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A new species and a new record in the *Agaricales* from Sri Lanka

Aseni N Ediriweera[1,2,3,a], Pietro Voto[4,b], Samantha C Karunarathna[5,c], Jaturong Kumla[6,7,d], Vinodhini Thiyagaraja[8,e], Madumali K Wijesooriya[9,f], Kasun S Wadduwage[9,g], Wenhua Lu[5,h], Steven L Stephenson[10,i], Xu Jianchu[1,3,j,*]

[1]Centre for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China
[2]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[3]CIFOR-ICRAF China Program, World Agroforestry Centre, 132 Lanhei Road, Kunming
[4]Via Garibaldi 173, I-45010 Villadose (RO), Italy
[5]Center for Yunnan Plateau Biological Resources Protection and Utilization | College of Biological Resource and Food Engineering | Qujing Normal University | Qujing, Yunnan 655011 | P.R. China
[6]Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand
[7]Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
[8]Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand
[9]Department of Biosystems Technology, Faculty of Technology, University of Ruhuna, Matara 81000, Sri Lanka
[10]Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701

[a]aseniediriweera@gmail.com; https://orcid.org/0009-0004-5876-7615
[b]pietrovoto@libero.it; https://orcid.org/0000-0003-1922-1324
[c]samanthakarunarathna@gmail.com
[d]jaturong_yai@hotmail.com; http://orcid.org/0000-0002-3673-6541
[e]vino.thiyagaraja@gmail.com
[f]kanchanawijesooriya0601@gmail.com; http://orcid.org/0009-0005-7696-0141
[g]samirawadduwage@gmail.com; https://orcid.org/0009-0005-0798-8060
[h]luwh9742@126.com
[i]slsteph@uark.edu; http://orcid.org/0000-0002-9207-8037
[j]jxu@mail.kib.ac.cn; http://orcid.org/0000-0002-2485-2254

*Corresponding author: jxu@mail.kib.ac.cn

Key words:
Agaricales
Internal Transcribed Spacer
Macrofungi
Phylogeny
Taxonomy
Tropics
Wet-zone

Abstract: Sri Lanka is one of the global biodiversity hotspots, and the island is characterized by rich and unique assemblage of fungi. However, the fungi of the country are poorly known, with less than 10% of the taxa having been described thus far. Studies of macrofungi are comparatively more numerous than those of microfungi due to relative importance. Nevertheless, most studies have been based only on morphological characterization of taxa. Several morpho-molecular based studies have been recently carried out, and these have yielded novel taxa and new records of macrofungi from Sri Lanka. The study reported herein focused on the macrofungi (mushrooms) in the wet zone of Sri Lanka. All fresh samples were collected from three districts (Galle, Kalutara and Matara) that represent two provinces (Southern, and Western). The samples were investigated based on both morphological and molecular analyses. The new species, *Candolleomyces ruhunensis*, is described from the family *Psathyrellaceae* and *Crepidotus striatus*, new to Sri Lanka, from *Crepidotaceae*. Sequence data from the ITS gene region were used to construct maximum likelihood (ML) and Bayesian inference analyses. The morphology of each taxon is illustrated with pictures, drawings and full descriptions.

INTRODUCTION

Agaricales is one of the best known groups of fungi to science; its taxa have been recorded as saprotrophs, symbionts and parasites. They occur in diverse habitats from the arctic to the tropics (Laala *et al*. 2018; Luna-Fontalvo *et al*. 2021). *Agaricales* are characterized by a fleshy fruiting body with an umbrella and a laminar, porous, or venous hymenophore. The order encompasses 44 families that accommodate more than 16,000 taxa (Wijayawardene *et al.* 2022; Luna-Fontalvo *et al.*2021). *Agaricales* also include numerous macro-delicacies rich in carbohydrates, proteins and vitamins B and D which are good for human health. Several members of the genera *Pleurotus*, *Agaricus*, *Macrocybe*, and *Termitomyces* have both medicinal and edible properties (Hobbs 1996; Naeem *et al.* 2020; Kumar *et al*. 2021). On the other hand, several taxa such as *Amanita phalloides* and *Mycena polygramma* contain mushroom toxins that are highly detrimental to humans (Yagan *et al*. 2020; Luna-Fontalvo *et al*. 2021).

Several studies (Berkley & Broom 1870, 1871, 1873; Petch 1908a, b, 1910, 1913, 1915a, b, 1916a, b, c, 1917a, b, 1919, 1922, 1923, 1924a, b, c, d, 1925; Petch & Bisby 1950; Cesati 1879; Höehnel 1908, 1909, 1914) have been reported on the *Agaricales* of Sri Lanka, and these include 513 taxa from 50 genera. Species of *Agaricus*, *Entoloma*, *Hygrophorus*, *Inocybe*, *Lepiota*, *Marasmius*, and *Pleurotus* have been identified most frequently, based only on morphology (Karunarathna *et al*. 2012a, b). Most of those historical collections are deposited in the Royal Botanical Gardens, Peradeniya, Sri Lanka, and the Herbarium at Kew. Nevertheless, no reliable, detailed statistics have yet been generated on the assemblage of *Basidiomycetes* from Sri Lanka (Karunarathna *et al*. 2012).

The present paper describes a novel taxa, *Candolleomyces ruhunensis*, of *Candolleomyces*, and a new record of *Crepidotus striatus* reported from the wet zone of Sri Lanka. These taxa have been investigated based on evidence from morphology and phylogenetic analyses. Both maximum likelihood (ML) and Bayesian analysis were carried out using the ITS and LSU gene regions to determine their phylogenetic placements. Macro and micro-morphological characteristics are described with the aid of images and detailed descriptions including ecology and distribution.

MATERIALS AND METHODS

Collection sites

Specimens of mushrooms were collected from different areas of the country's wet zone, which include three districts (Matara, Galle and Kalutara) of two provinces (Southern and Western). The sampling areas are located in the southwestern portion of Sri Lanka, which receives a mean annual rainfall of over 2,500 mm, with a strong contribution of the south-west monsoons. The mean annual temperature ranges from 28–33°C while the relative humidity ranges from 85–91% (Department of Meteorology of Sri Lanka 2022). The specimens were collected from home gardens, agricultural lands, bare lands, roadsides, and public places.

Sample Collection

Fresh basidiomata were collected from 2020 and 2021. Specimens were photographed in the natural habitat and after being separating from the habitat, using a Can-on XD5 digital camera. Collected basidiomata were cleaned as much as possible to remove soil or attached debris and wrapped separately in aluminum foil to prevent spore contamination, damage, and mixing up of basidiomata of different taxa. Specimens were taken to the laboratory for morphological studies.

Morphological Studies

Macro-morphological characteristics such as size, shape, and structure of the pileus and stipe were recorded. The colour terminology used for macro-morphological identification follows Kornerup & Wanscher (1978). The specimens were dried with a portable dryer at 40°C for 24–48 hours and sealed in zip-lock plastic bags containing silica gel as a desiccant to control humidity. All the herbarium specimens were deposited in the Herbarium of Kunming Institute of Botany (HKAS), Kunming, China.

Micro-morphological observations of dry specimens were carried out with free hand sections. Slides were prepared with distilled water. In addition, 3–5% KOH, Congo red, and 3–5% NH4(aq) were used to check some

morphological characters where necessary. Morphological characters were observed and photographed using a compound light microscope (Nikon Model Eclipse Ci–s) attached to a Canon 550D digital camera. The measurements were taken with the Tarosoft (R) Image Frame Work pro-gram, while images used for figures were processed with Adobe Photoshop CS3 (Version 15.0.0, Adobe®, San Jose, CA, USA) extended version 10.0 (Adobe Systems, San Jose, CA, USA).

DNA Extraction, PCR Amplification, and Sequencing

The genomic DNA of each specimen was extracted from dried samples using a Bio-spin Fungus Genomic DNA Extraction Kit (Bioer Technology Co., Ltd., Hangzhou, P.R. China). The nuclear ribosomal internal transcribed spacer (nrITS) and Large subunit (nrLSU) regions were amplified using the primer pair ITS5/ITS4 and LROR/LR5 (White *et al.* 1990; Vilgalys & Hester 1990). The amplification process was carried out for total volume of 25 µL comprising 1.0 µL of template DNA, 9.5 µL of double-distilled water, 1.0 µL of each primer, and 12.5 µL of 2× Power Taq PCR Master Mix. The latter consisted of a premixed, ready to use solution that included 0.1 Units/ µL Taq DNA polymerase, 500 µm of dNTP mixture each (dATP, dCTP, dGTP, and dTTP), 20 mM of Tris–HCl pH 8.3, 100 mM KCl, 3 mM of MgCl2, stabilizer, and enhancer. During the polymerase chain reaction (PCR), each sample underwent 35 cycles according to the following settings: denaturation (95°C, 30 s), annealing (52°C, 30 s), extension (72°C, 1 min), and final extension (72°C, 10 min). Amplified products were con-firmed on a 1% agarose gel electrophoresis stained with ethidium bromide. The amplified PCR fragments were sent to a commercial sequencing provider (Beijing Bai Mai Hui Kang Biological Engineering Technology Co., P.R. China). The nucleotide sequence data were deposited in GenBank.

Sequence Alignment and Phylogenetic Analyses

The Basic Local Alignment Search Tool (BLAST) of the National Center for Biotechnology Information (NCBI) was used for the preliminary identification of the sequences data. Sequences were assembled using Seqman (Swindell & Plasterer 1997). The closely related sequences for each taxon were obtained from Genbank with consideration of recent literature. Sequences were automatically generated with MAFFT v. 7 (Katoh & Standley 2013) and terminal ends of sequences and ambiguous regions were trimmed manually using BioEdit v. 7.0.5.2 (Hall 1999) and excluded from the dataset. The phylogenetic web tool "ALTER" was used to convert sequence alignment from FASTA to PHYLIP for RAxML analysis and from FASTA to NEXUS format for Bayesian analysis (Glez-Peña *et al*. 2010). Maximum likelihood (ML) analysis was performed using RAxML-HPC2 on XSEDE (8.2.10) in CIPRES Science Gateway V. 3.3 with 1000 separate runs using the GTR+I+G model of evolution iterations. The optimal nucleotide substitution models used for Bayesian analysis were independently selected for each locus under the Akaike information criterion (AIC). Bayesian analysis was conducted with MrBayes v. 3.1.2 (GTR+I+G model) to evaluate posterior probabilities (PP) by Markov chain Monte Carlo sampling (BMCMC). Sequences for each strain were aligned using Clustal X (Thompson *et al*. 1997). Six simultaneous Markov chains were run for 2,000,000 generations, and trees were sampled every 1000 generations, resulting in 2000 trees. The first 25% of the trees, representing the burning phase of the analyses, were discarded, while the remaining 75% of the trees were used to calculate PP in the majority rule consensus tree. The ITS sequence data were analyzed using ML and Bayesian analyses. Trees were displayed in FigTree v1.4.0 (Rambaut 2012) and then copied to Microsoft PowerPoint 2013 and converted to jpeg files using Adobe Photoshop CS3 Extended 10.0 (Adobe Systems, San Jose, CA, USA).

RESULTS

Trees of similar topologies were constructed in MLand Bayesian analyses and the ML tree was taken to present the results. The results of our phylogenetic analyses show that *C. ruhunensis* is a new species, in accordance with its morphological characteristics, supported with high bootstrap values in combined phylogram of ITS and LSU: 94% in ML and 0.96 in PP (Figure 3).

TAXONOMY

Candolleomyces ruhunensis A.N. Ediriweera, P. Voto, S.C. Karunarathna & J. Kumla sp. nov. (Figure 1-2)

Figure 1. Candolleomyces *ruhunensis* (HKAS123158, holotype): (a-c) mature basidiomes; scale bars = 0.5 cm

Typus: Sri Lanka, Southern province, Matara, premises of the University of Ruhuna; saprotrophic on soil with decaying leaf litter and woody debris in a wetland in tropical climate; 2nd January 2021, A.N. Ediriweera, Herb. HKAS123158; GenBank ITS accession number: ON685315; Index Fungorum IF 555865.

Etymology. The specific epithet derives from "Ruhuna", where the specimen was first detected from premises of the University of Ruhuna, Sri Lanka.

Diagnosis: *Candolleomyces ruhunensis* is characterized by 2–3.5 cm wide pileus, fugacious veil, lamellae not darkening with age, elliptic to oval, spores of (6.12) 6.65–8.30 (8.51) × (4.21) 4.43–5.94 (6.48) µm, basidia of 12–22 × 5–10 µm, utriform to subcylindraceous or sublageniform cheilocystidia of 23–28.2 × 7.1–8 µm, absence of pleurocystidia.

Macroscopic characters

Basidiomata small.

Pileus (primordia not observed) 20 – 35 mm across, paraboloid to convex when young, broadly convex to campanulate at maturity, margin thin, slightly eroded or slightly plicate and striate; surface bald, smooth, deep orange (6A8) to corn yellow (4A5) or light brown (6D8), brownish grey (6F8) at centre, chocolate brown (6F4) when dried; veil of fugacious, dispersed, white (1A1) to yellowish white (1A3) flocci up to center and around the margin, also scarcely appendiculate.

Lamellae crowded, with three tiers of lamellulae (2, 4 and 5 mm), adnate, thin, 2 mm height, yellowish white (2A2), dull yellow (3B3), not darkening with age; edge equal.

Stipe 40 – 55 × 3 mm, slender, cylindrical, equal, fragile, hollow, white (1A1) or pale yellow (1A3), slightly squamulose towards the base; annulus absent.

Context very thin (2 mm or less), pale yellow (1A4) to light yellow (4A5). Odour indistinct, taste not tested.

Microscopic characters

Basidiospores (n = 40) (6.12) 6.65 – 8.30 (8.51) × (4.21) 4.43 – 5.94 (6.48) µm, on average 7.39 × 5.04 µm, Q = (1.31) 1.37 – 1.59 (1.64), on average 1.46, in face view elliptic to oval, base rounded, in side view adaxially flattened to indistinctly subphaseoliform, thick-walled, smooth, hyaline to sub-hyaline in water and in NH_4, inamyloid, prominent with hyaline to sub-hyaline oil drops; germ pore absents or an indistinct callus.

Basidia 12.0 – 22.0 × 5.0 – 10.0 µm, clavate, 4-spored, hyaline.

Pleurocystidia absent.

Cheilocystidia 23.0 – 28.2 × 7.1 – 8.0 µm, utriform to sometimes subcylindraceous or sublageniform, apex obtuse to broadly rounded, hyaline, abundant; paracystidia small to sometimes voluminous, numerous.

Pileipellis composed of a 2–3 layers paraderm of subglobose, weakly pigmented cells 30.3 – 41.0 µm broad.

Clamp connections present.

Ecology and habitat: saprotrophic, gregarious, growing on soil mixed with decaying coconut leaf litter and woody debris in wet humus soil in a wet soil in tropical climate.

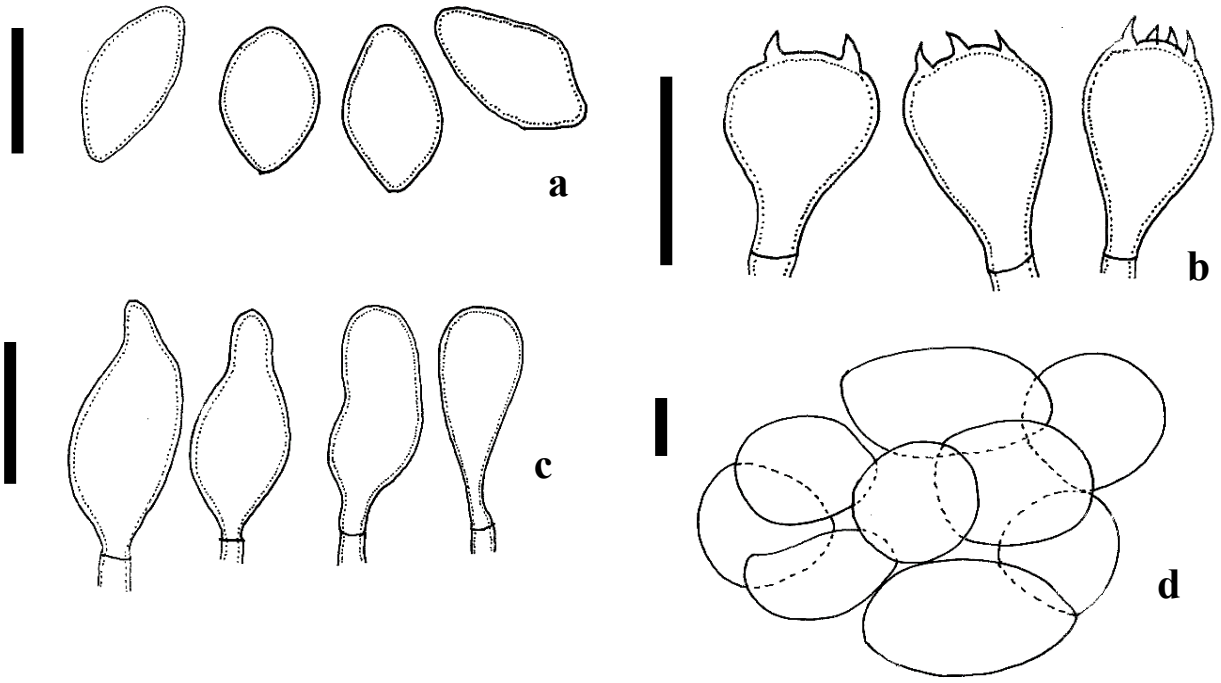


Figure 2. *Candolleomyces ruhunensis* (HKAS123158, holotype): (a) basidiospores; (b) basidia; (c) cheilocystidia; (d) pileipellis. Scale bars: (a) = 5 µm, (b) = 10 µm, (c) = 20 µm, (d) = 10 µm

NOTES

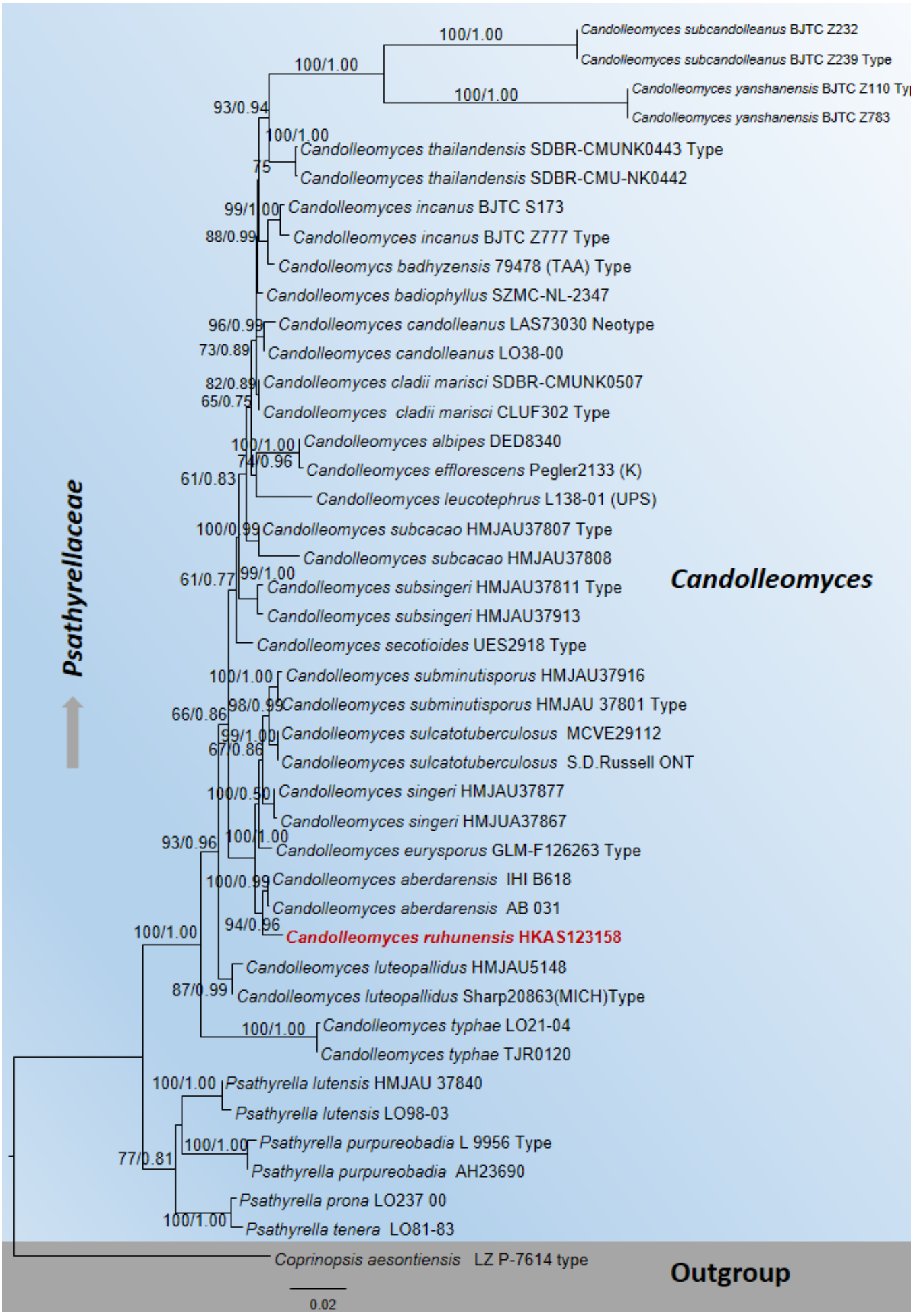
Candolleomyces ruhunensis is characterized by absence of pleurocystidia, which includes it in *Psathyrella* sect. *Spintrigerae* (Fr.) Konrad & Maubl. following a different systematics (e.g. Örstadius, Ryberg & Larsson 2015), hyaline, not phaseoliform spores mostly lacking a germ pore, distinctly utriform cheilocystidia, habitat on woody material in an equatorial climate, and a medium, not minute, habit. *Candolleomyces aberdarensis* A. Melzer, Kimani & R. Ullrich, described from Kenya (central Africa), shares several characteristics but differs in very minute habit and differently shaped spores [7.5 – 8 (8.8) × 4.4 – 5.0 µm] having a higher quotient (1.6 – 1.75). This species is the closest taxon on a molecular basis with an identity between 97.94% – 98.09%. (see Figure 3 and Table 1).

The North American *Candolleomyces singeri* A.H. Sm. lacks truly differentiated cheilocystidia. *Candolleomyces sulcatotuberculosus* (J. Favre) Einhell, described from Europe, has a pileus distinctly striate and radially sulcate with age, and grows in moist to wet sites on debris of hygrophilous plants.

Candolleomyces cacao Desjardin & B.A. Perry and *Psathyrella atricastanea* (Murrill) A.H. Sm., from the equatorial African and American belt, have darker and ocellate pilei, and narrower spores.

The voucher *Psathyrella candolleana*, strain BRPCL, accession number MT658050, deposited by J. Xu, has a strong identity (99.27 – 99.41%, query cover 97 – 95%) with our materials. It was collected in China, associated with leaves of *Broussonetia papyrifera*, and may reveal a larger diffusion of *Candolleomyces ruhunensis* in Southeast Asia.

Figure 3 (below). RAxML analysis based on the ITS and LSU sequence data of *Candolleomyces ruhunensis*. Bootstrap support values for ML equal to or greater than 65%, and Bayesian posterior probabilities (BP) equal to or greater than 0.95 are given as ML/BP above the nodes. The tree is rooted with *Coprinopsis aesontiensis*. The newly obtained strain is indicated in red.


Psathyrellaceae
Candolleomyces
Outgroup
100/1.00
Candolleomyces subcandolleanus BJTC Z232
Candolleomyces subcandolleanus BJTC Z239 Type
100/1.00
Candolleomyces yanshanensis BJTC Z110 Ty
Candolleomyces yanshanensis BJTC Z783
93/0.94
100/1.00
Candolleomyces thailandensis SDBR-CMUNK0443 Type
75
Candolleomyces thailandensis SDBR-CMU-NK0442
99/1.00
Candolleomyces incanus BJTC S173
88/0.99
Candolleomyces incanus BJTC Z777 Type
Candolleomycs badhyzensis 79478 (TAA) Type
Candolleomyces badiophyllus SZMC-NL-2347
96/0.99
Candolleomyces candolleanus LAS73030 Neotype
73/0.89
Candolleomyces candolleanus LO38-00
82/0.89
Candolleomyces cladii marisci SDBR-CMUNK0507
65/0.75
Candolleomyces cladii marisci CLUF302 Type
100/1.00
Candolleomyces albipes DED8340
74/0.96
Candolleomyces efflorescens Pegler2133 (K)
61/0.83
Candolleomyces leucotephrus L138-01 (UPS)
100/0.99
Candolleomyces subcacao HMJAU37807 Type
Candolleomyces subcacao HMJAU37808
61/0.77
99/1.00
Candolleomyces subsingeri HMJAU37811 Type
Candolleomyces subsingeri HMJAU37913
Candolleomyces secotioides UES2918 Type
100/1.00
Candolleomyces subminutisporus HMJAU37916
98/0.99
Candolleomyces subminutisporus HMJAU 37801 Type
66/0.86
99/1.00
Candolleomyces sulcatotuberculosus MCVE29112
67/0.86
Candolleomyces sulcatotuberculosus S.D.Russell ONT
100/0.50
Candolleomyces singeri HMJAU37877
Candolleomyces singeri HMJUA37867
93/0.96
100/1.00
Candolleomyces eurysporus GLM-F126263 Type
100/0.99
Candolleomyces aberdarensis IHI B618
Candolleomyces aberdarensis AB 031
94/0.96
100/1.00
Candolleomyces ruhunensis HKAS123158
Candolleomyces luteopallidus HMJAU5148
87/0.99
Candolleomyces luteopallidus Sharp20863(MICH)Type
100/1.00
Candolleomyces typhae LO21-04
Candolleomyces typhae TJR0120
100/1.00
Psathyrella lutensis HMJAU 37840
Psathyrella lutensis LO98-03
100/1.00
Psathyrella purpureobadia L 9956 Type
77/0.81
Psathyrella purpureobadia AH23690
Psathyrella prona LO237 00
100/1.00
Psathyrella tenera LO81-83
Coprinopsis aesontiensis LZ P-7614 type
0.02

Species	Collection ID	ITS	LSU
Candolleomyces aberdarensis	AB 031	MH880928	MH880928
C. aberdarensis	IHI B618	MK421517	MK421517
C. albipes	DED8340	KX017209	
C. badhyzensis	79478 (TAA) Type	KC992883	KC992883
C. badiophyllus	SZMC-NL-2347	FN430699	FM876268
C. cacao	SFSU DED 8339 Type	NR148106	
C. cacao	FP1R4	KU847452	
C. candolleanus	LAS73030 Neotype	KM030175	KM030175
C. candolleanus	LO38-00	DQ389720	
C. cladii-marisci	CLUF302 Type	MK080112	
C. cladii-marisci	SDBR-CMUNK0507	MZ145228	
C. effibulata	LO37-96 Type	DQ389672	DQ389672
C. efflorescens	Pegler2133 (K)	KC992941	
C. eurysporus	GLM-F126263 Type	MT651560	MT651560
C. incanus	BJTC Z777 Type	ON042759	ON042766
C. incanus	BJTC S173	ON042760	ON042767
C. leucotephrus	LÖ138-01 (UPS)	KC992885	KC992885
C. luteopallidus	Sharp20863 (MICH) Type	KC992884	KC992884
C. luteopallidus	HMJAU5148	MG734736	MW301084
C. ruhunensis	HKAS123158	ON685315	to be submitted
C. secotioides	UES2918 Type	KR003281	KR003282
C. singeri	HMJUA37867	MG734718	MW301088
C. singeri	HMJAU37877	MW301073	MW301091
C. subcacao	HMJAU37807 Type	MW301064	MW301092
C. subcacao	HMJAU37808	MW301065	MW301093
C. subcandolleanus	BJTC Z239 Type	ON042755	ON042762
C. subcandolleanus	BJTC Z232	ON042756	ON042763
C. subminutisporus	HMJAU37801 Type	MW301066	MW301094
C. subminutisporus	HMJAU37916	MW301067	MW301095
C. subsingeri	HMJAU37811 Type	MG734715	MW301097
C. subsingeri	HMJAU37913	MG734725	MW301098
C. sulcatotuberculosus	MCVE29112	MF326002	
C. sulcatotuberculosus	S.D. Russell ONT	OP643311	
C. trinitatensis	TL9035 (C)	KC992882	KC992882
C. trinitatensis	ADK4162 (BR)	KC992886	KC992886
C. yanshanensis	BJTC Z783	ON042757	ON042764
C. yanshanensis	BJTC Z110 Type	ON042758	ON042765
C. tuberculatus	ADK3564	KC992934	KC992934
C. tuberculatus	Mushroom Observer # 315413	MH497604	
C. subminutisporus	HMJAU 37801 Type	NR_173318	
C. subminutisporus	X114	MK304138	
C. typhae	LO21-04	DQ389721	DQ389721

C. typhae	TJR0120	OK346575	
C. thailandensis	SDBR-CMU-NK0442	MZ145232	
C. thailandensis	SDBR-CMUNK0443 Type	MZ146874	
Psathyrella lutensis	LO98-03	DQ389685	DQ389685
P. lutensis	HMJAU 37840	MG734748	
P. prona	LO237 00	KJ939634	
P. pseudogracilis	LO172-02	DQ389675	DQ389675
P. pseudogracilis	CBS 166.47	MH856200	
P. purpureobadia	L 9956 Type	NR_119670	
P. purpureobadia	AH23690	KR261436	
P. tenera	LO81-83	KC992849	
Coprinopsis aesontiensis	LZ P-7614 type	NR_158339	KY554752

Table 1. Taxa information and GenBank accession numbers of ITS and LSU sequences of *Candolleomyces* specimens used in the molecular phylogenetic analysis.

Crepidotus striatus T. Bau & Y.P. Ge (Figures 4, 5)
Mycosystema 39(2): 251 (2020)

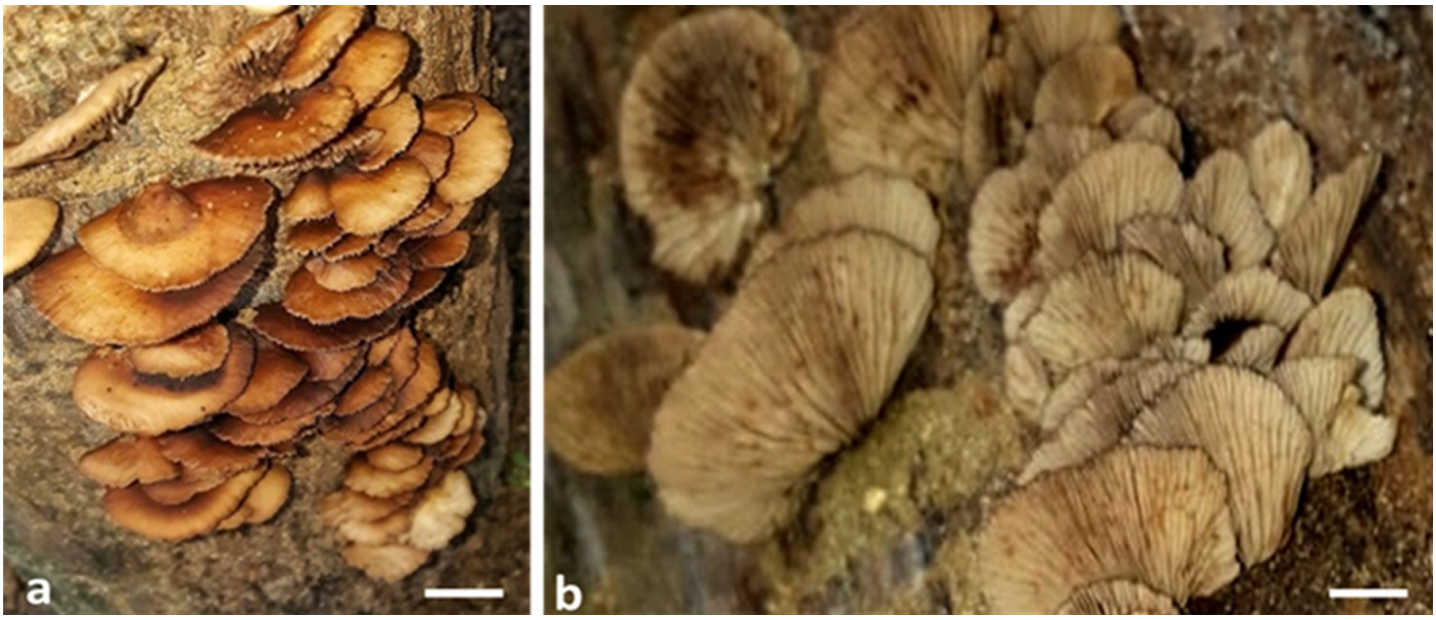


Figure 4. *Crepidotus striatus* (HKAS123160) (a,b): mature basidiomata in situ; scale bars = 2 cm

Macroscopic characters

Basidiomata small to medium, sessile.

Pileus fleshy, 2 – 4 mm of thickness, 10 – 32 mm across, hemispherical, pleurotoid or petaloid, occasionally with an umbo close to the attachment point; surface initially whitish (1A1-2), then butter yellow (4A5), yolk yellow (4B8) to brownish yellow (5C8), at maturity yellowish brown (5E8) close to the margin and in the middle, rust brown (6E8) at the attachment point, drying to light brown (6D8), smooth, slender, slightly pubescent, sticky, moist and slimy; margin slightly striate, plicate to sometimes lobed, sharp, concolorous with pileus surface.

Lamellae crowded, sinuate, dull yellow (3B3) to muddy brown and straw yellow (3B4) with maturity, lamellulae intermingled with 2-3 different lengths of 6, 2 and 2.2 mm, moist and fragile; edge smooth, even.

Stipe absent.

Context thin, 3 mm of thickness, whitish grey; odor distinct, taste not tested.

Microscopic characters

Basidiospores 7.5 – 8.4 × 4.9 – 5.4 µm, Q = 1.30 – 1.55, in front view elliptic, in side view adaxially flatted to sub-elliptic, light brown in water, thick-walled, with a guttule or yellowish to brown colour contents; germ pore visible, central, 1 – 2 µm of diam.

Basidia 4-spored and 2-spored, 16 – 22 × 5.0 – 7.7 µm, clavate to cylindraceous or subululiform, thin-walled, sub-hyaline to hyaline in water or 5% KOH, with a dark brown to light brown content.

Hymenium gelatinized. *Subhymenium* pseudoparenchymatous.

Hymenophoral trama regular, composed of thin-walled, hyaline, 2.5 – 4.0 µm wide hyphae.

Lamella edge heteromorphous with scattered cheilocystidia.

Cheilocystidia 18.0 – 34.0 × 9.5 – 17.6 µm, slender to thickset, clavate, versiform to lageniform or cylindric-clavate, fusoid, often mucronate or with a long flexuous neck, hyaline, thin-walled. *Pleurocystidia* absent.

Pileipellis composed of a gelatinized cutis with thin-walled hyphae of 13.0 – 30.0 × 4.0 – 10.0 µm, yellowish in mass in ammonia. *Pileal trama* composed of thin-walled, hyaline, 6.1 – 10.0 µm wide hyphae,

Clamp connections not found.

Ecology and habitat: saprotrophic, caespitose, growing on a decaying huge woody trunk.

Collection examined: Sri Lanka, Southern province, Galle, Kanneliya; 29th August 2021, collectors G.P Pathirana and A.N. Ediriweera; Herbarium voucher code: HKAS123160; GenBank ITS Accession Number: ON704093.

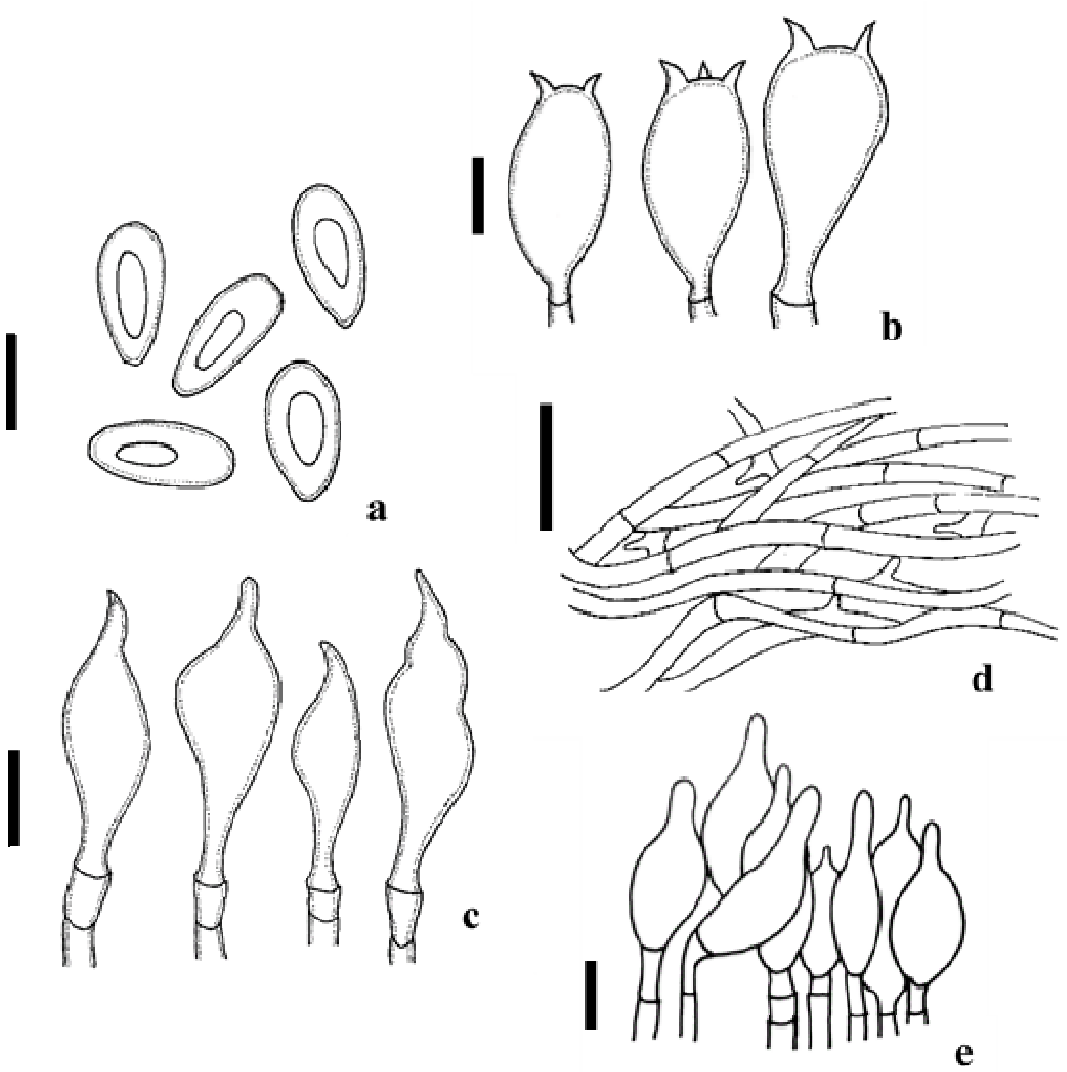


Figure 5. *Crepidotus striatus* (HKAS123160). (a) basidiospores; (b) basidia; (c) cheilocystidia; (d) pileipellis; (e) lamellae edge. Scale bars: (a) = 5 µm, (b) = 5 µm, (c) = 6 µm, (d) = 10 µm, (e) = 10 µm

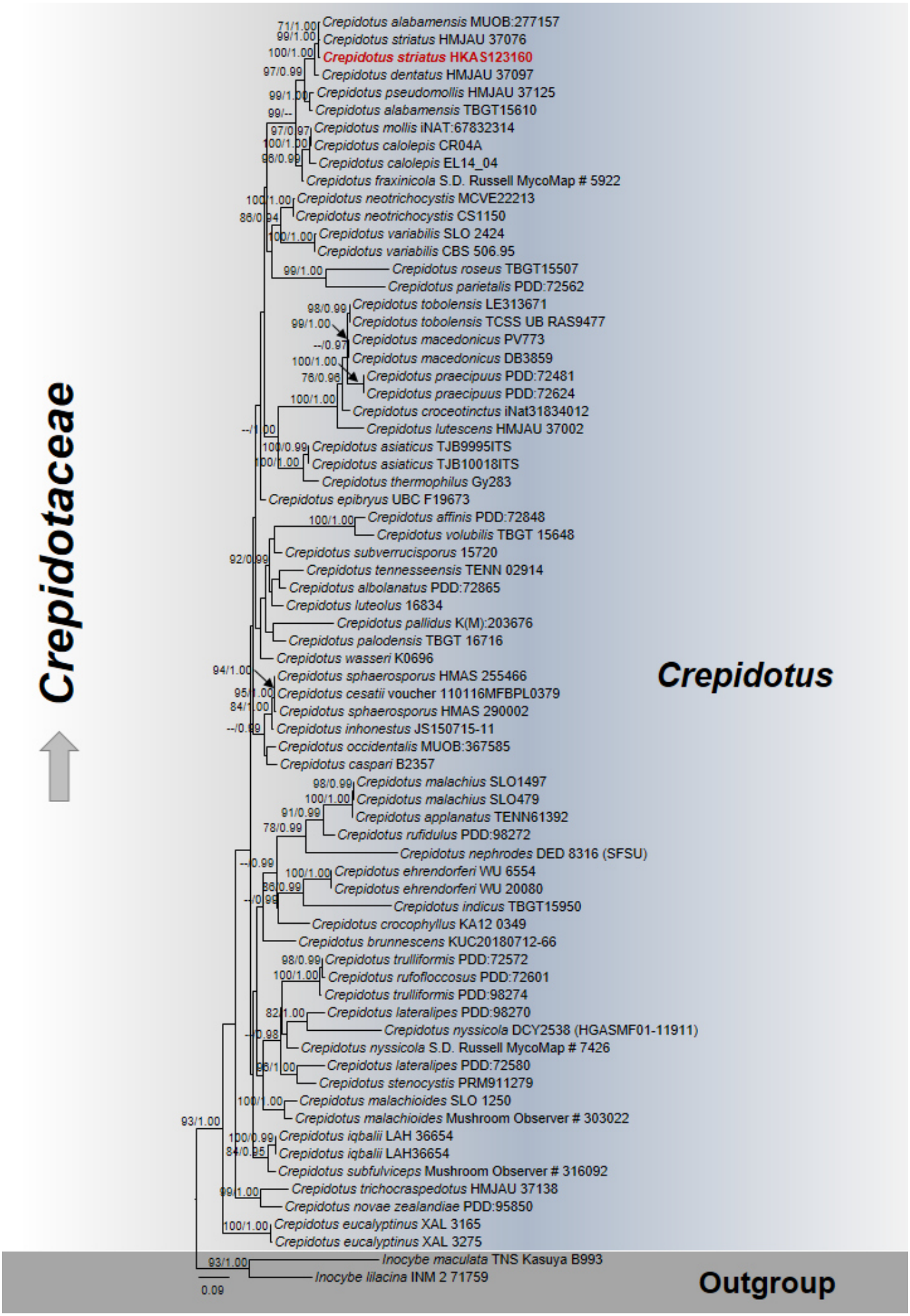

Crepidotaceae
Crepidotus
Outgroup
Crepidotus alabamensis MUOB:277157
Crepidotus striatus HMJAU 37076
Crepidotus striatus HKAS123160
Crepidotus dentatus HMJAU 37097
Crepidotus pseudomollis HMJAU 37125
Crepidotus alabamensis TBGT15610
Crepidotus mollis iNAT:67832314
Crepidotus calolepis CR04A
Crepidotus calolepis EL14_04
Crepidotus fraxinicola S.D. Russell MycoMap # 5922
Crepidotus neotrichocystis MCVE22213
Crepidotus neotrichocystis CS1150
Crepidotus variabilis SLO 2424
Crepidotus variabilis CBS 506.95
Crepidotus roseus TBGT15507
Crepidotus parietalis PDD:72562
Crepidotus tobolensis LE313671
Crepidotus tobolensis TCSS UB RAS9477
Crepidotus macedonicus PV773
Crepidotus macedonicus DB3859
Crepidotus praecipuus PDD:72481
Crepidotus praecipuus PDD:72624
Crepidotus croceotinctus iNat31834012
Crepidotus lutescens HMJAU 37002
Crepidotus asiaticus TJB9995ITS
Crepidotus asiaticus TJB10018ITS
Crepidotus thermophilus Gy283
Crepidotus epibryus UBC F19673
Crepidotus affinis PDD:72848
Crepidotus volubilis TBGT 15648
Crepidotus subverrucisporus 15720
Crepidotus tennesseensis TENN 02914
Crepidotus albolanatus PDD:72865
Crepidotus luteolus 16834
Crepidotus pallidus K(M):203676
Crepidotus palodensis TBGT 16716
Crepidotus wasseri K0696
Crepidotus sphaerosporus HMAS 255466
Crepidotus cesatii voucher 110116MFBPL0379
Crepidotus sphaerosporus HMAS 290002
Crepidotus inhonestus JS150715-11
Crepidotus occidentalis MUOB:367585
Crepidotus caspari B2357
Crepidotus malachius SLO1497
Crepidotus malachius SLO479
Crepidotus applanatus TENN61392
Crepidotus rufidulus PDD:98272
Crepidotus nephrodes DED 8316 (SFSU)
Crepidotus ehrendorferi WU 6554
Crepidotus ehrendorferi WU 20080
Crepidotus indicus TBGT15950
Crepidotus crocophyllus KA12 0349
Crepidotus brunnescens KUC20180712-66
Crepidotus trulliformis PDD:72572
Crepidotus rufofloccosus PDD:72601
Crepidotus trulliformis PDD:98274
Crepidotus lateralipes PDD:98270
Crepidotus nyssicola DCY2538 (HGASMF01-11911)
Crepidotus nyssicola S.D. Russell MycoMap # 7426
Crepidotus lateralipes PDD:72580
Crepidotus stenocystis PRM911279
Crepidotus malachioides SLO 1250
Crepidotus malachioides Mushroom Observer # 303022
Crepidotus iqbalii LAH 36654
Crepidotus iqbalii LAH36654
Crepidotus subfulviceps Mushroom Observer # 316092
Crepidotus trichocraspedotus HMJAU 37138
Crepidotus novae zealandiae PDD:95850
Crepidotus eucalyptinus XAL 3165
Crepidotus eucalyptinus XAL 3275
Inocybe maculata TNS Kasuya B993
Inocybe lilacina INM 2 71759
0.09

Figure 6 (above). RAxML analysis based on the ITS sequence data of *Crepidotus striatus*. Boot-strap support values for ML equal to or greater than 65%, and Bayesian posterior probabilities (BP) equal to or greater than 0.95 are given as ML/BP above the nodes. The tree is rooted with *Inocybe lilacina* and *Inocybe maculata*. The newly obtained strain is indicated in red.

NOTES

Our new collection formed a distinct clade with *C. striatus*, *C. alabamensis* Murrill and *C. dentatus* T. Bau & Y.P. Ge with an high bootstrap (98% ML) support. The base pair comparison between them and our collection revealed a 0.62 %, 0.46 % and 2.0 % difference respectively (see Figure 6 and Table 2).

Crepidotus striatus, very recently described from China (Yu-Peng & Bau 2020), shares all qualitative characters with our collection: gelatinized pileus and gills, crowded gills, a striate pileus margin, basidia also 4-spored or mainly 2-spored, a tropical to sub-tropical habitat (the type of *C. striatus* was found in Nanning City, China, on the tropic of cancer), lageniform cheilocystidia, spore shape, and structure of the pileipellis. A slight deviation in the dimensional parameters of spores, basidia and cheilocystidia falls within a normal range of intraspecific quantitative variability in a recently described and still little known species.

Table 2. Taxa information and GenBank accession numbers of ITS sequences of *Crepidotus* specimens used in the molecular phylogenetic analysis.

Species	Collection ID	ITS
Crepidotus affinis	PDD:72848	KY827291
C. alabamensis	Muob:277157	OL142283
C. alabamensis	TBGT15610	MK459545
C. albolanatus	PDD 72865 type	NR_159820
C. albolanatus	PDD 72865 type	KY827292
C. applanatus	TENN61392 clone C5	FJ596805
C. applanatus	TENN61392 clone C4	FJ596804
C. asiaticus	TJB10018ITS paratype	MF077339
C. asiaticus	TJB9995ITS paratype	MF077337
C. brunnescens	KUC20180712-66	MN197898
C. calolepis	CR04A	KF879617
C. calolepis	EL14_04	FJ904178
C. caspari	B2357	MW722982
C. cesatii	110116MFBPL0379	MW554348
C. croceotinctus	iNat31834012	MN498116
C. crocophyllus	KA12-0349	KR673424
C. dentatus	HMJAU 37097 type	NR_173279
C. ehrendorferi	WU:6554 type	MH780918
C. ehrendorferi	WU:20080	MH780919
C. epibryus	UBC F19673	HM240524
C. eucalyptinus	XAL 3275	KT715782
C. eucalyptinus	XAL 3165	KT715780
C. fraxinicola	S.D. Russell MycoMap # 5922	MN906146
C. fraxinicola	S.D. Russell MycoMap 6297	MK560109
C. indicus	TBGT15950 paratype	MK370662
C. inhonestus	JS150715-11	KX963787

C. iqbalii	LAH 36654 type	NR_173306
C. iqbalii	LAH 36654 type	MT973498
C. lateralipes	PDD:98270 isotype	KY827295
C. luteolus	16834	JF907963
C. lutescens	HMJAU 37002 type	NR_158400
C. macedonicus	PV773	MH780921
C. macedonicus	DB3859	MH780922
C. malachioides	SLO 1250 type	NR_132047
C. malachioides	Mushroom Observer # 303022	MK607561
C. malachius	SLO479	MF621033
C. malachius	SLO1497	MF621032
C. mollis	iNAT:67832314	MW676780
C. neotrichocystis	MCVE22213 type	MT055895
C. neotrichocystis	CS1150	OL672745
C. nephrodes	DED 8316 (SFSU)	KX017200
C. novae-zelandiae	PDD:95850	HQ533046
C. nyssicola	DCY2538 (HGASMF01-11911)	MZ413059
C. occidentalis	MUOB:367585	OK376745
C. pallidus	K(M):203676	MZ159614
C. palodensis	BGT16716 type	MH84489
C. parietalis	PDD:72562	KY827320
C. praecipuus	PDD:72481	KY827311
C. praecipuus	PDD:72624	KY827312
C. pseudomollis	HMJAU 37125 type	NR_173280
C. roseus	TBGT15507	MK567976
C. rufidulus	PDD 98272 type	NR_159823
C. rufidulus	PDD:98272 isotype	KY827319
C. rufofloccosus	PDD 72601 type	NR_159822
C. rufofloccosus	PDD:72601	KY827296
C. sphaerosporus	HMAS 255466	MK966515
C. sphaerosporus	HMAS 290002	MK966514
C. stenocystis	PRM911279	MF621030
C. striatus	HMJAU 37076 type	MH320742
C. striatus	HMJAU 37076 type	NR_173281
C. striatus	HKAS123160	ON704093
C. subfulviceps	Mushroom Observer # 316092	MH484051
C. subverrucisporus	MVCE15720	JF907961
C. tennesseensis	TENN 029144 type	NR_119720
C. tennesseensis	TENN 029144 type	FJ601806
C. thermophilus	Gy283	MF163183
C. tobolensis	LE313671	OL739885
C. tobolensis	TCSS UB RAS9477 paratype	MK522392
C. trichocraspedotus	HMJAU 37138 type	NR_173282

C. trichocraspedotus	HMJAU 37138 type	MH320743
C. trulliformis	PDD:72572 type	KY827297
C. trulliformis	PDD:98274 isotype	KY827298
C. variabilis	CBS 506.95	OL687124
C. variabilis	SLO 2424	MT055894
C. volubilis	TBGT15648 type	MH845231
C. wasseri	K0696 type	MW72298
Inocybe lilacina	INM 2 71759	KF680277
I. maculata	TNS Kasuya B993	KF680276

DISCUSSION

In the present study the new taxon *Candolleomyces ruhunensis* from *Psathyrellaceae* is introduced and a rare occurrence of the recently described *Crepidotus striatus* is reported. Based on a molecular biological evidence and on morphological differentiation (Hopple & Vilgalys 1999; Moncalvo *et al*. 2002; Matheny *et al*. 2006) *Candolleomyces* was recently separated from the genus *Psathyrella* inside which, in a different classification (Örstadius, Ryberg & Larsson 2015), it is treated as section *Spintrigerae*.

Several *Psathyrella* species have been reported from Sri Lanka which had not been identified to the species level (Ediriweera *et al*. 2014). Therefore *C. ruhunensis* is the first *Candolleomyces* species reported from Sri Lanka. Nevertheless, the highest number of *Candolleomyces* have been reported from China (Yan 2018; Bau and Yan 2021) which approximately amount to one third of the total number of *Candolleomyces* species reported worldwide.

Several species of *Crepidotus*, including *C. reversus* (Berk. & Broome) Sacc. and *C. citrinus* Petch, have been described and reported in previous studies from Sri Lanka (Pegler 1986). The report of *C. striatus* in the present study is the second ever finding of *C. striatus* after it was described from China (Yu-Peng & Bau 2020) in 2020 and first time to report from Sri Lanka.

The diversity of mushrooms in Sri Lanka is hardly explored even though the country is rich in diversity. Most familiar species with medicinal and culinary values naturally occur in home gardens, agricultural lands, forest borders and other disturbed areas, where they are known as a result of the traditional knowledge and experiences of villagers (Caron 1995; Rajapakse 2014; Hewage 2015). Thus, those species are known by their local names, which are highly synonymized based on macro-morphological characteristics and their habitats. Those locally known species are also just a handful of the island's total diversity. Hence, it is not fallacious to mention that Sri Lanka's diversity of mushrooms needs considerable more attention in order to identify its immense values and to derive the maximum output from this natural resource.

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REFERENCES

Bau T, Yan J-Q (2021) Two new rare species of *Candolleomyces* with pale spores from China. *MycoKeys* 80:149–161 https://doi.org/10.3897/mycokeys.80.67166

Berkeley MJ, Broome CE (1870) On some species of the genus *Agaricus* from Ceylon. *Transactions of the Linnean Society of London* (series 1) 27:149–152

Berkeley MJ, Broome CE (1871) The Fungi of Ceylon (*Hymenomycetes* from *Agaricus* to *Cantharellus*). *Transactions of the Linnean Society of London, Botany* 9:494 – 567

Berkeley MJ, Broome CE (1873) Enumeration of the Fungi of Ceylon. Part 2., containing the remainder of the *Hymenomycetes*, with the remaining established tribes of Fungi. *Transactions of the Linnean Society* 14(73):29–64

Caron CM (1995) The role of non-timber tree products in household food procurement strategies: profile of a Sri Lankan village. *Agroforestry Systems* 32(2):99–117

Cesati V (1879) Mycetum in itinere Borneensi lectorum a cl. Od. Beccari enumeratio curis Vincentii Cesati s. o. *Atti della R. Accademia delle Scienze Fisiche e Matematiche*, Ser. 1 8(3):1–28

Department of Meteorology, Sri Lanka https://www.meteo.gov.lk/index.php?lang=en (accessed 12th Apr 2022)

Ediriweera SS, Wijesundera RLC, Nanayakkara LMC, Weerasena OVDSJ (2014) Macrofungi from the Sigiriya wilderness in Sri Lanka. *Journal of Mycopathologycal Research* 52:47–51

Glez-Peña D, Gómez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D (2010) ALTER: program-oriented conversion of DNA and protein alignments. *Nucleic acids research* 38(Web Server issue):W14–18 doi: 10.1093/nar/gkq321

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/ NT. *Nucleic Acids Symposium Series* 41:95–98

Hewage D (2015) Traditional Knowledge of Edible Wild Mushrooms in a Village Adjacent to the Sinharāja Forest. *J. Royal Asiatic Society of Sri Lanka* 60:77–95

Hobbs C (1996) Medicinal Mushrooms: An Exploitation of Tradition, Healing and Culture. Botanica Press, Santa Cruz

Höehnel F (1908) Fragmente zur Mykologie (V. Mitteilung, Nr. 169 bis 181). *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften in Wien Mathematisch-Naturwissenschaftliche Classe* 117:1–48

Höehnel FXR von (1909) Fragmente zur Mycologie (VI. Mitteilung, Nr. 182 bis 288). *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften in Wien Mathematisch-Naturwissenschaftliche Classe*, Abt. 1 118:275–452

Höehnel F (1914) Fragmente zur Mycologie (XVI. Mitteilung, Nr. 813 bis 875). *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften in Wien Mathematisch-Naturwissenschaftliche Classe*, Abt. 1 123:49–155

Hopple JS, Vilgalys R (1999) Phylogenetic relationships in the mushroom genus *Coprinus* and dark-spored allies based on sequence data from the nuclear gene coding for the large ribosomal subunit RNA: Divergent domains, outgroups, and monophyly. *Molecular Phylogenetics and Evolution* 13:1–19 https://doi.org/10.1006/mpev.1999.0634

Karunarathna SC, Udayanga D, Maharachchikumbura SN, Pilkington M, Manamgoda DS, Wijayawardene DNN, Ariyawansa HA, Bandara AR, Chukeatirote E, McKenzie EHC, Hyde KD (2012) Current status of knowledge of Sri Lankan mycota. *Current Research in Environmental and Applied Mycology* 2:18–29 Doi 10.5943/cream/2/1/2

Karunarathna SC, Yang ZL, Raspé O, Ko Ko TW, Vellinga EC, Zhao RL, Bahkali AH, Chukeatirote E, Degreef J, Callac P, Hyde KD (2012) *Lentinus giganteus* revisited: new collections from Sri Lanka and Thailand. *Mycotaxon* 118:57–71

Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. *Molecular Biology and Evolution* 30:772–780

Kornerup A, Wanscher JH (1978) Methuen Handbook of Colour, London, UK: Methuen

Kumar H, Bhardwaj K, Sharma R, Nepovimova E, Cruz-Martins N, Dhanjal DS, Singh R, Chopra C, Verma R, Abd-Elsalam KA, et al. (2021) Potential usage of edible mushrooms and their residues to retrieve valuable supplies for industrial applications. *Journal of Fungi* **7**(6), 427 https://doi.org/10.3390/jof7060427

Laala GE, Raja MU, Gardezi SRA, Irshad G, Akram A, Bodlah I (2018) Study of macrofungi belonging to order *Agaricales* of Poonch District Azad Jammu and Kashmir (AJK). *Pure Applied Biology* **8**:27–33

Luna-Fontalvo JA, Barrios A, Abaunza C, Ramírez-Roncallo K, Negritto MA (2021) New records of *Agaricaceae* (*Agaricales*, *Basidiomycota*) from Colombia. Check List. **17**:1383–1393

Matheny PB, Curtis JC, Hofstetter V, Aime MC, Moncalvo JM, Ge ZW, Yang ZL, Slot JC, Ammirati JF, Baroni TJ, Bougher NL, Hughes KW, Lodge DJ, Kerrigan RW, Seidl MT, *et al*. (2006) Major clades of *Agaricales*: A multi-locus phylogenetic overview. *Mycologia* **98**:982–995 https://doi.org/10.1080/15572536.2006.11832627

Moncalvo JM, Vilgalys R, Redhead SA, Johnson JE, James TY, Aime MC, Hofstetter V, Verduin SJW, Larsson E, Baroni TJ, Thorn RG, Jacobsson S, Clèmencon H, Miller OK (2002) One hundred and seventeen clades of euagarics. *Molecular Phylogenetics and Evolution* **23**:357–400 https://doi.org/10.1016/S1055-7903(02)00027-1

Naeem MY, Ugur S, Rani S (2020) Emerging Role of Edible Mushrooms in Food Industry and Its Nutritional and Medicinal Consequences. *European Journal of Food Science and Technology* **4**:6–23

Örstadius L, Ryberg M, Larsson E (2015) Molecular phylogenetics and taxonomy in *Psathyrellaceae* (*Agaricales*) with focus on psathyrelloid species: introduction of three new genera and 18 new species. *Mycological Progress* **14**(5/25):1–42

Pegler DN (1986) Agaric flora of Sri Lanka. *Kew Bulletin Additional Series* 12:1–519

Petch T (1908a) The *Phalloideae* of Ceylon. *Annals of the Royal Botanical Gardens, Peradeniya* **4**:139–184

Petch T (1908b) The genus *Endocalyx*, Berkeley and Broome. *Annals of Botany, London* **22**:389–400

Petch T (1910) Revisions of Ceylon fungi (Part II). *Annals of the Royal Botanical Gardens, Peradeniya* **4**: 373–444

Petch T (1913) Termite fungi: a résumé. *Annals of the Royal Botanical Gardens, Peradeniya* **5**:303–341

Petch T (1915a) The pseudosclerotia of *Lentinus similis* and *Lentinus infundibuliformis*. *Annals of the Royal Botanical Gardens, Peradeniya* **6**:1–18, 1 tab.

Petch T (1915b) Horse-hair blights. *Annals of the Royal Botanical Gardens, Peradeniya* **6**:43–68, 6 tabs

Petch T (1916a) A preliminary list of Ceylon polypori. *Annals of the Royal Botanical Gardens, Peradeniya* **6**(2):87–144

Petch T (1916b) Ceylon lentini. *Annals of the Royal Botanical Gardens, Peradeniya* **6**(2):145–152

Petch T (1916c) Revisions of Ceylon fungi (Part IV). *Annals of the Royal Botanical Gardens, Peradeniya* **6**:153–183

Petch T (1917a) Additions to Ceylon fungi. *Annals of the Royal Botanical Gardens, Peradeniya* **6**(3):195–256.

Petch T (1917b) Revisions of Ceylon fungi (Part V). *Annals of the Royal Botanical Gardens, Peradeniya* **6**(4):307–355

Petch T (1919) Revisions of Ceylon fungi (Part VI). *Annals of the Royal Botanical Gardens, Peradeniya* **7**(1):1–44

Petch T (1922) Additions to Ceylon fungi II. *Annals of the Royal Botanical Gardens, Peradeniya* **7**(4):279–322

Petch T (1923) The diseases of the Tea Bush. MacMillan & Co. Ltd. London, UK, 220 pp.

Petch T (1924a) Thread blights. *Annals of the Royal Botanical Gardens, Peradeniya* **9**(1):1–45, tabs I-IX

Petch T (1924b) Revisions of Ceylon fungi (Part. VII). *Annals of the Missouri Botanical Gardens, Peradeniya* **9**(2):119–184

Petch T (1924c) Ceylon pink-spored agarics. *Annals of the Missouri Botanical Gardens, Peradeniya* **9**(1):201–216

Petch T (1924d) *Agaricaceae* pleuropodes *Zeylanicae*. *Annals of the Missouri Botanical Gardens, Peradeniya* **9**(1):217–227

Petch T (1925) Additions to Ceylon fungi III. *Annals of the Royal Botanical Gardens, Peradeniya* **9**(3):313–328

Petch T, Bisby GR (1950) The fungi of Ceylon. Peradeniya Manual 6, Colombo, Government Publication Bureau. Sri Lanka: 111 pp.

Rajapakse JC (2014) Status of edible and medicinal mushroom research in Sri Lanka. *Proceedings of the 8th International Conference on Mushroom Biology and Mushroom Products* (ICMBMP8)

Rambaut A (2012). FigTree v1. 4.0. University of Oxford, Oxford, UK.

Swindell SR, Plasterer TN (1997) Seqman: contig assembly. *In*: Swindell. Sequence data analysis guidebook. Methods in Molecular Biology 70:75–89. Springer, Totowa (NJ)

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X Windows Interface: Flexible Strategies for Multiple Sequence Alignment Aided by Quality Analysis Tools. *Nucleic Acids Research* 25(24):4876–4882

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172:4238–4246

White TJ, Bruns TD, Lee S, Taylor JW (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky J, White TJ (eds) PCR protocols: a guide to methods and applications. Academic Press, London, 482 pp.

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J (2022) Outline of Fungi and fungus-like taxa – 2021. *Mycosphere* 13:53–453 Doi 10.5943/mycosphere/13/1/2

Yagan O, Senel E, Kayir S (2020) Mushroom toxicity in academic literature: Holistic analysis of the global publications on mushroom poisoning between 1975 and 2019. *Journal of Clinical Medicine of Kazakhstan* 6:48–52

Yan JQ (2018) Taxonomy and molecular phylogeny of *Psathyrella* and related genera in China. Dissertation. Jilin Agricultural University.

Yu-Peng GE, Bau T (2020) Descriptions of six new species of *Crepidotus* from China. Mycosystema 39:238 – 255