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Candolleomyces albipes (Psathyrellaceae) - A New Asian Record

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ABSTRACT

During our extensive study on the psathyrelloid fungi of Kerala State, India, a remarkable, lesser-known species of Candolleomyces was collected several times from the dead trunks of Artocarpus. Morphological and nrITS-based phylogenetic studies identified it as Candolleomyces albipes. Based on collections made in Kerala State, India, an updated description of the species is presented. This is the first-ever report of this species from the Asian region.

Keywords: Kerala, nrITS, Phylogeny, *Psathyrella*

INTRODUCTION

In 2020, *Candolleomyces* D. Wächt. & A. Melzer was recognized as a separate genus within the dark-spored agaric genus *Psathyrella* (Fr.) Quél., based on thorough specimen analysis, including morphological and multi-gene phylogenetic studies. *Candolleomyces* macro-morphologically resembles *Psathyrella*; it can be distinguished micro-morphologically by the absence of pleurocystidia. *Candolleomyces* is a relatively small genus with 60 species known worldwide (Nayana and Pradeep 2023a, 2023b, 2024; Ahmad *et al.* 2024; Han *et al.* 2024; Haqnawas *et al.* 2024). The highest diversity of the genus is found in the Asian region, with thirteen species reported from India (Nayana and Pradeep 2023a, 2023b, 2024).

In an investigation on the diversity of psathyrelloid mushrooms of Kerala State, India, basidiomes of an apparently psathyrelloid fungus were spotted on several occasions on dead *Artocarpus* tree trunks in Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI) campus. Detailed morphological and molecular studies confirmed it as *Candolleomyces albipes* (Murrill) D. Wächt. & A. Melzer. An updated account of the species is provided based on the current collections from Kerala State, India.

MATERIALS AND METHODS

Morphological studies

Candolleomyces specimens collected from Kerala State, India, were used for the macromorphological descriptions. Specimens for this study were collected by the authors during the monsoon months (May-December) in 2020-2022 from the forests of the JNTBGRI campus. The JNTBGRI campus is situated in the southern part of Kerala State (southern India), and the forests are part of the Western Ghats. Photographs of basidiomata were made in the field using a digital camera (Canon EOS 70D DSLR). Color codes follow Kornerup & Wanscher (1978). Dried specimens were used for the microscopic study, and characters were studied on hand-cut sections stained with 1% Congo red, mounted in 3% aqueous KOH. Microcharacters were examined, photographed and measured under an Olympus CX43 optical microscope at 600X. Twenty basidiospores and 10 each of basidia, cystidia and hyphae per collection were measured for length and width. Basidiospore measurements include both the mean and the standard deviation for both the length (avL) and the width (avW), together with the range of spore quotient (Q, length/width ratio) and its mean value (Qm). Basidiospore measurements exclude the hilar appendix. All materials examined are deposited at the Mycological Herbarium of Jawaharlal Nehru Tropical Botanic Garden and Research Institute, Thiruvananthapuram [TBGT (M)].

DNA extraction, PCR and sequencing

DNA extraction from the specimens of *Candolleomyces* was carried out using the protocols described by Izumitsu *et al.* (2012). The primer sets ITS1/ITS4 (White *et al.* 1990) were used to amplify the rDNA ITS region. The procedures followed for PCR amplification and sequencing are based on the methodology outlined by Kumar *et al.* (2018). Amplified products were confirmed by agarose gel electrophoresis and sequenced in a commercial facility. The newly generated sequences are deposited in GenBank (https://www.ncbi.nlm.nih.gov/genbank).

Sequence alignment and phylogenetic analysis

Molecular phylogenetic analysis was performed using nrITS sequences. The nrITS sequences

newly generated from the Kerala collections along with those retrieved from GenBank were aligned using the MAFFT web tool (www.ebi.ac.uk/Tools/msa/mafft/) with default settings. The data matrix consisted of 42 sequences from 32 taxa, including the outgroup, *Coprinopsis aesontiensis* A. Melzer, Ferisin & Dovana, following Ediriweera *et al.* (2023). The aligned data matrix was then imported into BioEdit v7.2.6.1 (Hall 1999) for manual modification. Maximum likelihood (ML) analysis was performed on the web platform http://iqtree.cibiv.univie.ac.at (Trifinopoulos *et al.* 2016) with 1000 ultrafast bootstrap replicates. The transition model with equal frequency (TIM2+F+I+G4) was selected automatically as the best-fit substitution model as per the BIC score on the same web platform. The phylogram inferred from ML analysis is displayed with MEGA X (Kumar *et al.* 2016).

RESULTS

Molecular phylogeny

The final dataset containing 42 nrITS sequences from 32 taxa of *Candolleomyces,* including the newly generated sequences (PQ615686; PQ615687), was included in the ML phylogenetic analyses. Molecular phylogenetic tree inferred from the ML analysis illustrates the relative placement of *Candolleomyces albipes* (Murrill) D. Wächt. & A. Melzer with other closely related *Candolleomyces* species (**Figure 1**). *Candolleomyces albipes* from India clusters with *C. albipes* from Africa (KX017209) with 100% ML bootstrap support, thus confirming the conspecificity.

Figure 1: Maximum likelihood tree generated from nrITS sequence data. Bootstrap values are indicated above/below branches. *Candolleomyces albipes* from India are indicated in bold.

TAXONOMY

Candolleomyces albipes (Murrill) D. Wächt. & A. Melzer, *Mycol. Progr.* 19(11): 1230 (2020)

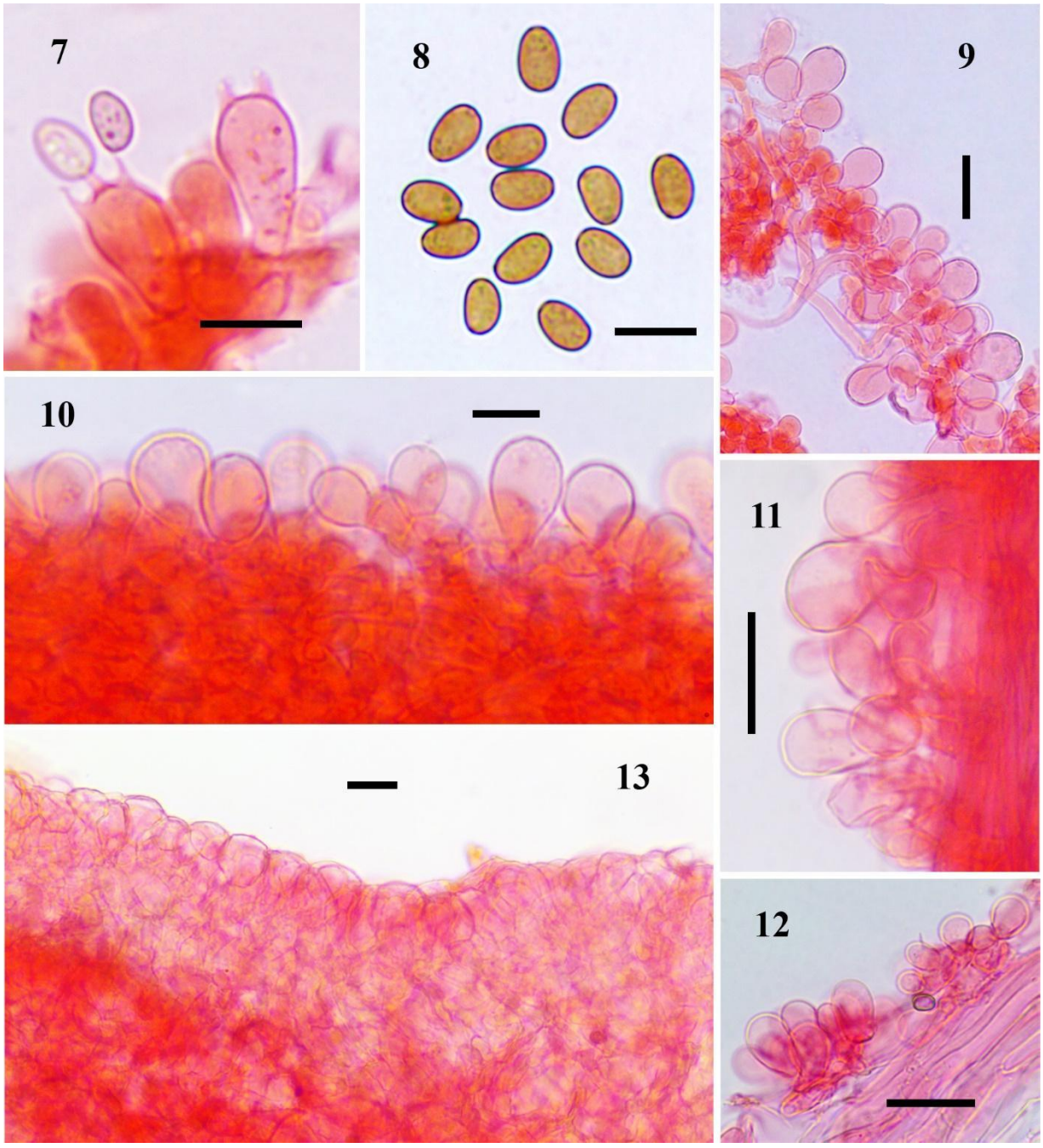
Astylospora albipes Murril *[as 'Atylospora']* *Mycologia* 10(1): 22 (1918)

Psathyra albipes (Murrill) Murrill, *Mycologia* 10(1): 33 (1918)

Psathyrella albipes (Murrill) A.H. Sm., *Mem. N. Y. Bot. Gdn* 24: 283 (1972) **Figures. 2–13**

Basidiomata small, thin. Pileus 8–24 mm diam., convex, broadly convex, plano-convex to applanate; surface white when young, becoming greyish orange to greyish brown (5B2/5B4/5C5/6C2/6D3) with minute white evanescent squamules, pellucid striate up to the disc, hygrophanous, rugulose on drying, shiny, dry; margin straight, appendiculate when young.

Figures 2–6: *Candolleomyces albipes.* 2–4. Habit *in-situ*; 5–6. Lamellae view. Scale bars: 2–6=10 mm.



Figures 7–13: ***Candolleomyces albipes***. 7. Basidia; 8. Basidiospores; 9–10. Cheilocystidia; (e) 11–12. Caulocystidia; 13. Pileipellis. Scale bars: 7–9=10 µm; 10–13=20 µm.

Discussion

Candolleomyces albipes is notable for its small fruiting bodies, greyish orange pileus, evanescent pileal veil, basidiospores with a broad germ pore, clavate cheilocystidia and lignicolous habitat. It was originally described by Murrill (1918) from Jamaica as *Astylospora albipes* (as *Atylospora albipes*), and later, Smith (1972), based on his studies on the type, made a new combination, viz., *Psathyrella albipes*. In an extensive specimen analysis coupled with morphological and multigene studies on Psathyrellaceae led to the redesignation of *Psathyrella albipes* as *Candolleomyces albipes* (Wächter and Melzer 2020). In addition to the type, *C. albipes* have also been reported from São Tomé, Africa (Desjardin and Perry 2016). This species is so far not reported from the Asian continent, and thus the present record of *C. albipes* from tropical India has phytogeographic significance.

In terms of morphology, the specimens documented from Africa and the original type description closely match our collection of *C. albipes*. Using the nrITS sequences from the current collections [TBGT(M)18042; TBGT(M)18823], a BLASTn search showed 100% sequence similarity with *C. albipes* (KX017209) from Africa. The presence of clavate to subglobose caulocystidia, somewhat larger basidiomata, larger basidiospores and habitat on dead wood of *Artocarpus* species are the variations observed in the Indian collections and can be considered as additional features. This variation could be due to the eco-physiological and geographic conditions prevailing in the current location.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

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