Plant and Fungal Systematics 71(1): 91–96, 2026
DOI: https://doi.org/10.35535/pfsyst-2026-0010

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

Coccocarpia aptrootii, a new lichen species from Mauritius

Paul Diederich[1*], Damien Ertz[2] & Einar Timdal[3]

Article info

Received: 28 Feb. 2026
Revision received: 15 Jun. 2026
Accepted: 23 Jun. 2026
Published: 31 Jul. 2026

Associate Editor

Harrie Sipman

Abstract. A new species of *Coccocarpia* is described from Mauritius based on morphological and molecular evidence. The species is corticolous and currently known from four localities in parkland and natural mountain forest habitats. It is characterized by comparatively large thallus lobes, a distinctly pruinose upper surface, and abundant laminal isidia that are initially subspherical and later elongate into cylindrical to coralloid structures. Phylogenetic analysis of nuclear ITS rDNA sequences places the Mauritian material as a distinct lineage within *Coccocarpia*, not nested within any currently sampled species-level clade. The combined morphological distinctiveness and molecular differentiation support its recognition as a new species, here described as *Coccocarpia aptrootii*. This discovery further demonstrates that species diversity in *Coccocarpia* remains underestimated, particularly in tropical regions.

Key words: Indian Ocean, lichens, molecular phylogeny, new species, taxonomy

Introduction

The lichen genus *Coccocarpia* Pers. (*Peltigerales*, *Ascomycota*) comprises foliose, predominantly tropical lichens associated with cyanobacteria as photobionts. Species of the genus are typically corticolous or saxicolous and are characterized by a heteromerous thallus with distinctive rhizines and often well-developed vegetative propagules. Despite its relatively conspicuous morphology and wide tropical distribution, the taxonomy of *Coccocarpia* has long been considered difficult because of extensive morphological variation and the limited number of stable diagnostic characters.

The first comprehensive worldwide revision of the genus was provided by Arvidsson (1983), who recognized 28 species based primarily on morphological and anatomical characters. Several additional taxa have subsequently been described, but species delimitation within *Coccocarpia* has remained problematic, partly because many species have been regarded as broadly distributed and morphologically variable. In particular, combinations of characters such as thallus lobe morphology and size, and the structure of vegetative propagules have often shown considerable overlap among taxa.

During fieldwork in Mauritius, material of *Coccocarpia* was collected that showed a unique combination of morphological characters not matching any species recognized in the global revision of the genus or in subsequent taxonomic treatments. These specimens are characterized by comparatively broad thallus lobes, a distinctly pruinose upper surface, and abundant laminal isidia that are initially subspherical and later elongate, becoming cylindrical to coralloid and never flattened. No species currently described in the genus is known to possess this combination of characters.

Recent molecular phylogenetic studies have profoundly changed our understanding of species diversity and evolution within *Coccocarpia* (Coca et al. 2025). A global phylogenetic analysis based on multiple genetic markers demonstrated that the genus is monophyletic, but that many traditionally recognized species represent polyphyletic assemblages. The study further suggested that the diversity of the genus has been vastly underestimated and that it may contain well over 150 species worldwide. The phylogeny also revealed strong geographical structuring, with major lineages largely restricted to the Paleotropics, the Neotropics, or showing pantropical distributions, and suggested an origin of the genus in tropical Australasia–Oceania during the Late Cretaceous.

In order to clarify the taxonomic placement of the Mauritian material, we generated ITS sequence data from a representative specimen and incorporated it into a phylogenetic framework based on previously published datasets. The resulting analyses demonstrated that the Mauritian populations form a distinct lineage that is not conspecific with any sequenced species of *Coccocarpia*.

[1] National Museum of Natural History, 25 rue Munster, L-2160 Luxembourg, Luxembourg
[2] Meise Botanic Garden, Department of Research, Nieuwelaan 38, 1860 Meise, Belgium, and Fédération Wallonie-Bruxelles, Service général de l'Enseignement supérieur et de la Recherche scientifique, rue A. Lavallée 1, 1080 Bruxelles, Belgium
[3] Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, 0318 Oslo, Norway
[*] Corresponding author e-mail: paul.diederich@education.lu

Additional herbarium studies revealed further specimens collected in Mauritius, indicating that this taxon is not restricted to a single locality, but is apparently widespread on the island.

Based on the combined morphological, anatomical, and molecular evidence, we describe this material here as a new species of *Coccocarpia*. The new species contributes to the growing evidence that species diversity in the genus is higher than previously assumed and highlights the importance of regional sampling in tropical areas for understanding the global diversity of cyanobacterial lichens.

Material and methods

Molecular techniques

A well-preserved herbarium specimen, ten months old, was used for DNA isolation. Hand-cut thallus sections were subjected to direct PCR following Ertz et al. (2015). The material was placed directly into microtubes containing 20 µl H_2O. Amplification reactions were prepared in a final volume of 50 µl, including the lichen material, as described in Ertz et al. (2018). A fragment of ~0.6 kb of the nuclear ribosomal DNA internal transcribed spacer region (ITS1, 5.8S, ITS2) (nucITS) was amplified using primers ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990). PCR cycling conditions for nucITS were: (1) 10 min at 95°C; (2) 35 cycles of 45 s at 95°C, 1 min at 52°C, 75 s at 72°C; and (3) a final extension of 10 min at 72°C. Both strands were sequenced by Macrogen® using the amplification primers. Sequence fragments were assembled with Sequencher v. 5.3 (Gene Codes Corporation, Ann Arbor, Michigan).

Taxon selection and phylogenetic analyses

One new nucITS sequence was generated for this study (GenBank accession number PZ381589; voucher: Diederich 18312). The closest matches were identified using megablast searches in GenBank. Additional representatives of *Coccocarpia* were selected from Coca et al. (2025) to represent the principal clades recovered in that study (Fig. 1). The selection prioritized sequences that were assigned to named species, thereby excluding those labelled "sp.", except for sequences originating from the African continent, as they are geographically closer to our new species. Sequences were aligned using MAFFT v. 7.505 (Katoh et al. 2002) on the CIPRES Science Gateway (Miller et al. 2010) and manually refined in Mesquite v. 4.01 (Maddison & Maddison 2025). Ambiguously aligned regions and incomplete sequence ends were delimited manually and excluded.

The final alignment comprised 70 terminals and 594 unambiguously aligned positions (File S1). *Sticta lobarioides* was selected as the outgroup, following the phylogeny of *Coccocarpia* presented by Coca et al. (2025). Best-fit substitution models were evaluated under the Akaike Information Criterion (AIC) using jModelTest v. 2.1.6 (Darriba et al. 2012). The GTR+I+G model was selected for the nucITS dataset. Maximum Likelihood (ML) analysis was conducted in RAxML v. 8.2.12 (Stamatakis 2014) via the CIPRES Science Gateway, using the GTRGAMMA model and 1,000 rapid bootstrap replicates. Bootstrap values (ML-BS) were mapped onto the best-scoring ML tree. Nodes with ML-BS ≥ 70 were considered well supported and are indicated by thicker branches (Fig. 1). The tree was visualized in FigTree v. 1.4.4 (Rambaut 2018).

Results

Phylogenetic analysis

The principal, well-supported lineages of the phylogenetic tree correspond to those recovered by Coca et al. (2025). The backbone topology is relatively well resolved and comprises two major clades: (1) a Paleotropical lineage extending from *Coccocarpia dissecta* [Thailand] to *C. dissecta* [USA]; and (2) a second lineage subdivided in a Neotropical clade (from *C. erythroxyli* [Puerto Rico] to *C. erythroxyli* [Colombia]) and a larger clade extending from *C. glaucina* to *C. palmicola*. *Coccocarpia epiphylla*, *C. erythroxyli*, *C. palmicola* and *C. dissecta* are recovered as polyphyletic. The new species is placed within the clade extending from *C. glaucina* to *C. palmicola*, where it occupies a distinct and isolated position. It is more closely related to sequences originating from Eastern Paleotropics than to African ones, but the relationships are mostly poorly supported.

Taxonomy

Coccocarpia aptrootii Diederich, Ertz & Timdal, sp. nov. (Fig. 2)

MycoBank MB 863770

Diagnosis: Distinguished from *Coccocarpia smaragdina* and *C. pruinosa* by the presence of numerous subspherical to cylindrical or coralloid laminal isidia.

Type: Mauritius, Plaines Wilhems distr., Curepipe, Curepipe Botanic Gardens, 20.3244°S, 57.5136°E (±100 m), 565 m, on bark of trees, 30 Jul. 2016, P. Diederich 18312 (MAU – holotype; BR – isotype).

Etymology. The epithet honors our friend Dr André Aptroot, in recognition of his outstanding contributions to lichenology.

Description. Thallus orbicular, loosely attached, up to 6 cm diam., foliose, lobate. Lobes greyish to bluish grey, 2–4 mm wide, adjacent to imbricate, broadly cuneate to flabellate, apically often rounded, not elongate, slightly concave to slightly convex, occasionally incised; lobe margins slightly recurved; accessory lobules not observed. Upper surface ± smooth, never wrinkled, distinctly and uniformly pruinose over the entire lobe surface, radially faintly striate or not. Pruina white. Isidia abundant, laminal, developing in the center of lobes, always leaving a narrow marginal zone devoid of isidia; initially almost subspherical, later vertically elongating and becoming subcylindrical, terete, never flattened, simple or coralloid-branched, concolorous with the thallus or slightly

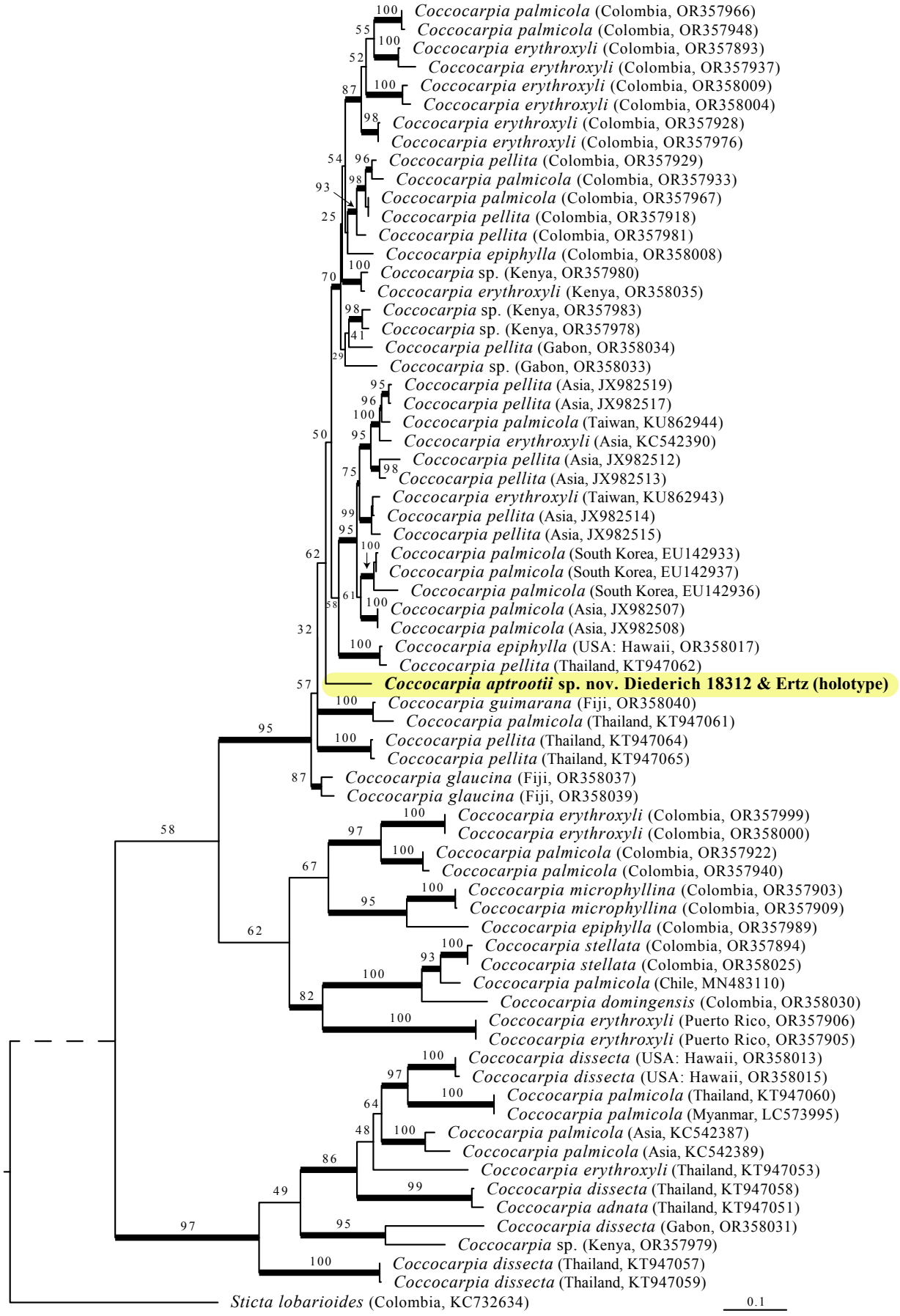

Figure 1. Phylogeny of *Coccocarpia*, with *Sticta lobarioides* as outgroup, inferred from nucITS sequences using Maximum Likelihood analysis in RAxML. Bootstrap values (ML-BS) are shown near internal branches. Branches with ML-BS ≥70 are drawn thicker. The newly generated sequence is shown in bold and highlighted in color. The length of the branch represented by a dashed line was reduced by 50% for editing reason. Species names are followed by geographic origin and GenBank accession number.

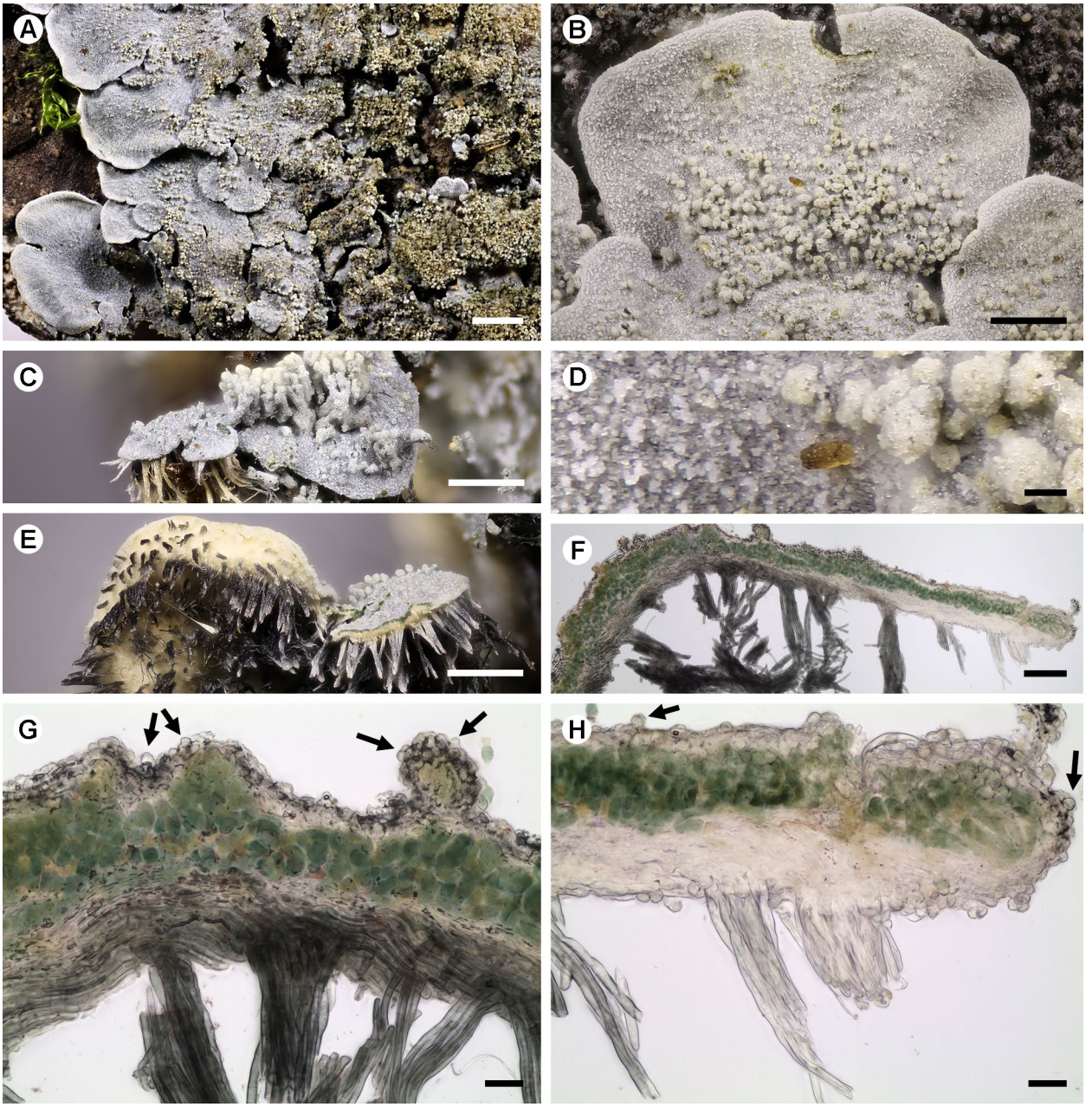

Figure 2. *Coccocarpia aptrootii* (A, holotype; B–H, Diederich 19140). A – pruinose thallus covered with isidia; B – pruinose thallus lobe with young, subspherical to shortly cylindrical, laminal isidia; C – thallus lobe with subcylindrical, coralloid isidia and cream-colored marginal rhizines; D – thallus surface at high magnification, showing cellular pruina and young isidia; E – section through a lobe, showing pale to slightly greyish rhizines (right) and an ochraceous lower lobe surface with dark grey to blackish rhizines (left); F – section through a thallus lobe in water, showing colorless marginal and dark grey central rhizines; G – enlargement of F, showing the upper cortex, photobiont layer, scarcely distinguishable greyish medulla and lower cortex, and the ontogeny of young isidia; H – same as G, showing a colorless medulla and lower cortex, and colorless rhizines. Arrows in G and H indicate cells forming the pruina. Scale bars: A = 1 mm; B, C, E = 0.5 mm; D = 50 µm; F = 100 µm; G, H = 20 µm. Photos: P. Diederich.

paler, when old, occasionally apically broken and then appearing darker, 50–100 µm diam., up to 500 µm tall. Lower surface cream near the margins, centrally with an ochraceous tinge, densely rhizinate. Rhizines cream when young, later basally cream and apically grey to blackish, distinct, initially simple or entangled, later becoming fibrillose, rarely projecting beyond the lobe margins. Apothecia and pycnidia unknown.

Anatomy. Thallus 80–150 µm thick. Upper cortex colorless, 10–18 µm thick, consisting of 2–4 layers of cells 6–11 µm diam. Epicortex absent. Pruina on the upper cortex composed of scattered, rounded cells with a granular surface, 5–8 µm diam. Photobiont cyanobacterial. Photobiont layer 30–80 µm thick; photobiont cells 10–15 µm diam. Medulla and lower cortex hardly distinguishable, together 35–47 µm thick, composed of 10–13 layers of rather densely compacted, horizontal hyphae; colorless near the lobe margins, dark grey to blackish centrally; hyphae 4–7 µm thick. Rhizines colorless near the lobe margins, centrally dark grey to blackish, composed of densely compacted, vertical hyphae, 4–7 µm thick.

Chemistry. Thallus K–, C–, KC–, UV–; no substances detected by TLC.

Ecology and distribution. All known specimens are corticolous on bark of unidentified trees, occurring both in parkland habitats and in natural mountain forests. Currently known from four localities in Mauritius.

Notes. Owing to the densely pruinose thallus and the form and size of the lobes, this species closely resembles *Coccocarpia smaragdina* Pers., originally described from Mariana Islands and rather common in Mauritius, from which it is readily distinguished by the constant presence of subspherical to subcylindrical or coralloid, laminal isidia. The similar *C. pruinosa* L. Arvidss., described from Réunion and also known from Mauritius (Diederich & Ertz 2020), differs in having rounded, flattened isidia (Arvidsson 1983). The only other known *Coccocarpia* species with pruinose lobes is *C. rottleri* (Ach.) L. Arvidss., described from the East Indies, which is distinguished by much narrower lobes, 0.1–0.6 mm wide, and the presence of accessory lobules. The new species has been collected at the type locality (Curepipe Botanic Gardens) in 1991, 2016 and 2019. Some morphological variability was observed among these collections, particularly in the development of radial striation of the upper surface. In the holotype specimen, the lobes are distinctly radially striate, whereas in other collections the striation is present, but less pronounced. We interpret this variation as phenotypic variability within a single species; however, this character merits attention when additional populations are discovered.

Additional specimens examined. MAURITIUS. Plaines Wilhems distr.: Same locality as type, 20.3251°S, 57.5139°E (±200 m), on bark of trees, 9 Sept. 2019, P. Diederich 19140 & D. Ertz 24178 (BR; MAU); ibid., 4 Nov. 1991, H. Krog & E. Timdal MAU 02/04 (O L-21129); Macchabee Forest, along road from Le Pétrin to Mt Bris Fer, 20°23′S, 57°26′E, 600 m, corticolous, 21 Nov. 1991, H. Krog & E. Timdal MAU 63/01 (O L-22127). Rivière Noire distr.: Black River Gorges National Park, along trail from Plaine Champagne towards Piton de la Petite Rivière Noire, 20.4213°S (±700 m), 57.4195°E (±200 m), 630–700 m, corticolous, 5 Aug. 2016, P. Diederich 19548 (BR; MAU). Savanne distr.: Mt Cocotte, SE of the peak, along the road towards Bassin Blanc, 20°26′S, 57°28′E, 620 m, corticolous, 9 Nov. 1991, H. Krog & E. Timdal MAU 29/02 (O L-21501).

Discussion

The combination of morphological, anatomical, and molecular evidence demonstrates that the Mauritian material represents a distinct evolutionary lineage within *Coccocarpia*. The new species is morphologically diagnosable and genetically differentiated from all sequenced taxa currently available. Its discovery further supports the view that species diversity in *Coccocarpia* has been underestimated and that island systems such as Mauritius may harbor previously overlooked lineages. Continued regional sampling, combined with multilocus phylogenetic approaches, will be essential to resolve species boundaries and evolutionary relationships within this morphologically plastic and phylogenetically complex genus.

Acknowledgments

P. D. and D. E. are grateful to all those who facilitated their fieldwork in Mauritius, assisted during excursions, and provided the necessary collecting permits. We particularly thank Cláudia Baider and Kersley Pynee (The Mauritius Herbarium, Réduit), Vincent Florens (University of Mauritius, Réduit), Kevin Ruhomaun, Parmananda Ragen and Mario Allet (National Parks and Conservation Service, Réduit), and Zayd Jhumka (Forestry Service, Curepipe) for their support and collaboration. Collecting and transport of specimens were conducted under permits FD No. 971/A/III (Forestry Service, Curepipe, 25 Jul. 2016) and NP57/1 V5 (National Parks and Conservation Service, Réduit, 28 Jul. 2016). We also thank Wim Baert for his assistance with the molecular laboratory work.

ORCID

Paul Diederich https://orcid.org/0000-0003-0357-7414
Damien Ertz https://orcid.org/0000-0001-8746-3187
Einar Timdal https://orcid.org/0000-0003-4524-0617

Supplementary electronic materials

File S1. ITS alignment of *Coccocarpia* sequences. Sequence headers indicate the GenBank accession numbers followed by the taxon names. Regions that were excluded from the analyses are provided. Download file

References

Arvidsson, L. 1983 [‘1982’]. A monograph of the lichen genus *Coccocarpia*. *Opera Botanica* 67: 1–96.

Coca, L. F., Lumbsch, H. T., Marcado-Díaz, J. A., Widhelm, T. J., Goffinet, B., Kirika, P. & Lücking, R. 2025. Diversity, phylogeny, and historical biogeography of the genus *Coccocarpia* (lichenized *Ascomycota*: *Peltigerales*) in the tropics. *Molecular Phylogenetics and Evolution* 206: 108312. https://doi.org/10.1016/j.ympev.2025.108312

Darriba, D., Taboada, G. L., Doallo, R. & Posada, D. 2012. jModelTest2: more models, new heuristics and parallel computing. *Nature Methods* 9: 772. https://doi.org/10.1038/nmeth.2109

Diederich, P. & Ertz, D. 2020. First checklist of lichens and lichenicolous fungi from Mauritius, with phylogenetic analyses and description of new taxa. *Plant and Fungal Systematics* 65(1): 13–75. https://doi.org/10.35535/pfsyst-2020-0003

Ertz, D., Tehler, A., Irestedt, M., Frisch, A., Thor, G. & van den Boom, P. 2015. A large-scale phylogenetic revision of *Roccellaceae* (*Arthoniales*) reveals eight new genera. *Fungal Diversity* 70: 31–53. https://doi.org/10.1007/s13225-014-0286-5

Ertz, D., Sanderson, N., Łubek, A. & Kukwa, M. 2018. Two new species of *Arthoniaceae* from old-growth European forests, *Arthonia thoriana* and *Inoderma sorediatum*, and a new genus for *Schismatomma niveum*. *The Lichenologist* 50: 161–172. https://doi.org/10.1017/S0024282917000688

Gardes, M. & Bruns, T. D. 1993. ITS primers with enhanced specificity for basidiomycetes, application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2: 113–118. https://doi.org/10.1111/j.1365-294X.1993.tb00005.x

Katoh, K., Misawa, K., Kuma, K. & Miyata, T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research* 30: 3059–3066. https://doi.org/10.1093/nar/gkf436

Maddison, W. P. & Maddison, D. R. 2025. Mesquite: a modular system for evolutionary analysis. Version 4.01. Available from: https://www.mesquiteproject.org

Miller, M. A., Pfeiffer, W. & Schwartz, T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceedings of the Gateway Computing Environments Workshop (GCE), 14 Nov. 2010, New Orleans, pp. 1–8. https://doi.org/10.1109/GCE.2010.5676129

Rambaut, A. 2018. FigTree v1.4.4. Available from: https://tree.bio.ed.ac.uk/software/figtree/

Stamatakis, A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30: 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

White, T. J., Bruns, T., Lee, S. B. & Taylor, J. W. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis, M. A., Gelfand, D. H., Sninsky. J. J. & White, T. J. (eds), *PCR Protocols: a Guide to Methods and Applications*. New York: Academic Press, pp. 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1