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Original Article

# Four new records of *Agaricales* for the Iranian mycobiota from Dalahu County, Western Iran

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## ABSTRACT

The agaric mycobiota of western Iran remains insufficiently explored despite recent advances in fungal diversity studies across the country. During mycological surveys conducted in Dalahu County, Kermanshah Province, basidiomata were collected from forested habitats, grasslands, and orchards. Species identification was achieved through an integrative taxonomic approach combining detailed macromorphological and micromorphological observations with phylogenetic analyses based on nuclear ribosomal ITS sequences. Four species, *Coprinopsis strossmayeri* (*Psathyrellaceae*), *Collybia mongolica* (*Clitocybaceae*), *Meottomyces dissimulans* (*Tubariaceae*), and *Mycena zephirus* (*Mycenaceae*), are reported for the first time from Iran. Comprehensive descriptions of macro- and micromorphological characteristics, ecological notes, specimen data, and phylogenetic relationships are provided for each taxon. The phylogenetic analyses supported the placement of the examined collections within their respective species and complemented the morphological evidence used for species delimitation. These new records considerably expand the known geographical distribution of the four taxa and contribute to a better understanding of the diversity of *Agaricales* in Iran. Furthermore, the results emphasize the importance of integrative taxonomy for documenting fungal biodiversity and highlight Dalahu County as a valuable yet understudied region with significant potential for future mycological investigations.

**KEYWORDS**
*Collybia mongolica, Coprinopsis strossmayeri,* ITS rDNA*, Meottomyces dissimulans, Mycena zephirus.*

## INTRODUCTION

The order *Agaricales* Underw. represents one of the largest and most diverse groups of macrofungi within the phylum *Basidiomycota* (Hyde et al. 2024). Members of this order exhibit remarkable morphological and ecological diversity and include saprophytic, ectomycorrhizal, and pathogenic taxa. Due to their ecological significance and economic importance, species of *Agaricales* have received considerable attention in taxonomic, ecological, and phylogenetic studies during recent decades (Vizzini et al. 2019, Kalichman et al. 2020). These fungi play essential roles in nutrient cycling and the stability of forest ecosystems, while several species are recognized as edible, poisonous, medicinal, or industrially important fungi (Ryberg and Matheny 2012, Sudharsan et al. 2023, Costa et al. 2026).

Phylogenetic studies based on molecular data have substantially improved our understanding of evolutionary relationships within *Agaricales* and have resulted in major taxonomic revisions involving numerous genera and families within the order (Matheny et al. 2006, Zhao et al. 2017). Currently, more than 40,000 species are recognized within *Agaricales* (Vizzini et al. 2019, Kalichman et al. 2020). Multilocus molecular analyses have clarified the phylogenetic placement of many problematic taxa and highlighted the importance of integrating classical morphological studies with DNA-based phylogenetic approaches for accurate species identification and classification.

The identification of these macrofungi, as a fundamental field of study, not only contributes to biodiversity assessment but also provides a basis for diverse investigations on edible, poisonous, medicinal, and mycorrhizal fungi, fungal metabolites, and other related biological studies. Although scattered studies on macrofungi identification in Iran have contributed significantly to documenting fungal diversity, such investigations become considerably more effective

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when conducted as focused regional surveys aimed at characterizing the fungal flora of specific geographical areas. Owing to its diverse climatic conditions and heterogeneous ecosystems, Iran harbors considerable fungal diversity; however, the diversity of *Agaricales* remains insufficiently explored in many regions of the country.

Western Iran, particularly Kermanshah Province, hosts diverse habitats, including forests, mountainous regions, orchards, grasslands, and semi-natural ecosystems that provide suitable environmental conditions for macrofungi. The first systematic studies on macrofungi identification in Kermanshah Province were conducted during 2009–2010 by Fadavi and colleagues (Fadavi et al. 2013, Fadavi et al. 2015). Subsequently, Seidmohammadi and co-workers carried out extensive investigations in the Qalajeh region, resulting in the introduction of numerous new records for the Iranian mycobiota (Seidmohammadi et al. 2018a, Seidmohammadi et al. 2018b, Seidmohammadi et al. 2019a, Seidmohammadi et al. 2019b, Seidmohammadi et al. 2021). Despite these studies, comprehensive investigations on the diversity of *Agaricales* remain limited in many parts of western Iran, including Dalahu County. Therefore, the present study aimed to investigate the diversity of *Agaricales* in Dalahu County, western Iran, using morphological characteristics together with ITS-rDNA sequence analyses. The findings of this study contribute to a better understanding of fungal biodiversity in Iran and provide baseline data for future taxonomic, ecological, and phylogenetic studies on *Agaricales*.

## MATERIALS AND METHODS

### Sampling and Morphological Identification

To investigate the diversity of agaric fungi in Dalahu County, Kermanshah Province, specimens were systematically collected from a range of habitats between 2020 and 2022. Field sampling was concentrated in spring and autumn, coinciding with peak rainfall and the active growth period of agaric fungi. Surveyed habitats included mountainous regions, forests, orchards, and grasslands. GPS coordinates were recorded for each collection site to ensure precise georeferencing and to facilitate subsequent ecological analyses.

Specimens were promptly examined to preserve their fresh morphological features. Thin hand-cut sections of the gills, cap, and stipe were prepared and mounted in water for microscopic analysis. Micromorphological characteristics, including spores, basidia, cystidia, and pileipellis structure, were observed, measured, and documented using an Olympus BX51 light microscope equipped with a digital imaging system. For quantitative analyses, 25–30 structures per specimen were randomly selected to determine average dimensions and assess variability.

Specimens were identified by comparison with comprehensive taxonomic literature and recent studies to ensure accurate classification (Hansen and Knudsen 1992). The status of the identified species as new records for Iran was assessed through a review of the available taxonomic literature, particularly the national checklist of Iranian agarics and boletes (Ghobad-Nejhad et al. 2020). Both currently accepted scientific names and their relevant taxonomic synonyms were considered to verify the absence of previous records from Iran. Representative specimens of each newly recorded species for the Iranian mycobiota were deposited in the fungal herbarium at the Iranian Research Institute of Plant Protection, Tehran, for long-term preservation and future reference. Additional examined material was retained in the authors' collection.

### DNA Extraction and PCR Amplification

Genomic DNA was isolated from selected fungal specimens using the Fungal DNA Extraction Kit (Denazist Asia, Iran) following the manufacturer’s protocol. The internal transcribed spacer (ITS) region was amplified with the primer pair ITS1F/ITS4. PCR reactions were assembled with approximately 50 ng of template DNA, 2 µL of each primer (10 µM working concentration; 0.4 µM final concentration), and 25 µL of 2× ready-to-use master mix (Sinagen, Iran) to a final volume of 50 µL.

Thermal cycling was carried out in a Biometra T-personal thermocycler (Germany) with the following program: initial denaturation at 95 °C for 2 minutes, followed by 35 cycles consisting of 95 °C for 40 seconds (denaturation), 57 °C for 40 seconds (annealing), and 72 °C for 50 seconds (extension), concluding with a final extension at 72 °C for 10 minutes. PCR products were separated on 1% agarose gels, stained with Red Gel, and visualized under UV light to verify amplification.

Successful PCR products were purified and submitted for sequencing by Microsynth (Switzerland). Raw sequences were manually edited using BioEdit software, and the finalized sequences were deposited in GenBank (http://www.ncbi.nlm.nih.gov/genbank) for public access.

### Phylogenetic Analyses

To investigate evolutionary relationships, the newly generated ITS sequences were compared with valid sequences retrieved from GenBank, prioritizing sequences from published studies, using the BLAST algorithm to identify the closest matches. Multiple sequence alignments were performed using MAFFT version 7 via the online server (Katoh and Standley 2013), with manual adjustments made to optimize alignment accuracy. Phylogenetic trees were constructed using the maximum likelihood (ML) method under the Tamura-Nei substitution model in MEGA 12.1.4 software**,** and branch support was evaluated with 1000 bootstrap replicates to assess the reliability of clades.

## RESULTS AND DISCUSSION

During surveys conducted between 2020 and 2022 across various habitats in Dalahu County, a total of 104 agaric fungal specimens were collected. The identified specimens belonged to 20 genera and 26 species. Among these, four species, namely *Collybia mongolica*, *Coprinopsis strossmayeri*, *Meottomyces dissimulans*, and *Mycena zephirus* represent new records for the fungal flora of Iran.

These results demonstrate the rich diversity of agaric fungi in the region and underscore the presence of previously unreported species, expanding the known distribution of these taxa. The identification of these newly recorded species enhances our understanding of the regional mycobiota and provides a solid foundation for further ecological, taxonomic, and phylogenetic investigations. The findings also highlight the ecological significance of Dalahu County as a reservoir of fungal biodiversity, encompassing diverse habitats ranging from forests and grasslands to orchards and mountainous areas. Detailed morphological descriptions and illustrations of these four newly recorded species are presented below in alphabetical order:

***Collybia mongolica*** (S. Imai) Z.M. He & Zhu L. Yang, Fungal Diversity 123: 35 (2023). Fig 1

Macroscopic Features: Pileus initially convex, becoming plane to slightly infundibuliform at maturity, 2–9 cm in diameter, glabrous, yellowish-cream to pale ochre, with a distinctly paler margin (Fig. 1A). Lamellae adnexed to emarginate, sometimes with a shallow decurrent tooth, crowded, pale cream when young, becoming light coffee-brown at maturity (Fig. 1B). Spore print white. Stipe central, cylindrical, solid, 2–4 cm long, whitish-cream, smooth to slightly fibrillose toward the base.

Microscopic Features: Basidia clavate, tetrasporic, measuring 32.25–43.89 × 6.47–9.72 µm (Fig. 1C). Basidiospores ovate to broadly ovate, hyaline, thin-walled, smooth to finely verrucose, measuring 6.68–8.26 × 4.89–5.79 µm (Fig. 1D). Cystidia absent. Clamp connections present. Pileipellis composed of repent cylindrical hyphae, forming a cutis to weakly gelatinized ixocutis. See Table 1 for comparison with published descriptions.

Specimen examined: IRAN, Kermanshah Province, Dalahu, grassland habitat, 1624 m a.s.l., 34°28′50″ N, 46°09′12″ E, 14 April 2020, collected by Sabah Ziaei, identified by Saeed Abbasi, voucher 18934, GenBank accession no. PX632812.

Notes: *Collybia mongolica* occurs solitary to gregarious on humus-rich soils, mainly in grasslands and cultivated fields. It has been reported predominantly from the Mongolian Plateau, particularly northern China and Mongolia (Yu et al. 2011, Lu et al. 2018). The Iranian collection therefore represents a notable extension of its documented geographical distribution. Morphologically, the species is characterized by a pale yellowish-cream pileus, white spore print, and ovate to broadly ovate, finely verrucose basidiospores. It resembles *C. irina*, but the latter differs in its more slender stipe and smaller basidiospores. The morphological characteristics of the Iranian specimen agree with previous descriptions (Yu et al. 2011, Dong and Bau 2013). Originally treated in the genus *Leucocalocybe*, this species is now classified as *C. mongolica* following the treatment of *Leucocalocybe* as a subgenus of *Collybia* (He et al. 2023).

BLASTn comparison of the ITS sequence of the Iranian specimen (PX632812) showed 99.85% sequence identity with GenBank accession KC413944, representing the documented Chinese collection HMJAU:24941 of *Collybia mongolica* (formerly *Leucocalocybe mongolica*; Yu et al. 2011).

The ITS-based phylogenetic analysis placed the studied specimen (PX632812) within the *Collybia mongolica* lineage with 99% bootstrap support (Fig. 2). The Iranian collection clustered with previously published sequences of *C. mongolica* and was clearly separated from closely related taxa, including *C. irina*, *C. phyllophila*, and *C. sordida*. The phylogenetic placement is congruent with the morphological characteristics observed in the examined material, particularly pileus morphology and basidiospore shape and dimensions. The combined morphological and molecular evidence supports the assignment of the examined specimen to *C. mongolica.*

**Table 1.** Morphological comparison of *Collybia mongolica* from Iran with published descriptions.

| Morphological character | Present study | Published description |
|---|---|---|
| Pileus diameter (cm) | 2–9 | 1.5–7 |
| Pileus color | Yellowish-cream to pale ochre | White, yellowish at centre |
| Lamellae | Adnexed to emarginate | Sinuate |
| Basidiospores (µm) | 6.68–8.26 × 4.89–5.79 | 6–9 × 5–7 |
| Basidia (µm) | 32.25–43.89 × 6.47–9.72 | 32–45 × 6–10 |
| Spore ornamentation | Smooth to finely verrucose | Finely verruculose |
| Pileipellis | Cutis to weakly gelatinized ixocutis | Repent epicutis of radial hyphae |
| Clamp connections | Present | Present |

Reference: Yu et al. (2011), under *Leucocalocybe mongolica*. Microscopic measurements are in µm (length × width).

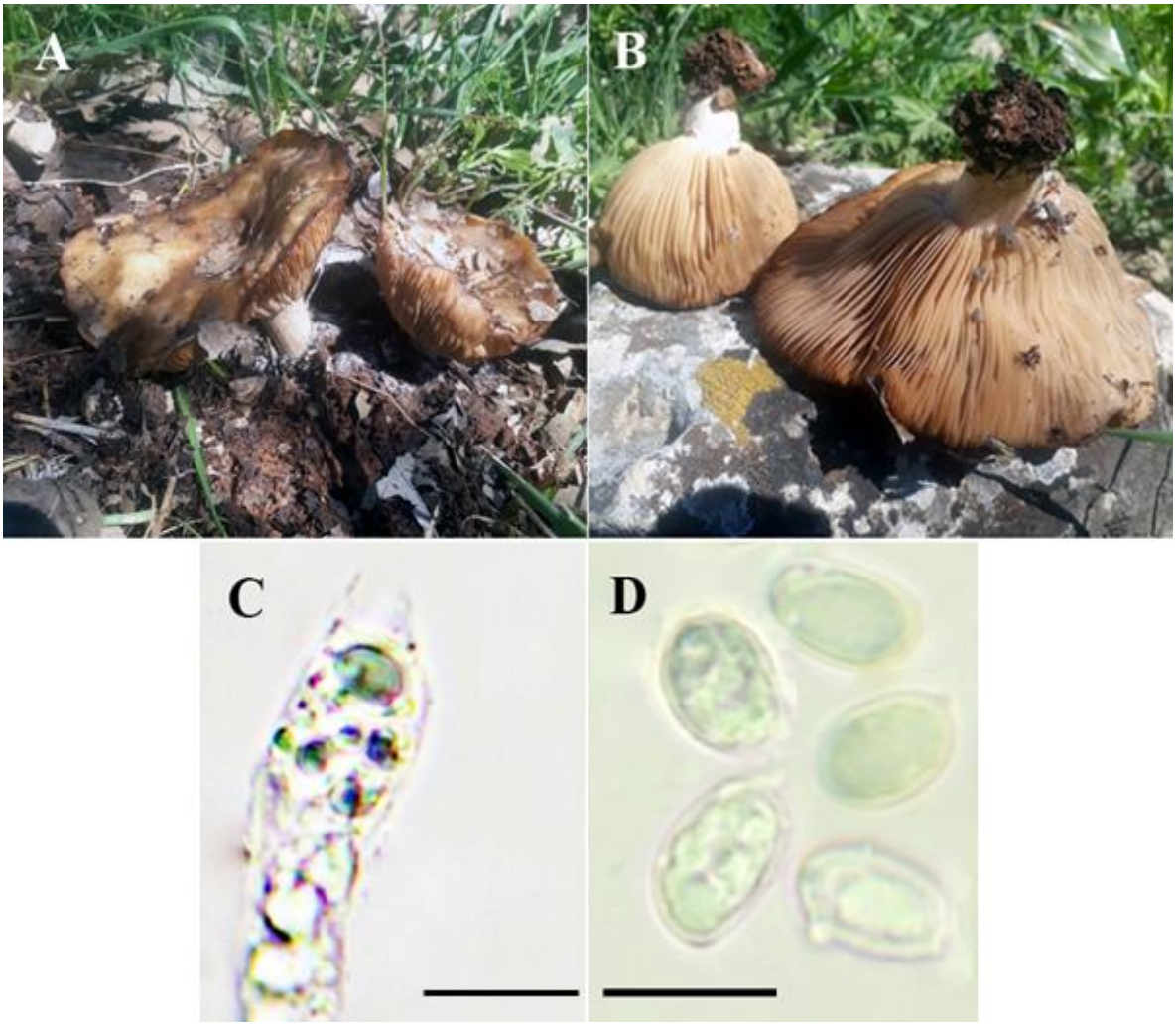



**Fig. 1.** *Collybia mongolica*. (A) basidiomata in situ, (B) mature basidiomata with lamellae, (C) basidium, (D) basidiospores. Scale bars: (C, D) = 10 µm.

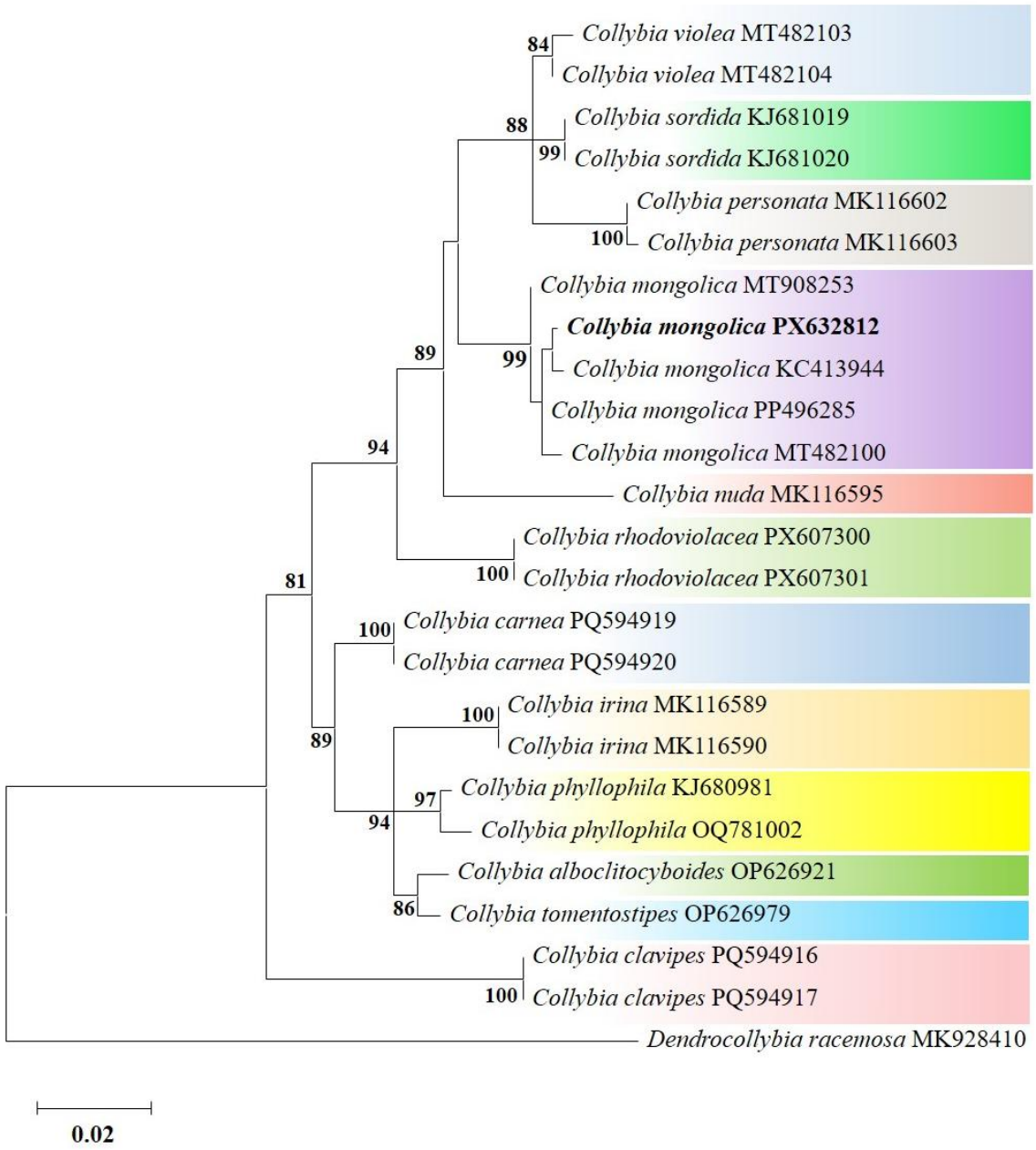



**Fig. 2.** Maximum likelihood phylogenetic tree inferred from ITS sequence data showing the placement of the studied specimen of *Collybia mongolica* (PX632812, shown in bold). Bootstrap support values (>70%) are indicated at the nodes. The analyzed specimen clusters within the *C. mongolica* lineage and is separated from closely related taxa. The tree was rooted using *Dendrocollybia racemosa* (GenBank accession no. MK928410) as the outgroup.

***Coprinopsis strossmayeri*** (Schulzer) Redhead, Vilgalys & Moncalvo, Taxon 50 (1): 231 (2001). Fig. 3

Macroscopic Features: Pileus initially cylindrical to ovoid, becoming conical and finally broadly campanulate at maturity, 3–5 cm in diameter. Surface covered with white to cream fibrillose squamules, becoming progressively fragmented and darker toward the pileus disc. Pileus pale gray to ochraceous, with a distinctly darker brownish center and a paler margin (Fig. 3A, B). Lamellae crowded, free, initially whitish-pink, becoming grayish-brown and finally black at maturity. Spore print dark brown to black. Stipe cylindrical, slightly tapering toward the apex, white, fibrous to subfibrillose, 5–10 cm long.

Microscopic Features: Basidia clavate, tetrasporic, measuring 24.10–32.27 × 8.66–10 µm (Fig. 3C, D). Basidiospores ellipsoid to ovoid, smooth, reddish-brown, with a distinct central germ pore, measuring 8.06–9.59 × 5.05–6.14 µm (Fig. 3E). Pleurocystidia abundant, elongate, fusiform, lageniform to utriform, measuring 120–225 × 24–54 µm (Fig. 3F, G). Cheilocystidia fusiform to broadly ovate and elongate, measuring 80–110 × 16–22 µm (Fig. 3H). Pileus surface composed of globose cells (Fig. 3I). Clamp connections present (Fig. 3J). See Table 2 for comparison with published descriptions.

Specimen examined: IRAN, Kermanshah Province, Dalahu-Gahvare, on decayed tree trunk, 1560 m a.s.l., 34°20′06″ N, 46°24′57″ E, 1 May 2020, collected by Sabah Ziaei, identified by Saeed Abbasi, voucher 18933, ITS sequence GenBank accession no. PX633024.

Notes: *Coprinopsis strossmayeri* is a lignicolous species that typically produces clustered basidiomata on decaying, fragmented, or fallen wood. Its distinguishing characteristics include a conspicuous whitish, felty veil that breaks into patches or scales on the pileus, smooth basidiospores with a distinct germ pore, and elongate cheilocystidia. Orange-brown rhizomorphs at the stipe base have also been reported for this species (Prydiuk and Lomberg 2021). The species may be confused with *C. atramentaria* and *C. romagnesiana*. However, *C. atramentaria* generally has an almost smooth pileus, whereas *C. romagnesiana* develops reddish-brown veil scales (Prydiuk and Lomberg 2021). The morphological features of the Iranian collection are generally consistent with published descriptions (El Akil et al. 2014, Douglas et al. 2020, Prydiuk and Lomberg 2021). Its basidiospore, basidial, and cystidial measurements largely overlap those reported by Douglas et al. (2020), although some differences are evident when compared with Prydiuk and Lomberg (2021). These variations should be interpreted in the context of the reported morphological variability within the *C. strossmayeri* aggregate (Table 2).

BLASTn comparison of the ITS sequence of the Iranian specimen (PX633024) showed 99.70% sequence identity with GenBank accession FJ185161, corresponding to the Armenian isolate 15-2C of *Coprinopsis strossmayeri* reported by Badalyan et al (2011).

The ITS phylogeny recovered the studied specimen (PX633024) within the *Coprinopsis strossmayeri* clade, which received 96% bootstrap support. The Iranian collection clustered with sequences of *C. strossmayeri* previously reported in published studies and was clearly separated from closely related taxa (Fig. 4). This phylogenetic placement is consistent with the morphological characteristics observed in the examined material. The combined morphological and phylogenetic evidence supports the recognition of the examined specimen as *C. strossmayeri*.

**Table 2.** Morphological comparison of *Coprinopsis strossmayeri* from Iran with published descriptions.

| Morphological character | Present study | Published description |
|---|---|---|
| Pileus diameter (cm) | 3–5 | Up to 6 |
| Pileus color | Pale grey to ochraceous, darker centre | Pale grey to ochraceous-grey, darker centre |
| Veil | White to cream fibrillose squamules | Whitish, felty veil forming patches |
| Basidiospores (µm) | 8.06–9.59 × 5.05–6.14 | 8.1–10.6 × 4.7–6.1 |
| Germ pore | Central | Central |
| Basidia (µm) | 24.10–32.27 × 8.66–10 | 22–31 × 7–9.5 |
| Cheilocystidia (µm) | 80–110 × 16–22 | 36–101 × 14–20 |
| Pleurocystidia (µm) | 120–225 × 24–54 | 125–220 × 28–63 |
| Clamp connections | Present | Present |

Reference: Douglas et al. (2020). Microscopic measurements are in µm (length × width).

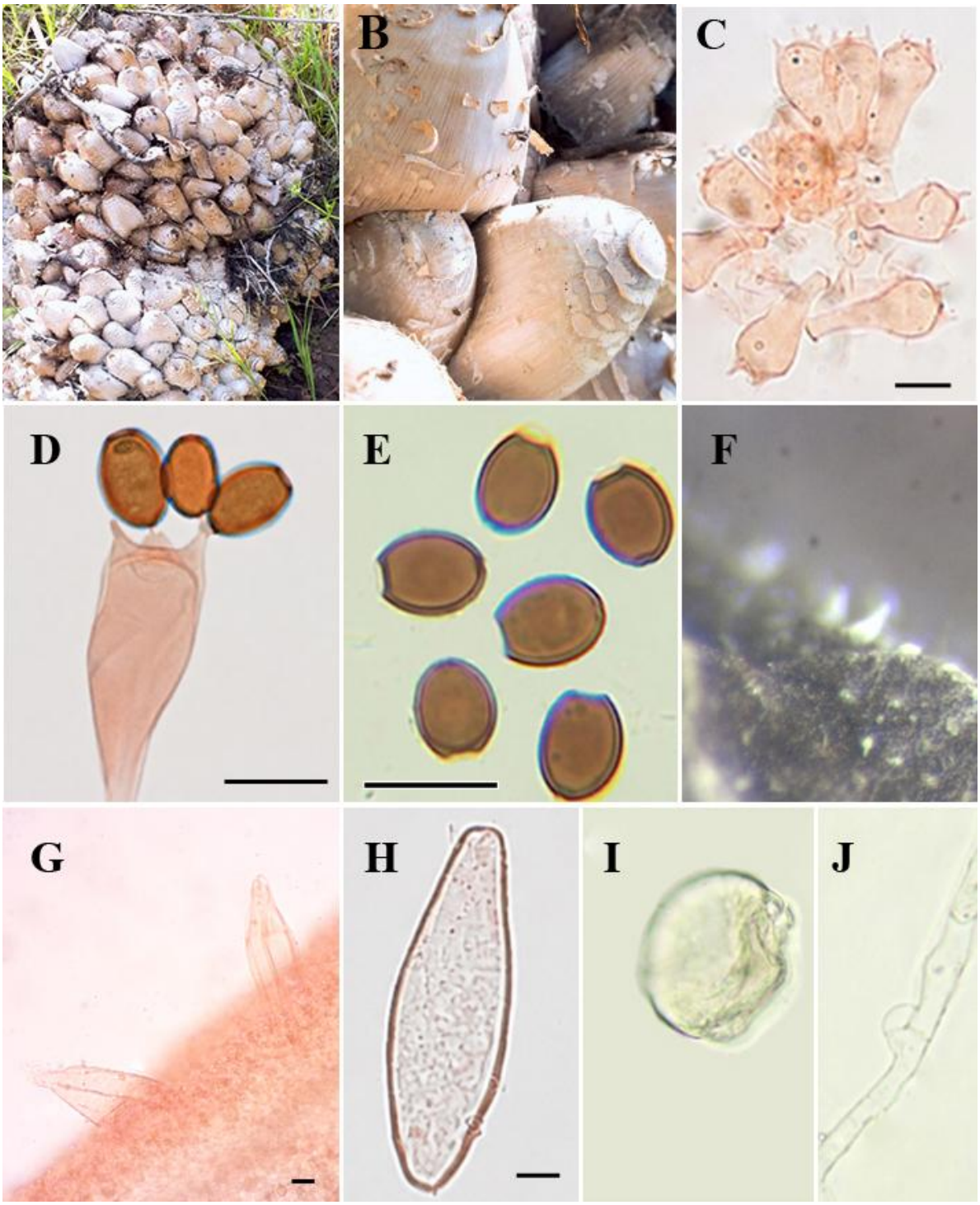



**Fig. 3.** Macroscopic and microscopic features of *Coprinopsis strossmayeri*. (A) Basidiomata in natural habitat, (B) Mature basidiomata showing fibrillose pileal squamules, (C) Basidia, (D) Basidium bearing basidiospores, (E) Basidiospores, (F, G) Pleurocystidia, (H) Cheilocystidium, (I) Pileus surface cell, (J) Clamp connection. Scale bars: (C–E, G, H) = 10 µm.

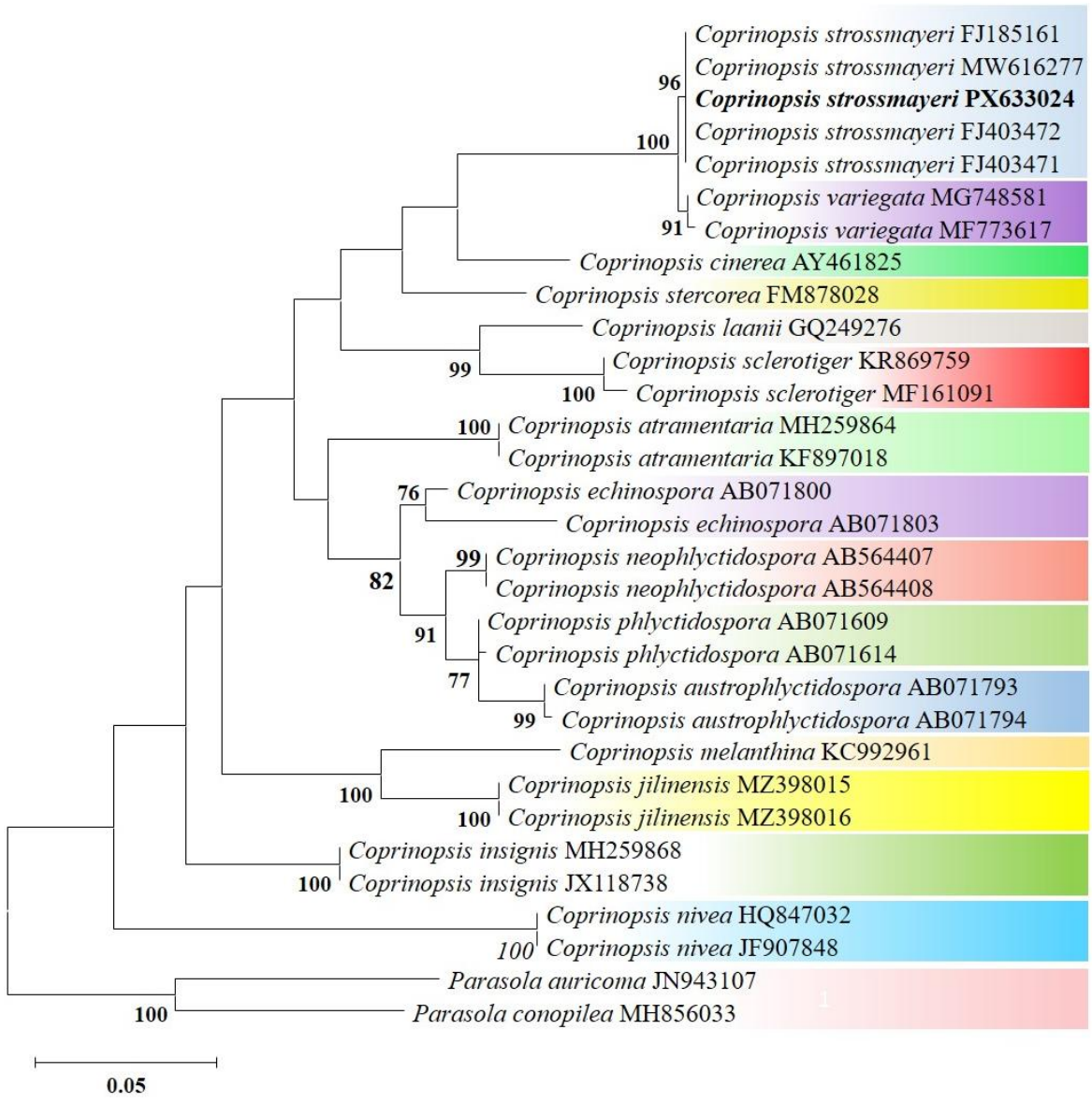



**Fig. 4.** Maximum likelihood phylogenetic tree inferred from ITS sequence data showing the placement of the studied specimen of *Coprinopsis strossmayeri* (PX633024, shown in bold). Bootstrap support values (>70%) are indicated at the nodes. The analyzed specimen clusters within the *C. strossmayeri* lineage and is separated from closely related taxa. The tree was rooted using *Parasola auricoma* and *P. conopilea* as outgroup taxa.

***Meottomyces dissimulans*** (Berk. & Broome) Vizzini, Rivista Micol. 51 (1): 63 (2008). Fig. 5

Macroscopic Features: Pileus initially hemispherical, becoming convex to broadly convex with age, 1–4 cm in diameter, moist, striate, and slightly translucent at the margin. Surface brown when young, becoming yellowish-brown to ochraceous at maturity, often viscid to greasy, fading upon drying (Fig. 5A). Lamellae adnate to slightly decurrent, initially whitish-cream, becoming grayish-brown to pale brown at maturity (Fig. 5B). Spore print yellowish-cream. Stipe central, cylindrical, slightly clavate toward the base, white to ochre-yellow, fibrillose, solid when young, becoming hollow with age.

Microscopic Features: Basidia cylindrical to narrowly clavate, tetrasporic, measuring 23.45–32.94 × 5.74–8.00 µm (Fig. 5C). Basidiospores ovate to broadly ovate, in lateral view ellipsoid to slightly fusiform, yellowish-ochre, thin- to moderately thick-walled, with indistinct germ pore, measuring 6.73–8.35 × 4.00–5.18 µm (Fig. 5D). Cheilocystidia cylindrical to subclavate, thin-walled, often with a small apical projection and basal constriction, 28.64–59.82 × 6.34–8.9 µm (Fig. 5E). Pleurocystidia absent. Pileipellis an ixocutis composed of gelatinized, repent, cylindrical hyphae. Clamp connections present in all tissues. See Table 3 for comparison with published descriptions.

Specimens examined: IRAN, Kermanshah Province, Dalahu-Gahvare, on decayed wood, 34°19′35″ N, 46°24′39″ E, ca. 1548 m a.s.l., 26 December 2021, Sabah Ziaei leg., Saeed Abbasi det., voucher 18935 (GenBank accession no. PX632810). IRAN, Kermanshah Province, Dalahu-Gahvare, on decayed leaves, 34°19′36.5″ N, 46°24′39.4″ E, ca. 1548 m a.s.l., 26 December 2021, Sabah Ziaei leg., Saeed Abbasi det., voucher D54 (authors' collection; GenBank accession no. PZ501689).

Notes: *Meottomyces dissimulans* is a saprotrophic agaric occurring on leaf litter, decaying wood, and other plant debris, particularly in humid habitats. The species has been documented in Europe, where its small, inconspicuous, brownish basidiomata may easily be overlooked (Legon 2012). The Iranian collections, obtained from decaying wood and leaves, are consistent with its reported ecology and extend its documented geographical distribution to western Iran.

Taxonomically, the species has undergone several nomenclatural changes since its original description as *Agaricus dissimulans*, having previously been assigned to genera such as *Pholiota*, *Hemipholiota*, and *Phaeogalera* (Holec 2001, Holec 2003). Its placement in *Pholiota* as *P. oedipus* was considered inconsistent with morphological features such as the absence of chrysocystidia, a hygrophanous pileus, and characteristic cheilocystidia. Its current placement in *Meottomyces* is supported by morphological and molecular evidence (Vizzini 2008).

Diagnostic characteristics include small basidiomata, a viscid brown pileus, a yellowish-cream spore print, the absence of pleurocystidia, and cylindrical to subclavate cheilocystidia. Although superficially similar to certain species of *Tubaria*, *M. dissimulans* can be distinguished by the combination of these characteristics. The morphological features of the Iranian collections agree well with previous descriptions (Noordeloos 1999, Knudsen and Vesterholt 2008, Noordeloos 2011, Halama and Rutkowski 2016), supporting their identification as *M. dissimulans*.

BLASTn comparisons of the ITS sequences of the two Iranian specimens of *Meottomyces dissimulans* (PX632810 and PZ501689) revealed 99.37% sequence identity with the reference sequence MW692353, representing a previously documented specimen of *M. dissimulans* included in the phylogenetic study by Li et al. (2023).

The ITS-based phylogenetic analysis placed the two studied specimens (PX632810 and PZ501689) within the *Meottomyces dissimulans* lineage with 100% bootstrap support (Fig. 6). The Iranian collections clustered with other sequences of *M. dissimulans* and formed a well-supported clade distinct from closely related taxa, including *M. striatulus* and species of *Tubaria*. The phylogenetic placement was congruent with the morphological characteristics observed in the examined material, particularly the viscid pileus, yellowish-cream spore print, basidiospore morphology, and cheilocystidial features. The combined morphological and phylogenetic evidence supports the assignment of the examined specimens to *M. dissimulans.*

**Table 3.** Morphological comparison of *Meottomyces dissimulans* from Iran with published descriptions.

| Morphological character | Present study | Published description |
|---|---|---|
| Pileus diameter (cm) | 1–4 | 0.5–3 |
| Pileus color | Brown to yellowish-brown or ochraceous | Dark brown to yellow-brown or pale olivaceous-brown |
| Pileus surface | Moist, viscid to greasy, with a striate margin | Hygrophanous, greasy to viscid, sometimes striate |
| Basidiospores (µm) | 6.73–8.35 × 4.00–5.18 | 6.6–8.6 × 4.3–5.4 |
| Basidia (µm) | 23.45–32.94 × 5.74–8.00 | 23.3–34.2 × 6.8–8.8 |
| Cheilocystidia (µm) | 28.64–59.82 × 6.34–8.90 | 29.6–61.4 × 5.3–8.2 |
| Pleurocystidia | Absent | Absent |
| Pileipellis | Gelatinized ixocutis | Ixocutis |
| Germ pore | Indistinct | Absent or indistinct |

Reference: Halama and Rutkowski (2016). Microscopic measurements are in µm (length × width).

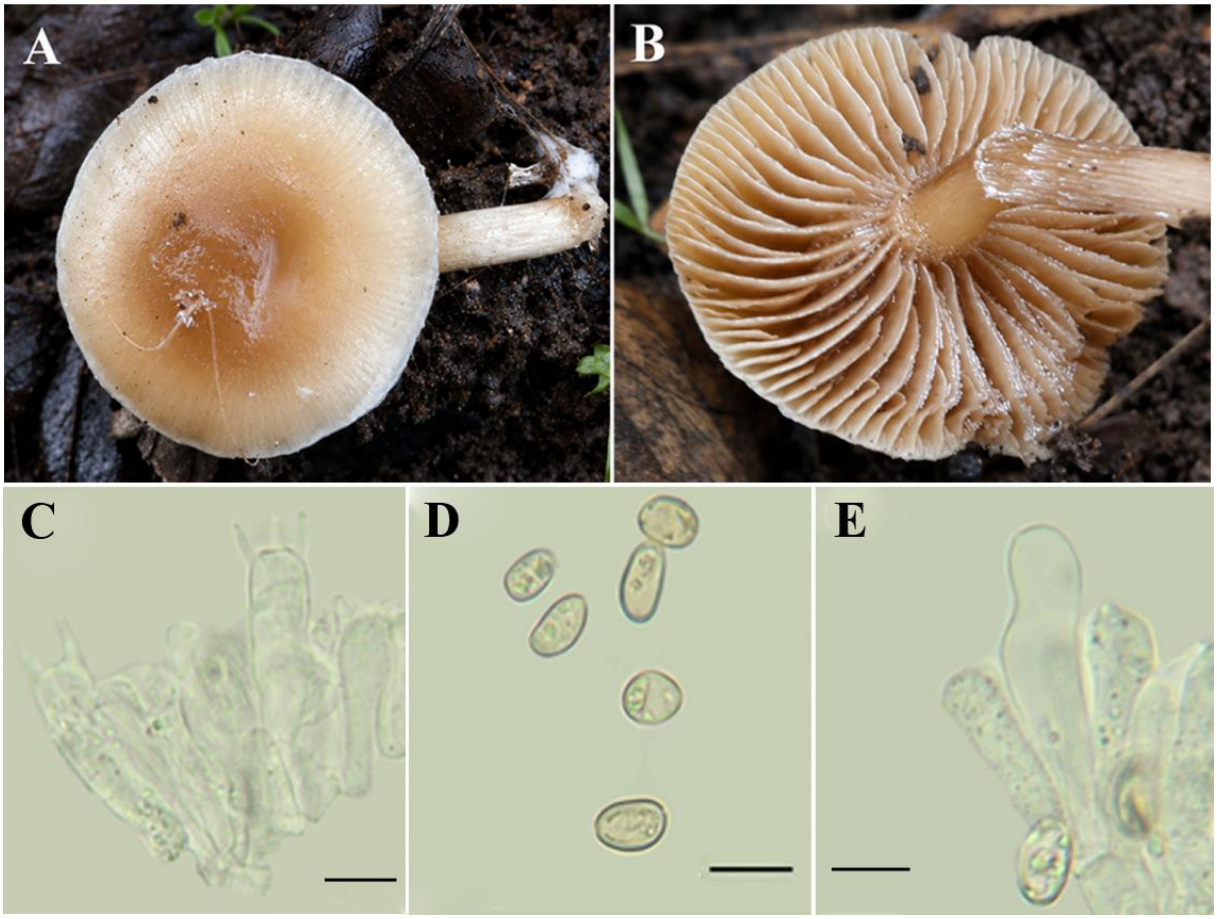



**Fig. 5.** *Meottomyces dissimulans*: (A) basidioma in situ, (B) lamellae, (C) basidia, (D) basidiospores, (E) cheilocystidia. Scale bars: (C–E) = 10 µm.

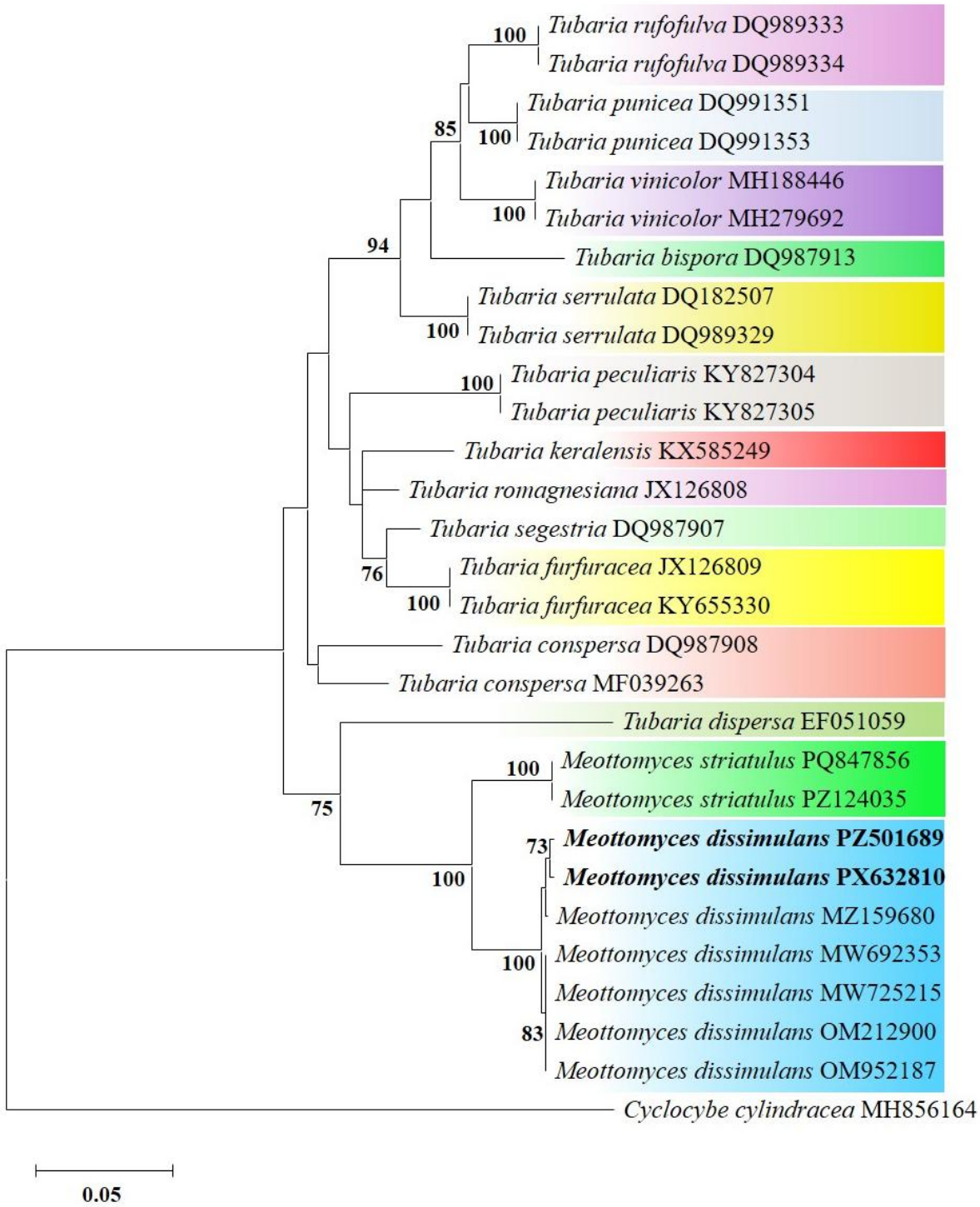



**Fig. 6.** Maximum likelihood phylogenetic tree inferred from ITS sequence data showing the placement of the two studied specimens of *Meottomyces dissimulans* (PX632810 and PZ501689, shown in bold). Bootstrap support values (>70%) are indicated at the nodes. The analyzed specimens cluster within the *M. dissimulans* lineage and are separated from closely related taxa. The tree was rooted using *Cyclocybe cylindracea* as the outgroup.

***Mycena zephirus*** (Fr.) P. Kumm., Führer Pilzk.: 110 (1871). Fig. 7

Macroscopic Features: Pileus initially conical to bell-shaped, becoming broadly convex to flat at maturity, 1.5–3 cm in diameter, distinctly striate, glabrous, white to beige, often developing reddish-brown discoloration with age (Fig.

7A). Lamellae distant, adnexed with a slight depression near stipe attachment, whitish-pink, with interspersed short lamellae (lamellulae), often showing reddish-brown spotting at maturity (Fig. 7B). Spore print white to cream. Stipe central, cylindrical, slightly enlarged toward apex, fragile, hollow, 2–5 cm long, silvery-white, with a reddish-brown base becoming darker with age.

Microscopic Features: Basidia clavate, tetrasporic, measuring 28.08–35.65 × 7.29–10.07 µm (Fig. 7D). Basidiospores ovate to cylindrical, hyaline, thin-walled, measuring 8.00–10.09 × 5.19–6.34 µm (Fig. 7E). Cheilocystidia highly variable, ventricose, clavate to fusiform, apically mucronate, occasionally with an acuminate apex, measuring 47.61–70.85 × 8.35–15.48 µm (Fig. 7F, G). Pleurocystidia similar in morphology, measuring 76.50–90.21 × 14.24–23.64 µm (Fig. 7H). Clamp connections present. Pileipellis composed of smooth to slightly ornamented hyphae with rare excrescences. See Table 4 for comparison with published descriptions.

Specimen examined: IRAN, Kermanshah Province, Dalahu, on an oak (*Quercus* sp.) trunk in a forested habitat, 1685 m a.s.l., 34°24′18″ N, 46°17′42″ E, 22 November 2020, collected by Sabah Ziaei, identified by Saeed Abbasi, voucher 18936, GenBank accession no. PX632676.

Notes: *Mycena zephirus* is a saprotrophic species reported mainly from temperate forests in Europe and East Asia, particularly coniferous and mixed forests, although it also occurs in broad-leaved forest habitats (Legon and Henrici 2005, Park et al. 2017). The Iranian specimen was collected on an oak (Quercus sp.) trunk in a forested area of western Iran, providing an additional record of the species in association with a broad-leaved tree. Morphologically, *M. zephirus* is characterized by a pale, distinctly striate pileus that develops reddish-brown discoloration with age, distant lamellae with interspersed lamellulae, a slender silvery-white stipe, and elongated basidiospores. These features, together with the morphology of the cheilocystidia and pleurocystidia, are consistent with published descriptions (Mertens 2009, Park et al. 2017). The species resembles other pale-colored members of *Mycena*, including *M. erminea*, *M. eburnea*, *M. algeriensis*, and *M. valida*, but can be differentiated by a combination of pileus coloration, growth habit, basidiospore morphology, and cystidial characteristics. The Iranian collection extends the documented geographical distribution of *M. zephirus* to western Iran.

BLASTn comparison of the ITS sequence of the Iranian specimen (PX632676) showed 98.90% sequence identity with GenBank accession MT497550, associated with the documented Chinese specimen HMJAU 43106 of *Mycena zephirus* (Na and Bau 2020).

The ITS-based phylogenetic analysis recovered the studied specimen (PX632676) within the *Mycena zephirus* lineage with 98% bootstrap support (Fig. 8). The Iranian collection clustered with other sequences of *M. zephirus* and was clearly separated from closely related taxa, including *M. abramsii, M. crocata*, and *M. haematopus*. The phylogenetic placement was congruent with the morphological characteristics observed in the examined material, particularly the striate pileus, distant lamellae, basidiospore morphology, and characteristic cystidial features. The combined morphological and phylogenetic evidence supports the taxonomic placement of the examined specimen in *M. zephirus.*

**Table 4.** Morphological comparison of *Mycena zephirus* from Iran with published descriptions.

| Morphological character | Present study | Published description |
|---|---|---|
| Pileus diameter (cm) | 1.5–3 | 1.5–2 |
| Pileus color | White to beige, becoming reddish-brown | White to beige, becoming reddish-brown |
| Stipe length (cm) | 2–5 | 2–2.5 |
| Basidiospores (µm) | 8.00–10.09 × 5.19–6.34 | 8.5–10.4 × 5.3–6.6 |
| Basidia (µm) | 28.08–35.65 × 7.29–10.07 | 28.7–36.3 × 7.6–10.6 |
| Cheilocystidia (µm) | 47.61–70.85 × 8.35–15.48 | 47.8–71.1 × 7.9–15.7 |
| Pleurocystidia (µm) | 76.50–90.21 × 14.24–23.64 | 77–89.4 × 14–22.3 |
| Pileipellis | Smooth to slightly ornamented hyphae | Smooth or rarely excrescent |
| Clamp connections | Present | Present |

Reference: Park et al. (2017). Microscopic measurements are in µm (length × width).

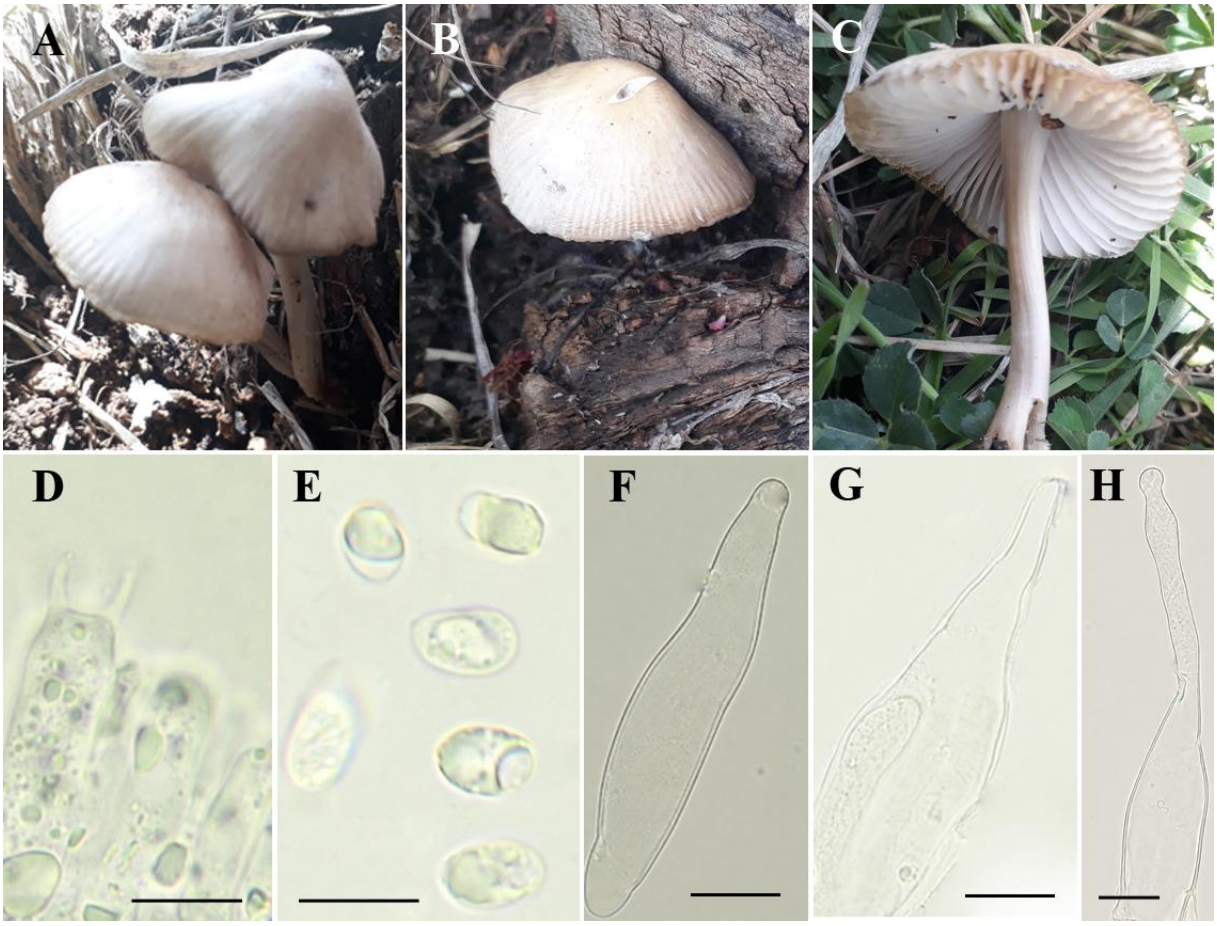



**Fig. 7.** *Mycena zephirus*: (A–C) basidiomata in natural habitat showing pileus and lamellae, (D) basidia, (E) basidiospores, (F–G) cheilocystidia, (H) pleurocystidia. Scale bars: (D–H) = 10 µm.

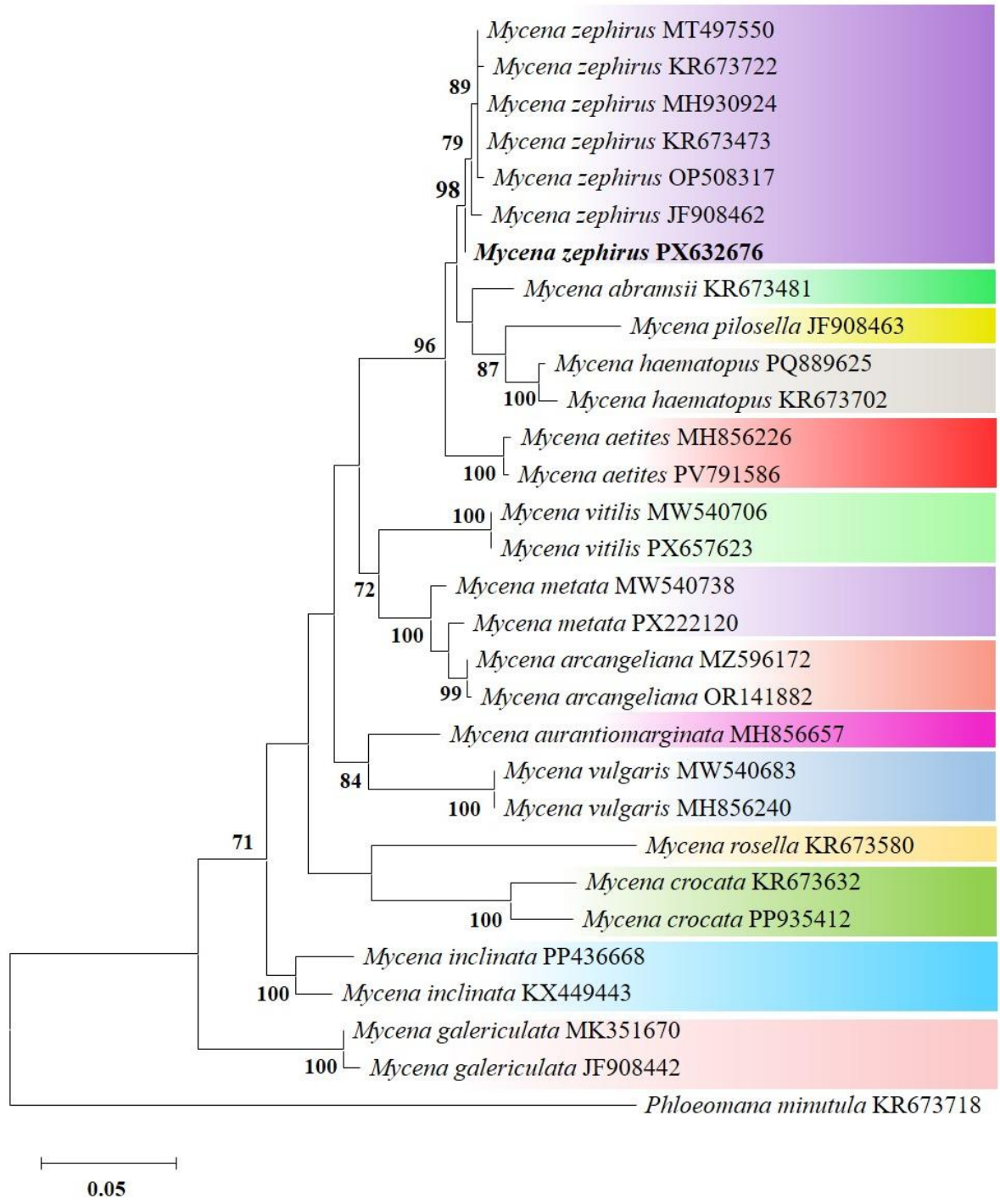



**Fig. 8.** Maximum likelihood phylogenetic tree inferred from ITS sequence data showing the placement of the studied specimen of *Mycena zephirus* (PX632676, shown in bold). Bootstrap support values are indicated at the nodes. The analyzed specimen clusters within the *M. zephirus* lineage and is separated from closely related taxa. The tree was rooted using *Phloeomana minutula* as the outgroup.

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## AUTHOR CONTRIBUTION

Sabah Ziaei conducted the investigation, field sampling, morphological and molecular analyses, data collection, and preparation of the original draft. Saeed Abbasi contributed to the conceptualization and methodology of the study, supervised the research, performed species identification and phylogenetic analyses, validated and interpreted the data, reviewed and edited the manuscript, and administered the project. Elham Seidmohammadi assisted with the molecular analyses, sequence submission to GenBank, data validation, and review and editing of the manuscript.

## DATA AVAILABILITY

The ITS sequences generated during this study are available in GenBank under the accession numbers listed in the manuscript. All other data supporting the findings of this study are available from the corresponding author upon reasonable request.

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## DECLARATION

The authors declare that they have no competing interests.

## ETHICAL APPROVAL

Ethics approval was not required for this study because it did not involve humans or animals.

## REFERENCES

Badalyan SM, Szafranski K, Hoegger PJ, Navarro-González M, Majcherczyk A, … et al. 2011. New Armenian Wood-Associated Coprinoid Mushrooms: *Coprinopsis strossmayeri* and *Coprinellus* aff. *radians*. Diversity. 3(1): 136-54. https://doi.org/10.3390/d3010136.

Costa JM, Santos MI, Guiné RPF. 2026. Ecology and Diversity of Edible and Medicinal Mushrooms Across Different Habitats. In: Advances in Mushroom Research: Breakthroughs and Future Directions. (Giri B, Gunwal I, Mago P, Kapoor R, Raseetha S, eds): 23-81. Springer Nature Singapore, Singapore.

Dong D, Bau T. 2013. A study on the taxonomic position of *Tricholoma mongolicum*. Journal of Fungal Research. 11 (3): 172-175. https://www.cabidigitallibrary.org/doi/full/10.5555/20133321418.

Douglas B, Schafer D, Liimatainen K, Champion D. 2020. *Coprinopsis strossmayeri* agg. new to Britain. Field Mycology. 21(1): 5-10. https://doi.org/10.1016/j.fldmyc.2020.01.004.

El Akil M, Touhami AO, Benkirane R, Doura A. 2014. Étude de quelques champignons coprinoïdes de la forêt domaniale du site minier Jerada (Nord-Est du Maroc) dont *Coprinellus bipellis* et *Coprinopsis strossmayeri* sont nouvelles pour la flore fongique du Maroc. Journal of Applied Biosciences. 82: 7389-402. https://doi.org/10.4314/JAB.V82I1.9.

Fadavi S, Abbasi S, Asef MR. 2015. A contribution to the identification of agaric fungi of Kermanshah, W Iran (2): Families *Agaricaceae, Inocybaceae, Pluteaceae* and *Polyporaceae*. Rostaniha. 16(1): 1-16. https://doi.org/10.22092/botany.2015.101976.

Fadavi S, Asef MR, Abbasi S. 2013. A contribution to the identification of agaric fungi of Kermanshah province, W Iran: Families *Bolbitiaceae*, *Entolomataceae* and *Strophariaceae*. Rostaniha 14 (2): 95-107. https://doi.org/10.22092/botany.2014.101279.

Ghobad-Nejhad M, Langer E, Antonín V, Gates G, Noroozi J, … et al. 2020. The gilled fungi and boletes of Iran: diversity, systematics, and nrDNA data. Mycologia Iranica. 7 (1): 1-43. https://doi.org/10.22092/mi.2021.123456.

Halama M, Rutkowski R. 2016. *Meottomyces dissimulans* (*Agaricales, Basidiomycota*), new for Poland. Polish Botanical Journal. 61(1): 167-72. https://doi.org/10.1515/pbj-2016-0006.

Hansen L, Knudsen H. 1992. Nordic macromycetes Volume 2: *Polyporales*, *Boletales*, *Agaricales*, *Russulales*: Nordsvamp, Denmark.

He Z-M, Chen Z-H, Bau T, Wang G-S, Yang ZL. 2023. Systematic arrangement within the family *Clitocybaceae* (*Tricholomatineae, Agaricales*): phylogenetic and phylogenomic evidence, morphological data and muscarine-producing innovation. Fungal Diversity. 123(1): 1-47. https://doi.org/10.1007/s13225-023-00527-2.

Holec J. 2001. The genus *Pholiota* in central and western Europa. Libri Botanici. 20: 1-220.

Holec J. 2003. Taxonomy and nomenclature of *Pholiota dissimulans* with respect to *Phaeogalera oedipus*. Sydowia. 55: 77-85. https://www.cabidigitallibrary.org/doi/full/10.5555/20033141289.

Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ, Johnston PR, … et al. 2024. The 2024 Outline of Fungi and fungus-like taxa. Mycosphere. 15(1): 5146-6239. https://doi.org/10.5943/mycosphere/15/1/25.

Kalichman J, Kirk PM, Matheny PB. 2020. A compendium of generic names of agarics and Agaricales. Taxon. 69(3): 425-47. https://doi.org/10.1002/tax.12240.

Katoh K, Standley DM. 2013. MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Molecular Biology and Evolution. 30(4): 772-80. https://doi.org/10.1093/molbev/mst010.

Knudsen H, Vesterholt J. 2008. Funga Nordica Vol. 1. Agaricoid, Boletoid and Cyphelloid genera. Nordsvamp, Denmark.

Legon N. 2012. Fungal portraits No. 49: *Meottomyces dissimulans*. Field Mycology. 13(1): 3-7. https://doi.org/10.1016/j.fldmyc.2011.12.002.

Legon NW, Henrici A. 2005. Checklist of the British & Irish *Basidiomycota*. Royal Botanic Gardens, Kew, UK.

Li J, Yang W, Ren J, Cao B, Zhu X, … et al. 2023. A New Species *Agrocybe striatipes*, also a Newly Commercially Cultivated Mushroom with Highly Nutritional and Healthy Values. Journal of Fungi. 9(3): 383. https://doi.org/10.3390/jof9030383.

Lu T, Bao H, Bau T. 2018. Genetic diversity and population structure of endemic mushroom *Leucocalocybe mongolica* in Mongolian Plateau uncovered by EST-SSR markers. Biotechnology & Biotechnological Equipment. 32(5): 1195-204. https://doi.org/10.1080/13102818.2018.1510743.

Matheny PB, Curtis JM, Hofstetter V, Aime MC, Moncalvo J-M, … et al. 2006. Major clades of *Agaricales*: a multilocus phylogenetic overview. Mycologia. 98(6): 982-95. https://doi.org/10.1080/15572536.2006.11832627.

Mertens C. 2009. *Mycena zephirus*, espèce méconnue en Belgique? Revue du Cercle de Mycologie de Bruxelles–n. 9: 20-26.

Na Q, Bau T. 2020. Ten new records of *Mycena* from China. Mycosystema. 39(9): 1783-808. https://doi.org/10.13346/j.mycosystema.200214.

Noordeloos M. 1999. *Strophariaceae*. In: Flora Agaricina Neerlandica. (Bas C, Kuyper TW, Noordeloos ME, Vellinga EC, eds), 4: 27-107. Balkema, Netherlands.

Noordeloos M. 2011. *Strophariaceae* s.l. Fungi Europaei 13. Edizioni Candusso, Alassio, Italy.

Park MS, Cho HJ, Kim NK, Park JY, Lee H, … et al. 2017. Ten new recorded species of macrofungi on Ulleung Island, Korea. Mycobiology. 45(4): 286-96. https://doi.org/10.5941/MYCO.2017.45.4.286.

Prydiuk MP, Lomberg ML. 2021. First record of *Coprinopsis strossmayeri* (*Psathyrellaceae*) in Ukraine: morphological and cultural features. Czech Mycology. 73(1): 45-58. https://doi.org/10.33585/cmy.73104.

Ryberg M, Matheny PB, eds. 2012. Asynchronous origins of ectomycorrhizal clades of *Agaricales*. Proceedings of the Royal Society, Series B, Biological Sciences. The Royal Society, London.

Seidmohammadi E, Abbasi S, Asef M. 2021. New *Entoloma* species from Iran. Mycologia Iranica. 8(1): 35-42. https://doi.org/10.22043/MI.2022.356768.1206.

Seidmohammadi E, Abbasi S, Asef MR. 2018a. First report of *Pluteus cinereofuscus* for mycobiota of Iran. Rostaniha. 19(2): 192-5. https://doi.org/10.22092/botany.2019.124052.1126.

Seidmohammadi E, Abbasi S, Asef MR. 2018b. Morphological and molecular characterization of coprinoid fungi newly recorded for the mycobiota of Iran. Cellular and Molecular Biology. 64(15): 78-83. https://doi.org/10.14715/cmb/2017.64.15.13.

Seidmohammadi E, Abbasi S, Asef MR. 2019a. The first report of *Panaeolus olivaceus* and *Panaeolus guttulatus* from Iran. Taxonomy and Biosystematics. 11: 23-30. https://doi.org/10.22108/tbj.2020.118170.1093.

Seidmohammadi E, Abbasi S, Asef MR, Jamali S. 2019b. New records of *Pezizales* from Kermanshah Province. Nova Biologica Reperta. 6(1): 88-95. https://doi.org/10.29252/nbr.6.1.88.

Sudharsan MS, Rajagopal K, Banu N. 2023. An Insight into Fungi in Forest Ecosystems. In: Plant Mycobiome: Diversity, Interactions and Uses. (Rashad YM, Baka ZAM, Moussa TAA, eds): 291-318. Springer International Publishing, Switzerland.

Vizzini A. 2008. Novitates genera *Meottomyces* (*Agaricales, Strophariaceae*). Rivista di Micologia. 51(1): 63-6.

Vizzini A, Consiglio G, Marchetti M. 2019. *Mythicomycetaceae* fam. nov.(*Agaricineae, Agaricales*) for accommodating the genera *Mythicomyces* and *Stagnicola*, and *Simocybe parvispora* reconsidered. Fungal systematics and evolution. 3(1): 41-56. https://doi.org/10.3114/fuse.2019.03.05.

Yu X-D, Deng H, Yao Y-J. 2011. *Leucocalocybe*, a new genus for *Tricholoma mongolicum* (*Agaricales, Basidiomycota*). African Journal of Microbiology Research. 5(31): 5750-6. https://doi.org/10.5897/AJMR11.1228.

Zhao R-L, Li G-J, Sánchez-Ramírez S, Stata M, Yang Z-L, et al. 2017. A six-gene phylogenetic overview of *Basidiomycota* and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. Fungal Diversity. 84(1): 43-74. https://doi.org/10.1007/s13225-017-0381-5.

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مقاله کامل

# چهار گزارش جدید از راسته *Agaricales* برای میکوبیوتای ایران از شهرستان دالاهو، غرب ایران

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## چکیده

با وجود پیشرفت‌های اخیر در مطالعات تنوع قارچی ایران، تنوع قارچ‌های کلاهک‌دار غرب کشور، به‌ویژه شهرستان دالاهو در استان کرمانشاه، همچنان به‌طور کامل شناخته نشده است. در این پژوهش، طی بررسی‌های میدانی در زیستگاه‌های جنگلی، مراتع و باغ‌ها، نمونه‌هایی از قارچ‌های راسته *Agaricales* جمع‌آوری و با استفاده از رویکردی تلفیقی شامل بررسی دقیق ویژگی‌های ماکروسکوپی و میکروسکوپی و همچنین تحلیل‌های فیلوژنتیکی مبتنی بر توالی ITS rDNA شناسایی شدند. چهار گونه شامل *Coprinopsis strossmayeri* از خانواده *Psathyrellaceae*، *Collybia mongolica* از *Clitocybaceae*، *Meottomyces dissimulans* از *Tubariaceae* و *Mycena zephirus* از *Mycenaceae* برای نخستین بار از ایران گزارش می‌شوند. برای هر گونه، توصیف‌های کامل ریخت‌شناسی، ویژگی‌های بوم‌شناختی، اطلاعات نمونه‌های بررسی‌شده و روابط فیلوژنتیکی ارائه شده است. نتایج تحلیل‌های فیلوژنتیکی جایگاه نمونه‌های بررسی‌شده را در کنار شواهد ریخت‌شناختی روشن ساخته و در تعیین حدود گونه‌ها نقش مکمل ایفا کردند. این گزارش‌ها دامنه پراکنش شناخته‌شده این چهار گونه را گسترش داده و دانش موجود درباره تنوع قارچ‌های راسته *Agaricales* در ایران را غنا می‌بخشند. همچنین، نتایج این پژوهش اهمیت استفاده از رویکرد تلفیقی در مستندسازی تنوع زیستی قارچ‌ها را نشان داده و شهرستان دالاهو را به‌عنوان یکی از مناطق ارزشمند و کمتر مطالعه‌شده برای پژوهش‌های آینده قارچ‌شناسی معرفی می‌کنند.

**واژگان کلیدی:** *Collybia mongolica*، *Coprinopsis strossmayeri*، ITS rDNA، *Meottomyces dissimulans*، *Mycena zephirus*.



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