	M71_consensus2	Brazil	MK953343	–	–	Leal-Dutra *et al*. 2020
Pterula sp.	M112_consensus1	Brazil	MK953337	MK953435	MK944340	Leal-Dutra *et al*. 2020
Pterula sp.	M112_consensus2	Brazil	MK953338	–	–	Leal-Dutra *et al*. 2020
Pterula sp.	KM141379	Puerto Rico	MK953344	–	–	Leal-Dutra *et al*. 2020
Pterula subulata	KM145950	Italy	MK953346	–	–	Leal-Dutra *et al*. 2020
Pterula subulata	KM167186	Sweden	MK953347	–	–	Leal-Dutra *et al*. 2020
Pterula verticillata	KM27119	Brunei	MK953348	–	–	Leal-Dutra *et al*. 2020
Pterula vinacea	DED7255	Indonesia	–	FJ648337	–	Dentinger *et al*. 2009
Pterulicium brunneosetosum	M35_clone5	Brazil	MK953365	–	–	Leal-Dutra *et al*. 2020
Pterulicium brunneosetosum	M35	Brazil	MK953366	MK953452	MK944353	Leal-Dutra *et al*. 2020

.....continued on the next page

TABLE 1. (Continued)

Taxon	Voucher specimen	Country	ITS	LSU	*rpb2*	Reference
Pterulicium caricispendulae	KM155784	UK	MK953367	–	–	Leal-Dutra *et al*. 2020
Pterulicium crassisporum	KM57972	Cameroon	MK953368	–	–	Leal-Dutra *et al*. 2020
Pterulicium echo	DJM302	Trinidad	DQ494693	AY629315	GU187805	Matheny *et al*. 2006; Binder *et al*. 2010
Pterulicium epiphyllum	DJM1347	Singapore	–	FJ648342	–	Dentinger *et al*. 2009
Pterulicium fasciculare	KM167225	Australia	MK953349	–	–	Leal-Dutra *et al*. 2020
Pterulicium fasciculare	KM167227	Malaysia	MK953350	–	–	Leal-Dutra *et al*. 2020
Pterulicium lilaceobrunneum	M89	Brazil	MK953352	MK953441	–	Leal-Dutra *et al*. 2020
Pterulicium lilaceobrunneum	M117	Brazil	MK953351	MK953440	MK944343	Leal-Dutra *et al*. 2020
Pterulicium secundirameum	BZL44	Brazil	MK953353	MK953400	MK944373	Leal-Dutra *et al*. 2020
Pterulicium secundirameum	M50	Brazil	MK953354	MK953442	MK944344	Leal-Dutra *et al*. 2020
Pterulicium sp.	KM167228	Malaysia	MK953357	–	–	Leal-Dutra *et al*. 2020
Pterulicium sp.	KM167233	Sierra Leone	MK953358	–	–	Leal-Dutra *et al*. 2020
Pterulicium subsimplex	M33	Brazil	MK953363	MK953450	MK944351	Leal-Dutra *et al*. 2020
Pterulicium subsimplex	M77	Brazil	MK953364	MK953451	MK944352	Leal-Dutra *et al*. 2020
Pterulicium sprucei	F60	Brazil	MK953360	MK953446	MK944348	Leal-Dutra *et al*. 2020
Pterulicium sprucei	M91	Brazil	MK953362	MK953448	MK944350	Leal-Dutra *et al*. 2020
Pterulicium xylogenum	Harsh s.n.	India	–	FJ648339	–	Dentinger *et al*. 2009
Pterulicium xylogenum	KM167222	Bangladesh	MK953387	–	–	Leal-Dutra *et al*. 2020
Pterulicium xylogenum	**MFLU24-0325**	**Thailand**	**PQ036930**	**PQ035118**	**–**	**This study**
Pterulicium xylogenum	**MFLU24-0326**	**Thailand**	**PQ036931**	**PQ035119**	**–**	**This study**
Pterulicium xylogenum	**MFLU24-0327**	**Thailand**	**PQ035113**	**PQ035120**	**–**	**This study**
Pterulicium xylogenum	**MFLU24-0328**	**Thailand**	**PQ035114**	**PQ035121**	**PQ505627**	**This study**
Pterulicium xylogenum	**MFLU24-0329**	**Thailand**	**PQ035115**	**PQ035122**	**–**	**This study**

Results

Phylogenetic analyses

The combined phylogenetic dataset of LSU, ITS and *rpb*2 contained 29 *Pterulaceae* species. After editing and trimming, the analyzed dataset contained a total of 2,104 characters including gaps (LSU+5.8S = 991; ITS1+ITS2 = 441; *rpb*2 = 672). Topologies of the single-gene phylogenies were similar to the one generated from the combined dataset. Further, the individual phylogenetic trees generated based on combined genes using ML and Bayesian analyses shared a similar topology, with no supported conflict. The RAxML analysis of the combined dataset produced the best-scoring tree with a final ML optimization log-likelihood value of -10080.85.

The phylogenetic tree (Figure 1) included *Phaeopterula* Henn. (1904) as the outgroup, *Pterula* and *Pterulicium*. The monophyly of the latter two genera was highly supported (MLBS = 100% and BIPP = 1.0). Our collections of *Pterulicium* clustered with two strains of *Ptm. xylogenum* (Harsh s.n., KM167222), with strong statistical support (MLBS = 100% and BIPP = 1.0) and 0 or close to 0 branch lengths. *Pterula siamensis* sequences clustered within the *Pterula* clade and were closely related to *P. vinacea* Corner (1950) (DED7255) with moderate ML support (MLBS = 85%, BIPP < 0.90). The tree topology obtained from the combined phylogenetic analysis in this study is consistent with previous research (Leal-Dutra *et al*. 2020).

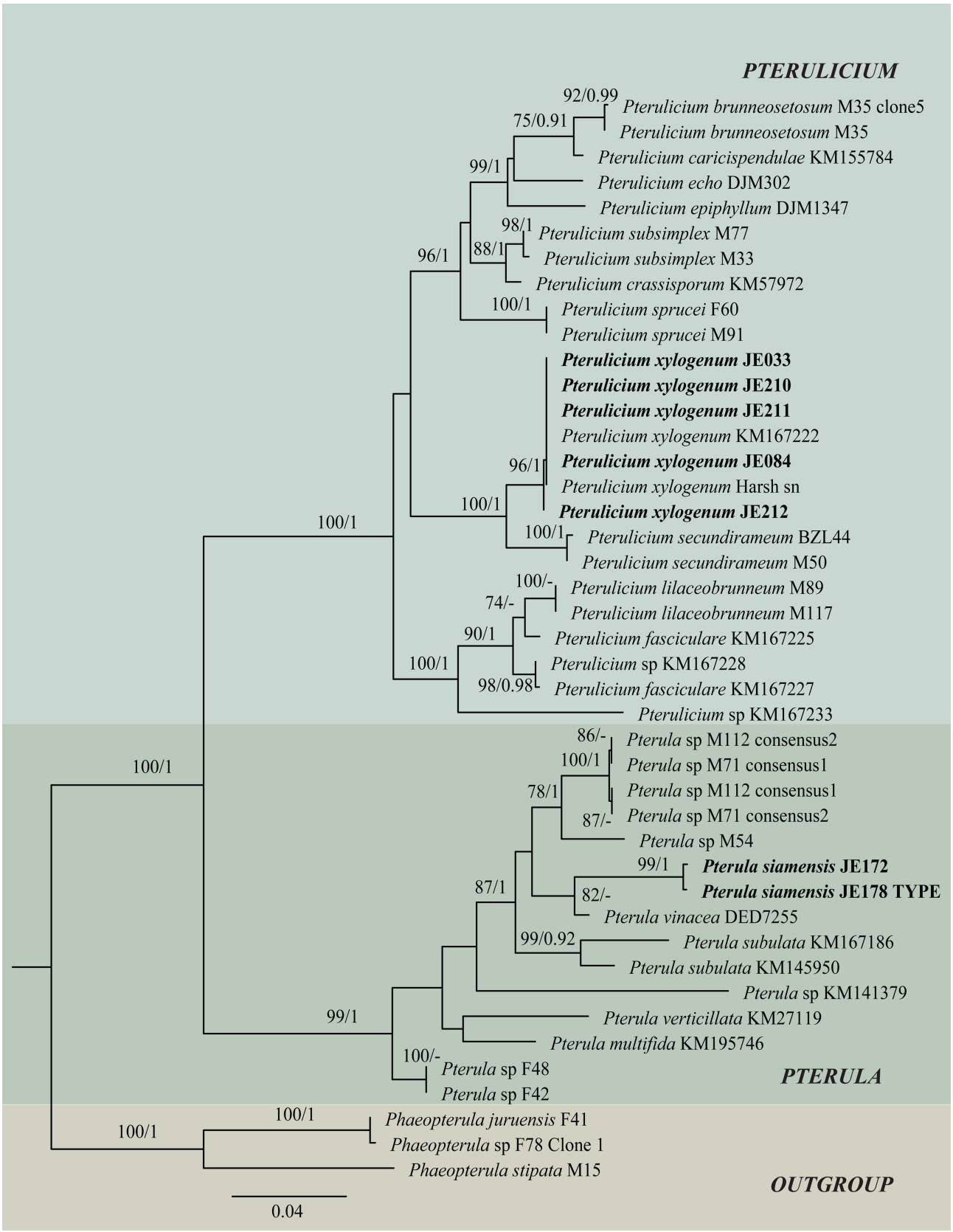

FIGURE 1. RAxML tree based on analysis of a combined dataset of LSU+5.8S, ITS1+ITS2, and *rpb*2 sequences. Maximum likelihood bootstrap proportion (MLBS) ≥ 70% and the Bayesian posterior probability (BIPP) ≥ 0.90 are indicated above the branches as MLBS /BIPP. The tree is rooted to *Phaeopterula juruensis*, *Phaeopterula stipata* and *Phaeopterula* sp.

Taxonomy

Pterula siamensis Appad. & Raspé, *sp. nov.* Figure 2
Mycobank number: MB 854785

Etymology:—Refers to Siam, the former name of Thailand, where the species was discovered.

Holotype:—THAILAND: Chiang Rai Province: Mae Chan District, San Sai, 20.149899°N–99.920525°E, elev. 480 m, on dead bamboo culms, branches, and leaves, 21 September 2023, *M.A. Appadoo JE178* (MFLU24-0323).

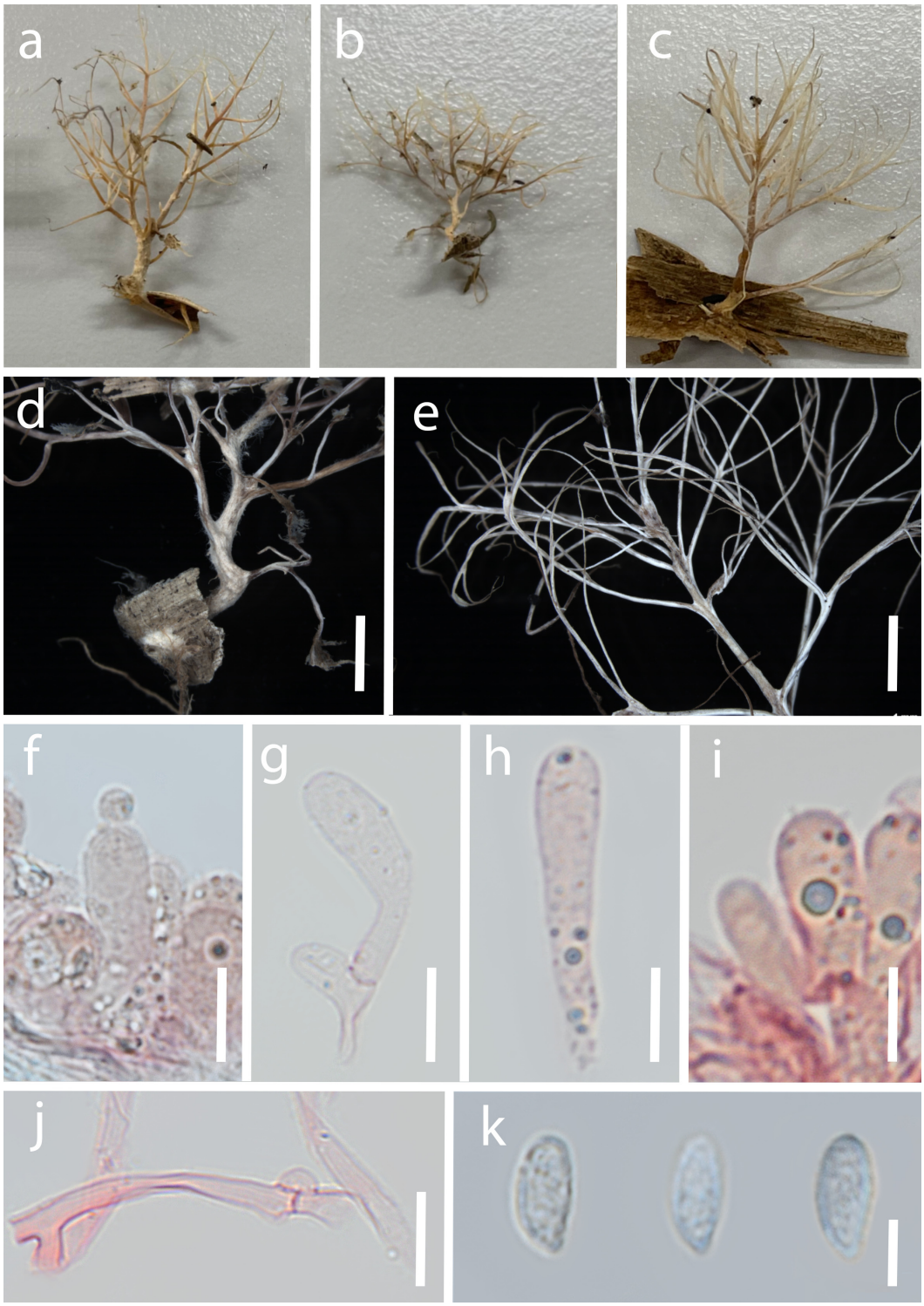

FIGURE 2. Pterula siamensis (MFLU24-0323, holotype). a–e Basidiomes. f. Capitate cystidium. g. Cystidium. h. Basidiole. i. Basidium. j. Generative hyphae with clamp connection. k. Basidiospores. Scale bars: a = 5 m, b = 500 µm, c = 500 µm, d = 500 µm, e = 100 µm, f–j = 10 µm, k = 5 µm.

Diagnosis:—*Pterula siamensis* is characterized by a coriaceous stipe with flexuous, concolorous tips and cylindrical, sometimes capitate cystidia. It differs from *Pterula verticillata* Corner (1950), which has a fleshy, translucent stipe and cystidia with a rostrate apex.

Gene sequences (from holotype):—PQ035116 (ITS), PQ035124 (LSU) and PQ505629 (*rpb*2)

Basidiomes 1.9–2.6 × 1–2.5 cm, gregarious or solitary, erect, dendroid, monopodial or multiaxial, decurrent (spreading branching with weak central stem dominance), axes with 4–5 tiers of 2–9 branches, light grey-brown when fresh and pale cinereous to fuscous brown when dried, pruinose. *Stipe* 5–8 × 0.7–1.5 mm, simple, cylindrical, rigid, sometimes twisted, arising from rhizoids covered with mycelial fibrils when fresh, smooth when dried. *Branches* sublateral 2–3 times dividing into widely spread, appearing cristate branchlets 7.03–13–18 mm long, 0.2–0.4 mm wide, curved ascending branches, flexuous at the tip, tapering into subulate tip; axils subacute to acute.

Basidiospores [70,3,3] 6.2–7.2–8.3 × 3.1–3.8–4.4 µm Q = (1.47–)1.54–1.92–2.23(–2.29), amygdaliform, smooth, hyaline, inamyloid, non-dextrinoid. *Basidia* 20.9–23.3–28.2 × 6.5–7.5–8.5 µm, cylindrical, hyaline, smooth, 4-sterigmate. *Cystidia* hyaline, cylindrical, sometimes capitate, thin-walled, inamyloid, non-dextrinoid. *Hyphal system* dimitic; skeletal hyphae 3.3–6.7 (mean = 5.41) µm, of even width, with a thick wall (0.6–1.5 µm), hyaline to pale ochraceous; generative hyphae 3–5.6 (mean = 4.2) µm, hyaline, thin-walled with clamp connections

Ecology and distribution:—Gregarious or solitary on dead bamboo culms, branches and leaves in bamboo-dominated forest, during August to September. Currently known only from the type locality in Chiang Rai Province, Thailand.

Additional specimen examined:—THAILAND: Chiang Rai Province, Mueang Chiang Rai District, Baan Pasang Wiwat Community Forest, 20.045767°N–99.854183°E elev. 440 m, on dead bamboo culms and branches, 22 August 2023, *M.A. Appadoo JE172* (MFLU24-0324); gene sequences PQ035117 (ITS), PQ035123 (LSU) and PQ505628 (*rpb*2).

Notes:—Morphologically, *Pterula siamensis* closely resembles *P. verticillata*. However, there are significant differences between the two species. *Pterula verticillata* is fleshy and translucent, with the main axis comprising 2–6 tiers of 3–4 branches, with paler, whitish ascending tips (Senthilarasu 2013). In contrast, *P. siamensis* features a coriaceous and sturdy stipe, with axes in 4–5 tiers of 2–9 branches, with flexuous, concolorous tips. Additionally, *P. siamensis* can be distinguished by its cylindrical, sometimes capitate cystidia, whereas *P. verticillata* produces cystidia with a rostrate apex (Senthilarasu 2013).

Pterula siamensis also differs from other bamboo-associated species, such as *P. capillaris* (Lév.) Sacc. 1888. *Pterula capillaris* produces larger basidiomes, reaching up to 5 cm in height, with penicillate and compressed tips. In contrast, *P. siamensis* is less bushy, with cylindrical tips that taper into a needle-like shape.

According to our phylogenetic tree (concatenated LSU+5.8S, ITS1+ITS2, *rpb*2 data), the closest species to our collection is *Pterula vinacea* with moderate support (MLBS = 85%, BIPP < 0.9). The morphology of *P. siamensis* contrasts with that of *P. vinacea* by being much smaller in size (1.9–2.6 × 1–2.5 cm compared to 7 × 6 cm) and by its light grey-brown color, as opposed to the vinaceous color of *P. vinacea.*

Pterulicium xylogenum (Berk. & Broome) Corner 1950: 538 Figure 3
Mycobank number: MB 304549

Basidiomes 0.9–1.8 × 1–1.5 cm, gregarious, fasciculate to connate, growing in clusters from a subiculum-like patch 1.5–3 cm in diam., erect, slender, simple, sparingly branched to very bushy, pale yellowish cinereous to fuscous brown, powdery when dry. *Stipe* 0.2–0.5 mm, thick, simple, cylindrical, rigid, smooth when dried, sometimes appearing anastomosing from the incomplete separation of initially connate stipes embedded in the white covering tissue (when dry). Branchlets in 2–6 tiers, last tiers often looking verticillate, 0.1–0.4 cm wide, tapering into a subulate, flexuous tip; axils subacute to acute.

Basidiospores [30,3,3] (8.4–)8.9–10.8–13.1(–13.3) × (5.2–)5.3–6.1–7.1(–7.4) µm, Q = (1.4–)1.49–1.77–2.01(–2.04), amygdaliform, smooth, hyaline, inamyloid, non-dextrinoid. *Basidia* (24.3–)24.6–33.3–48.4(–49.5) × (7.4–)8–10.7–13.2(–13.5) µm cylindrical, clavate, hyaline, contents dense, smooth, 4-sterigmate. *Cystidia* (30.3–)31.8–39.3–46.2(–46.5) × (6.3–)6.3–7.6–10.9(–11.1) µm hyaline, cylindrical, fusiform, subventricose, thin-walled, inamyloid, non-dextrinoid. *Hyphal system* dimitic; skeletal hyphae 3.4–4.3–5.6 µm broad, of even width, with thick smooth walls (0.5–1.6 µm thick), hyaline to pale brown, aseptate to occasionally septate; generative hyphae 2.1–3.5–4.8 µm broad, hyaline, thin-walled with clamp connections.

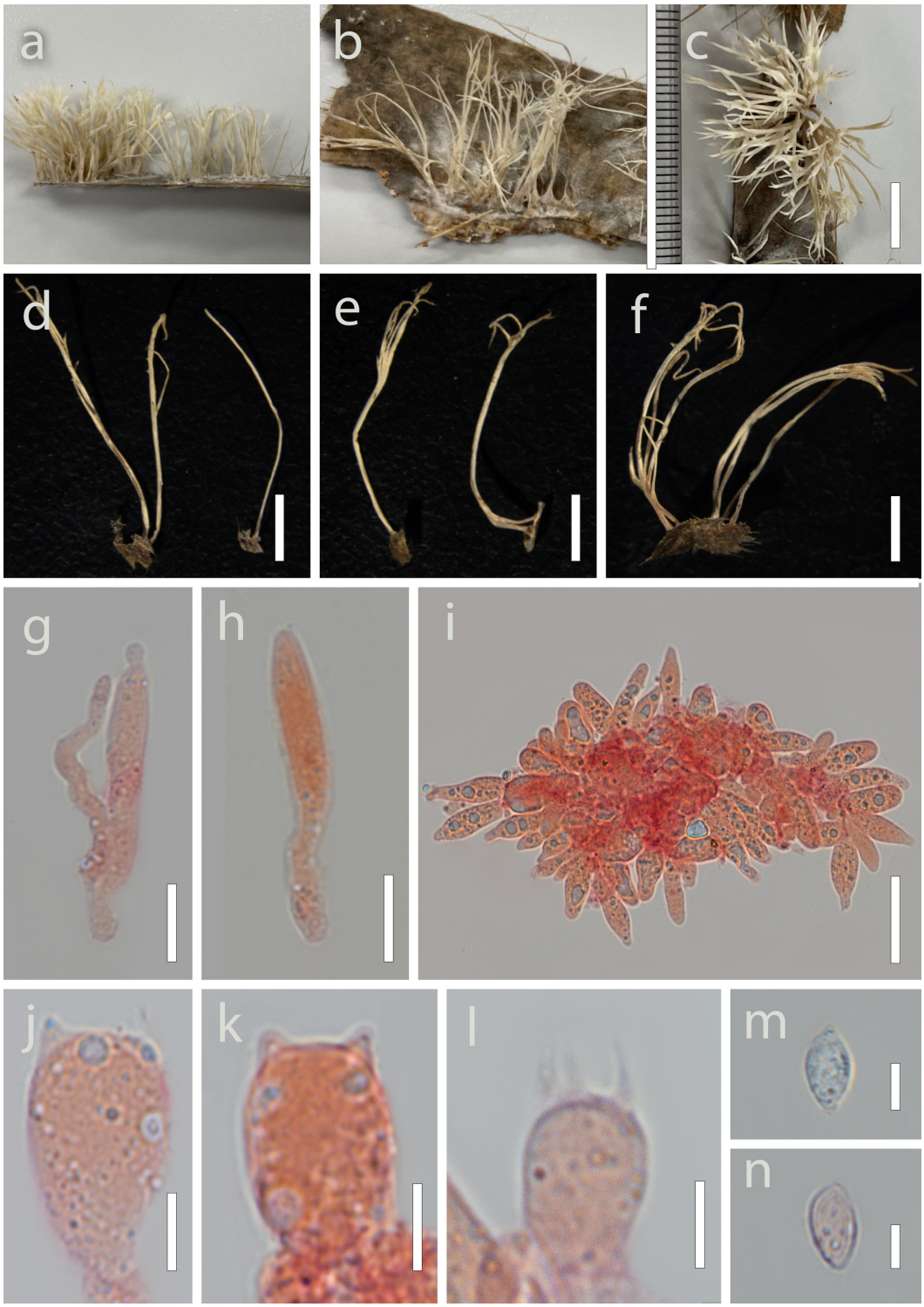

FIGURE 3. *Pterulicium xylogenum* (MFLU24-0327). a–f Basidiomes. g–i. Cystidia. j–l. Basidia. m–n Basidiospores. Scale bars: Scale bars: c–f = 4 mm, g–h = 10 µm, i = 40 µm, j–l= 10 µm, m–n = 5 µm.

Ecology and distribution:—On dead and recently cut bamboo culms, branches, leaves and sheaths as well as dead leaf-sheaths and trunks of various palms. Known from India, the Philippines, Malaysia, Sri Lanka, Thailand, and Uganda.

Specimens examined:—THAILAND: Chiang Rai Province, Mueang Chiang Rai District, Baan Pasang Wiwat Community Forest, 20.045767°N–99.854183°E, elev. 440 m, on dead bamboo culms and branches, 08 December 2022, *M.A. Appadoo JE0033* (MFLU24-0325). Chiang Rai Province, Mae Chan District, San Sai Subdistrict 20.149899°N–99.920525°E, elev. 480 m, on dead bamboo culms, branches, and leaves, 03 July 2023, *M.A. Appadoo JE0084*, (MFLU24-0326). Chiang Rai Province, Mueang Chiang Rai District, Mae Fah Luang University, 20.084072°N–100.490275°E,

elev. 420 m, on recently cut bamboo culms and sheaths, 11 December 2023, *O. Raspé JE210* (MFLU24-0327), *JE211* (MFLU24-0328), *JE212* (MFLU24-0329); gene sequences PQ036930, PQ036931, PQ035113, PQ035114, PQ035115 (ITS), PQ035118, PQ035119, PQ035120, PQ035121, PQ035122 (LSU), and PQ505627 (*rpb*2).

Notes:—Our collections of *Pterulicium* were identified as *Ptm. xylogenum* based on both morphological and phylogenetic evidence. Morphologically, the characteristics of our specimens are aligned with the species description provided by Corner (1950). Key features such as the basidiome structure, spore morphology, and other macroscopic and microscopic traits match the detailed description of *Ptm. xylogenum.* Phylogenetically, our collections cluster with other strains of *Ptm. xylogenum* with high statistical support (MLBS =100%, BIPP = 1.0). The biogeographical context of our collection from Thailand is consistent with the known distribution of *Ptm. xylogenum*, which has been recorded in India, the Philippines, Malaysia, Sri Lanka, and Uganda (Corner 1950, Harsh *et al*. 2005). These regions share similar tropical and subtropical climates, supporting the ecological consistency of our identification. Therefore, based on comprehensive morphological and phylogenetic evidence, as well as biogeographical consistency, our collection is confirmed to be *Ptm. xylogenum*.

Discussion

Pterula is characterized by intricately branched, coralloid basidiomes that range from fleshy to tough (Corner 1950). The new species we introduce in this paper, *P. siamensis*, fits well within this genus and is distinct from all other *Pterula* species based on morpho-molecular assessments. The discovery of *Pterula siamensis* is particularly noteworthy considering that the *Pterulaceae* from Thailand previously included only seven species (Chandrasrikul *et al*. 2011). This highlights the potential for further exploration of this family in diverse habitats across the country.

Morphologically, *Pterula siamensis* closely resembles *P. verticillata* but can be differentiated by several key characteristics: *P. siamensis* has a coriaceous stipe with flexuous, concolorous tips and cylindrical cystidia, whereas *P. verticillata* does not exhibit these specific traits (Corner 1950, Senthilarasu 2013). Phylogenetically, *P. siamensis* forms a distinct clade with strong statistical support (MLBS > 99%, BIPP = 1.0). When compared to its closest phylogenetic relative, *P. vinacea*, *P. siamensis* is smaller and has a light grey-brown coloration, in contrast to the vinaceous color of *P. vinacea* (Corner 1950).

In addition to the discovery of *Pterula siamensis,* we also report the first record of *Pterulicium xylogenum* in Thailand. This species has been previously documented in India, Malaysia, Sri Lanka, the Philippines, and Uganda (Corner 1950, Harsh *et al*. 2005). The consistency of *Ptm. xylogenum*'s presence in Thailand with similar ecological conditions and bamboo species across these regions suggests a broader geographical distribution. Despite our observations showing no evidence of pathogenicity associated with *P. xylogenum* in Thailand, its presence raises important considerations regarding its potential economic implications for bamboo, a crucial resource in the region. Understanding the ecological interactions and possible threats posed by this species is essential for effective management and conservation strategies (Corner 1952b, Harsh *et al*. 2005)

In conclusion, our findings contribute valuable new information to the taxonomy and distribution of the Pterulaceae. The discovery of *Pterula siamensis* and the first record of *Pterulicium xylogenum* in Thailand highlights the rich fungal biodiversity yet to be fully explored. Notably, while previous records of Pterulaceae have primarily been associated with soil or deciduous plants (Chandrasrikul *et al*. 2011), our observations mark the first occurrence of these fungi on bamboo in Thailand. This underscores the need for further exploration of fungal species in bamboo forests, as their ecological roles may be crucial, particularly considering their potential threats to important cash crops. Continued studies on fungi in Southeast Asia are essential for understanding and preserving this biodiversity.

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