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RESEARCH ARTICLE

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Descriptions of 19 Unrecorded Species Belonging to *Sordariomycetes* in Korea

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ABSTRACT

A survey of fungal diversity in soil and freshwater habitats in Korea isolated several species of the class *Sordariomycetes*. Morphological characteristics and multigene phylogenetic analyses showed that these species represented new records for Korea. Herein, we report the descriptions, illustrations, and molecular phylogeny of 19 species previously undescribed in Korea, including *Achaetomiella virescens*, *Arxotrichum gangligerum*, *Caespitomonium euphorbiae*, *Comoclathris typhicola*, *Gamsia aggregata*, *Luteonectria nematophila*, *Paramyrothecium sinense*, *Parasarocladium debruynii*, *Pleurocordyceps agarica*, *Pyrenochaetopsis sinensis*, *Scedosporium boydii*, *Scedosporium dehoogii*, *Scedosporium minutisporum*, *Striatibotrys rhabdosporus*, *Trichocladium crispatum*, *Trichoderma azevedoi*, *Trichoderma longifialidicum*, *Xepicula leucotricha*, and *Xylomelasma sordida*.

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1. Introduction

Ascomycota, the largest phylum of fungi, contains three subphyla, namely *Saccharomycotina* (budding yeasts), *Pezizomycotina* (filamentous fungi), and *Taphrinomycotina* (fission yeasts), and 92,725 described species [1]. *Sordariomycetes* is an important class of ascomycetes characterized by non-lichenized, perithecial ascomata, and inoperculate unitunicate or non-fissitunicate asci; this class has a variety of growth forms and can colonize a wide range of hosts [2,3].

Recently, classification of *Sordariomycetes* has changed considerably owing to the rapid increase in the availability of fungal deoxyribonucleic acid (DNA) sequence data [3–5]. Consequently, the species and numbers of *Sordariomycetes* are being continually updated [6]. Currently, *Sordariomycetes* comprises seven subclasses, 46 orders, and 172 families [6]. Members of *Sordariomycetes* have a cosmopolitan distribution and accommodate mostly terrestrial taxa but have also been reported in freshwater habitats [2,7,8].

Species of *Sordariomycetes* are considered among the most chemically inventive fungi and produce a wide array of secondary metabolites with diverse properties [9,10]. Therefore, *Sordariomycetes* spp. may impact humans positively (e.g., enzyme production, anticancer, antioxidant, antibacterial, or antimalarial activities) or negatively (e.g., mycotoxin production, human pathogens) [9,10]. Other examples of positive contributions include the production of sordarin-type diterpene glycosides, which selectively inhibit fungal protein synthesis through interaction with the elongation factor 2 [11], and the production of immunosuppressant drug cyclosporins by *Tolypocladium inflatum* [12]. In addition, some species, such as *Trichoderma* are considered economically important as biocontrol agents [13]. In contrast, harmful trichothecene mycotoxins are produced by members of *Sordariomycetes*, including genera *Fusarium*, *Myrothecium*, *Spicellum*, *Stachybotrys*, *Cephalosporium*, *Trichoderma*, and *Trichothecium* [14]; other toxic alkaloids, including ergot, are produced by the genera *Claviceps* and *Epichloë* [15,16].

Although many undescribed *Sordariomycetes* spp. have recently been reported in Korea [17–27], there are still a large number of *Sordariomycetes* spp. that have not been found and described in Korea.

This article aims to contribute to the knowledge about the diversity of members of *Sordariomycetes* in Korea through the description and illustration of new records and interesting taxa. Herein, we report 19 species belonging to class *Sordariomycetes* based on phylogenetic analyses combined with morphological

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characteristics that have not previously been documented in Korea.

2. Materials and methods

2.1. Sample collection, fungal isolation, and morphological studies

Soil and freshwater samples were collected from different areas in Korea. The samples were taken to the laboratory using zip-lock plastic bags within an icebox and kept in cold storage at 4 °C until isolation. The procedures used to isolate the fungal strains from the soil and freshwater samples were according to the methods of Nguyen et al. [21,22,28]. Potato dextrose agar (PDA) (Difco™, Becton, Dickinson and Company, Franklin Lake, NJ) and malt extract agar (MEA) (20 g of malt extract and 20 g of agar in 1 L of deionized water), with antibiotics (streptomycin with the final concentration of 50 ppm) were used. The strains isolated were purified and sub-cultured on PDA. All the pure isolates were maintained in PDA slant tubes and 20% glycerol at −80 °C at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, South Korea. The strains were also deposited at the Culture Collection of the Nakdonggang National Institute of Biological Resources (NNIBR), Sangju, South Korea, and the Collection of the National Institute of Biological Resources (NIBR), Incheon, South Korea, and the Collection of the Honam National Institute (HNIBR), Mokpo, South Korea.

For morphological identification, the fungal strains isolated in this study were inoculated onto PDA, MEA, corn meal agar (CMA) (Difco™, Becton, Dickinson and Company, Franklin Lake, NJ), oatmeal agar (OA) (30 g of oatmeal and 20 g of agar in 1 L of deionized water), and synthetic low nutrient agar (SNA) (1 g KH_2PO_4, 1 g KNO_3, 0.5 g $MgSO_4{\cdot}7H_2O$, 0.5 g KCl, 0.2 g glucose, 0.2 g sucrose, and 20 g agar in 1 L of deionized water). Mycelial fragments were removed from the cultures, and then placed on microscope slides in the presence of lactic acid (60% v/v) for morphological examination. Photomicrographs of the fungal structures were captured using an Olympus BX53 compound microscope (Tokyo, Japan), and images were recorded with a DP74 Olympus digital camera.

2.2. Extraction of DNA, polymerase chain reaction, purification, and sequencing

Fungal isolates were grown on PDA for seven days (d) at 25 °C and fresh mycelium was scraped from the living culture and transferred to 1.5 mL microcentrifuge tubes. The total genomic DNA was extracted using a Solg™ genomic DNA preparation kit (SolGent Co. Ltd., Daejeon, South Korea) according to the manufacturer's protocol. The DNA template amplifications were performed by polymerase chain reaction (PCR) using primer pairs, ITS5/ITS4 [29], V9G/LS266 [30,31] for the internal transcribed spacer (ITS) region, LR0R/LR5 [32] for the large subunit (LSU), Bt2a/Bt2b [33], T1/T22 [34], T10/T22 [35] for β-tubulin gene (*BenA*), RPB2-5F and RPB2-7cR [36], RPB2-5F2/RPB2AM-7R [37,38] for RNA polymerase II second largest subunit gene (*RPB2*), and EF1-983/EF1-2218 [39] for elongation factor 1-alpha gene (*tef*). The PCR amplifications were performed as described by Nguyen et al. [22,40,41]. Successful PCR products were sent to Macrogen Inc. (Daejeon, South Korea) for sequencing.

2.3. Sequence alignment and phylogenetic analyses

Obtained sequences were subjected to the Basic Local Alignment Search Tool (BLAST) search in GenBank (National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), Bethesda, MD; https://blast.ncbi.nlm.nih.gov/Blast.cgi). Sequences of each locus were aligned using Multiple Alignment using Fast Fourier Transform (MAFFT) v. 7 software (http://mafft.cbrc.jp/alignment/server) with default parameters [42], which were then confirmed manually using Molecular Evolutionary Genetics Analysis (MEGA) v. 7 [43]. Phylogenetic reconstructions by maximum-likelihood (ML) were carried out using Randomized Axelerated Maximum Likelihood for high-performance computing (RAxML-HPC2) on XSEDE on the online CIPRES Portal (https://www.phylo.org/portal2) with a default general time reversible (GTR) substitution matrix and 1000 rapid bootstraps. The trees were visualized and edited in FigTree v.1.4.3 [44].

3. Results

3.1. Phylogenetic analysis

A combined ITS, *BenA* and *RPB2* sequences analysis indicates that the strains CNUFC CHS2-10, CNUFC NHW16, and CNUFC SN35-44 isolated in this study clustered with type species of *Achaetomiella virescens*, *Arxotrichum gangligerum*, and *Trichocladium crispatum*, respectively, with strong statistical support (ML = 100%) (Figure 1). Combined phylogenetic analyses of ITS and LSU rDNA placed the strains CNUFC SN35-81, CNUFC 120603, and CNUFC

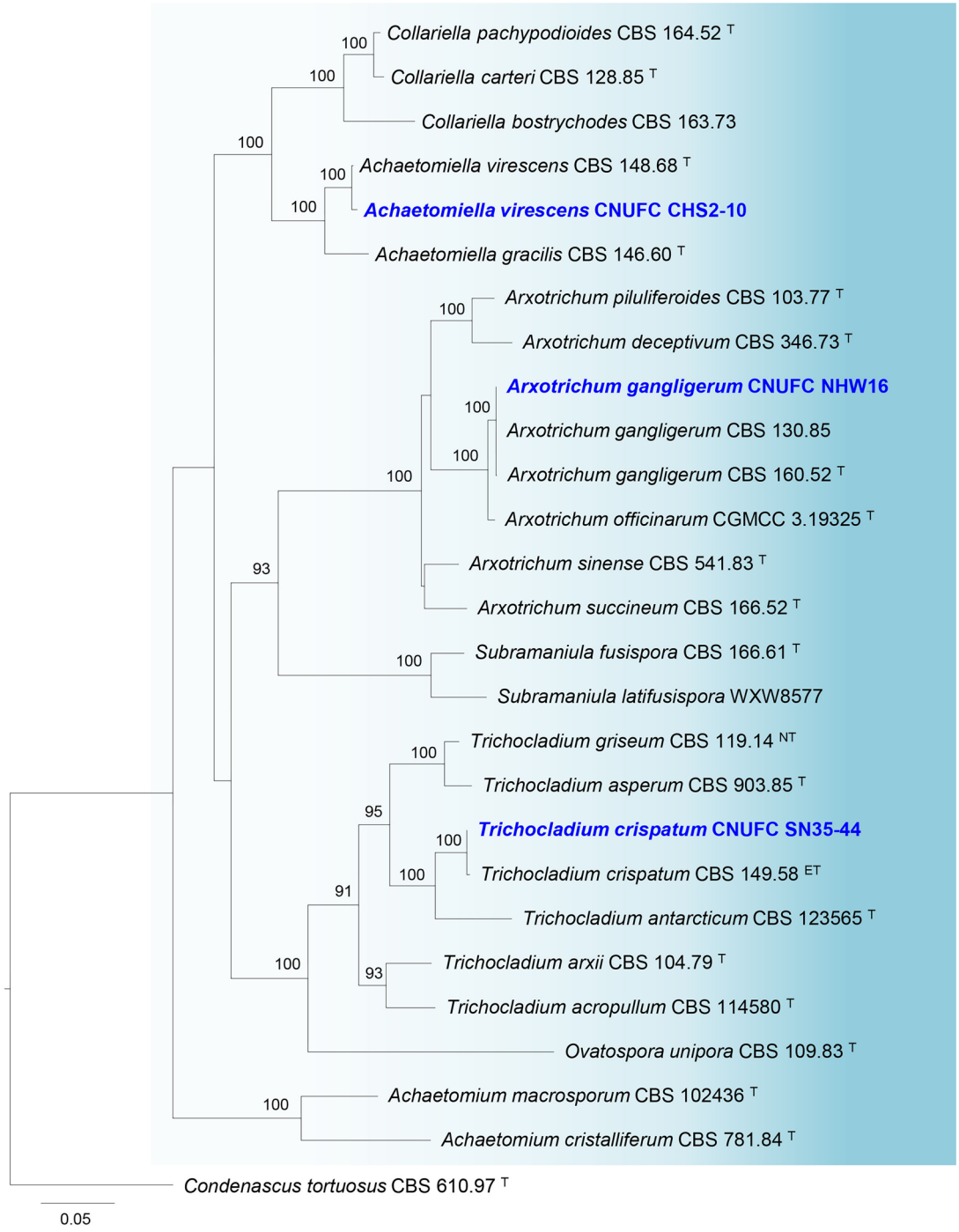

Figure 1. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS, *BenA* and *RPB2* sequence data for *Achaetomiella virescens* CNUFC CHS2-10, *Arxotrichum gangligerum* CNUFC NHW16, *Trichocladium crispatum* CNUFC SN35-44, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Condenascus tortuosus* CBS 610.97 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type, ex-epitype, and ex-neotype strains are indicated by superscript T, ET, and NT, respectively.

IS159 with the type species *Caespitomonium euphorbiae*, *Comoclathris typhicola*, and *Gamsia aggregata*, respectively (Figures 2–4). Strain CNUFC ROS20 clustered with the type strain and other strains of *Luteonectria nematophila* (Figure 5). Strain CNUFC 110505 and CNUFC AMS8 were grouped with the type strain of *Paramyrothecium sinense* and *Parasarocladium debruynii*, respectively, with 100% ML support (Figures 6 and 7). Strains CNUFC 032307 and CNUFC SLJ4 clustered with strains of *Pleurocordyceps agarica* (YHCPA1303, YHHPA1305, and YHCPA1305) and the type strain of *Pyrenochaetopsis sinensis*, respectively (Figures 8 and 9). Strains CNUFC FW8-2, CNUFC JF214-5, and CNUFC GCW112 clustered with the type species of *Scedosporium boydii*, *S. dehoogii*, and *S. minutisporum*, respectively (Figure 10). Strain CNUFC UCIS4 was grouped with the type strain *Striatibotrys*

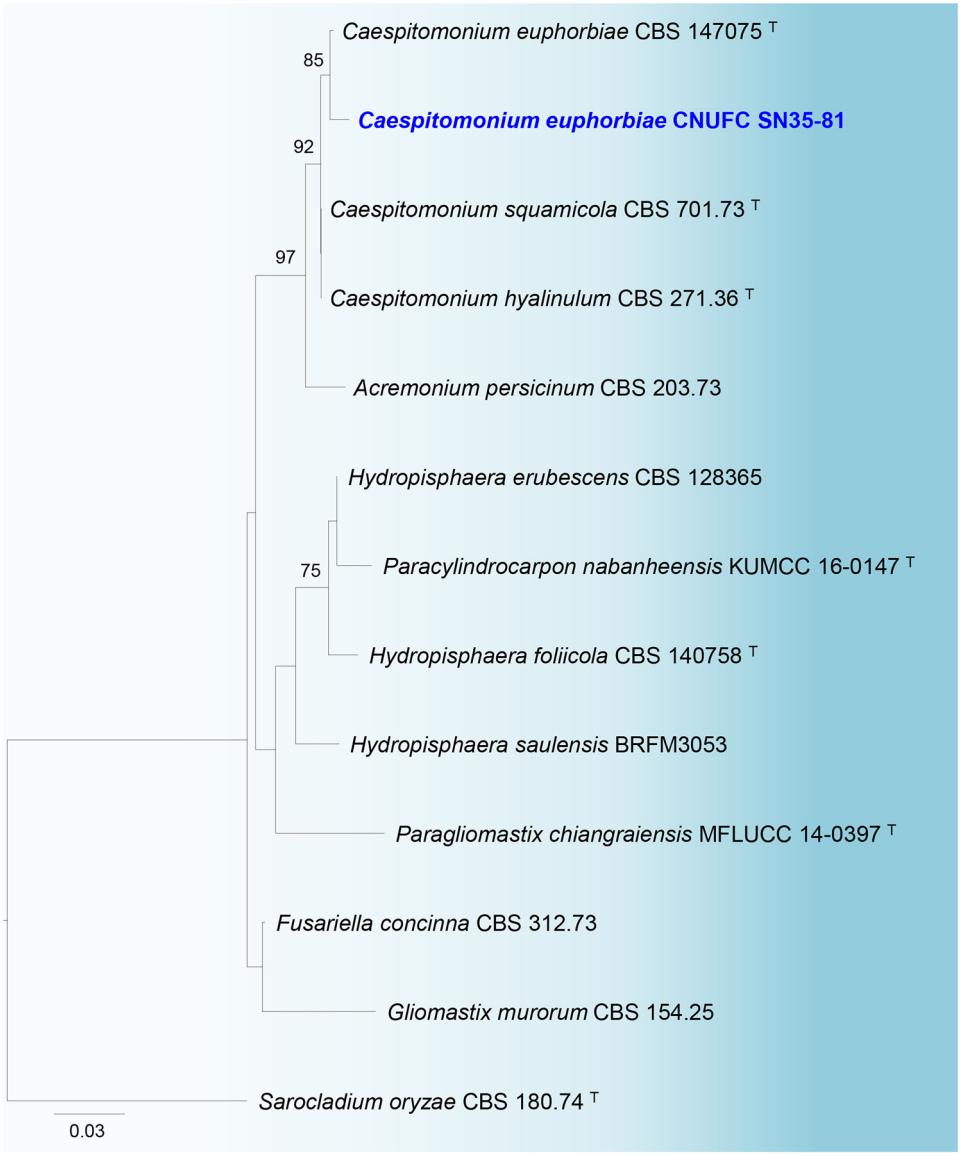

Figure 2. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Caespitomonium euphorbiae* CNUFC SN35-81, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Sarocladium oryzae* CBS 180.74 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

rhabdosporus CBS 528.80 with 100% ML support (Figure 11). Strains CNUFC FH2-1 and CNUFC NYS2-12 clustered with the type strains of *Trichoderma azevedoi* and *T. longifialidicum*, respectively (Figure 12). Strains CNUFC JDCW16-1 and CNUFC JAS1-39 were grouped with strains of *Xepicula leucotricha* and *Xylomelasma sordida*, respectively (Figures 13 and 14).

3.2. Taxonomy

Achaetomiella virescens Arx, The genera of fungi sporulating in pure culture: 247. 1970. MycoBank MB 308086 (Figure 15).

Description – Hyphae hyaline, aseptate, 3.5–6.0 µm wide. Ascomata globose or ovoid, brown to black, (95–)122–189.5 × (85.5–)96–178 µm. Ascomatal wall yellowish brown. Ascomatal hairs straight, septate, 69–177 × 2.5–3.5 µm. Ascospores fusiform, brown, smooth-walled, 10.5–14.5 × 6–7 µm.

Culture characteristics – Colony on PDA radial sulcate, white to yellow to grayish, floccose, reverse moderate yellow, reaching 46 mm in diameter after 7 d at 25 °C. Colony on CMA white, sparse aerial mycelia, but ascomata abundantly produced, reverse uncolored, reaching 44 mm in diameter after 7 d at 25 °C. Colony on OA white to light bluish gray, reaching 39 mm in diameter after 7 d at 25 °C.

Material examined – Republic of Korea, Jeollabuk-do, Iksan-si, Yongdong-myeon, Gusan-ri, from a soil sample, May 13 2023, culture CNUFC

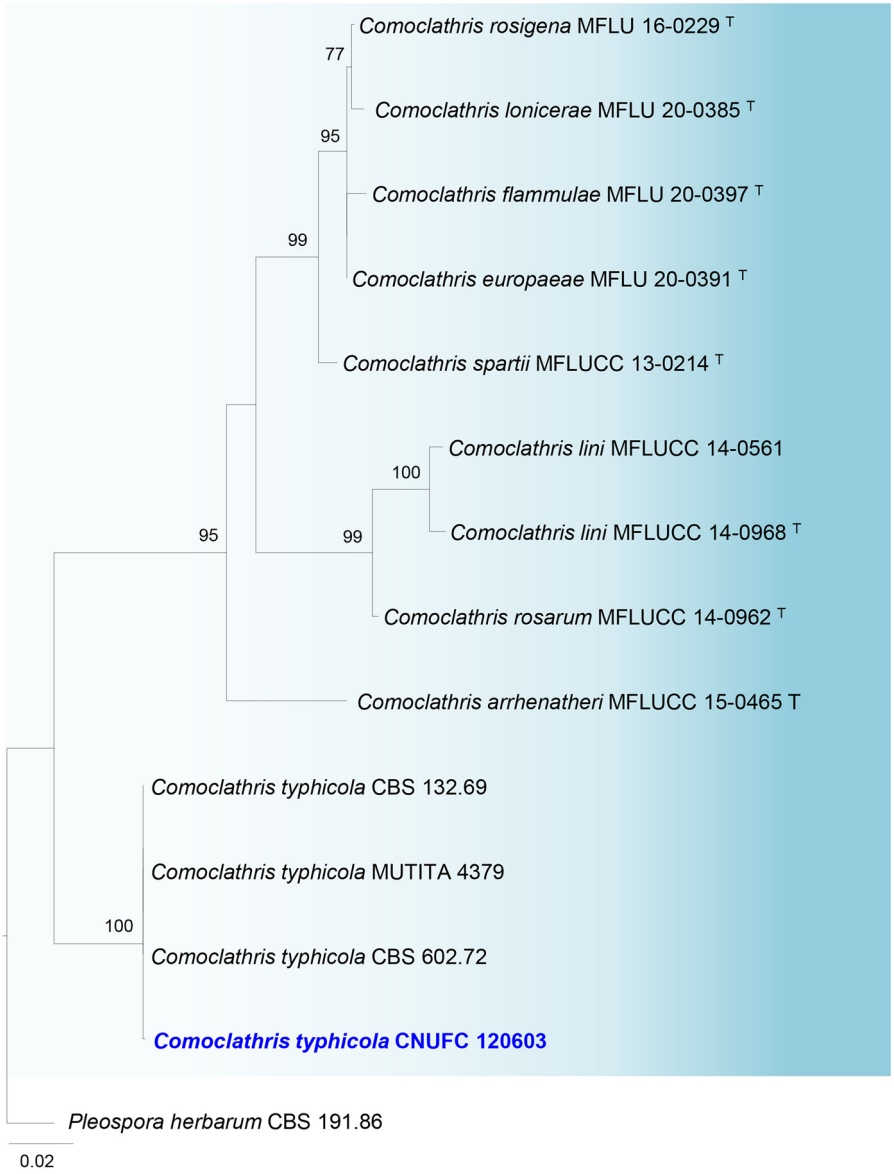

Figure 3. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Comoclathris typhicola* CNUFC 120603, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Pleospora herbarum* CBS 191.86 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

CHS2-10 = NIBRFGC000511440, GenBank numbers: ITS = PQ311723, *BenA* = PQ453027.

Notes – *Ach. virescens* has been reported from agricultural soil in Pakistan and wheat straw compost in Ludhiana, Punjab [45,46]. Phylogenetic analysis placed the CNUFC CHS2-10 grouped with the *Ach. virescens* CBS 148.68 ex-type strain (Figure 1). The isolation of *Ach. virescens* from soil in Korea is a new record.

Arxotrichum gangligerum (L.M. Ames) X. Wei Wang & Houbraken, Stud. Mycol. 101: 151. 2022. MycoBank MB 830918 (Figure 16).

Description – Ascomata covered by aerial mycelium together with conidial structures, solitary or aggregated, black, ovoid or ellipsoidal, 179–306 × 143–193 µm. Ascomatal wall brown. Ascomatal hairs are numerous, long, unbranched, spirally coiled in the upper part, brown, 134–172 µm long. Asci clavate or fusiform, containing eight irregularly arranged ascospores, 24.5–43 × 11–15.5 µm. Ascospores avoid or limoniform at the biapiculate at both ends, 11–13 × 7–8.5 µm.

Culture characteristics – Colony on PDA moderate to strong yellow, reverse yellow with black patches, producing vivid yellow exudates diffusing into the medium, reaching 54 mm in diameter after 7 d at 25 °C. Colony on OA floccose, light yellow, reverse yellow green, reaching 57 mm in diameter after 7 d at 25 °C. Colony on CMA with sparse white aerial hyphae, rapidly developing ascomata, reverse uncolored, reaching 48 mm in diameter after 7 d at 25 °C.

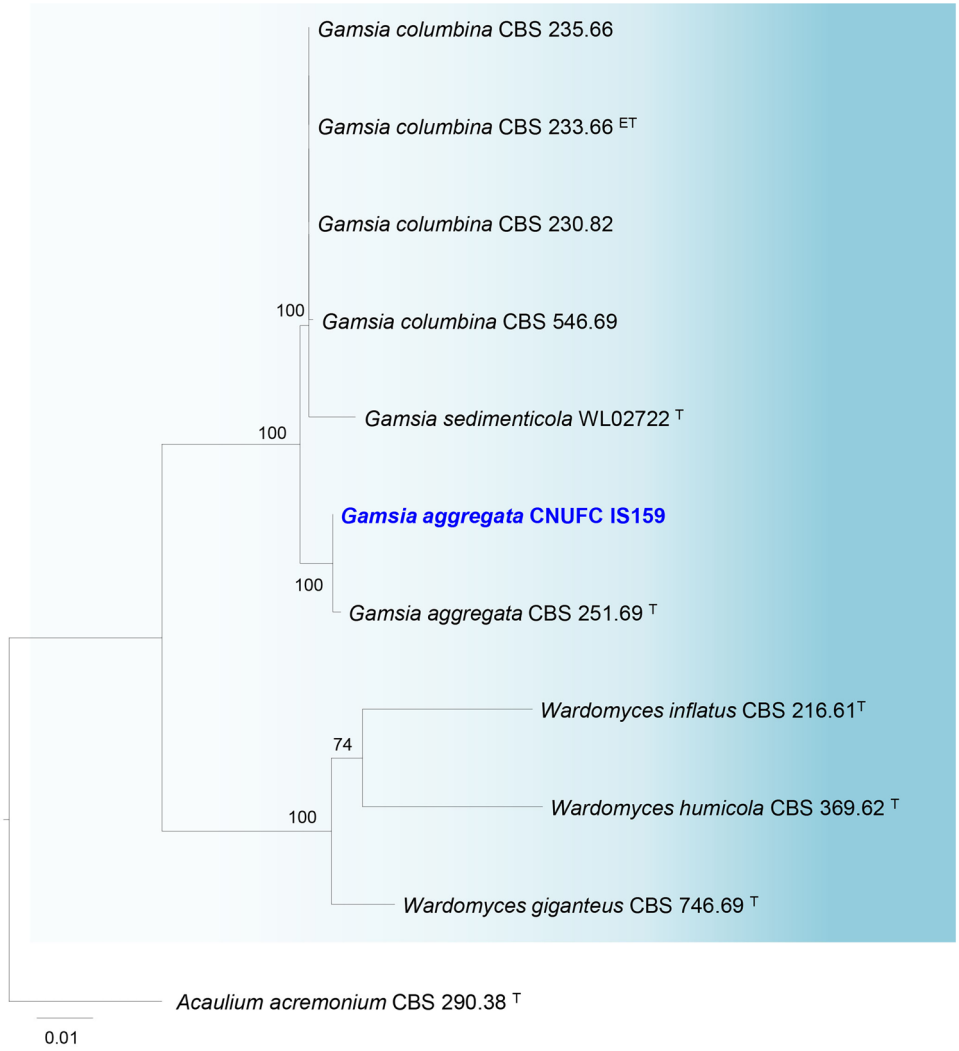

Figure 4. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Gamsia aggregata* CNUFC IS159, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Acaulium acremonium* CBS 290.38 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

Material examined – Republic of Korea, Jeollanam-do, Goheung gun, from a freshwater sample, September 21 2023, culture CNUFC NHW16 = NNIBRFG54713, GenBank numbers: ITS = PQ311 722, *BenA* = PQ453026.

Notes – *Arx. gangligerum* has been reported from rabbit dung in Canada and wood samples under test conditions in a tropical testing chamber in the USA [46]. Phylogenetic analysis grouped the CNUFC NHW16 strain with the ex-type strain of *Arx. gangligerum* CBS 160.52 (Figure 1). The material described here matches closely with *Arx. gangligerum* as described by Wang et al. [46]. The isolation of *Arx. gangligerum* from freshwater in Korea is the first report of this species in freshwater and is also a new record in Korea.

Caespitomonium euphorbiae Crous, Persoonia 47: 183. 2021. MycoBank MB 841777 (Figure 17).

Description – Conidiophores solitary to aggregated, subcylindrical, hyaline, smooth, 52–103 × 2.5–4 µm. Phialides subcylindrical, borne in whorls, or solitary, 20–34 × 2–3 µm. Conidia hyaline, aseptate, ellipsoid, smooth, base with truncate hilum, 4–5.5 × 2–2.5 µm.

Culture characteristics – Colony on PDA, white to moderate orange-yellow, floccose, reverse brown, reaching 42 mm in diameter after 14 d at 25 °C. Colony on OA floccose with concentric ring, white to light yellowish brown, reverse moderate yellowish pink, reaching 46 mm in diameter after 14 d at 25 °C. Colony on CMA flat, sparse to moderate aerial mycelium, sporulation abundant on the surface of the medium, reverse uncolored, reaching 44 mm diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Gyeonggi-do, Goyang-si, from a soil sample, August 7 2022, culture

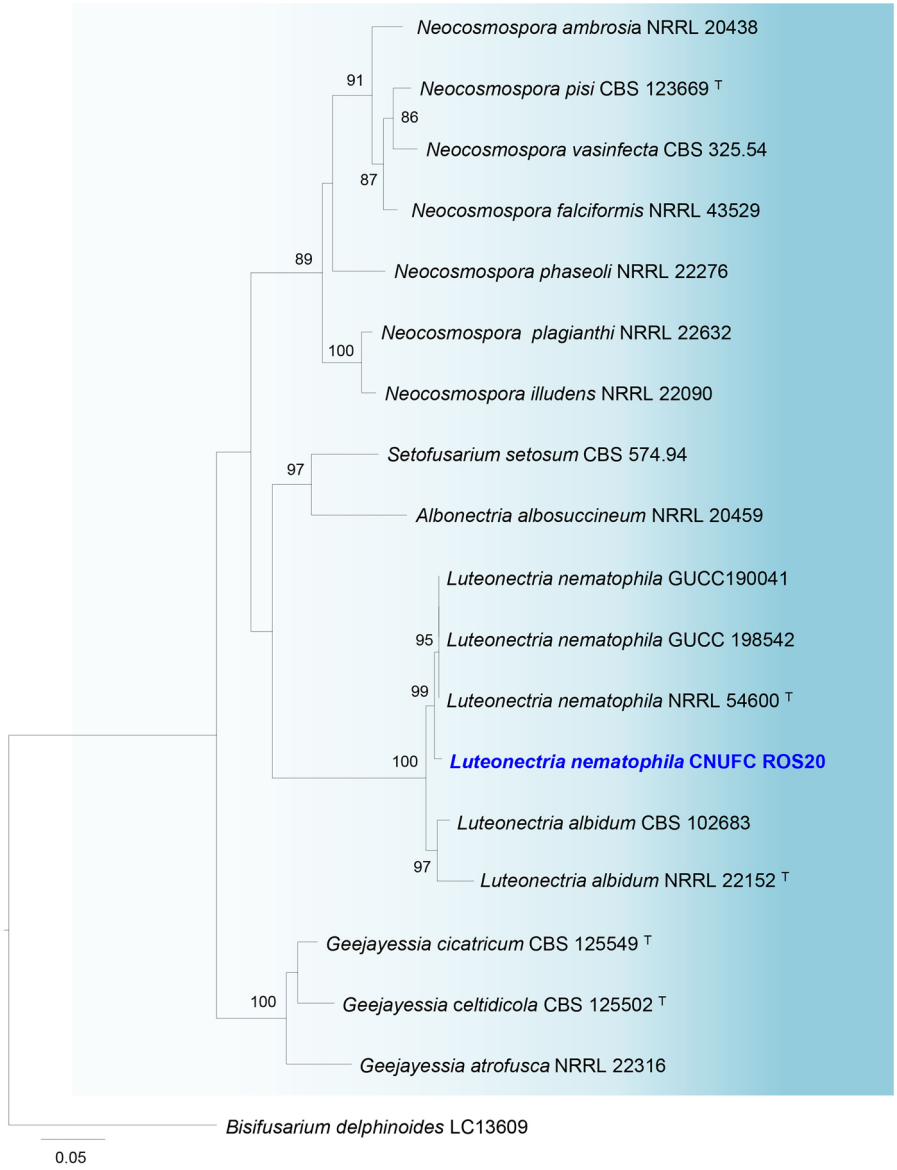

Figure 5. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and *RPB2* sequence data for *Luteonectria nematophila* CNUFC ROS20, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Bisifusarium delphinoides* LC13609 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

CNUFC SN35-81 = NIBRFGC000511439, GenBank numbers: ITS = PQ311724, LSU = PQ443749.

Notes – *C. euphorbiae* has been reported from *Euphorbia* sp. in Namibia [47]. Phylogenetic analysis indicates that our strain consistently clustered with the ex-type strain CBS 147075. Our strain has similar conidia and phialides morphology to *C. euphorbiae* [47]. The isolation of *C. euphorbiae* from soil is the first report of this species from soil and also is a new record in Korea.

Comoclathris typhicola (Cooke) Ariyaw. & K.D. Hyde, Fungal Diversity 71: 105. 2015. MycoBank MB 550954 (Figure 18).

Basionym: *Sphaeria typhicola* Cooke [as "typhaecola"], Grevillea 5 (35): 121 (1877).

Synonyms: *Clathrospora typhicola* (Cooke) Höhn., Ann. Mycol. 16 (1–2): 88 (1918), *Macrospora typhicola* (Cooke) Shoemaker & C.E. Babc., Can. J. Bot. 70 (8): 1644 (1992), *Pleospora typhicola* (Cooke) Sacc., Reliq. Libert 2: no. 152 (1881), *Pyrenophora typhicola* (Cooke) E. Müll., Sydowia 5(3–6): 256 (1951).

Description – Ascomata yellowish-creamy, globose to subglobose, solitary, scattered or aggregated in small groups, 65–154 × 64–150 µm. Ascomatal wall pale brown. Conidia elliptical, or ovate to oblong, hyaline, smooth-walled, aseptate, 3.5–5 × 2–2.5 µm.

Culture characteristics – Colony on PDA flat to umbonate, with flocculent aerial mycelium, olivaceous greenish, reverse greenish-black, reaching 74 mm in diameter after 7 d at 25 °C. Colony on OA floccose, light olive gray, with abundant aerial

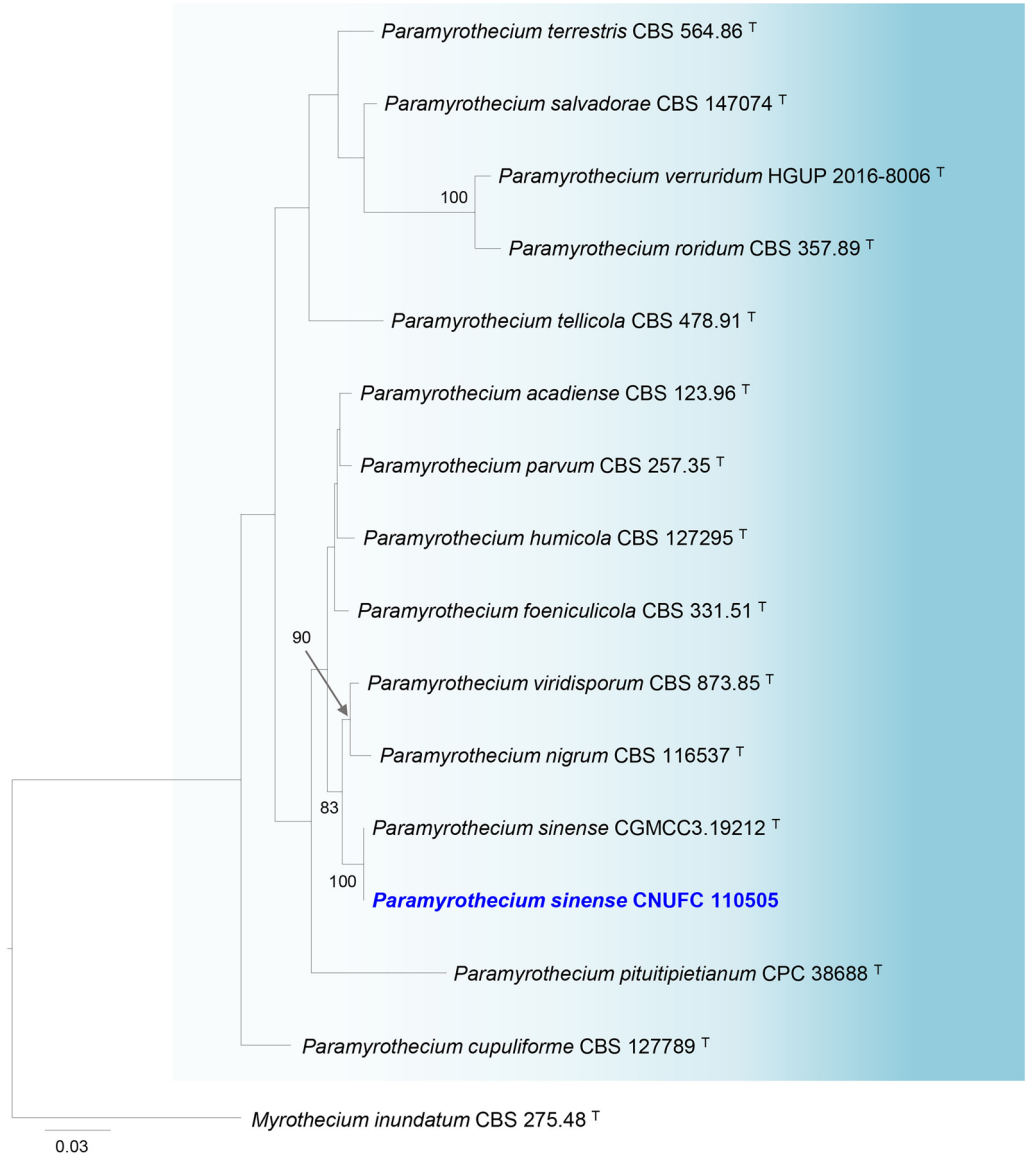

Figure 6. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and *BenA* sequence data for *Paramyrothecium sinense* CNUFC 110505, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Myrothecium inundatum* CBS 275.48 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

mycelium and smooth margin, reaching 62 mm in diameter after 7 d at 25 °C. Colony on CMA flat or slightly raised at center, mycelium mostly immersed, aerial mycelium sparse, good sporulation, reverse uncolored, reaching 59 mm in diameter after 7 d at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Cheongyang-gun, Cheongyang-eup, from a freshwater sample, August 14 2021, culture CNUFC 120603 = NNIBRFG46694, GenBank numbers: ITS = PQ311725, LSU = PQ443743.

Notes – In the phylogenetic analyses, CNUFC 120603 clustered with *Co. typhicola* (CBS 132.69, CBS 602.72, and MUTITA 4379) (Figure 3). *Comoclathris typhicola* has been found on *Typha angustifolia* in the Netherlands [48], *Posidonia oceanica* in Italy [49], and *Typha latifolia* L. in Iran [50]. The isolation of *Co. typhicola* from freshwater in Korea is the first report of this species in freshwater and also the first record of *Co. typhicola* in Korea.

Gamsia aggregata (Malloch) Kiffer & M. Morelet, Annales de la Société des Sciences Naturelles et d'Archéologie de Toulon et du Var. 47: 93.1995. MycoBank MB 413101 (Figure 19).

Synonym: *Wardomyces aggregatus* Malloch, Can. J. Bot. 48: 883. 1970.

Description – Hyphae hyaline, septate, 1.5–4 µm wide, smooth-walled. Conidiophores reduced to conidiogenous cells, subcylindrical to cylindrical, hyaline, smooth-walled. Conidia aseptate, broadly ellipsoidal to ovoid, with truncate at base, rounded

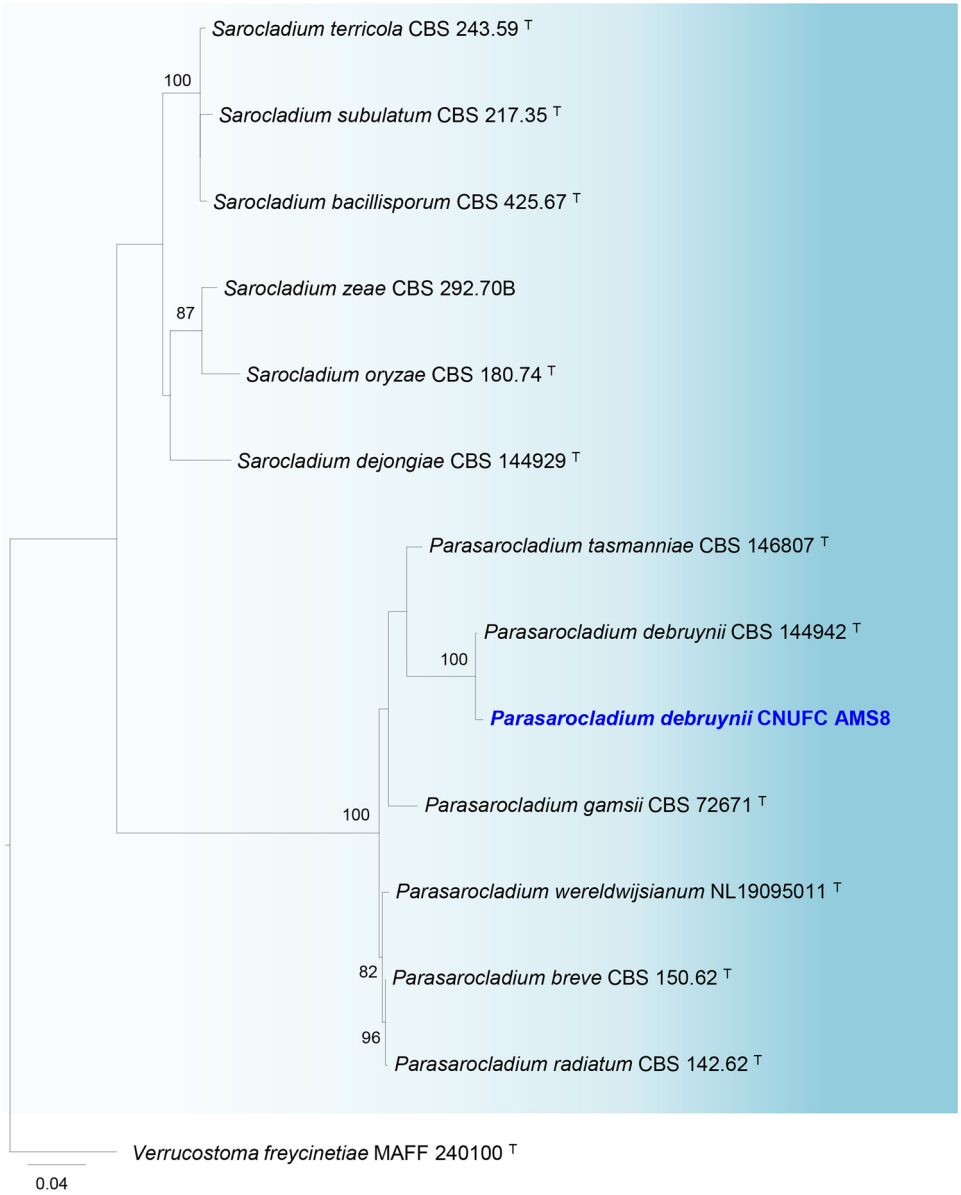

Figure 7. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Parasarocladium debruynii* CNUFC AMS8, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Verrucostoma freycinetiae* MAFF 240100 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

at apex, dark brown, 6.5–9.5 × 2.7–3.5 µm, smooth and thick-walled.

Culture characteristics – Colony on PDA sulcate, dark grayish green, with a white regular margin, slow growing, reverse grayish green, reaching 28 mm in diameter after 14 d at 25 °C. Colony on CMA flat, with spare aerial mycelia, light olive gray to grayish olive at the center, white near margin, reaching 37 mm in diameter after 14 d at 25 °C. Colony on OA dark olive green, floccose, reverse olive grey, reaching 35 mm in diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Jeollanam-do, Jindo-gun, September 5 2023, culture CNUFC IS159 = NIBRFGC000511443, GenBank numbers: ITS = PQ311726, LSU = PQ443744.

Notes – *Gamsia aggregata* has been reported from the dung of carnivores in USA [51,52], and from soil in this study. *Gamsia aggregata* is similar to *G. aggregata* (Malloch) Kiffer & M. Morelet in the shape of the conidia, but differs in that these structures are larger in *G. aggregata* CNUFC IS159 [51,52]. In the phylogenetic analyses, our strain clustered with the ex-type of with *G. aggregata* CBS 251.69 with 100% MLBS support. This is the first record of *G. aggregata* isolated in Korea.

Luteonectria nematophila (Nirenberg & Hagedorn) Sand.-Den. & L. Lombard, Studies in Mycology 98 (no. 100116): 60. 2021. MycoBank MB 838666 (Figure 20).

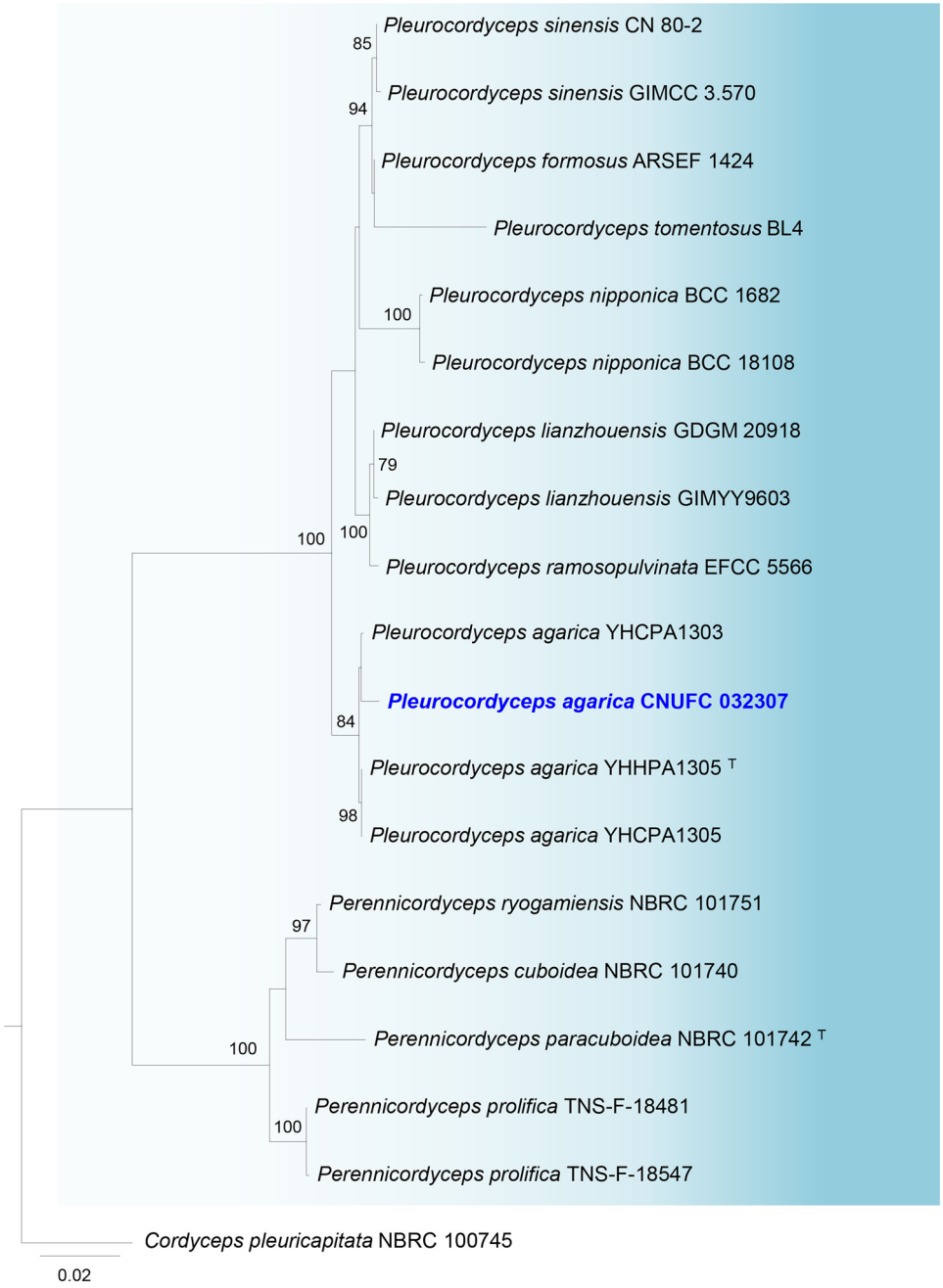

Figure 8. Maximum-likelihood phylogenetic tree inferred from combined dataset of LSU and *tef* sequence data for *Pleurocordyceps agarica* CNUFC 032307, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Cordyceps pleuricapitata* NBRC 100745 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

Basionym: *Fusarium nematophilum* Nirenberg & Hagedorn, Nachrichtenbl. Deutsch. Pflanzenschutzdienstes 60: 214. 2008.

Description – Conidiophores borne on aerial mycelia, erect, hyaline, unbranched, often reduced to conidiogenous cells, up to 178.5 µm long. Conidiogenous cells, hyaline, smooth, straight or slightly curved, cylindrical, 10–41 × 3.5–4.5 µm. Macroconidia straight to curved, wider at the middle or apical, tapering toward the base, usually 3-septate, hyaline, smooth-walled, (30–)33–40 × 5.5–7.0 µm. Chlamydospores globose to subglobose to broadly ellipsoid, 8.5–12.5 × 5.5–9 µm.

Culture characteristics – Colony on PDA light yellow, slightly raised at the center, with abundant aerial mycelium, reverse pale yellow, reaching 33 mm in diameter after 7 d at 25 °C. Colony on SNA white, flat, sparse aerial mycelium with entire margin, reverse white, reaching 40 mm in diameter after 7 d at 25 °C. Colony on MEA velvety, white to cream, reaching 38 mm in diameter after 7 d at 25 °C.

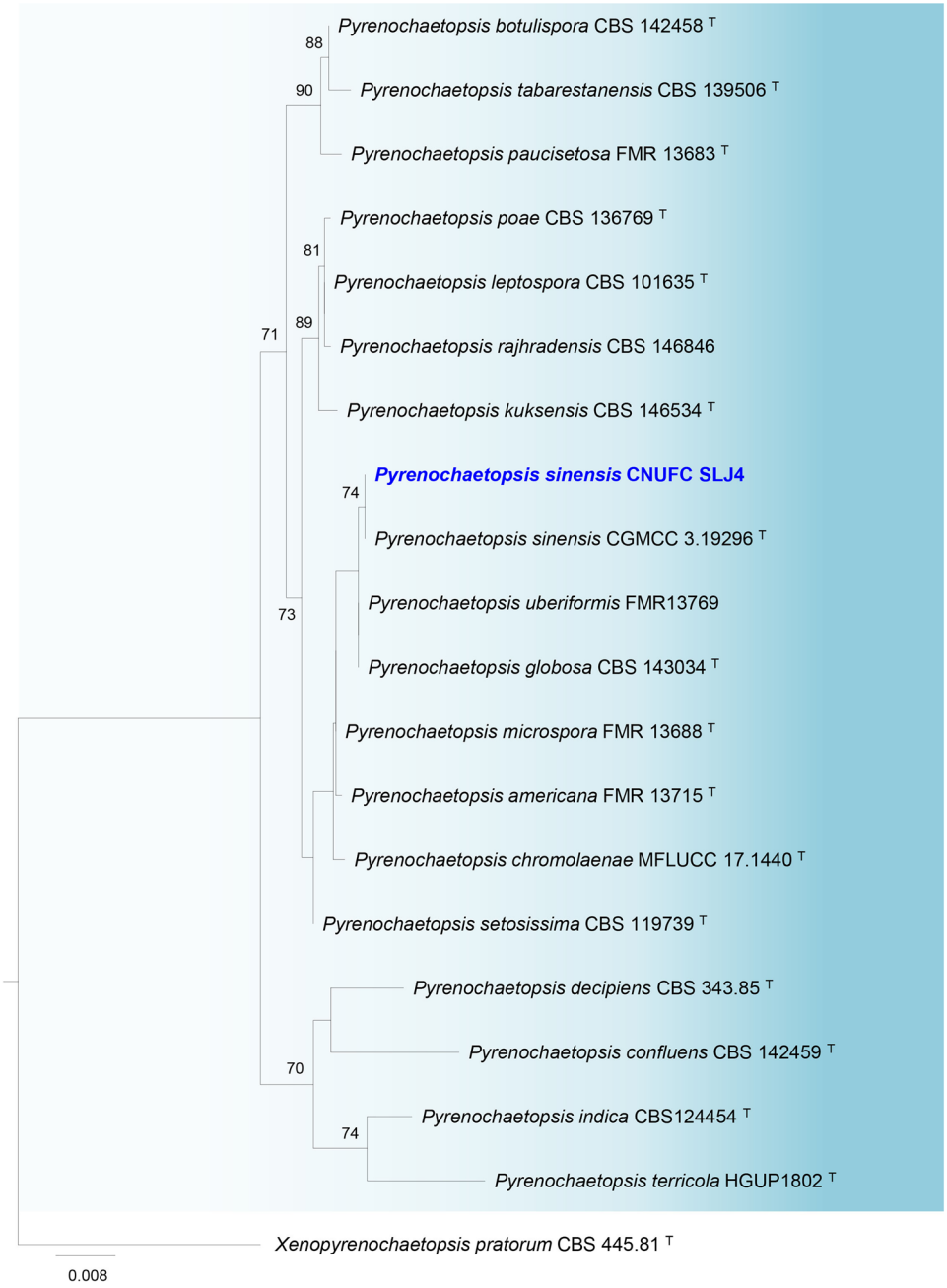

Figure 9. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Pyrenochaetopsis sinensis* CNUFC SLJ4, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Xenopyrenochaetopsis pratorum* CBS 445.81 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

Material examined – Republic of Korea, Jeollanam-do, Goheung gun, from a soil sample, April 27 2022, culture CNUFC ROS20 = HNIBRFG7463, GenBank numbers: ITS = PQ459451, *RPB2* = PQ453020.

Notes – In the phylogenetic analyses, *L. nematophila* CNUFC ROS20 was close to the type strain and other strain of *L. nematophila* (Figure 5). *L. nematophila* was found in soil with roots of *Hedera helix* in Germany [53,54], roots of *Rosa roxburghii* in China [55], and from soil in this study. Our strain shares similar conidial morphology to *L. nematophila* NRRL 54600 (ex-type culture); however, conidia of the type strain of *L. nematophila* (29–43 × 6.1–8.2 µm) are slightly larger compared with the conidia of strain CNUFC ROS20 [(30–)33–40 × 5.5–7.0 µm] [53].

Paramyrothecium sinense J.M. Liang, G.S. Li & L. Cai, MycoKeys 51: 44. 2019. MycoBank MB 829698 (Figure 21).

Description – Conidiomata sporodochial, stromatic, superficial, cupulate, scattered or gregarious, oval or irregular in outline, without a setose fringe surrounding a green to black agglutinated slimy mass of conidia. Conidiogenous cells cylindrical to subcylindrical, hyaline, smooth-walled, straight to

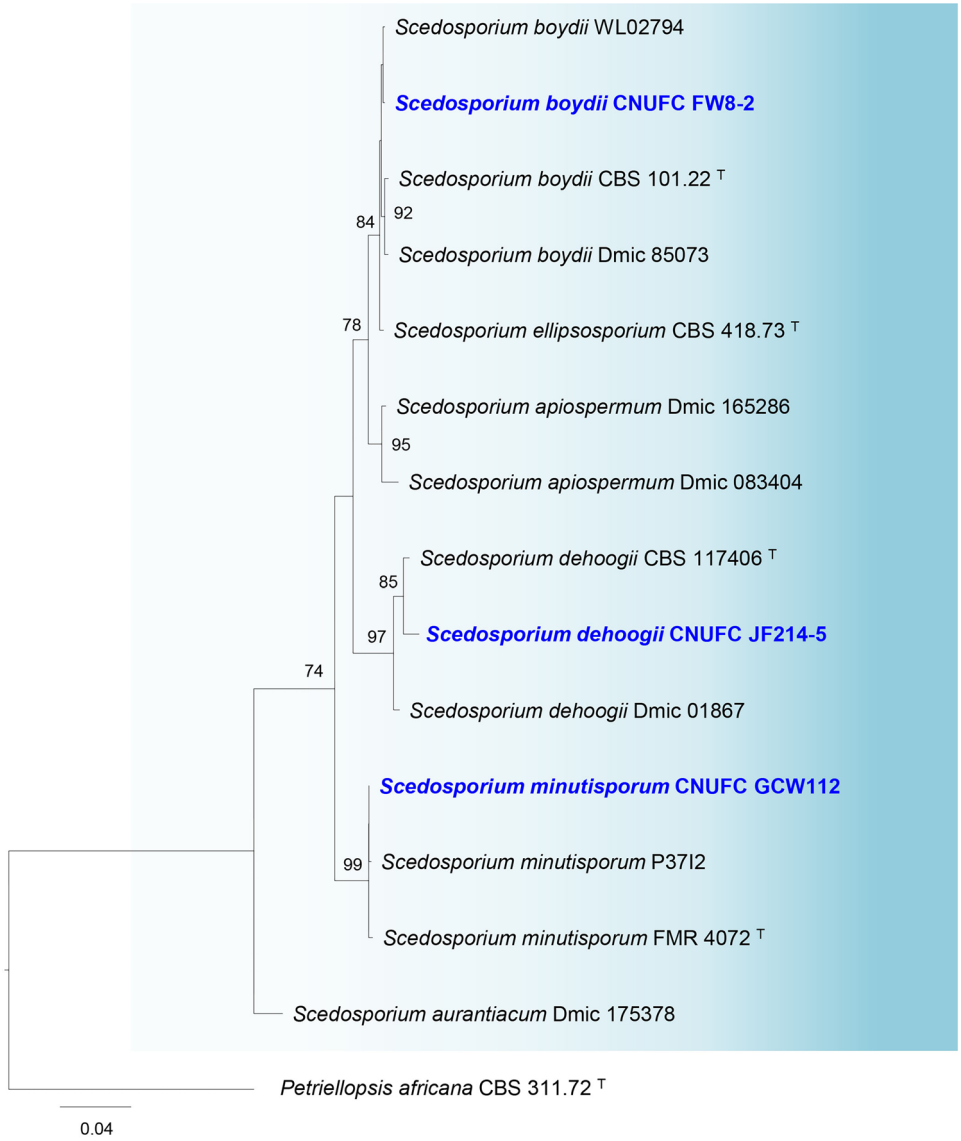

Figure 10. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and *BenA* sequence data for *Scedosporium boydii* CNUFC FW8-2, *Scedosporium dehoogii* CNUFC JF214-5, *Scedosporium minutisporum* CNUFC GCW112, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches or near the nodes. *Petriellopsis africana* CBS 311.72 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

slightly curved, 6–10.5 × 1.5–2.5 µm. Conidia aseptate, hyaline, smooth-walled, cylindrical to ellipsoidal, (4–)5–6.5 × 1.5–2(–2.5) µm.

Culture characteristics – Colony on PDA initially white, then filled with dark green masses, slightly folded in the center, reverse light orange, reaching 35 mm in diameter after 7 d at 25 °C. Colony on CMA white, sparse aerial mycelium, with no sporulation, reaching 39 mm in diameter after 7 d at 25 °C. Colony on OA, initially white moderate yellowish pink, forming concentric rings, reverse pale yellow, reaching 36 mm in diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Cheongyang-gun, Cheongyang-eup, from a freshwater sample, August 14 2021, culture CNUFC 110505 = NNIBRFG46705, GenBank numbers: ITS = PQ312628, *BenA* = PQ453028.

Notes – In the phylogenetic analyses, our strain clustered with the type strain (CGMCC3.19212) of *P. sinense* (Figure 6). Our strain shared similar characteristics of conidiogenous cells and conidia identical to the ex-type strain *P. sinense* (CGMCC3.19212). *P. sinense* from Korea presents slightly smaller conidia compared with the material cited in Liang et al. [56] [(4–)5–6.5 × 1.5–2(–2.5) vs. 6–7 × 2–3 µm]. The

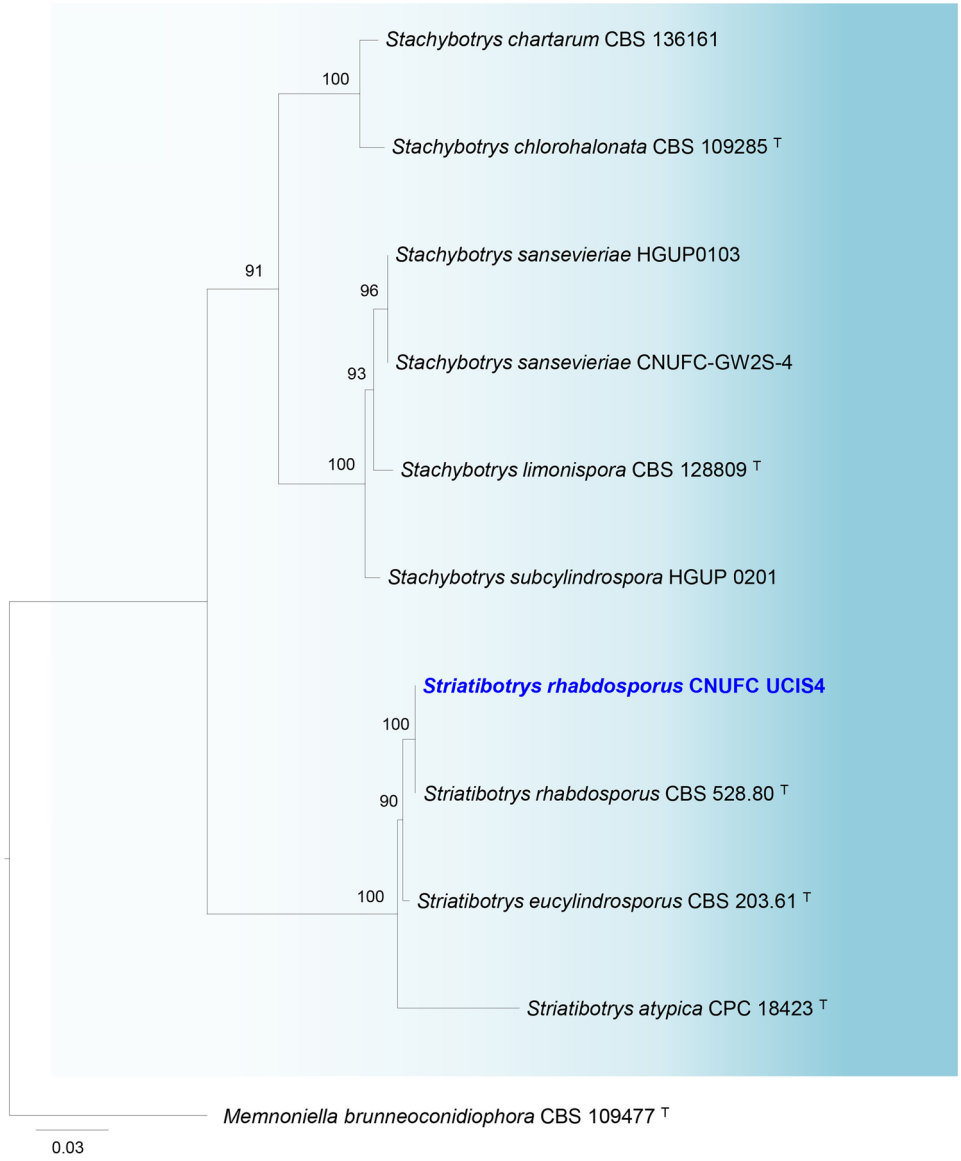

Figure 11. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and *RPB2* sequence data for *Striatibotrys rhabdosporus* CNUFC UCIS4, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Memnoniella brunneoconidiophora* CBS 109477 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

type strain and our strain were isolated from soil. This is the second world record of *P. sinense* and the first report of this species in Korea.

Parasarocladium debruynii L. Lombard, Persoonia 41: 343. 2018. MycoBank MB 828217 (Figure 22).

Description – Conidiophores erect, arising directly from vegetative hyphae, simple or poorly branched, hyaline, smooth-walled, aseptate, up to 65 µm long. Conidiogenous cells arising laterally from hyphae or in terminal pairs, aseptate, cylindrical to subcylindrical, smooth-walled, 9.5–15.5 × 1.5–3 µm. Conidia ellipsoidal to fusiform, some elliptical flattened at one side, 3.5–5.5 × 2–3 µm, hyaline, smooth-walled.

Culture characteristics – Colony on PDA rare aerial mycelium, dense, moderate yellowish pink, reverse pale yellow, reaching 32 mm in diameter after 7 d at 25 °C. Colony on MEA, without aerial mycelium, uncolored, reaching 50 mm in diameter after 7 d at 25 °C. Colony on OA, moderate yellowish pink, reverse uncolored, reaching 25 mm in diameter after 7 d at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Taean-gun, Anmyeon-eup, from a soil sample, April 20 2022, culture CNUFC AMS8 = HNIBRFG7461, GenBank numbers: ITS = PQ312629, LSU = PQ443745.

Notes – *Parasarocladium debruynii* was isolated from soil in the Netherlands [57]. Our strain was isolated from soil in Korea. Our strain shares similar conidiophores, conidiogenous cells, and conidia characteristics. However, conidia of type strain of *Pa. debruynii* (3–5 × 1–2 µm) are narrower compared with the conidia of strain CNUFC AMS8 (3.5–5.5 × 2–3 µm)

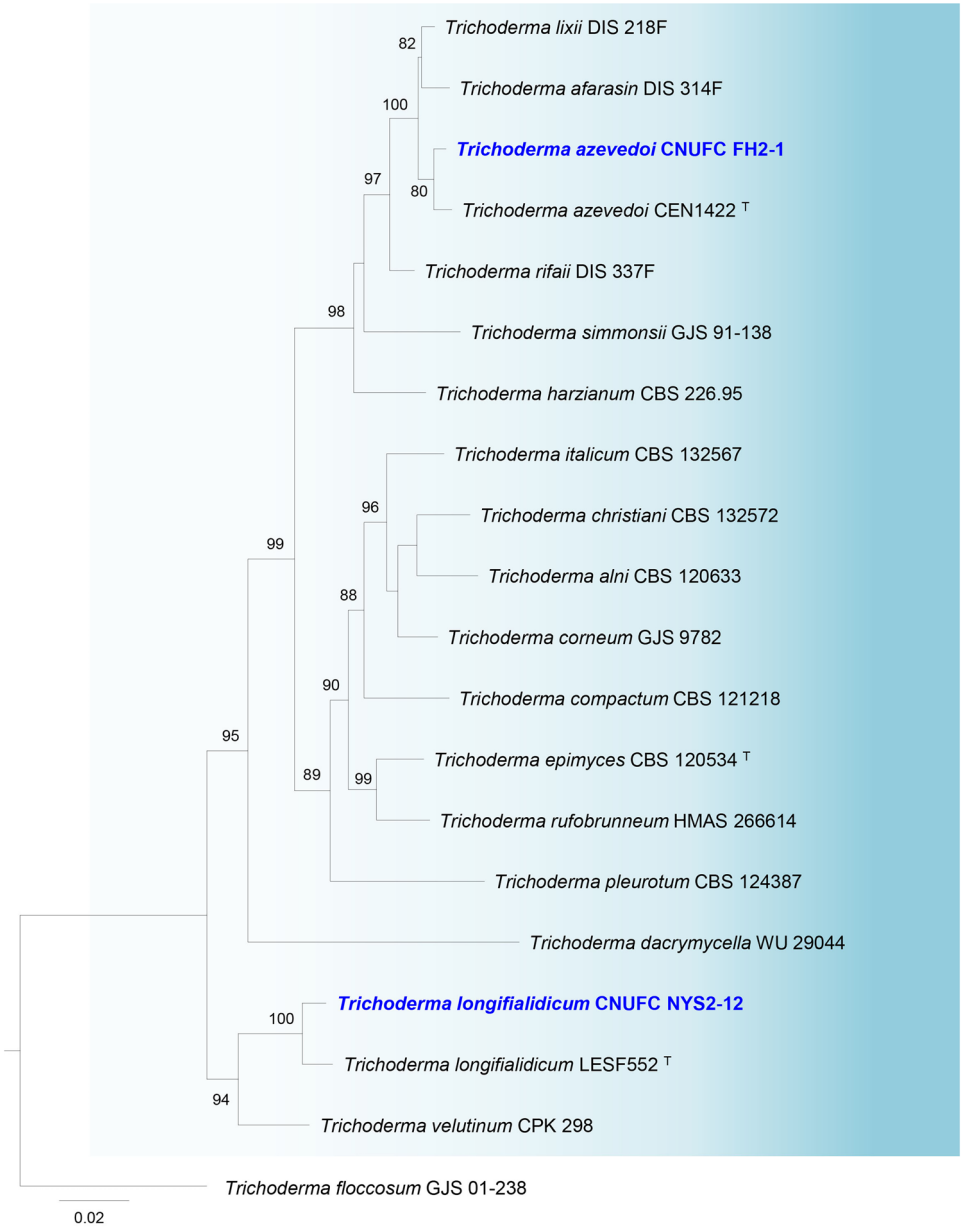

Figure 12. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS, *RPB2*, and *tef* sequence data for *Trichoderma azevedoi* CNUFC FH2-1, *Trichoderma longifialidicum* CNUFC NYS2-12, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above or below branches. *Trichoderma floccosum* GJS 01-238 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

[57]. Phylogenetic analysis indicates that our strain clustered with ex-type strain CBS 144942 (Figure 7). Therefore, we report the strain isolated as a new record of *Pa. debruynii* in Korea.

Pleurocordyceps agarica (Hong Yu bis & Y.B. Wang) Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang, P.M. Kirk & Y.J. Yao, Journal of Systematics and Evolution 59 (5): 1076. 2021. MycoBank MB 570677 (Figure 23).

Basionym: *Polycephalomyces agaricus* Hong Yu bis & Y.B. Wang Mycol. Progr. 14 (No. 70): 4 (2015).

Description – *Synnemata* solitary, light yellow, cylindrical, non-branched, distribution at the edge. Hyphae hyaline, branched, smooth-walled. Phialides hyaline, smooth-walled, 1.5–2.5 × (4.5–)6–10.5(–13) µm. α-conidia globose to subglobose, smooth-walled, 1.7–2.3 µm in diameter. β-conidia fusiform, smooth-walled, 3–5.5 × 1.5–2 µm.

Culture characteristics – Colony on PDA light yellow, margin entire, reverse pale yellow, reaching 46 mm in diameter after 14 d at 25 °C. Colony on OA white, reverse light yellow at center with a white margin, reaching 38 mm in diameter after 14 d at 25 °C. Colony on CMA aerial mycelia sparse, colorless, reverse also colorless, reaching 50 mm after 14 d at 25 °C.

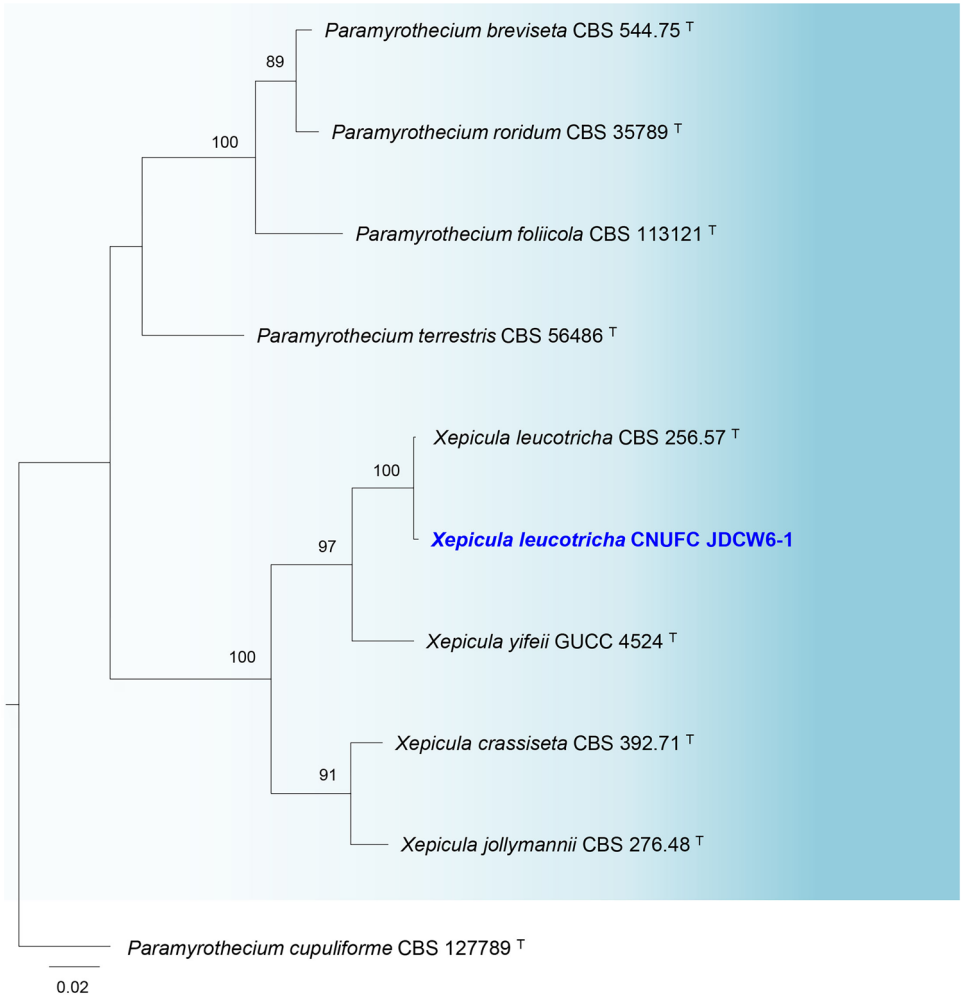

Figure 13. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and *RPB2* sequence data for *Xepicula leucotricha* CNUFC JDCW6-1, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Paramyrothecium cupuliforme* CBS 127789 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

Material examined – Republic of Korea, Chungcheongnam-do, Cheongyang-gun, Cheongyang-eup, February 22 2021, from soil sample, culture CNUFC 032307 = NIBRFGC000508971, GenBank numbers: LSU = PQ443746, *tef* = PQ453030.

Notes – *Pleurocordyceps agarica* has been found on the stroma of *Ophiocordyceps* spp. associated with the melolonthid larva buried in the soil in China [58,59] and from soil in this study. Multigene phylogeny showed that the strain CNUFC 032307 clustered with other strains of *Pl. agarica* (YHCPA1303, YHHPA1305, and YHCPA1305) (Figure 8). This is the first record of the species for Korea.

Pyrenochaetopsis sinensis G.S. Li, J.M. Liang & L. Cai, Fungal Diversity 96: 65. 2019. MycoBank MB 556011 (Figure 24).

Description – Hyphae hyaline to brown, smooth-walled, septate, 1.5–3 µm wide. Conidiomata pycnidial, brown, solitary, superficial on PDA, globose to ovoid, 158.5–357 × 153.5–306 µm. Pycnidial wall brown. Conidia hyaline, aseptate, ellipsoidal to cylindrical, 3.5–4 × 1.5–2 µm.

Culture characteristics – Colony on PDA flattened, dark green, with an entire edge, reverse brownish grey, reaching 26 mm in diameter after 7 d at 25 °C. Colony on CMA flattened, spare aerial mycelia, green in the center, reverse uncolored, reaching 28 mm in diameter after 7 d at 25 °C. Colony on OA, floccose, raised at the center, white to green-white, reverse dark grayish green, reaching 31 mm in diameter after 7 d at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Cheongyang-gun, Cheongyang-eup, from a soil samples, February 22 2021, culture CNUFC SLJ4 = NIBRFGC000508973, GenBank numbers: ITS = PQ312630, LSU = PQ443747.

Notes – Multigene phylogeny showed that the strain CNUFC SLJ4 clustered with type strain of *Py. sinensis* (CGMCC 3.19296) (Figure 9). *Py. sinensis* has been isolated from the rhizosphere soil of *Poa*

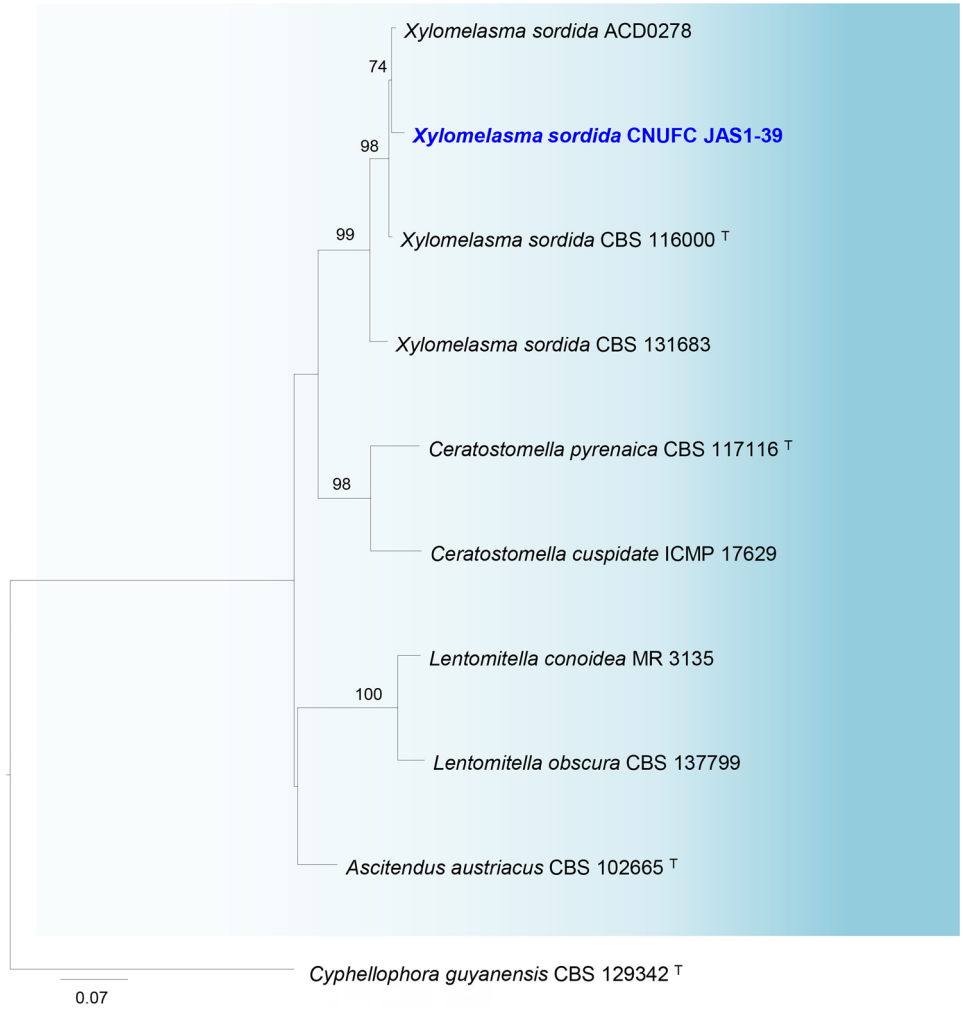

Figure 14. Maximum-likelihood phylogenetic tree inferred from combined dataset of ITS and LSU sequence data for *Xylomelasma sordida* CNUFC JAS1-39, and related species. Bootstrap support values for maximum-likelihood (MLBS) higher than 70% are indicated above branches. *Cyphellophora guyanensis* CBS 129342 was used as the outgroup. The newly generated sequences are in blue bold font. Ex-type strains are indicated by superscript T.

pratensis (Poaceae) in China [60], and also from soil in this study. This is the first record for Korea.

Scedosporium boydii (Shear) Gilgado, Gené, Cano & Guarro, Journal of Clinical Microbiology 46 (2): 770. 2008. MycoBank MB 538387 (Figure 25).

Description – Synnemata not observed. Hyphae hyaline, branched, smooth-walled. Conidiogenous cells arising terminally or laterally from hypha, hyaline, smooth-walled, cylindrical, 7–15.5 × 1.5 – 2 µm. Conidia ellipsoidal to obovoid, hyaline, smooth-walled, (5)6–10 (–12.5) × (2–)3.5–6 µm.

Culture characteristics – Colonies on PDA cottony to lanose, white in outer ring, grayish green, reverse moderate yellow-green, reaching 36 mm in diameter after 14 d at 25 °C. Colony on CMA white, with sparse aerial mycelium, reverse uncolored, reaching 51 mm in diameter after 14 d at 25 °C. Colony on OA floccose, pale grey near the center, with a white regular margin, reverse light yellow, reaching 39 mm in diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Daejeon, Hanbat Arboretum, from a freshwater sample, February 15 2020, culture CNUFC FW8-2 = NNIBR FG31715, GenBank numbers: ITS = PQ312631, *BenA* = PQ453029.

Notes – *S. boydii* has been found in soil in Thailand, Austria, and Zaire, and sputum with cystic fibrosis and lung disease in France, mycetoma in humans (male) in the USA [61]. This is the first report of *S. boydii* from a freshwater sample.

Scedosporium dehoogii Gilgado, Cano, Gené & Guarro, J. Clin. Microbiol. 46 (2): 768. 2008. MycoBank MB 538388 (Figure 26).

Description – Synnemata not observed. Conidiogenous cells arising laterally from hyphae, hyaline, smooth-walled, cylindrical, (5–)11–28.5 × 1.5–3(–3.5) µm. Conidia obovoid, hyaline to brown, smooth-walled, (5–)6.5–9 × 3.5–5 µm.

Culture characteristics – Colonies on PDA cottony, white to pale green, reverse olive green, reaching

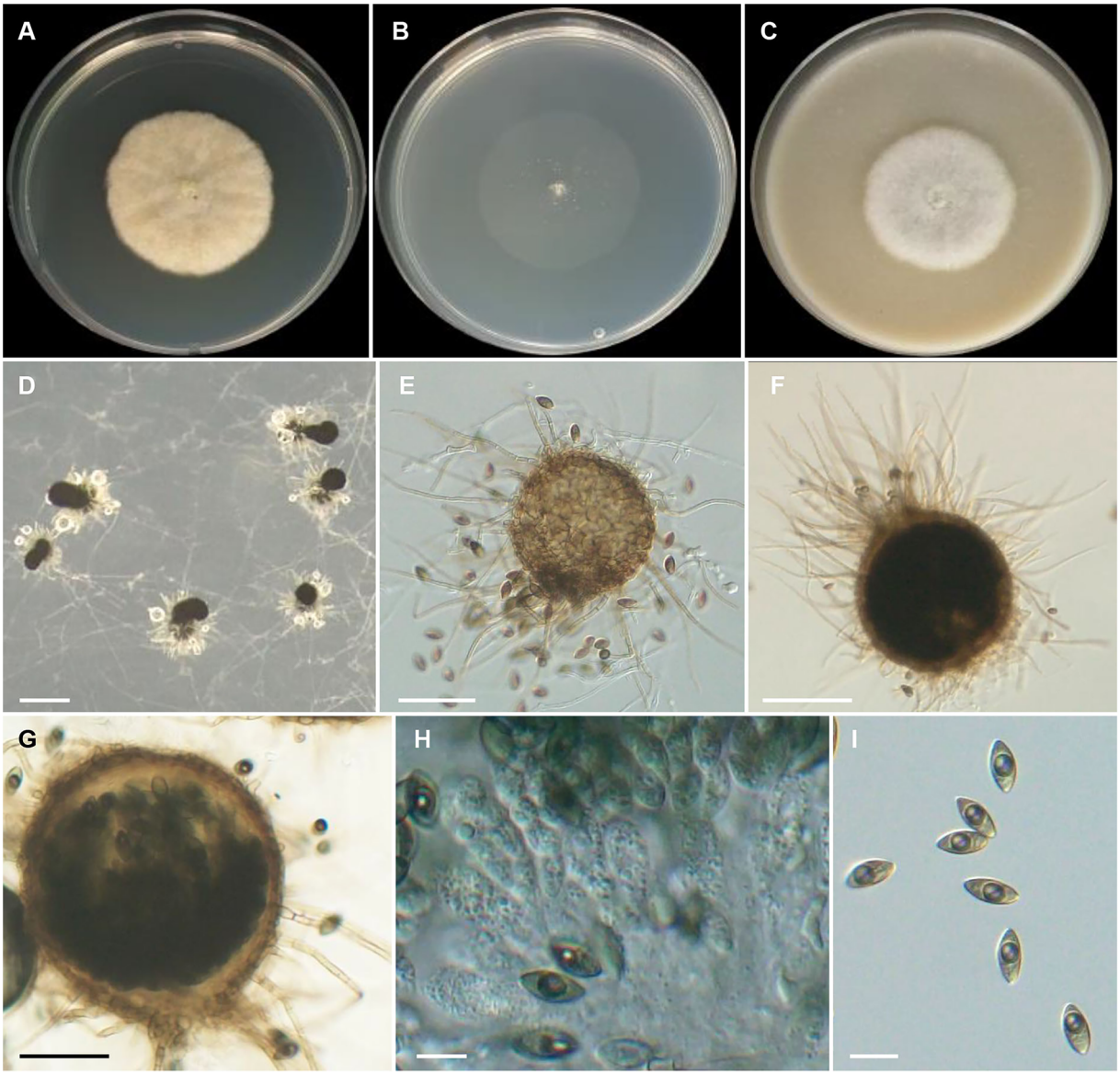

Figure 15. Morphology of *Achaetomiella virescens* CNUFC CHS2-10. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D) ascomata on CMA; (E–G) young and mature ascomata and ascomatal hairs; (H) asci; (I) ascospores. Scale bars: D = 200 µm; E–G = 50 µm; H, I = 10 µm.

31 mm in diameter after 14 d at 25 °C. Colony on CMA with sparse aerial mycelium, uncolored, reaching 51 mm in diameter after 14 d at 25 °C. Colony on OA cottony, white, reverse olive green, reaching 48 mm in diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Jeju Island, from a freshwater sample, April 16 2021, culture CNUFC JF214-5 = NNIBRFG46713, GenBank numbers: ITS = PQ312632, *BenA* = PQ476233.

Notes – Phylogenetic analysis placed our strain close to the ex-type strain (CBS 117406) and other strain (Dmic 01867) of *S. dehoogii* (Figure 10). *S. dehoogii* has been found in soil in Iran, Taiwan, Thailand, Mexico, India, Chile, Australia, Austria, and the Netherlands [62–69]. This is the first report of this species from Korea and also the first report from a freshwater sample.

Scedosporium minutisporum (Gilgado, Gené, Cano & Guarro) Lackner & de Hoog, Fungal Diversity 67: 9. 2014. MycoBank MB 807326 (Figure 27).

Description – Synnemata brown, erect, 343–908 µm long, producing cylindrical to clavate conidia 6–8.5 × 2.6–3.2 µm. Conidiogenous cells hyaline, cylindrical, producing ellipsoidal to elongate conidia, light brown, smooth-walled, 6.5–12(–14) × 3–5.5 µm. Ascomata solitary, non-ostiolate, globose to subglobose, light brown to black, 75–119.5 µm diameter. Ascospores unicellular, light brown, smooth-walled, ellipsoidal, 5.5–8.5 × 3–4.5 µm.

Culture characteristics – Colonies on PDA cottony, grayish-white, reverse brownish gray, reaching 48 mm in diameter after 14 d at 25 °C. Colony on CMA white, with sparse aerial mycelium, reverse uncolored,

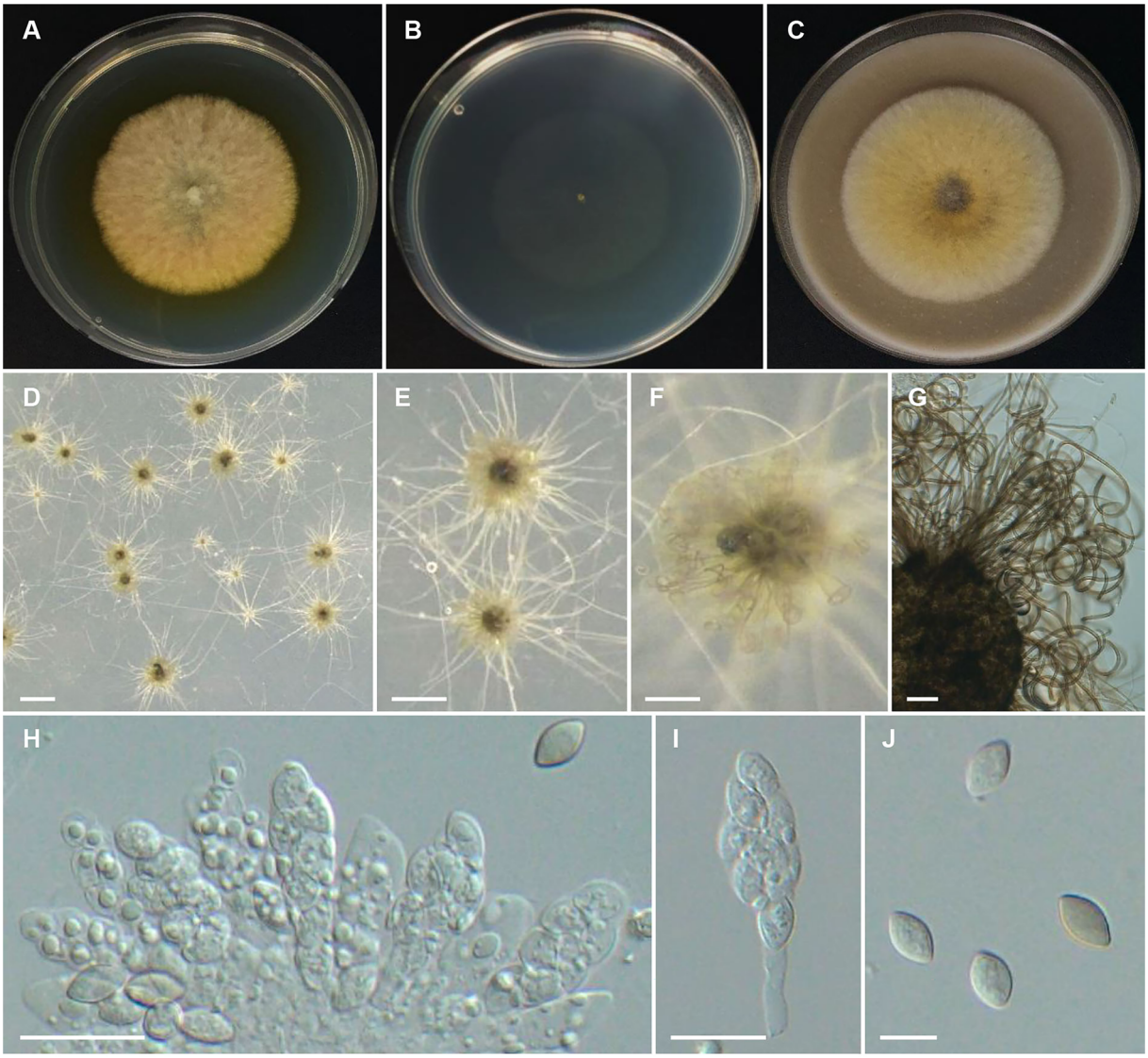

Figure 16. Morphology of *Arxotrichum gangligerum* CNUFC NHW16. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) ascomata on CMA; (G) ascomata and ascomatal hairs mounted in lactic acid; (H, I) asci; (J) ascospores. Scale bars: D = 500 µm, E = 200 µm, F = 100 µm, G–I = 20 µm, J = 10 µm.

reaching 55 mm in diameter after 14 d at 25 °C. Colony on OA cottony, zonate, grayish at the center, white toward the periphery, reverse grayish olive green at the center, and pale green toward the periphery, reaching 68 mm in diameter after 14 d at 25 °C. Strain developed abundant ascomata on PDA and CMA.

Material examined – Republic of Korea, Jeollabuk-do, Gochang-gu, from a freshwater sample, February 17 2023, culture CNUFC GCW112 = NNIBRFG54724, GenBank numbers: ITS = PQ312633, *BenA* = PQ476234.

Notes – In the phylogenetic analyses, our strain clustered with the ex-type strain (FMR 4072) and other isolate (P37I2) of *S. minutisporum* (Figure 10). Our strain CNUFC GCW112 shares similar morphology to the ex-type species *S. minutisporum*. However, our strain has longer synnemata compared to the material cited by Gilgado et al. [70]. *S. minutisporum* has been reported from patients with cystic fibrosis in France and soil samples from France, Austria, Netherlands, Australia, and Thailand, and bark beetle galleries from Iran [71,72]. This is the first report of this species from Korea and also the first report from a freshwater sample.

Striatibotrys rhabdosporus L. Lombard & Crous, Persoonia 36: 226. 2016. MycoBank MB 821468 (Figure 28).

Description – Ascomata not observed. Conidiophores erect, single or in groups, septate, straight or slightly flexuous, smooth, olivaceous to brown, 49–103.5 × 3.5–5 µm, bearing 2–6 conidiogenous cells. Conidiogenous cells phialidic, clavate, hyaline to brown, smooth, 9–11.5 × 4–5.5 µm. Conidia ellipsoidal to subcylindrical, pale brown, smooth-walled, 12–15 × 3.5–4.5 µm.

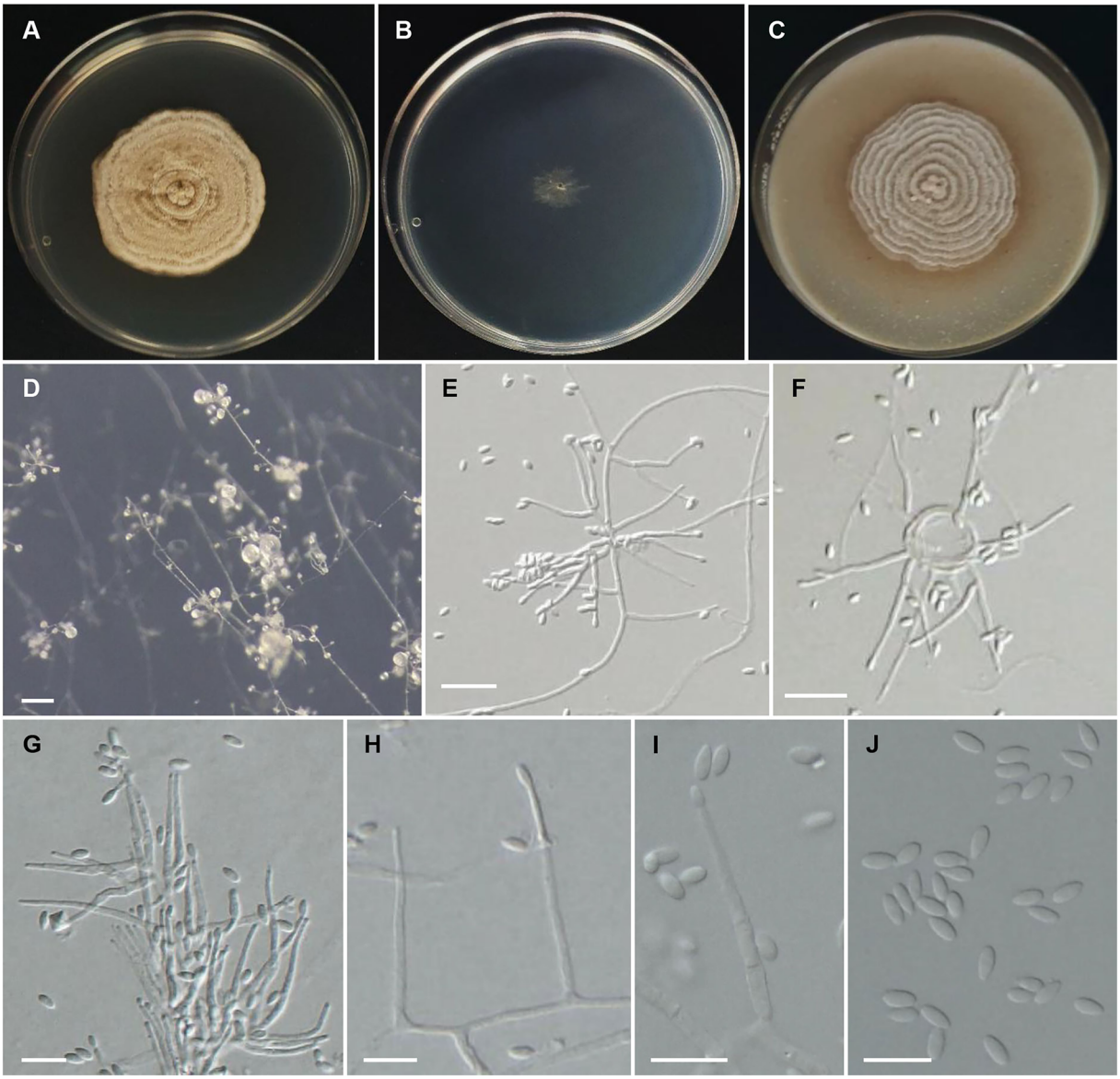

Figure 17. Morphology of *Caespitomonium euphorbiae* CNUFC SN35-81. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–I) conidiophores and phialides; (J) conidia. Scale bars: D = 100, E, F = 20 µm, G–J = 10 µm.

Culture characteristics – Colony on PDA with abundant aerial mycelium, reverse light yellow to pale yellow, reaching 51 mm in diameter after 14 d at 25 °C. Colony on CMA with sparse aerial mycelium, reaching 55 mm in diameter after 14 d at 25 °C. Colony on OA floccose aerial mycelium, reverse dark reddish brown, reaching 60 mm in diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Ulleung Island, from a soil sample, October 20 2021, culture CNUFC UCIS4 = NIBRFGC000510095, GenBank numbers: ITS = PQ312702, *RPB2* = PQ453021.

Notes – *Striatibotrys rhabdosporus* has been reported from soil in Germany and Switzerland, plant debris in Spain, petiole of *Caltha palustris* in USA, asbestos cement tile on building roof in Belgium [73], and from soil in this study. Combined phylogenetic analyses of ITS and *RPB2* placed the strain CNUFC UCIS4 with the type species *St. rhabdosporus* CBS 528.80 with high statistical support (ML = 100%) (Figure 11). *Striatibotrys rhabdosporus* from Korea presents longer conidiophore and conidia compared to the material cited Lombard et al. [73].

Trichocladium crispatum (Fuckel) X. Wei Wang & Houbraken, Stud. Mycol. 93: 137. 2018. MycoBank MB 824467 (Figure 29).

Description – Ascomata superficial on the aerial mycelium, observed after 4 weeks, dark grey to black, nearly spherical to ovoid, (69–)76–203 × (59.5–)62–194 µm. Ascomatal wall brown. Terminal hairs straight at the base, spirally coiled at the apex, 3.5–6 µm diameter at the base, dark brown. Asci cylindrical, 36–52 × 7.5–9.5 µm, containing six to

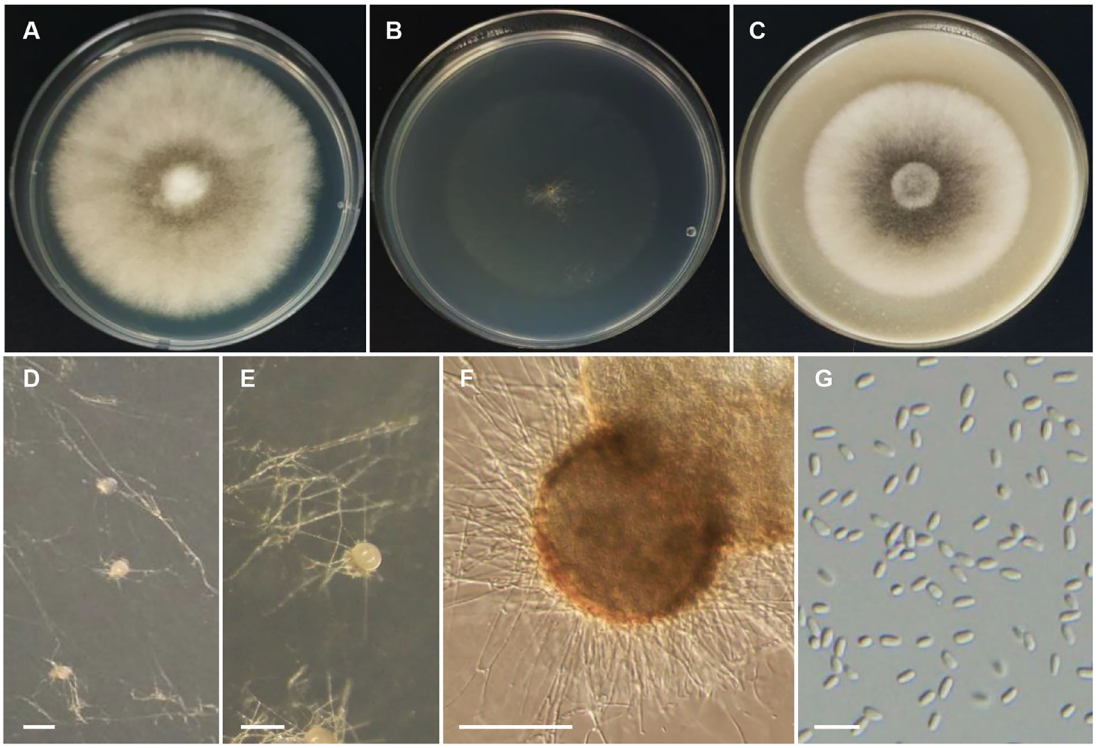

Figure 18. Morphology of *Comoclathris typhicola* CNUFC 120603. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D, E) ascomata forming on CMA; (F) ascomata and conidia; (G) conidia. Scale bars: D, E = 200 µm, F = 100 µm, G = 10 µm.

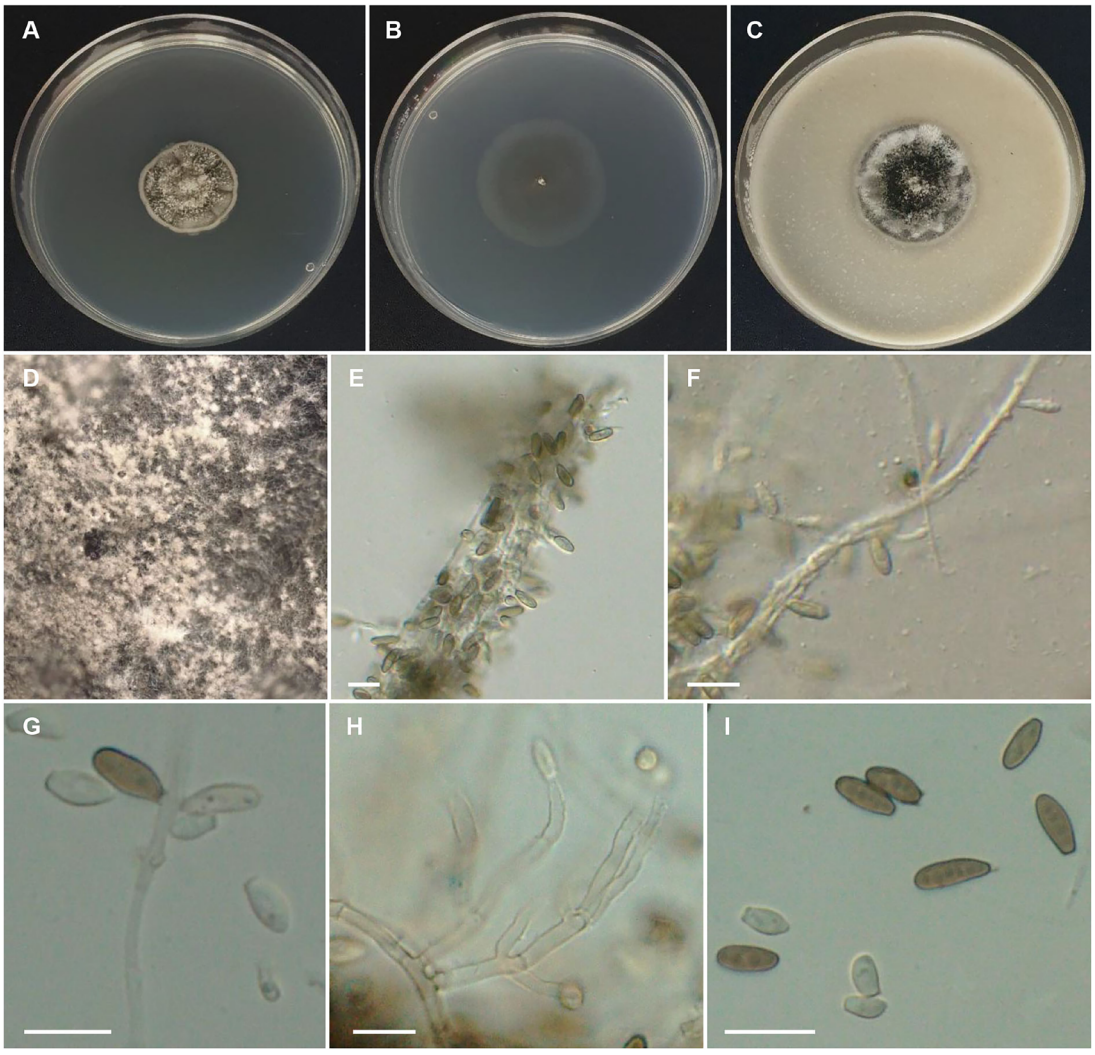

Figure 19. Morphology of *Gamsia aggregata* CNUFC IS159. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D) texture on PDA; (E–H) conidiophores, conidiogenous cells, and conidia; (I) conidia. Scale bars = 10 µm.

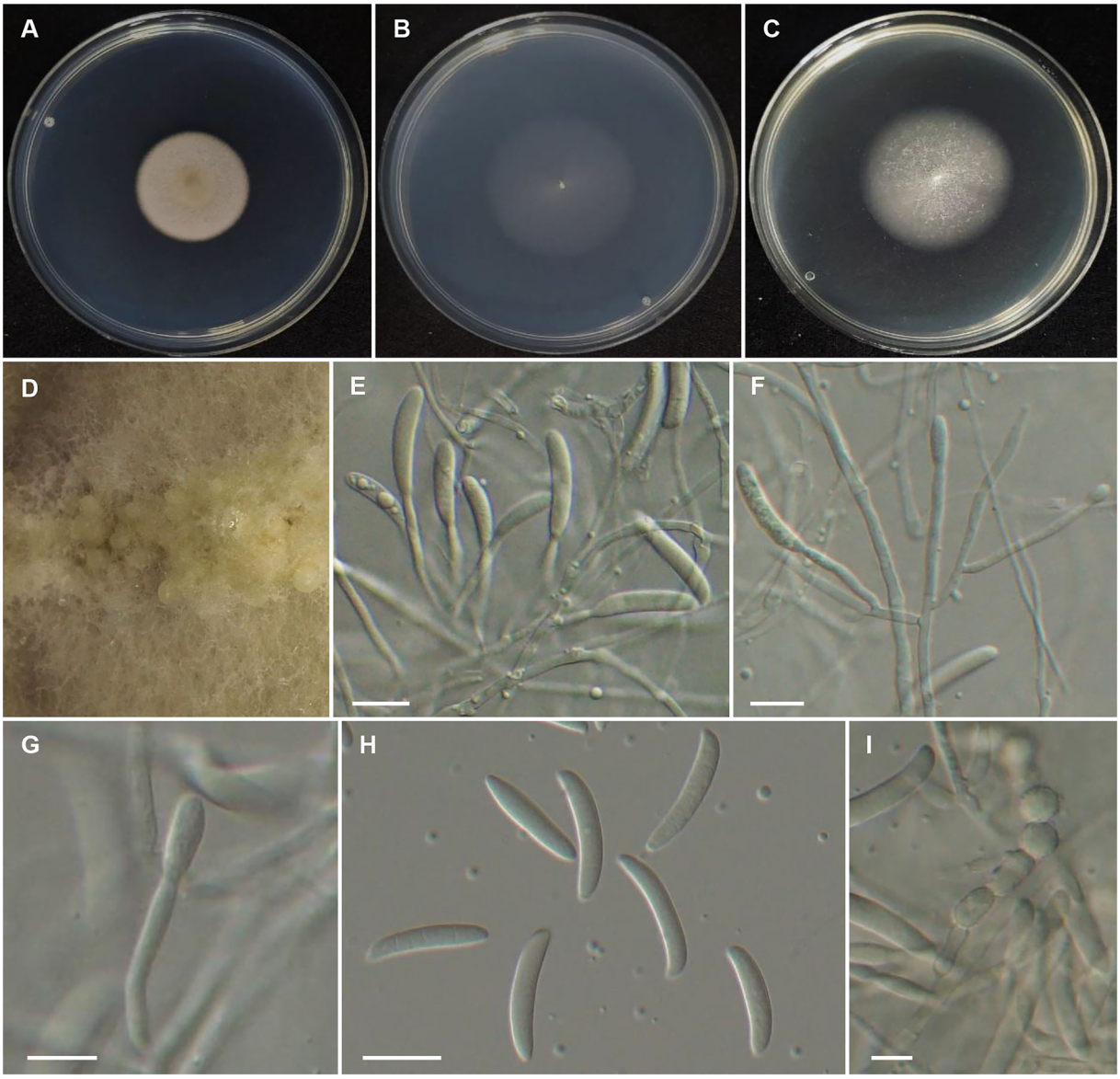

Figure 20. Morphology of *Luteonectria nematophila* CNUFC ROS20. (A) colony on PDA; (B) colony on SNA; (C) colony on MEA; (D) sporodochia on PDA; (E) sporodochial conidiophores; (F) branched conidiophores; (G) monophialides; (H) macroconidia; (I) chlamydospores. Scale bars: E, F, H = 20 µm, G, I = 10 µm.

seven ascospores. Ascospores reddish brown, broad ovate to limoniform, 8.5–9.5 × 5–6.5 µm.

Culture characteristics – Colony on PDA cottony, greenish-yellow, reverse citrine, reaching 52 mm in diameter after 14 d at 25 °C. Colony on OA, floccose, light greenish-yellow near center, white at the edge, reverse yellow-green, reaching 67 mm in diameter after 14 d at 25 °C. Colony on CMA, aerial mycelia sparse, colorless, reverse colorless, reaching 55 mm diameter after 14 d at 25 °C.

Material examined – Republic of Korea, Gyeonggi-do, Goyang-si, August 7 2022, culture CNUFC SN35-44 = NIBRFGC000511450, GenBank numbers: ITS = PQ312703, *RPB2* = PQ453022.

Notes – *Trichocladium crispatum* has been reported from agricultural soil in the Netherlands, estuarine sediment in Germany [74], and soil in this study. The phylogenetic analysis based on multi-gene indicates that our strain clustered together with the ex-type strain *T. crispatum* CBS 149.58 (Figure 1). Our strain is similar to *T. crispatum* CBS 149.58 in shape of ascomata and ascospores [74]. Based on the phylogeny and morphological characteristics, the strain CNUFC SN35-44 was identified as *T. crispatum* and this is the first record of *T. crispatum* in Korea.

Trichoderma azevedoi M.C. Valadares-Inglis & P.W. Inglis, PLOS One 15 (3): e0228485, 11. 2020. MycoBank MB 830305 (Figure 30).

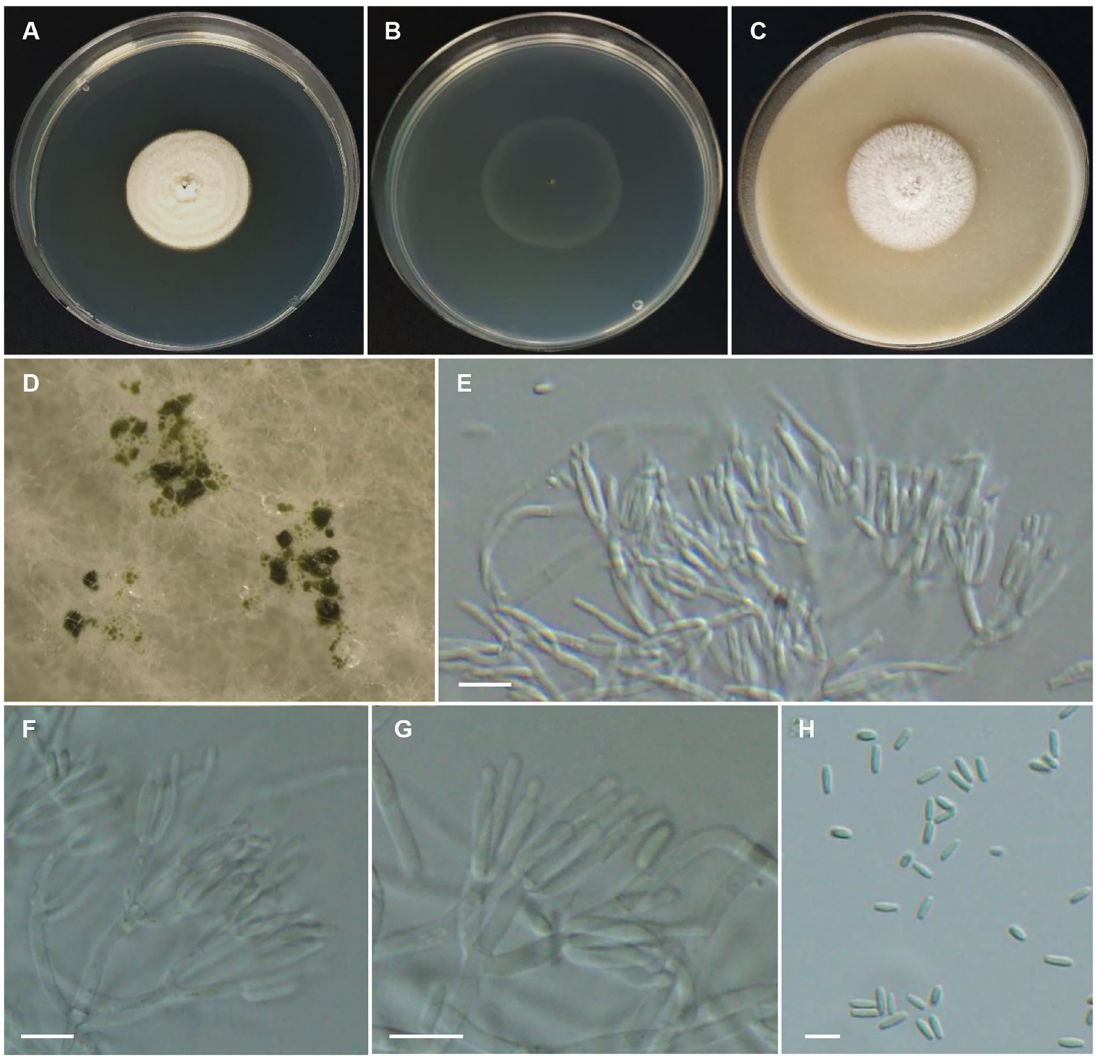

Figure 21. Morphology of *Paramyrothecium sinense* CNUFC 110505. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D) conidiomata on PDA; (E–G) conidiophores and conidiogenous cells; (H) conidia. Scale bars = 10 µm.

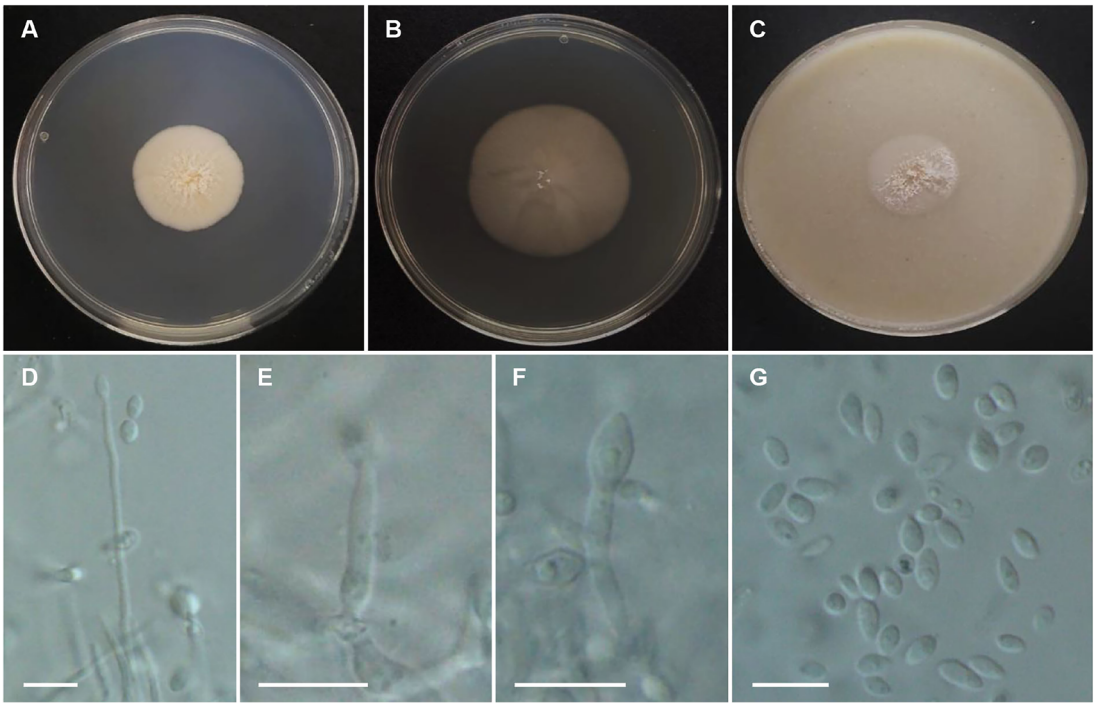

Figure 22. Morphology of *Parasarocladium debruynii* CNUFC AMS8. (A) colony on PDA; (B) colony on MEA; (C) colony on OA; (D) conidiophore; (E, F) conidiogenous cells; (G) conidia. Scale bars = 10 µm.

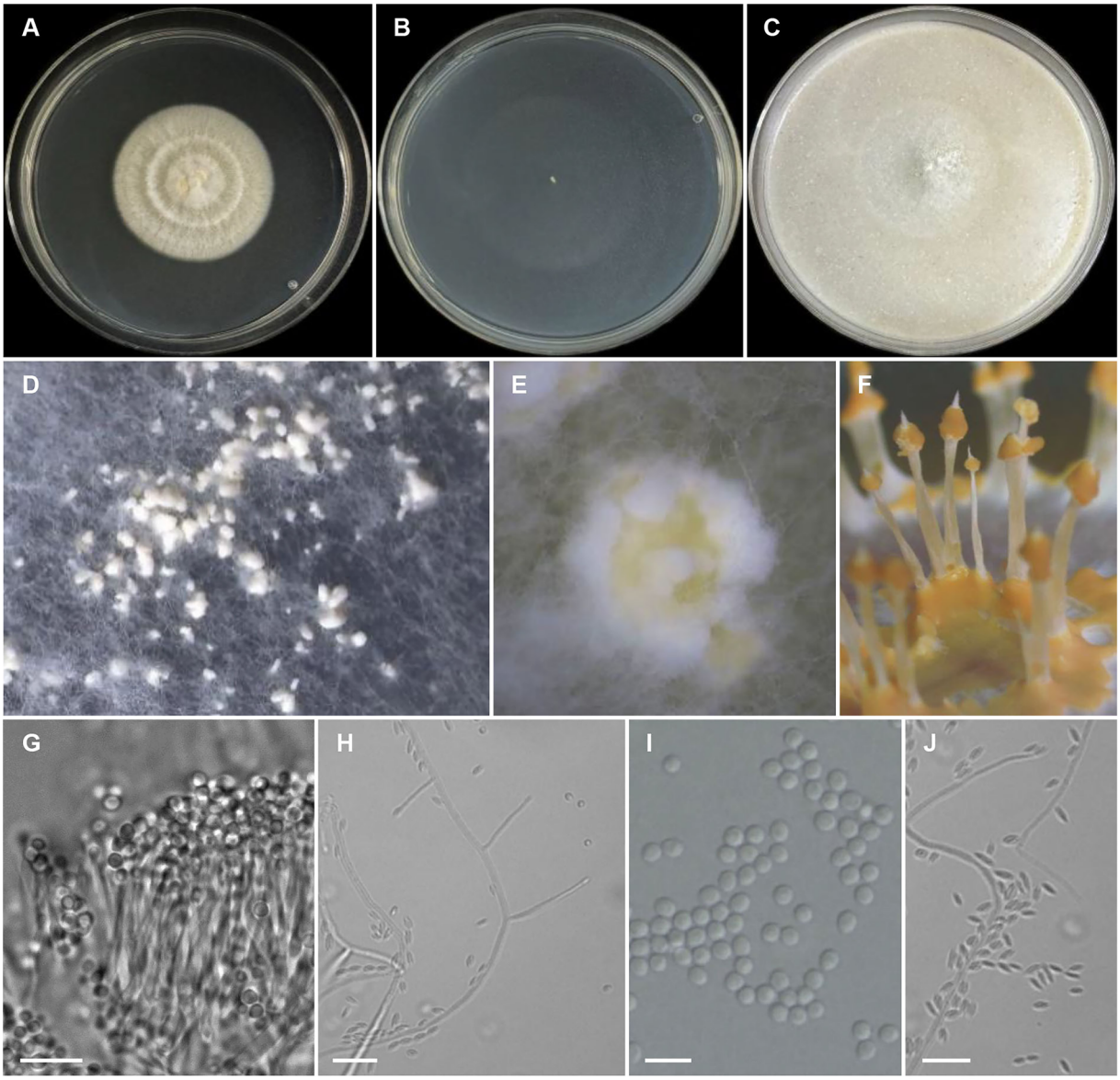

Figure 23. Morphology of *Pleurocordyceps agarica* CNUFC 032307. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D, E) conidial masses on PDA; (F) synnemata on the PDA; (G) α-phialides; (H) β-phialides; (I) α-conidia; (J) β-conidia. Scale bars: G, H, J = 10 µm, I = 5 µm.

Description – Hyphae hyaline. Conidiophores erect, mostly 2.5–3 µm wide, with short secondary branches. Phialides arising singly or in whorls of 2–4, flask-shaped with a narrow neck, 5.5–9(–10) × 2–3(–3.5) µm. Conidia subglobose to ovoid, green in mass, smooth-walled, 2.5–3(–3.5) µm diameter. Chlamydospores abundant, globose to subglobose, terminal or intercalary, smooth-walled, 5–8.5 µm diameter.

Culture characteristics – Colony on PDA rapidly growing, aerial hyphae abundant, initially white, soon becoming greenish yellow, reverse pale greenish yellow, reaching 74 mm in diameter after two days at 25 °C. Colony on CMA green, aerial hyphae sparse, abundant chlamydospores, reverse uncolored, reaching 57 mm in diameter after two days at 25 °C. Colony on OA slow growing, green appearing around the point of inoculation, and white near the margin, strong sporulation, reaching 66 mm in diameter after two days at 25 °C.

Material examined – Republic of Korea, Jeollanam-do, Jeungdo, Ujeon reservoir, from a freshwater sample, May 3 2022, culture CNUFC FH2-1 = HNIBRFG2982, GenBank numbers: ITS = PQ312704, *RPB2* = PQ453 023, *tef* = PQ453031.

Notes – *Trichoderma azevedoi* was first reported from an onion crop soil in Brazil [75]. Our strain was isolated from freshwater. This is the first report of this species from freshwater and also is a new record in Korea.

Trichoderma longifialidicum Q.V. Montoya, L.A. Meirelles, P. Chaverri & A. Rodrigues. 2016. MycoBank MB 814488 (Figure 31).

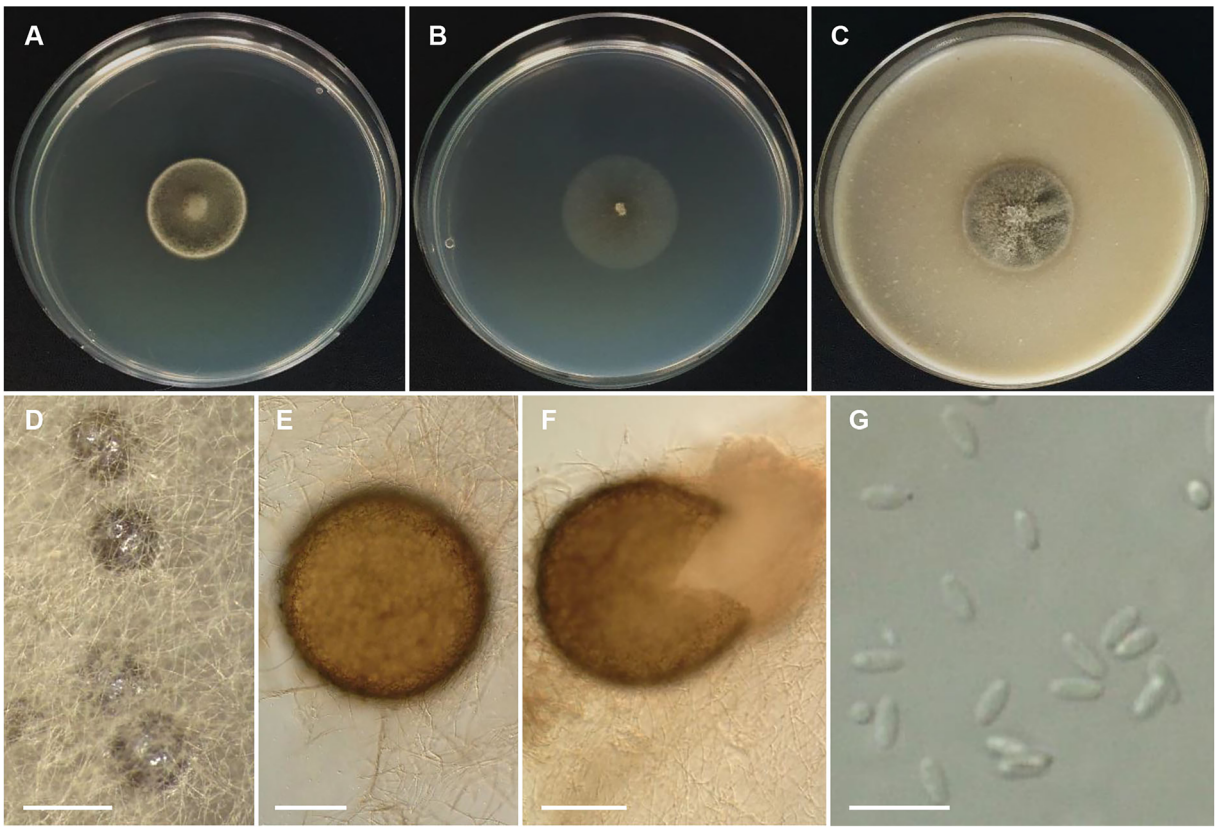

Figure 24. Morphology of *Pyrenochaetopsis sinensis* CNUFC SLJ4. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D) pycnidia forming on PDA; (E, F) mature pycnidia; (G) conidia. Scale bars: D = 500 µm, E, F = 100 µm, G = 10 µm.

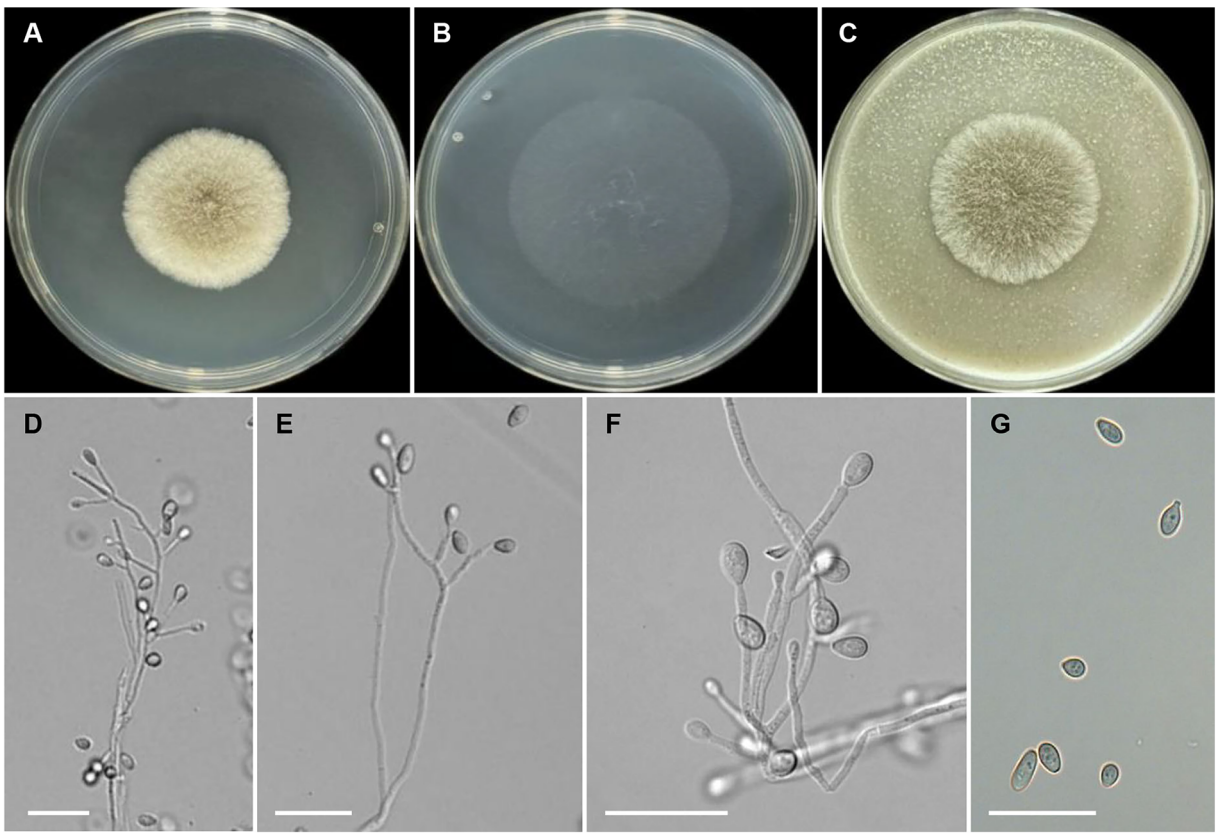

Figure 25. Morphology of *Scedosporium boydii* CNUFC FW8-2. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) conidiogenous cells; (G) conidia. Scale bars = 20 µm.

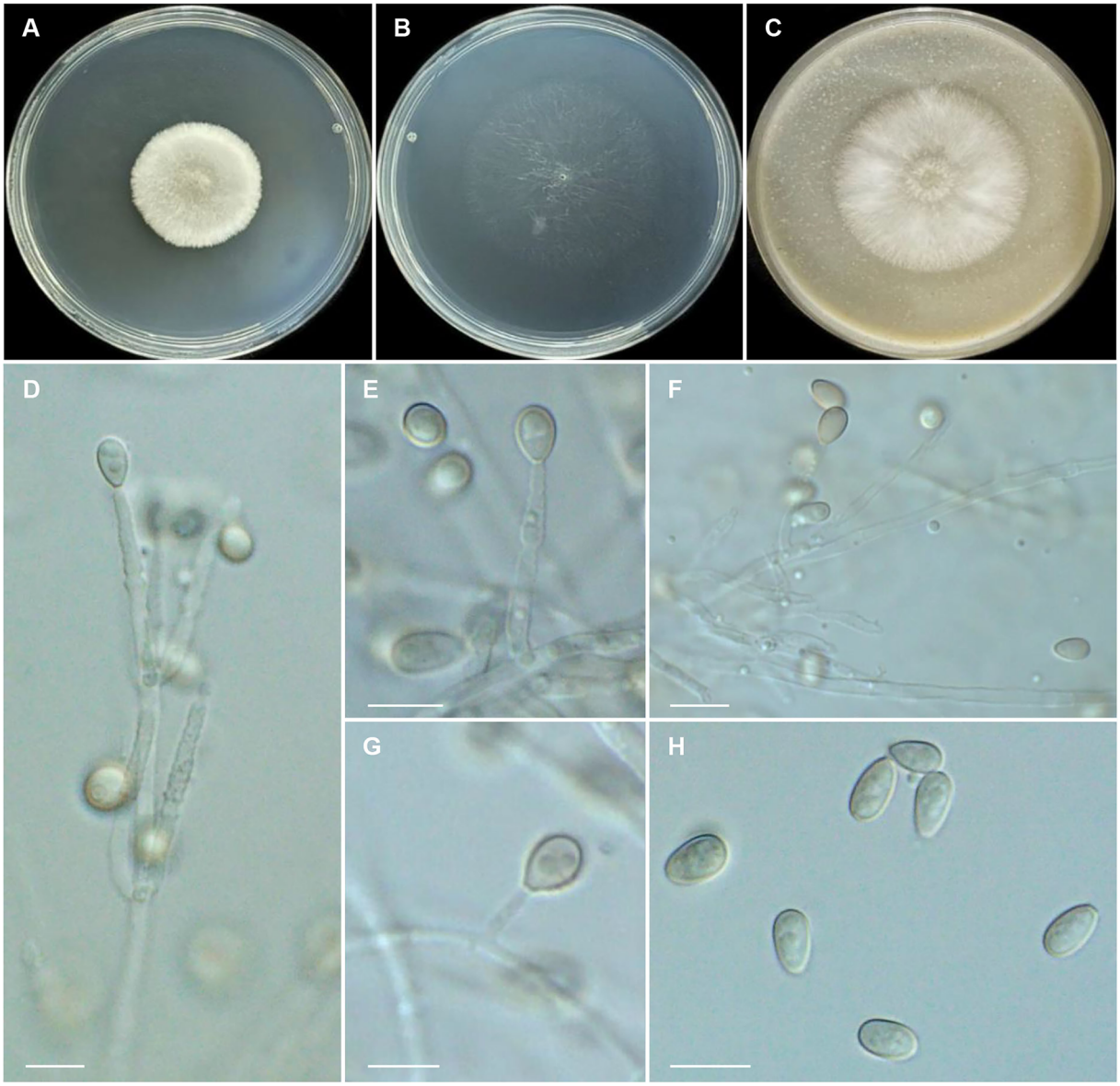

Figure 26. Morphology of *Scedosporium dehoogii* CNUFC JF214-5. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–G) conidiogenous cells; (H) conidia. Scale bars = 10 µm.

Description – Hyphae hyaline, up to 3.5 µm wide. Conidiophores straight or slightly curved, with short branches near the tip. Phialides paired or in whorls of three, flask-shaped with cylindrical at the tip, 6–18 × 1.5–3 µm. Conidia are mostly ellipsoidal, some globose, green in mass, smooth-walled, 2.0–3.0 × 2.5–3.0 µm. Chlamydospores intercalary, smooth-walled, hyaline, up to 10 µm wide.

Culture characteristics – Colony on PDA similar to colony on OA, cotton-like, initially white, gradually turning green, reaching 72 mm (on PDA), and 59 mm (on OA) in diameter after two days at 25 °C. Colony on CMA, sparse aerial mycelia, forming a few large pustules, light yellow, reaching 61 mm in diameter after two days at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Cheongyang-gun, Cheongyang-eup, from a soil sample, December 11 2021, culture CNUFC NYS2-12 = NIBRFGC000510093, GenBank numbers: ITS = PQ312705, *RPB2* = PQ453025, *tef* = PQ453032.

Notes – *Trichoderma longifialidicum* was first found from attine ants in the USA and introduced as a new species by Montoya et al. [76]. The strain CNUFC NYS2-12 was isolated from soil in this study and is phylogenetically related to type strain LESF552 with 100% MLBS support (Figure 12). Furthermore, our strain shares similar features of phialides and ellipsoidal conidia with *Tr. longifialidicum* LESF552. Therefore, based on the phylogeny and morphological characteristics, our strain CNUFC NYS2-12 has been identified as *Tr. Longifialidicum*, which is a new record in Korea.

Xepicula leucotricha (Peck) Nag Raj, Coelomycetous anamorphs with appendage-bearing conidia: 980. 1993. MycoBank MB 359685 (Figure 32).

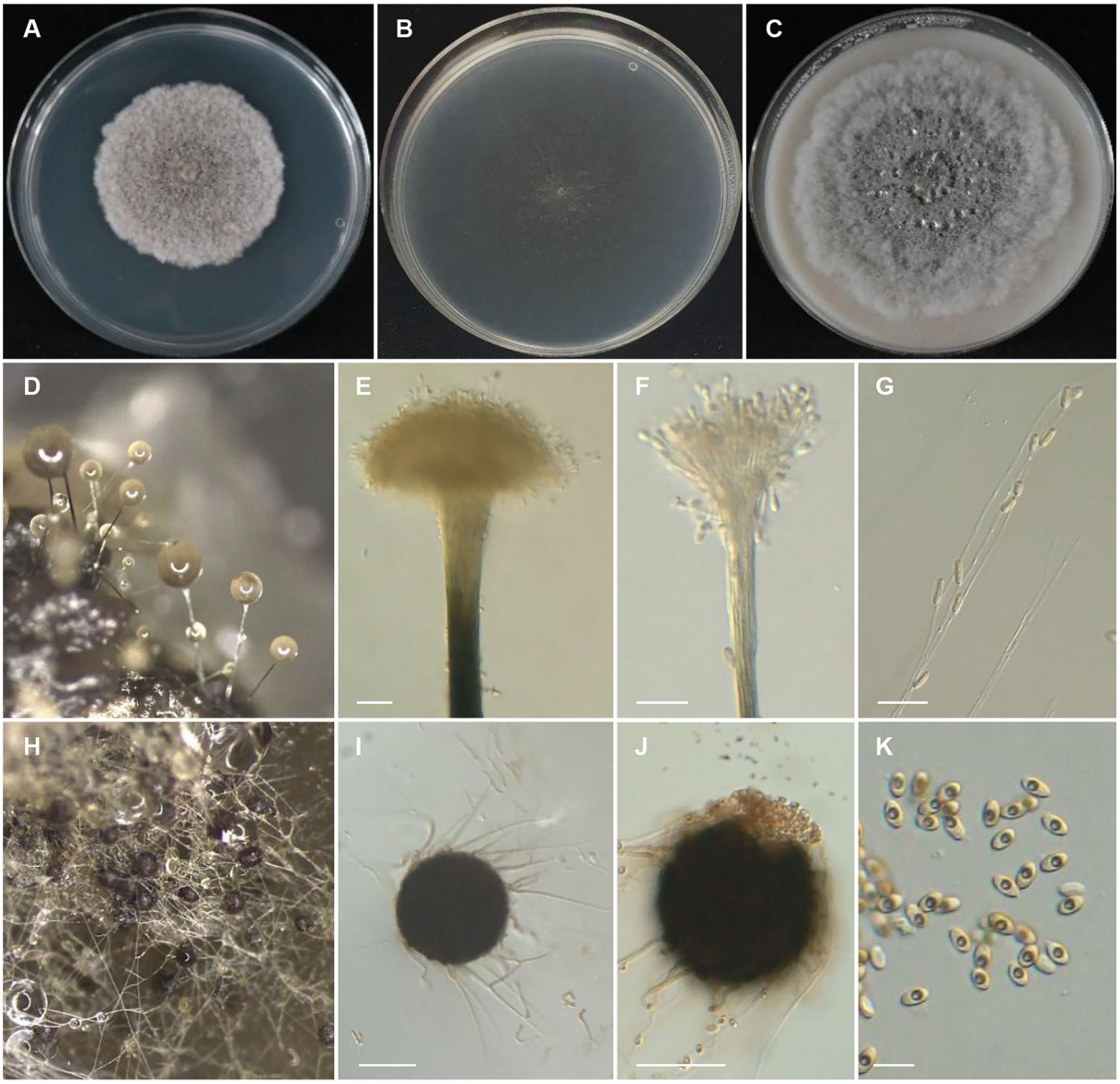

Figure 27. Morphology of *Scedosporium minutisporum* CNUFC GCW112. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) synnematous conidiomata; (G) conidiogenous cells and conidia; (H–J) ascomata; (K) ascospores. Scale bars: E–G = 20 µm, I, J = 50 µm, K = 10 µm.

Description – Sporodochia stromatic, superficial, scattered to gregarious, oval to elongate. Setae simple, unbranched, straight, septate, hyaline to light green, smooth-walled, dark green near the base 106–354 × 3.0–4.5 µm. Conidiogenous cells phialidic, hyaline, smooth, cylindrical, 7–12 × 2.5–3 µm. Conidia hyaline to pale green, cylindrical, smooth-walled, 7–9 × 1.5–2.5 µm.

Culture characteristics – Colony on PDA radially sulcate, moderate to strong yellow, yellow pigments, reverse moderate orange yellow, reaching 25 mm in diameter after 7 d at 25°C. Colony on OA floccose, light yellow, reverse pale greenish yellow, reaching 48 mm in diameter after 7 d at 25°C. Colonies on CMA floccose, white, reaching 33 mm in diameter after 7 d at 25°C.

Material examined – Republic of Korea, Jeollanam-do, Jangseong-gun, Jangseong-eup, Yonggang-ri, from a freshwater sample, March 10 2023, culture CNUFC JDCW6-1 = NNIBRFG46721, GenBank numbers: ITS = PQ312706, *RPB2* = PQ453024.

Notes – *Xepicula leucotricha* has been reported from soil in Brazil, Colombia, and India [73]. Phylogenetic analysis placed the CNUFC JDCW6-1 grouped with type strain of *X. leucotricha* CBS 256.57 as a single lineage (Figure 13). The isolation of *X. leucotricha* from freshwater in Korea is the first report of this species from freshwater and a new record in Korea.

Xylomelasma sordida Réblová, Mycologia 98 (1): 88. 2006. MycoBank MB 501369 (Figure 33).

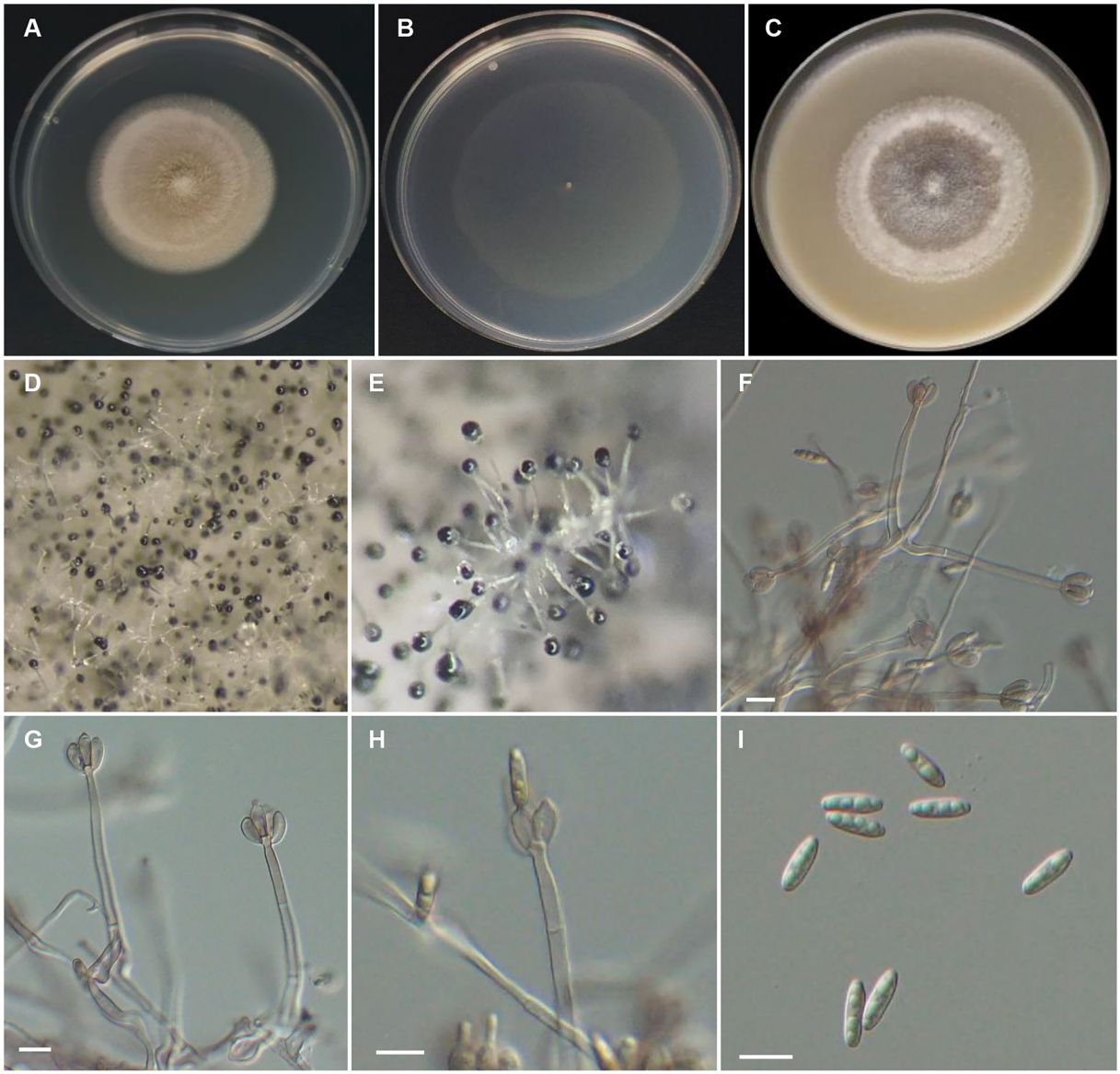

Figure 28. Morphology of *Striatibotrys rhabdosporus* CNUFC UCIS4. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D, E) conidiophores on PDA; (F–H) conidiophores and conidiogenous cells; (I) conidia. Scale bars = 10 µm.

Description – Hyphae hyaline to brown, septate, branched, smooth-walled, sometimes swollen, 2.5–5.0 µm wide, forming a constricting ring. Ascomata scattered, globose to subglobose, immersed, dark brown, (50–)71–105 µm in diameter.

Culture characteristics – Colonies on PDA olive-brown, cottony at the center, margin filamentous, reverse dark grayish-blackish green, reaching 48 mm in diameter after 7 d at 25 °C. Colonies on OA, light olive gray to grayish green, reverse dark grayish green, reaching 41 mm in diameter after 7 d at 25 °C. Colonies on CMA, flat with slightly raised at center, aerial mycelium aggregated into slimy masses, small pellets, reverse uncolored, reaching 50 mm in diameter after 7 d at 25 °C.

Material examined – Republic of Korea, Chungcheongnam-do, Gongju-si, Jeongan-myeon, March 15 2021, from a soil sample, culture CNUFC JAS1-39 = NIBRFGC000510137, GenBank numbers: ITS = PQ466863, LSU = PQ443748.

Notes – *Xylomelasma sordida* has been reported from the wood of *Alnus glutinosa* in the Czech Republic and Southern Moravia [77], and on the dead parts of coppiced *Ulmus* spp. in deciduous forests in Norway [78]. Phylogenetic analysis placed the CNUFC JAS1-39 grouped with the other strain of *Xy. sordida* (Figure 14). Therefore, we identify our strain as *Xy. sordida*. The isolation of *Xy. sordida* from the soil in Korea was the first report of this species from soil and also is a new record in Korea.

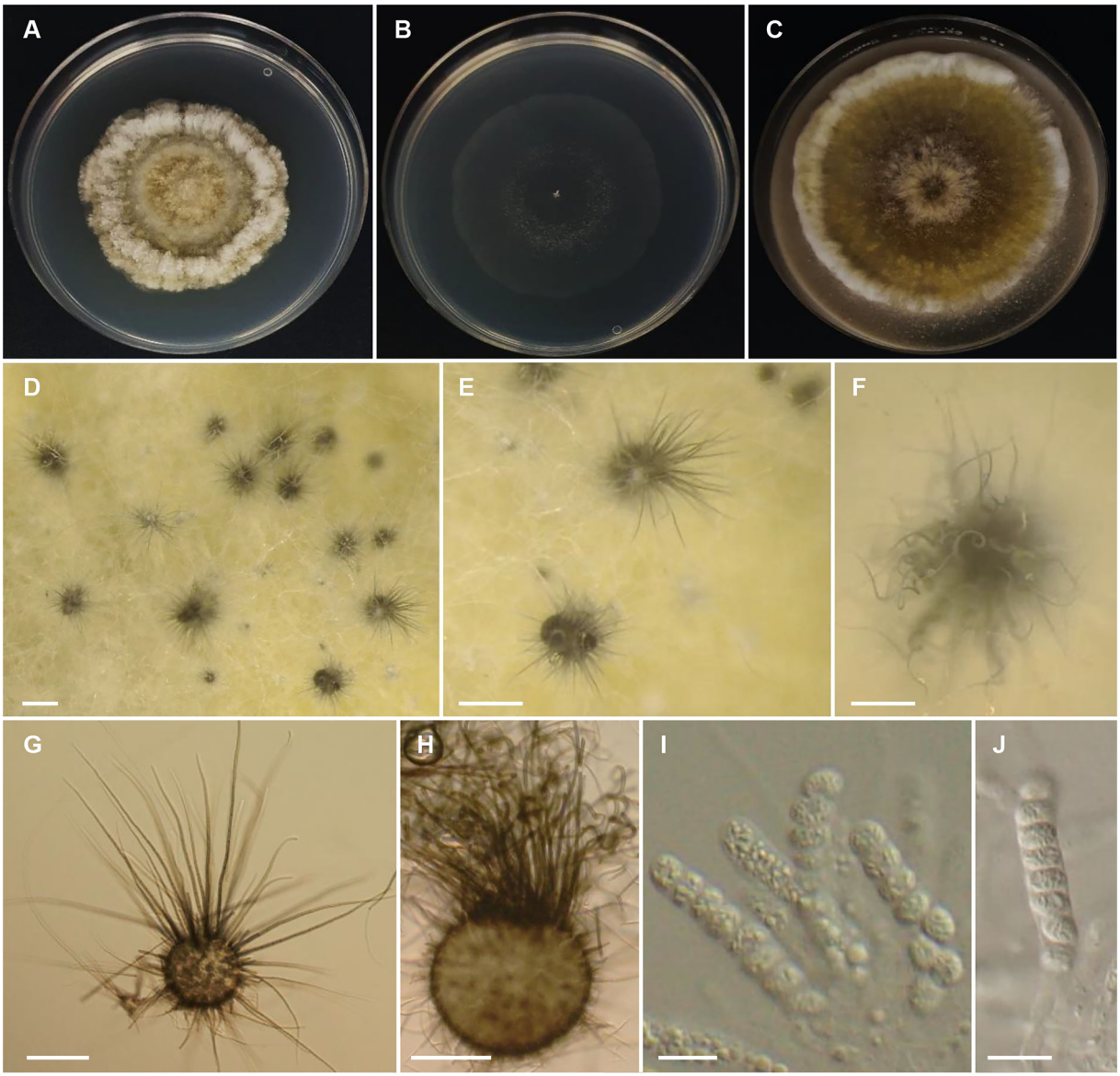

Figure 29. Morphology of *Trichocladium crispatum* CNUFC SN35-44. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) ascomata and ascomatal hairs on PDA; (G, H) ascomata and ascomatal hairs mounted in lactic acid; (I, J) asci and ascospores. Scale bars: D–F = 200 µm, G, H = 100 µm, I, J = 10 µm.

4. Discussion

The results presented in this study were obtained by combining morphological and molecular data. The phylogenetic analyses demonstrated the presence of *Ach. virescens*, *Arx. gangligerum*, *C. euphorbiae*, *Co. typhicola*, *G. aggregata*, *L. nematophila*, *P. sinense*, *Pa. debruynii*, *Pl. agarica*, *P. sinensis*, *S. boydii*, *S. dehoogii*, *S. minutisporum*, *St. rhabdosporus*, *T. crispatum*, *Tr. azevedoi*, *Tr. longifialidicum*, *X. leucotricha*, and *Xy. sordida* for the first time in Korea.

Documenting fungal species, whether they are new or new host records, is an important contribution to diversity and taxonomy knowledge, and provides essential information for accurate fungal species identification and potential metabolite identification and evaluation. In this study, 13 of the 19 species identified, including *Ach. virescens*, *Arx. gangligerum*, *C. euphorbiae*, *G. aggregata*, *L. nematophila*, *P. sinense*, *Pa. debruynii*, *Pl. agarica*, *Py. sinensis*, *T. crispatum*, *Tr. azevedoi*, *Tr. longifialidicum*, and *Xy. sordida*, have only been reported from a few countries. In addition, seven of the 19 species were reported from freshwater environments for the first time, including *Arx. gangligerum*, *Co. typhicola*, *P. sinense*, *S. boydii*, *S. dehoogii*, *S. minutisporum*, and *Tr. azevedoi*. Therefore, the findings of this study contributed to the knowledge of the geographic distribution of *Sordariomycetes* spp. and can improve our understanding of the distribution of these microorganisms in ecosystems.

Scedosporium spp. are ubiquitous and emerging opportunistic mold pathogens found in various natural habitats and hosts [79,80]. Previously, *S. boydii*

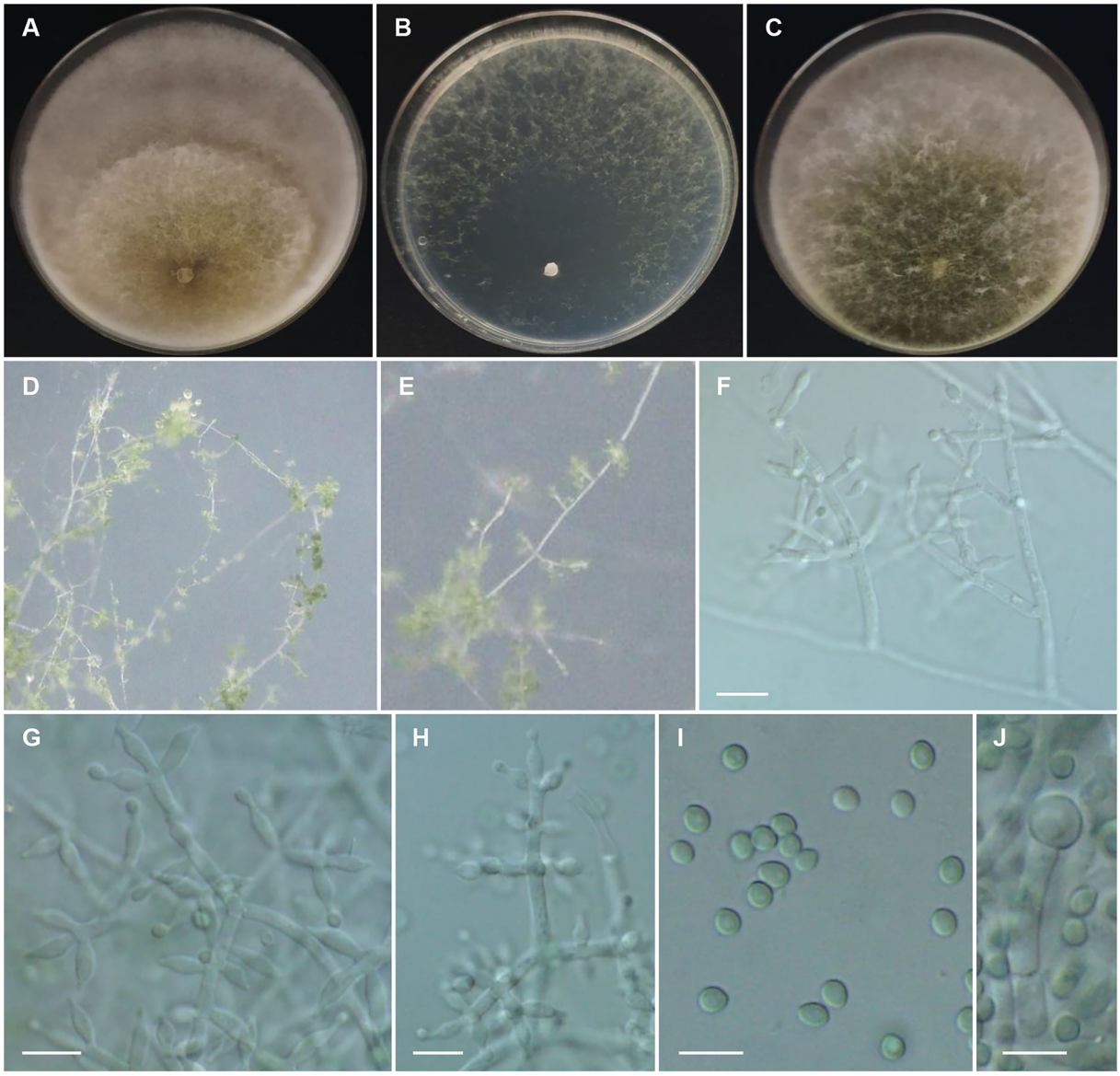

Figure 30. Morphology of *Trichoderma azevedoi* CNUFC FH2-1. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D, E) conidiophores; (F–H) conidiophores and phialides; (I) conidia; (J) conidia and chlamydospore. Scale bars = 10 μm.

has been reported in the USA, Thailand, Austria, and the Republic of Zaire [61]; *S. dehoogii* has been identified in Thailand, Mexico, India, Chile, Australia, and Netherlands [62–69] and *S. minutisporum* has been found in France, Australia, Austria, and Thailand [71,72]. The three species, *S. boydii*, *S. dehoogii*, and *S. minutisporum*, found in freshwater samples from Korea suggest that these species may have a worldwide distribution. Other studies have reported that *Scedosporium* spp. possess many biological activities, such as being antitumor, antimicrobial, insecticidal, and antidiabetic [81]. For example, a novel compound, AS-183, produced by *Scedosporium* sp. SPC-15549 inhibits acyl-CoA: cholesterol acyltransferase (ACAT) [82]. The three species of *Scedosporium* isolated in this study may have highly valuable attributes that could be the focus of future research.

Species of the family *Chaetomiaceae* are medically and economically important [45,83]. For example, Han et al. [84] have recently identified tricrilactones A–H from *T. crispatum*; these are potent antiosteoporosis macrolides with distinctive ring skeletons. Some of the fungi found in Korea in this study belonged to the family *Chaetomiaceae*, including *Ach. virescens*, *Arx. gangligerum*, and *T. crispatum*. Therefore, there is a need for further research to explore the metabolites from these species.

Numerous studies have reported that species in the genus *Trichoderma* produce a variety of secondary metabolites during growth and are recognized worldwide as biocontrol agents of plant diseases [85]. Recently, Silva et al. [86] demonstrated that *Tr. azevedoi* CEN1241's volatile organic compound profiles changed with colony age and altered the ability of the biocontrol agent to suppress *Sclerotinia*

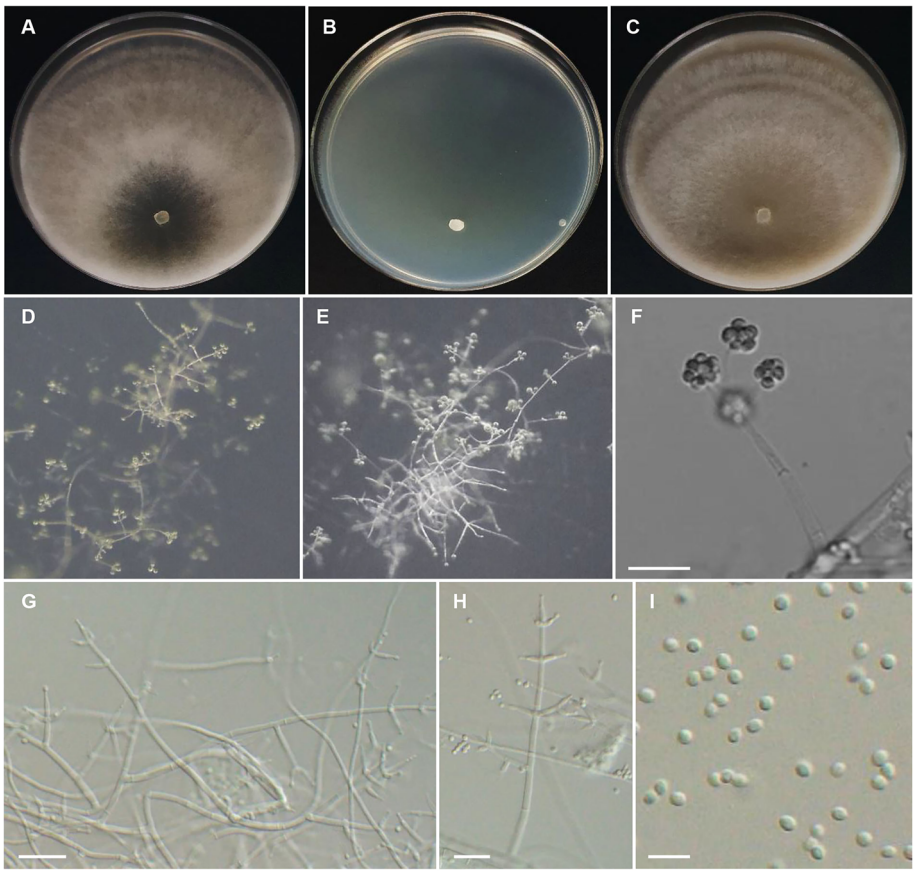

Figure 31. Morphology of *Trichoderma longifialidicum* CNUFC NYS2-12. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) Conidiophores; (G, H) conidiophores and phialides; (I) Conidia. Scale bars: F = 40 μm, G, H = 20 μm, I = 10 μm.

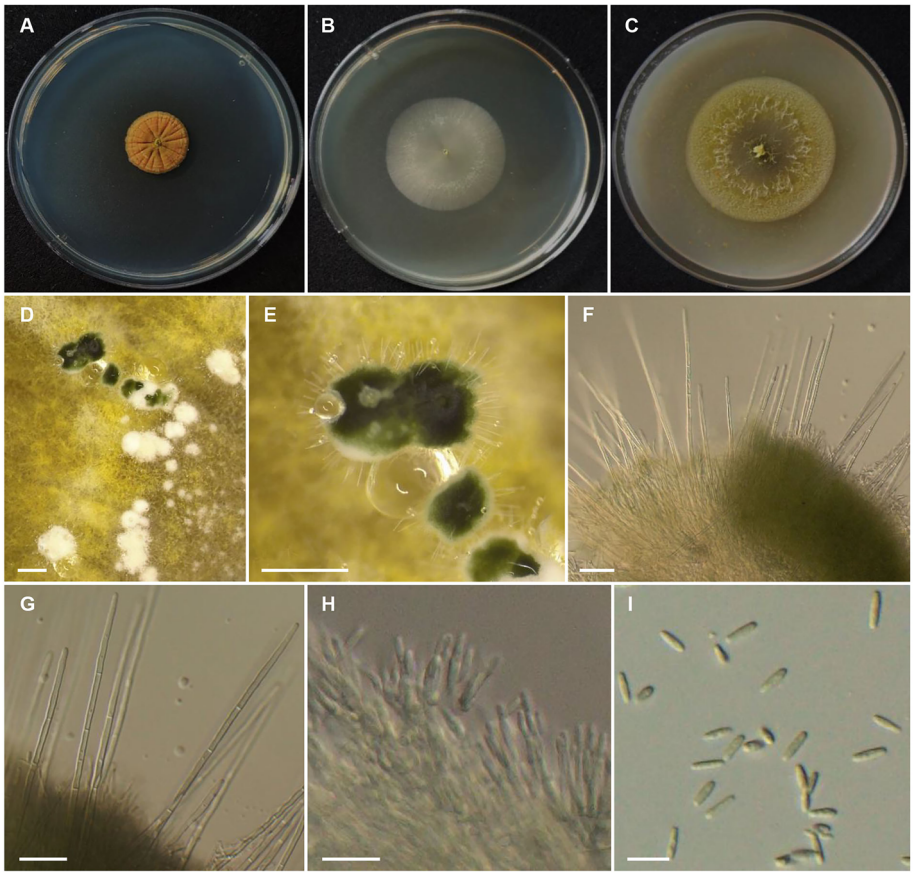

Figure 32. Morphology of *Xepicula leucotricha* CNUFC JDCW6-1. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D, E) sporodochial conidiomata on PDA; (F, G) setae; (H) conidiophores and conidiogenous cells; (I) conidia. Scale bars: D, E = 500 μm, F, G = 50 μm, H = 20 μm, I = 10 μm.

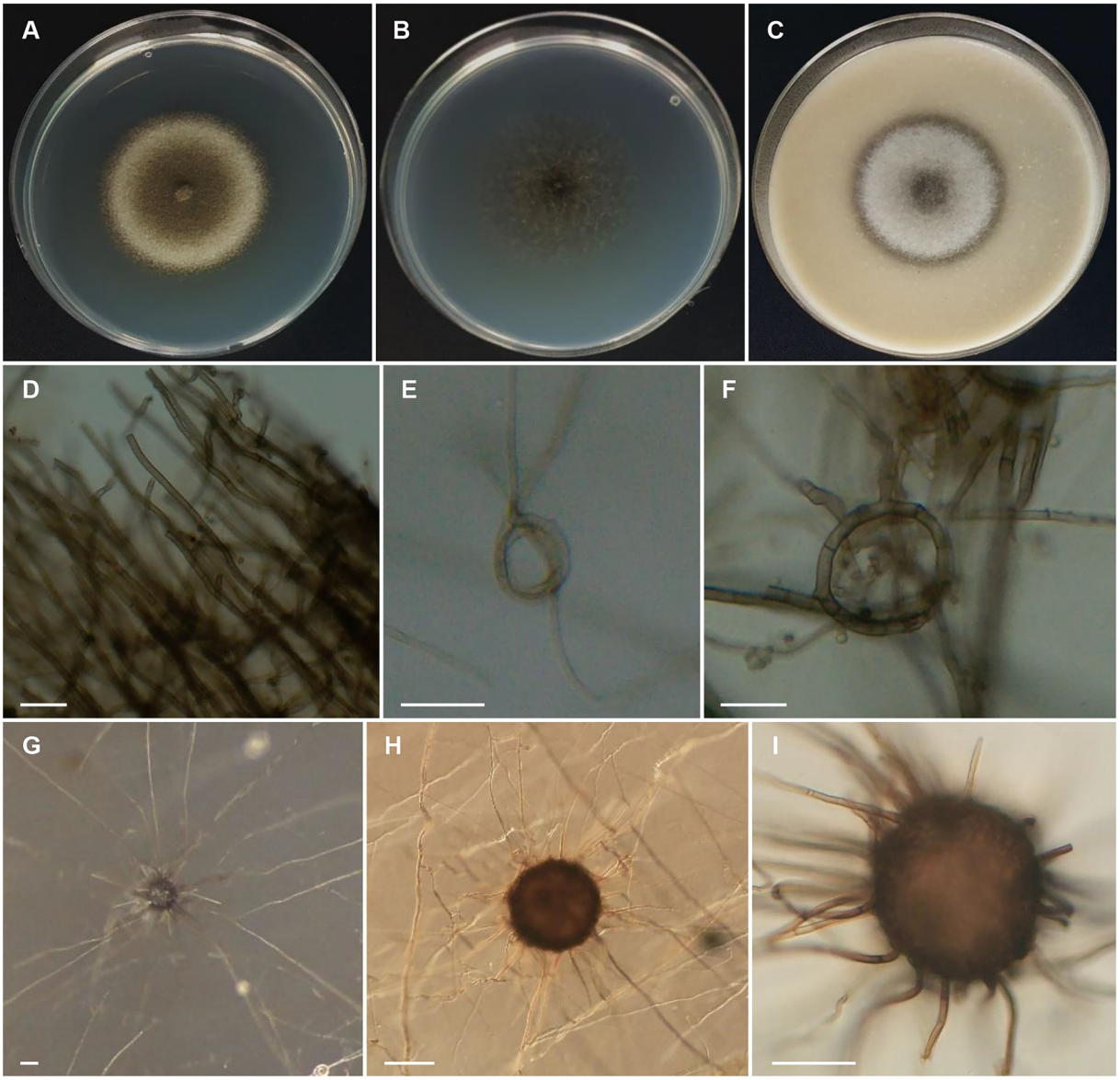

Figure 33. Morphology of *Xylomelasma sordida* CNUFC JAS1-39. (A) colony on PDA; (B) colony on CMA; (C) colony on OA; (D–F) hyphae and coiled hyphae; (G–I) ascomata on CMA. Scale bars: D–F = 20 µm, G–I = 50 µm.

sclerotiorum. The two *Trichoderma*, *Tr. azevedoi* and *Tr. longifialidicum* obtained in this study could be promising biocontrol agent candidates.

Species of *Pleurocordyceps* exhibit significant potential to produce a diverse range of secondary metabolites. Some researchers have reported that *Pl. nipponicus* and *Pl. phaothaiensis* contain antibacterial, antioxidant, antitumorigenic, anti-inflammatory, and antimicrobial compounds [87–89]. Therefore, there is a need for further studies to explore the metabolites from the *Pl. agarica* isolated from Korea in this study.

According to a recent report, there are 2.5 million species of fungi globally [90]. However, only 156,000 species of fungi have been formally described and are accepted in the fungal kingdom currently [90], highlighting the potential for unraveling novel fungal taxa in largely untapped ecosystems.

The findings of this study provide additional insights into fungal diversity in the class *Sordariomycetes* in Korea. Further studies will increase our understanding of the occurrence, distribution, and host (substrate) of the fungal group in Korea.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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