Article received 26 August 2025, accepted 11 October 2025, additional images received 8 October 2025

First record of *Mystagaricus brunneolilacinus* (*Basidiomycota*, *Agaricaceae*) in the Dominican Republic

Claudio Angelini[a,b,*], Alfredo Justo[c]

[a]Herbario Jardín Botánico Nacional Dr. Rafael Ma. Moscoso, Santo Domingo, Dominican Republic
[b]Via dei Cappuccini 78/8, I-33170 Pordenone, Italy
[c]New Brunswick Museum, 277 Douglas Avenue, Saint John, NB E2K 1E5, Canada

*Corresponding author: claudio_angelini@libero.it

Key words:
Fungi
Agaricales
First record
Caribbean

Abstract: Based on morphological and molecular data, we document the presence of *Mystagaricus brunneolilacinus* in natural forested areas of the Dominican Republic. This taxon was originally described from a tropical greenhouse in Hungary, and so far has only been reported from similar habitats in Austria, Canada, Germany and Spain. Our collections represent the first confirmed record of this species in its putative natural habitat in Mesoamerica.

INTRODUCTION

Tropical greenhouses in temperate areas of Europe and North America provide an ideal habitat for lepiotoid fungi native to the tropics (Vellinga 2004). In many cases, the species recorded in these environments have been first described based on temperate collections and only later they have been found in their native tropical environments, e.g. *Leucocoprinus heinemannii* Migliozzi (Justo *et al.* 2020), *Leucoagaricus rubroconfusus* Migliozzi & Coccia (Justo, Angelini & Bizzi 2021) and *Coprinopsis calospora* (Bas & Uljé) Redhead, Vilgalys & Moncalvo (Voto & Angelini 2025).

Leucoagaricus brunneolilacinus Babos was originally described from a tropical greenhouse in Hungary (Babos 1980). It was subsequently reported from similar habitats in Austria, Germany and Canada (Radnóti *et al.* 2025). It has also been recorded in Spain growing in a flower pot (Jiménez Antonio & Reyes García 2021) and in an outdoor garden (Conca & Garrido-Benavent 2024). The new genus *Mystagaricus* V. Papp, Radnóti & Dima has recently been proposed to accommodate *L. brunneolilacinus*, based on its morphological characteristics and the results of multi-gene phylogenetic analyses (Radnóti *et al.* 2025). These authors have hypothesised a Palaeotropical origin for the genus *Mystagaricus*, based on the geographic distribution of its closest relatives, since no tropical collections of *M. brunneolilacinus* (Babos) V. Papp, Radnóti & Dima were known at the time.

Here we report and describe in detail two collections of *M. brunneolilacinus* from the Dominican Republic. Their identity is confirmed by their morphological characteristics and DNA (ITS, *rbp2*) sequences.

MATERIALS AND METHODS

Morphological study

Basidiocarps were photographed in the field using a Nikon Coolpix 8400 camera and subsequently dried. Collections were studied using standard procedures for morphological examination of lepiotaceous fungi (Candusso & Lanzoni 1990; Vellinga 2001). Microscopic observations were made on a Meiji Techno 4000 microscope. Descriptive terms for morphological features follow Vellinga (1988, 2001). The neutral term “pileus covering” is used for all covering layers of the pileus following Vellinga (2001). The notation N = x/y indicates that measurements were made from x basidiospores across y collections. Spore values are reported as an interval, with extreme values (less than 2%) shown in parentheses. The following abbreviations were used in the descriptions: avl for average length, avw for average width, Q for quotient of length and width, and Qav for average quotient.

Molecular study

ITS and *rpb2* sequences for the Dominican collections were generated at ALVALAB (Oviedo, Spain) and UNITE (University of Tartu, Estonia), with primers ITS1F/ITS4 (White *et al.* 1990; Gardes &Bruns 1993) and bRPB2-6F/bRPB2-7R (Matheny *et al.* 2007) respectively, and were deposited in the Genbank (Sayers *et al.* 2021) and UNITE (Abarenkov *et al.* 2023) public databases respectively. We assembled separate ITS and *rpb2* datasets

based on the results of Radnóti *et al.* (2025), with *Eriocybe chionea* as an outgroup. Sequences for both datasets were aligned using MAFFT 7 (Katoh & Standley 2013) under the strategy FFT-NS-i. Sequences used in this study are listed in Table 1. Alignment files were inspected, manually trimmed and corrected in AliView (Larsson 2014). A concatenated ITS + *rpb2* dataset was used for the phylogenetic analysis. We ran a maximum likelihood (ML) analysis using RaxML HPC2, v. 8.2.12 (Stamatakis 2014) under a GTRGAMMAI model with 1000 bootstrap (BS) replicates, using the resources at the CIPRES Science Gateway (Miller *et al.* 2010) (Figure 5).

RESULTS

Phylogenetic analyses

The Dominican collections of *M. brunneolilacinus* appear in a well-supported clade with the European collections of the same species in the ITS + *rpb2* phylogeny (Figure 5). There is some internal variation in the ITS sequences, mostly caused by 4 ambiguous or variable nucleotide positions. The *rpb2* sequence of ANGE differs only in 1-2 nucleotide positions with respect to the rpb2 sequences of the European collections. The collection MFLU090129 from Thailand, initially identified as "*Lepiota* aff. *fuscovinacea*", appears as sister to *M. brunneolilacinus*. As indicated in Radnóti *et al.* (2025), this collection probably represents a yet-undescribed species of *Mystagaricus*.

Taxonomy

Mystagaricus brunneolilacinus (Babos) V. Papp, Radnóti & Dima (Figure 1)
Mycol. Progr. 24(no. 54): 10 (2025)

Basionimo: *Leucoagaricus brunneolilacinus* Babos, *Annls hist.-nat. Mus. natn. hung.* 72: 81 (1980)

Macroscopic characters

Pileus 30 – 90 mm in diameter, hemispherical, then plano-convex, and finally flattened, without an umbo; surface dry, purplish brown, vinaceous, strongly fibrillose-squamose, with distinct, leathery scales on the disc, elsewhere woolly-fibrillose scaly, with a tendency to radially split with age, showing the white context underneath; margin projecting beyond the gills, often with overhanging velar remnants.
Lamellae crowded, lamellulae abundant; up to 3 mm broad, free; white, immediately becoming pink-apricot and then brown-pink if rubbed; edges entire, smooth.
Stipe 50 – 110 × 7 – 12 mm, cylindrical, often curved, sometimes slightly widened towards the base; white, floccose at the apex, otherwise entirely with vinaceous, purplish brown fibrillose-lanuginose zig-zagged zones, above and below the annulus.
Annulus pendant, thin, membranaceous, with the surface covered with the same fibrils that cover the stipe, whitish with vinaceous tinges, often absent because it remains completely attached to the pileus margin.
Context thin, white in the pileus, whitish and turning orange and then dark brown when cut in the stipe.
Smell unpleasant.

Microscopic characters

Basidiospores (N = 40/2) ellipsoid to oblong, smooth, hyaline, (3.5) 4.0–4.8 (5.0) × (2.2) 2.5–3.0 (3.2) µm, avl × avw = 4.56 × 2.8 µm, Q = (1.33) 1.4 – 1.66 (1.72), Qav = 1.62 µm, dextrinoid in iodine, metachromatic in Cresyl Blue; germ pore not observed.
Basidia 15.5 – 18 × 5 – 6 µm, 4-spored, clavate.
Cheilocystidia 15 – 20 × 3 – 7 µm, cylindrical to clavate.
Pleurocystidia not observed.
Pileus covering a cutis made up of long, cylindrical, septate, branching hyphae with terminal elements up to 70 × 6.5 µm, smooth or with granular incrustations and purple-brown intracellular pigment in water.
Clamp connections not observed.

Habit, habitat and distribution: often gregarious to caespitose; growing among leaf litter or accumulations of plant refuse; in coastal or hilly broadleaved forests.

Figure 1. *Mystagaricus brunneolilacinus*. First row: fresh specimens in their natural habitat; second row: (left) detail of the pileal surface, (centre) and (right) cross section; third row: (left) to (right) cheilocystidia, spores, structure of pileipellis.

Figure 2 and 3. *Mystagaricus brunneolilacinus*. Guatemala, Peten, Loc. El Remate (author Camila Samara)

Material examined: Dominican Republic. Puerto Plata, Cabarete, Loc. See Horse Runch, six specimens with caespitose growth on litter in a coastal forest with almond trees near, among a pile of tree prunings, 26 Mar. 2020, *legit C. Angelini* (personal fungarium n. ANGE1296); Puerto Plata, Sosúa, Loc. Monkey Jungle, one specimen growing on litter in a natural hill forest with various broadleaf trees, 15 Feb. 2024, *legit C. Angelini* (personal fungarium n. ANGE1872).

NOTES

The genus *Mystagaricus* is characterized by its medium-sized pilei with purplish brown, woolly or felty covering over ivory white surface, consisting of long, branching purple elements, and stipes ornamented with vinous, fibrillose-lanuginose ± zig-zagged girdles above and below a pendant annulus (Radnóti *et al*. 2025).

M. brunneolilacinus is characterized by its slender appearance and medium size; (sub) caespitose habit; a strongly fibrillose-scaly pileus with purplish-brown scales on an ivory-white ground surface; a stipe covered with zigzag, fibrillose-downy, purple-vinaceous belts, with a pendant purple ring above and below; an immediate intense orange-red color change of the gills and context; dextrinoid and metachromatic spores; and the absence of clamp connections.

Its external appearance somewhat resembles the European *Lepiota fuscovinacea* F.H. Møller & J.E. Lange or the Caribbean (Martinique) *L. ianthinosquamosa* Pegler, but both species are smaller, with an ephemeral and fleeting ring, an unchanging white context, non-metachromatic spores, and abundant clamp connections.

The herbarium voucher MFLU090129 from Northern Thailand, labeled as "*Lepiota* aff. *fuscovinacea*", represents a taxon with white spores, without clamp connections, and a floccose fibrillose vinaceous gray pileus covering (Vellinga, Sysouphanthong & Hyde, 2011). In the phylogenetic analyses this collection appears as the sister-taxon to *M. brunneolilacinus*, with the ITS sequences of both taxa having 94% similarity. This collection is presumed to represent an undescribed *Mystagaricus* species.

The collections reported and described in this study extend the global distribution of *M. brunneolilacinus* to the Caribbean and, having personal knowledge of its presence also in Guatemala (Figure 2, 3) and Puerto Rico (Figure 4), we believe that the species is more widely distributed in the Mesoamerica. However, additional sequenced collections are needed for confirmation.

Based on the geographic distribution of its closest relatives (*Pseudolepiota*, *Xanthagaricus*), Radnóti *et al.* (2025) suggested a biogeographic origin in Palaeotropical Asia for *Mystagaricus*. Our data add another piece of the biogeographical puzzle for the genus and indicate that a Mesoamerican origin cannot be ruled out, at least for *M. brunneolilacinus*.

Figure 4. *Mystagaricus brunneolilacinus*. Puerto Rico, Quebradillas, Loc. Mirador de Guajataca (author Kurt Miller)

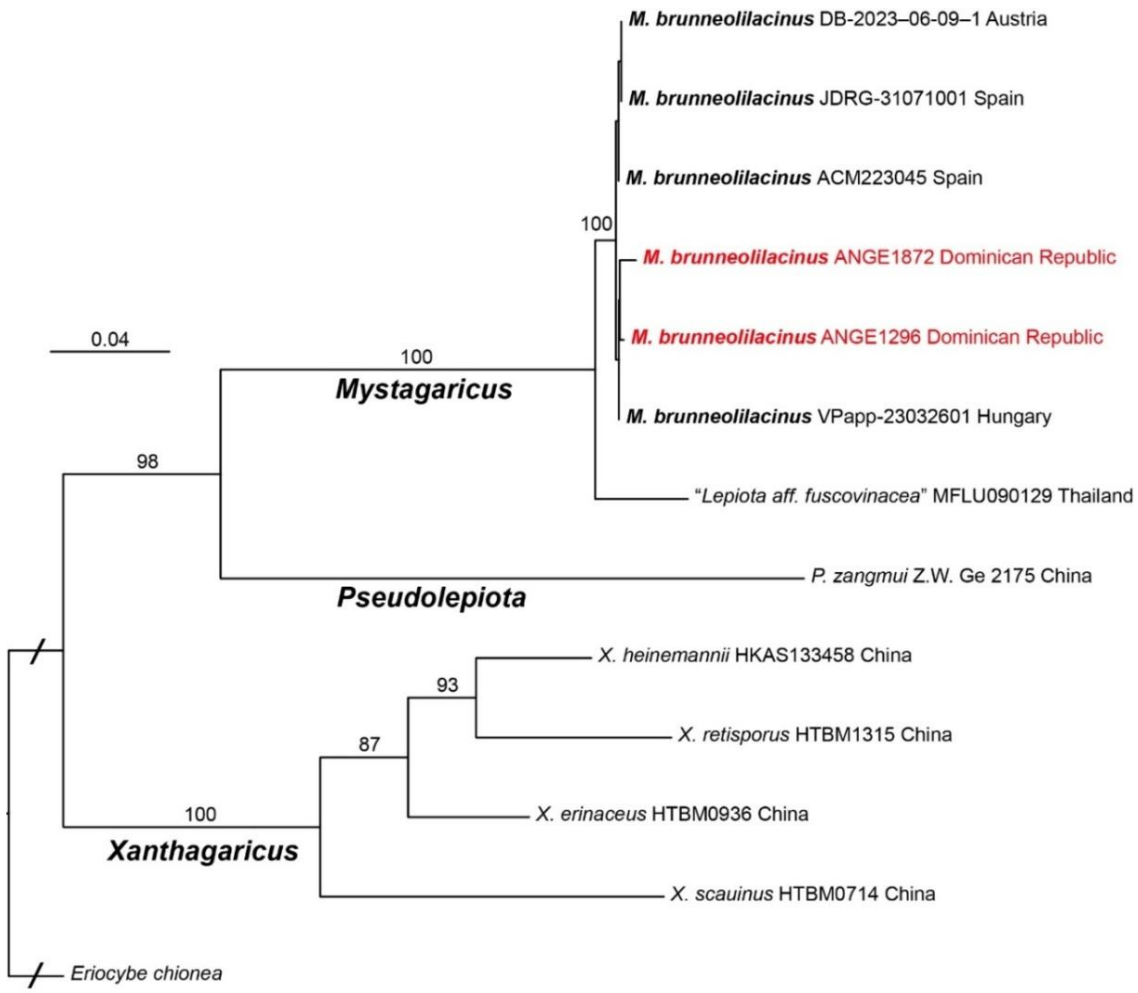

Figure 5. Maximum Likelihood (ML) best tree based on the ITS + rpb2 dataset. Bootstrap support values ≥ 70% are shown on the branches. A slash (/) indicates branches with reduced length for graphical representation.

Taxon	Collection	Country	ITS	*rpb2*
Eriocybe chionea	ecv3560	Thailand	HM488752	HM488800
Mystagaricus brunneolilacinus	ANGE 1296	Dominican Republic	PX171990	PX207708
Mystagaricus brunneolilacinus	ANGE 1872	Dominican Republic	UDB07676645	-
Mystagaricus brunneolilacinus	DB-2023–06-09–1	Austria	PV659895	PV657075
Mystagaricus brunneolilacinus	VPapp-23032601	Hungary	PV659894	PV657074
Mystagaricus brunneolilacinus	JDRG-31071001	Spain	OK582196	-
Mystagaricus brunneolilacinus	ACM223045	Spain	PQ129437	-
"Lepiota aff. *fuscovinacea"*	MFLU090129	Thailand	HM488758	-
Pseudolepiota zangmui	Z.W. Ge 2175	China	KY768928	KY768929
Xanthagaricus erinaceus	HTBM0936	China	PP736704	PP746788
Xanthagaricus heinemannii	HKAS133458	China	PP736714	PP746799
Xanthagaricus retisporus	HTBM1315	China	PP736662	PP746797
Xanthagaricus scauinus	HTBM0714	China	PP736700	PP746787

Table 1. Sequences used in the phylogenetic analysis

REFERENCES

Abarenkov, K; Nilsson, RH; Larsson, K-H; Taylor, AFS; May, TW; Frøslev, TG; Pawlowska, J; Lindahl, B; Põldmaa, K; Truong, C; Vu, D; Hosoya, T; Niskanen, T; Piirmann, T; Ivanov, F; Zirk, A; Peterson, M; Cheeke, TE; Ishigami, Y; Jansson, AT; Jeppesen, TS; Kristiansson, E; Mikryukov, V; Miller, JT; Oono, R; Ossandon, FJ; Paupério, J; Saar, I; Schigel, D; Suija, A; Tedersoo, L; Kõljalg, U (2023) The UNITE database for molecular identification and taxonomic communication of fungi and other eukaryotes: sequences, taxa and classifications reconsidered. *Nucleic Acids Research* **52**(D1):D791–D797

Babos, M (1980) Studies on Hungarian *Lepiota* s.l. species, V. *Ann. Hist.-Nat. Mus. Natl. Hung*. **72**:81–84

Candusso, M; Lanzoni, G (1990) *Lepiota* s.l. *Fungi europaei* 4. Saronno, Italy: Giovanna Biella. 743 p.

Conca, A; Garrido-Benavent, I (2024) *Leucoagaricus brunneolilacinus* Babos, a novelty for the Valencian fungal checklist. *Butlletí de la. Societat Micològica Valenciana* **28**:71–84

Gardes, M; Bruns, TD (1993) ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. *Mol Ecol* **2**:113–118

Jiménez Antonio, F; Reyes García, JD (2021) Especies Interesantes XXVII. *Lactarius* **29**:20–37

Justo, A; Angelini, C; Bizzi, A (2021) The genera *Leucoagaricus* and *Leucocoprinus* in the Dominican Republic. *Mycologia* **113**(2):348–389

Justo, A; Angelini, C; Bizzi, A; Tatti, A; Vizzini, A (2020) Three new cryptic Caribbean species in the *Leucocoprinus heinemannii* complex (*Agaricaceae*, *Agaricales*). *Mycological Progress* **19**(12):1445–1457

Katoh, K; Standley, DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* **30**:772–780

Larsson, A (2014) AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics* **30**:3276–3278

Matheny, PB; Wang, Z; Binder, M; Curtis, JM; Lim, YW; Nilsson, RH; Hughes, KW; Hofstetter, V; Ammirati, JF; Schoch, CL; Langer, E; Langer, G; Mclaughlin, DJ; Wilson, AW; Frøslev, T; Ge, ZW; Kerrigan, RW; Slot, JC; Yang, ZL; Baroni, TJ; Fischer, M; Hosaka, K; Matsuura, K; Seidl, MT; Vauras, J; Hibbett, DS (2007) Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (*Basidiomycota*, *Fungi*). *Mol Phylogenet Evol* **43**:430–451

Miller, MA; Pfeiffer, W; Schwartz, T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceeding of the Gateway Computing Environments Workshop (GCE), 14 Nov 2010. New Orleans, LA.; Los Alamitos, CA: IEEE Computer Society. p. 1–8

Radnóti, Á; Dima, B; Halász, K; Krisai-Greilhuber, I; Kovács, GM; Papp, V (2025) *Mystagaricus*, a new genus within the core *Agaricaceae* to accommodate *Leucoagaricus brunneolilacinus* described from a tropical greenhouse in Hungary. *Mycol Progress* **24**(no. 54):1–18

Sayers, EW; Cavanaugh, M; Clark, K; Pruitt, KD; Schoch, CL; Sherry, ST; Karsch-Mizrachi, I (2021) GenBank. *Nucleic Acids Res.* **49**:D92–D96

Stamatakis, A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**:1312–1313

Vellinga, EC (1988) Glossary. In: Bas, C; Kuyper, TM; Noordeloos, ME; Vellinga, EC eds. *Flora Agaricina Neerlendica* Vol. 1. Rotterdam, The Netherlands: A.A. Balkema. p. 54–64

Vellinga, EC (2001) *Leucocoprinus, Leucoagaricus*. In: Noordeloos, ME; Kuyper, TM; Vellinga, EC eds. *Flora Agaricina Neerlendica*. Vol. 5. Lisse, The Netherlands: A. A. Balkema. p. 76–108

Vellinga, EC (2004) Ecology and distribution of Lepiotaceous fungi (*Agaricaceae*)—a review. *Nova Hedwigia* **78**:273–299

Vellinga, EC; Sysouphanthong, P; Hyde, KD (2011) The family *Agaricaceae*: phylogenies and two new white-spored genera. *Mycologia* **103**(3):494–509

Voto, P; Angelini, C (2025) Third report of coprinoid fungi (*Psathyrellaceae*, *Agaricales*) in the Dominican Republic with notes on *Coprinopsis clastophylla*, rhacophylloid taxa and the *Coprinopsis afronivea* complex. *MycolObs* **11**:38–68

White, TJ; Bruns, T; Lee, S; Taylor, JW (1990) Amplification and direct sequencing of fungal ribosomal RNAgenes for phylogenetics. In: Innis, MA; Gelfand, DH; Sninsky, JJ; White, TJ eds. PCR protocols: a guide to methods and applications. New York: Academic Press.p. 315–322