

Fungal Systematics and Evolution: FUSE 11

Jonathan Cazabonne^{1*}, Danny Haelewaters^{2,3,4}, İsmail Acar⁵, Eman Alhomaidi⁶, Mona Saleh Al Tami⁷, Nourin Aman^{8,9}, Vadim Alexandrovich Iliushin¹⁰, Anam Aslam¹¹, Lok Ranjan Bhatt¹², Muhammad Bilal Bin Majeed¹³, Ram Chandra Poudel¹⁴, Sujan Chaudhary¹², Shivani Digra¹⁵, Francesco Dovana¹⁶, Laurent Dufosse¹⁷, Giuliano Ferisin¹⁸, Aneeqa Ghafoor¹⁹, Sana Hanif¹¹, Hira Ijaz²⁰, Aamna Ishaq¹¹, Sana Jabeen²⁰, Halide Karabıyık²¹, Abdul Nasir Khalid⁸, Irina Yuryevna Kirtsideli¹⁰, Munazza Kiran²², Deegendra Khadka¹⁴, Anand Mallik²³, Hugo Madrid^{24,25}, Jean-Marc Moncalvo^{9,26}, Nicole Scott²⁷, Abdul Rehman Niazi¹⁹, Skarma Nonzom¹⁵, Rijan Ojha^{28,29}, Inna Gennadievna Pankova¹⁰, Sudeep Rai^{28,23}, Abdul Razaq¹¹, Mohammad Ataullah Siddiqui¹⁴, Manita Shyaula¹², Hana Ševčíková³⁰, Aisha Umar⁸, Sadiq Ullah³¹, Muhammad Usman^{8,32}, Irmgard Krisai-Greilhuber³³

¹ Institut de recherche sur les forêts, Université du Québec en Abitibi-Témiscamingue, Rouyn-Noranda, QC, Canada

² Research Group Mycology, Department of Biology, Ghent University, 9000 Ghent, Belgium

³ Faculty of Science, University of South Bohemia, 370 05 České Budějovice, Czechia

⁴ Biology Centre of the Czech Academy of Sciences, Institute of Entomology, 370 05 České Budějovice, Czechia

⁵ Van Yüzüncü Yıl University, Başkale Vocational School, Department of Organic Agriculture, Van, Türkiye

⁶ Department of Biology, College of Science, Princess Nourah bint Abdulrahman University, P.O. Box 84428, Riyadh 11671, Saudi Arabia

⁷ Department of Biology, College of Science, Qassim University, Qassim, Saudi Arabia

⁸ Institute of Botany, Quaid-e-Azam Campus, University of the Punjab, Lahore 54590, Pakistan

⁹ Department of Natural History, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario M5S 2C6, Canada

¹⁰ Komarov Botanical Institute of the Russian Academy of Sciences, 197022, St. Petersburg, Russia

¹¹ Department of Biological Sciences, Faculty of Fisheries and Wildlife, University of Veterinary and Animal Sciences, Ravi Campus, Pattoki, Pakistan

¹² Biological Resource Unit, Faculty of Science, Nepal Academy of Science and Technology, Lalitpur 44700, Nepal

¹³ Department of Animal Breeding and Genetics, Faculty of Animal Production and Technology, University of Veterinary and Animal Sciences, Ravi Campus, Pattoki, Pakistan

¹⁴ Molecular Biotechnology Unit, Faculty of Science, Nepal Academy of Science and Technology, Lalitpur 44700, Nepal

¹⁵ Department of Botany, University of Jammu, Baba Saheb Ambedkar Road, Gujarbasti, Jammu, Jammu and Kashmir 180006, India

¹⁶ Dipartimento di Bioscienze, Biotecnologie e Ambiente (DBBA), Campus Universitario "Ernesto Quagliariello", Università degli Studi di Bari "Aldo Moro", Via Orabona 4, 70125 Bari, Italy

¹⁷ CHEMBIOPRO Laboratoire de Chimie et Biotechnologie des Produits Naturels, ESIROI Agroalimentaire, Université de La Réunion, Saint-Denis, Ile de La Réunion, France

¹⁸ Associazione Micologica Bassa Friulana, via Vespucci 7, 33052 Cervignano del Friuli, Italy

¹⁹ Institute of Botany, Quaid-e-Azam Campus, University of the Punjab, Lahore, 54590, Pakistan

²⁰ Department of Botany, Division of Science and Technology, University of Education, Township, Lahore-54770, Punjab, Pakistan

²¹ Trakya University, Arda Vocational School, Department of Food Processing, Edirne, Türkiye

²² Department of Botany, University of Education, Lahore, Pakistan

²³ Department of Botany, Degree Campus, Tribhuvan University, Biratnagar 56613, Nepal

²⁴ Escuela de Tecnología Médica, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Av. Alemania 281, 4801043 Temuco, Chile

²⁵ Centro para la Resiliencia, Adaptación y Mitigación (CReAM), Universidad Mayor, Av. Alemania 281, 4801043 Temuco, Chile

²⁶ Department of Ecology and Evolutionary Biology, University of Toronto, 25 Willcocks Street, Ontario M5S 3B2, Canada

²⁷ Escuela de Tecnología Médica, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Camino La Pirámide 5750, 8580745 Huechuraba, Santiago, Chile

²⁸ Biodiversity Research and Conservation Society, Kathmandu 44600, Nepal

²⁹ Center for Integrative Conservation and Yunnan Key Laboratory for Conservation of Tropical Rainforests and Asian Elephants, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan 666303, China

³⁰ Department of Botany, Moravian Museum, Zelný trh 6, CZ - 659 37 Brno, Czechia

³¹ Department of Botany, Dr. Khan Shaheed Government Degree College, Kabal, Swat, Khyber Pakhtunkhwa, Pakistan

³² The Natural History Museum, Cromwell Road, London, SW7 5BD, United Kingdom

³³ Department of Botany and Biodiversity Research, University of Vienna, 1030 Wien, Austria

* e-mail: cazabonne.jonathan@gmail.com

Cazabonne J., Haelewaters D., Acar İ., Alhomaidi E., Al Tami M.S., Aman N., Iliushin V.A., Aslam A., Bhatt L.R., Majeed M.B.B., Poudel R.C., Chaudhary S., Digra S., Dovana F., Dufossé L., Ferisin G., Ghafoor A., Hanif S., Ijaz H., Ishaq A., Jabeen S., Karabiyk H., Khalid A.N., Kirtsideli I.Y., Kiran M., Khadka D., Mallik A., Madrid H., Moncalvo J.-M., Scott N., Niazi A.R., Nonzom S., Ojha R., Pankova I.G., Rai S., Razaq A., Siddiqui M.A., Shyaula M., Ševčíková H., Umar A., Ullah S., Usman M. & Krisai-Greilhuber I. (2025) Fungal Systematics and Evolution: FUSE 11. – *Sydowia* 77: 315–383.

In this 11th contribution to the Fungal Systematics and Evolution series published by *Sydowia*, the authors formally describe four species: *Dothidea nigricans* from Antarctica; *Ganoderma punjabicum*, *Lepiota penguiniformis* and *Leucococybe papillatus* from Pakistan. The following new country records are reported: *Entoloma noordeloosii* from Czechia, *Hebeloma lindae* from Türkiye, *Paxillus ammoniavirescens* from Pakistan, *Plectosphaerella plurivora* from Chile, *Sparassis latifolia* from Pakistan, *Talaromyces fusiformis* on *Elaeagnus angustifolia* from India, and *Trichaleurina javanica* on *Shorea robusta* from Nepal.

Keywords: 4 new species, 7 new records, Agaricaceae, Dothideaceae, Entolomataceae, integrative taxonomy, Marasmiaceae, Paxillaceae, Polyporaceae, Pyronemataceae, Sparassidaceae, Strophariaceae, Trichocomaceae, Trichosphaeriaceae.

Materials and methods

Sample collection, isolation, and specimen examination

For the *Dothidea* Fr. study, timber samples from which *D. nigricans* was isolated were collected in abandoned polar station buildings on Heiss Island in Franz Josef Land, Arkhangelsk Oblast, Russian Federation (80°34' N, 57°41' E) in August 2021. Nine oak wood samples were collected into individual sterile plastic tubes and stored for 1 month at 5 °C, then frozen at 20 °C. *Dothidea nigricans* was first isolated by direct inoculation of substrate fragments (wood) onto Sabouraud dextrose agar (SDA), following the methods of Guinea et al. (2005) and Dudka et al. (1982). To obtain a pure culture, single-spore isolation was performed using a 0.05 % Tween 80 solution (Samson et al. 2014). As a result, two strains of *D. nigricans* were isolated, namely DI-209 and ID-316b. The strain DI-209 was deposited in the All-Russian Collection of Microorganisms (VKM), Pushchino, Russia, under No. VKM F-5012, and a dried type culture is preserved in the Mycological Herbarium of the Komarov Botanical Institute, St. Petersburg, Russia (LE), under No. LE F-350178. For morphological analysis, the two isolates (DI-209 and ID-316b) were cultivated on Czapek agar (CZ) (Raper & Thom 1949), malt extract agar (MEA) (Samson et al. 2010) and SDA (Guinea et al. 2005). The isolates were inoculated on 9 cm Petri dishes and incubated at 21 °C in darkness for 21 days. To assess temperature-dependent growth patterns, inoculated CZ, MEA and SDA plates were incubated at 4, 6, 8, 12, 16, 18, 25, 27 and 30 °C for 21 days. Colony color was determined using the ISCC-NBS Centroid Color Charts (Kelly 1964), following the recommendations of Nováková et al. (2012). Micro-morphological features were examined with a Carl Zeiss Axio Imager A1 microscope.

For the *Ganoderma* P. Karst study, specimens were collected during the monsoon season of 2018

from areas surrounding District Lahore, Punjab Province, Pakistan. Lahore, located in the north-eastern part of the country, is the second-largest city in Pakistan (Ghouri et al. 2022). The subsoil of this region is alluvial, composed of sand, silt, and clay (Khan et al. 2022). Fresh basidiomata were photographed in situ. Macroscopic features were recorded from the fresh basidiomata (e.g., color, texture, laccate appearance). Specimens were dried by placing them in front of a hot air fan set at 40–45 °C, then stored at –20 °C for two weeks, and finally sealed in polyethylene bags. Color descriptions follow the Munsell Color System (Munsell Color Company 1954). For microscopic examination, sections of dried tissues (i.e., a free hand section from upper and lower surface of basidiomata) were rehydrated in 5 % KOH and stained with 1 % Congo Red. Microscopic observations were made using a compound light microscope at 100× magnification (MX4300H, Meiji Techno Co., Ltd., Japan). At least 35 measurements were recorded for each microscopic structure using the Piximètre software (Henriot & Cheypne 2020). Basidiospores dimensions are presented as length range × width range, followed by mean length × mean width ± standard deviation, and the length/width ratio (Q). Dried specimens were deposited at the Lahore herbarium (LAH) of the University of the Punjab, Pakistan.

The specimen of *Lepiota* (Pers.) Gray was collected from Nimakai, Kabal Tehsil, Swat District, Khyber Pakhtunkhwa, Pakistan. The climate of this region ranges from warm semi-arid (BSH) to humid subtropical (Cfa), with some areas classified as temperate continental (Dwb) according to the Köppen-Geiger climate classification system (Arnfield 2024). Vegetation in the area includes West Himalayan moist temperate and dry temperate forests. Moist temperate forests are characterized by the presence of *Quercus dilatata* Royle, *Q. incana* Roxb., and *Q. semecarpifolia* Sm. Other plant species found in these forests are *Abies pindrow* Royle, *Acer caesium*

Wall. ex Brandis, *Cedrus deodara* (Roxb. ex D. Don) G. Don, *Diospyros lotus* L., *Juglans regia* L., *Juniperus macropoda* Boiss., *Olea ferruginea* Royle, *Picea smithiana* Boiss., *Pinus roxburghii* Sarg., *P. wallichiana* A.B. Jacks., *Pistacia integerrima* J.L. Stewart and *Taxus wallichiana* Zucc. In contrast, dry temperate forests of Swat are dominated by *Q. bal-lota* Desf., *Pinus gerardiana* Wall ex D. Don and *Betula utilis* D. Don (Ahmad et al. 2015). The specimen was photographed at the collection site, morphological features were noted, and the collection was dried using a fan heater. Key macroscopic characteristics—including pileus size, shape, and color; lamellae attachment and coloration; and presence and type of annulus on the stipe—were noted using Vellinga's terminologies (Vellinga 2001). Colors were determined using the Munsell color chart mobile application (<https://munsell.com/color-blog/tag/color-app/>). An EU 2230436 microscope with a 100x objective lens was used to observe micro-morphological features. The material was mounted with 5 % KOH for rehydration and Congo red for staining hyaline tissues. Measurements were recorded using the Calibrated Motic Images Plus 2.0 software, with a minimum of 20 measurements per observed structure. The symbol '(a-)b-c(-d)' was used to indicate the basidiospore size, where 'b-c' represented 90 % of measured values, and 'a' and 'd' indicated extreme values. 'Q' denoted the length-to-width ratio of a single basidiospore from the side view, while 'avQ' represented the average 'Q' value for all specimens. Other microstructural measurements included the range between extreme length and width measurements. The specimen was deposited in the Herbarium at the Department of Botany, University of Education, Lahore, Pakistan (UEH).

For the *Leucoinocybe* Singer ex Antonín, Borov., Holec & Kolařík study, two specimens were collected in the Pabbi reserve forest, Punjab, Pakistan, during the monsoon of 2020. Basidiomata were found growing solitary, on loamy forest soil. Macroscopic description was made by examining fresh basidiomatas and photographs were taken at the collection site. Color codes are according to Munsell Color (1994). Microscopic observations were made from slides prepared from the dried material mounted in 5 % KOH and Congo red stain, and made under a compound microscope (Zeiss, Axio-lab, Germany) with an attached digital camera (Axio-cam 208) to capture images. For each collection, a total of 30 basidiospores, basidia, cystidia, and hyphae were measured. Basidiospore dimensions are expressed as length × width. The arithmetic mean of the length and width of each measured basidiospore

is included in the measurements. The length/width ratios (Q) were computed and displayed as the mean ± standard deviation with the range of Q values (Qmin-Qmax). The specimen was deposited at the Cryptogamic Herbarium (TRTC) of the University of Toronto, Ontario, Canada.

The macroscopic description of *Entoloma* (Fr.) P. Kumm. is based on observations of fresh material. The micro-morphological characters are based on the study of fresh and dried material. Dry basidiomata were rehydrated in distilled water or KOH (10%) before observation and mounted in aqueous Congo Red. Q indicates the quotient of length and width of the spores in sideview. In the basidiospore dimension notation, (a-)b-c(-d), b-c is the range including 95 % of the measured values, with (a) and (d) being the extreme values. Q indicates the quotient of length and width of the spores in sideview. Qav represents the mean length/width quotient for all measured spores. For all microscopic structures, 30 elements were measured. Voucher specimen is deposited at the Moravian Museum (BRNM), Brno, Czechia. Color abbreviations follow the RAL Design color range system (<https://www.ralcolorchart.com/ral-design>). The drawings in Fig. 11 were edited in GNU Image Manipulation Program (GIMP) v.2.10.2.

For the *Hebeloma* (Fr.) P. Kumm. study, seven specimens were collected in 2024 from the Terzioğlu campus of Çanakkale Onsekiz Mart University, Türkiye, where *Pinus brutia* Ten. (Fig. 13) dominates. Specimens were photographed in situ using a Canon 60D digital camera. Microcharacters of the collected specimens were examined under a light microscope (Leica DM500: Germany). Each microscopic character (spores, basidia, cheilocystidia, and caulocystidia) was measured at least 40 times to obtain reliable results. Standard chemical reagents, including 5 % potassium hydroxide (KOH) and Melzer's reagent, were used for microscopical preparations. Illustrations of microscopic structures were prepared using the CorelDRAW Graphics Suite 2022 (64-bit) (Corel Corporation, Ottawa, Canada) drawing program and scanning electron microscope (SEM) images of basidiospores were obtained using a ZEISS GeminiSEM 300 (Bozzola & Russell, 1999). The morphology of macro- and microscopic characters (e.g., spores, basidia, cheilocystidia, caulocystidia) was estimated by following the literature defined by Vesterholt (2005), Vesterholt et al. (2014), Carrasco-Hernandez et al. (2015), Beker et al. (2016, 2017), Grilli & Brugaletta (2016), Acar et al. (2022), Akata et al. (2023), and Lambert et al. (2024). After the identification process, speci-

mens were dried and deposited in the Fungarium of the Department of Biology, Faculty of Science, Van Yüzüncü Yıl University, Türkiye (VANF Acar 1757 and Acar 1866).

Specimens of *Paxillus* Fr. were collected from the Kharmang valley in Gilgit Baltistan between September 2022 and July 2023. The species was found at a high altitude along the northeastern border of India and Pakistan (ca. 35.3° N, 76.5° E). The valley is located at an altitude of approximately 3000 to 5000 m a.s.l. and is home to diverse plant communities, including juniper, pine, and spruce trees, along with many different herbs, fruit orchards, aquatic plants and bushes, and a rich fungal diversity. Annual precipitation ranges from 83 to 208 mm and mainly occurs during spring and late summer (Hussain et al. 2024). *Paxillus ammoniavirescens* specimens were collected at one sampling site using a knife and photographed in situ. After proper labelling, specimens were placed in a zipper-sealed plastic bag and transported to the laboratory for heat drying and further analysis. Specimens were dried to a final moisture content of ~5 %. The hand-free section of lamellae was prepared in 5 % KOH and observed under a compound microscope (S/N – EU 2230391 euromex). Morphological features, including the pileus' size, shape, and color, lamellae attachment and color, and presence and type of annulus on the stipe, were documented. For each morphological feature, a minimum of 20 measurements was recorded. Color determination was conducted using the Munsell color chart (<https://munsell.com/color-blog/tag/color-app/>). Voucher specimens were deposited in the Herbarium of the University of Education, Lahore, Pakistan (UEH).

For the *Plectosphaerella* Kleb. study, a sample of decaying branches, leaves and bark of an unidentified plant was collected in Santiago, Chile. Plant samples were placed in plastic bags, kept in a refrigerator at 4–7 °C, and processed within 24 h of collection. Materials were incubated in moist chambers at room temperature and periodically examined under a stereomicroscope over a 1-month period for signs of fungal growth. To obtain a pure culture, conidia were transferred directly from colonies observed on a decaying leaf to malt extract agar (MEA; Merck, Germany) plates using a sterile dissection needle. Morphological features of the isolated fungus were studied on MEA and Sabouraud agar (Merck, Germany) after 7 days at 25 °C. Semipermanent microscope slides were mounted on lactophenol cotton blue (Sigma-Aldrich, Oakville, Canada) to observe and describe micromorphological characteristics. Conidial dimensions are given

as length × width with ranges followed by mean values ($\bar{x}$) and the number of measurements (n) indicated in parentheses. The studied strain, HM 230, is preserved at the fungal strain collection of Hugo Madrid (HM) at the Medical Technology School of Universidad Mayor, Temuco, Chile.

Basidiomata of *Sparassis* Fr. species were collected during 2020–2021 as part of a study aimed at exploring the macrofungal diversity in the Abbottabad district of Khyber Pakhtunkhwa (Pakistan). Basidiomata were collected, vouchered, and photographed in their natural habitats using a Nikon D70S digital camera. Morphological features such as size, shape and surface features of different parts of the basidiomata were recorded in the field from the fresh specimens. Colors were designated according to Munsell (1975). The microscopic structures were observed on dried material using 5 % KOH, Congo red and Melzer's reagent. Melzer's reagent was used to demonstrate color changes of basidiospores. At least 20 basidiospores from each collection and similarly basidia, hymenial and stipe elements were measured using Scope Image 9.0(X5). The given spore dimensions in parentheses include both the extremes, mean, and the standard deviation for both the length and width. The range of spore quotient (Q) was also calculated. The following abbreviations were used: avl = average length, avw = average width, Q = length/width ratio of basidiospores (Sher et al. 2018). The collected specimens were deposited in the herbarium (LAH) of the Institute of Botany, University of the Punjab, Lahore, Pakistan.

For the *Talaromyces* C.R. Benj. study, isolates were obtained from a wild host plant growing in the cold arid regions of Kargil, Ladakh, India (34°33'14" N, 76°08'06"E). Healthy plant samples were collected aseptically in pre-sterilized, autoclaved polyethylene bags and transported to the laboratory. Samples were processed within 24–48 hours after collection for endophyte isolation following the method of Petrini & Fisher (1986), with slight modifications. Fresh berries of the plant were washed repeatedly under running tap water, then surface-sterilized in 70 % ethanol (1 min), 2 % sodium hypochlorite (2 min), and again in 70 % ethanol (1 min). Treated fresh berry samples were dried between sterile filter paper sheets in a laminar airflow chamber. Each berry was sectioned into small segments with the help of a sterile blade and placed on potato dextrose agar (PDA) in Petri dishes. Plates were incubated at 28±2°C for 7 days to allow for the growth of endophytic fungi. Emerging endophyte colonies were further cultured and purified for sub-

sequent morphological and molecular characterization. The colonization frequency (CF) of the isolate was calculated by using the following formula:

$$\text{CF \%} = \frac{\text{number of infected tissue segments}}{\text{Total number of segments inoculated}} \times 100.$$

The isolated fungus was grown on two different media, *viz.*, PDA and Czapek yeast extract agar (CYA). After sufficient growth of the fungal mycelium on nutrient media, characteristic features of colony, including color, texture, diameter, exudate and pigment formation, were recorded. Micromorphological details were studied by mounting fungal mycelium in lactophenol cotton blue stain and using transparent tape. Line drawings were prepared with the aid of a camera lucida (Erma, Japan) attached to a compound light microscope (Magnus, India model no. HB 043295). Different microscopic structures of the fungal isolate, including hyphae, stipe, metulae, phialides and conidia, were measured using an ocular micrometer. The anatomy of the isolate was studied under a compound microscope (Leica DM2000) equipped with image analysis software. The pure culture of the isolate of *T. fusiformis* (ELS-F4) has been deposited in the Microbial Culture Collection (MCC) center (also known as the National Centre for Microbial Resource [NCMR]), Pune, India, under accession number MCC10205.

For the *Trichaleurina* Rehm study, 5 specimens were collected on a decaying twig of *Shorea robusta* on 18 June 2023 in Raja-Rani Community Forest, Morang District, Koshi Province, Nepal. Specimens were photographed in their natural habitat and collected in paper envelopes. The specimens were oven-dried at 37 °C for 2 days. One representative, mature specimen was deposited at the National Herbarium and Plant Laboratories (KATH), Nepal, under the collection number MRN1 (Fig 1). For microscopic examination, temporary slides were prepared from fresh material. No mounting chemicals were used for staining and microscopic observations were conducted in H₂O. Microscopic structures were observed under a compound microscope (model Magnus MLX-TR) and photographed using an iPhone 12 Pro Max. Ascocarps of *T. javanica* were cleaned and washed with distilled water to remove any residual materials, then oven-dried at 35°C to constant weight and ground into a fine powder using a mixer. One gram of the resulting powder was extracted with 10 mL of methanol in a shaking incubator (37°C, 100 rpm) for 24 h. The obtained mixture was filtered through Whatman No. 1 filter paper. Residues were extracted again with an addi-

tional 10 ml of methanol using the same procedure. The filtrates were combined, evaporated to dryness at 40 °C using a rotary evaporator, and the resulting extract was stored at 4 °C for subsequent analyses (Al-Harrasi et al. 2014). Total phenolic content was measured using a modified version of the Folin-Ciocalteu assay (Singleton & Rossi 1965). Briefly, 50 µl of ascocarp extract was mixed with 150 µl of Folin-Ciocalteu's phenol reagent. After 3 min, 150 µl of 20 % sodium carbonate solution was added, and the mixture was diluted to a final volume of 1,500 µl using Milli-Q water. The reaction mixture was incubated in the dark for 90 min, and the absorbance was read at 725 nm using an Epoch Microplate spectrophotometer (BioTek Instruments, Winooski, VT, USA). A standard curve was established using gallic acid concentrations ranging from 0 to 500 µg/mL, yielding a regression equation of $y = 0.0021x + 0.0596$ ($R^2 = 0.9962$). Phenolic content was expressed as milligrams of gallic acid equivalents (GAEs) per 100 g of extract. Total flavonoid content was measured using a modified aluminum chloride (AlCl₃) colorimetric method (Woisky & Salatino 1998). Briefly, 100 µL of ascocarp extract was added to an equal volume of 2 % AlCl₃·H₂O solution. The mixture was incubated in the dark for 1 h, after which the absorbance was recorded at 415 nm using an Epoch Microplate spectrophotometer (BioTek Instruments, Winooski, VT, USA). A calibration curve was constructed using quercetin standards that ranged from 0 to 500 µg/ml, yielding the regression equation $y = 0.0011x + 0.0941$ ($R^2 = 0.9909$). Flavonoid content was expressed as milligrams of quercetin equivalents (QAE) per 100 g of extract. The antioxidant activity of the ascocarp extract was determined using the DPPH (1,1-diphenyl-2-picrylhydrazyl) free radical-scavenging assay (Baliyan et al. 2022). Briefly, 0.9 ml of freshly prepared methanolic solution of 0.1 mM DPPH was added to 0.3 ml of ascocarp extract at various concentrations. The mixture was incubated in the dark for 30 min at room temperature to complete the reaction, after which the absorbance was measured at 517 nm using an Epoch Microplate spectrophotometer (BioTek Instruments, Winooski, VT, USA). Radical scavenging activity (RSA) was calculated using the

following formula: $\text{RSA (\%)} = \left(\frac{A-B}{A} \right) \times 100$, where A =

Absorbance of DPPH solution without extract; and B = Absorbance of the DPPH solution mixed with the ascocarp extract. Antioxidant activity was expressed as IC₅₀, defined as the extract concentration (µg/ml) required to inhibit 50 % of the DPPH radi-

cals. All assays were carried out in triplicate. Data were processed in Microsoft Excel and presented as mean $\pm$ standard deviation.

DNA extraction, PCR amplification, and sequencing

For the *Dothidea* study, the pure cultures of DI-209 and ID-316b were grown on SDA at 21 °C for 14 days. Genomic DNA was extracted using a DiamondDNA Plant kit (ABT, Russia, Barnaul), according to the manufacturer's instructions. The D1/D2 region of 28S rDNA (LSU) was amplified using PCR-primers NL-1 (5'-GCATATCAATAAGCG-GAGGAAAAG-3') and NL-4 (5'-GGTCCGTGTTT-CAAGACGG-3') (O'Donnell 1993). PCR amplification conditions were as follows: an initial denaturation at 94 °C for 2 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 55 °C for 1 min, and extension at 72 °C for 2 min, with a final extension step at 72 °C for 5 min. The internal transcribed spacer rDNA region (ITS1-5.8S-ITS2) was amplified using PCR-primers ITS1 (5'-TCCGTAG-GTGAACCTTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (White et al. 1990). PCR amplification conditions were as follows: an initial denaturation at 95 °C for 2 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, and extension at 72 °C for 1 min, with a final extension step at 72 °C for 10 min. For the amplification of the partial second largest subunit of RNA polymerase II (*RPB2*), primers 5F_Eur (5'-GAY-GAY-CGK-GAY-CAY-TTC-GG-3') and 7CR_Eur (5'-CCC-ATR-GCY-TGY-TTR-CCC-AT-3') were used (Houbraken & Samson 2011). PCR amplification conditions were as follows: an initial denaturation at 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 52 °C for 30 s, and extension at 72 °C for 1 min, with a final extension step at 72 °C for 10 min. ITS, LSU and *RPB2* sequences were deposited in GenBank (Tab. 1).

Genomic DNA of *Ganoderma* was extracted from two basidiomata (LAH036551, LAH036552) using the modified CTAB protocol from Doyle & Doyle (1987). The nuclear ribosomal internal transcribed spacer (ITS) region was amplified using the primers ITS1 and ITS4 (White et al. 1990). PCR reaction mixture (25 μ l) comprised *Taq* polymerase (12.5 μ l), 2 $\times$ Master Mix with Standard Buffer (1 μ l), each primer of 10 μ M (1 μ l), ddH₂O (9.5 μ l), and DNA template (1 μ l). PCR amplification was performed with the following thermal cycling conditions: initial denaturation at 94 °C for 4 min; fol-

lowed by 40 cycles of denaturation at 94 °C for 1 min, annealing at 55 °C for 1 min, and extension at 72 °C for 1 min; with a final extension at 72 °C for 10 min. PCR products were purified and Sanger sequencing was outsourced to Tsing Ke Biotechnology Co., Ltd. (Beijing, China). The two ITS sequences were deposited in GenBank (Tab. 1).

Genomic DNA of *Lepiota* was extracted following the CTAB method (Gardes & Bruns 1993, Bruns 1995). PCR amplification of the ITS region was carried out using the primers ITS1F and ITS4 (White et al. 1990), following the thermal cycler conditions described by Gardes & Bruns (1993). The resulting PCR products were purified and sequenced using Sanger sequencing by the Beijing Genomics Institute (BGI), P. R. China. The ITS sequence was deposited in GenBank (Tab. 1).

Genomic DNA was extracted from dried basidiomata of *Leucoiocybe* following Gardes & Bruns (1993), with a few modifications. The internal transcribed spacer (ITS) region of the nuclear ribosomal RNA gene array was amplified using the primers ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990). PCR amplifications were performed in a 20 μ l reaction volume containing 12 μ l of PCR 2X Master Mix (Wizsolutions, New Jersey, USA), 5 μ L of double-distilled water, 1 μ l of MgCl₂, and 1 μ l of each primer. Thermocycling conditions were as follows: initial denaturation at 94 °C for 5 min; 35 cycles of 94 °C for 1 min, 53 °C for 1 min, and 72 °C for 1 min; and a final extension at 72 °C for 18 min. PCR products were visualized on a 1 % agarose gel stained with 3 μ l of ethidium bromide. Amplified products were sequenced by TsingKe Biological Technology Co. (Beijing, China). Sequences were deposited in GenBank (Tab. 1).

Genomic DNA was extracted from dried *E. noordeლოსii* basidioma using the CTAB protocol (Doyle & Doyle 1987). The ITS region was amplified with primers ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990). The sequence was generated commercially by M. Sochor (VÚRV, Olomouc, Czechia) following the molecular methods described in Ševčíková et al. (2021). The sequence was assembled and edited in Geneious version 11.1.5 (Kearse et al. 2012) and then submitted to GenBank (Tab. 1).

Genomic DNA was extracted from two specimens of *Hebeloma* (Acar 1757 and Acar 1866) using the CTAB method following the protocol described by Rogers & Bendich (1994) and Dizkırıcı et al. (2019a, 2019b, 2022). The purity and quantity of the isolated DNA were evaluated using a NanoDrop2000c UV-Vis Spectrophotometer (Thermo

Tab. 1. Details of sequences and isolates included in the BLAST searches and phylogenetic analyses for the new species and interesting reports.

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEFI	Reference(s)
<i>Amauroderma rude</i>	GDGM25736	China	KF372587			Li & Yuan (2015)
<i>Auricularia heimuer</i>	Cui 7105	China	KM396777			Wu et al. (2014)
<i>Auricularia heimuer</i>	Cui 7101	China	KM396776			Wu et al. (2014)
<i>Coniozoma leucospermi</i>	CBS:111289	South Africa, <i>Leucospermum conocarpodendron</i>	EU552113	EU552113		Marincowitz et al. (2008)
<i>Dothidea berberidis</i>	CBS 186.58	India	KC800752	EU167601		da Hora Júnior et al. (2014)
<i>Dothidea eucalypti</i>	CBS:143417, T	Australia, leaves of <i>Eucalyptus dalympheana</i>	MG386106	NR_156390		Crous et al. (2017b)
<i>Dothidea hippophaeos</i>	CBS 188.58	Unknown	DQ678048	AF027763	DQ677942	Thambugala et al. (2014)
<i>Dothidea insculpta</i>	CBS:189.58, T	France	MH869284	AF027764	DQ247792	Vu et al. (2019)
<i>Dothidea insculpta</i>	KNU-SOT5	South Korea, <i>Prunus serrulata</i>	LC591853	LC591852		Moe et al. (2021)
<i>Dothidea insculpta</i>	MFUCC 13-0686	Italy, dead branch of <i>Clematis vitalba</i>	KM388551	KM388543		Thambugala et al. (2014)
<i>Dothidea kunmingensis</i>	YG-2021a	China, <i>Jasminum nudiflorum</i>	MZ571163	MZ571163		Gao et al. (2021)
<i>Dothidea muelleri</i>	CBS 191.58, T	Switzerland, <i>Daphne striata</i>	EU167593	MH857751		Simon et al. (2009), Vu et al. (2019)
<i>Dothidea muelleri</i>	CBS:192.58	Switzerland, <i>Daphne striata</i>	MH869285	MH857752		Vu et al. (2019)
<i>Dothidea nigricans</i>	VKM F-5012 (DI-209), T	Russia, Franz Josef Land, timber of abandoned buildings of polar station	OR801565	OP961959	OR810751	This study
<i>Dothidea nigricans</i>	ID-316b	Russia, Franz Josef Land, timber of abandoned buildings of polar station	PP993970	PP993961	PQ000247	This study
<i>Dothidea noxia</i>	CBS:171.34, T	The Netherlands	MH866956	MH855477		Vu et al. (2019)
<i>Dothidea sambuci</i>	AFTOL-ID 274	Unknown, freshwater	AY544681	DQ491505	DQ522854	Thambugala et al. (2014)
<i>Dothidea sambuci</i>	CBS 198.58, T	Switzerland, <i>Acer pseudoplatanus</i>	AF382387	AY930109	KT216559	Jeewon et al. (2002), Ismail et al. (2016)
<i>Dothiora cactacearum</i>	CBS 142492	USA, Cactaceae (ornamental)	KY929176	KY929143		Crous et al. (2017a)
<i>Dothiora ceratoniae</i>	CBS 477.69, T	Spain, <i>Ceratonia siliqua</i>	KF251655	KF251151	MF951419	Quaedvlieg et al. (2013)
<i>Dothiora ribesia</i>	CPC 30689	Germany, twig of <i>Ribes rubrum</i>	KY929174	KY929141		Crous et al. (2017a)
<i>Endoconidioma euphorbiae</i>	CPC:38649	South Africa, <i>Euphorbia mauritanica</i>	MW883810	MW883417	MW890060	Crous et al. (2021)
<i>Endoconidioma populi</i>	UAMH 10297, T	Canada, <i>Populus tremuloides</i>	NG_059198	NR_121303		Tsunedo et al. (2008)
<i>Endoconidioma rosae-hissaricae</i>	TASM 6106, T	Uzbekistan, <i>Rosa hissarica</i>	NG_059269	NR_157516		Wanasinghe et al. (2018)
<i>Entoloma aff. sinuatum</i>	TRTC156546	Canada	JN021019			Dentinger et al. (2011)
<i>Entoloma atrosericeum</i>	K69 310 G262084, T	France	LN850607			Kokkonen (2015)
<i>Entoloma atrosericeum</i>	GG160811	Sweden	MZ868968			Reschke et al. (2022)
<i>Entoloma boreale</i>	106/09 TUR, T	Finland	LN850624			Kokkonen (2015)

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEFI	Reference(s)
<i>Entoloma brunneipes</i>	TENN9029, T	USA	LN850621			Kokkonen (2015)
<i>Entoloma brunneorugulosum</i>	KaiR691, T	Panama	MZ611676			Reschke et al. (2022)
<i>Entoloma</i> cf. <i>carolinianum</i>	IBUG Montanez222	Mexico	MZ869010			Reschke et al. (2022)
<i>Entoloma</i> cf. <i>spadiceum</i>	TENN 070791	USA, Tennessee	MF686497			Matheny & Sanchez-Garcia, unpublished
<i>Entoloma</i> cf. <i>rhodopolium</i>	DB03-06-2018-3	Hungary	MZ868960			Reschke et al. (2022)
<i>Entoloma festivum</i>	L:Rommelaars_17-Jul.2004, T	The Netherlands	MZ869009			Reschke et al. (2022)
<i>Entoloma festivum</i>	L:Rommelaars_17-Jul.2004, T	The Netherlands	MZ869009			Reschke et al. (2022)
<i>Entoloma leucocarpum</i>	MEN701, T	The Netherlands	MZ868970			Reschke et al. (2022)
<i>Entoloma lividoalbum</i>	GE12-025	France	MZ868957			Reschke et al. (2022)
<i>Entoloma lupinum</i>	13/14 TUR, T	Finland	LN850570			Kokkonen (2015)
<i>Entoloma mediorobustum</i>	PA728	Panama	MZ611688			Reschke et al. (2022)
<i>Entoloma mediorobustum</i>	JR064, T	Panama	MZ611635			Reschke et al. (2022)
<i>Entoloma myrmecophilum</i> (as <i>Rhodophyllus myrmecophilus</i>)	K398, T	France	LN850462			Kokkonen (2015)
<i>Entoloma nidorosum</i>	FR2016708	France	MZ868995			Reschke et al. (2022)
<i>Entoloma noordeloosii</i>	OAK_PLOT15	Hungary, <i>Quercus</i>	UDB0786449			R. Henrik Nilsson, unpubl.
<i>Entoloma noordeloosii</i>	WU18780, T	Austria	MZ868962			Reschke et al. (2022)
<i>Entoloma noordeloosii</i>	BEECH_PLOT21	Germany, <i>Fagus sylvatica</i>	UDB0782631			R. Henrik Nilsson, unpubl.
<i>Entoloma noordeloosii</i>	TUE002403	Georgia, Soil DNA	UDB05326574			R. Henrik Nilsson, unpubl.
<i>Entoloma noordeloosii</i>	O-F-256343	Norway	UDB07673644			Gunnhild Marthinsen, unpubl.
<i>Entoloma noordeloosii</i>	WU:39739	Unknown	MZ868963			Reschke et al. (2022)
<i>Entoloma noordeloosii</i>	BRNM 825859 (HS21-8-10-15)	Czech Republic, forest with <i>Quercus</i>, <i>Fraxinus</i> and <i>Ulmus</i>	PQ656722			This study
<i>Entoloma noordeloosii</i> (as <i>Entoloma</i> sp.)	LM5650	Hungary, mycorrhizal root tip of <i>Quercus petraea</i>	KM576401			Suz et al. (2014)
<i>Entoloma noordeloosii</i> (as <i>Uncultured Entoloma</i>)	H05IK20	Germany, Thuringia	HF675366			Kapturska et al., unpubl.
<i>Entoloma noordeloosii</i> (as <i>Uncultured Entoloma</i>)	Ir3	Iran	FR852296			Bahram et al. (2012)
<i>Entoloma noordeloosii</i> (as <i>Uncultured Entoloma</i>)	clone_15859	Spain, ectomycorrhizal root tip of <i>Fagus sylvatica</i>	MW282430			Rodríguez-Uña et al. (2024)
<i>Entoloma noordeloosii</i> (as <i>Uncultured Entoloma</i>)	clone_13357	Spain, ectomycorrhizal root tip of <i>Fagus sylvatica</i>	MW282600			Rodríguez-Uña et al. (2024)
<i>Entoloma noordeloosii</i> (as <i>Uncultured fungus</i>)	BR-K2_A11	Switzerland, ectomycorrhizal root tip of <i>Fagus sylvatica</i>	KX886002			de Witte et al. unpubl.
<i>Entoloma noordeloosii</i> (as <i>Uncultured fungus</i>)	clone F87	Poland	MH834479			Wilgan et al. (2020)
<i>Entoloma nubooeculatum</i>	KaiR687, T	Panama	MZ611675			Reschke et al. (2022)

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEFI	Reference(s)
<i>Entoloma paludicola</i>	K178125, T	United Kingdom	LN850517			Kokkonen (2015)
<i>Entoloma pruinotum</i>	KaiR533, T	Panama	MZ611656			Reschke et al. (2022)
<i>Entoloma pseudorhodopolium</i>	KUB102, T	Japan	LC088042			Kondo et al. 2017
<i>Entoloma radicipes</i>	42 14 TUR, T	Finland	LN850585			Kokkonen (2015)
<i>Entoloma rhodopolium</i>	213/14 TUR, T	Sweden	LN850494			Kokkonen (2015)
<i>Entoloma rivulare</i>	703/12 TUR, T	Finland	LN850544			Kokkonen (2015)
<i>Entoloma sericatum</i>	237/11	Finland	LN850445			Kokkonen (2015)
<i>Entoloma serpens</i>	410/09 TUR, T	Finland	LN850526			Kokkonen (2015)
<i>Entoloma sinuatum</i>	J.Vauras 8181F	Finland	KC710116			Morgado et al. (2013)
<i>Entoloma subarcticum</i>	JHP-596 C6271	Greenland	LN850473			Kokkonen (2015)
<i>Fuscohypha expansa</i>	CBS 418.89, T	Martinique, tuber of <i>Dioscorea</i> sp.	LR026715			Giraldo & Crous (2019)
<i>Galerina paludosa</i>	BHS2010-09	USA	HM856641			B.H. Seitzman & D.S. Hibbet, unpubl.
<i>Galiella rufa</i>	OMDL iNat # 171102969	USA	OR825613.1			Canan et al. (2024)
<i>Ganoderma adspersum</i>	PF263	Italy	JN176908			Hapuarachchi et al. (2018)
<i>Ganoderma aridicola</i>	Dai 12588	South Africa	KU572491			Du et al. (2023)
<i>Ganoderma aridicola</i>	BJFC Dai 12588	South Africa	NR152914			Xing et al. (2016)
<i>Ganoderma boninense</i>	WD 2028 (FFPRI)	Japan	KJ143905			Zhou et al. (2015)
<i>Ganoderma boninense</i>	WD 2085	Japan	KJ143906			Zhou et al. (2015)
<i>Ganoderma casuarinicola</i>	Dai 16336	China	MG279173			Du et al. (2023)
<i>Ganoderma casuarinicola</i>	Dai 16337	China	MG279174			Du et al. (2023)
<i>Ganoderma casuarinicola</i>	Dai 16339	China	MG279176			Xing et al. (2018)
<i>Ganoderma casuarinicola</i>	Dai 16338	China	MG279175			Xing et al. (2018)
<i>Ganoderma enigmaticum</i>	Dai 15970	South Africa	KU572486			Du et al. (2023)
<i>Ganoderma enigmaticum</i>	CBS 139792	South Africa	NR132918			Xing et al. (2016)
<i>Ganoderma enigmaticum</i>	Dai 15971	South Africa	KU572487			Du et al. (2023)
<i>Ganoderma fornicatum</i>	KR20	India	FJ655474			I. Arulpandi & P.T. Kalaichelvan, unpubl.
<i>Ganoderma lobatum</i>	JV 0402/24	USA	KF605677			Hapuarachchi et al. (2018)
<i>Ganoderma lucidum</i>	GICN04	Italy	AM906058			Guglielmo et al. (2007)
<i>Ganoderma lucidum</i>	Dai11593 (IFP)	Finland	JQ781852			Cao et al. (2012)
<i>Ganoderma mastoporium</i>	TNMF0018835	China	JX840351			Wang et al. (2022)
<i>Ganoderma mastoporium</i>	TNMF-F0018783	China	JX840350			Wang et al. (2022)
<i>Ganoderma neojaponicum</i>	AS5.542	China	AY593867			Wang & Yao (2005)
<i>Ganoderma orbiforme</i>	GACP1408 1329	China	MH106877			Hapuarachchi et al. (2018)
<i>Ganoderma orbiforme</i>	GACP1408 1235	China	MH106875			Hapuarachchi et al. (2018)

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEF1	Reference(s)
<i>Ganoderma pakistanicum</i>	PBD322	Pakistan	MZ518792			Umar et al. (2021)
<i>Ganoderma pakistanicum</i>	PBD321	Pakistan	MZ518789			Umar et al. (2021)
<i>Ganoderma punjabicum</i>	LAH036551 (3BDIII), T	Pakistan	PV821352			This study
<i>Ganoderma punjabicum</i>	LAH036552 (PBDPII), T	Pakistan	PV821353			This study
<i>Ganoderma ramosissimum</i>	xsd08085	China	FJ478127			J. Jiang, X. Cao, G. Zhao, Y. Sun, X. Ju, T. Yin, Q. Miao & C. Li, unpubl.
<i>Ganoderma ramosissimum</i>	xsd08032	China	EU918700			J. Jiang, X. Cao, X. Ju, Y. Sun, T. Yin, J. Peng & F. Chen, unpubl.
<i>Ganoderma sinense</i>	GS92	China	DQ424982			Su et al. (2007)
<i>Ganoderma sinense</i>	GS175	China	DQ425014			Su et al. (2007)
<i>Ganoderma zonatum</i>	FL-02 (TNM)	USA	KJ143921			Zhou et al. (2015)
<i>Ganoderma zonatum</i>	FL-03 (TNM)	USA	KJ143922			Zhou et al. (2015)
<i>Grifola frondosa</i>	ZW-Clarku 005	USA, Massachusetts	AY218415			Wang et al. (2004)
<i>Hebeloma aanenii</i>	HJB13734	Poland	KM390766			Eberhardt et al. (2015)
<i>Hebeloma aestivale</i>	HJB11764	United Kingdom	KT218365			Grilli et al. (2016)
<i>Hebeloma alboerumpens</i>	JVG1090114	Spain	JQ751220			Eberhardt et al. (2013)
<i>Hebeloma alpinum</i>	MONT:CLC2855	USA, Montana	MK281073			Cripps et al. (2019)
<i>Hebeloma birrus</i>	795	Italy	JF908029			Osmundson et al. (2013)
<i>Hebeloma bulbiferum</i>	HJB13522	France	KT218439			Grilli et al. (2016)
<i>Hebeloma celatum</i>	HJB14250	France	KT218468			Grilli et al. (2016)
<i>Hebeloma clavulipes</i>	LY:BR69-22	France	KX765771			Beker et al. (2016)
<i>Hebeloma clavulipes</i>	HJB13094	France	KY271857			Beker et al. (2016)
<i>Hebeloma cylindrosporum</i>	VANF45A	Türkiye	MW131677			Acar et al. (2021)
<i>Hebeloma danicum</i>	IK-H0170	Poland	KX687198			Kalucka et al. (2016)
<i>Hebeloma danicum</i>	S:F93697	Sweden	KX765811			Beker et al. (2016)
<i>Hebeloma dunense</i>	KRAM:F57434	Poland	KT071022			Eberhardt et al. (2015)
<i>Hebeloma dunense</i>	IK-H0361	Poland	KX687202			Kalucka et al. (2016)
<i>Hebeloma duracinoides</i>	JMT-22101108	France	OQ832781			J.M. Trendel, unpubl.
<i>Hebeloma erumpens</i>	JoV1071029-8, BCN	Barcelona	EU570187			Eberhardt et al. (2009)
<i>Hebeloma grandisporum</i>	KRAM:F47189	Romania	KT071023			Eberhardt et al. (2015)
<i>Hebeloma immutabile</i>	SAT-09-262-13	USA, Alaska	MZ054340			S.A. Trudell & J.F. Ammirati, unpubl.
<i>Hebeloma laterinum</i>	X34	Czech Republic	HF678211			Sácký et al. (2014)
<i>Hebeloma laterinum</i>	IK-H0070	Poland	KX687214			Kalucka et al. (2016)
<i>Hebeloma laterinum</i>	F-3440	Sweden	PQ652580			P. Fritzon & B. Bravander, unpubl.
<i>Hebeloma leucosarz</i>	K:K(M)52712	United Kingdom	KT218469			Grilli et al. (2016)

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEFI	Reference(s)
<i>Hebeloma lindae</i>	Acar 1757	Türkiye	PQ891843			This study
<i>Hebeloma lindae</i>	Acar 1866	Türkiye	PV150655			This study
<i>Hebeloma lindae</i>	HJB10955	Spain	OQ100474			Eberhardt et al. (2023)
<i>Hebeloma lindae</i>	HJB13395	Spain	OQ100475			Eberhardt et al. (2023)
<i>Hebeloma lindae</i>	HJB13409	Spain	OQ100476			Eberhardt et al. (2023)
<i>Hebeloma lindae</i>	HJB14798	Italy	OQ100494			Eberhardt et al. (2023)
<i>Hebeloma lindae</i>	HJB14112	Greece	OQ100533			Eberhardt et al. (2023)
<i>Hebeloma lindae</i>	BR5020184115555, T	Spain	NR185378			Beker et al. (2016)
<i>Hebeloma lutense</i>	P:59.232	France	KM390775			Eberhardt et al. (2015)
<i>Hebeloma mesophaeum</i>	HJB10683	United Kingdom	KT218307			Grilli et al. (2016)
<i>Hebeloma mesophaeum</i>	HJB11130	Switzerland	MK305922			Cripps et al. (2019)
<i>Hebeloma nanum</i>	PRM:PRM153761	Czech Republic	KX765798			Beker et al. (2016)
<i>Hebeloma nanum</i>	HJB18171	Canada	ON202540			Eberhardt et al. (2022)
<i>Hebeloma nauseosum</i>	BR5020184122478	Italy	KX765763			Beker et al. (2016)
<i>Hebeloma odoratissimum</i>	BR5020184121440	Belgium	KX765765			Beker et al. (2016)
<i>Hebeloma olympianum</i>	MICH:60198	USA	OQ100515			Eberhardt et al. (2023)
<i>Hebeloma pumilum</i>	C:D-F-40666	Denmark	KX765808			Beker et al. (2016)
<i>Hebeloma pumilum</i>	JE:no_number	Germany	KX765809			Beker et al. (2016)
<i>Hebeloma pusillum</i>	L:WBS9648	France	KM390767			Eberhardt et al. (2015)
<i>Hebeloma radicosum</i>	BR<BEL>:BR5020184113490	France	KX765800			Beker et al. (2016)
<i>Hebeloma sacchariolenis</i>	HJB9020	United Kingdom	KT218216			Grilli et al. (2016)
<i>Hebeloma sacchariolenis</i>	BP:B. Dima DB4918	Hungary	KT591541			Soop et al. (2016)
<i>Hebeloma salicicola</i>	VANF1079-H1	Türkiye	OR122311			Acar et al. (2024)
<i>Hebeloma sinapizans</i>	JV95-515	Denmark	JQ751194			Eberhardt et al. (2013)
<i>Hebeloma sinapizans</i>	VANF476T2	Türkiye	OK356903			Kalmer et al. (2022)
<i>Hebeloma sordescens</i>	C:JV84-1371	Denmark	KX765787			Beker et al. (2016)
<i>Hebeloma subtortum</i>	ML17/9.12.12	Cyprus	OQ100307			Eberhardt et al. (2023)
<i>Hebeloma syrjense</i>	H:H4004	Finland	KX765795			Beker et al. (2016)
<i>Hebeloma theobrominum</i>	ROHB:925 LQ	Italy	JX275966			Eberhardt et al. (2013)
<i>Hebeloma uliferum</i>	HJB12867	Macedonia	KT218416			Grilli et al. (2016)
<i>Hebeloma velutipes</i>	HJB9377	United Kingdom	JQ751204			Eberhardt et al. (2013)
<i>Hebeloma vesterholtii</i>	HJB11869	Italy	FJ943240			Eberhardt & Beker (2010)
<i>Kabatina thujae</i>	CBS 238.66, T	Germany	NG_064053 NR_156189			Vu et al. (2019)
<i>Lepiota alba</i>	PAM95082604	France	KT315649			Vidal et al. (2015)
<i>Lepiota alba</i>	KUN-HKAS 90371	China	MN810115			Hou & Ge (2020)
<i>Lepiota attenuata</i>	MFLU090199	Thailand	MN240412			P. Sysouphanthong, unpubl.
<i>Lepiota attenuata</i>	HKAS50110	China	EU681776			Liang et al. (2011)

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<i>Lepiota aurantiopileae</i>	LAH37661	Pakistan	OQ282887			Asif et al. (2024)
<i>Lepiota brunneogranulosa</i>	LAH:36803	Pakistan	NR_184481			Asif et al. (2022)
<i>Lepiota</i> cf. <i>erminea</i>	HMAS61597	China	MK651624			F.Yu, J.F. Liang, J. Song, B. Chen & X.Y. Pan, unpubl.
<i>Lepiota</i> cf. <i>erminea</i>	HKAS52674	China	MK651626			F.Yu, J.F. Liang, J. Song, B. Chen & X.Y. Pan, unpubl.
<i>Lepiota</i> cf. <i>erminea</i>	12-VI-1972, N. S. Weber 2947 (MICH)	USA	AY176357			Vellinga (2004)
<i>Lepiota</i> cf. <i>erminea</i>	AG2042	USA	MT908259			S.L. Miller & A. Gongloff, unpubl.
<i>Lepiota</i> cf. <i>erminea</i>	MO502871	USA	OR336138			T.A. Clements, unpubl.
<i>Lepiota clypeolaria</i>	Taxon 334	USA	MW899495			S.P. Brown., M. Shahrtash, A.E. Tucker, J. Knoepp, C.E. Stokes & R. Baird, unpubl.
<i>Lepiota clypeolaria</i>	Taxon 331	USA	MW899494			S.P. Brown., M. Shahrtash, A.E. Tucker, J. Knoepp, C.E. Stokes & R. Baird, unpubl.
<i>Lepiota clypeolaria</i>	TRTC156939	Canada	JN021057			Dentinger et al. (2011)
<i>Lepiota clypeolaria</i>	M.M. Rogers, 4-XI-2000	USA	AF390999			Vellinga (2001)
<i>Lepiota clypeolaria</i>	17-IX-1990, E.C. Vellinga 1683 (L)	Germany	AY176361			Vellinga (2004)
<i>Lepiota clypeolaria</i>	MHHNU32567	China	ON248481			z.J. Jiang, unpubl.
<i>Lepiota clypeolaria</i>	2018-69(HGASMF01-13555)	China	MZ128816			M. Wang, unpubl.
<i>Lepiota clypeolarioides</i>	MCVE:16904	USA	FJ998407			M. Garbelotto, L. Baker, E. Crocker, K. Haden, M. Kozanitis, R. Linzer, S. Mascheretti, L. Mizzan, T. Osmundson, K. Peay, G. Robich & D. Schmidt, unpubl.
<i>Lepiota cortinarius</i>	HKAS 46095	China	EU416306			Liang et al. (2010)
<i>Lepiota cortinarius</i>	MCVE:16811	USA	FJ998404			M. Garbelotto, L. Baker, E. Crocker, K. Haden, M. Kozanitis, R. Linzer, S. Mascheretti, L. Mizzan, T. Osmundson, K. Peay, G. Robich & D. Schmidt, unpubl.
<i>Lepiota cortinarius</i>	25-IX-1999, R.E. Tulloss (UCB)	USA	AY176468			E.C. Vellinga, unpubl.
<i>Lepiota elseae</i>	AH40487	Spain	KP640556			Caballero et al. (2015)
<i>Lepiota elseae</i>	AC1456	Spain	KP640557			Caballero et al. (2015)
<i>Lepiota erminea</i>	S38	Germany	OL527680			Sarawi et al. (2022)
<i>Lepiota erminea</i>	6-XI-1998 E.C. Vellinga 2290 (L)	The Netherlands	AY176470			E.C. Vellinga, unpubl.

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<i>Lepiota geocarpa</i>	UTC247364	USA	HQ020412			Kropp et al. (2012)
<i>Lepiota geophana</i>	UTC253060	USA	HQ020411			Kropp et al. (2012)
<i>Lepiota geophana</i>	Trappe 17584	USA	HQ020410			Kropp et al. (2012)
<i>Lepiota kuehneriana</i>	HKAS45881	China	MK651627			F.Yu, J.F. Liang, J. Song, B. Chen & X.Y. Pan, unpubl.
<i>Lepiota kuehneriana</i>	HKAS46027	China	MK651628			F.Yu, J.F. Liang, J. Song, B. Chen & X.Y. Pan, unpubl.
<i>Lepiota laevigata</i>	PAM14110916	France	KT315652			Vidal et al. (2015)
<i>Lepiota lilacea</i>	SJ109_Lepiota	Pakistan	MT974254			Naseer et al. (2022)
<i>Lepiota magnispora</i>	HAY-F-005480	USA	PP578065			G. D'Elia, H. Singer, N. Thysell, C. Schwarz, M. Quark, B.A. Perry, K. Buegeleisen, W. Cardimona, D. Tighe, D. Lyons, S. Pickell, M. Hackney, S. Hickey, R. Diaz, A. Tupac, T. Bright, G. Stark, B. Vardeh, J. Hockert, M. Torres-Grant, A. Rockefeller, S. Jakob, S. Ostuni, S. Squazzo, I. Bednash, V. Warhol, J. Paulin, W. Hut-ton, W. Ho, L. Morgan, J. Quintero, G. Mueller, R. Stevenson, L. Hart, P.O. Kaishian, A. DeMartino, J. Williams & M. Williamson, unpubl.
<i>Lepiota magnispora</i>	NAMPA1805-22	USA	OP225556			A. Anglin, H. Young, D. Reeck, J. Dodge, S. Jakob, H. Johnson, H. Singer, & M. Kuzmina, unpubl.
<i>Lepiota magnispora</i>	UBC F-24565	Canada	MF955053			M. Berbee, A. Bazzicalupo, C. Schwartz, B. van der Meer & P. Kroeger, unpubl.
<i>Lepiota magnispora</i>	Z.L. Yang 2521, 16-IX-1998, China, Yunnan Prov., Yiliang Co., Muga Township, Sanjiangkon Nature Reserve (HKAS)	USA	AF391006			Vellinga (2001)
<i>Lepiota magnispora</i>	personal:Koukichi Maruyama:FY161021-7	Japan	LC549681			K. Maruyama & N. Murakami, unpubl.
<i>Lepiota magnispora</i>	Mushroom Observer 390697	USA	MT075537			T.A. Clements, unpubl.
<i>Lepiota magnispora</i>	MAK:UTK27	Pakistan	OR632354			M. Azeem & I. Ahmad, unpubl.
<i>Lepiota magnispora</i>	MFLU090124	Thailand	MN240411			P. Sysouphanthong, unpubl.

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<i>Lepiota magnispora</i>	E.C. Vellinga 1412, 25-IX-1988, Lxembourg, Marienthal (L)	USA	AF391020			Vellinga (2001)
<i>Lepiota magnispora</i>	S21	Germany	OL527676			Sarawi et al. (2022)
<i>Lepiota mengei</i>	UTC00253524	USA	MN810131			Hou & Ge (2020)
<i>Lepiota metulispora</i>	HMAS61859	China	EU681778			Liang et al. (2011)
<i>Lepiota ochraceodisca</i>	PAM02111802	France	KT315648			Vidal et al. (2015)
<i>Lepiota oreadiformis</i>	110117MFBPL0136	China	MW554391			H. Zhou, unpubl.
<i>Lepiota pakistanensis</i>	OQ954776	Pakistan	LAH37846			Rehman et al. (2024)
<i>Lepiota pakistanensis</i>	OQ954777	Pakistan	LAH37847			Rehman et al. (2024)
<i>Lepiota pallidiochracea</i>	HKAS:45579	China	NR_158462			Liang & Yang (2011)
<i>Lepiota penguiniiformis</i>	UEH-F0033	Pakistan	PQ456114			This study
<i>Lepiota spheniscispora</i>	UC<USA-CA>:1860005	USA	NR_119448			Vellinga (2001)
<i>Lepiota squamulodiffracta</i>	CA21	Dominican Republic	KR022006			Justo et al. (2015)
<i>Lepiota sublaevigata</i>	PAM02081205	France	KT315650			Vidal et al. (2015)
<i>Lepiota thrombophora</i>	HKAS48451	China	EU681779			Liang et al. (2011)
<i>Lepiota thrombophora</i>	HKAS41003	China	EU681780			Liang et al. (2011)
<i>Lepiota</i> sp.	personal:Koukichi Maruyama:FY160906-5	Japan	LC549683			K. Maruyama & N. Murakami, unpubl.
<i>Lepiota</i> sp.	personal:Koukichi Maruyama:FY191001-96	Japan	LC549686			K. Maruyama & N. Murakami, unpubl.
<i>Lepiota</i> sp.	personal:Koukichi Maruyama:FY180903-23	Japan	LC549684			K. Maruyama & N. Murakami, unpubl.
<i>Lepiota</i> sp.	personal:Koukichi Maruyama:FY180919-62	Japan	LC549685			K. Maruyama & N. Murakami, unpubl.
<i>Lepiota</i> sp.	iNaturalist # 98675764	USA	OP455771			S.D. Russell, unpubl.
<i>Lepiota</i> sp.	PUL:00036506	USA	OM522724			S.D. Russell, unpubl.
<i>Lepiota</i> sp.	iNaturalist # 98318627	USA	OP455718			S.D. Russell, unpubl.
<i>Leucoincocybe auricoma</i>	HKAS41510	China	DQ490647			Matheny et al. (2006)
<i>Leucoincocybe auricoma</i>	HKAS126433	China	OQ025169			J.W. Liu, unpubl.
<i>Leucoincocybe lenta</i>	OKA-TR-M498	Türkiye	MN701624			O. Kaygusuz, H. Sevcikova, E. Battistin & I. Turkecul, unpubl.
<i>Leucoincocybe lenta</i>	OKA-TR-M500	Türkiye	MN701625			O. Kaygusuz, H. Sevcikova, E. Battistin & I. Turkecul, unpubl.
<i>Leucoincocybe lenta</i>	OKA-TR-M427	Türkiye	MN701623			O. Kaygusuz, H. Sevcikova, E. Battistin & I. Turkecul, unpubl.
<i>Leucoincocybe lishuiensis</i>	FFAAS0113	China	MW424490			Na et al. (2021)
<i>Leucoincocybe lishuiensis</i>	FFAAS0111	China	MW424488			Na et al. (2021)

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<i>Leucoinocybe papillatus</i>	TRTC176854	Pakistan	OP497984			This study
<i>Leucoinocybe papillatus</i>	TRTC176855	Pakistan	OP497986			This study
<i>Leucoinocybe</i> sp.	GDGM80114	China	MZ667477			X. Chen, unpubl.
<i>Leucoinocybe</i> sp.	GDGM79543	China	MZ667475			X. Chen, unpubl.
<i>Leucoinocybe</i> sp.	GDGM80184	China	MZ667478			X. Chen, unpubl.
<i>Leucoinocybe</i> sp.	GDGM80113	China	MZ667476			X. Chen, unpubl.
<i>Leucoinocybe</i> sp.	LAH37831	Pakistan	OQ998346			M. Usman & A.N. Khalid, unpubl.
<i>Leucoinocybe subglobispora</i>	FFAAS1035	China	OR238887			Na et al. (2024)
<i>Leucoinocybe subglobispora</i>	FFAAS1034	China	OR238886			Na et al. (2024)
<i>Leucoinocybe sulcata</i>	CAL 1246	India	KR029720			Latha et al (2015)
<i>Leucoinocybe taniae</i>	D	Italy	HM191743			Malysheva & Morozova (2011)
<i>Leucoinocybe taniae</i>	LE262757	Russia	HM191745			Malysheva & Morozova (2011)
<i>Leucoinocybe taniae</i>	IB	Italy	LT854058			Antonin et al. (2019)
<i>Leucoinocybe taniae</i>	GDOR	Italy	HM191744			Malysheva & Morozova (2011)
<i>Leucoinocybe taniae</i>	B-4064	Italy	LT854057			Antonin et al. (2019)
<i>Mycena</i> sp.	Ghobad-Nejhad 134	Iran	MT535730			M. Ghobad-Nejhad, E. Langer, & J. Hellmann-Clausen, unpubl.
<i>Mycena</i> sp.	PK2021-5-10	Unknown	OK643829			j.Z. Qiu, unpubl.
<i>Neocy lindroseptoria pistaciae</i>	CBS:471.69, T	Spain, Pistacia lentiscus	MH871115	KF251152	KF252161	Quaedvlieg et al. (2013), Vu et al. (2019)
<i>Neophaeocryptopus cyrtisi</i>	MFLUCC 14-0970, T	Italy, Cytisus scoparius	NG_059643	NR_148094		Li et al. (2016)
<i>Neophaeocryptopus spartii</i>	MFLU 15-3470, T	Italy, Spartium junceum	NG_064456	NR_157480		Hyde et al. (2017)
<i>Oligoporus rennyi</i>	KEW 57	Unknown	AY218416			Wang et al. (2004)
<i>Paramycocentrospora acericola</i>	IRAN 4551C, T	Iran, on seedlings of Acer velutinum	ON212673	NR_187001		Bakhshi & Braun (2022)
<i>Parillus adelphus</i>	TL:127-0003	France	NR158830			Jargeat et al. (2016)
<i>Parillus adelphus</i>	/	France	KU163510			Jargeat et al. (2016)
<i>Paxillus ammoniavirescens</i>	UEH-F40047	Pakistan	PP758271			This study
<i>Paxillus ammoniavirescens</i>	UEH-F40048	Pakistan	PQ461142			This study
<i>Parillus ammoniavirescens</i>	IB1997_0980, T	Italy	JN661718			E.C. Vellinga, unpubl.
<i>Parillus ammoniavirescens</i>	AB 18-11-128	France	ON322967			Mycoseq, unpubl.
<i>Parillus ammoniavirescens</i>	iNaturalist.org/254230753	United kingdom	PQ810796			F. Verenciano Benito, unpubl.
<i>Parillus ammoniavirescens</i>	Ik-00188	Poland	KX610698			Kalucka et al. (2016)
<i>Parillus ammoniavirescens</i>	Ik-00554	Poland	KX610700			Kalucka et al. (2016)
<i>Parillus ammoniavirescens</i>	M56	Hungary	MW354998			M. Csizmar, P. Cseh, B. Dima & Z. Bratek, unpubl.

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<i>Parillus ammoniavirescens</i>	Patricia Jargeat: UPS12.1	France	KF261420			Jargeat et al. (2014)
<i>Parillus cuprinus</i>	Cas10.3	France	KF261379			Jargeat et al. (2014)
<i>Parillus cuprinus</i>	Car10.1	France	KF261371			Jargeat et al. (2014)
<i>Parillus involutus</i>	Jean-Paul Chaumeton:B121140.1	France	KF261368			Jargeat et al. (2014)
<i>Parillus involutus</i>	Herve Gryta: CA10.B2	France	KF261393			Jargeat et al. (2014)
<i>Parillus obscurosporus</i>	Jean-Paul Chaumeton:B121029	France	KF261367			Jargeat et al. (2014)
<i>Parillus obscurosporus</i>	Jean-Paul Chaumeton:B121012	France	KF261386			Jargeat et al. (2014)
<i>Parillus olivellus</i>	TL:127-0004	France	NR158829			Jargeat et al. (2016)
<i>Parillus olivellus</i>	PAM07103001	France	KU163489			Jargeat et al. (2016)
<i>Parillus orientalis</i>	HKAS63615	China	KF372876			Gelardi et al. (2014)
<i>Parillus orientalis</i>	ZT13437	China	KF372877			Gelardi et al. (2014)
<i>Parillus rubicundulus</i>	Orton_2905	UK	KU163502			Jargeat et al. (2016)
<i>Parillus rubicundulus</i>	/	France	JQ890294			Roy et al. (2013)
<i>Penicillium chrysogenum</i>	CBS 306.48	USA	NR 077145			Thom (1910)
<i>Phaeocryptopus nudus</i>	CBS 268.37, T	Canada, <i>Abies balsamea</i>	EF114701	EU700371	GU357745	Schoch et al. (2009), Winton et al. (2007)
<i>Phloeomana speirea</i>	PRM:860810	Czech Republic	LT671446			Holec & Kolarik (2017)
<i>Plectosphaerella alismatis</i>	CBS 113362, T	The Netherlands, <i>Alisma plantago-aquatica</i>	LR026794			Giraldo & Crous (2019)
<i>Plectosphaerella citrulli</i>	CBS 131741, T	Italy, root of <i>Citrullus lanatus</i>	LR026796			Giraldo & Crous (2019)
<i>Plectosphaerella citrulli</i>	CBS 131740	Italy, root of <i>Cucumis melo</i>	LR026795			Giraldo & Crous (2019)
<i>Plectosphaerella cucumerina</i>	CBS 131739, T	Italy, collar of <i>Cucumis melo</i>	HQ238980			Carlucci et al. (2012)
<i>Plectosphaerella delsorboi</i>	CBS 116708, T	Italy, <i>Curcuma alismatifolia</i>	LR026810			Giraldo & Crous (2019)
<i>Plectosphaerella endophytica</i>	YMF 1.04701, T	China, <i>Hydrilla verticillata</i>	MW024054			Yang et al. (2021)
<i>Plectosphaerella guizhouensis</i>	CGMCC 3.19658, T	China, soil	MK880441			Zhang et al. (2019)
<i>Plectosphaerella hanneae</i>	CBS 144925, T	The Netherlands, garden soil	LR590201			Giraldo et al. (2019)
<i>Plectosphaerella humicola</i>	CBS 423.66, T	Zaire, soil	LR026811			Giraldo & Crous (2019)
<i>Plectosphaerella melonis</i>	CBS 489 96, T	Japan, root of <i>Cucurbita melo</i>	LR026812			Giraldo & Crous (2019)
<i>Plectosphaerella nauculaspora</i>	CGMCC 3.19656, T	China, soil	MK880439			Zhang et al. (2019)
<i>Plectosphaerella niemeijerum</i>	CBS 143233, T	The Netherlands, soil	PV391292			Crous et al. (2017b)
<i>Plectosphaerella oligotrophica</i>	CBS 440.90	Brazil, soil	LR026814			Giraldo & Crous (2019)
<i>Plectosphaerella oratosquillae</i>	NJM0662, T	Japan, <i>Oratosquilla oratoria</i>	AB425974			Duc et al. (2009)
<i>Plectosphaerella pauciseptata</i>	CBS 131744, T	Italy, collar of <i>Cucumis melo</i>	LR026815			Giraldo & Crous (2019)

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<i>Plectosphaerella pauciseptata</i>	CBS 131745	Italy, root of <i>Solanum esculentum</i>	LR026816			Giraldo & Crous (2019)
<i>Plectosphaerella plurivora</i>	CBS 131742, T	Italy, Apex turion of <i>Asparagus officinalis</i>	LR026829			Giraldo & Crous (2019)
<i>Plectosphaerella plurivora</i>	HM 230	Chile, decaying plant material	PV535341			This study
<i>Plectosphaerella populi</i>	CBS 139623, T	Germany, <i>Populus nigra</i>	KR476750			Crous et al. (2015)
<i>Plectosphaerella ramiseptata</i>	CBS 131861, T	Italy, root of <i>Solanum esculentum</i>	LR026832			Giraldo & Crous (2019)
<i>Plectosphaerella ramiseptata</i>	CBS 131743	Italy, collar of <i>Citrullus lanatus</i>	LR026831			Giraldo & Crous (2019)
<i>Plectosphaerella sichuanensis</i>	YMF 1.05081, T	China, <i>Stuckenia pectinata</i>	MW027539			Yang et al. (2021)
<i>Plectosphaerella sinensis</i>	ACC39145, T	China, stem of <i>Cucumis melo</i>	KX527888			Su et al. (2017)
<i>Plectosphaerella slobbergiarum</i>	CBS 147227, T	The Netherlands, soil	MW883443			Crous et al. (2021)
<i>Plectosphaerella tabeijun-koae</i>	BRIP 74929a, T	Australia, soil	OR122287			Tan & Shivas (2023)
<i>Plectosphaerella verschoorii</i>	CBS 144924, T	Netherlands, garden soil	LR590240			Giraldo et al. (2019)
<i>Plectosphaerella vigrensis</i>	CBS 150722, T	Poland, leaf spots on <i>Impatiens noli-tangere</i>	OR539695			Crous et al. (2023)
<i>Rhizosphaera kalkhoffii</i>	CBS 280.38	USA, <i>Picea pungens</i>	EF114706	EU700375		Winton et al. (2007)
<i>Rhizosphaera kobayashii</i>	ATCC 46389	Japan, <i>Pinus pumila</i>	AF462432			Thambugala et al. (2014)
<i>Rhizosphaera macrospora</i>	CBS 208.79, T	France, <i>Abies alba</i>	NG_064115	NR_166003		Vu et al. (2019)
<i>Rhizosphaera merioides</i>	JE334-1	Canada	MH873614	ON784014		Vu et al. (2019)
<i>Rhizosphaera minteri</i>	RFSS_2-4_M	United Kingdom, <i>Picea sitchensis</i>		ON784042		Taylor & Koukol (2023)
<i>Rhizosphaera oudemansii</i>	CBS 226.83, T	Canada, <i>Pseudotsuga menziesii</i>	EF114707	EU700366		Winton et al. (2007)
<i>Rhizosphaera pini</i>	DAOMC:251499	Canada, house dust	KY654326	KY659500		Humphries et al. (2017)
<i>Rhizosphaera pinicola</i>	CAA 1007, T	Spain, <i>Pinus nigra</i>		MW732245		Monteiro et al. (2022)
<i>Rhizosphaera pseudotsugae</i>	CBS 101222, T	Germany, fading needles of <i>Pseudotsuga menziesii</i>		EU700369		Taylor & Koukol (2023)
<i>Scleroconidioma sphagnicola</i>	UAMH 9731, T	Canada, <i>Sphagnum fuscum</i>		NR_121294		Schoch et al. (2014)
<i>Sparassis brevipes</i>	MBUH-ILKKA96-1044/ss24	Germany	AY218441			Wang et al. (2004)
<i>Sparassis crispa</i>	MBUH-PIRJO&ILKKA94-1587/ss5	France	AY218427			Wang et al. (2004)
<i>Sparassis crispa</i>	MBUH-DORISLABER/ss25	Germany	AY218442			Wang et al. (2004)
<i>Sparassis cystidiosa</i>	Desjardin 7410	Thailand	AY256891			Desjardin et al. (2004)
<i>Sparassis cystidiosa</i> f. <i>flabelliformis</i>	HKAS59857	China, Yunnan, Tengchong	JQ743080			Zhao et al. (2013)
<i>Sparassis cystidiosa</i> f. <i>flabelliformis</i>	HKAS59855	China, Yunnan, Tengchong	JQ743078			Zhao et al. (2013)

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<i>Sparassis cyrtidiosa</i> f. <i>flabelliformis</i>	HKAS59856	China, Yunnan, Tengchong	JQ743079			Zhao et al. (2013)
<i>Sparassis latifolia</i>	LAH28820	Pakistan	OM417067			This study
<i>Sparassis latifolia</i>	LAH26721	Pakistan	OM417066			This study
<i>Sparassis latifolia</i>	HKAS59356	China	JN387102			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS59357	China	JN387103			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS59355	China	JN387101			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS55938	China	JN387098			Zhao et al. (2013)
<i>Sparassis latifolia</i>	DAI10269	China	JQ743077			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS55937	China	JN387097			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HMJAU5301	China	JQ743074			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HMJAU2955	Russia	JQ743073			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS59358	China	JN387100			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HKAS59854	Japan	JQ743071			Zhao et al. (2013)
<i>Sparassis latifolia</i>	HMJAU2007	China	JQ743072			Zhao et al. (2013)
<i>Sparassis latifolia</i>	DAI12549	China	JQ743076			Zhao et al. (2013)
<i>Sparassis radicata</i>	TENN50232/ss32	USA, Tennessee	AY218449			Wang et al. (2004)
<i>Sparassis radicata</i>	UBC-F12464/ss26	Canada	AY218443			Wang et al. (2004)
<i>Sparassis spathulata</i>	zw-clarku002/ss8	USA, New Hampshire	AY218429			Wang et al. (2004)
<i>Sparassis spathulata</i>	zw-clarku004/ss11	USA, Massachusetts	AY218432			Wang et al. (2004)
<i>Sparassis spathulata</i>	zw-clarku001/ss7	USA, Massachusetts	AY218428			Wang et al. (2004)
<i>Sparassis subalpina</i>	HKAS55269	China	JN387096			Zhao et al. (2013)
<i>Sparassis subalpina</i>	HKAS57488	China	JN387093			Zhao et al. (2013)
<i>Sparassis subalpina</i>	HKAS57511	China	JN387094			Zhao et al. (2013)
<i>Sparassis subalpina</i>	HKAS55936	China	JN387095			Zhao et al. (2013)
<i>Stylodothis puccinioides</i>	HMAS 285382	China, dead wood	OQ170850	OQ534230		G.C Ren, in press; L. Yao, unpubl.
<i>Talaromyces aurantiacus</i>	CBS 314.59	USA, soil	NR103681			Samson et al. (2011)
<i>Talaromyces calidicanius</i>	CBS 112002	Taiwan, soil	NR103665			Samson et al. (2011)
<i>Talaromyces duclauxii</i>	CBS 322.48	France, canvas	NR121526			Samson et al. (2011)
<i>Talaromyces duclauxii</i>	MRn6	Egypt, water	PP029083			Yilmaz et al. (2014)
<i>Talaromyces fusiformis</i>	CBS 140637	China, air	NR169911			Chen et al. (2016)
<i>Talaromyces fusiformis</i>	MCC10205 (ELS-F4)	India, endophyte	PP345605			This study
<i>Talaromyces fusiformis</i>	TBS21201	China, stool	MK805488			Xu et al. (2021)
<i>Talaromyces fusiformis</i>	XG-337	China, endophyte	PQ721761			Li et al. (2025)
<i>Talaromyces haitouensis</i>	CGMCC-3.16101	China	NR177564			Han et al. (2021)
<i>Talaromyces haitouensis</i>	HR 1-7	China	MZ045695			Ren et al. (2024)

Species name	ID (status, strain, isolate, voucher)	Country, isolation source	ITS	LSU	TEFI	Reference(s)
<i>Talaromyces piceae</i>	CBS:361.48	The Netherlands	MH856392			Vu et al. (2019)
<i>Talaromyces piceae</i>	NRRL 1051	USA	KF196893			Peterson & Jurjevic (2013)
<i>Talaromyces primulinus</i>	CBS 321.48	USA	NR145151			Samson et al. (2011)
<i>Talaromyces primulinus</i>	H21	USA	OQ438031			Samson et al. (2011)
<i>Talaromyces viridulus</i>	CBS 252.87	Australia, soil	NR103663			Samson et al. (2011)
<i>Trichaleurina javanica</i>	MRN1	Nepal	PV807968			This study
<i>Trichaleurina javanica</i>	TNM F8917	Taiwan	KF418251			Carbone et al. (2013b)
<i>Trichaleurina javanica</i>	TNM F11338	Taiwan	KF418253			Carbone et al. (2013b)
<i>Trichaleurina javanica</i>	TUR-A 198586	Seychelles	KF418257			Carbone et al. (2013b)
<i>Trichaleurina javanica</i>	MRNo502	Thailand	LC176769			J. Sittthipol, T. Malimas, N. Chaiyawan, L. Chatanon, K. Niwasabutra, P. Taweet-eptaikul, Y. Insumran, W. Klinhom, B. Wannissorn, B. Fungsin & C. Poonsiri, unpubl.
<i>Trichaleurina javanica</i>	KSRF-0019	India	MF476196			Patel et al. (2019)
<i>Trichaleurina javanica</i>	FIPIA-DEP57	Indonesia	PP728051			I.P. Putra, O.D. Nurhayat & M.T. Sibero, unpubl.
<i>Trichaleurina tenuispora</i>	TNM F4705	Taiwan	KF418243			Carbone et al. (2013b)
<i>Trichaleurina tenuispora</i>	TNM F20790	Taiwan	KF418248			Carbone et al. (2013b)
<i>Trichaleurina tenuispora</i>	TNS-F-31213	Japan	KF418250			Carbone et al. (2013b)
<i>Trichaleurina tenuispora</i>	JBRI-M23-004	South Korea	OR852464			S.H. Lee, unpubl.
<i>Trichaleurina tenuispora</i>	JBRI-M23-114	South Korea	OR852522			S.H. Lee, unpubl.
<i>Trichaleurina tenuispora</i>	Dai 27294	China	PV191116			K.-Y. Luo & Y.-C. Dai, unpubl.

¹ Herbarium abbreviations follow Index Herbariorum (Thiers continuously updated)² T: type

Scientific, USA). The isolated genomic DNA was stored in a deep freezer (-20°C) before PCR amplification. Amplification of ITS rDNA selected as the target region was performed in 25 μl reaction mixture containing: 10 μM concentration of each primer (ITS 1 and ITS 4), 5 U/ μl Taq DNA polymerase (FIREPol[®], Solis Biodyne, Estonia), sterile water, 10 ng/ μl of genomic DNA, 10x PCR buffer, 25 mM MgCl_2 , and 10 mM dNTP (White et al. 1990; Akata et al. 2024). The primer sequences were ITS1: 5'-TC-CGTAGGTGAACCTGCGG-3' and ITS4: 5'-TC-CTCCGCTTTATTGATATATGC-3'. Amplification products (amplicons) were confirmed by agarose gel electrophoresis (90 min at 100-volt current). A one-step PCR was performed to amplify a region of approximately 700 base pairs. PCR products were purified using the HighPrep[™] PCR Clean-up System (AC-60005) purification kit for single-banded samples, following the manufacturer's instructions. Bidirectional Sanger sequencing was performed by Macrogen (Netherlands) using an ABI 3730XL Sanger sequencer and BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA) (Chen et al. 2014). The two newly generated ITS rDNA sequences from the Turkish collections of *H. lindae* were deposited in GenBank with accession numbers PQ891843 and PV150655 (Tab. 1).

Gills of collected specimens of *Paxillus* were crushed in 3 ml CTAB buffer, following the method of Doyle & Dickson (1987) with some modifications. The complete internal transcribed spacer (ITS) region of the nuclear ribosomal DNA—comprising ITS1, 5.8S, and ITS2—was amplified through an optimized polymerase chain reaction (PCR) (Gardes & Bruns 1993) using the fungal-specific primer pair ITS1F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'), along with Taq polymerase (White et al. 1990). A reaction mixture of 25 μL was prepared according to Gardes & Bruns (1993). The PCR product was sent to Beijing Tsingke Biotech (China) for sequencing. ITS sequences have been deposited in GenBank (Tab. 1).

Genomic DNA of *Plectopshaerella* was extracted from a fungal colony of isolate HM 230 grown on MEA for 1 week at 25°C , using the Fast DNA Kit (Bio 101, Vista, CA) following the manufacturer's instructions. The internal transcribed spacer (ITS) region was amplified and sequenced with the primer pair ITS5/ITS4 (White et al. 1990). The amplification was carried out following the illustra PuReTaq Ready-To-Go PCR beads protocol (Amersham, Buckinghamshire, UK), with 0.5 μM of both primers, 1 μl of diluted template DNA and water to ob-

tain a final reaction volume of 25 μl . The amplification program included an initial denaturation at 94°C for 5 min, followed by 35 cycles of denaturation at 95°C for 30 s, annealing for 1 min at 50°C , and extension for 1 min at 72°C , with final extension at 72°C for 7 min. PCR amplification success was checked on 2 % agarose gels with GelRed fluorescent nucleotide stain (Merck Millipore, Burlington, MA). Purification of PCR products and Sanger sequencing were outsourced to Macrogen (Seoul, South Korea). Amplicons were bidirectionally sequenced and consensus sequences were obtained from forward and reverse reads using the SeqTrace software (Stucky 2012). The ITS sequence was deposited in GenBank (Tab. 1).

Genomic DNA was extracted directly from the clean part of each specimen of *Sparassis* using a modified 2 % CTAB method (Gardes & Bruns 1993). The ITS-nrDNA region (Internal Transcribed Spacer of the nrDNA) was amplified using the primer pair ITS1F (forward primer) (Gardes & Bruns 1993) and ITS4 (reverse primer) (White et al. 1990). The PCR amplification was carried out as follows: initial denaturation (94°C for 1 min), 35 cycles (94°C for 1 min; 53°C for 1 min; 72°C for 1 min), and a final extension (72°C for 8 min). PCR products were visualized on 1 % agarose gel with ethidium bromide through Gel documentation system (Sambrook & Russel 2001). PCR products were sent for sequencing to Tsingke, China. ITS sequences were submitted to GenBank (Tab. 1).

Genomic DNA of *Talaromyces* was extracted using the standard chloroform-phenol extraction method described by Sambrook et al (1989). The ITS region was amplified using the universal primers ITS1 (5'-TCC GTA GGT GAA CCT GCG G-3') and ITS4 (5'-TCC TCC GCT TAT TGA TAT GC-3') (White et al. 1990). PCR amplification was performed using a thermal cycler with an initial denaturation at 95°C for 4 min, followed by 35 cycles of denaturation at 95°C for 1 min, annealing at 50°C for 15 s, and extension at 72°C for up to 1 min. Each cycle also included an additional extension step at 72°C for 30 s. A final extension was performed at 72°C for 6 min. The amplified PCR products were purified by PEG-NaCl precipitation and sequenced bidirectionally (from both ends to ensure reading each position twice) on an ABI[®] 3730XL robotic DNA sequencer (Applied Biosystems, Inc., USA) following the manufacturer's instructions. Sequences were assembled using the Lasergene package v18.0.3 (<https://www.dnastar.com/workflows/genomics/>) and subjected to BLAST analysis using the NCBI database. The consensus ITS sequence

was deposited in GenBank under the accession number PP345605 (Tab. 1).

Genomic DNA was extracted from an air-dried specimen of *Trichaleurina* (different from KATH166569) using the NucleoSpin® Soil DNA Extraction Kit (Macherey-Nagel GmbH & Co.), following the manufacturer's instructions. Concentration and purity of the extracted DNA were assessed using a µDrop Plate on a Multiskan™ Sky Microplate Spectrophotometer (Thermo Fisher Scientific Inc., USA). Extracted DNA was stored at -20 °C. PCR amplification of the Internal Transcribed Spacer (ITS) region was performed using the primer pairs ITS-1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS-4 (5'-TCCTCCGCTTATTGATATGC-3') (Nilsson et al. 2015; White et al. 1990). PCR reactions were carried out in an ABI Veriti 96-well thermal cycler (Applied Biosystems™, USA) with the following conditions: initial denaturation at 94 °C for 4 min; 35 cycles of denaturation at 94 °C for 40 s, annealing at 56 °C for 60 s, and extension at 72 °C for 70 s; followed by a final extension at 72 °C for 7 min. PCR products were resolved on a 1.5 % (w/v) agarose gel via electrophoresis at 70 V for 60 min and visualized under ultraviolet (UV) illumination. PCR products were initially purified using the SAP-Exo Kit (Jena Biosciences, Germany) to remove excess primers and unincorporated nucleotides. Sanger sequencing was performed using the Big-Dye™ Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems™, USA), following the dideoxy chain termination method (Sanger et al. 1977). After an additional purification step with 3M sodium acetate (NaOAc), single-stranded DNA samples were loaded into an Applied Biosystems™ 3500xL Genetic Analyzer for sequencing. The ITS sequence was deposited in GenBank (Tab. 1).

Phylogenetic analyses

For the *Dothidea* study, sequences were trimmed, edited and assembled in BioEdit version 7.1.9. The resulting sequences were submitted to the NCBI GenBank and compared with existing sequences using BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). For phylogenetic analyses, *Phaeocryptopus nudus* (Peck) Petr. (CBS 268.37) was chosen as the outgroup. LSU (578 sites/274 variable), ITS (428 sites/234 variable) and *RPB2* (951 sites/714 variable) sequences were combined, resulting in a final dataset with 1957 aligned positions. The concatenated LSU+ITS+*RPB2* data matrix contained 38 isolates representing 33 species within *Dothideaceae* and *Dothioraceae*. Ex-type or holotype-derived

reference sequences from previous studies deposited at NCBI were included whenever available (Tab. 1). Multiple sequence alignment was performed with ClustalW (Larkin et al. 2007), including sequences from other *Dothideaceae* species. Phylogenetic reconstruction was carried out using the Maximum Likelihood (ML) based on the Tamura-Nei model (Tamura & Nei 1993) in MEGA XI (Kumar et al. 2018). Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining (NJ) and BIONJ algorithms to a matrix of pairwise distances estimated using the Tamura-Nei model (Gascuel 1997). The tree topology with the highest log-likelihood value was selected. Confidence levels in nodes were determined using 1000 bootstrap replicates.

For the *Ganoderma* study, generated ITS sequences were first subjected to BLAST searches in NCBI GenBank, resulting in a final ITS database comprising 31 sequences of 15 closely related *Ganoderma* species. The sequence of *Amauroderma rude* (KF372587) was selected as the outgroup taxon (Li et al. 2015). Consensus sequences were generated from ITS1 and ITS4 reads using BioEdit v.7.2.5 (Hall 1999) and aligned (678 positions in length) using ClustalX v.2.1 (Larkin et al. 2007) and MAFFT v.10 (Katoh & Standley 2013). Phylogenetic analyses were performed using MEGA v. 10 and the CIPRES Science Gateway web server (Miller et al. 2010), employing RAXML-HP2 on XSEDE v.8.2.10 (Stamatakis 2014) under the GTRCAT substitution model. All positions containing gaps are treated as missing data. Node support was assessed through ML bootstrapping with 1,000 replicates. The resulting phylogenetic tree was visualized in FigTree v.1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>) and modified in Inkscape v.0.91 (Free Software Foundation, Boston, MA) for final presentation.

For the *Lepiota* study, sequences were assembled in BioEdit version 7.2.5 (Hall 1999). Closely related sequences were retrieved from GenBank for phylogenetic analysis, excluding those with insufficient query coverage in the BLAST results. The phylogenetic tree included published sequences of species' closest relatives with corresponding GenBank accessions. The final aligned dataset contained a total of 63 ITS sequences, including three sequences from *L. sect. Lilacea*, i.e., *L. lilacea* Bres. (MT974254), *L. brunneogranulosa* Asif, Izhar, Haqnawaz, Niazi & Khalid (NR_184481) and *L. aurantiopileae* Asif, Izhar, Haqnawaz, Niazi & Khalid (OQ282887) as outgroup taxa (Justo et al. 2015). Multiple sequence alignment was performed with the online MUSCLE tool at EMBL-EBI (<https://www.ebi.ac.uk/jdispat>

cher/msa/muscle). The best-fit nucleotide substitution model was selected prior to phylogenetic reconstruction. The evolutionary history was inferred by using ML based on the Tamura 3-parameter model (Tamura 1992). A discrete Gamma distribution was used to model evolutionary rate differences among sites, with 1000 bootstrap replicates, in MEGA version 11 software (Tamura et al. 2021). Bayesian inference was conducted using BEAST v. 1.8.2 (Drummond et al. 2012). The XML input file was generated using BEAUti v1.8.2 (Drummond et al. 2012), and log files were examined in Tracer v1.6 (Rambaut et al. 2014) to ensure that effective sample size (ESS) values exceeded 200 for all parameters. The monitored parameters included posterior, likelihood, prior, tree length, and substitution model components such as base frequencies and gamma shape, as well as clock rate parameters e.g., strict or relaxed clock mean rate. These results confirmed adequate sampling and reliable parameter estimation. Log files were combined using LogCombiner 1.8.2 (Drummond et al. 2012). An ultrametric maximum-clade-credibility (MCC) tree was summarized using TreeAnnotator v. 1.8.2 (Drummond et al. 2012). FigTree v. 1.4.2 (Rambaut 2012) was used for phylogenetic tree visualization.

For the *Leucoinocybe* study, the resulting ITS sequences were used as queries in BLAST searches against the NCBI database. Hits with a percent identity above 85 % and an E-value of zero were selected and downloaded. Sequence alignment was conducted in MUSCLE v3.6 (Edgar 2004) via the EMBL-EBI web server (<https://www.ebi.ac.uk/Tools/msa/muscle/>), then visualized and manually adjusted in AliView (Larsson 2014). The best-fit ML model, TPM2+F+G4, was selected according to the Bayesian Information Criterion (BIC) using ModelFinder (Kalyaanamoorthy et al. 2017) via the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) (Nguyen et al. 2015). Statistical support for branches was calculated from 1,000 bootstrap replicates. The resulting phylogenetic tree was visualized in FigTree v1.4.0 (Rambaut 2012) and edited for presentation in Adobe Illustrator CS5 and Adobe Photoshop 7.0.

Based on the BLASTn results in NCBI (<https://www.ncbi.nlm.nih.gov/genbank/>) and the UNITE (Abarenkov et al. 2010) database, and according to the outcomes of recent phylogenetic studies on *Entoloma* subg. *Entoloma*, forty-one sequences were selected for the dataset used (see Tab. 1). *Entoloma festivum* (GenBank: MZ869009) was used as an outgroup. Sequences were aligned using MAFFT version 7.450 (Katoh & Standley 2013) with default

parameters in Geneious version 11.1.5. ML was inferred with IQ-TREE ver. 1.6.12 (Nguyen et al. 2015) under IQ-TREE web server (Trifinopoulos et al. 2016). The TPM2+F+G4 models were selected for our alignment using ModelFinder (Kalyaanamoorthy et al. 2017). Clade support for the ML analyses was assessed using an SH-aLRT test with 1000 replicates and 100 replicates of the standard bootstrap (BS).

For the *Hebeloma* study, sanger sequencing data obtained using the ITS1/ITS4 primer pair were assembled with DNAMAN version 10 (Lynnon Biosoft Corporation, Québec, Canada). Consensus sequences were subsequently subjected to BLASTn searches to assess sequence similarity and preliminary species identification (Altschul et al. 1990). Based on BLASTn results, an additional 53 ITS sequences were retrieved from GenBank, resulting in a dataset of 55 sequences representing 36 *Hebeloma* species and one outgroup taxon, *Galerina paludosa* (Tab. 1). Multiple sequence alignment was performed using the Markov Chain Monte Carlo (MCMC) algorithm implemented in MrBayes v3.2.7a software (Ronquist et al. 2012). The probability distribution of phylogenetic trees was sampled using the MCMC + MC³ algorithm. Within phylogenetic analyses, the GTR+I+ Γ model was applied as a nucleotide substitution model with uniform ratios (Höhna et al. 2017; Barba-Montoya et al. 2020). To evaluate node support, a bootstrap analysis with 1,000 replicates was applied as described by Felsenstein (1985).

For the *Paxillus* study, the consensus sequences were constructed from forward and reverse sequences using BioEdit (Hall 1999). These sequences were queried using the Basic Local Alignment Search Tool (BLAST) against the NCBI GenBank database (<http://www.ncbi.nlm.nih.gov/genbank>). Reference sequences of closely related taxa, preferably from published sources, were retrieved from GenBank. The Genus *Auricularia* was selected as an outgroup from previously published literature (Du et al. 2020). Sequences were aligned using ClustalW and manually adjusted in Molecular Evolutionary Genetics Analysis Version 11 (MEGA-11) (Tamura et al. 2021). Phylogenetic reconstruction was carried out using ML under the Kimura 2-parameter model with gamma distribution (K2+G), using 1000 bootstrap replicates. The resulting tree, consisting of 722 aligned nucleotide positions, was visualized in FigTree v1.4.4 and further refined in Adobe Illustrator 88 v1–1.6.

For the *Plectopshaerella* study, the phylogenetic reconstruction was based on an ITS dataset that in-

cluded 27 strains of *Plectosphaerella* spp. and one strain of *Fuscohypha expansa* Giraldo López & Crous (CBS 320.64) as outgroup (Tab. 1). ITS sequences were aligned with the MUSCLE webserver (<http://www.ebi.ac.uk/Tools/msa/muscle/>, Edgar 2004) and then adjusted manually with a text editor. After excluding ambiguous regions, an alignment of 434 bp was obtained. Phylogeny reconstructions were performed with the NJ and ML methods using MEGA XI (Kumar et al. 2018), using the best DNA substitution model chosen by that software (i.e., K2 + G) according to the BIC. The statistical support for the groupings was assessed by bootstrap analysis of 1000 replicates. The ITS sequence alignment generated during this study was deposited in Figshare (<https://doi.org/10.6084/m9.figshare.28821632>). The generated phylogeny was edited with Microsoft PowerPoint.

For the *Sparassis* study, bidirectional sequences of the ITS region were assembled using the BioEdit software (Hall 1999). Highly similar ITS sequences were retrieved using Basic Local Alignment Search Tool (BLAST) analysis from NCBI GenBank. The final dataset consisted of 30 sequences of *Sparassis* spp. and two outgroup taxa, *Grifola frondosa* (AY218415) and *Oligoporus rennyi* (AY218416) (Zhao et al. 2013) (Tab. 1). Maximum percent identity and query coverage of sequences with related taxa were noted. Multiple sequences (including sequences retrieved from GenBank) were aligned using webPRANK multiple alignment software with default parameters (Löytynoja & Goldman 2010). All sequences were trimmed at their ends to nearly equal length using BioEdit. The phylogenetic tree was constructed in MEGA 7.0 (Kumar et al. 2016), using ML based on Kimura 2-parameter, with 1000 rapid bootstrap replicates. The model of evolution was selected by searching for the best DNA model for ML analysis in MEGA 7.0 (Kumar et al. 2016).

For the *Talaromyces* study, the closest hits were retrieved from the GenBank database using BLAST searches (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), resulting in a final dataset comprising 16 nrDNA ITS-5.8S-ITS2 sequences, including that of the studied isolate (Tab. 1). *Penicillium chrysogenum* Thom was used as the outgroup (Fig. 28). Prior to phylogenetic analysis, all sequences were aligned using MAFFT v7 (Katoh et al. 2019; <https://mafft.cbrc.jp/alignment/server/index.html>). The resulting alignment was edited as needed in BioEdit v7.2 (Hall 1999). The phylogenetic tree was constructed using ML under the Tamura–Nei model (Tamura & Nei 1993), as implemented in

MEGA XI, with bootstrap support values based on 1000 replicates. In our phylogenetic analyses, it also formed a well-supported clade with three ITS sequences representing *T. fusiformis* (NR169911, MK805488, PQ721761) with a bootstrap support value of 100 %.

For the *Trichaleurina* study, sequence chromatograms obtained from Sanger sequencing were assembled into a consensus contig using Sequencher® v4.1.4 DNA sequence analysis software (Gene Codes Corporation, Ann Arbor, MI, USA). The assembled sequence was then subjected to a BLAST search against the GenBank database (<https://blast.ncbi.nlm.nih.gov/>) to identify closely related matched species for further phylogenetic analysis. The retrieved sequences, along with the outgroup taxa *Galiella rufa* (OR825613.1), were aligned with MAFFT v7.505 (Katoh & Standley 2013). The best-fit substitution model was determined using ModelFinder v2.2 under the Akaike Information Criterion (AIC) (Kalyaanamoorthy et al. 2017). A ML phylogenetic tree was inferred using IQ-TREE v2.2.0, using the K3P+G4 substitution model with 1000 bootstrap replicates to assess branch support (Nguyen et al. 2015). The tree was visualized and edited using the Interactive Tree of Life (iTOL) web server (Letunic & Bork 2024).

Taxonomy

Ascomycota, Dothideomycetes, Dothideales, Dothideaceae

Dothidea nigricans V. A. Iliushin, I. Y. Kirtsideli & I. G. Pankova, **sp. nov.** – Figs. 1, 2
MycoBank no.: MB 850996

Diagnosis. – Distinguished from all other *Dothidea* species by its ellipsoid or almost spherical, even lemon-shaped conidia, the absence of conidiomata, and the gradual blackening of colonies during cultivation.

Holotypus. – RUSSIA. Franz Josef Land, Hayes Island, 80°34'N, 57°41'E, from timber of abandoned polar station buildings, 1 August 2021. isol. I.G. Pankova. 2022, (LE F-350178; holotype, dried culture; ex-type culture VKM F-5012). Sequences ex-type culture: OP961959 (ITS), OR801565 (LSU), OR810751 (*RPB2*).

Description. – Hyphae towards colony center melanized, dark brown, smooth to lightly roughened, rapidly developing into chlamydospores. – Chlamydospores brown, lightly rough-walled, globose to subglobose, septate to aseptate, 7.0–13.5 µm in diam. – Conidiogenous cells undifferentiated, hyaline, smooth-walled, 4.0–7.0 × 2.0–4.0 µm, producing conidia percurrently from short lateral denticles not exceeding

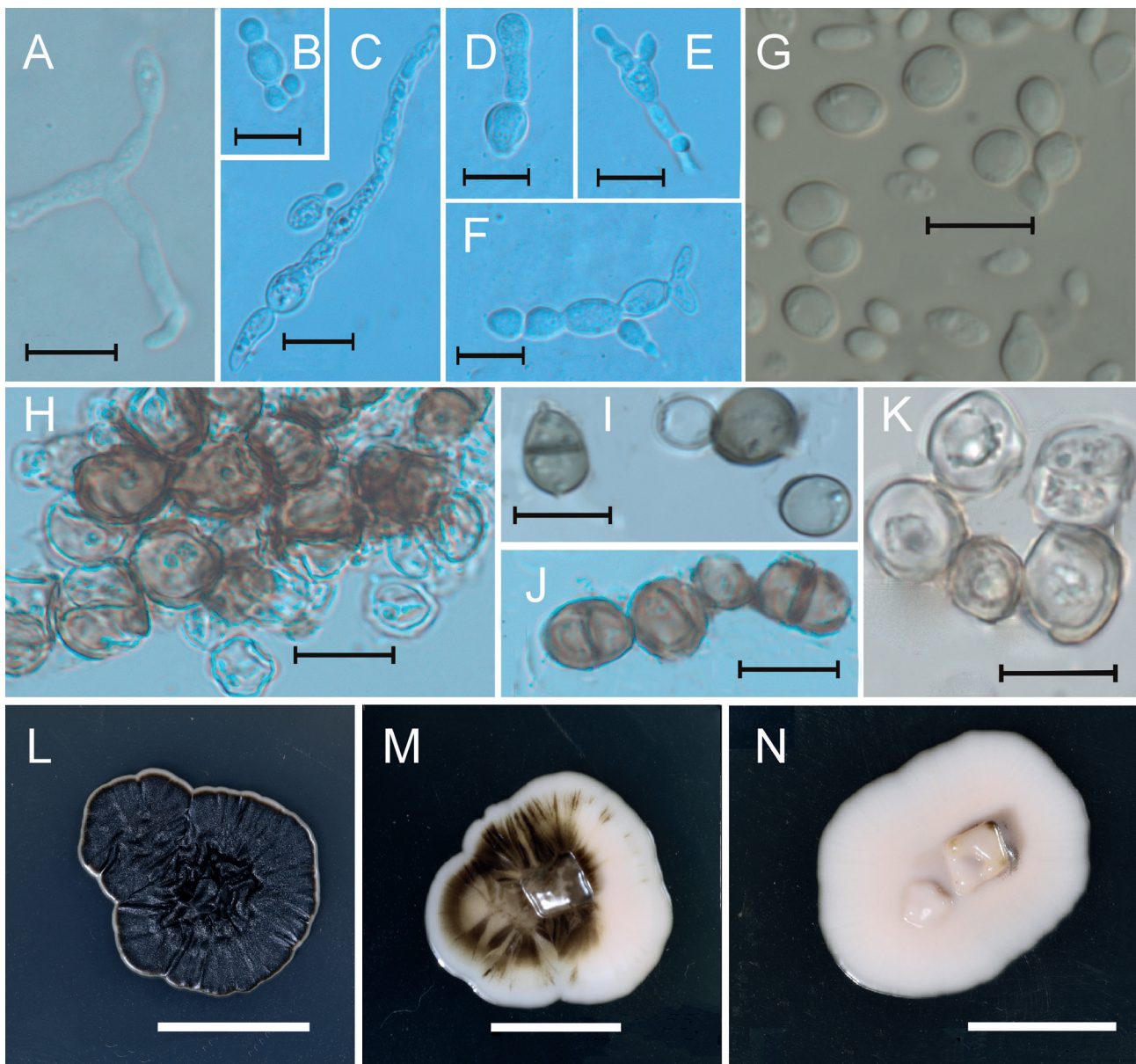


Fig. 1. *Dothidea nigricans* (VKM F-5012, ex-type culture). **A, C.** Hyphae. **B, D, E, F.** Conidia and conidiogenic cells with some yeast-like budding occurring. **G.** Conidia. **H, I, J, K.** Chlamydospores. Colony of *D. nigricans* on MEA (**L**), SDA (**M**) and CZ (**N**) after 3 weeks at 21 °C. Bars **A-K** 10 μ m, **L-N** 10 mm.

1 μ m long. – Conidia often yeast-like, hyaline, smooth-walled, aseptate, ellipsoidal or subglobose to lemon-shaped, $3.5\text{--}7.0 \times 1.5\text{--}4.0 \mu\text{m}$, microcyclic conidiation occurring at one or sometimes both ends of conidia.

Culture characteristics (in darkness, 21°C, 21 d). – Colonies on MEA slow growing, 14–18 mm in diam., non-zonate, surface leathery, crusty, wrinkled, lacking aerial mycelium; brownish black (#28201c) to olive black (#25241d); at the be-

ginning of cultivation (the first 3–4 days) light yellow (#f8de7e); exudates absent; reverse light olive gray (#8a8776) to olive gray (#57554c). – Colonies on CZA slow growing, 11–15 mm in diam., yeast-like, non-zonate, smooth and slimy, light yellow (#f8de7e); exudates absent; reverse light yellow (#f8de7e). – Colonies on SDA slow growing, 17–20 mm in diam., yeast-like, non-zonate, smooth and slimy, light yellow (#f8de7e), gradually darkening to dark olive brown (#3b3121); exudates absent;

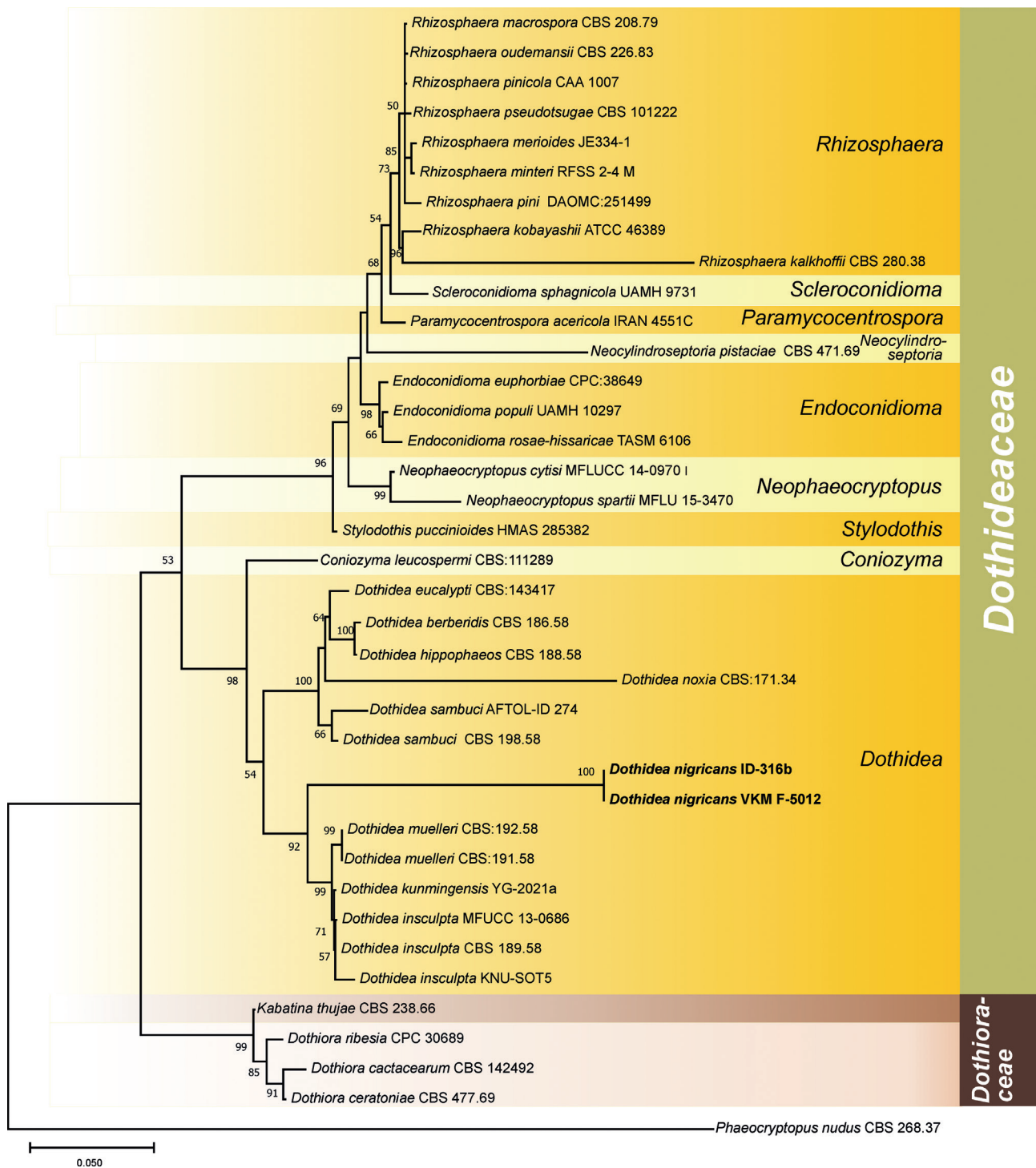


Fig. 2. Phylogenetic tree based on maximum likelihood (ML) analysis of concatenated LSU+ITS+RPB2 sequences showing relationships of *D. nigricans* to other *Dothideaceae* species. Tree root *Phaeocryptopus nudus* (CBS 268.37). Bootstrap percentages >50 % given at the nodes. Scale bar indicating number of substitutions per site. The new species *D. nigricans* (VKM F-5012 and ID-316b) in bold.

reverse gradually darkening to dark olive brown (#3b3121). The lower the cultivation temperature,

the later the colonies begin to darken. Growth temperature range: 6–27 °C. Optimum: 21–23 °C.

Etymology. – The Latin epithet “nigricans” refers to the blackening of colonies after several days of cultivation.

Habitat and distribution. – Known only from timber of abandoned polar station buildings on Hayes Island, Franz Josef Land, Russia.

Notes. – BLAST analysis reveals that the LSU sequences of both strains of *D. nigricans* share 91 % similarity with a LSU sequence of *D. insculpta* Wallr. (DQ247802), as well as similar levels of homology with other species of the Dothideaceae, including *Neocylindroseptoria pistaciae* (Quaedvlieg, Verkley & Crous) K. M. Thambugala & K. D. Hyde (NG_057996; 93 % similarity) and *Neophaeocryptopus cytisi* Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde (KU248849; 93 % similarity). Based on a BLAST analysis of the ITS region of strains DI-209 and ID-316b, *D. nigricans* is most closely related to *Endoconidioma euphorbiae* Crous (MW175351) and *Coniozyma leucospermi* (Crous & Denman) Crous (MT816430), with 85 % similarity to both sequences. Partial *RPB2* sequences of both *D. nigricans* strains also share 85 % similarity with that of *D. insculpta* (AF107800). The concatenated ML phylogenetic tree based on LSU, ITS, and *RPB2* shows that *D. nigricans* clustered adjacent to a clade containing *D. insculpta* (KNU-SOT5, MFUCC 13-0686, CBS 189.58), *D. kunmingensis* Ying Gao, Gentekaki & Monkai (YG-2021a) and *D. muelleri* Loeffler (CBS:192.58, CBS:191.58) (Fig. 2). Interestingly, the ITS sequences of both *D. nigricans* strains show 99.8 % similarity (100 % coverage) with two sequences from uncultured strains of unidentified Ascomycetes isolated from house dust in Finland (FR682365 and AM901815). This suggests that our novel species has likely been previously detected in environmental samples, but has not been described or named until the present study. These results also underscore the considerable yet undescribed diversity within the Dothideaceae that remains to be formally described through integrative taxonomic efforts.

Although species of the genus *Dothidea* are morphologically diverse (Thambugala et al. 2014), most of the described diversity corresponds to teleomorphs. In contrast, *D. nigricans* is an anamorphic species. Morphologically, *D. nigricans* is relatively similar in some features to the recently described anamorphic species *D. kunmingensis* from southwest China (Gao et al. 2021). Both species have similar conidiogenous cells. However, the two species differ in the shape of their conidia. *D. nigricans* produces ellipsoid or nearly spherical, even lemon-shaped, conidia, while *D. kunmingensis* has nearly

spherical to ovoid conidia. Moreover, *D. nigricans* does not produce conidiomata, while *D. kunmingensis* is a coelomycete. The gradual blackening of colonies during cultivation is a characteristic not present in other members of the *Dothidea*.

Species of the genus *Dothidea* are known to play important roles as wood decomposers and plant pathogens (Crous et al. 2017b; Gao et al. 2021). They have been reported from a variety of substrates (e.g., leaves, dead wood, stems, fresh water) and across a wide range of geographical regions (Shoemaker et al. 2003, Thambugala et al. 2014). In the Arctic, wood is often of anthropogenic origin. Thus, abandoned wooden buildings—no longer in use for several decades—represent introduced substrates that are frequently colonized by fungi (Kirtsideli 2020). Fungi isolated from such woody substrates are typically adapted to cold environments, as long-term exposure to low temperatures selects for microfungi capable of decomposing wood under extreme conditions at high latitudes (Pankova et al. 2023). Growth tests confirmed that *D. nigricans* is capable of growth at 6 °C, therefore supporting its classification as a psychrotolerant (psychrotrophic) species (Hassan et al. 2016). This study demonstrates that human-introduced wood in cold climatic zones may contain previously unidentified diversity of microfungi. These undescribed taxa or strains represent promising avenues for studying adaptive strategies of microfungi in low-temperature conditions. In particular, they can serve as model organisms for investigating the molecular mechanisms of cold resistance and the evolutionary processes shaping fungal diversity in extreme environmental conditions.

Authors: V.A. Iliushin, I.Y. Kirtsideli & I.G. Pankova

Basidiomycota, Agaricomycetes, Polyporales, Polyporaceae

Ganoderma punjabicum A. Umar, **sp. nov.** – Figs. 3, 4
Mycobank no.: MB 859780

Holotypus. – PAKISTAN. Punjab Province, District Lahore, 31.5497° N, 74.3436° E, 210 m a.s.l., on exposed surface roots of *Polyalthia longifolia* (Sonn.) Thwaites, 12 July 2018, *leg.* A. Umar, 3BDIII (LAH036551; holotype). GenBank Sequence: PV821352 (ITS).

Description. – Basidiomata sessile to substipitate, solitary, verrucose, spirally curled. – *Pileus* 22–23 × 17–20 cm, laccate to non-laccate, dimidiate to flabelliform, unevenly thick and wrinkled margins, maroon-brown zones (2.5YR 3/6) showing streaks, creamy yellowish margins (10YR 8/6). – *Stipe* absent or stout, forming a hard crust.

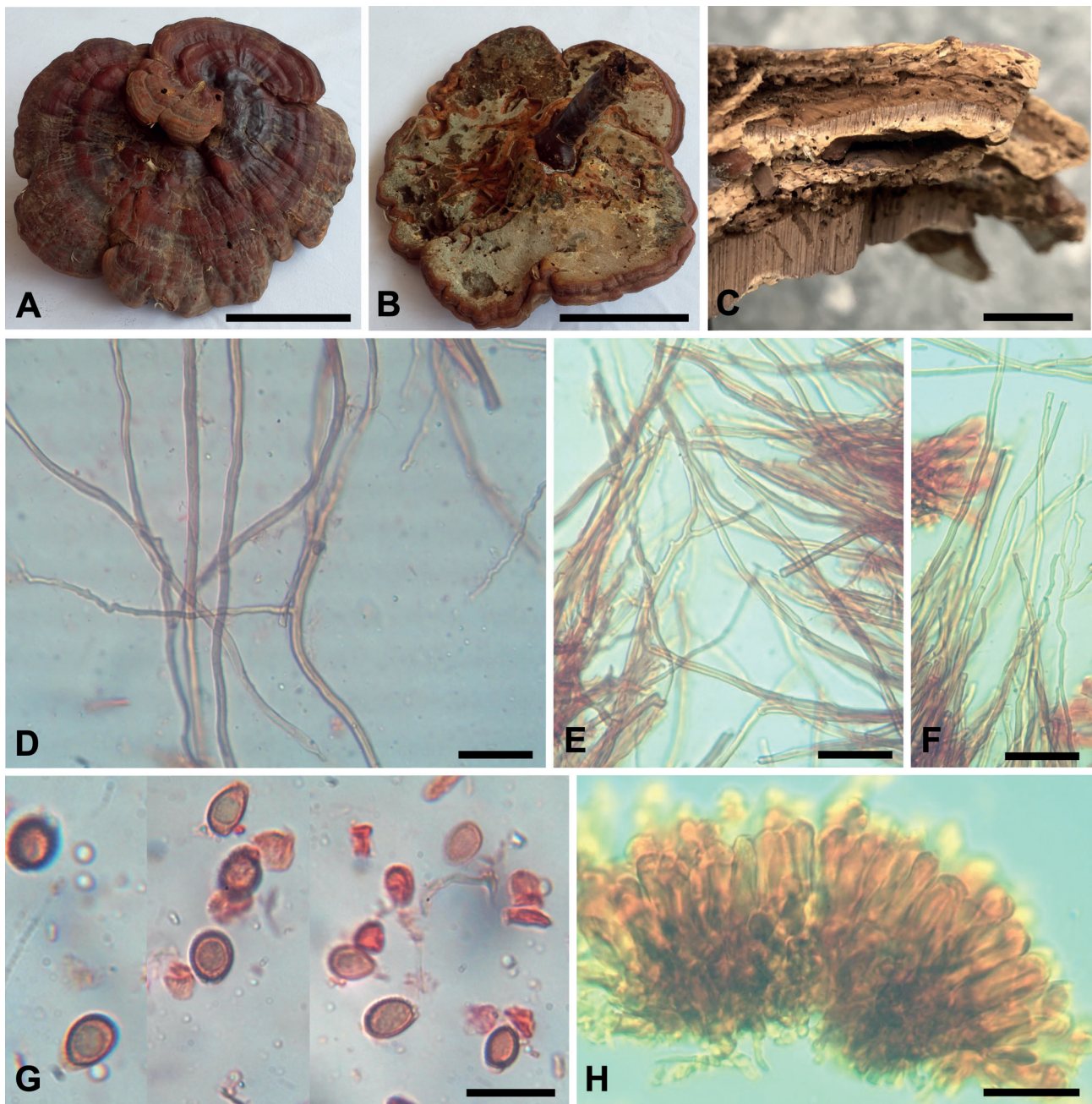


Fig. 3. *Ganoderma punjabicum* (3BDIII, holotype). **A.** Basidiomata, top view; **B.** Basidiomata, lower view, with stipe and pore surface; **C.** Section showing context (color and tubes); **D.** Generative hyphae; **E.** Binding hyphae; **F.** Skeletal hyphae; **G.** Basidiospores; **H.** Cutis section showing cylindrical crustohymeniderm cells. Bars **A–B** 2 cm, **C** 0.5 mm, **D–F** 5 µm, **G–H** 10 µm.

– Pores greyish white (7.5GY 7/2). – Tubes 0.9–1 mm long, stratified, slightly woody, light brown (5YR5/8) to dark chocolate brown (7.5YR 4/6). – Context 0.7 mm thick, non-homogenous, stratified, dry, fibrous to corky, yellowish brown (2.5Y 8/8). – Trimitic hyphal system 1) generative hyphae (clamped, septate, branched, thin-

walled); 2) skeletal (simple, thick-walled); 3) binding hyphae (thin, hyaline). – Basidiospores (8.0–)9.24–8.88 × 5.76–5.23 µm ($\bar{L}$ = 8.55, $\bar{W}$ = 5.44, Q = 1.57, n = 35), ellipsoid, rough in appearance, bitunicate, echinulate; exosporium yellowish brown (2.5Y 8/6), endosporium greenish (5Y 6/6), with thick echinulae and highly thickened inter-wall pil-

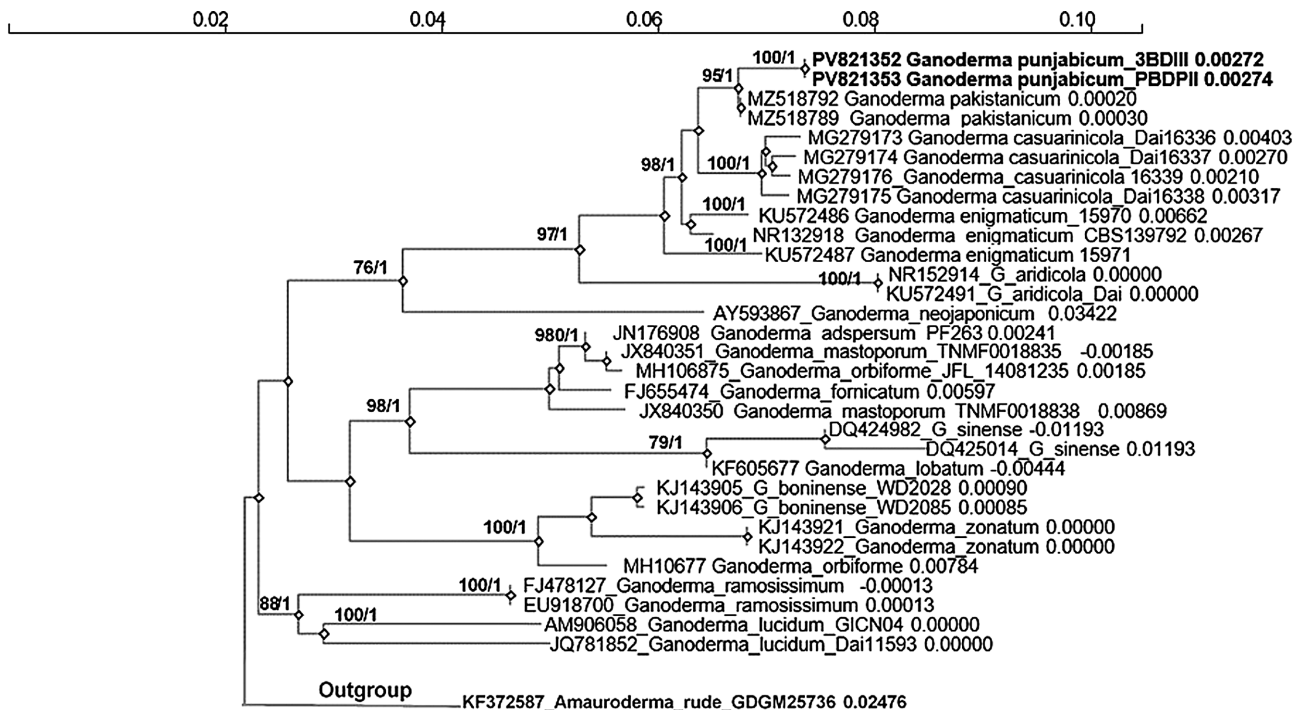


Fig. 4. Maximum likelihood (ML) phylogenetic tree of *Ganoderma punjabicum* sp. nov. and related species based on an ITS dataset of 32 sequences. Analysis performed using RAxML. Tree root *Amauroderma rude*. For each node, bootstrap support values from ML analysis (MLBS ≥ 70) and Bayesian posterior probabilities (BIPP ≥ 0.7) indicated above the branches. Sequences of *G. punjabicum* generated during this study in bold.

lars. – Basidia 16–27 $\times$ 9–10 μ m, smooth, ellipsoid, tapered base, four sterigmata. – Crustohymeniderm cells 67.35–45.10 $\times$ 8.91–6.07 μ m, with broader semicircular apices. – Pileipellis a cutis; amyloid reactions absent.

Etymology. – Epithet refers to the location where the holotype was collected (Punjab Province, Pakistan).

Habitat and distribution. – On exposed old roots of *Polyalthia longifolia* (Sonn.) Thwaites. Thus far reported only from Pakistan (Punjab, Lahore).

Additional material examined. – PAKISTAN. Punjab Province, District Lahore, PCSIR (Pakistan Council of Scientific and Industrial Research), 31.5204° N, 74.3587° E, 217 m a.s.l., scattered in organic soil, 25 July 2019, leg. A. Umar, PBDPII (LAH036552; paratype). GenBank: PV821353 (ITS)

Notes. – Based on our phylogenetic analyses, the ITS sequences from the two Pakistani specimens formed a well-supported (100 %) and distinct clade that is closed to *Ganoderma pakistanicum* (MZ518792, MZ518789), *Ganoderma casuarinicola* (MG279173, MG279174, MG279176, MG279175), *G. enigmaticum* (KU572486, NR132918, KU572487) and *G. aridicola* (NR152914, KU572491) (Fig. 4).

The neighboring species within this clade hence signified that *G. punjabicum* is a distinct species based on both morphological differences and distinct geographic origin; e.g., *G. casuarinicola*, *G. enigmaticum* (Xing et al. 2018), and *G. aridicola* have been described from South Africa (Xing et al. 2016), while *G. pakistanicum* (Umar et al. 2021) and *G. punjabicum* were collected from Punjab, Pakistan.

Ganoderma punjabicum, *G. pakistanicum*, *G. casuarinicola*, *G. aridicola*, and *G. enigmaticum* share some morphological characteristics, including a laccate to strongly laccate upper pileus surface. However, *G. punjabicum* can be easily distinguished from *G. pakistanicum* by its spirally curled, homogeneously maroon-brown basidiomata with distinct growth streaks, while *G. pakistanicum* has uneven, horny, lobate, and irregularly shaped basidiomata with maroon to yellowish, unequally thickened margins. *Ganoderma casuarinicola* produces brownish-red to yellowish-brown basidiomata with a yellowish, shiny crust marked by growth zones (Zhou et al. 2015), which further helped to separate it from *G. punjabicum*. Similarly, *G. enigmaticum* shows a golden-yellow pileus lacking furrows (Coetzee et al. 2015), while *G. aridicola* is

characterized by a dark brown to black pileus (Xing et al. 2016), both of which contrast with the pileus coloration of *G. punjabicum*. Furthermore, basidiomata are sessile in *G. aridicola*, while being substipitate to stipitate in *G. pakistanicum*, *G. casuarinicola* and *G. punjabicum*. The tubes of *G. pakis-*

tanicum are long (1.0–1.2 cm), unstratified, woody-hard, and greyish brown to dark chocolate brown, whereas in *G. punjabicum*, they are smaller, stratified, slightly woody, and range from light brown to dark chocolate brown. The context in *G. pakistani-*

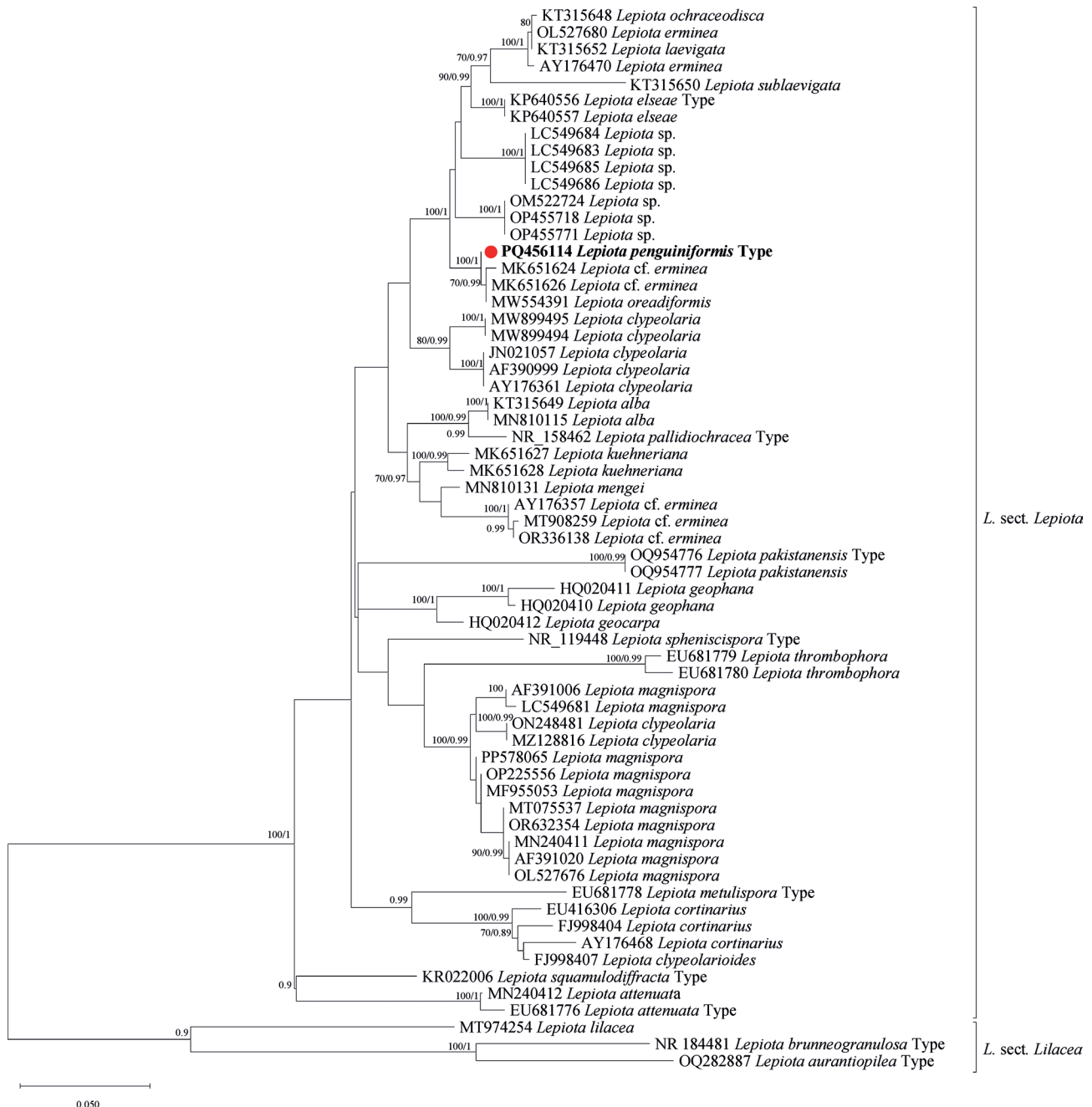


Fig. 5. Phylogeny of selected *Lepiota* species from an ITS dataset with three sequences belonging to *L. sect. Lilacea* as outgroup. Section designations following Justo et al. (2015). Tree with the highest log likelihood (–4359.21) shown, resulting from ML inference performed in MEGA11. Nodes with maximum likelihood values exceeding 70 % and Bayesian inference values surpassing 0.9 considered statistically significant (MLB/BPP = 100/0.99). GenBank accession numbers given for each taxon. Sequence generated from the collected specimen marked in bold with a red bullet.

while in *G. punjabicum* it is non-homogeneous, stratified, and composed of brown, light brown and yellowish-brown layers. Black melanoid bands are absent from the context of both *G. casuarinicola* and *G. punjabicum*.

Anatomically, the binding and skeletal hyphal systems differ markedly between *G. pakistanicum* and other closely related *Ganoderma* species. In *G. pakistanicum*, cuticular cells are clavate to rounded-lobulate, with stout and septate lateral branches, while in *G. punjabicum*, *G. casuarinicola*, *G. enigmaticum*, and *G. aridicola*, they are broader with semicircular ends. The basidiospores of *G. punjabicum* are larger than those of *G. pakistanicum* ($8.2\text{--}8.9 \times 5.0\text{--}5.8 \mu\text{m}$; Umar et al. 2021). In comparison, the broadly ellipsoid basidiospores of *G. casuarinicola* ($8.3\text{--}9 \times 5\text{--}6 \mu\text{m}$; Xing et al. 2018) and the ellipsoid basidiospores of *G. enigmaticum* ($8\text{--}11 \times 3.5\text{--}6 \mu\text{m}$; Coetzee et al. 2015) are smaller than those of *G. punjabicum*. In contrast, the spores of *G. aridicola* ($9\text{--}11.5 \times 5.3\text{--}6.9 \mu\text{m}$; Xing et al. 2016) are slightly larger than those observed in our specimens. Morpho-anatomical and phylogeny inferred from sequences support that the specimens collected from Pakistan represent a new species within the *G. lucidum* complex.

Authors: A. Umar, E. Alhomaidi, M.S. Al Tami & L. Dufosse

Basidiomycota, Agaricomycetes, Agaricales, Agaricaceae

Lepiota penguiniformis Ijaz & Jabeen, **sp. nov.** – Figs. 5–7

Mycobank no.: MB856211

Diagnosis. – Differs from *Lepiota elseae* by its applanate pileus, a fibrillose stipe with minutely pubescent apex and relatively smaller ($8.8\text{--}10.3 \times 3.8\text{--}4.4 \mu\text{m}$) penguin-shaped basidiospores without guttules.

Holotypus. – PAKISTAN. Khyber Pakhtunkhwa, Swat District, Kabal Tehsil, Nimakai, $34^{\circ}54'9''$ N, $72^{\circ}17'36''$ E, 1500–1700 m a.s.l., on loamy soil, under broad leaf vegetation, 30 July 2023, Sadiq Ullah 95, H46 (UEH-F0033; GenBank for ITS: PQ456114).

Description. – **Pileus** 4.5 cm broad, broadly convex to applanate, light brown (2.5Y8/3), brittle; surface dry, rough, scurfy, and scaly, with dense squamules at the center becoming progressively sparse towards the margin; central disc covered with brown (7.5YR4/2) squamules, becoming dull over an off-white (5Y9/2) context; margin irregular, slightly split, light brown (2.5Y8/3). – **Lamellae** free, crowded, margin even, slightly ventricose, off-white (5Y9/2); lamellulae frequently present, variable lengths, concolorous with lamel-



Fig. 6. *Lepiota penguiniformis* (UEH-F0033, holotype). **A, B.** Fresh basidiomata. Bars **A, B** 1 cm.

lae. – **Stipe** 8×0.9 cm, central, becoming narrower (0.6 cm) towards apex; surface fibrillose, minutely pubescent from apex, dry; off-white having yellowish brown (5Y8/4) patches at base. – **Annulus** rudimentary, partial veil remnants present, off-white. – **Context** off-white, no color change when exposed to air. Taste and odor not observed. – **Basidiospores** $[20/1/1]$ $(8.0)8.8\text{--}10.3(10.8) \times (3.4)3.8\text{--}4.4(4.8) \mu\text{m}$, $avl \times avw = 9.5 \times 4.1 \mu\text{m}$, $Q = 2.2\text{--}2.8$, $avQ = 2.5$, elongate to cylindrical or penguin-shaped, with straight abaxial side and a suprahilar depression in side view, distinctly narrowed at the apex, without germ pore, fusiform to sub-cylindrical in frontal view, smooth, slightly thick-walled, non-guttulate, apiculus prominent, hyaline in 5 % KOH, pinkish-red in Congo red. – **Basidia** $(21.6)22.5\text{--}28.7(30.2) \times (7.5)7.7\text{--}8.9(9.2) \mu\text{m}$, $avl \times avw = 25.6 \times 8.3 \mu\text{m}$, clavate, 2–4 sterigmata, smooth, thin-walled. – **Pleurocystidia** absent. – **Cheilocystidia** $(16.8)17.5\text{--}20.4(22) \times (4.7)4.9\text{--}6.4(7.8) \mu\text{m}$, clavate, septa at base, basal cell rarely present, smooth, thin-walled. – **Pileipellis** a trichodermial palisade of elongate, apically attenuate terminal elements, often with some short elements, hyphae $(3)3.3\text{--}5.3(5.6) \mu\text{m}$ wide, pigment parietal and intracellular in upper part, sometimes in basal part of elements, septate, branched, clamp connections rarely present. – **Stipitipellis** trichoderm, hyphae $(2.7)2.9\text{--}4.3(4.8) \mu\text{m}$ wide, septate, branched, clamp connections rarely present. All tissues hyaline in 5 % KOH.

Etymology. – The specific epithet “*penguiniformis*” (Latin) refers to the penguin-shaped basidiospores.

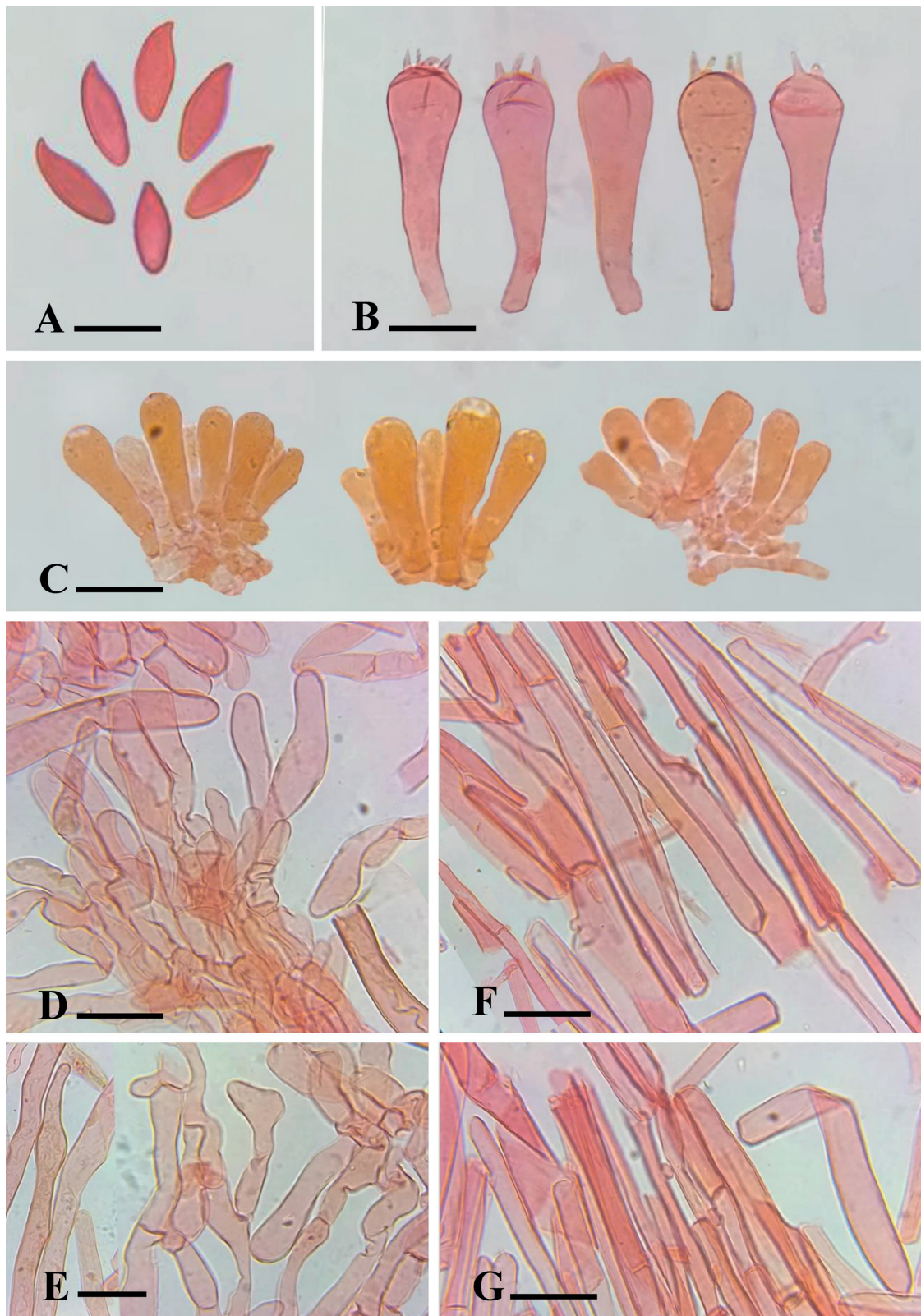


Fig. 7. Microscopic characters of *Lepiota penguiniformis* (UEH-F0033, holotype). **A.** Basidiospores; **B.** Basidia; **C.** Cheilocystidia; **D.** Pileal elements; **E.** Pileipellis hyphae; **F, G.** Stipitipellis hyphae. Bars **A–G** 10 µm.

Habitat and distribution. – Found solitary on a loamy soil in temperate forests under broad leaf vegetation dominated by *Quercus* spp. Thus far only known from Pakistan (this study).

Notes. – *Lepiota* is a widely distributed genus of saprobic fungi with more than 550 species described globally (Singer 1986, Ahmad et al. 1997, Kirk et al. 2008, Liang et al. 2011, Liang & Yang 2011, Razaq et al. 2012, 2013, 2014, Nawaz et al. 2013, Qasim et al. 2015, 2016, Sysouphanthong et al. 2016, Bashir et al. 2020, Niazi et al. 2021, Asif et al. 2022, Haqnawaz et al. 2022, Kaygusuz 2022, Naseer et al. 2022, Razzaq et al. 2022, Azeem et al. 2024, Rehman et al. 2024, Asif et al. 2024, Asif & Saba 2025, Pious & Kumar 2025, Sarawi et al. 2025). In Pakistan, more than 33 species have been reported and only four species belong to *L. sect. Lepiota* (Ahmad et al. 1997, Razaq et al. 2012, 2013, 2014, Nawaz et al. 2013, Qasim et al. 2015, 2016, Bashir et al. 2020, Niazi et al. 2021, Asif et al. 2022, Haqnawaz et al. 2022, Naseer et al. 2022, Razzaq et al. 2022, Azeem et al. 2024, Rehman et al. 2024, Asif et al. 2024, Asif & Saba 2025).

During this study, a new species of *Lepiota*, *L. penguiniformis*, was described from a temperate forest in Pakistan. The ITS sequence of 690 base pairs from our Pakistani collection (UEH-F0033) showed 99.4–99.51 % similarity in BLAST with sequences of *Lepiota oreadiformis* Velen. (MW554391) and *L. cf. erminea* (MK651626) from China. The final alignment consisted of 727 positions, out of which 392 sites were conserved, 296 were variable, 214 were parsimony informative and 77 were singletons. The phylogenetic tree obtained via Bayesian inference displayed a topology consistent with that of the ML analysis across all sequence datasets. Therefore, only the ML tree is shown, with both ML bootstrap values and Bayesian posterior probabilities (BPP) indicated at each node. Nodes with ML support values exceeding 70 % and BPP values surpassing 0.9 were considered statistically significant (Fig. 5). The ITS sequence from our collection formed a distinct lineage within *L. sect. Lepiota*, clustering alongside misidentified sequences of *L. oreadiformis* (MW554391) and *L. cf. erminea* (MK651624, MK651626) with strong statistical support (100 ML/1 BPP), thus confirming its status as a novel taxon.

Morphologically, *L. penguiniformis* is characterized by its applanate, scurfy pileus bearing dense brown squamules at the center, becoming scattered towards the irregular, split margin; a fibrillose stipe with a minutely pubescent apex; distinctive, penguin-shaped basidiospores ($8.8\text{--}10.3 \times 3.8\text{--}4.4 \mu\text{m}$), lacking guttules and a germ pore; and a pileipellis forming a basal subhymeniform layer of trichoderm

with apically attenuate terminal cells, often with some short elements having intracellular pigmentation. *Lepiota elseae* A. Caball., Vizzini, G. Muñoz & Contu, reported from Spain, is a morphologically similar species to *L. penguiniformis* but differs in having a pileus with brown-pinkish tinges, rare claviform elements not forming a subhymeniform layer beneath the long cylindrical pileus covering elements, and relatively larger basidiospores ($12\text{--}16.8 \times 4.6\text{--}6.5 \mu\text{m}$). It is found in small groups, terrestrial, on *Quercus ilex* litter in Mediterranean maquis (Caballero et al. 2015). *Lepiota erminea* (Fr.) P. Kumm., reported from several Asian and European countries, grows in grasslands on calcareous soil, in thermophilous shrublands, and at sunny forest margins (Wasser 1985, Vellinga 2001, Gminder 2003, Legon et al. 2005, Kosakyan et al. 2008). It differs from *L. penguiniformis* by its white, campanulate, glabrous pileus, with a silky margin lacking squamules, and larger fusiform basidiospores ($11\text{--}12 \times 4\text{--}6 \mu\text{m}$) (Massee 1902). *Lepiota oreadiformis* occurs solitary or in small groups in grasslands, at roadsides, rarely in deciduous forests, terrestrial and widespread globally, but rare in Europe (Vellinga 2001, Lange 2012). It is different from *L. penguiniformis* by its pale pileus surface lacking distinct and contrasting squamules, fusiform-amygdaliform basidiospores ($12.8\text{--}15 \times 4.1\text{--}5.5 \mu\text{m}$) with both spore sides convex and larger in profile, and pileipellis composed of non-septate hyphae (Vellinga 2001, Četković et al. 2021). *Lepiota pakistansis* A. Rehman, Afshan, Usman, & Khalid is a recently published taxon from Pakistan found gregariously on sandy soil, rich in leaf litter under *Dalbergia sissoo* Roxb. ex DC. This species is distinguished from *L. penguiniformis* by its ochraceous to light brown cottony squamules forming rings on floccose creamy white pileus with light brown central disk, a squamulose stipe, and relatively larger basidiospores ($10.3\text{--}11.7 \times 4.7\text{--}5.8 \mu\text{m}$) (Rehman et al. 2024). Based on morpho-anatomical differences and molecular phylogenetic analysis of ITS nrDNA sequences, we showed that this species is distinct from already known taxa within the genus *Lepiota*.

Authors: H. Ijaz, S. Ullah, S. Jabeen

Basidiomycota, Agaricomycetes, Agaricales, Marasmiaceae

***Leucoinocybe papillatus* Aman, Khalid & Moncalvo, sp. nov.** – Figs. 8–10

MycoBank no: MB847845

Holotypus. – PAKISTAN. Punjab Province, Pabbi reserve forest, saprobic, on loamy forest soil, 23 August 2020, *leg.*



Fig. 8. *Leucoinocybe papillatus* (TRTC176854, holotype: **A, B**; TRTC176855, paratype: **C, D**). Basidiomata. Bars 1 cm.

N. Aman & M. Usman, TRTC176854 (MU237; holotype). GenBank accession number OP497986 (ITS).

Description. – *Basidioma* inocyboid, small. Pileus 2.6–16.0 mm in diam., campanulate with a distinct papilla, mustard brown (7.5 YR 6/8), turning light brown (10 YR 6/6) towards the margin; surface dry and granular; margin reflexed. Lamellae sinuate, off-white. Stipe 25.4–26.5 × 1.8–1.9 mm, central, cylindrical. Annulus absent. Volva sub-bulbous. Basidiospores 4.8–7.4 µm × 3.9–5.8 µm, Q (mean) = 1.3 ± 0.4 , ellipsoid, smooth, amyloid. Basidia 20–28.3 × 5.1–5.4 µm, 4-spored, clavate. Cheilocystidia 30.8–53.3 × 4.1–8.3 µm, narrowly clavate, scattered, thin-walled. Pleuro-

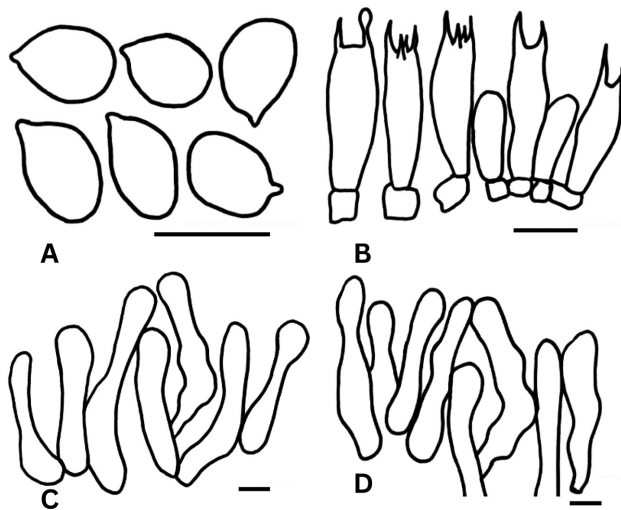


Fig. 9. *Leucoinocybe papillatus* (TRTC176854, holotype) **A.** Basidiospores **B.** Basidia **C.** Caulocystidia **D.** Pileocystidia. Bars 10 µm.

cystidia absent. Pileipellis a cutis, composed of cylindrical, thin-walled hyphae, 4.9–9.1 µm wide, with clamp connections. Pileocystidia 34.6–70.4 × 3.5–10.0 µm, from narrowly cylindrical to narrowly lageniform and flexuous. Stipitipellis a cuticle of cylindrical, parallel, thick-walled, hyphae, 3.1–7.2 µm wide, with clamp connections. Caulocystidia 33.4–66.3 × 4.8–13.9 µm, thick-walled, narrowly cylindrical to narrowly lageniform.

Additional material examined. – PAKISTAN. Punjab Province, Pabbi reserve forest, saprobic, on loamy forest soil, 23 August 2020, leg. N. Aman & M. Usman, TRTC176855 (MU256; paratype). GenBank accession number OP497984 (ITS).

Etymology. – Referring to the presence of a papilla on the pileus.

Habitat and distribution. – Growing solitary on loamy forest soil. Known only from the Punjab Province, Pakistan.

Notes. – The genus *Leucoinocybe* belongs to the hydropoid clade containing eight genera, namely *Clitocybula*, *Megacollybia*, *Leucoinocybe*, *Hydropus*, *Trogia*, *Gerronema*, *Porotheleum* and *Lignomphalia* (Antonin et al. 2019). *Leucoinocybe* was previously considered part of *Clitocybula* due to morphological similarities, including the overall appearance of the basidiomata and microscopic features. However, it was later recognized as a distinct, monophyletic lineage (Antonin et al. 2019). The distinct position of *Leucoinocybe* is also supported by the presence of different types of cystidia, caulocystidia, and pileocystidia compared to other genera of the family *Porothaleaceae* (Kaygusuz et al. 2020). Currently, the genus *Leucoinocybe* comprises six species according to Index Fungorum (www.indexfungorum.org; accessed on 18 July 2025).

The ITS sequence of *Leucoinocybe papillatus* shows only 87 % similarity to *L. lenta* Singer ex Antonín, Borovička, Holec & Kolařík (GenBank acc. no.: MN701623, MN701624, MN701625) in a BLAST search in the NCBI database. *Leucoinocybe papillatus* forms a statistically well-supported (92 % bootstrap support), separate clade in our ITS-based phylogenetic analysis. ITS sequences of *L. papillatus* also grouped with an ITS sequence (GenBank acc. no.: OQ998346) labeled as *Leucoinocybe* sp. that was generated and submitted after the time-frame of the current study. It likely represents the same taxon, but the corresponding specimen was not morphologically described.

Leucoinocybe papillatus also exhibits the distinctive diagnostic characters of the genus *Leucoinocybe*, i.e., smooth and moderately large basidiospores; presence of cheilocystidia and caulocystidia; absence of pleurocystidia (or, if present, they resemble cheilocystidia); and presence or absence of pileipellis. In addition to occupying a different and well-supported position in the ITS phylogenetic tree, *L. lenta* differs morphologically from *L. papillatus* by having a convex pileus with a pinkish centre that fades to white toward the margin (Kaygusuz et al. 2020). In contrast, *L. papillatus* has a campanulate pileus with papilla, mustard brown at the centre and turning light brown towards the margin. *Leucoinocybe lishuiensis* Q. Na, H. Zeng & Y.P. Ge from China also differs from *L. papillatus* by having a pileus that transitions from hemispherical to campanulate during early development, uplifted or recurved pileus margins, adnexed to slightly decurrent lamellae, and a camel to brown pileus

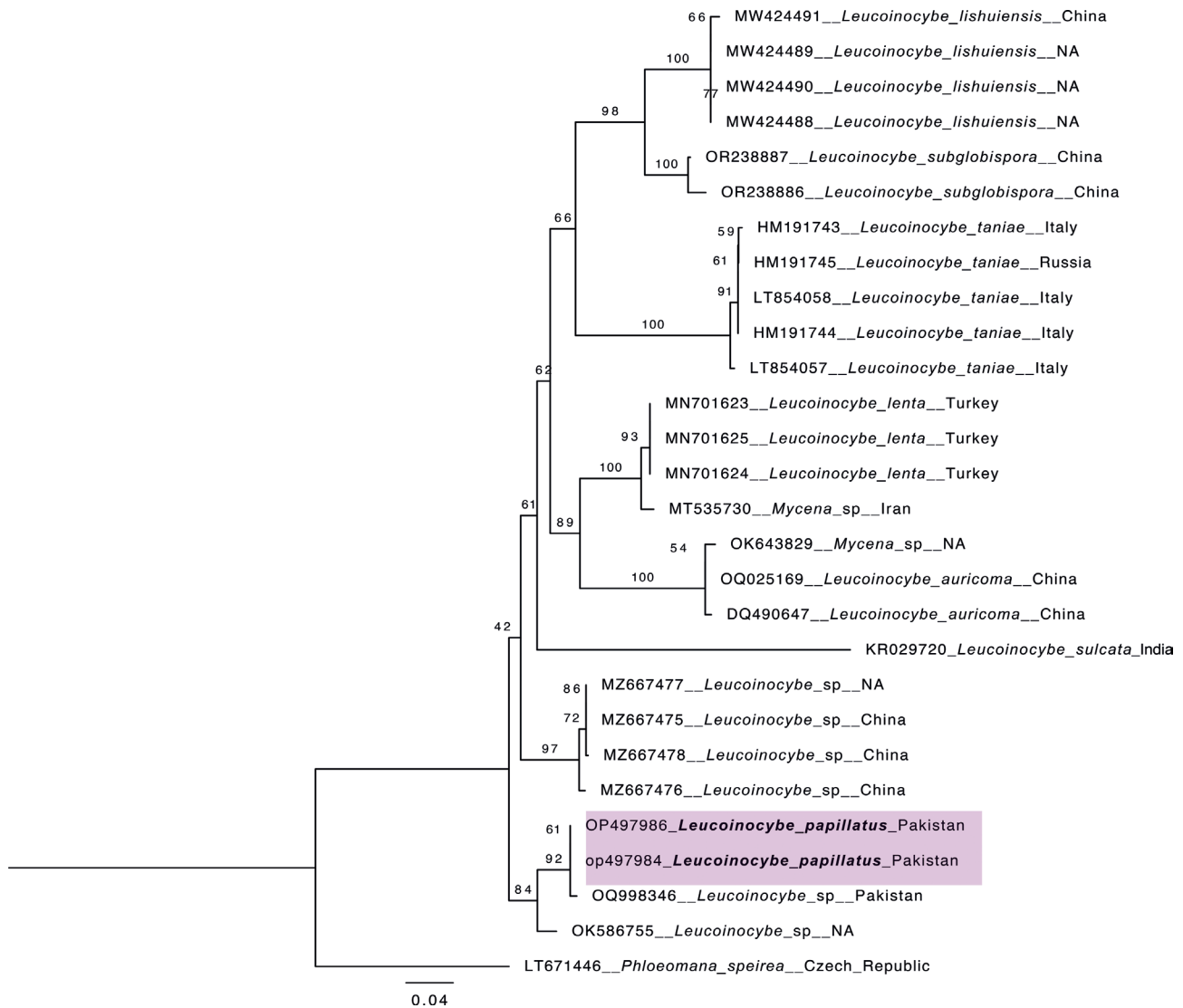


Fig. 10. Maximum likelihood phylogeny of *Leucoinocybe* inferred from ITS sequences using IQ-TREE (Nguyen et al. 2015). Typology resulting from the best-fit model TPM2+F+G4, selected according to the Bayesian Information Criterion. Tree root *Phloeomana speirea* (GenBank LT671446). GenBank numbers mentioned for each taxon. Newly generated sequences in bold. Scale bar representing 0.04 substitutions per site. (Note: GenBank OQ998346 added after the timeframe of this study.)

(Na et al. 2022). *Leucoinocybe sulcata* (K.N.A. Raj & Manim.) Antonin, Borov., Holec & Kolařík is also morphologically different, by having a convex to plano-convex pileus with a slight central depression and brownish-orange lamellae (Latha et al. 2015). *Leucoinocybe auricoma* (Har. Takah.) Matheny differs from *L. papillatus* by having a larger, golden to yellow-orange pileus and bigger, ovoid-ellipsoid basidiospores (Takahashi 1999), as compared to the narrowly ellipsoid basidiospores of *L. papillatus*. *Leucoinocybe subglobispora* Q. Na, & Y.P. Ge has subglobose to broadly ellipsoid basidiospores, as well as flexuous and subcapitate cheilo-

cystidia (Na et al. 2024), whereas *L. papillatus* has longer and narrower ellipsoid basidiospores and narrowly clavate cheilocystidia. Compared to *L. papillatus*, *L. taniae* (Vila) Antonín, Borov., Holec & Kolařík features a broader, convex to campanulate-convex pileus and cheilocystidia that are variable in shape, ranging from lageniform with long neck (sometimes forked) to sublageniform or fusoid (Malysheva & Morozova 2011), while *L. papillatus* has a campanulate pileus and narrowly clavate cheilocystidia.

Authors: N. Aman, M. Usman, A.N. Khalid, J.M. Moncalvo

Interesting taxonomical notes, new hosts, and geographical records

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma noordeloosii Hauskn., Österr. Z. Pilzk. 8: 149 (1999) – Figs. 11, 12

Material examined. – CZECHIA. Kanice, U Brněnky Nature Reserve, calcareous *Querceto-Carpinetum*, 18. August 2021, leg. H. Ševčíková (BRNM 825859).

Description. – Pileus 26–58 mm broad, plano-convex with broad umbo, undulate at margin in mature basidioma, hygrophanous, glabrous, slightly translucently striate at margin, beige to sand yellow (RAL1001–1002) with paler broad central umbo when young, oyster white (RAL1013) or light ivory (RAL1015) with darker central umbo, pallescent on drying. – Lamellae crowded, adnate-emarginate, up to 12 mm broad, white then pinkish with irregular concolorous edge. – Stipe

59–82 × 4–7 mm, cylindrical, white, innately longitudinally fibrillose, glabrous, base with white tomentum. – Flesh white. – Smell indistinctly sweet. – Taste mild, indistinct. – Basidiospores (7.5)8–10.0(10.5) × (5.8)6.2–7.8(8.0) µm, $Q = 1.15–1.50$, $Q_{av} = 1.32$ sub-isodiametrical to heterodiametrical, with 5–7 angles in side view. – Basidia 4-spored, 20–47 × 7–14 µm, narrowly clavate to clavate, clamped. – Lamellae edge fertile. – Cheilocystidia not detected in the examined basidiomata. – Pileipellis a cutis of (2)4–7 µm wide, cylindrical hyphae. – Pigment intracellular, pale brown, without incrustation. – Stipitipellis a cutis, caulocystidia absent. – Clamps numerous in the pileipellis and basidia.

Habitat and distribution. – In small group, in calcareous soil of *Querceto-Carpinetum*, in August. Thus far reported from Austria, Georgia, Germany, Hungary, Iran, Norway, Poland, Spain, Switzerland and now from Czechia (South Moravia).

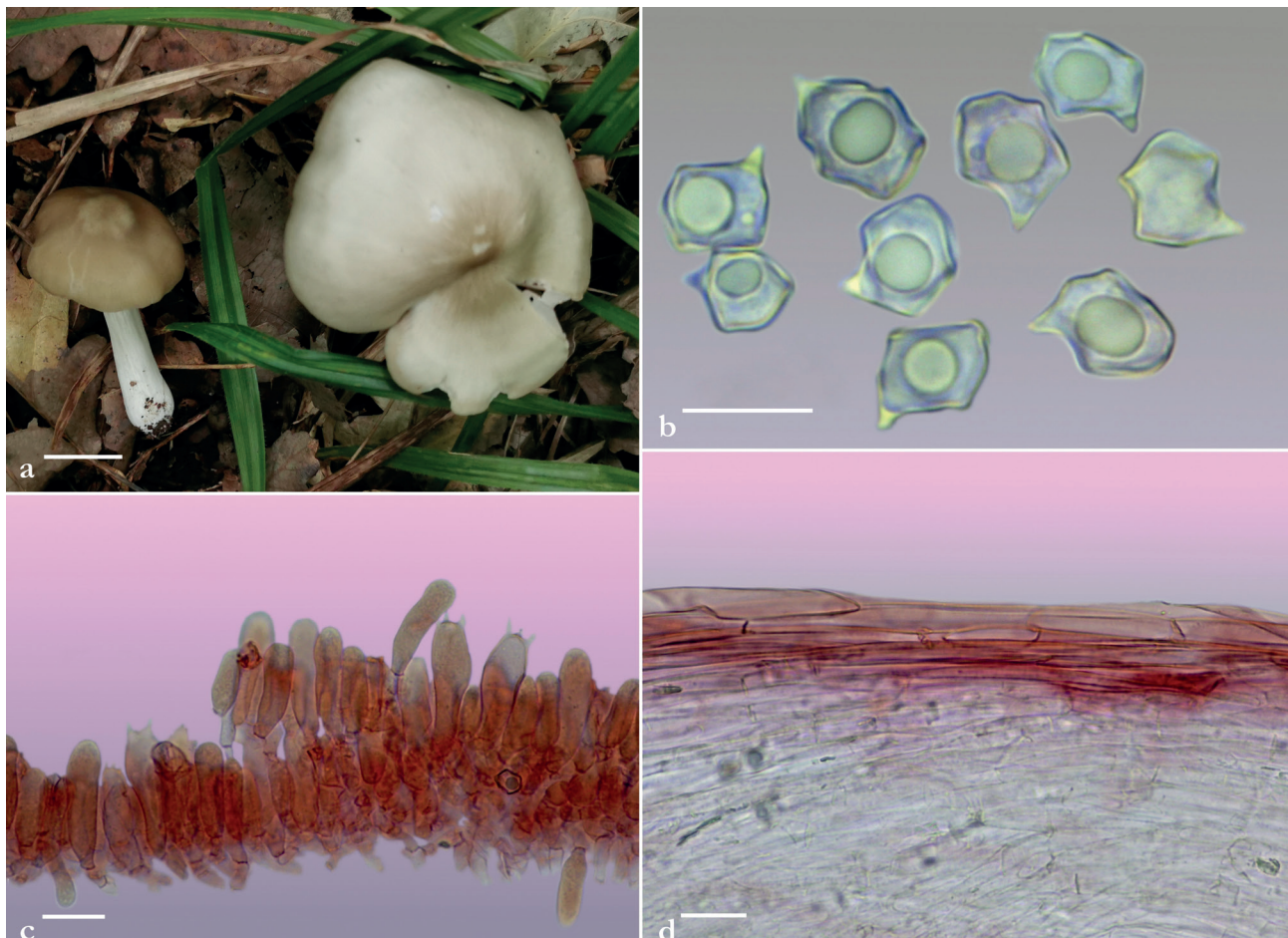


Fig. 11. *Entoloma noordeloosii* (BRNM 825859). **a.** Basidiomata *in situ*. **b.** Basidiospores. **c.** Lamellae edge section in Congo Red. **d.** Pileipellis hyphae from the centre of pileus in Congo Red. **a.** Bar 10 mm. **b–d.** Bars 10 µm.

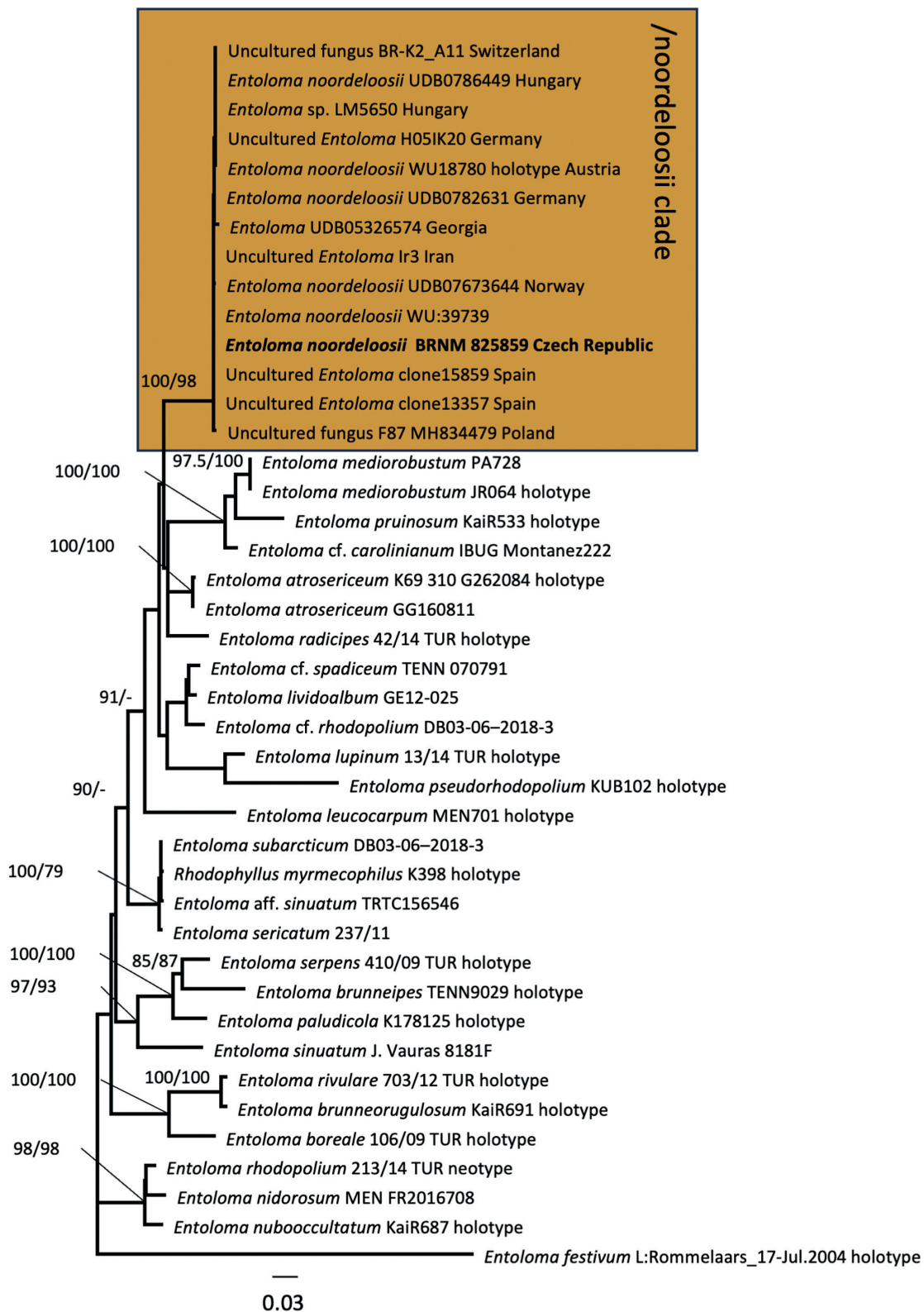


Fig. 12. Maximum Likelihood phylogram of species of *Entoloma* subg. *Entoloma* based on the alignment of ITS sequences. *E. festivum* used as outgroup. SH-aLRT support (%) ≥ 80 / bootstrap support (%) ≥ 70 given above the nodes. Bar = estimated changes/nucleotide.

Notes. – *Entoloma noordeloosii* belongs to the subgenus *Rhodopolia* (Fr.) Noordel. ex Kokkonen, which encompasses species classified within several sections, including *Rhodopolia* (Fr.) Noordel., *Polita* Noordel., *Pseudonolanea* Largent, *Typodochroa* Largent, and *Lividoalbum* Largent. This subgenus is characterized by five main features: (1) a hygrophanous pileus, typically smooth or occasionally faintly fibrillose; (2) a color range from brown to white, with yellowish, grey, or black tones being less common; (3) a stipe that is generally smooth or fibrillose, predominantly white, grey, or brown; (4) spores that are mostly subisodiametrical or broadly heterodiametrical, with well-defined angular edges; (5) the consistent presence of clamp connections (Kokkonen 2015).

According to Brandrud et al. (2018), *E. noordeloosii* is placed within the /*Sericatum* clade. However, the same authors note that this species shows morphological affinities with species belonging to the *Entoloma rhodopolium* complex.

Entoloma noordeloosii was originally described by Hausknecht (1999) from Austria. Typical basidiomata of *E. noordeloosii* are characterized by strongly hygrophanous pileus of variable color from yellowish brownish, pinkish brown to greyish-orange, which becomes whitish during dehydration, stipe generally yellowing at the base, basidiospores hetero-diametrical with 5–7 angles in side-view, and presence of cheilocystidia (Noordeloos 2004, Brandrud et al. 2018). The smell seems to be a variable character, ranging from faint farinaceous (Hausknecht 1999), nut-like to sweetish smell (Brandrud et al. 2018) or indistinct in our Czech collection. Brandrud et al. (2018) reported that this species appears uncommon, restricted to thermophilous deciduous forests, and has not yet been reported in secondary environments like parks. In our ML tree, the sequence from Czechia (BRNM 825859, GenBank: PQ656722) forms a well-supported clade (/noordeloosii) with thirteen other sequences (Fig. 12). Czech sequence (BRNM 825859) shows an identity of 99 % (894/899, for five “N”) compared to the *E. noordeloosii* holotype sequence. /noordeloosii clade includes samples from Austria, Czechia, Georgia, Germany, Hungary, Iran, Norway, Poland, Spain and Switzerland. The studied specimen is the first record from Czechia. The sequences KM576401, KX886002, MW282430 and MW282600 come from ectomycorrhizal root tips of *Fagus sylvatica* and *Quercus petraea*, highlighting the close association of *E. noordeloosii* with beech and oak. The Czech collection (BRNM 825859) fits well with the previous description except for the absence of true

cheilocystidia and fertile lamellae edge (Fig. 11). Noordeloos (2004), in his monograph on the genus *Entoloma* in Europe reported about *E. noordeloosii* “Lamella edge sterile or heterogeneous”, highlighting that cheilocystidia can vary in different collections. From the morphological point of view, *E. noordeloosii* is close to taxa belonging to *E. rhodopolium* (Fr.) P. Kumm. complex, which are characterized by “presence of more or less nitrous smell, usually a tomentose hirsute stipe base and no cystidia” (Brandrud et al. 2018). Among the species reported by Brandrud et al. (2018) within the /*Sericatum* clade, *Entoloma lividoalbum* occurs in similar habitats but is generally more robust and darker in color (never whitish when dry), typically exhibits a stronger farinaceous smell, and lacks cheilocystidia. In the case of *E. noordeloosii* basidiomata lacking cheilocystidia, the distinction between these two species must rely primarily on macromorphological and organoleptic characters.

In conclusion, only molecular analysis can lead to correct identification of *E. noordeloosii* in the presence of atypical samples without cheilocystidia or difficulty with rehydration of dry samples.

Authors: F. Dovana, G. Ferisin & H. Ševčíková

Basidiomycota, Agaricomycetes, Agaricales, Strophariaceae

Hebeloma section *Hebeloma*

Hebeloma lindae Beker & U. Eberh., in Beker, Eberhardt & Vesterholt, *Fungi europ.* (Alasio) 14: 457 (2016) – Figs. 13–19

Material examined. – TURKIYE. Çanakkale, Terzioğlu Campus, Safiye Hüseyin Elbi Girls’ Dormitory vicinity, 40°06’45” N, 26°25’54” E, 205 m, near *Pinus brutia* Ten, 17 January 2024, *leg.* I. Acar (Acar 1757); *ibid.*, 29 March 2024, *leg.* I. Acar (Acar 1866).

Description. – Pileus 35–70(100) mm in diam., usually convex, rarely broadly umbonate; margin smooth to wrinkled, inwardly curled when young, becoming concave at maturity, occasionally crenulate or sulcate, rarely fibrillose; color typically uniform, sometimes bi-colored, with a reddish-yellow with pinkish tones to dark pinkish buff center and a lighter-colored outer margin, sometimes ochraceous or cinnamon. – Pileus surface smooth, sometimes wrinkled or cracked, viscid when moist; turning reddish brown in KOH. – Lamellae emarginate, occasionally adnate, with 66–100 complete lamellae; spacing not recorded. – Lamellar edges mostly intact, showing minimal tearing; cream brown to pale tobacco brown;



Fig. 13. Research area. **A.** In situ photographs of the habitat of *Hebeloma lindae*, **B.** Leaves of *Pinus brutia*.

edge serrulate, whitish, fimbriate, white fimbriate edge often weakly developed. – *Cortina* not observed. – *Stipe* 30–75(110) × 6–12 mm {median} × 5–14 mm {basal}, usually cylindrical, sometimes tapering toward the base or clavate to bulbous; surface floccose, rarely fibrillose, floccose at apex or pruinose on the upper third, sometimes with deep-rooted structure, thick rhizoids at base absent, turns slightly reddish brown in KOH. – *Odor* pleasant, sweet, fruity. – *Context* fleshy, firm. – *Taste* mild. – *Basidiospores* 8.3–11.8(12.3) × 5.3–7(7.5) μm, (n = 40), Q = 1.46–1.79; amygdaloid, often brown, occasionally yellow or yellow-brown, guttulate, color code O2; P0, P1; D3. – *Basidia* 25–38 × 5.5–9 μm, four-spored. – *Cheilocystidia* 14–50 × 3–7 {apex width} × 3–6 {median width} × (2.4)2.8–7 μm {basal width}; often cylindrical, rarely ventricose; usually septate, sometimes clamped septa; short, bifurcate, branching or geniculate, rostrate or sinuate; rarely irregular. – *Pleurocystidia* not observed. – *Caulocystidia* similar in shape and size to cheilocystidia but slightly longer, reaching up to 110 μm. – *Pileipellis* two-layered; suprapellis an ixotomentocutis, 130 μm thick (when dried), hyphae 1.6–5 μm wide, hyaline, and occasionally with fine epiparietal pigments, terminal elements typically hyphoid, lower hyphae up to 5.5–6.3 μm wide; subpellis pale brownish-yellow,

distinguishable from the pileitrama by its distinct coloration, composed of densely interwoven, partially fused hyphoid hyphae, filamentous to allantoid, up to 20 μm wide. – *Stipitipellis* up to 11.2 μm wide, cylindrical, septate, with clamp connection.

Habitat and distribution. – Growing in coniferous dune woodlands with calcareous, sandy, or bare soils; scattered, solitary, and rarely gregarious. Primarily associated with *Pinus* (91.7%), but also recorded with *Quercus* (8.3 %) and once with *Cistus*. Most frequently recorded families associated with *H. lindae* are *Pinaceae* (86.7 %), *Fagaceae* (26.7 %), and *Cistaceae* (13.3 %) (Beker et al. 2016). Thus far reported from Greece, Italy, Spain, and Türkiye (this study).

Notes. – The two ITS sequences of our Turkish specimens shared 99.85 % similarity (96–99 % query cover) with an ITS sequence representing *H. lindae* (GenBank accession no. OQ100533), as well as 99.55 % similarity (96–99 % query cover) with the ITS sequence of the type material of *H. lindae* (GenBank accession no. NR_185378). Our Bayesian phylogenetic inference revealed 13 well-supported clades within *Hebeloma* (Fig. 14), with the Turkish collections placed in Sect. *Scabrispora*. The species *H. lindae*, *H. laterinum*, *H. olympianum*, *H. danicum*, *H. immutability*, *H. pumilum*, *H. birrus*, and *H.*

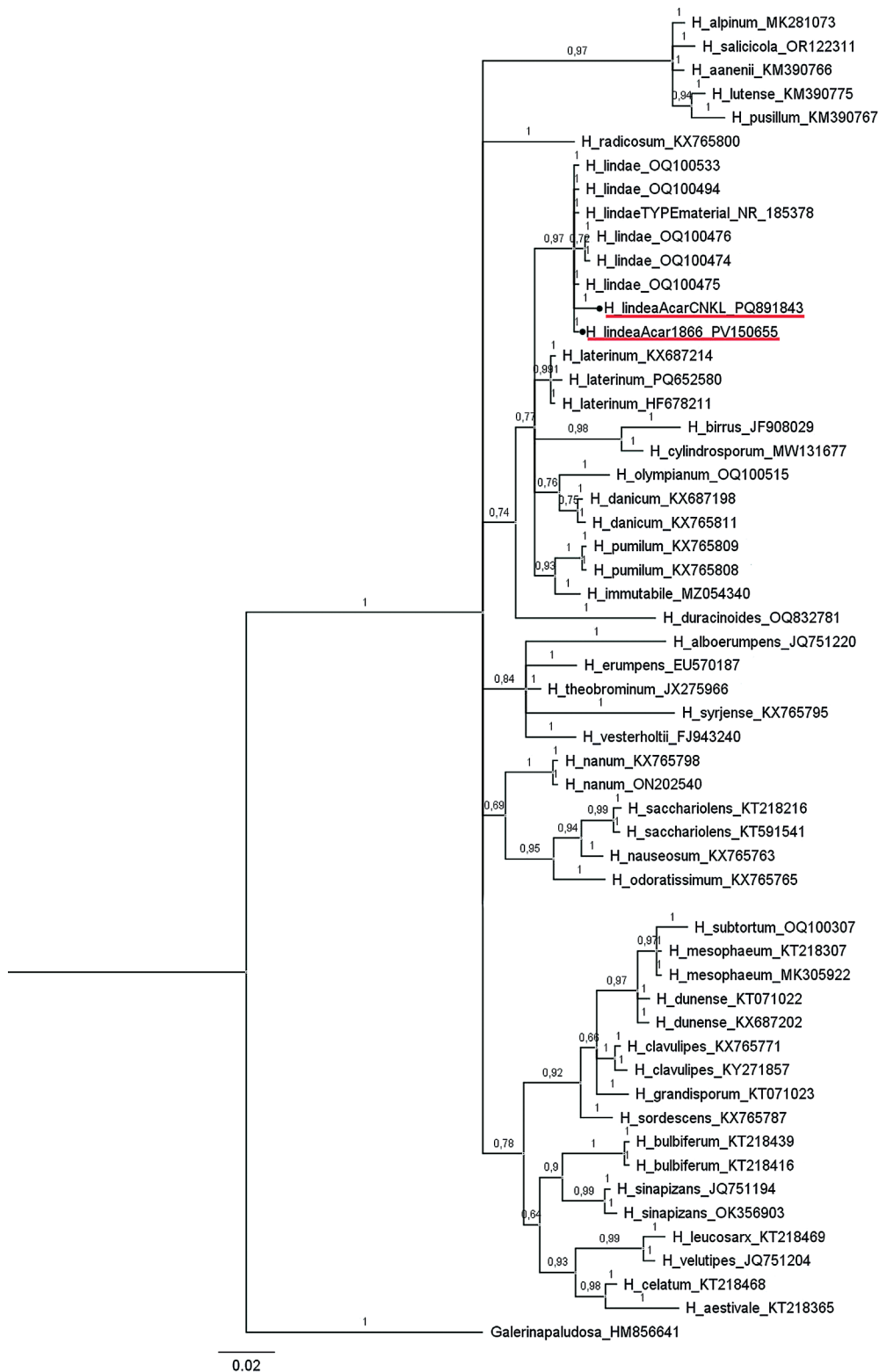


Fig. 14. Bayesian 50 % majority-rule consensus tree of *Hebeloma* species inferred from ITS rDNA sequence data using the Markov Chain Monte Carlo (MCMC) algorithm implemented in MrBayes v3.2.7a. Turkish specimens underlined in red. Bayesian posterior probability values (≥ 0.50) shown above the branches. *Galerina paludosa* used as the outgroup. Scale bar indicating the estimated number of substitutions per site.

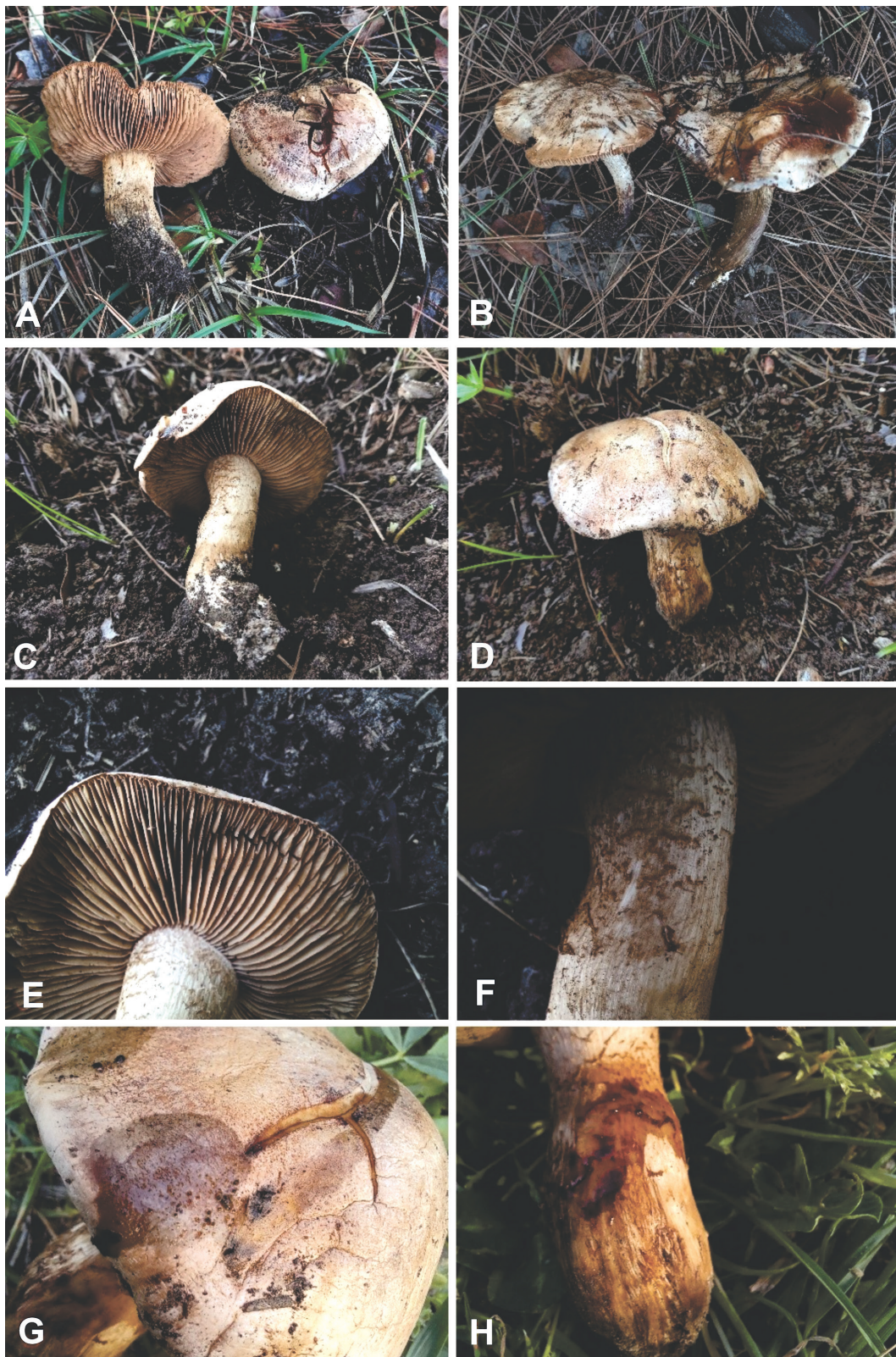


Fig. 15. Macrophotographies of Turkish specimens of *Hebeloma lindae* (Acar 1757, Acar 1866). **A–D.** Basidiomes in the field, **E.** Lamellae, **F.** Stipe, **G.** KOH reaction of the pileus, **H.** KOH reaction of the stipe.

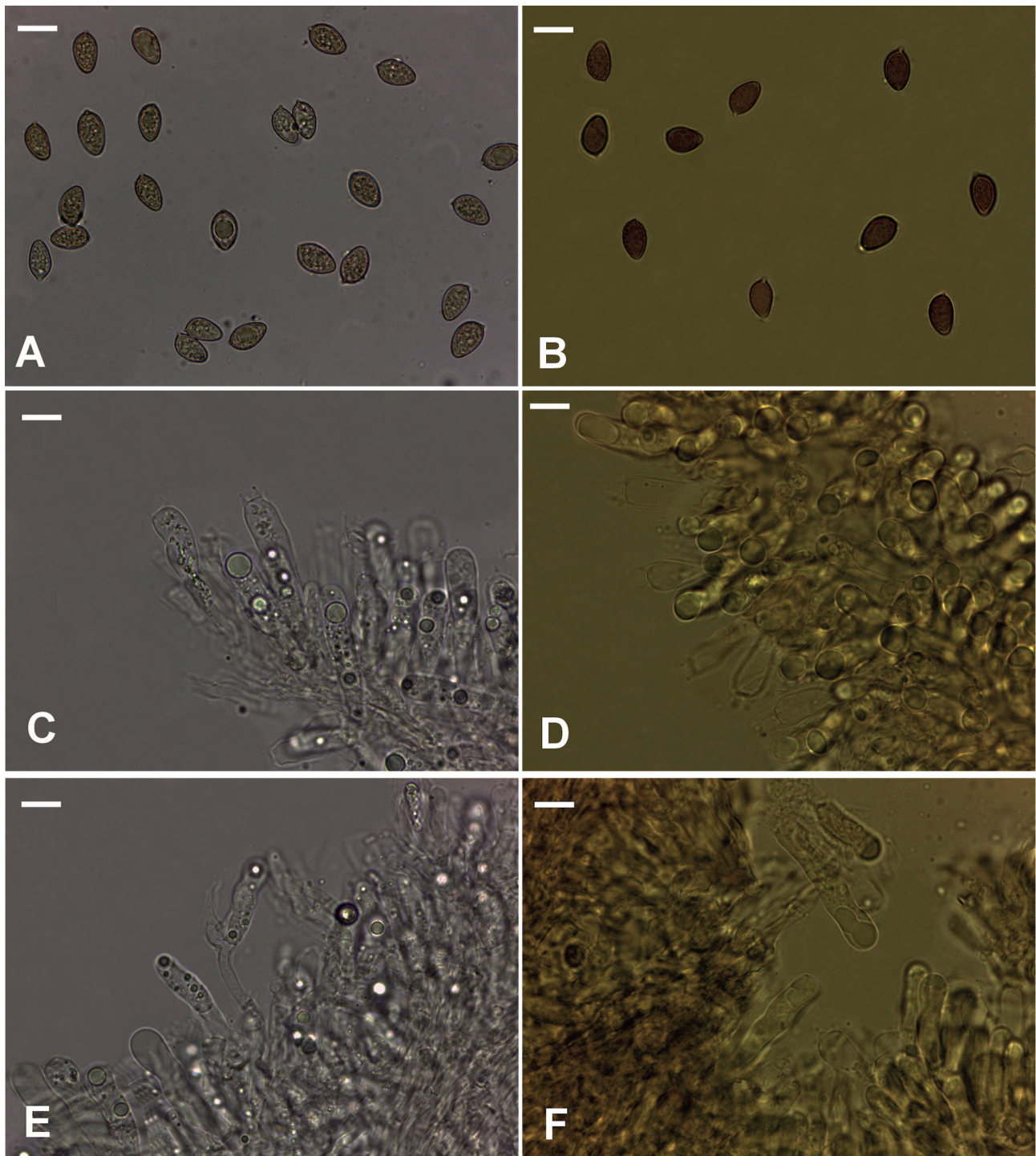


Fig. 16. Microphotographies of Turkish specimens of *Hebeloma lindae* (Acar 1757). **A–B.** Spores, **C–D.** Basidia, **E–F.** Cheilocystidia; **A, C, E.** in water, **B, D, F.** in Melzer's Reagent. Bars 10 µm.

cylindrosporum grouped together as expected (Bayesian posterior probability [BPP] = 0.77). Within this clade, the Turkish specimens of *H. lindae* were recovered as sister to *H. laterinum* (BPP =

0.99). These results confirm the identification of the Turkish collections as *H. lindae*.

The first specimens of the species *Hebeloma lindae* were initially misidentified as *H. catalaunicum*

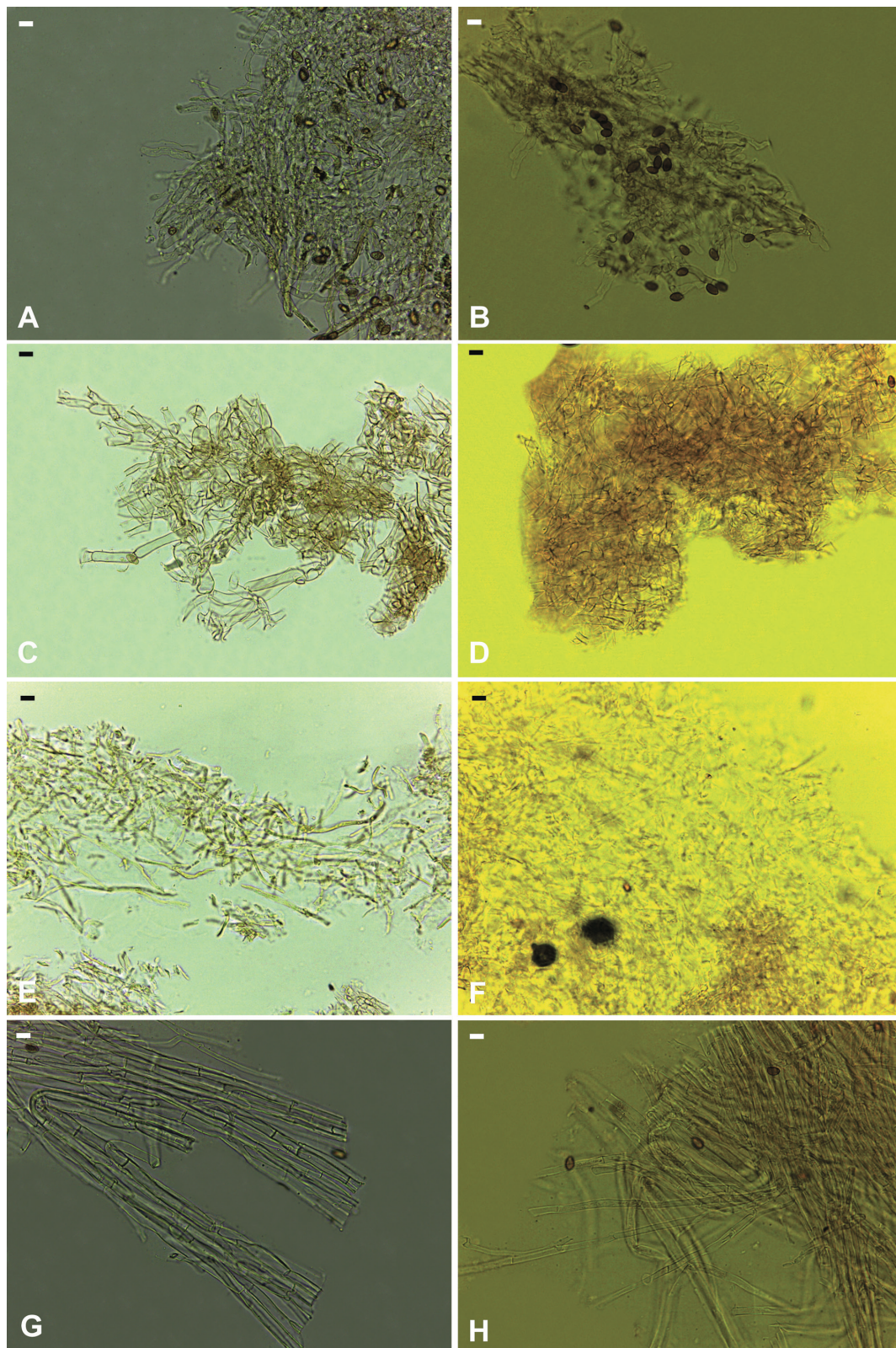


Fig. 17. Microphotographies of Turkish specimens of *Hebeloma lindae* (Acar 1757). **A–B.** Caulocystidia, **C–D.** Subpellis, **E–F.** Hyphae scattered within the gel matrix (pileipellis), **G–H.** Stipitipellis. **A, C, E, G.** in water, **B, D, F, H.** in Melzer's Reagent. Bars 10 µm.

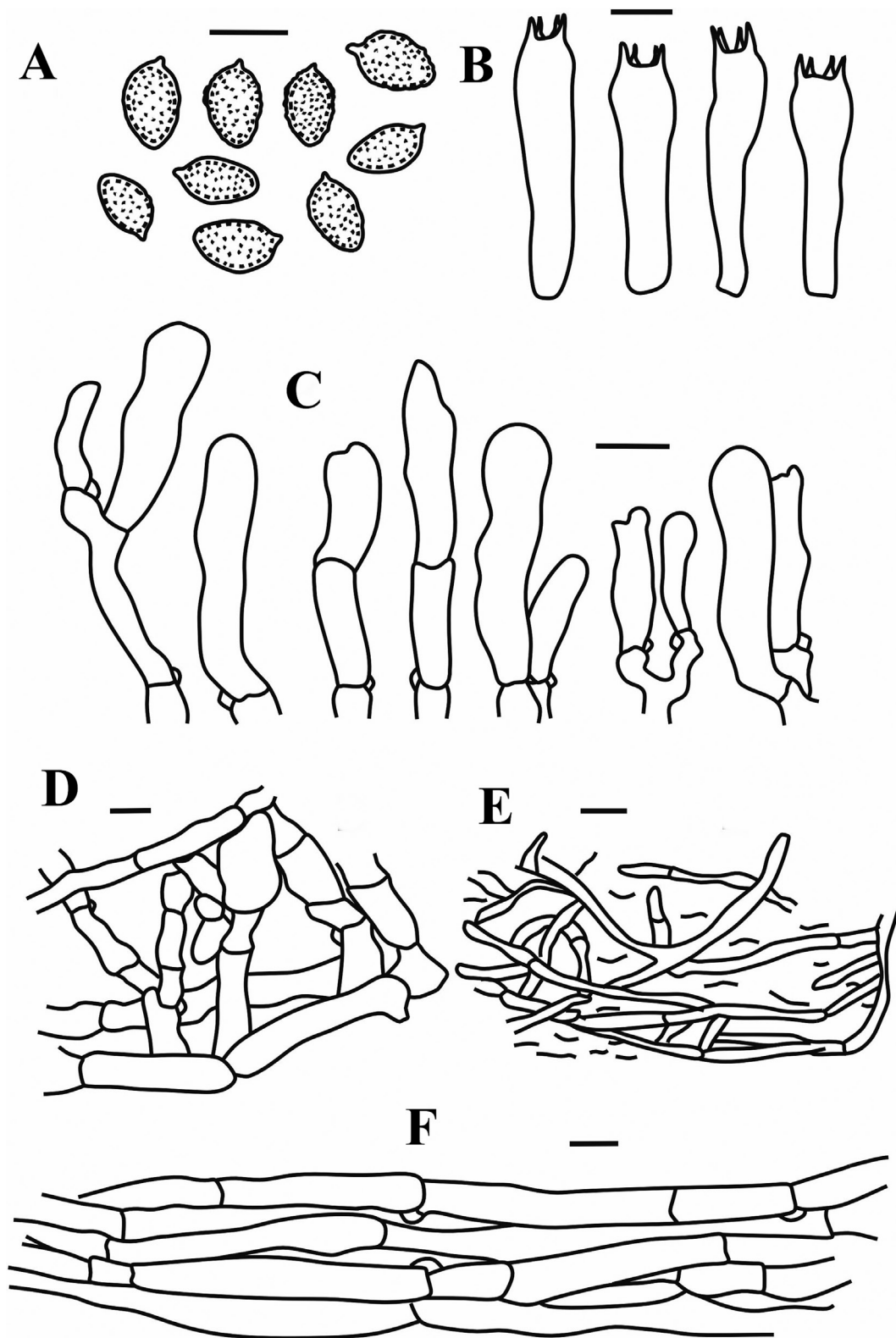


Fig. 18. Line drawings of microscopic features from Turkish specimens of *Hebeloma lindae* (Acar 1757, Acar 1866). **A.** Spores, **B.** Basidia, **C.** Cheilocystidia, **D.** Subpellis, **E.** Hyphae scattered within the gel matrix (pileipellis), **F.** Stipipellis. Bars 10 µm. Drawing İ. Acar.

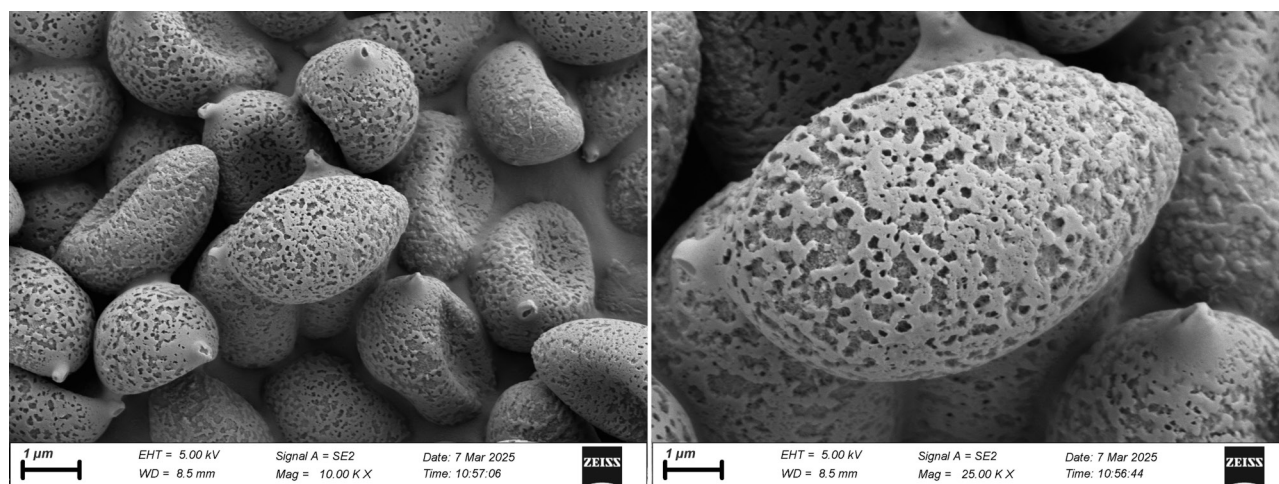


Fig. 19. Scanning microphotographs of basidiospores of *Hebeloma lindae*. Bar 1 µm.

based on preliminary investigations by H. Beker. However, the presence of velar remnants observed by the collector Emanuele Brugaletta raised doubts about this identification. A second collection from the same locality also showed traces of a spidery veil and some specimens showed the development of a rooting stipe. These findings strengthen the possibility that the material rather belongs to *Hebeloma* subsection *Scabrispora*. Although these specimens did not fully match any previously described species in this group, they were later recognized as *H. lindae* as described in the monograph of European *Hebeloma* species published by Beker et al. (2016) and further confirmed to belong to this species by both morphological and molecular evidence (Grilli & Brugaletta 2016).

The large size of *H. lindae*, its rooting tendency and floccose stipe lacking a ring are diagnostic features supporting its classification within sect. *Scabrispora*. Morphologically, it slightly resembles *H. laterinum*, but the stipe of *H. lindae* shows little color change. Microscopically, *H. lindae* can be distinguished from other species within *Hebeloma* subsect. *Scabrispora* by its relatively small, weakly ornamented spores with limited perispore loosening (spore code: O2; P0, P1), average spore length less than 11 µm and width greater than 5.7 µm, and Q value below 1.8. In addition, its cheilocystidia are relatively narrow, with average apical widths not exceeding 5.2 µm and basal widths not exceeding 6 µm, which are generally smaller than those observed in closely related species (Beker et al. 2016). Our molecular data also confirms the close relationship between *H. lindae* and *H. laterinum*, though our *H. lindae* ITS sequences (PQ891843 and

PV150655) show 98.37–98.38 % similarity (97–100 % query cover) with an ITS sequence of *H. laterinum* (GenBank accession no. KX687214) (Fig. 14).

The pileus diameter of the seven Turkish specimens examined in this study [35–70(100) mm] was larger than the ranges reported in the *Fungi Europaei* monograph [31–60(69) mm] and by Grilli & Brugaletta (2016) (24–42 mm), a difference thought to reflect phenotypic plasticity across geographic regions. The stipes of the Turkish specimens ranged from 30 to 110 mm, which is longer than those reported in Beker et al. (2016) [27–70(90) mm] and Grilli & Brugaletta (2016) (34–50 mm), thus indicating a broader size range in our material. In the present study, the pileus and stipe reacted to KOH by turning reddish brown and slightly reddish brown, respectively—a reaction not previously documented in earlier studies. Although no significant differences in micromorphological characters were observed, the size of the gelatinous hyphae in the pileus was slightly greater in our Turkish specimens (1.6–5 µm) compared to the 1.0–3.5 µm range reported by Grilli & Brugaletta (2016) (Tab. 2). Spore codes were consistent between the present study and the previously cited works on *H. lindae* (Tab. 2). As in previous descriptions, it was not possible to determine whether the fibrillose velar remnants on the stipe originated from a universal veil or a cortina.

Regarding mycorrhizal associations, *H. lindae* is thought to be primarily associated with *Pinus*; however, as already mentioned, our Turkish specimens have also been found near *Quercus* and *Cistus*. Sicilian specimens of *H. lindae* were collected in areas dominated by typical garrigue shrubs, with

Tab. 2. Comparison of macroscopic and microscopic characters of Turkish specimens of *Hebeloma lindae* and those reported in Beker et al. (2016) and Grilli & Brugaletta (2016; average measurements or ranges of averages underlined).

<i>H. lindae</i>	Beker et al. 2016	Grilli & Brugaletta 2016	This study
Pileus	(24)31–60(69) mm	27–35 mm	35–70(100) mm
KOH reaction of pileus	unspecified	unspecified	reddish brown
Stipe	(24)27–70(90) × 7–13(14) × (7)8–15(21) mm	34–50 × 7–8 mm	30–75(110) × 6–12 mm × 5–14 mm
KOH reaction of stipe	unspecified	unspecified	slightly reddish brown
Spores	(8.0)8.6–11.4(11.9) × (5.2)5.4– 6.9(7.0) µm	(9.6)9.7 10.7–11.1 12(12.8) × 5.5 6.2–6.3 6.8(7.2) µm	8.3–11.8(12.3) × 5.3– 7(7.5) µm
Basidia	25–36 × 6–9 µm	26 30.6 36 × 7.2 8.2 9.6 µm	25–38 × 5.5–9 µm
Cheilocystidia	(13)14–53(70) × (2.7)3.2–6.5(7.4) × 2.8–5.8(6.1) × (2.4)2.8–6.6(7.0) µm	21 38 53(56) × 4.0 5.5–5.6 7.0(7.2) × 3.2 4.3–4.4 5.6(6.0) × 3.0 4.8 7.0(7.2) µm	14–50 × 3–7 × 3–6 × (2.4)2.8–7 µm
Caulocystidia	up to 150 µm	reported to be of similar size to cheilocystidia	up to 110 µm
Subpellis	up to 20	6.4–20(28) µm	up to 20
Hyphae scattered within the gel matrix	size not specified	1.0–3.5 µm wide	1.6–5 µm wide
Stipitipellis	size not specified	size not specified	up to 11.2 µm wide
Spore code	O2, P0, P1, D3	O2, P0, P1, D3	O2, P0, P1, D3

species of *Cistus*, *Rosmarinus* and *Pistacia lentiscus*, as well as with *Pinus halepensis* and *Quercus coccifera* seedlings, found growing nearby (Grilli & Brugaletta, 2016). Consequently, without empirical evidence, it remains nearly impossible to determine with certainty the ectomycorrhizal status of *H. lindae* (Grilli & Brugaletta, 2016).

Collections cited in *Fungi Europaei* and those from Sicily were made in December, which was considered normal due to the Mediterranean climate. Grilli & Brugaletta (2016) emphasized that basidiomata could also occur in spring if conditions are suitable—a hypothesis confirmed by our study, in which *H. lindae* specimens were collected in January and March.

Although *H. lindae* had previously been reported only from Europe and considered a Mediterranean species (Beker et al. 2016, Grilli & Brugaletta, 2016), its occurrence in Çanakkale—an intercontinental city bordering the European continent and located along the Mediterranean coast—is not unexpected, as the region shares similar climatic conditions with the Mediterranean zone. This study thus provides the first confirmed record of *H. lindae* outside Europe and contributes to a better understanding of the geographical distribution of the genus *Hebeloma* at global scales.

Authors: İ. Acar & H. Karabıyık

Basidiomycota, Agaricomycetes, Boletales, Paxillaceae

Paxillus ammoniavirescens Contu & Dessì, in Dessì & Contu, Micol. Veg. Medit. 13(2): 123 (1999) – Figs. 20–23

Material examined. – PAKISTAN. Gilgit-Baltistan, Kharmang district, Mehdiabad, 2851 m a.s.l., on the soil in grass, 10 September 2022, *leg.* Ghulam Hussain (UEH-F40047; ITS GenBank accession number: PP758271); – *ibid.*, 2961 m a.s.l., on the soil in grass, 3 July 2023, *leg.* Ghulam Hussain (UEH-F40048; ITS GenBank accession number: PQ461142).

Description. – Pileus 6–7 cm in diam., convex, depressed from center, surface smooth, incurved from the margin and undulating, shiny, brown (Hue 10 YR). – Lamellae adnate, plane margins, crowded spacing, parallel tissue, lamellulae 2 tiers, yellow (Hue 25 YR). – Stipe 1.5–4 cm (l) × 0.7–1.7 cm (w), eccentric with rhizoids, smooth surface, yellow (Hue 25 YR). – Basidiospores (4)5–6(7) × (2)3–4(–5) µm on average $Q=1.67$, oblong in shape, germ pore, guttulate, apiculus not prominent, light brown in KOH. – Basidia 24–36 × 5–8 µm, narrowly uniform, thin-walled and smooth. – Cystidia (4)5–6(7) × (2)4–4(6) µm narrowly clavate. – Pileipellis hyphae 3–4 µm wide, irregular, septate. – Stipitipellis hyphae 2–3 µm wide, inverse, septate.

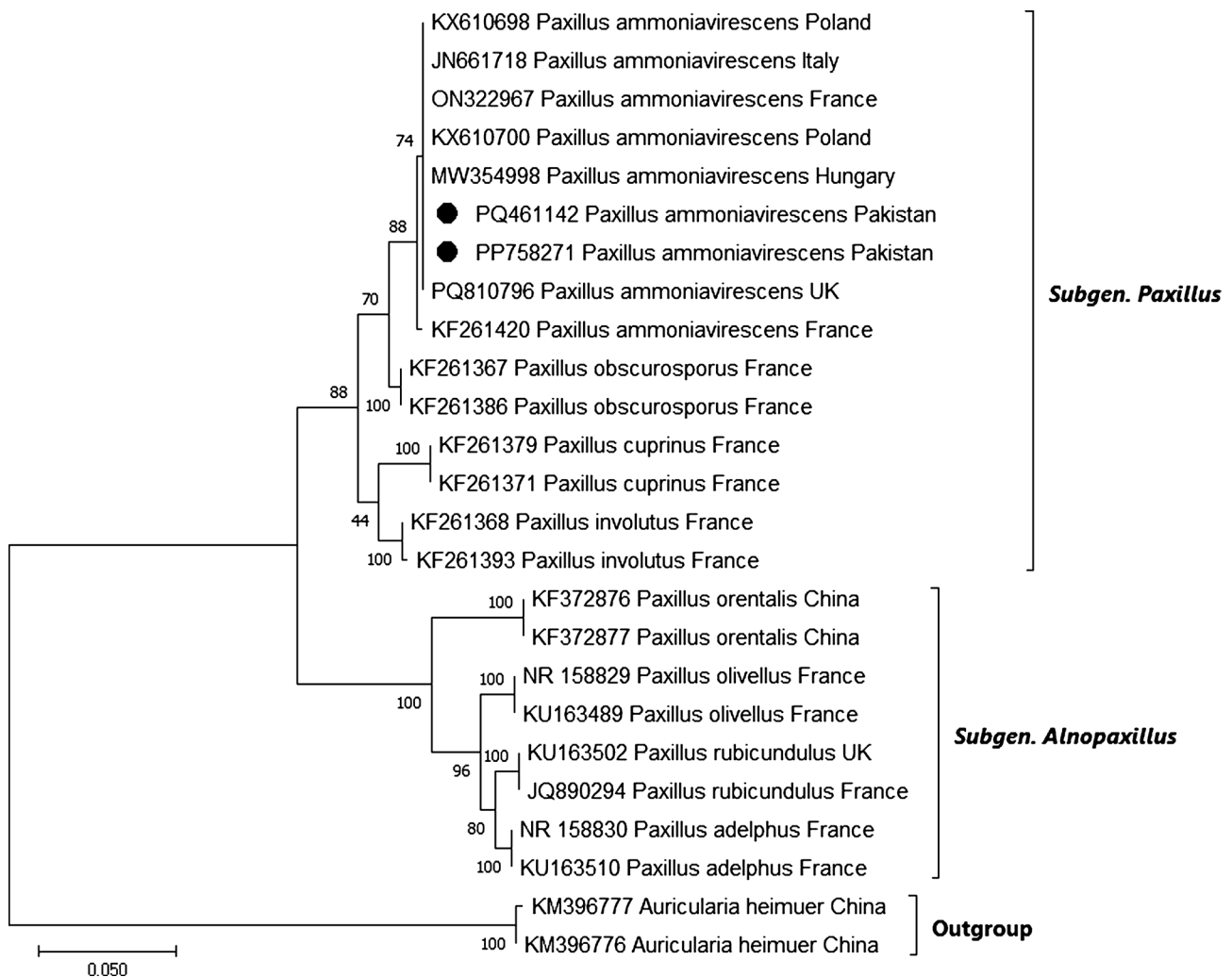


Fig. 20. Phylogeny of *Paxillus* reconstructed from an ITS dataset with *Auricularia* as outgroup. Tree generated by the MEGA Software using Maximum likelihood under the Kimura 2-parameter model with gamma distribution. Bootstrap support values ≥ 50 % indicated at the nodes. Scale bar indicating the number of substitutions per site. Sequences generated in this study highlighted with bullet signs.

Habitat and distribution. – On forest soil. Thus far reported from Argentina, Austria, Canada, Corsica, Estonia, Finland, France, England, Germany, India, Italy, Morocco, Netherlands, New Zealand, Poland, Russian Federation, Sardinia, Spain, Sweden, Türkiye, USA and Pakistan (this study).

Notes. – *Paxillus ammoniavirescens* is reported and described for the first time in Pakistan. Microscopic characters were compared with the description of the type specimen from Dessi & Contu (1999). It was described as having irregular and septate pileipellis hyphae, a yellowish-brown stipe which was typically central and straight, consisting of fusiform cystidia with a narrow appendage, yellowish brown short lamellae and growth on grass

without visible connection to wood. Contrary to the holotype material, the two collections from Pakistan present inverse and septate stipitipellis hyphae, as well as quite smaller cystidia (5–7 μm on average vs. 6–13 μm). On the other hand, the holotype and collections of *P. ammoniavirescens* from Pakistan share similar features, namely (i) the brown pileus can be completely smooth, convex, depressed from center, (ii) the short yellow lamellae present, (iii) the stipe is eccentric with rhizoids, smooth surface, yellow, (iv) cystidia are present in narrowly and clavate shape, (v) basidia are in narrowly uniform shape, (vi) basidiospores are oblong in shape, germ pore, gutulate, apiculus not prominent, light brown in KOH (Tab. 3).

Tab. 3. Morpho-anatomical comparison of studied collections of *Paxillus ammoniavirescens* with the holotype.

Collection No.	Pileus	Lamellae	Stipe	Basidiospores	Basidia	Cystidia	Pileipellis hyphae	Stipitipellis hyphae
Spain (holotype)	3–13 cm in diam., convex to flattened, sometimes slightly funnel-shaped; pale yellow, golden yellow to tawny brown	Dense, thin, separable from the flesh; forked and intermixed with short lamellula; golden yellow	Central and straight, 2–6.5 cm long, cylindrical; surface smooth; color similar to the pileus	Ellipsoid to ovoid, with slightly visible apiculus; featuring a large central guttule and smaller polar guttules; (6.49)6.80–8.07(9.56) × (4.35)4.59–5.31(5.60) µm	Clavate; 22–40 × 6–9 µm	Fusiform, with a narrow appendage; 6–13 µm long	Cylindrical hyphae with narrow walls, irregularly arranged, with frequent emergent tips; 3–5 µm wide	Not observed
Pakistan (UEH-F40047)	6–7 cm in diam., convex, depressed at center; surface smooth, margin incurved and undulating; golden yellow to brown	Adnate, with plane margins; crowded; arranged in two tiers; tissue parallel; yellow	1.5–4 cm long, 0.7 cm wide; eccentric with rhizoids; surface smooth; yellow	Oblong, with germ pore and guttules present, apiculus not prominent; (5)6–7(8) × (2)4–5(5) µm Q=1.75	Narrowly clavate; 24–36 × 5–8 µm	Narrowly clavate, smooth, thin-walled; (4)5–6(–7) × (2)4–4(–6)µm	Irregular, septate; 3–4 µm wide	Inverse, septate; 2–3 µm wide
Pakistan (UEH-F40048)	Somewhat rounded to slightly depressed in the center; surface glossy, smooth, with inwardly curved and gently undulating margins; warm brown	Loosely joined, densely arranged, smooth with flat edges; aligned nearly parallel; pale yellow to golden tint	2–4 cm long, 1.7 cm wide; off-center with rhizoid-like extensions; surface even, untextured; soft yellow	Elongated with nearly prominent apiculus; germ pore present; pale brown in KOH; (4)5–6(7) × (2)3–4(5) µm Q=1.67	Slightly narrow and uniform; 25–37 × 6–9 µm	Narrow and slightly club-shaped, smooth; (5)6–7(7) × (3)4–5(–6)	Irregular, septate; 3–5 µm wide	Inverse septate; 2–4 µm wide

In our phylogeny, the studied collections were found clustering with reference sequences of *P. a46mmoniavirescens* (MW354998, KF261420) with strong bootstrap support (BS = 92 %). All *Paxillus* sequences included in the analysis formed two well-supported clades (BS>70 %) corresponding to the subgenus *Paxillus* (*P. ammoniavirescens* Contu &

Dessi, *P. obscurusporus* C. Hahn, *P. cuprinus* Jargeat, Gryta, J.-P. Chaumeton & Vizzini, *P. involutus* (Batsch) Fr.) and subgenus *Alnopaxillus* (*P. orentalis* Gelardi, Vizzini, E. Horak & G. Wu, *P. olivellus* P.-A. Moreau, J.-P. Chaumeton, Gryta & Jargeat, *P. rubicundulus*, P.D. Orton, *P. adelphus* J.-P. Chaumeton, Gryta, Jargeat & P.-A. Moreau) (Fig. 20). BLAST

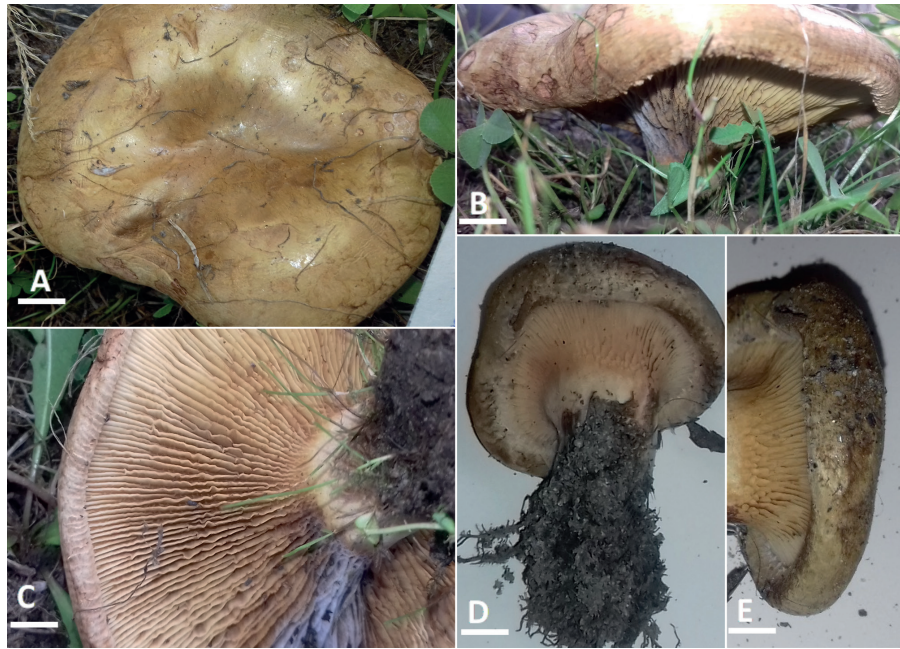


Fig. 21. *Paxillus ammoniavirescens* (UEH-F40047; UEH-F40048) **A.** Pileus upper surface, **B.** Gills arrangement, **C.** Margins of gills, **D–E.** Stipe with lamellae attachment. Bars 1 cm.

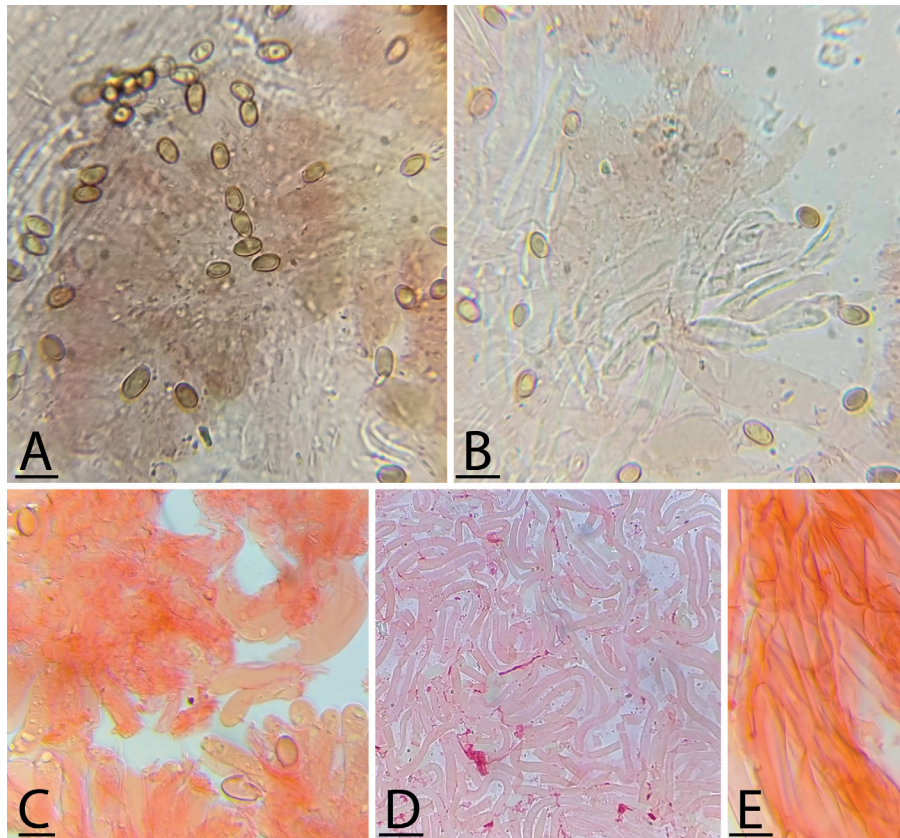


Fig. 22. Microscopic features of *Paxillus ammoniavirescens*. **A.** Basidiospores; **B.** Basidia; **C.** Cystidia; **D.** Pileipellis hyphae; **E.** Stipitipellis hyphae. Bars **A** 11 μm , **B** 22 μm , **C** 4 μm , **D** 35 μm , **E** 8 μm .

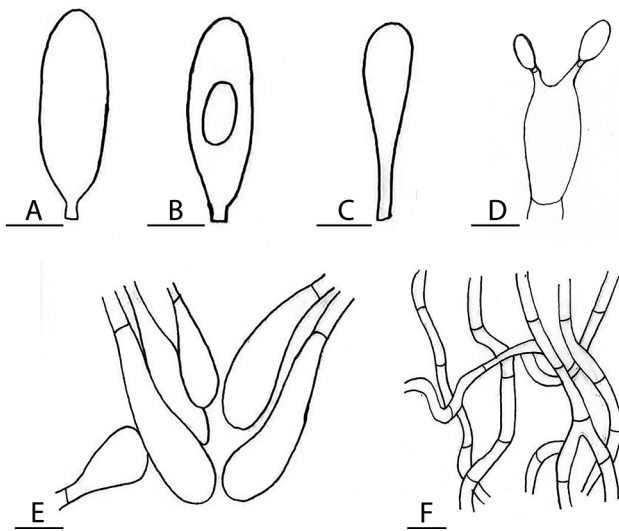


Fig. 23. Line drawings of microscopic features of *Paxillus ammoniavirescens* (UEH-F40047). **A.** Oblong basidiospore; **B.** Germ pore; **C.** Narrowly clavate cystidia **D.** Basidia (barrel-shaped) **E.** Stipitipellis hyphae (inverse and septate); **F.** Pileipellis hyphae (irregular and septate). Bars **A, B** 1.5 μm , **C** 1.7 μm , **D** 11.5 μm , **E** 0.7 μm , **F** 15.5 μm . Drawing S. Hanif.

results showed that the two ITS sequences of 715 and 706 base pairs obtained from the studied collections showed 98–99 % similarity with sequences of *P. ammoniavirescens* from Hungary (MW354998, 100 % query coverage), France (ON322967, 100 % query coverage; KF261420, 70 % query coverage), Poland (KX610698 and KX610700, 100 % query coverage), UK (PQ810796, 100 % query coverage) and Italy (JN661718, type, 90 % query coverage). Both morphological and molecular data confirm the identification of our two Pakistani specimens as *P. ammoniavirescens*.

Authors: S. Hanif, A. Aslam, A. Razaq, M.B.B. Majeed, M. Kiran, A. Ishaq

Ascomycota, Sordariomycetes, Trichosphaeriales, Trichosphaeriaceae

Plectosphaerella plurivora A.J.L. Phillips, A. Carlucci & M.L. Raimondo, in Carlucci, Raimondo, Santos & Phillips, Persoonia 28: 44 (2012) – Figs. 24, 25

Material examined. – CHILE. Región Metropolitana, Santiago, Campus Huechuraba, Universidad Mayor, from unidentified decaying leaf, 27 April 2015, leg. H. Madrid (culture HM 230).

Description. – Vegetative hyphae septate, branched, straight to flexuous, hyaline, smooth and thin-walled, 1–4 μm wide, forming strands and coils, with anastomoses. – Conidiophores solitary, simple to rarely branched, hyaline,

line, smooth and thin-walled, mostly reduced to conidiogenous cells. – Conidiogenous cells monophialidic, subcylindrical to lageniform, sometimes ventricose, straight to sinuous, 7–21 $\times$ 1.5–3 μm ($n = 30$, $x = 12.5 \times 2.2 \mu\text{m}$), usually with a conspicuous cylindrical collarette. – Conidia cylindrical to fusiform, hyaline, smooth, thin-walled, sometimes asymmetrical, one-celled or 1-septate, often with a minute apiculus at each pole, aseptate conidia 4.5–9 $\times$ 2–3.5 μm ($n = 30$, $x = 6.8 \times 2.3 \mu\text{m}$), septate conidia 7–9.5 $\times$ 2–3 μm ($n = 30$, $x = 7.9 \times 2.3 \mu\text{m}$). – Chlamydospores not observed. – Sexual morph not observed.

Culture characteristics (25 °C, 7 days). – Colonies on MEA reaching 36 mm diam., cottony to funiculose, white, with a fimbriate margin; reverse yellowish with light-orange tinges. – Colonies on Sabouraud agar reaching 25 mm in diam., glabrous and sulcate towards the periphery, but with abundant, coarse mycelial tufts at the center, off-white to cream; reverse yellowish.

Habitat and distribution. – Associated with soil and various plant hosts, including *Asparagus officinalis* (asparagus), *Citrullus lanatus* (watermelon), *Lolium perenne* (ryegrass), *Nicotiana tabacum* (cultivated tobacco), *Ocimum basilicum* (basil), *Panax notoginseng* (notoginseng), *Petroselinum sativum* (parsley), *Solanum lycopersicum* (tomato), and *Solanum tuberosum* (potato). Thus far reported from Australia, New Zealand, Belgium, Germany, Italy, Netherlands, Scotland, Spain, USA, Argentina, Japan, and Chile (Carlucci et al. 2012, Raimondo & Carlucci 2018, Giraldo & Crous 2019, Han et al. 2019, Girardi et al. 2023, this study).

Notes. – The genus *Plectosphaerella* currently includes 24 recognized species, most of which are associated with plants and soil (Zhang et al. 2019, Yang et al. 2021, Crous et al. 2023). Many species are pathogenic to economically important crops, often causing significant yield losses (Carlucci et al. 2012). In addition, a few *Plectosphaerella* species are known to cause opportunistic infections in animals. These include cases of keratitis in humans (Kamada et al. 2012, Russello et al. 2021, Kiriya et al. 2022, Raghavan et al. 2024), a probable mixed disseminated infection in a dog, which also involved *Lecythophora canina* (Troy et al. 2013), and hyalohyphomycosis in the mantis shrimp *Oratosquilla oratoria* (Duc et al. 2009).

Strain HM 230 (Figs. 1, 2), a hyaline, phialidic fungus with a simple conidiogenous apparatus and elongate conidia typical of *Plectosphaerella* (Seifert et al. 2011, Carlucci et al. 2012), was isolated during a taxonomic study of conidial fungi occurring on plant material in central Chile. BLAST

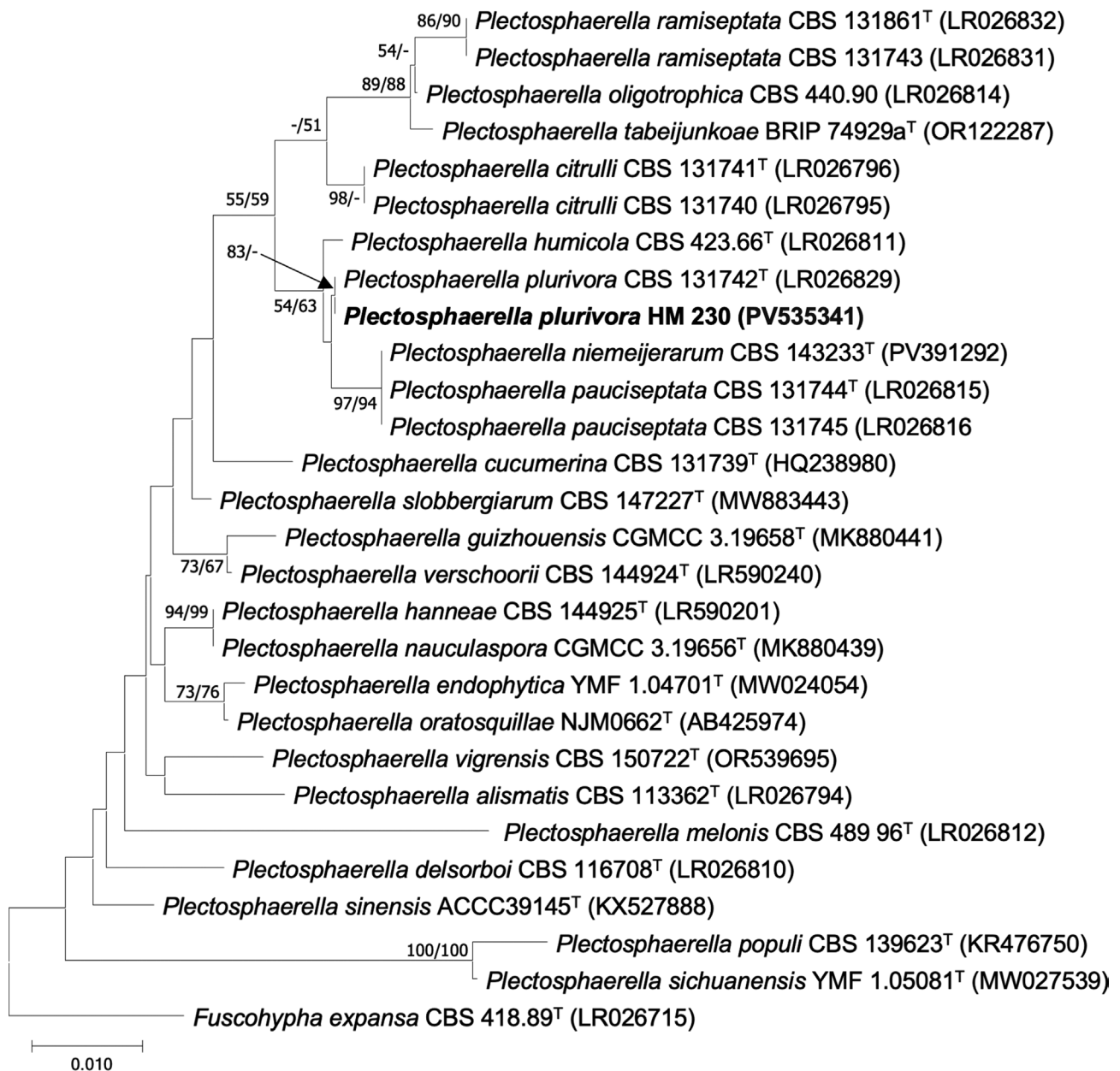


Fig. 24. Phylogeny of *Plectosphaerella* spp. reconstructed from an ITS sequence dataset. The topology was inferred using the Neighbor-Joining method performed in MEGA X. Bootstrap values ≥ 50 from Neighbor-Joining and Maximum Likelihood analyses are shown at the internal nodes in the format NJ/ML. T indicates ex-type strains. The Chilean isolate of *P. plurivora* is shown in boldface. *Fuscohypha expansa* was used as the outgroup.

searches with ITS sequences revealed that its closest matches were strains of *P. plurivora*, including CBS 131742 (ex-type strain, GenBank accession number LR026829, 100 % identical), CBS 642.63 (GenBank accession number MH858371, 100 % identical) and CBS 101607 (GenBank accession number MH862743, 100 % identical). Other close matches were *P. niemeijerum* CBS 143233 (ex-

type strain, GenBank accession number PV391292, 99.62 % id.), *P. slobbergiarum* CBS 147227 (ex-type strain, GenBank accession number MW883443, 98.90 % id.), *P. tabeijunkoae* BRIP 74929 (ex-type strain, GenBank accession number OR122287, 98.71 % id.), and *P. cucumerina* CBS 131739 (ex-type strain, GenBank accession number HQ238980, 98.25 % id.). In a phylogeny reconstruction based on

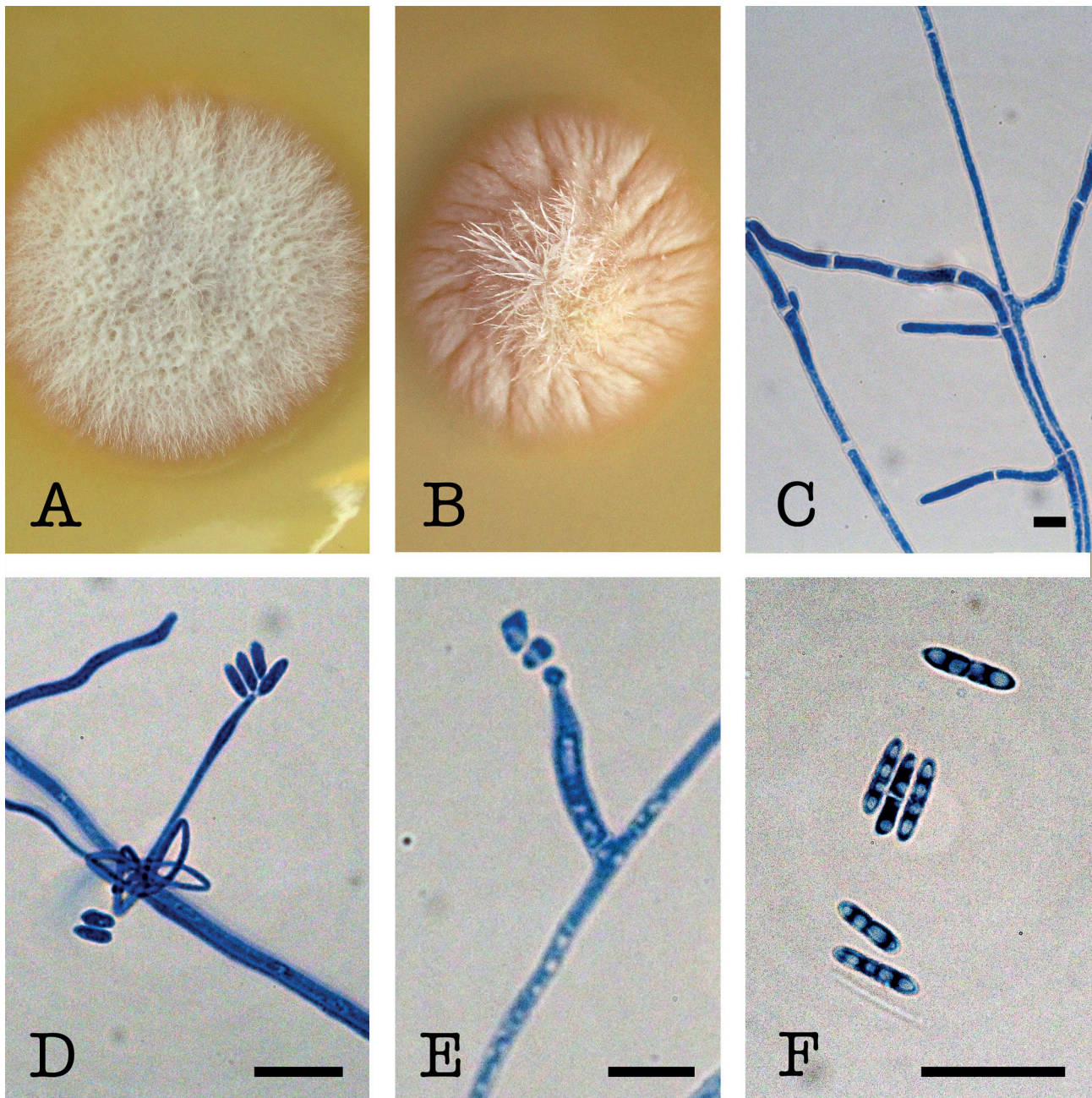


Fig. 25. *Plectosphaerella plurivora* (HM 230). **A, B.** Colonies (front face) on malt extract agar and Sabouraud agar, respectively, after 7 d at 25 °C. **C.** Anastomosing hyphae. **D, E.** Conidiophores, conidiogenous cells and conidia. **F.** Conidia. Bars **C, F** 10 µm, **D** 20 µm, **E** 5 µm.

ITS sequences, which included strains of all *Plectosphaerella* species currently represented in GenBank, the Chilean strain HM 230 grouped with *P. plurivora* CBS 131742 (Fig. 24).

This represents the first record of *P. plurivora* from Chile (Lazo 1996, Mujica et al. 1980, Minter & Peredo López 2006). Considering that this species has been associated with plant diseases in a variety

of hosts in other countries (Carlucci et al. 2012, Giraldo & Crous 2019), its presence in Chile may be of phytopathological relevance. Moreover, this finding may also be of biotechnological interest, since *P. plurivora* has recently been identified as a potential biocontrol agent against phytopathogenic nematodes (Girardi et al. 2023).

Authors: H. Madrid & N. Scott

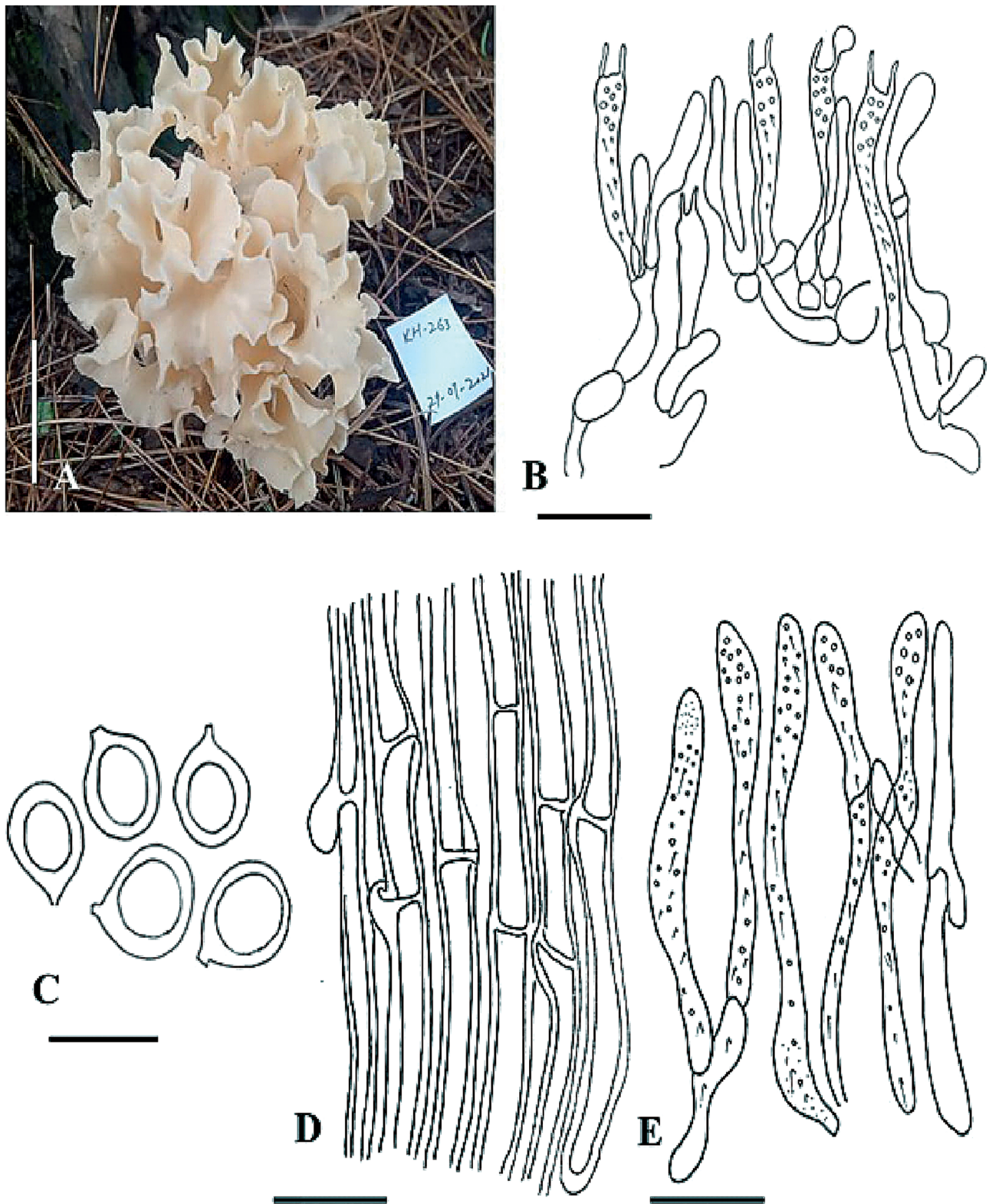


Fig. 26. Macro-micromorphological features of *Sparassis latifolia* collections (OM417067-OM417066). **a.** Basidiomata; **b.** Basidia and basidioles; **c.** Basidiospores; **d.** Hyphae in the trama of flabellum; **e.** Subhymenial hyphae. Bars **a** 30mm, **b-e** 5µm. Drawing Aneeqa Ghafoor.

Basidiomycota, Agaricomycetes, Polyporales, Sparassidaceae

Sparassis latifolia Y.C. Dai & Zheng Wang, in Dai, Wang, Binder & Hibbett, *Mycologia* 98(4): 586 (2006) – Figs. 26, 27

Material examined. – PAKISTAN. Khyber Pakhtunkhwa, Abbottabad district, Ayubia National Park, 2400 m a.s.l., under *Abies pindrow*, 28 August 2020, leg. A.R. Niazi, KH-263 (LAH28820). Ibid., Kuza Gali, 2452 m a.s.l., under

Abies pindrow, 26 July 2021, leg. A.R. Niazi & Aneeqa Ghafoor, SC-1 (LAH26721).

Description. – Basidiomata stipitate, consisting of a central mass from which various loosely arranged flabellae arise. – Flabellae broad, dissected and slightly contorted, soft and creamy white to light yellowish (8/3 Hue 10 YR) when fresh, while pale ochraceous (8/3 Hue 25 YR) to light brown and leathery when dry; solitary, 385–

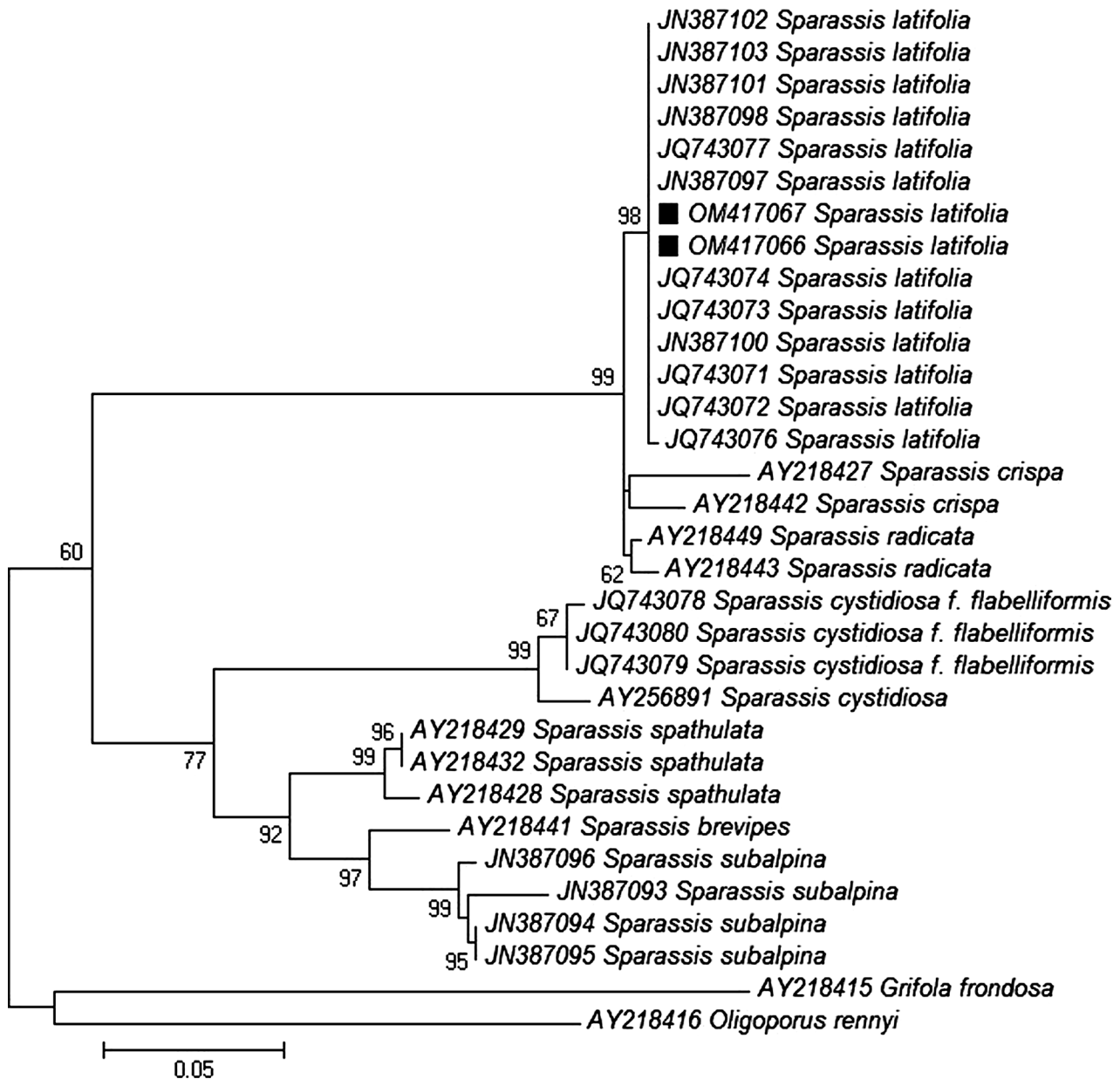


Fig. 27. Phylogeny of the *Sparassis* genus reconstructed from an ITS dataset. Topology result of Maximum Likelihood inference in MEGA 7.0 based on Kimura 2-parameter, with 1000 rapid bootstrap replicates. Bootstrap support values shown adjacent to each node. Sequences representing the Pakistani specimens indicated with a black square. Tree rooted using *Grifola frondosa* and *Oligoporus rennyi*.

392 mm in diam. – Margin smooth, wavy and sometimes tooth-like. – Stipe 18–21 mm in diam. – Basidiospores $(4.4)4.9 - 5.1(5.3) \times (3.0)3.0 - 3.5(3.6) \mu\text{m}$, $\text{avl} \times \text{avw} = 4.9 \times 3.3 \mu\text{m}$, $Q = 1.5$, broadly ellipsoid to sometimes ellipsoid, hyaline. – Basidioles $11.2-36.5 \times 3.4-6.8$, $\text{avl} \times \text{avw} = 21.1 \times 5.0 \mu\text{m}$, narrowly clavate. – Basidia $24.1-34.8 \times 3.7-5.8 \mu\text{m}$, $\text{avl} \times \text{avw} = 30.9 \times 5.0 \mu\text{m}$, clavate to narrowly clavate, 4-spored, with clamp connections. – Subhymenial hyphae $2.9-6.7 \mu\text{m}$, cylindrical, interwoven, thin-walled. – Trama of flabellum a system composed of septate, clamped, thin-walled, interwoven, colorless and hyaline hyphae, $3.6 - 9.0 \mu\text{m}$ in diam. – Cystidia not found. – Odor pleasant. – Taste not observed.

Habitat and distribution. – Solitary, growing in moist temperate coniferous forests under *Abies pindrow* at an altitude of above 2400 m a.s.l., Pakistan. Soil pH 6–8.4. Thus far reported from China, Korea, Japan, Russia and Pakistan (Hanif et al. 2024, this study). In Pakistan, it is known only from the Himalayan moist temperate forests, near *Pinus wallichiana* and *Abies pindrow*.

Notes. *Sparassis latifolia* was first described as a new species in the genus *Sparassis* by Dai et al. (2006). This species is characterized by a broad flabellae (up to 30 cm in diam.), azonate, stipitate; a white to cream hymenophore and small basidiospores ($4.5-5.5 \times 3.5-4.0 \mu\text{m}$) (Zhao et al. 2013). The aligned ITS1-5.8S-ITS2 region comprised 666 sites, of which 341 were conserved and 325 variable; 230 sites were parsimony informative and 95 were singleton variants. In the inferred phylogenetic tree, three in-group clades were formed and the Pakistani collections of *S. latifolia* nested within specimens of the same taxon from China (JN387097, JQ743074, JQ743077, JN387098, JN387101, JN387103, JN387102, JN387100, JQ743072, JQ743076), Russia (JQ743073), and Japan (JQ743071) (Fig. 27) (Zhao et al. 2013). There are only two nucleotide differences between Pakistani and Chinese sequences (JN387097, JQ743074). Macro-micromorphological features also confirm the identification of our collections as representing *Sparassis latifolia*. However, minor variations in the color and size of the basidiomata were observed compared to the holotype description, which may be attributed to differences in specimen maturity and ecological conditions. We had presented *S. latifolia* as a new record from Pakistan in 2022 and submitted its DNA sequences to GenBank and got accession numbers. Our first attempt to publish this finding in a journal was rejected. We then sent it to another journal, where it was under review for two

years. Unfortunately, during this time, Hanif et al. (2024) also reported *S. latifolia* from Pakistan in 2024. Therefore, we are now reporting it again as the second record of this species in Pakistan.

Key to the known species of *Sparassis* from Asia

- 1 Hyphae in the trama of the flabellum without clamp connections *S. subalpina*
 - 1* Hyphae in the trama of the flabellum with abundant clamp connections
 - 2 Flabellae broad (up to 30 cm in diam.), azonate, stipitate; hymenophore white to cream; basidiospores $4.5-5.5 \times 3.5-4.0 \mu\text{m}$ *S. latifolia*
 - 2* Flabellae broad (10–15 cm in diam.), rosette; hymenophore dark greyish brown; basidiospores $7-9 \times 6-7 \mu\text{m}$
 - 3 Cystidia common *S. cystidiosa* f. *cystidiosa*
 - 3* Cystidia absent *S. cystidiosa* f. *flabelliformis*
- Authors: A. Ghafoor & A.R. Niazi

Ascomycota, Eurotiomycetes, Eurotiales, Trichomaceae

Talaromyces fusiformis A.J. Chen, Frisvad & Samson, in Chen, Sun, Houbraken, Frisvad, Yilmaz, Zhou & Samson, Stud. Mycol. 84: 139 (2016) – Figs. 28, 29

Material examined. – INDIA. Kargil, Ladakh, $34^{\circ}33'14''\text{N}$, $76^{\circ}08'06''\text{E}$, from the healthy tissues of the fruit of *Elaeagnus angustifolia*, growing in cold arid land, 01 September 2023, leg. Skarma Nonzom (MCC10205).

Description. – Hyphae smooth, septate, branched, $1.6-2 \mu\text{m}$ in diam. – Conidiophores biverticillate, symmetrically branched; stipe smooth, $20.8-88 \times 2.4-3.2 \mu\text{m}$. – Metulae appressed, hyaline, 3–4 per conidiophore, $9.6-16 \times 2.4-3.2 \mu\text{m}$. – Phialides acerose, 3–4 per metula, $11.2-12.8 \times 1.6-2.4 \mu\text{m}$. – Conidia ellipsoidal to fusiform, hyaline, $1.6-3.2 \times 1.6-2.4 \mu\text{m}$. – Sexual morph not observed.

Culture characteristics ($28 \pm 2^{\circ}\text{C}$, 7 days). – Colonies on PDA reaching 30 mm in diam.; growth moderately deep, margin entire; surface yellowish at the centre, whitish at the periphery, turning green after sporulation; reverse yellowish brown; no soluble pigments produced; exudates golden yellow. – Colonies on CYA reaching 28 mm in diam.; growth moderately deep, entire margin; surface light yellowish at the centre, becoming green after sporulation, later turning greenish yellow; texture slightly floccose; reverse orange-yellow with white periphery; exudates light yellow; no soluble pigments produced.

Habitat and distribution. – Endophytic in the fruit of *Elaeagnus angustifolia*. So far reported from China, Malaysia, Korea and India.

Notes. – The nrDNA ITS sequence of our isolate ELS-F4 showed 99.48 % similarity to the type material of *Talaromyces fusiformis* (NR169911) after BLAST searches in the GenBank database. Based on both morphological and molecular analysis, the identity of the current isolate (ELS-F4) is confirmed as *T. fusiformis*.

Talaromyces fusiformis has previously been reported from only four countries: China, Malaysia, Korea and India. It has been isolated from various habitats such as air, soil, sand, stool, and the human body (Chen et al. 2016, Singh et al. 2021, Xu et al. 2021, Yee et al. 2022, Cui et al. 2022, Nguyen & Lee 2023, Li et al. 2025). To date, no reports have docu-

mented its occurrence as a plant endophyte from India. The present isolate therefore represents the first record of *T. fusiformis* as an endophyte from a high-altitude medicinal plant, with a colonization frequency of 6.6 %.

Currently, approximately 268 species of *Talaromyces* are recognized according to Index Fungorum (www.indexfungorum.org; accessed on 10th October 2024), of which 84 species belong to section *Talaromyces* (Wang & Zhuang, 2022). To the best of our knowledge, *T. fusiformis* has a limited known global distribution and has been rarely reported since its original description in 2016 (Chen et al. 2016). The present isolate adds to the growing number of recent records and is of particular interest due to its ability to colonize a plant host as an endophyte in an extreme, high-altitude habitat. A

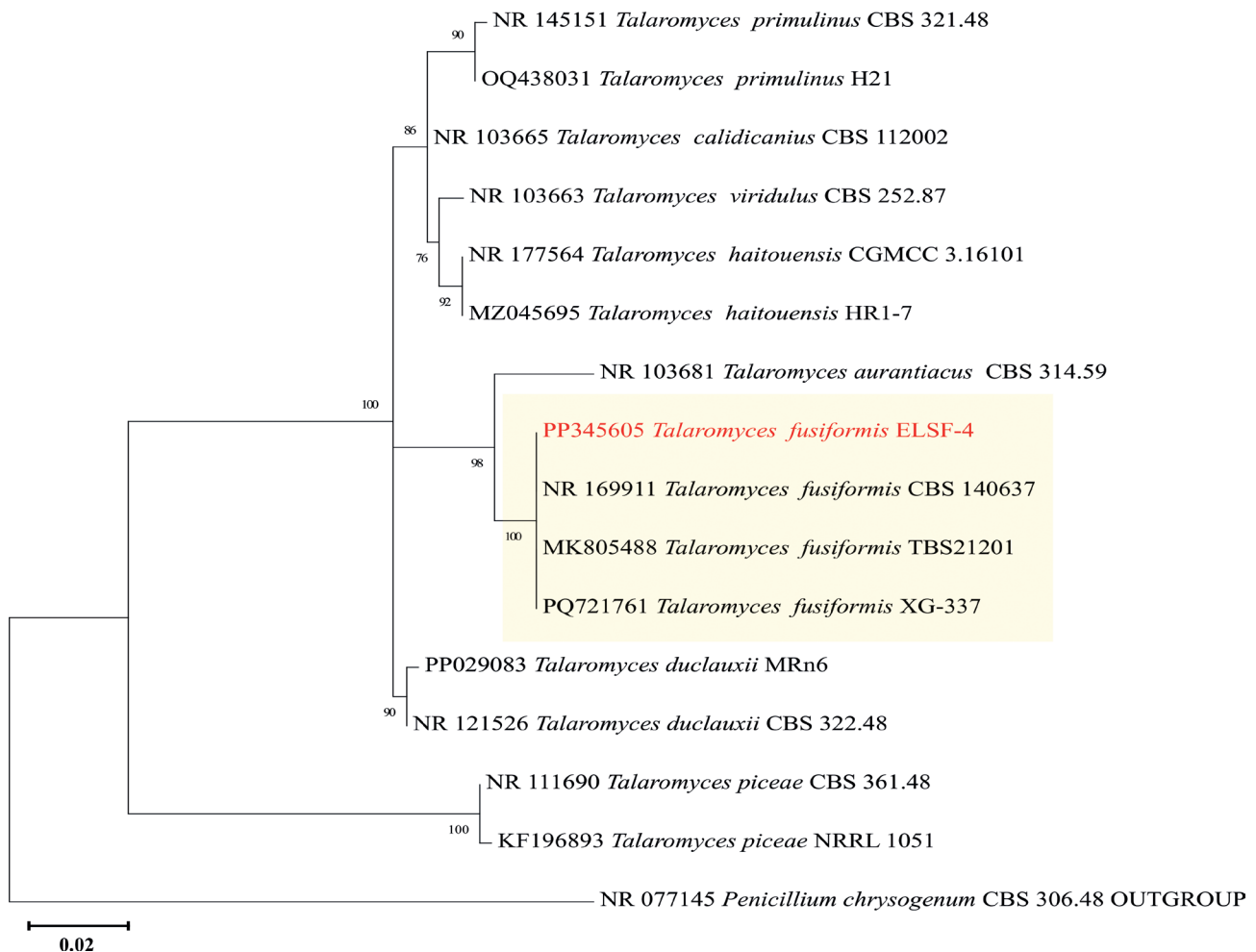


Fig. 28. Phylogenetic relationship of *Talaromyces fusiformis* inferred from Maximum Likelihood analysis of ITS sequences using Tamura–Nei model. Authentic bootstrap values (>50) shown on the left side of the branches at each node. Isolate from our study highlighted in red. Scale bar indicating the number of substitutions per site.

Tab. 4. Distribution pattern and characteristic features of *Talaromyces fusiformis*.

S. No.	Source	Morphology				Country	Reference
		Cultural characters		Microscopic features			
		Colony	Exudates	Branching	Penicillus		
1	Air	Surface-light yellow and reverse-orange with yellowish brown margin	light yellow exudates	Biverticillate	Stipe 42-70 × 2.5-4 µm, Metulae 12-15 × 2.5-4 µm, Phialides 11-15 × 2-3 µm, Conidia 3-4 × 2-3 µm	China	Chen et al. (2016)
2.	Dermatophytes (human)	NM	NM	NM	NM	India	Singh et al. (2021)
3.	Stool	NM	NM	NM	NM	China	Xu et al. (2021)
4.	Sand	Surface Yellowish in color and reverse- orange in color	Absent	Biverticillate	Conidia- 2.1-3.8 µm	Malaysia	Yee et al. (2022)
5.	Gut (of <i>Crocothemis servilia</i> , dragonfly)	NM	NM	NM	NM	China	Cui et al. (2022)
6.	Soil	Surface-greyish green and reverse-yellowish brown with pale yellow to white margins	Absent	Biverticillate	Stipe 76-142 × 2.5-3.0 µm, Metulae 9-14 × 2.5-3.0 µm, Phialides 8.5-13.5 × 2-3 µm, conidia 2.5-4.0 × 2.0-2.5µm	Korea	Nguyen & Lee (2023)
7.	Endophyte (host <i>Hypocoum leptocarpum</i>)	NM	NM	NM	NM	China	Li et al. (2025)
8.	Endophyte (present isolate)	Surface- greenish yellow and reverse-orange-yellow with white margins	Light yellow exudates formed	Biverticillate	Stipe 20.8-88 × 2.4-3.2 µm, Metulae 9.6-16 × 2.4-3.2 µm, Phialides 11.2-12.8 × 1.6-2.4 µm, Conidia 1.6-3.2 × 1.6-2.4 µm	India	This study

NM – not mentioned

comparative overview of the species reported from different habitats is provided in Tab. 4. Our study further demonstrates the ecological versatility of *T. fusiformis*. Such adaptability may be linked to its ability to produce diverse metabolites, potentially supporting its survival across varied and often harsh environments (Ameen et al. 2024). To date, the ecological role of *T. fusiformis* when associated

with plant hosts remains poorly understood; however, its occurrence in a high-altitude medicinal plant may suggest a potentially beneficial interaction, possibly aiding the host in coping with oligotrophic conditions and environmental stress. This hypothesis needs to be further tested in future studies.

Authors: S. Digra & S. Nonzom

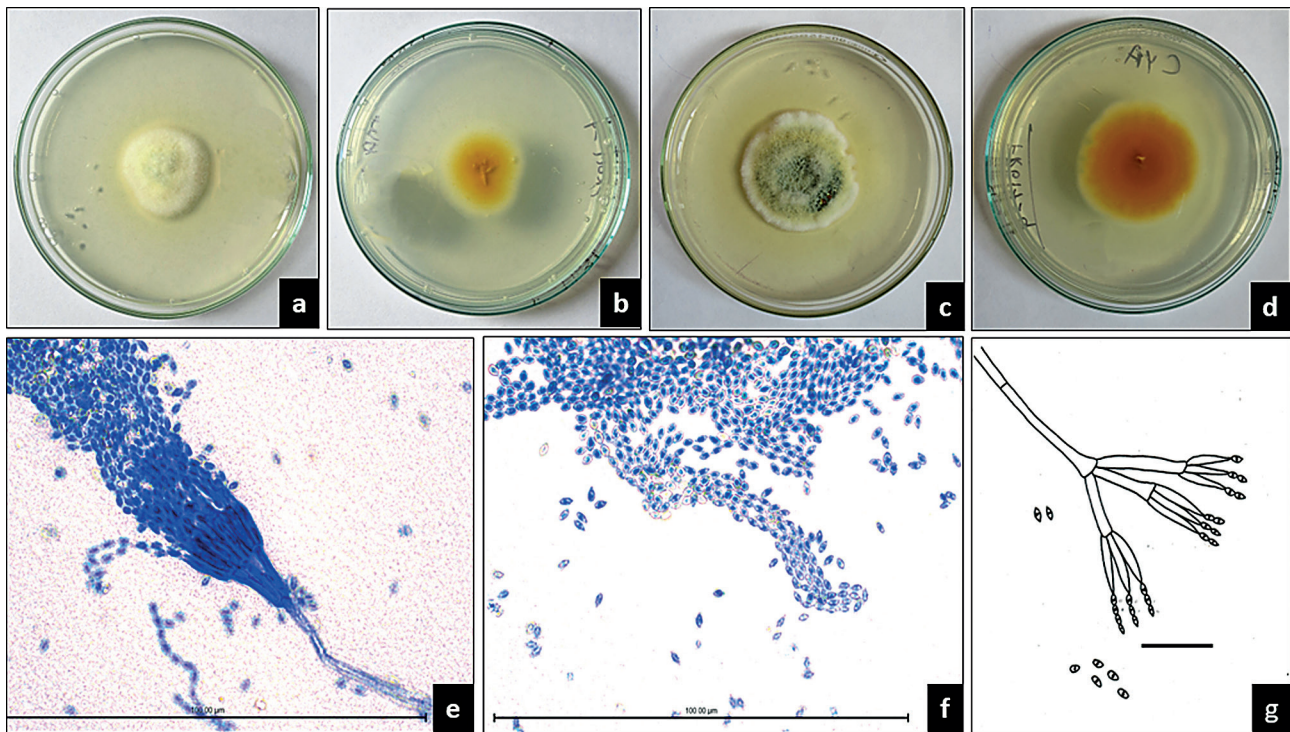


Fig. 29. *Talaromyces fusiformis* (ELS-F4). **a-b.** Colonies on PDA (front; reverse) **c-d.** Colony on CYA (front; reverse) **e.** Stipe with metulae, phialides and conidia **f.** Conidia **g.** Line drawings of stipe, metulae, phialides and conidia. Bars **e-f** 100 μm , **g** 10 μm . Drawings by Shivani Digra.

Ascomycota, Pezizomycetes, Pezizales, Pyrenomataceae

Trichaleurina javanica (Rehm) M. Carbone, Agnello & P. Alvarado, *Ascomycete.org* 5(1): 6 (2013) – Figs. 30–33

Material examined. – NEPAL. Koshi Province, Morang District, Raja-Rani community forest, 26°44'54.64"N, 87°28'54.31"E; on fallen dead branches of *Shorea robusta*, 470 m a.s.l., 18 June 2023, leg. S. Rai, D.B. Rai & B. Gautam, KATH (KATH166569).

Basionym. – *Sarcosoma javanicum* Rehm, *Hedwigia* 32: 226 (1893)

Description. – Apothecia 2.8–4.1 cm in width and 2.5–5.0 cm in height, resembling a drum with light brown at the top surface, leathery texture, no odor, inner tissue like jelly, outer surface ranging in color from blackish-brown to grey-brown, cylindrical or tapering downward, sparse hair covering along the cup's rim, cavity at the base containing a colorless, and odorless jelly fluid. – Ascospores (19.9)21–29(30.6) $\times$ (11)11.3–13(13.5) μm , on average $28.5 \times 12.3 \mu\text{m}$, $Q = (1.56–2.57)$, $Q_{av} = 2.08$, $N = 20$, elliptical, elongated, cylindrical, with distinct oil droplets. – Paraphyses filamentous, 9.9–11.6 μm in diam., extending beyond the asci. –

Hypothecium 3.33–5.3 μm in diam., gelatinized hyphae. – Excipulum erect, septate, dark septa, wall layer appearing dark.

Habitat and distribution. – Apothecia found either solitary or in small clusters (3–5 ascomycarpes) on fallen dead branches of *Shorea robusta*. Thus far recorded from China, Malaysia, India, Indonesia, Philippines, Seychelles, Taiwan, Singapore, Thailand, Australia, Madagascar and Nepal (this study).

Notes. – The collected specimen from Nepal closely resembles specimens of *T. javanica* previously documented from India (Patel et al. 2019, Hermawan et al. 2020, Kumar et al. 2021), with only minor differences observed in its macroscopic and microscopic features. The apothecia were found both solitary and in clusters, cup-shaped and having a leathery texture. The inner tissue of the apothecia was gelatinous and smoothly rubbery in texture, while the outer surface varied in color from blackish brown to grey-brown. The presence of a hairy outer surface giving the apothecia a velvety appearance is a distinguishing characteristic of the genus *Trichaleurina* (Carbone et al. 2013b). Similar descriptions of *T. javanica* apothecia were observed



Fig. 30. Digitized image of the herbarium specimen of *Trichaleurina javanica* stored in the database of the National Herbarium and Plant Laboratories (KATH), Nepal. Barcode number KATH166569.

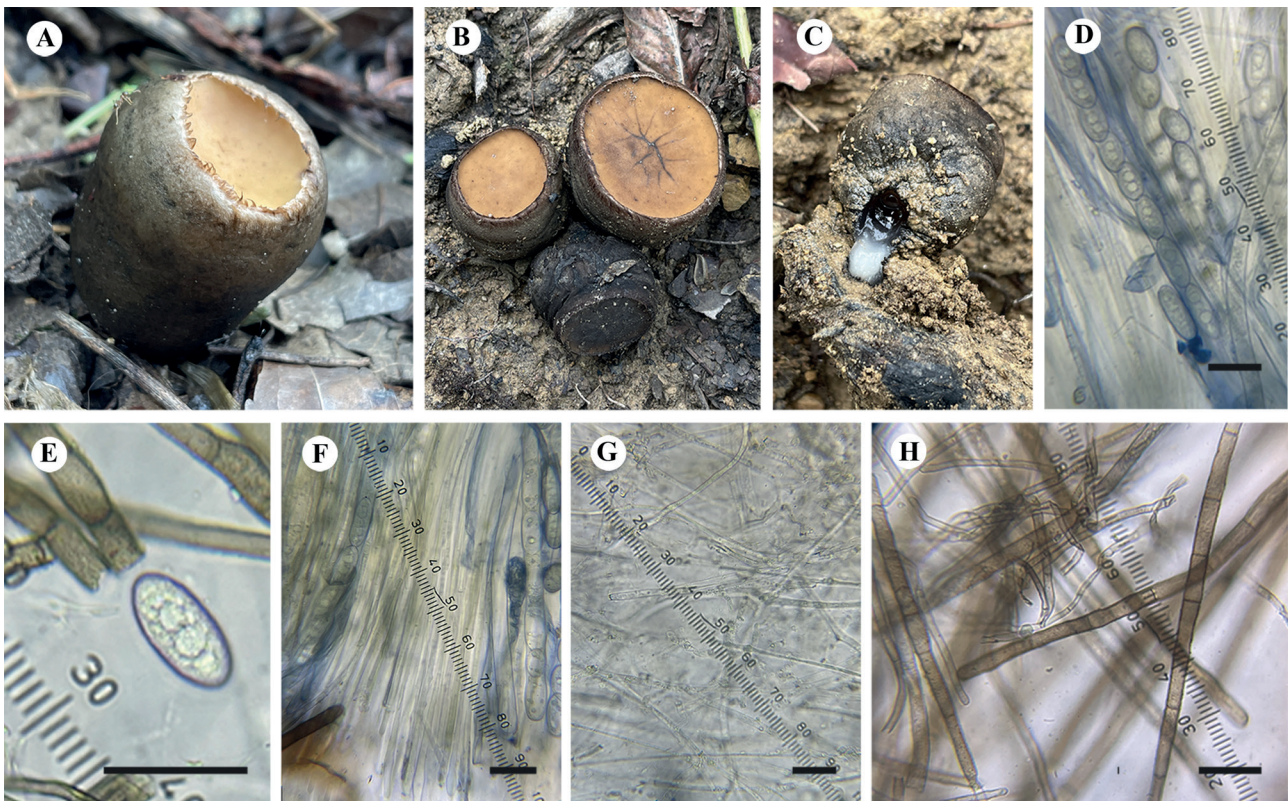


Fig. 31. *Trichaleurina javanica*. **A.** Habit (young apothecium). **B.** Mature apothecium on the branch of *Shorea robusta*. **C.** Fluid in cavity at the base of the apothecium. **D.** Ascus bearing ascospore. **E.** Enlarged single ascospore in water. **F.** Paraphysis with irregularity in its wall layer. **G.** Gelatinized hyphae of the hypothecium. **H.** Excipulum containing septate hyphae. Bars D–E 33.3 µm.

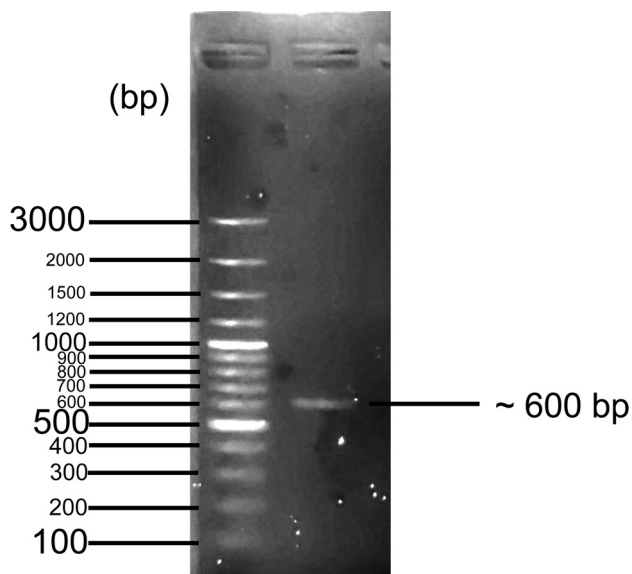


Fig. 32. Gel electrophoresis of PCR product showing a clear, single band at approximately 600 bp in the sample lanes. GeneRuler 100 bp Plus DNA Ladder (Thermo Scientific) used as a molecular size reference.

by previous studies (Kumar et al. 2021). Moreover, Patel et al. (2019) recorded apothecial dimensions of 2.5–8 cm in width and 2–6 cm in height, while Kumar et al. (2021) reported measurements ranging from 5.2–7.8 cm in width and 5.5–6.5 cm in height. These values are consistent with those recorded in the present study.

The ascospore dimensions of *T. javanica* observed in this study are smaller than those reported for *T. tenuispora* (Hermawan et al. 2020), but closely match the measurements previously described for *T. javanica* (Patel et al. 2019). In our specimens, ascospores were slender, slightly curved, and heterogeneous in shape and size. The upper spores were wider, shorter, and slightly rounded or spherical, whereas the lower spores were longer, slender or elliptical. This observation aligns with the descriptions of *T. javanica* in the literature, which also emphasize the heterogeneity in ascospore morphology, with upper spores being shorter and wider than the longer, slender lower spores (Carbone et al. 2013a, Carbone et al. 2013b). Hence, based on our morpho-

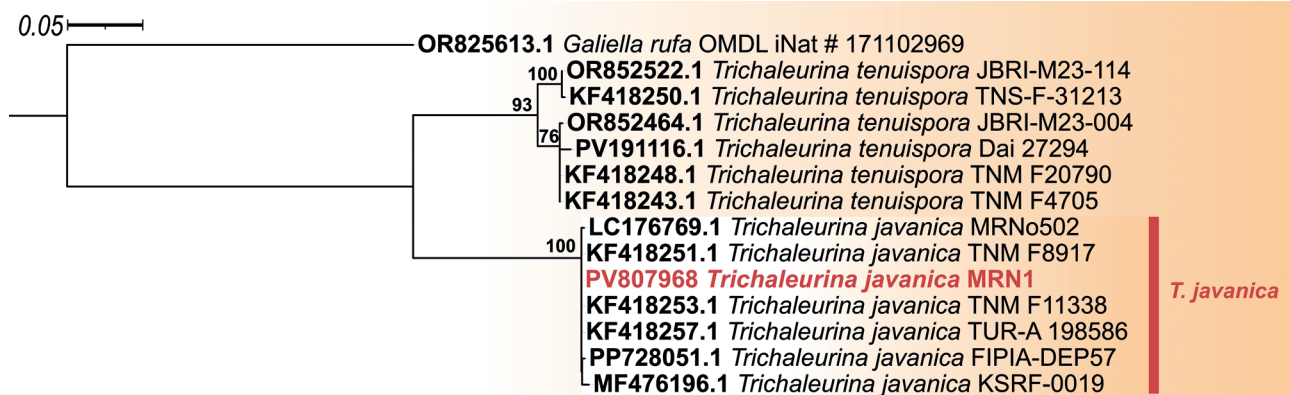


Fig. 33. Maximum likelihood phylogeny of selected *Trichaleurina* species reconstructed from an ITS dataset using *Galiella rufa* (OR825613.1) as outgroup. Tree topology with the highest log likelihood ($-\ln L = -1760.884$) is shown, as inferred with IQ-TREE v2.2.0. For each node, ML bootstrap support values $>70\%$ are indicated. The sequence generated from our sample is highlighted in bold red. Scale bar indicates the expected number of substitutions per site.

logical examination, we conclude that the specimens described in the present study represent *T. javanica*, a member of the class *Pezizomycetes* (Ascomycota).

PCR amplification yielded an amplicon of approximately 600 base pairs. The final sequence length was determined to be 583 base pairs (Fig. 32). BLAST analysis revealed a 100 % sequence similarity between our generated ITS sequence and *T. javanica* TNM F11338 from Taiwan (GenBank accession no. KF418253.1), with 100 % query coverage (Fig. 33). In our phylogenetic analysis, our specimen from Nepal clustered in a well-supported clade comprising six sequences of *T. javanica* (GenBank accession no. LC176769.1, KF418251.1, KF418253.1, KF418257.1, PP728051.1, and MF476196.1), with a bootstrap value of 100 %. Both morphology and molecular analyses confirm the identification of our specimens from Nepal as *T. javanica*. Furthermore, our phylogenetic analysis highlights the genetic integrity of this species across different geographical regions. These results open new opportunities for more research on the evolutionary history of *T. javanica* and its interaction with the environment.

Phenolic compounds are an important group of secondary metabolites in plants, known for their role in protection against oxidative stress (Kumar & Goel 2019). Mushrooms have also been shown to contain diverse phenolic compounds with potent radical-scavenging properties (Janciauskiene 2020). The presence of phenols and flavonoids in mushrooms suggests they are a potential source of bioactive compounds with anti-inflammatory, anticancer, immunomodulatory, and other pharmacologically relevant properties (Lin et al. 2016). For compari-

son, methanolic extracts in different *Pleurotus* species have shown total phenolic contents ranging from 22.67 to 36.03 mg/g and flavonoid contents from 1.19 to 2.94 $\mu\text{g/g}$ (Babu et al. 2014), while *Schizophyllum commune* was reported to have 143.21 mg GAE/100g and 91.55 mg QAE/100g (Dawadi et al. 2023). Similarly, several wild mushrooms from Nepal—including *Laetiporus sulphureus*, *Polypore* sp., *Trametes elegans*, *Trichaptum biforme*, *Lenzites betulina*, *Stereum complicatum*, *Trametes versicolor*, *Trichaptum subchartaceum*, and *Ganoderma Lucidium*—showed total phenolic and flavonoid contents ranging from 3.95 to 10.05 mg/ml and 2.14 to 11.36 mg/ml, respectively (Upadhyaya et al. 2017). In our study, total phenolic and flavonoid contents of *T. javanica* were found to be 498.7 ± 0.01 mg GAE/100g and 98.60 ± 0.02 mg QAE/100g, respectively. The IC₅₀ value was 2821 ± 0.02 $\mu\text{g/ml}$, thus indicating low antioxidant activity. According to Phongpaichit et al. (2007), IC₅₀ values between 10–50 $\mu\text{g/mL}$ indicate high antioxidant activities, whereas values greater than 100 $\mu\text{g/ml}$ indicate low antioxidant properties.

Authors: S. Rai, S. Chaudhary, A. Mallik, R. Ojha, M. Shyaula, M.A. Siddiqui, D. Khadka, R.C. Poudel, L.R. Bhatt

Acknowledgements

The editors are thankful for 15 reviewers whose relevant and detailed comments greatly improved the contributions from FUSE 11. The *Dothidea* study was carried out as part of the state assignment under the thematic plan of the Komarov Botanical Institute of the Russian Academy of Sciences (theme No. 12401310-0829-3), with financial support from the Ministry of Education and Science of the Russian Federation

(Agreement No. 075-15-2021-1056, dated September 28, 2021). The research was conducted using the equipment of the Core Facilities Center “Cell and Molecular Technologies in Plant Science” at the Komarov Botanical Institute RAS (St.-Petersburg, Russia). The *Ganoderma* study was funded by Princess Nourah bint Abdulrahman University Researchers Supporting Project (No. PNURSP2025R317), Princess Nourah bint Abdulrahman University, Riyadh, Saudi Arabia. The authors of the *Lepiota* study express their gratitude to Dr. Shaun Pennycook (Mycobibliophile/Research Associate, Manaaki Whenua-Landcare Research, Private Bag 92170, Auckland 1072, New Zealand) for his valuable nomenclatural suggestions. Special thanks are also extended to Mr. Usman Farooqi for his financial support in carrying out this research. The authors of the *Leuconocybe* study thank the Ontario Student Assistance Program (OSAP) for covering the cost of sequencing for this project. The studies of H.Š. were enabled by support provided to the Moravian Museum by the Ministry of Culture of Czechia as part of its long-term conceptual development program for research institutions (DKRVO, ref. MK000094862). The authors of the *Paxillus* study thank Mr. Ghulam Hussain, M. Phil Scholar (Department of Animal Breeding and Genetics), University of Veterinary and Animal Sciences, Lahore, Pakistan, for his assistance with field visits and sample collection. The authors of the *Sparassis* study are highly thankful to Dr. Muhammad Ali, Institute of Botany, University of the Punjab, Lahore, Pakistan, for his valuable pre-submission comments and suggestions to improve the manuscript. The authors of the *Talaromyces* study are thankful to the Head of the Department of Botany, University of Jammu for providing lab facilities. The first author is thankful to the University Grants Commission for providing financial assistance in the form of a Senior Research Fellowship (SRF). The authors of the *Trichaleurina* study thank Prof. Dr. Shiva Kumar Rai (Head of Department, Degree Campus, Tribhuvan University, Nepal) for providing lab facilities and for valuable input in reviewing and enhancing the manuscript. They also like to thank Mr. Desh Bhakta Rai for his support during fieldwork. J. Cazabonne acknowledges support from the Fonds de Recherche du Québec – Nature et technologies through a B2X doctoral research fellowship (<https://doi.org/10.69777/347942>, n°347942). D. Haelewaters is supported by the Czech Academy of Sciences (Lumina Quaeruntur Fellowship LQ200962501).

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(Manuscript accepted 18 August 2025; Corresponding Editors: D. Haelewaters and J. Cazabonne)

