The sexual morph of *Induratia coffeana*, a new record from Thailand

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Abstract
An induratia-like fungus was collected in Thailand from a deadwood piece of an unidentified plant. Phylogenetic analyses based on ITS, LSU, *rpb*2, and *β-tubulin* sequence data and morphological characteristics showed that the fungus is *Induratia coffeana*. *Induratia coffeana* differs from *I. ziziphi*, *I. thailandica* and *I. apiospora* by its 2-celled ascospores with equal divisions. Full description, illustrations, and a phylogenetic tree to show the placement of *I. coffeana* are provided. *Induratia coffeana* is reported herein as a new record for Thailand based on its sexual morph.

Keywords: *Ascomycota*, Phylogeny, Taxonomy, *Xylariales*

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Introduction

Endophytic fungi live within healthy living tissues of host plants, typically without causing any visible symptoms of disease (Hyde and Soytong 2008). Most endophytic fungi cannot produce sexual morphs on artificial media (Li et al. 2016, Tibpromma et al. 2018). The genus *Muscodor* Worapong et al. was described based on the *sterilia mycelia* of an endophytic species, *M. albus* Worapong et al. which was isolated from *Cinnamomum zeylanicum* (Worapong et al. 2001).

Over a decade, 22 species, including *M. albus*, have been described based on their morphology, DNA sequence data and volatile organic compounds (VOCs) (Worapong et al. 2001, 2002, Daisy et al. 2002a, b, Miller and Huhndorf 2005, Zhang et al. 2006, Mitchell et al. 2008, González et al. 2009, Suwannarach et al. 2010, 2013, 2010, Kudalkar et al. 2012, Meshram et al. 2013, 2014, 2015, 2017, Hongsanan et al. 2015, Saxena et al. 2015, Chen et al. 2019, Pena et al. 2019). *Muscodor* species are distinguished based on culture characteristics such as the formation of ropy mycelium, right-angle branching and cauliflower-like or nondescript structures. However, based on ITS, LSU, *rpb*2 and *β-tubulin* sequence data, Samarakoon et al. (2020) confirmed that *Muscodor* is a synonym of *Induratia* (the older, sexually typified genus) (Samuels et al. 1987) and placed it in *Induratiaceae* (*Xylariales*).

Induratia cinnamomi Samarak et al. (2020) (=*Muscodor cinnamomi* Suwannar et al.) was isolated as an endophyte living within a leaf of *Cinnamomum bejolghota* from northern Thailand (Suwannarach et al. 2010). Four new *Muscodor* species isolated from medicinal plants of northern Thailand were introduced based on morphological and physiological characteristics, and phylogenetic analysis of ITS sequence data (Suwannarach et al. 2013). All five new species from Thailand were described with sterile mycelia. Samarakoon et al. (2020) described two new species (*viz*., *I. thailandica* Samarak. et al. and *I. ziziphi* Samarak. et al.) from Thailand, with sexual morphs. *Induratia coffeana* (=*Muscodor coffeanum*) associated with the stems of *Coffea arabica* was introduced with a description of the sterile mycelium and phylogenetic analysis based on ITS sequences (Hongsanan et al. 2015). *Induratia coffeana* has been reported from Brazil as an endophytic fungus (Monteiro et al. 2017).

During an investigation of *Xylariales* in Thailand, one induratia-like fungus with sexual morph was collected. In this paper, we report it as *Induratia coffeana*, a new record for Thailand based on its sexual morphology, mycelial characteristics, and phylogenetic analyses.

Materials and methods

Collection and isolation

Samples of dead wood of an unidentified plant were collected from Chiang Rai, Thailand, and transported to the laboratory in paper bags. The morphological examination of specimens was carried out following the method of Stadler et al. (2014). Macro-morphological characters were examined and photographed using a digital camera fitted to the Olympus SZ61 stereo microscope (Olympus Corporation, Japan) (Senanayake et al. 2015). Morphological characteristics of asci ($n \geq 20$), ascospores ($n \geq 30$) mounted in water and Melzer's reagent were photographed using a digital camera fitted with Nikon Ni compound microscopy (Nikon Corporation, Japan) and measured with Tarosoft v. 0.9.0.7. Photomicrographs were arranged with Adobe Photoshop v. CS6. Single-spore isolation was performed following the method of Chomnunti et al. (2014). Culture characteristics on potato dextrose agar (PDA) medium were described (Worapong et al. 2001). The cultures were maintained in 2 mL screw cap micro-centrifuge tubes with 10 % glycerol at –20 °C, and those with sterile water were maintained at 4 °C. Herbarium specimens were deposited at the herbaria of Mae Fah Luang University (MFLU) and Guizhou Medical University, Guizhou, China (GMB). The cultures were deposited at Mae Fah Luang University Culture Collection (MFLUCC) and Guizhou Medical University Culture Collection (GMBC).

DNA extraction, PCR amplification and sequencing

Cultures were transferred to 2 % PDA medium and incubated at 25 °C for 15 days, till the hyphae covered the Petri dishes. Mycelium was scraped off the surface of the medium for DNA extraction. Total genomic DNA was extracted from fresh mycelia using BIOMIGA Fungus Genomic DNA Extraction Kit (GD2416) (Wijayawardene et al. 2013). The segments of the internal transcribed spacer region (ITS), *β-tubulin* gene, large-subunit ribosomal RNA gene (LSU), and RNA polymerase II subunit gene (*rpb*2) were amplified separately by primer pairs, ITS4/ITS5, T11/T22, LR0R/LR5 and RPB2-5f/RPB2-7Cr (Tanaka et al. 2009, Hsieh et al. 2010, Daranagama et al. 2015). PCR amplifications were performed following Li et al. (2015) and Su et al. (2016). Each reaction mixture comprised a 25 μL total volume, consisting of 19.75 μL of double-distilled water, 2.5 μL of 10× Taq buffer with $MgCl_2$, 0.5 μL of dNTP (10 mM each), 0.5 μL of each primer (10 μM), 0.25 μL Taq DNA polymerase (5 U/μL), and 1.0 μL of DNA template (Li et al. 2015). Amplified PCR products were transported to SinoGenoMax, Beijing, China, for DNA sequencing. The sequences obtained were deposited in GenBank. The closest sequences from NCBI BLAST results were downloaded for the phylogenetic tree construction (Table 1).

Sequence alignment and phylogenetic analyses

NCBI BLAST searches of ITS sequences revealed the closest hits to our strain. The sequences of the closest taxa and other taxa from Samarakoon et al. (2020) were downloaded and aligned using MAFFT (http://mafft.cbrc.jp/alignment/server/index.html). Alignments were improved manually using

Table 1 Names, codes, references and corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses of this study

Species	Code	GenBank accession numbers				References
		ITS	LSU	*rpb2*	*β-tubulin*	
Achaetomium macrosporum	CBS 532.94	KX976574	KX976699	KX976797	KX976915	Wang et al. (2016a)
Amphirosellinia nigrospora	HAST 91092308*	GU322457	N/A	GQ848340	GQ495951	Hsieh et al. (2010)
Annulohypoxylon truncatum	CBS 140778*	KY610419	KY610419	KY624277	KX376352	Kuhnert et al. (2017), Wendt et al. (2018)
Anthostomella formosa	MFLUCC 14-0170	KP297403	KP340544	KP340531	N/A	Daranagama et al. (2015)
A. obesa	MFLUCC 14-0171*	KP297405	KP340546	KP340533	N/A	Daranagama et al. (2015)
Anthostomelloides krabiensis	MFLUCC 15-0678*	KX305927	KX305928	KX305929	N/A	Tibpromma et al. (2017)
Apiospora hydei	CBS 114990*	KF144890	KF144936	N/A	KF144982	Crous and Groenewald (2013)
A. kogelbergensis	CBS 113333*	KF144892	KF144938	N/A	N/A	Crous and Groenewald (2013)
A. neosubglobosa	HKAS 96354*	KY356089	KY356094	N/A	N/A	Dai et al. (2016)
A. phragmitis	CPC 18900*	KF144909	KF144956	N/A	KF145001	Crous and Groenewald (2013)
Astrocystis sublimbata	HAST 89032207	GU322447	N/A	GQ844834	GQ495940	Hsieh et al. (2010)
Barrmaelia moravica	CBS 142769*	MF488987	MF488987	MF488996	MF489015	Voglmayr et al. (2018)
B. rappazii	CBS 142771*	MF488989	MF488989	MF488998	MF489017	Voglmayr et al. (2018)
B. rhamnicola	CBS 142772*	MF488990	MF488990	MF488999	MF489018	Voglmayr et al. (2018)
Biscogniauxia nummularia	MUCL 51395*	KY610382	KY610427	KY624236	KX271241	Wendt et al. (2018)
B. repanda	ATCC 62606	KY610383	KY610428	KY624237	KX271242	Wendt et al. (2018)
Brunneiperidium involucratum	MFLUCC 14-0009*	KP297399	KP340541	KP340527	KP406610	Daranagama et al. (2015)
Camillea obularia	ATCC 28093	KY610384	KY610429	KY624238	KX271243	Wendt et al. (2018)
Chaetomium elatum	CBS 374.66	KC109758	KC109758	KF001820	KC109776	Wang et al. (2016b)
Clypeosphaeria mamillana	CBS 140735*	KT949897	KT949897	N/A	N/A	Jaklitsch et al. (2016)
Collodiscula leigongshanensis	GZUH 0107*	KP054281	KP054282	KR002588	KR002587	Li et al. (2015)
Creosphaeria sassafras	STMA 14087	KY610411	KY610468	KY624265	KX271258	Wendt et al. (2018)
C. sassafras	CBS 119001	KU683754	N/A	KU684308	KU684126	U'Ren et al. (2016)
C. ligniota	CBS 273.87*	KT425232	KT425297	KT425362	KT425167	Trouillas et al. (2015)
C. subcutanea	CBS 240.87*	KT425233	KT425298	KT425363	KT425168	Trouillas et al. (2015)
Daldinia concentrica	CBS 113277	AY616683	KY610434	KY624243	KC977274	Kuhnert et al. (2014)
D. loculatoides	CBS 113279*	AF176982	KY610438	KY624247	KX271246	Wendt et al. (2018)
Diabolocovidia claustri	CBS 146630	MT373367	MT373350	N/A	N/A	Crous et al. (2020)
Diatrype disciformis	AFTOL-ID 927*	N/A	DQ470964	DQ470915	N/A	Spatafora et al. (2006)
Dematophora buxi	JDR 99	GU300070	N/A	GQ844780	GQ470228	Hsieh et al. (2010)
D. necatrix	HAST 89062904	EF026117	KF719204	GQ844779	EF025603	Hsieh et al. (2010)
Emarcea castanopsidicola	CBS 117105*	AY603496	MK762717	MK791285	MK776962	Duong et al. (2004)

E. eucalyptigena	CBS 139908*	KR476733	MK762718	MK791286	MK776963	Crous et al. (2015)
Entalbostroma erumpens	ICMP 21152*	KX258206	N/A	KX258204	KX258205	Johnston et al. (2016)
Entoleuca mammata	JDR 100	GU300072	N/A	GQ844782	GQ470230	Hsieh et al. (2010)
Entosordaria perfidiosa	CBS 142773*	MF488993	MF488993	MF489003	MF489021	Voglmayr et al. (2018)
E. quercina	CBS 142774*	MF488994	MF488994	MF489004	MF489022	Voglmayr et al. (2018)
Eutypa lata	AFTOL-ID 929*	N/A	DQ836903	DQ836889	N/A	Zhang et al. (2006)
Graphostroma platystomum	CBS 270.87*	JX658535	DQ836906	KY624296	HG934108	Zhang et al. (2006)
Hypomontagnella monticulosa	MUCL 54604*	KY610404	KY610487	KY624305	KX271273	Wendt et al. (2018)
Hypoxylon fragiforme	MUCL 51264*	KC477229	NG_066364	KY624277	KX271282	Stadler et al. (2013)
Induratia alba	MONT 620*	AF324336	N/A	N/A	N/A	Worapong et al. (2001)
I. alba	9-6	HM034857	HM034865	N/A	HM034844	Zhang et al. (2010)
I. brasiliensis	LGMF 1256*	KY924494	N/A	MF510171	N/A	Pena et al. (2019)
I. camphorae	NFCCI 3236*	KC481681	N/A	N/A	N/A	Meshram et al. (2017)
I. cinnanomi	BCC 38842*	GQ848369	N/A	N/A	N/A	Suwannarach et al. (2010)
I. coffeana	COAD 1842*= CDA739	KM514680	N/A	KP862881	N/A	Hongsanan et al. (2015)
I. coffeana	COAD 1900	KP862879	N/A	KP862880	N/A	Hongsanan et al. (2015)
I. coffeana	**MFLUCC13-0159**	**MK634693**	**MK634694**	**MK644942**	**MK644943**	**This study**
I. crispans	MONT 2347*	EU195297	N/A	N/A	N/A	Mitchell et al. (2008)
I. darjeelingensis	NFCCI 3095*	JQ409997	N/A	N/A	N/A	Saxena et al. (2014)
I. equiseti	JCM 18233*	JX089322	N/A	N/A	N/A	Suwannarach et al. (2013)
I. fengyangensis	CGMCC 2863	HM034855	HM034861	HM034851	HM034842	Zhang et al. (2010)
I. fengyangensis	CGMCC 2862*	HM034856	HM034859	HM034849	HM034843	Zhang et al. (2010)
I. ghoomensis	NFCCI 3234*	KF537625	N/A	N/A	N/A	Meshram et al. (2015)
I. indica	NFCCI 3235*	KF537626	N/A	N/A	N/A	Meshram et al. (2015)
I. kashayum	NFCCI 2947*	KC481680	N/A	N/A	N/A	Meshram et al. (2013)
I. musae	JCM 18230*	JX089323	N/A	N/A	N/A	Suwannarach et al. (2013)
I. oryzae	JCM 18231*	JX089321	N/A	N/A	N/A	Suwannarach et al. (2013)
I. rosea	MONT 2098*	AH010859	N/A	N/A	N/A	Worapong et al. (2002)
Induratia sp.	SMH 1255	MN250031	AY780069	N/A	AY780119	Miller and Huhndorf (2005)
I. strobelii	NFCCI 2907*	JQ409999	N/A	N/A	N/A	Meshram et al. (2014)
I. suthepensis	JCM 18232*	JN558830	N/A	N/A	N/A	Suwannarach et al. (2013)
I. suturae	MSUB 2380*	JF938595	N/A	N/A	N/A	Kudalkar et al. (2012)
I. thailandica	MFLUCC 17-2669*	MK762707	MK762714	MK791283	MK776960	Samarakoon et al. 2020
I. tigerensis	*Camphoric**	JQ409998	N/A	N/A	N/A	Saxena et al. (2015)
I. vitigena	MONT P-15*	AY100022	N/A	N/A	N/A	Daisy et al. (2002a)
I. yucatanensis	MEXU 25511*	FJ917287	N/A	N/A	N/A	González et al. (2009)
I. yunnanensis	CGMCC 3.18908*	MG866046	MG866038	MG866059	MG866066	Chen et al. (2019)

I. ziziphi	MFLUCC 17-2662*	MK762705	MK762712	MK791281	MK776958	Samarakoon et al. 2020
Kretzschmaria deusta	CBS 163.93	KC477237	KY610458	KY624227	KX271251	Stadler et al. (2013)
Lopadostoma dryophilum	CBS 133213*	KC774570	KC774570	KC774526	MF489023	Jaklitsch et al. (2014)
L. turgidum	CBS 133207*	KC774618	KC774618	KC774563	MF489024	Jaklitsch et al. (2014)
Nemania abortiva	BISH 467*	GU292816	N/A	GQ844768	GQ470219	Hsieh et al. (2010)
N. primolutea	HAST 91102001*	EF026121	N/A	GQ844767	EF025607	Hsieh et al. (2010)
Obolarina dryophila	MUCL 49882	GQ428316	GQ428316	KY624284	GQ428322	Pažoutová et al. (2010)
Podosordaria mexicana	WSP 176	GU324762	N/A	GQ853039	GQ844840	Hsieh et al. (2010)
Poronia punctata	CBS 656.78*	KT281904	KY610496	KY624278	KX271281	Senanayake et al. (2015), Wendt et al. (2018)
Sarcoxylon compunctum	CBS 359.61	KT281903	KT281898	KY624230	KX271255	Senanayake et al. (2015), Wendt et al. (2018)
Sordaria fimicola	CBS 508.50	AY681188	AF132330	DQ368647	DQ840087	Miller and Huhndorf (2005), Tang et al. (2009)
Stilbohypoxylon elaeicola	HAST 94082615	GU322440	N/A	GQ844827	GQ495933	Hsieh et al. (2010)
Vamsapriya bambusicola	MFLUCC 11-0477*	KM462835	KM462836	KM462834	KM462833	Dai et al. (2014)
V. indica	MFLUCC 12–0544*	KM462839	KM462840	KM462841	KM462838	Dai et al. (2014), Jiang et al. (2018)
Xylaria adscendens	JDR 865	GU322432	N/A	GQ844818	GQ487709	Hsieh et al. (2010)
X. arbuscula	CBS 126415	KY610394	KY610463	KY624287	KX271257	Fournier et al. (2011)
X. bambusicola	WSP 205*	EF026123	N/A	GQ844802	AY951762	Hsieh et al. (2010)
X. cubensis	JDR 860	GU991523	N/A	GQ848365	GQ502700	Hsieh et al. (2010)
X. discolor	HAST 131023*	JQ087405	N/A	JQ087411	JQ087414	Hsieh et al. (2010)
X. hypoxylon	CBS 122620*	AM993141	KM186301	KM186302	KM186300	Daranagama et al. (2015)

Notes: *: cultures from type materials or herbaria. N/A: no available sequences

BioEdit 7.2.3 (Hall 1999). The individual alignment datasets of ITS, LSU, *rpb*2 and *β-tubulin* were concatenated. Phylip file for RAxML analysis and Nexus file for Bayesian analysis were exported using ALTER (http://sing.ei.uvigo.es/ ALTER/) (Glez-Peña et al. 2010). Maximum likelihood (ML) analysis was carried out on the CIPRES Science Gateway v.3.3 (http://www.phylo.org/portal2; Miller et al. 2010) using RAxML v.8.2.8 at the RAxML-HPC BlackBox tool (Stamatakis et al. 2008). The likelihood of the final tree was evaluated and optimized under GTRGAMMA+I model. The best-scoring tree was selected with a final ML optimization likelihood value of -59548.017972. Bootstrap support (BS) values in ML analysis were calculated from 500 replicates. RAxML bootstrap support values equal to or more than 75 % were shown on each node (Fig. 1).

Bayesian analysis was implemented with MrBayes v.3.2.2 (Ronquist et al. 2012). The best-fitting substitution model for the Bayesian analysis (BY) was determined with MrModeltest version 2.2 and GTR+I+G was chosen as the substitution model (Posada and Crandall 1998, Nylander 2004). Posterior probabilities (PP) (Rannala and Yang 1996) were determined by Markov Chain Monte Carlo sampling (MCMC) (Ronquist and Huelsenbeck 2003). Six simultaneous Markov chains were initially run for 30 $\times 10^6$ generations, and for every 1000th generation, a tree was sampled. All sampled topologies beneath the asymptote (20 %) were discarded. The remaining trees were used to calculate the PP in the majority rule consensus tree. Posterior probabilities equal to or greater than 0.95 were provided at each node (Fig. 1). Phylogenetic trees were visualized with FigTree v.1.4.0 (Rambaut, 2010) and annotated by software of Microsoft Office PowerPoint and Adobe Photoshop v.CS6.

Results

Phylogenetic analyses

The phylogenetic tree (Fig. 1) based on the combined ITS, LSU, *rpb2* and *β-tubulin* sequence data revealed that *Induratia* species belong to the family *Induratiaceae*. Strains COAD 1842, COAD 1900 and MFLUCC13-0159 of *I. coffeana* clustered together with high statistical support values (87 %/ 0.99).

Taxonomy

Induratia coffeana (A.A.M. Gomes, Pinho & O.L. Pereira) Samarak., Thongbai, K.D. Hyde & M. Stadler, Fungal Diversity 101:193 (2020) **Fig. 2**

Synonym: *Muscodor coffeanus* A.A.M. Gomes, Pinho & O.L. Pereira [as 'coffeanum'], Cryptog. Mycol. 36(3):368 (2015)

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Saprobic on dead bark of an unidentified plant. **Sexual morph:** *Ascomata* developing beneath raised blackened areas, with a central erumpent cone-shaped papilla, scattered or gregarious, solitary, immersed, visible as slightly raised, blackened, dome-shaped areas, coriaceous, in vertical section 580–650 µm diam., 380–450 µm high, subglobose to globose, immersed beneath a clypeus. *Clypeus* black, comprising intracellular brown hyphae. *Ostioles* papillate on the centre, black. *Peridium* 35–50 µm thick, comprising several layers of brown-walled angular cells, walls dark brown at the inside. *Paraphyses* 3–5 µm, hyaline, unbranched, septate, lacking mucilage. *Asci* 140–320 × 7–11.5 µm ($\bar{x}$= 234 × 9 µm, n=20), 8-spored, unitunicate, cylindrical, short-pedicellate, apically rounded, with a J+, wedge apical apparatus, 4–5 µm high, 1.5–2 µm broad. *Ascospores* 18.5–22.5 × 6–8 µm ($\bar{x}$= 20.5 × 6.5 µm, n=30), overlapping uniseriate, hyaline, bicellular, fusiform, ellipsoid-equilateral, with one median slightly constricted septum, with rounded ends, smooth-walled, with the hat-like sheathes on the ends, lacking germ slit and appendage. **Asexual morph**: undetermined.

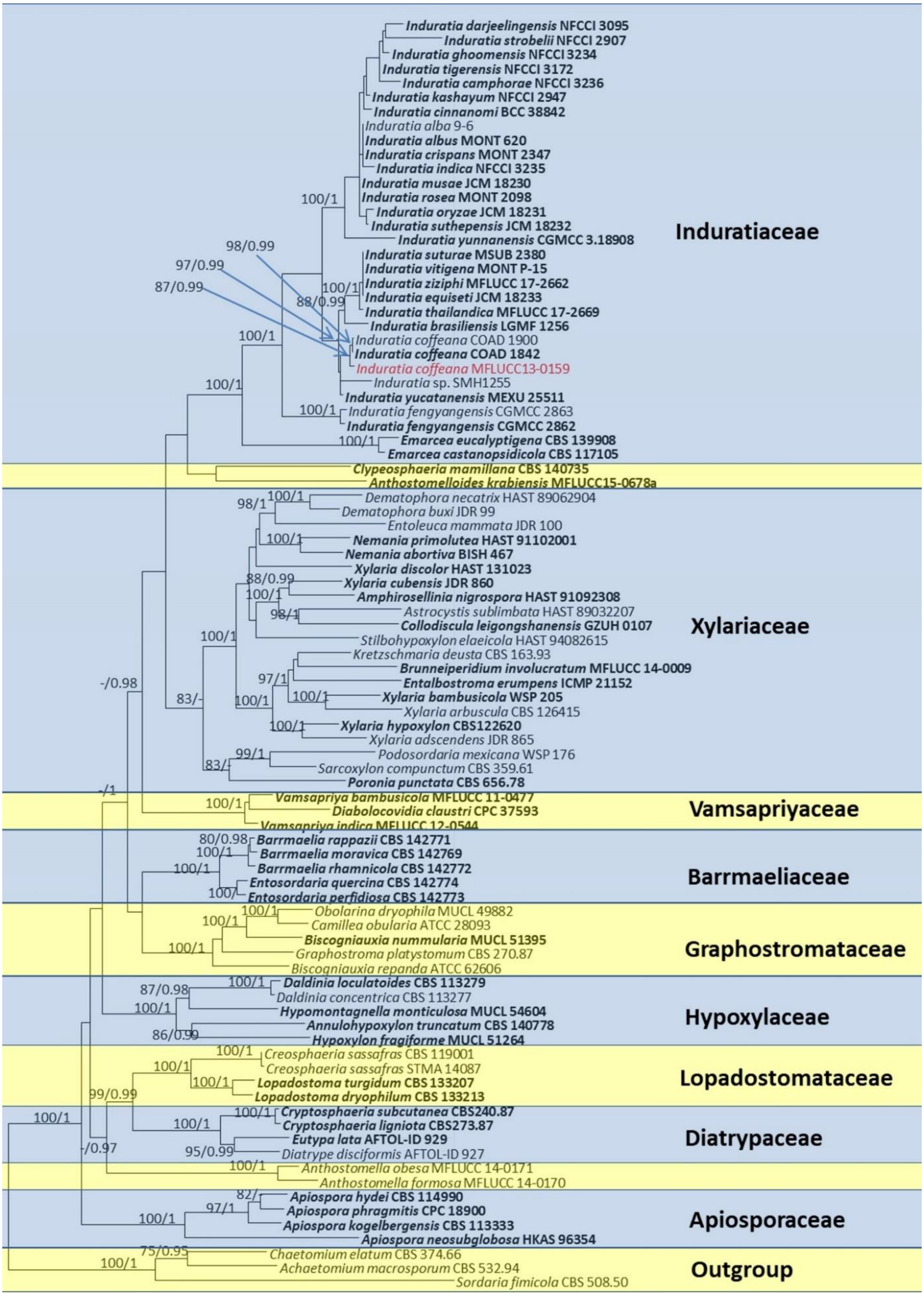

Figure 1. Phylogenetic tree based on a combined ITS, LSU, *rpb*2, and *β-tubulin* dataset. Numbers above each branch represent maximum likelihood bootstrap values (≥75 %) and Bayesian posterior probabilities (≥0.95). Hyphen (-) means a value lower than 75 % (BS) or 0.95 (PP). The tree was rooted to *Sordaria fimicola*, *Achaetomium macrosporum* and *Chaetomium elatum*. Type materials are marked in bold. The new strain is marked in red.

Culture characteristics: Colonies grew slowly on PDA, reaching 4.0 cm diam. after one week at 25 ºC, white, cottony, flat, low, and dense, with slightly wavy margin. Fructifications were not observed in culture. Hyaline hyphae (1.0–4.5 µm diam.), thin-walled, septate, branched, frequently intertwining forming rope-like strands 3.5–13.0 µm wide, and coils (11–18 µm diam.). No conidia and sporulation structures were observed under laboratory conditions (Fig. 3).

Material examined: Thailand, Chiang Rai city, Khun Kon Waterfall, on a deadwood piece of an unidentified plant, October, 2012, Q.R. Li, T17 (MFLU12-2129, GMB312; living cultures, MFLUCC13-0159, GMBC312).

Notes – Phylogenetic tree of multiple loci confirmed that the strain MFLUCC13-0159 clustered within a branch that contains strain COAD 1842, the type material of *I. coffeana* (Samarakoon et al. 2020). We identified our strain (MFLUCC13-0159) as the species of *I. coffeana* based on the morphological features and molecular data. The ITS and *rpb*2 comparisons of MFLUCC13-0159 and *I. coffeana* COAD 1842 show 99.4 % (485/488, 0 gaps) and 98.7 % (838/849, 1 gap) similarities, respectively. The dimensions of hyphae and coils of MFLUCC13-0159 are consistent with those of *I. coffeana* (Hongsanan et al. 2015). *Induratia coffeana* has 2-celled ascospores with equal divisions, which differs from *I. ziziphi*, *I. thailandica* and *I. apiospora* (Samuels et al. 1987, Samarakoon et al. 2020).

Discussion

The genus *Muscodor* (current name: *Induratia*) was described based on morphological characteristics, LSU and ITS sequences of *M. albus* (current name: *Induratia albus*). In subsequent studies, 22 species that produce only mycelium have been identified and reported with ITS sequence data (Worapong et al. 2001, 2002, Daisy et al. 2002a, b, Miller and Huhndorf 2005, Zhang et al. 2006, 2010, Mitchell et al. 2008, González et al. 2009, Suwannarach et al. 2010, 2013, Kudalkar et al. 2012, Meshram et al. 2013, 2014, 2017, Hongsanan et al. 2015, Saxena et al. 2015, 2017, Chen et al. 2019, Pena et al. 2019). Production of volatile compounds was used as a feature for species identification in several studies, such as Zhang et al. (2010), Meshram et al. (2013), Saxena et al. (2015). *Induratia thailandica* and *I. ziziphi* were introduced with sexual morphs, and *Induratia* was proposed as the accepted name over *Muscodor* based on molecular phylogenetic studies of ITS, LSU, *rpb*2 and *β-tubulin* sequence data (Samarakoon et al. 2020). In this study, we describe the sexual morph of *I. coffeana* from Thailand for the first time. *Induratia coffeana* was introduced as an endophytic fungus with a full description and illustration of the sterile mycelium by Hongsanan et al. (2015). The species is characterized by immersed ascomata with a central erumpent cone-shaped papilla and a papillate ostiole, unitunicate asci with a J+, wedge apical apparatus mounted Melzer's reagent and fusiform, 2-celled ascospore with one median constricted septum (Figure 2).

Induratia was found to produce mixtures of volatile compounds that are active against many plant-pathogenic fungi and bacteria (Strobel et al. 2001, Suwannarach et al. 2013). Meanwhile, the composition of volatile compounds has been used as one feature for species identification (Zhang et al. 2010, Kudorka et al. 2012, Suwannarach et al. 2013, Samarakoon et al. 2020). A large number of *Induratia* species were published with their VOCs, although there are some problems in using secondary metabolites as species identification features, such as imperfect compound database, inconsistent fermentation conditions, and difficulty in obtaining standard compounds (Suwannarach et al. 2010, 2013, Meshram et al. 2015, 2017, Samarakoon et al. 2020). In this paper, although we did not use VOCs profiling, the identification is supported by the morphology and molecular data.

Figure 2 *Induratia coffeana* (MFLU12-2129) A, B. Ascomata on wood, C. Longitudinal section of an ascoma, C. Paraphyses, E. Asci in Melzer's reagent with wedge, J+, apical apparatus, F–G. Culture on PDA H–K. Asci (stained in Melzer's reagent), L–O, Ascospores in water with a thin mucilaginous sheath on the ends (N, O stained in Melzer's reagent). Scale bars: A= 1000 µm, B=500 µm, C=100 µm, D, E, L–O =5 µm, F, G=1 cm, H–K=10 µm.

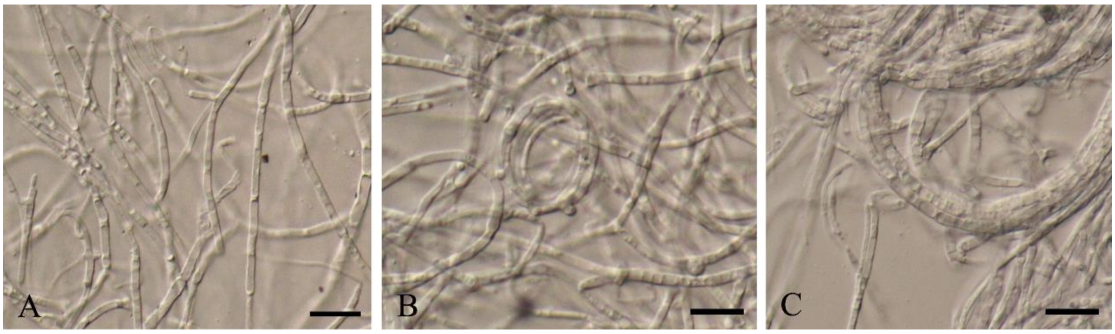

Figure 3 Morphological characters of *Induratia coffeana* (MFLUCC13-0159) on PDA medium. A. Sterile hyphae, B. Hyphal coil, C. Ropy mycelium. Bar. A–C=10 um.

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Conflict of interest
Authors declare no conflict of interest.

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