Plant and Fungal Systematics 70(2): 65–74, 2025
DOI: https://doi.org/10.35535/pfsyst-2025-0007

ISSN 2544-7459 (print)
ISSN 2657-5000 (online)

Yunnanomyces syagri sp. nov. (*Sympoventuriaceae*, *Venturiales*) on *Syagrus coronata*, an endemic Brazilian palm

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Article info
Received: 5 Jun. 2025
Revision received: 18 Aug. 2025
Accepted: 24 Aug. 2025
Published: 6 Nov. 2025

Associate Editor
Julia Pawłowska

Abstract. While surveying saprotrophic microfungi on *Syagrus coronata* (*Arecaceae*), an endemic palm in Brazil, an unusual fungus was identified occurring on the dead leaves of this plant. Morphologically, it showed the key traits of *Yunnanomyces*, including semi-macronematous conidiophores, integrated conidiogenous cells and globose to subglobose, ellipsoidal or irregularly shaped muriform conidia. Phylogenetic analyses using ITS, LSU, SSU, and *rpb2* locus sequences confirmed its placement as a unique lineage among described species of *Yunnanomyces*, leading us to introduce it as *Yunnanomyces syagri* sp. nov.

Key words: hyphomycetes, new species, phylogeny, tropical fungi

Introduction

Sympoventuriaceae is represented by *Sympoventuria* Crous & Seifert as the type genus, is characterized by its saprobic lifestyle, both teleomorph and anamorph are described, and is characterized by the presence of subglobose ascomata, asci 8-spored, bitunicate, subcylindrical. The anamorph has conidiophores reduced to conidiogenous cells, that are terminal or lateral, integrated, sympodial, and conidia solitary or occurring in branched or unbranched chains. Additionally, it includes sympodiella-like, fusicladium-like asexual representatives and *Veronaeopsis* species (Zhang et al. 2011). In recent years, several genera have been added to *Sympoventuriaceae*, bringing the total number to 22 and including a mixture of asexual, sexual, and sterile morphs.

Among them, *Sympoventuria* Crous & Seifert, *Veronaeopsis* Arzanlou & Crous, and fusicladium-like species, are characterized by their hyphomycetous asexual morphs exhibiting rhexolytic secession of conidia. Several investigations, including topics such as ecology, geographic distribution, and species diversity (Crous et al. 2014; Machouart et al. 2014; Pratibha & Prabhugaonkar 2016; González-Domínguez et al. 2017; Tibpromma et al. 2018; Zhang et al. 2019; Shen et al. 2020) have contributed to our understanding of *Sympoventuriaceae*, culminating in its re-evaluation by Wei et al. (2022).

The generic name *Yunnanomyces* was first introduced by Tibpromma et al. (2018) to accommodate *Y. pandanicola* Tibproma & K.D. Hyde, collected on dead leaves of *Pandanus amaryllifolius* Roxb. (*Pandanaceae*) in China. Later, Zhang et al. (2019) described *Y. phoenicis* S.N. Zhang & J.K. Liu, from dead rachides and leaves of *Phoenix paludosa* Roxb. (*Arecaceae*) in Thailand. Two additional new species represented only by sexual morph, *Y. sexualis* Z.Y. Zhang, Heng Pan & Y.F. Han isolated from soil samples in China and *Y. mangrovei* S.N. Zhang, K.D. Hyde & Jian K. Liu, collected on submerged leaves and rachis of *Phoenix paludosa* in Thailand, were proposed by Zhang et al. (2024b) and Zhang et al. (2024a), respectively. In the same year, three novel asexual species were proposed, *Y. hagahagaensis* Crous from leaf spots of *Sideroxylon inerme* L. (*Sapotaceae*) in South Africa, *Y. panamaensis* Crous from leaf litter in Panama (Crous et al. 2024), and *Y. muriformis* Y.R. Sun, N.G. Liu & K.D. Hyde collected on a decaying branch of *Dracaena trifasciata* (Prain) Mabb. (*Ruscaceae*) in Thailand (Liu et al. 2024).

The asexual morphs of *Yunnanomyces* are characterized by mononematous, fasciculate, branched or

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unbranched and hyaline to subhyaline conidiophores. Conidiogenous cells are holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, and hyaline to subhyaline. Conidia are acrogenous, globose to broadly oval, flattened, one-cell thick, muriform and yellow-brown to brown (Tibpromma et al. 2018). The sexual morphs show scattered to gregarious, almost superficial ascomata, subglobose to globose, ellipsoidal, orange-brown and dark brown to black. Asci are 8-spored, bitunicate, cylindric-clavate, straight or curved, sessile or slightly truncate, apically rounded with an ocular chamber. Ascospores are biseriate, fusoid-ellipsoidal, subhyaline to hyaline, 1-septate, constricted at the septum or not, smooth-walled, guttulate and surrounded or not by a mucilaginous sheath (Zhang et al. 2024a, b).

Several studies have investigated microfungi on *Syagrus coronata* (Mart.) Becc. (*Arecaceae*) in Brazil, revealing a promising potential for fungal diversity (Souza et al. 2008; Vitória et al. 2020; da Silva & Vitória 2024). This palm tree, commonly referred to as "licuri" or "licurizeiro", is a species native to northeastern Brazil and commonly found in semiarid regions, where it plays an important ecological role within the Caatinga ecosystems. Apart from its ecological significance, it also holds economic importance as the local communities use it for crafting various products (Andrade et al. 2015; de Lima et al. 2020). During a survey of microfungi occurring on this palm tree an intriguing fungus was collected on dead leaves and exhibit morphological characteristics related to the asexual morphs of *Yunnanomyces*. The fungus was further isolated and based on integrating its morphology and multi-locus phylogeny, we introduce a new species to accommodate it.

Materials and methods

Sampling site and morphological identification

Field work around the campus of Universidade Estadual de Feira de Santana (Bahia, Brazil) to collect dead leaf samples of *S. coronata* was carried out in July 2023. Samples were prepared following the method outlined by Castañeda-Ruiz et al. (2016) and observed daily for 21 days under a Leica S8APO stereomicroscope (Leica, Germany) to verify fungal development. Isolation was conducted by transferring conidia to Petri dishes containing CMCA media (30 g of Cornmeal extract, 30 g of Carrot extract, 13 g of agar per H_2O) and incubated at room temperature (approximately 25°C). Microscope slides with fungal reproductive structures were prepared using either polyvinyl alcohol or lactophenol (Waller et al. 2002). The reproductive structures were measured at 1000 × using an Olympus BX-51 light microscope equipped with differential interference contrast (DIC), an Olympus DP25 camera, and cellSens Imaging Software (Olympus Corporation, Tokyo, Japan). The *Yunnanomyces* strain is deposited in the Coleção de Culturas e Microrganismos da Bahia (CCMB) of the State University of Feira de Santana, Bahia, Brazil and Herbarium exsiccates are deposited in the Herbário (HUEFS) of the State University of Feira de Santana, Bahia, Brazil.

DNA extraction, PCR amplification and sequencing

Colonies were cultured on CMCA medium for up to 30 days at ±25°C in a natural light-dark cycle and used for DNA extraction. Mycelial were removed and transferred to an extraction tube. Genomic DNA was extracted using the DNeasy® Plant Mini Kit (Qiagen), according to the manufacturer's instructions. The primers ITS4/ITS5 (White et al. 1990), LR0R/LR5 (Vilgalys & Hester 1990; Vilgalys & Sun 1994), NS1/NS4 (White et al. 1990) and fRPB2-5f/fRPB2-7cR (Liu et al. 1999), were used to amplify the first and second internal transcribed spacer regions along with the intervening 5.8S ncDNA (ITS), the nuclear ribosomal large subunit (LSU) of rDNA, nuclear ribosomal small subunit (SSU) of rDNA, and a fragment of the RNA polymerase second largest subunit (*rpb2*), respectively. Amplification reactions were performed according to Barreto et al. (2023). For *rpb2*, the amplification cycles were used as described by Yilmaz et al. (2021). PCR products were purified with polyethylene glycol 20% (PEG) (Paithankar & Prasad 1991) and sequenced with the same set of primers at the Fundação Oswaldo Cruz (Fiocruz), Bahia, Brazil.

Phylogenetic analyses

DNA consensus sequences were assembled using BioEdit v. 5.0.9 (Hall 1999) and compared with NCBI GenBank (see https://blast.ncbi.nlm.hih.gov) data using the BLASTn tool. Following Tibpromma et al. (2018) and Zhang et al. (2019), we constructed a combined dataset (ITS-LSU-SSU-*rpb2*) with sequences of species belonging to *Sympoventuriaceae*, *Venturiales*. Each matrix was individually aligned using default parameters on MAFFT software (https://mafft.dbrc.jp/alignment/server/; Katoh & Standley 2013) and concatenated. The Maximum Likelihood analysis (ML) was performed via IQ-TREE (v. 1.6.12, https://www.iqtree.org/; Nguyen et al. 2015). The analysis involved 100 ML searches, starting from one randomized stepwise addition parsimony tree. Branch support was calculated using the Ultrafast bootstrap method (Hoang et al. 2018) with 1,000 replications. To determine the best-fit evolutionary model and best partition strategy for the dataset, ModelFinder (Kalyaanamoorthy et al. 2017) was employed within the IQ-TREE (v. 1.6.12, https://www.iqtree.org/ModelFinder/), based on the Akaike information criterion (AICc). Bayesian inference (BI) analysis was conducted using MrBayes (v. 3.2.7a) in the CIPRES Science Gateway (http://www.phylo.org/; Miller et al. 2010), employing a Markov Chain Monte Carlo (MCMC) algorithm. The models and partitions were the same as those used in the ML analysis. Four independent Metropolis-coupled MCMC chains were run twice, with 10 million generations, and trees were saved every 1,000th generation. A burn-in of 25% was set for the initially sampled trees, and the remaining trees were used to reconstruct a 50% majority-rule consensus tree and calculate Bayesian posterior probabilities (BPP) of the clades. The phylogenetic tree was visualized via FigTree (v. 1.4.4, http//tree.bio.ed.ac.uk/; Rambaut 2012) and edited using Inkscape (v. 1.1.1, www.inkscape.org).

The bootstrap support (BS ≥ 70%) and Bayesian posterior probability (BPP ≥ 0.95) values were plotted at the nodes. The newly generated sequences were deposited at GenBank, and others retrieved from GenBank are presented in Table 1. The final alignment was deposited in Figshare (https://figshare.com/; https://doi.org/10.6084/m9.figshare.26844292).

Table 1. GenBank accession numbers of taxa used in the phylogenetic analysis. Newly generated sequences and strain are in bold.

Taxa	Source	GenBank accession number				References
		ITS	LSU	SSU	*rpb2*	
Bellamyces quercus	CBS 46217 T	MK810901	MK810788	–	MK887796	Shen et al. (2020)
Clavatispora thailandica	MFLUCC 100107	MH065721	KF770458	MH062967	–	Boonme et al. (2014)
Echinocatena arthrinioides	CBS 144202	MH107890	MH107937	–	–	Crous et al. (2018a)
Fuscohilum rhodense	CBS 121641 T	MK810909	MK810796	–	MK887802	Shen et al. (2020)
Fuscohilum sicilianum	CBS 105.85 T	MK810910	MK810797	–	MN091924	Shen et al. (2020)
Guizhoumyces acicularis	GUCC 18195 T	MZ503724	MZ503757	MZ503650	MZ546866	Wei et al. (2022)
Guizhoumyces acicularis	GUCC 18152	MZ503723	MZ503756	MZ503649	MZ546865	Wei et al. (2022)
Helicopsis olivacea	CBS 728.83	MH861681	MH873393	AY856925	–	Vu et al. (2019)
Matsushimaea fasciculata	CBS 167.97 T	LT962397	LT962402	–	–	Unpublished
Matsushimaea fasciculata	GUCC 18239	MZ503725	MZ503758	MZ503651	MZ546867	Wei et al. (2022)
Matsushimaea monilioides	CBS 143867 T	LT883468	LT883469	–	–	Crous et al. (2018b)
Melnikomyces longisporus	HUGP 18226 T	MT731290	MT731291	MT731289	–	Wei et al. (2020)
Melnikomyces thailandicus	CBS 145767 T	MN794374	MN794351	–	–	Hernández-Restrepo et al. (2020)
Melnikomyces vietnamensis	CBS 136209 T	KJ869156	KJ869213	–	–	Crous et al. (2014)
Mycosisymbrium cirrhosum	GUFCC 18012	KR259883	KR259884	KR259885	KR349124	Pratibha & Prabhugaonkar (2016)
Mycosisymbrium cirrhosum	GUCC 1837	MZ503722	MZ503755	MZ503648	MZ546864	Wei et al. (2022)
Neocoleroa cameroonensis	CBS 129041 T	MK810902	MK810789	–	MK887797	Shen et al. (2020)
Neocoleroa metrosideri	ICMP 21139 T	KU131678	KU131677	–	–	Johnston & Park (2016)
Neofusicladium eucalypti	CBS 128216 T	MK810903	MK810790	–	MK887798	Shen et al. (2020)
Neofusicladium eucalypticola	CBS 141301 T	MK810904	MK810791	–	MK887799	Shen et al. (2020)
Neofusicladium eucalypticola	CBS 143427	MK810905	MK810792	–	–	Shen et al. (2020)
Neofusicladium regnans	CBS 143411 T	MG386066	MG386119	–	–	Shen et al. (2020)
Neofusicladium regnans	CBS 144605	MK442628	MK442563	–	–	Crous et al. (2019)
Parafusicladium amoenum	CBS 254.95 T	MK810906	MK810793	–	–	Shen et al. (2020)
Parafusicladium intermedium	CBS 110746 T	MK810907	MK810794	–	MK887800	Shen et al. (2020)
Parafusicladium paraamoenum	CBS 141322 T	MK810908	MK810795	–	MK887801	Shen et al. (2020)
Pinaceicola cordae	CBS 126959 T	MK810911	MK810798	–	–	Shen et al. (2020)
Pinaceicola cordae	CBS 675.82	MK810912	MK810799	–	–	Shen et al. (2020)
Pinaceicola cordae	CBS 143494	MK810913	MK810800	–	–	Shen et al. (2020)
Pinaceicola pini	CBS 463.82 T	MK810915	MK810802	–	MK887804	Shen et al. (2020)
Pinaceicola pini	CBS 462.82	MK810914	MK810801	–	MK887803	Shen et al. (2020)
Pseudosigmoidea excentrica	CBS 469.95 T	HQ667543	KF282669	NG_065605	–	Samerpitak et al. (2014)
Pseudosigmoidea ibarakiensis	NBRC 107891 T	LC146758	LC146759	NG_078726	–	Unpublished
Scolecobasidium anellii	CBS 284.64 T	FR832477	KF156138	NG_062993	KF282684	Martin-Sanchez et al. (2012)
Scolecobasidium anomalum	CBS 131816 T	HE575201	KF156137	NG_062986	HE575205	Samerpitak et al. (2015)
Scolecobasidium blechni	CBS 146055 T	MN562134	MN567641	–	–	Martin-Sanchez et al. (2012)
Scolecobasidium constrictum	CBS 211.53 T	HQ667519	KF156148	NG_062994	KF282686	Machouart et al. (2014)
Scolecobasidium crassihumicola	CBS 120700	KJ867429	KJ867430	–	–	Samerpitak et al. (2015)
Scolecobasidium gamsii	CBS 239.78 T	KF156019	KF156150	NG_062991	–	Samerpitak et al. (2015)
Scolecobasidium icarus	CBS 536.69 T	HQ667524	KF156132	NG_062989	KF282700	Samerpitak et al. (2015)
Sterila eucalypti	CBS 144019 T	MK810918	MK810805	–	MK887807	Shen et al. (2020)
Sterila eucalypti	CPC 14942	MK810916	MK810803	–	MK887805	Shen et al. (2020)
Sterila eucalypti	CPC 14943	MK810917	MK810804	–	MK887806	Shen et al. (2020)
Sympoventuria capensis	CBS 120136 T	MK810921	MK810808	NG_061163	MK887810	Shen et al. (2020)
Sympoventuria capensis	CPC 12839	MK810922	MK810809	–	MK887811	Shen et al. (2020)
Sympoventuria capensis	CPC 12840	MK810923	MK810810	–	MK887812	Shen et al. (2020)
Sympoventuria melaleucae	CBS 143407 T	MG386059	MG386112	–	–	GenBank
Troposporella fumosa	CBS 351.94	MK810924	MH874121	–	–	Shen et al. (2020)
Troposporella monilipes	MUCL 19867	DQ351723	AY856871	AY856920	–	Tsui & Berbee (2010)
Tyrannosorus lichenicola	CBS 144018 T	MK810953	MK810838	–	MK887840	Shen et al. (2020)

Table 1. Continued.

Taxa	Source	GenBank accession number				References
		ITS	LSU	SSU	*rpb2*	
Veronaeopsis simplex	CBS 588.66 T	EU041820	EU041877	NG_061164	MN091925	Arzanlou et al. (2007)
Verruconis gallopava	CBS 437.64 T	HQ667553	KF156112	NG_062995	KF282689	Machouart et al. (2014); Samerpitak et al. (2014, 2015)
Verruconis mangrovei	NFCCI-4390 T	MN782361	NG_073757	NG_070311	MN231836	Unpublished
Verruconis panacis	CBS 142802 T	MF536882	MF536880	–	–	Zhang et al. (2018)
Verruconis pseudotricladiata	YMF1.04915 T	MK244396	MK248270	–	–	Qiao et al. (2019)
Venturia saliciperda	CBS 480.61 T	MK811007	MK810891	–	MK887886	Shen et al. (2020)
Yunnanomyces hagahagaensis	CPC 47671T	PQ498953	PQ499002	–	PQ497730	Crous et al. (2024)
Yunnanomyces mangrovei	SNT62T	–	PP621124	PP639251	PP780209	Zhang et al. (2024a)
Yunnanomyces muriformis	GZAAS 24-0053 T	PP657299	PP657341	–	–	Liu et al. (2024)
Yunnanomyces panamaensis	CPC 46559	PQ498939	PQ498988	–	PQ497727	Crous et al. (2024)
Yunnanomyces pandanicola	MFLUCC 17-2260 T	MH388369	MH376743	MH388333	MH412736	Tibpromma et al. (2018)
Yunnanomyces phoenicis	MFLUCC 19-0254 T	–	MK976738	MK976740	MK986484	Zhang et al. (2019)
Yunnanomyces phoenicis	MFLUCC 19-0253	–	MK976737	MK976739	MK986483	Zhang et al. (2019)
Yunnanomyces sexualis	ZY22.033 T	OR680512	OR680579	–	OR842929	Zhang et al. (2024b)
Yunnanomyces sexualis	ZY22.034	OR680513	OR680580	–	OR842930	Zhang et al. (2024b)
Yunnanomyces syagri	**CCMB 739 T**	**PP718673**	**PP718674**	**PP718675**	**PP747050**	**This paper**

"T" indicate the type species

Results

Phylogenetic results

The combined alignment included 64 sequences of members of *Sympoventuriaceae*, two sequences of *Tyrannosorus lichenicola* Crous, M.Shen &Y. Zhang ter (CBS 144018) and *Venturia saliciperda* J.Nüesch (CBS 480.61) used as outgroups. It contains 3,247 characters including gaps (ITS: 485; LSU: 753; SSU: 1230; *rpb2*: 779), of which 1,757 are conserved, 1,130 variables and 946 parsimony-informative. The evolutionary models for each partition were GTR+I+G for LSU and *rpb2*, SYM+I+G for ITS, and SYM+G for SSU. The best-scoring maximum likelihood tree had a final optimization likelihood value of $-ln = -28{,}781.993$. For Bayesian inference, the average standard deviation of split frequencies was 0.001938 after 10 million generations. The ML and BI analyses issued trees with the same topology (Fig. 1). In the combined dataset (ITS-LSU-SSU-*rpb2*), our strain (CCMB 739) forms a fully supported (100/1) unique lineage sister to *Y. hagahaensis* (CPC 47671).

Taxonomy

Diagnosis: Differs from other species of *Yunnanomyces* in having semi-macronematous, mononematous and branched conidiophores, and globose to subglobose, ellipsoidal conidia.

Yunnanomyces syagri G.G. Barreto, L.M.S. Lima, R.F. Castañeda & Gusmão, sp. nov. (Fig. 2)

MycoBank MB 855574

Type: Brazil, Bahia, Feira de Santana, State University of Feira de Santana, 22°24′51.9″S, 47°31′02.8″W, on dead leaves of *Syagrus coronata* (Mart.) Becc. (*Arecaceae*), 3 Jul. 2023, L.M.S. Lima (HUEFS 276450 – holotype; ex-type living culture CCMB 739).

Asexual morph. Colonies on natural substrate effuse, black, punctiform, granular. Mycelium partly superficial, partly immersed, hyaline, smooth. Conidiophores semi-macronematous, mononematous, septate, torulose, smooth, branched, thin-walled, hyaline to subhyaline, 15–24 × 2.5–4 µm. Conidiogenous cells monoblastic, integrated, terminal, determinate, cylindrical to lageniform, smooth, hyaline to subhyaline, 5–7.5 × 1.3–2.5 µm. Conidia abundant, solitary, dry, globose to subglobose, ellipsoidal or irregularly shaped, muriform, pale brown to brown, smooth, darkened septa when mature, constricted at some septa, 15–33 × 13–17 µm (n = 50). Schizolytic conidial secession. Sexual morph: unknown.

Culture characteristics. Colonies on CMCA after 21 days at 25°C, slow growing, flat, with white aerial mycelium in the center and towards the margin, pale brown to brown; margin entire, reverse brown. Mycelium hyaline, septate, branched. Conidial production is abundant in culture.

Etymology. Named after the host genus, *Syagrus* Mart.

Distribution. Known only from the type locality.

Habitat and ecology. Apparently palmicolous, recorded only from dead leaves of *S. coronata*.

Notes. Morphologically, the conidia of *Y. syagri* are similar to those of *Y. pandanicola* in terms of color and dimensions (15–33 × 13–17 µm vs. 20–25 × 13–18 µm). However, they differ significantly in shape: the conidia of *Y. syagri* are globose to subglobose and ellipsoidal, whereas those in *Y. pandanicola* tend to be globose to broadly ellipsoidal. Moreover, *Y. syagri* exhibits semi-macronematous, mononematous and torulose branched conidiophores, while *Y. pandanicola* possesses mononematous, fasciculate and unbranched conidiophores. Another species,

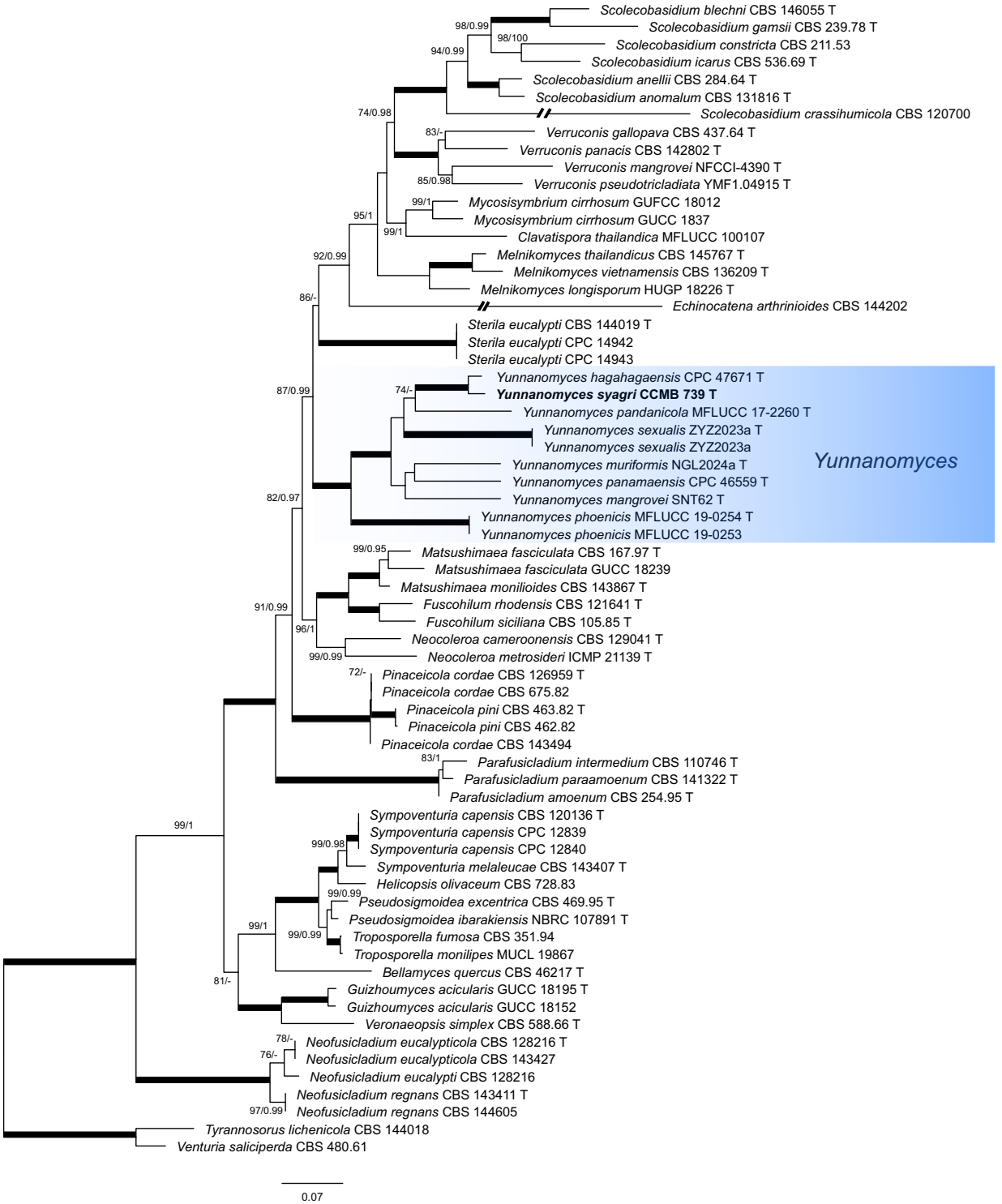

Figure 1. Maximum likelihood phylogenetic tree based on a combined ITS, LSU, SSU, and *rpb2* datasets of *Sympoventuriaceae* showing the placement of *Yunnanomyces syagri* within the family. Confidence values for MLBS ≥ 70% and BPP ≥0.95 are included near the nodes, with the "-" indicating a lack of statistical support. The scale bar represents the expected number of changes per site. Full statistical support (MLBS = 100% and BPP = 1.0) is indicated by thickened branches. The *Yunnanomyces syagri* CCMB 739 is in bold and the genus *Yunnanomyces* is highlighted in a blue color box. Ex-type strains are marked with a "T" after the culture number. The tree was rooted using sequences from *Tyrannosorus lichenicola* (CBS 144018) and *Venturia saliciperda* (CBS 480.61).

Y. phoenicis, has similar dimensions to those of *Y. syagri* (18–34 × 12–22 µm vs. 15–33 × 13–17 µm) (Table 2).

However, *Y. phoenicis* differs by the reduced conidiophores with darker, globose to broadly ellipsoidal conidia.

Based on phylogenetic data, *Y. hagahagaensis* appears to be the closest related species to *Y. syagri* and both formed a sister clade to *Y. pandanicola*, the type of *Yunnanomyces*. However, *Y. hagahagaensis* differs significantly from *Y. syagri* in morphology. It exhibitis features such as conidiogenous cells with sympodial development and subcylindrical conidia with truncated ends, which are 0–1-septate and arranged in branched chains. These characteristics do not align well with the generic concept of *Yunnanomyces*, making any detailed

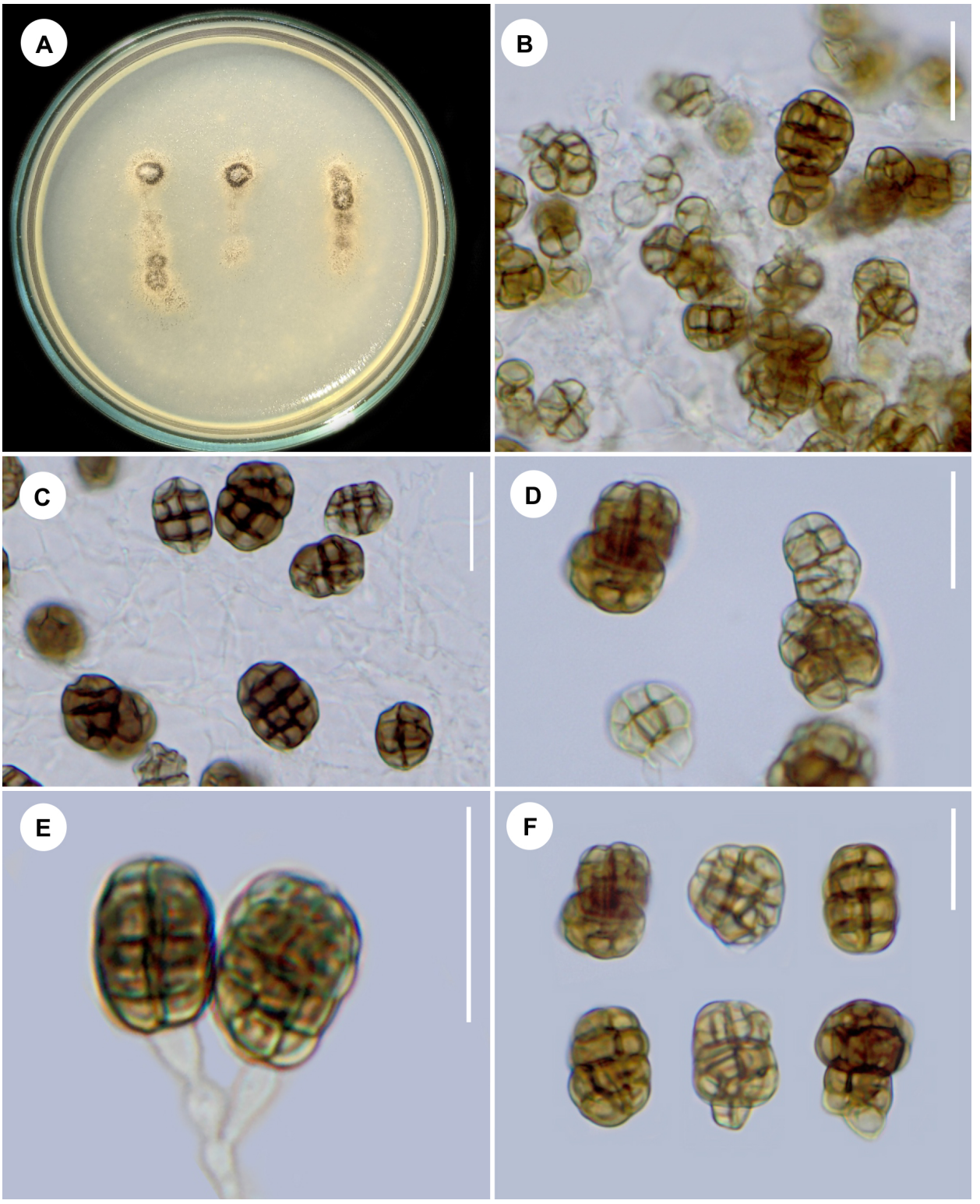

Figure 2. *Yunnanomyces syagri* (from holotype). A – colony on CMCA; B, C – hyphae with conidiogenous loci giving rise to conidia; D – young to mature conidia; E – conidiophores, conidiogenous cells with young conidia; F – conidia. Scales: B–F = 20 µm.

comparison unfeasible and pointing to contamination or data incongruence

Discussion

The genus *Yunnanomyces* is placed in *Sympoventuriaceae*, *Venturiales* (*Dothideomycetes*), a well-known group of fungi that comprises plant pathogens, saprobes and opportunistic species (Machouart et al. 2014; González-Domínguez et al. 2017; Shen et al. 2020; Wei et al. 2022). The genera included in *Sympoventuriaceae* are mainly known by their asexual morphs, many of which have septate or multiseptate conidia (Wei et al. 2022). Regarding taxa with multiseptate conidia, *Yunnanomyces* is the only genus that has muriform conidia, except for *Y. hagahagaensis* and *Y. panamaensis* (Crous et al. 2024). These two species were placed in *Yunnanomyces*, however the morphology of their conidiogenous cells with

Table 2. Synopsis of asexual morphs of *Yunnanomyces* species.

Species	Conidiophores (µm)	Conidiogenous cells (µm)	Conidia (µm)	References
Yunnanomyces hagahaensis	Micronematous to semi-macronematous, subcylindrical, erect, 3–40 × 1.5–3 µm	Polyblastic, sympodial, integrated, terminal, subcylindrical, pale brown, 3–25 × 1.5–2.5 µm	Subcylindrical, branched chains, 0–1-septate, pale brown, guttulate, (17–)20–27(–40) × 2.5–3 µm	Crous et al. (2024)
Yunnanomyces muriformis	Micronematous to semi-macronematous, mononematous, 1.5–3 µm wide	Monoblastic, integrated, terminal, subhyaline to pale brown	Subglobose to irregular ellipsoidal, muriform, verrucose, golden brown to golden dark brown, 11–19 × 7–11 µm	Liu et al. (2024)
Yunnanomyces panamaensis	Semi-macronematous, erect, unbranched, subcylindrical, 2–4-septate, 25–60 × 2.5–3 µm	Polyblastic, integrated, terminal, darker brown slightly roughened, 22–30 × 3 µm	Ellipsoid, 1-septate, brown, finely roughened, 5–6(–7) × 2–2.5 µm	Crous et al. (2024)
Yunnanomyces pandanicola	Macro, semi or micronematous, fasciculate, unbranched	2.5–5 × 1.5–5 µm	Globose to broadly oval, muriform, yellow-brown, 20–25 × 13–18 µm	Tibpromma et al. (2018)
Yunnanomyces phoenicis	Semi-macronematous	0.7–1.2 µm	Globose to broadly ellipsoidal, muriform, brown, 18–34 × 12–22 µm	Zhang et al. (2019)
Yunnanomyces syagri	Macro, semi or micronematous, branched, 15–24 × 2.5–4 µm	5–7.5 × 1.3–2.5 µm	Globose to subglobose, ellipsoidal, muriform, pale brown to brown, 15–33 × 13–17 µm	This study

sympodial development and subcylindrical conidia with truncated ends and darkened scars, suggests contamination or data mismatches and, further study or reexamination of their type materials are needed to investigate the placement of these species in *Yunnanomyces* or even a reanalysis of the type materials. The morphological characteristics of our strain matches well with the species described by Tibpromma et al. (2018) and Zhang et al. (2019). BLASTn searches in GenBank show that our strain has the closest matches of ITS sequence with *Yunnanomyces hagahagaensis* CBS 152291 (NR_199126.1) with identity of 94.78%, *Yunnanomyces sexualis* ZYZ-2023a (OR680512.1) with identity of 80.81% and *Fusicladium* sp. LSEM1156 (LC535820.1) with identity of 93.08%, whereas the LSU sequence matches *Y. pandanicola* MFLUCC 17-2260 (MH376743) with identity of 97.43% and *Y. phoenicis* MFLUCC 19-0253 (MK976737) with identity of 95%. Based on phylogenetic analyses, our strain clustered within the genus *Yunnanomyces*, forming a unique lineage among known species and closely related to *Y. pandanicola* and *Y. phoenicis* groups as a basal lineage within *Yunnanomyces* (ML-BS = 100/BP = 1), and it is easily differentiated in terms of phylogeny and morphology.

Yunnanomyces pandanicola was first collected in China (Tibpromma et al. 2018), whereas collections from Taiwan record it growing on *Ananas comosus* (L.) Merr. (*Bromeliaceae*) and on *Ficus ampelos* Burm.f. (*Moraceae*) (Facesoffungi 2020; Tennakoon et al. 2021). *Yunnanomyces mangrovei*, *Y. phoenicis* and now *Y. syagri* were collected on dead leaves of *Arecaceae* in Thailand and Brazil, respectively (Zhang et al. 2019; Zhang et al. 2024a). Despite being recorded occasionally outside the Asian continent, *Yunnanomyces* species are probably worldwide in distribution, occurring mostly on soil, dead leaves and rachides of monocotyledonous plants in China, Taiwan and Thailand (Tibpromma et al. 2018; Zhang et al. 2019; Tennakoon et al. 2021; Zhang et al. 2024a). *Yunnanomyces* was also recorded in South Africa on leaves of *Sideroxylon* and leaf litter in Panama (Crous et al. 2024), but their placement within the genus is probably the result of data mishandling or contamination. Here, we report the first occurrence of *Yunnanomyces* in Brazil on a palm host. This may imply a potential preference for *Arecaceae* hosts among *Yunnanomyces* species considering that *Y. mangrovei* and *Y. phoenicis* were also recorded on palms. However, further collections are needed to confirm a potentially wider distribution of the genus.

Acknowledgments

The authors thank the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brazil (CAPES, Finance Code 001) and the Programa de Pós-Graduação em Botânica – PPGBOT/UEFS. The authors extend their gratitude to Dr. Konstanze Bensch (Westerdijk Fungal Biodiversity Institute) for the nomenclatural review.

Author Contributions

L.F.P.G, undertook conceptualization; designed the study; L.M.S.L. collected sample; G.G.B. extracted DNA and PCR; conducted the experiments and phylogenetic analyses. L.F.P.G., G.G.B., J.D.P.B and L.M.S.L. prepared original draft; L.F.P.G, D.H.C.R and R.F.C.R., reviewed and edited the manuscript. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare no conflict of interest.

Declaration of Funding

This research was funded in part by the National Council for Scientific and Technological Development (CNPq, Proc. 312984/2018-9; Proc. 4072223/2023-1) and the Bahia State Research Support Foundation (FAPESB, APP 0023/2023).

Data Availability Statement

Sequence data were submitted to GenBank under the accession numbers provided in Table 1. Alignments are available

in Figshare. Herbarium specimen and strain are deposited in Herbário (HUEFS) of the State University of Feira de Santana, Bahia, Brazil and Coleção de Culturas e Microrganismos da Bahia (CCMB) of the State University of Feira de Santana, Bahia, Brazil.

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