

Notes of Five Wood-Decaying Fungi from Juwangsang National Park in Korea

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ABSTRACT

Wood-decaying fungi are essential decomposers in forest ecosystems. They decompose wood substrates by producing various lignocellulolytic enzymes, which have significant industrial and medical applications. A survey was conducted at the Juwangsang National Park from 2018 to 2019 to determine the diversity of macrofungi in Korea. Five previously unrecorded wood-decaying polyporoid and corticioid fungi were identified among the collected specimens: *Eichleriella sinensis*, *Hymenochaete anomala*, *Hyphoderma subsetigerum*, *Lyomyces orientalis*, and *Pseudowrightoporia crassihypha*. These species were identified based on morphological, molecular, and phylogenetic analyses of the internal transcribed spacer (ITS) and nuclear large subunit rDNA (nLSU) region. In this study, we provide detailed macro- and micro-morphological figures with phylogenetic trees to support the discovery of five new species in Korea.

ARTICLE HISTORY

Received 12 July 2023
Revised 29 November 2023
Accepted 20 December 2023

KEYWORDS

Wood-decaying fungi; polyporoid fungi; corticioid fungi; internal transcribed spacer; taxonomy

1. Introduction

Wood-decaying fungi play a crucial role in forest ecosystems by degrading wood-based materials and contributing to nutrient cycling [1]. They produce lignocellulolytic enzymes such as lignin peroxidase, manganese peroxidase, laccase, chitinase, cellulase, and hemicellulase, which breakdown lignin, cellulose, and hemicellulose [2,3]. These enzymes are applied to processes, such as pulping, wastewater treatment, and bioremediation of aromatic compounds [4,5]. In addition, wood-decaying fungi produce biologically active compounds that can be used for medicinal purposes [6].

Juwangsang National Park is located in the Gyeongsangbuk-do Province, Eastern Korea. Juwangsang was designated as a national park in 1976 due to its unique geological structures, such as welding facies and columnar joints [7]. Additionally, Juwangsang National Park has a representative vegetation of the mid-temperate zone dominated by pine and oak trees, which provides a suitable habitat for macrofungi [8,9]. A previous study reported 503 species in Juwangsang National Park [10]. However, these species were identified based on morphological traits, suggesting the necessity of DNA-based molecular analysis for accurate identification. Morphological characteristics are used to identify species and

determine their morphological evolution [11]. However, highly speciose groups or complex clades of fungi can be misidentified [12]. Thus, a DNA-based molecular analysis of the internal transcribed spacer (ITS) region is necessary. The ITS and nuclear large subunit rDNA (nLSU) regions in fungi are hyper-variable because of the rapid evolution in its rRNA gene, a significant barcode gap, and easy amplification [13]. Therefore, these regions have become the most popular region for fungal identification at the species level and was also applied in this study. We investigated the diversity of macrofungi in Juwangsang National Park from 2018 to 2019 and collected 406 macrofungal specimens during the survey. Consequently, we reported five previously unrecorded species [14]. Furthermore, we discovered five other species new to Korea. The identification results are supported by morphological and molecular analyses.

2. Materials and methods

2.1. Sampling

Juwangsang National Park (36°19'–36°27' N, 129°04'–129°14' E) is located across Cheongsong-gun and Yeongdeok-gun of Gyeongsangbuk-do province, South Korea. Fungal specimens were collected from

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2018 to 2019 along the trail near Dalgi Falls, Geumeungwangi, Jeolgol, and Jusan Reservoir. Collected specimens were dried at 60°C for 24 h and stored with silica gel to prevent contamination. The specimens were deposited in the Korea University Collection (KUC) and National Institute of Biological Resources (NIBR).

2.2. Molecular approach

DNA was extracted from the dried specimens using an AccuPrep® Genomic DNA Extraction Kit (Bioneer, Daejeon, South Korea). The ITS region was amplified with ITS1F/ITS4B, ITS5/ITS4, or ITS5/LR3 primer sets [15,16]. For *Eichleriella sinensis*, nLSU region was amplified with LR0R/LR5 primer set [17,18]. PCR product purification was conducted using the AccuPrep® PCR Purification Kit and AccuPrep® Gel Purification Kit (Bioneer, Daejeon, South Korea) following the manufacturer's instructions. MacroGen Inc. (Seoul, South Korea) performed DNA sequencing of amplified PCR products. Each sequencing result was edited using the SeqMan Lasergene package version 7.0.0 (DNASTar Inc., Madison, WI). The edited sequences were compared with sequences in GenBank using BLASTn v. 2.13.0. Reference sequences were obtained from the NCBI GenBank database (www.ncbi.nlm.nih.gov/genbank/) for phylogenetic analysis. Sequence alignment was conducted using MAFFT v. 7.453 [19]. Phylogenetic analysis was performed with ITS or ITS + nLSU combined datasets employing the maximum-likelihood (ML) method, which used RAXML-HPC2 on XSEDE v. 8.2.12 with GTR+G model and 1000 bootstrap replicates for tree inference [20]. The above phylogenetic analysis was performed using the CIPRES web portal [21]. Phylogenetic trees were edited using FigTree v. 1.4.3 and Adobe Illustrator CS6 (Adobe Systems Inc., San Jose, CA). Bootstrap support values >70% are indicated in the tree. The sequences of the five species are deposited in GenBank.

2.3. Morphological observation

Microscopic structures were observed using an Olympus BX51 light microscope (Olympus, Tokyo, Japan) and images were captured using a DP20 microscope camera (Olympus, Tokyo, Japan). Macroscopic images of each specimen were captured using Sony α 6500 camera (Sony, Tokyo, Japan). At least 20 basidia and basidiospores were detected. The specific color terms conform to those in Munsell Soil Color Book [22]. The following abbreviations

are used: L = mean spore length; W = mean spore width; Q = L/W ratio.

3. Results

A total of 406 macrofungal specimens were collected from Juwangsang National Park between 2018 and 2019. Among them, 252 specimens were identified as wood-decaying polyporoid or corticioid fungal species. These specimens were classified into seven orders, 27 families, 67 genera, and 133 species, including new species candidates. The order Polyporales (70 species, 52%) was the most abundant, followed by Russulales (25 species, 19%), and Hymenochaetales (24 species, 18%) (Figure 1). The most abundant species was *Irpex lacteus* (18 specimens), followed by *Trametes versicolor* (11 specimens), *Xylobolus peculiare* (nine specimens), and *Stereum hirsutum* (eight specimens). Six specimens (KUC20181101-43, KUC20180712-40, KUC20181101-24, KUC20190620-29, KUC20191011-08B, and KUC20191011-17B) were assigned to five unrecorded species candidates in Korea based on the ITS sequence homology. They were highly supported by high percentage of homology at 99–100% with reference sequences (Table 1). Meanwhile, KUC20181101-43 needed additional gene region (nLSU) for accurate identification. As a result, KUC20181101-43 (GenBank accession number: OR857463) showed 99% (729/730bp) homology with *E. sinensis* He4196 and 100% (730/730bp) homology with *E. sinensis* He5057. The phylogenetic analysis revealed that KUC20181101-43, KUC20180712-40, and KUC20190620-29 were clustered with *E. sinensis*, *Hym. anomala*, and *L. orientalis*, respectively, with 100% bootstrap values (Figures 2–4). KUC20191011-08B and KUC20191011-17B were identified to *P. crassihypha* (Figure 5). KUC20181101-24 was clustered in the *Hyp. subsetigerum* group (Figure 6). However, three specimens had low resolution (Figure 6 and 5).

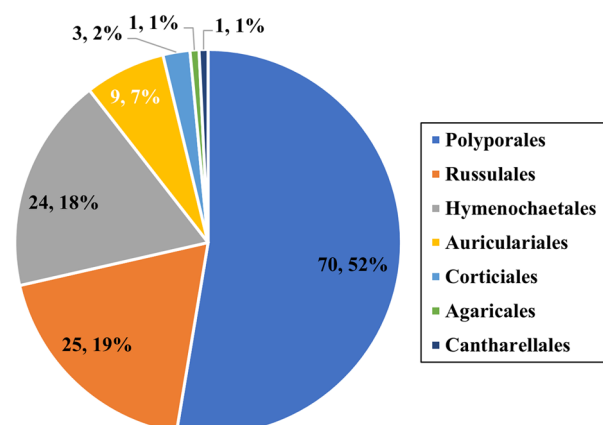


Figure 1. Diversity of wood-decaying fungi at the order level in Juwangsang National Park.

Table 1. Molecular identification of five unrecorded fungal species in Juwangsan National Park.

Specimen ID	Identity	Order	Sequence homology with Ref ^f	Gen. Acc. No. ^a for ITS	
				In this study	Ref ^f
KUC20181101-43	<i>Eichleriella sinensis</i>	Aur ^b	100% (511/511 bp)	OR150148	MH178254
KUC20180712-40	<i>Hymenochaete anomala</i>	Hym ^c	99% (596/597 bp)	OR150149	JQ279567
KUC20181101-24	<i>Hyphoderma subsetigerum</i>	Pol ^d	99% (546/552 bp)	OR150150	AJ534277 ^T
KUC20190620-29	<i>Lyomyces orientalis</i>	Hym	100% (345/345 bp)	OR150151	NR_169890 ^T
KUC20191011-08B	<i>Pseudowrightoporia crassihypha</i>	Rus ^e	99% (488/494 bp)	OR150152	NR_154620 ^T
KUC20191011-17B		Rus	99% (489/495 bp)	OR150153	NR_154620 ^T

^aGen. acc. no., GenBank accession number.

^bAur, Auriculariales.

^cHym, Hymenochaetales.

^dPol, Polyporales.

^eRus, Russulales.

^fRef, reference specimens.

^THolotype.

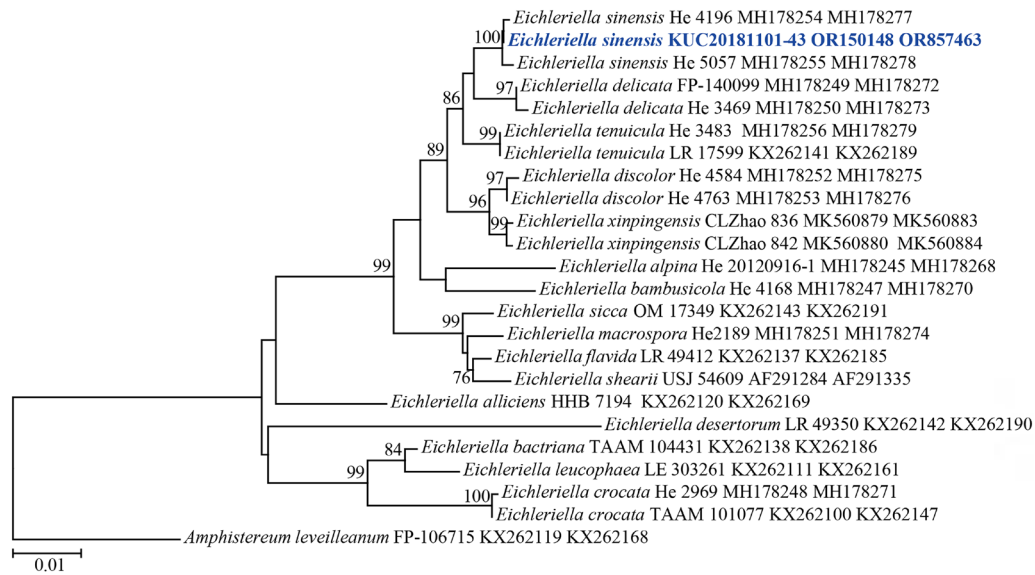


Figure 2. Maximum-likelihood tree of *Eichleriella sinensis* KUC20181101-43. The tree was constructed based on ITS+nLSU combined datasets of the genus *Eichleriella*. *Amphistereum leveilleianum* was used as an outgroup. The newly generated sequence is shown in blue and bold. Bootstrap support values more than 70% are shown. The numbers after scientific name indicate specimen ID and GenBank accession numbers (ITS and LSU regions).

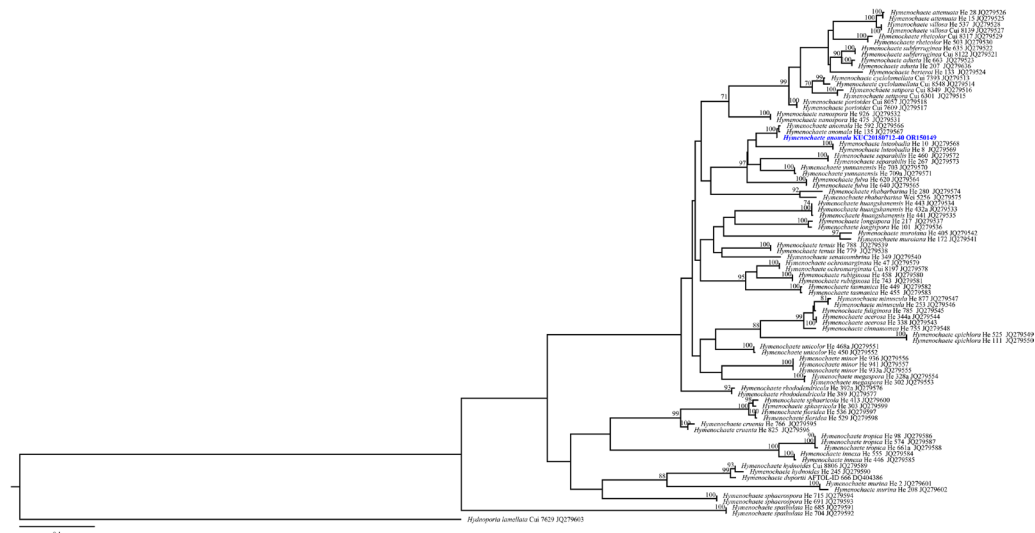


Figure 3. Maximum-likelihood tree of *Hymenochaete anomala* KUC20180712-40. The tree was constructed based on ITS sequence datasets of the genus *Hymenochaete*. *Hydnoporia lamellata* was used as an outgroup. The newly generated sequence is shown in blue and bold. Bootstrap support values more than 70% are shown. The numbers after scientific name indicate specimen ID and GenBank accession number (ITS region).

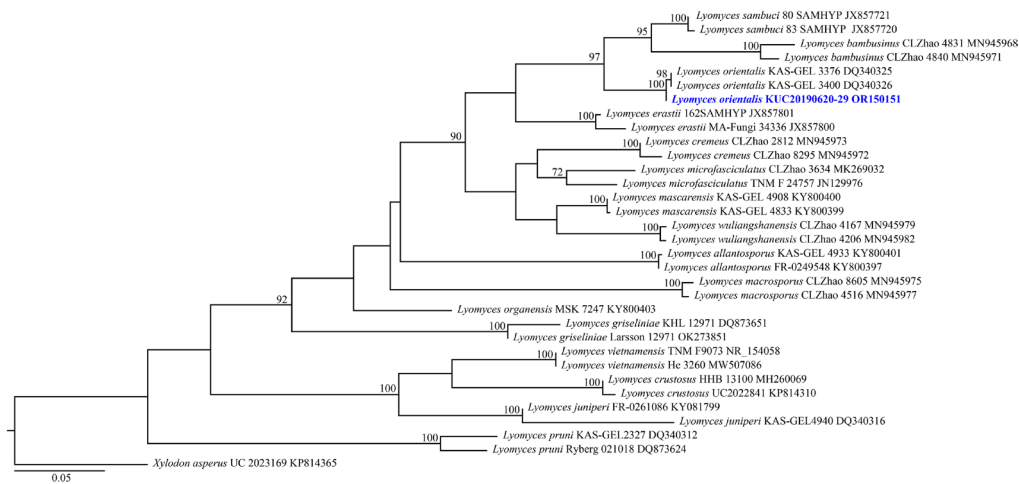


Figure 4. Maximum-likelihood tree of *Lyomyces orientalis* KUC20190620-29. The tree was constructed based on ITS sequence datasets of the genus *Lyomyces*. *Xylodon asperus* was used as an outgroup. The newly generated sequence is shown in blue and bold. Bootstrap support values more than 70% are shown. The numbers after scientific name indicate specimen ID and GenBank accession number (ITS region).

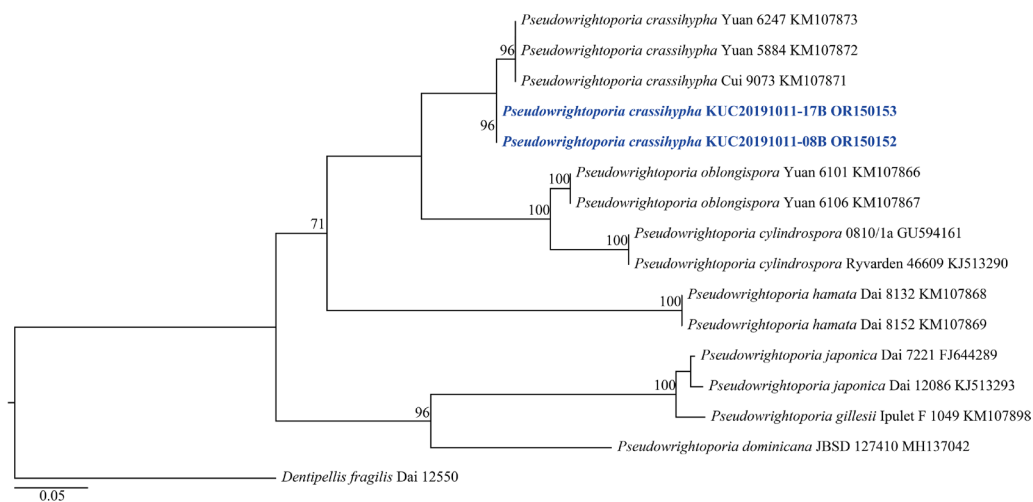


Figure 5. Maximum-likelihood tree of *Pseudowrightoporia crassihypha* KUC20191011-08B and KUC20191011-17B. The tree was constructed based on ITS sequence datasets of the genus *Pseudowrightoporia*. *Dentipellis fragilis* was used as an outgroup. The newly generated sequence is shown in blue and bold. Bootstrap support values more than 70% are shown. The numbers after scientific name indicate specimen ID and GenBank accession number (ITS region).

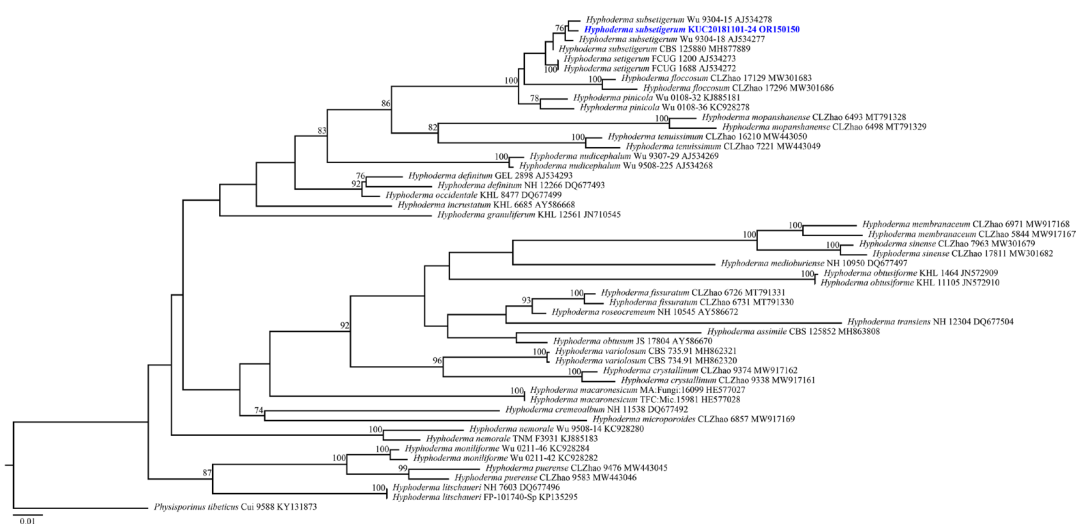


Figure 6. Maximum-likelihood tree of *Hyphoderma subsetigerum* KUC20181101-24. The tree was constructed based on ITS sequence datasets of the genus *Hyphoderma*. *Physisporinus tibeticus* was used as an outgroup. The newly generated sequence is shown in blue and bold. Bootstrap support values more than 70% are shown. The numbers after scientific name indicate specimen ID and GenBank accession number (ITS region).

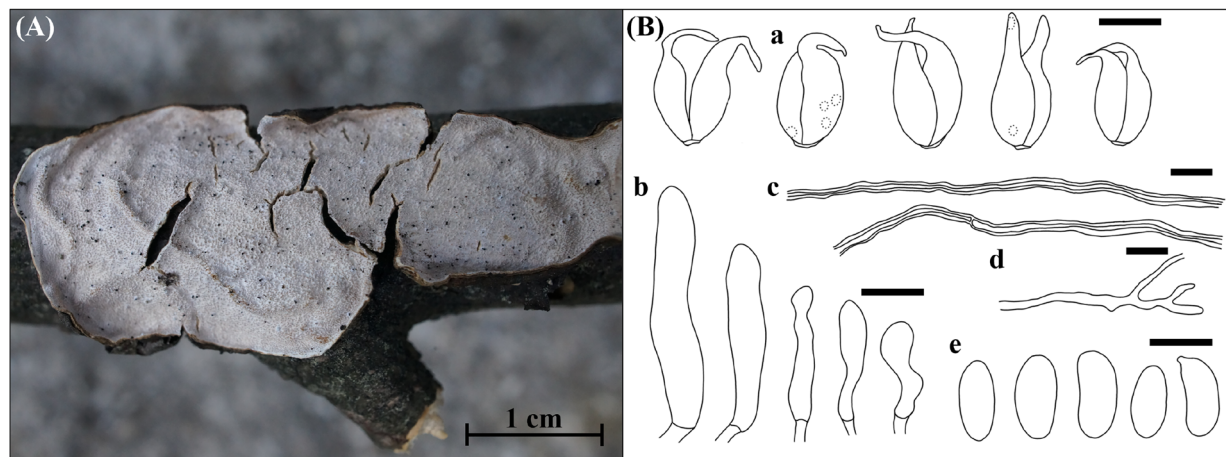


Figure 7. Morphological features of *Eichleriella sinensis* KUC20181101-43. (A) Basidiome; (B) Microscopic features, a. basidia; b. cystidia; c. skeletal hyphae; d. generative hyphae; e. basidiospores (Scale bars: A = 1 cm, B = 10 μ m).

4. Taxonomy

4.1. *Eichleriella sinensis* (Teng) S.H. He & Nakasone, *J. Fungi* 9 (3, no. 318): 16 (2023) [MB#847448] (Figure 7)

Korean name: Junggukgajakbeoseot.

Basidiome annual, resupinate, effused, covering up to 2 mm thick. *Hymenial surface* crustaceous, waxy, granulose, with some cracks, white (7.5YR, 8.5/1). *Hyphal system* dimitic. Generative hyphae frequently branched, thin-walled, hyaline, 2.1–3.2 μ m in diam. Skeletal hyphae septate, unbranched, thick-walled, brownish, 2.6–4.5 μ m. *Basidia* two-celled, ovoid, smooth, hyaline, with narrowly extended tips, containing few oil droplets, 16.8–27.1 \times 5.1–8.7 μ m. *Basidiospores* narrowly cylindrical, smooth, thin-walled, hyaline, 8.7–14.5 \times 3.9–6.4 μ m ($Q = 2.23$ –2.26). *Cystidia* rare, subcylindrical to clavate, smooth, thin-walled, hyaline, varying in length, 17.9–32.3 \times 4.5–6.6 μ m.

4.1.1. Specimen examined

Korea, Gyeongsangbuk-do, Cheongsong-gun, Juwangsan National Park, 36°22'19.0" N, 129°11'06.2" E, 388 m, mixed hardwood forest, occurring on hardwood branches near Jeolgol, November 1 2018, S. L. Kwon, KUC20181101-43 (NIBRFG0000514359).

4.1.2. Remarks

Eichleriella sinensis is characterized by a ceraceous and odontoid hymenial surface, cylindrical to narrowly cylindrical basidiospores, and a dimitic hyphal system with brownish, thick-walled skeletal hyphae [23], which matches KUC20181101-43. However, numerous and larger cystidia were observed in the original description (15–50(–70) \times 7.5–9(–12.5) μ m) [23]. In addition, four-celled basidia was described in the original description [23], which differs from our specimen. But two-celled basidia was observed

in *E. aculeobasidiata* [24], which is currently treated as synonym of *E. sinensis* [23]. This indicates that *E. sinensis* has two types of basidia: two-celled and four-celled. *E. sinensis* is morphologically similar with *E. tenuicula*, but *E. tenuicula* has larger allantoid basidiospores 16–21 \times 5.5–6.0 μ m ($Q = 2.91$ –3.50) [25].

4.2. *Hymenochaete anomala* Burt, *Annals of the Missouri Botanical Garden* 5: 358 (1918) [MB#101217] (Figure 8)

Korean name: Damgalsaeksonamubineulbeoseot.

Basidiome annual, resupinate, effused, adherent, covering up to 1 mm thick. *Hymenial surface* crustaceous, smooth, with many cracks, reddish brown (5YR, 5/4), with yellow (10YR, 7/6) margin when fresh, brown (7.5YR, 4/2) when dry. *Hyphal system* monomitic, generative hyphae frequently septate, moderately branched, without clamp connections, interwoven, thin-walled, hyaline, 1.8–3.7 μ m. *Setae* fusiform, subcylindrical, with an acute apex, smooth, bearing a wide lumen, thick-walled, projecting up to 25 μ m above the hymenium, yellowish red (5YR, 5/8), 29.0–65.4 \times 4.3–10.6 μ m. *Basidia* subcylindrical to clavate, four-spored, smooth, thin-walled, hyaline, with a basal clamp connection, 12.2–19.0(–21.0) \times 3.1–4.7 μ m; basidioles similar to basidia in shape. *Basidiospores* cylindrical to narrowly cylindrical, smooth, thin-walled, hyaline, 3.0–4.5(–4.8) \times 1.5–2.0(–2.3) μ m ($Q = 2$ –2.25). *Cystidia* absent.

4.2.1. Specimen examined

Korea, Gyeongsangbuk-do, Cheongsong-gun, Juwangsan National Park, 36°21'46.3" N, 129°11'18.5" E, 380 m, mixed hardwood forest, occurring on conifer branches near Jusan Reservoir, July 12 2018, S. L. Kwon, KUC20180712-40 (NIBRFG0000514362).

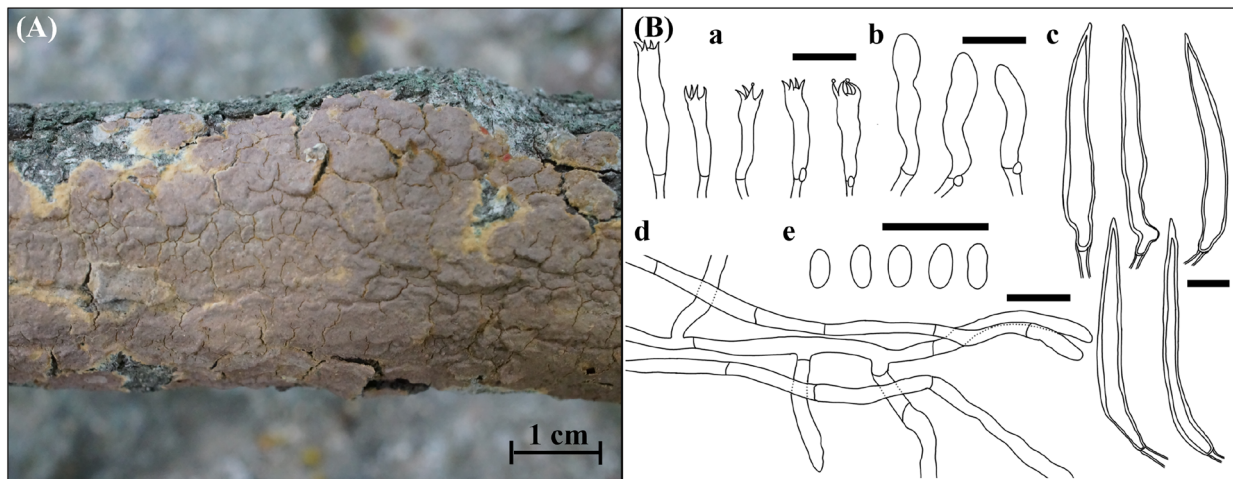


Figure 8. Morphological features of *Hymenochaete anomala* KUC20180712-40. (A) Basidiome; (B) Microscopic features, a. basidia; b. basidioles; c. setae; d. hyphae; e. basidiospores (Scale bars: A = 1 cm, B = 10 μ m).

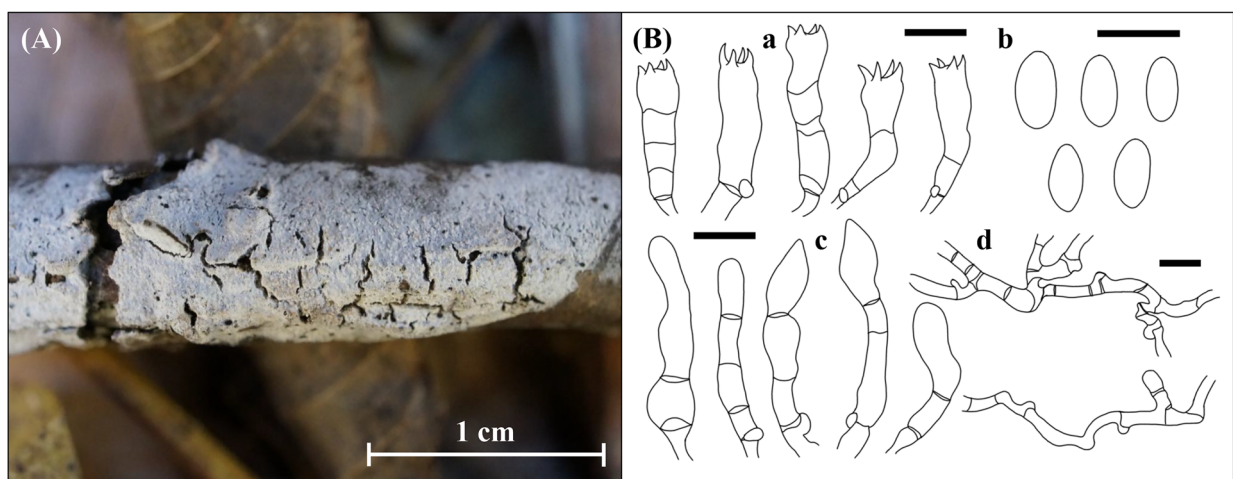


Figure 9. Morphological features of *Hyphoderma subsetigerum* KUC20181101-24. (A) Basidiome; (B) Microscopic features, a. basidia; b. basidiospores; c. septocystidia; d. hyphae (Scale bars: A = 1 cm, B = 10 μ m).

4.2.2. Remarks

Hymenochaete anomala is characterized by a crustaceous reddish-brown hymenial surface and thick-walled setae. Phylogenetically, *Hym. luteobadia* were the most closely related species. However, *Hym. luteobadia* has pileate basidiome, and numerous hyphidia with yellowish-brown granules [26,27]. Other closely related species (*Hym. separabilis*, *Hym. yunnanensis*, and *Hym. fulva*) had effused basidiomes. This indicates that morphological characteristics do not always correspond to phylogenetic relationships. *Hym. minor* exhibited micromorphological characteristics similar to *Hym. anomala*, but *Hym. minor* setae had encrustation at its apex [27].

4.3. *Hyphoderma subsetigerum* Sheng H. Wu, *Mycologia* 89 (1): 136 (1997) [MB#436877] (Figure 9)

Korean name: Dolgimokjaegoyakbeoseot.

Basidiome annual, resupinate, effused, thin.
Hymenial surface membranaceous, chalky, papillate,

with some cracks, white (2.5Y, 9.5/1), margin concolorous with main hymenial surface. *Hyphal system* monomitic, generative hyphae frequently septate, moderately branched, with frequent clamp connections, diverge in multiple orientations, thin-walled, hyaline, 3.0–4.7 μ m. *Basidia* fusiform, subcylindrical, four-spored, smooth, thin-walled, hyaline, with a basal clamp connection, 21.6–28.0 \times 4.4–7.1 μ m. *Basidiospores* cylindrical to narrowly cylindrical, smooth, thin-walled, hyaline, (7.8)8.0–11.0(–11.4) \times (3.7–)4.0–5.5(–5.6) μ m (Q = 2–2.03). *Septocystidia* cylindrical, sometimes with narrow apex, 2–4 septa with clamp connections, thin-walled, hyaline, 22.4–62.0 \times 4.6–6.3 μ m.

4.3.1. Specimen examined

Korea, Gyeongsangbuk-do, Cheongsong-gun, Juwangsang National Park, 36°26'26.0" N, 129°08'17.6" E, 405 m, mixed hardwood forest, occurring on hardwood branches near Dalgi Falls, November 1 2018, S. L. Kwon, KUC20181101-24 (NIBRFG0000514360).

4.3.2. Remarks

This species is characterized by a papillate-to-grand-inioid hymenial surface with cracks and smooth septocystidia. KUC20181101-24 has larger basidiospores than the original description ($6.0\text{--}8.0 \times 2.8\text{--}3.2 \mu\text{m}$). KUC20130718-46, and KUC20160721B-02 were identified as *Hyp. subsetigerum* in previous studies [28,29]; however, they were not reported owing to the absence of morphological analyses. Therefore, we classified KUC20181101-24 as an unknown species. *Hyp. subsetigerum* were grouped under *Hyp. setigerum* complex [30,31]. Morphologically, *Hyp. setigerum* have longer and wider basidiospores ($7.5\text{--}12.5 \times 3.5\text{--}5.0 \mu\text{m}$) than *Hyp. subsetigerum* [32]. Our specimens exhibited micromorphological characteristics similar to those of *Hyp. setigerum*. *Hyphoderma setigerum* was previously considered a species group because of the morphological variations among specimens from distinct regions [33,34]. According to an advanced phylogenetic study, *Hyp. subsetigerum* formed a separate group from *Hyp. setigerum* [30,31]. These two species have different geological distributions: *Hyp. subsetigerum* was observed to occur in Asia and *Hyp. setigerum* s.s. in Northern Europe [30]. This indicates that geological factors caused speciation within the *Hyp. setigerum* complex, leading to morphological and molecular variations [30].

4.4. *Lyomyces orientalis* Riebesehl, Yurchenko & Langer, *Mycological Progress* 16 (9): 874 (2017) [MB#819975] (Figure 10)

Korean name: Dongyangbaeksaekgoyakbeoseot.

Basidiome resupinate, effused, pellicular, covering up to 0.6 mm thick. *Hymenial surface* membranaceous, smooth, few projections, with frequent cracks, white (2.5Y, 9.5/1). *Hyphal system* monomitic, generative hyphae simple septate, unbranched, with clamp connections at all primary septa, interwoven, thin-walled, hyaline, $1.8\text{--}4.8 \mu\text{m}$. *Basidia* subcylindrical to clavate, four-spored, smooth, thin-walled, hyaline, sometimes bearing oil droplets, with a basal clamp connection, $16.2\text{--}20.5 \times 4.0\text{--}5.5 \mu\text{m}$. *Basidiospores* broadly ellipsoid, smooth, thick-walled ($0.3\text{--}0.4 \mu\text{m}$), hyaline, containing an oil droplet, $(5.0\text{--})5.2\text{--}6.0(\text{--}6.4) \times (3.7\text{--})4.0\text{--}5.0(\text{--}5.1) \mu\text{m}$ ($Q = 1.2\text{--}1.3$). *Cystidia* capitate, smooth, thin-walled, hyaline, $13.2\text{--}28.6 \times 2.1\text{--}6.6 \mu\text{m}$.

4.4.1. Specimen examined

Korea, Gyeongsangbuk-do, Cheongsong-gun, Juwangsang National Park, $36^{\circ}26'26.0''$ N, $129^{\circ}08'17.6''$ E, 405 m, mixed hardwood forest, occurring on

Pinus branches near Dalgi Falls, June 20 2019, S. L. Kwon, KUC20190620-29 (NIBRFG0000506081).

4.4.2. Remarks

Lyomyces orientalis is characterized by capitate cystidia and thick-walled basidiospores [35]. The morphological characteristics of KUC20190620-29 were similar to those in the original description [35]. In the phylogenetic tree, *L. orientalis* is closely related to *L. bambusinus* and *L. sambuci*. Similar to *L. orientalis*, *L. bambusinus* have slightly thick-walled ($0.3\text{--}0.4 \mu\text{m}$) basidiospores; however, *L. bambusinus* has two forms of cystidia; capitate and tapering, and smaller basidiospores $4.5\text{--}5.6(\text{--}5.8) \times 3.3\text{--}4.3(\text{--}4.5) \mu\text{m}$ [36]. *Lyomyces sambuci* differs from *L. orientalis* by having thin-walled and narrowly ellipsoid basidiospores of $4.5\text{--}6 \times 3\text{--}3.5 \mu\text{m}$, $Q = 1.55$ [35].

4.5. *Pseudowrightoporia crassihypha* Y.C. Dai, Jia J. Chen & B.K. Cui, *Persoonia* 37: 28 (2015) [MB#812227] (Figure 11)

Korean name: Neodomureunbaechakgumeongbeoseot.

Basidiome annual, resupinate, effused, orbicular, corky, poroid, up to 3 mm thick. *Hymenial surface* buff, ceraceous, yellow (10YR, 8/6) to very pale brown (10YR, 8/3). *Pores* circular to angular, 8–10 per mm, dissepiments thin, entire. *Hyphal system* dimitic, generative hyphae septate, sometimes branched, with few clamp connections, thin-walled, hyaline, $2.1\text{--}4.3 \mu\text{m}$. Skeletal hyphae dominant, aseptate, unbranched, without clamp connections, thick-walled, hyaline, $4.0\text{--}6.5 \mu\text{m}$. *Basidia* clavate to subclavate, four-spored, smooth, thin-walled, hyaline, with a basal clamp connection, $10.4\text{--}14.7 \times 4.1\text{--}5.7 \mu\text{m}$. *Basidiospores* broadly ellipsoid to ellipsoid, asperulate, thick-walled, hyaline, bearing an oil droplet, $(3.1\text{--})3.3\text{--}4.1(\text{--}4.3) \times (2.3\text{--})2.5\text{--}3.1(\text{--}3.3) \mu\text{m}$ ($Q = 1.30\text{--}1.34$). *Cystidia* clavate, smooth, thin-walled, hyaline, $15.5\text{--}23.3 \times 3.0\text{--}5.3 \mu\text{m}$.

4.5.1. Specimen examined

Korea, Gyeongsangbuk-do, Cheongsong-gun, Juwangsang National Park, $36^{\circ}24'44.5''$ N, $129^{\circ}10'17.2''$ E, 519 m, mixed hardwood forest, occurring on *Pinus* branches along Geumeungwangi trail, June 20 2019, S. L. Kwon, KUC20191011-08B (NIBRFG0000506161), occurring on dead branches along Geumeungwangi trail, June 20 2019, S. L. Kwon, KUC20191011-17B (NIBRFG0000506175).

4.5.2. Remarks

Pseudowrightoporia crassihypha is characterized by corky and yellowish basidiomes with pores, a dimitic

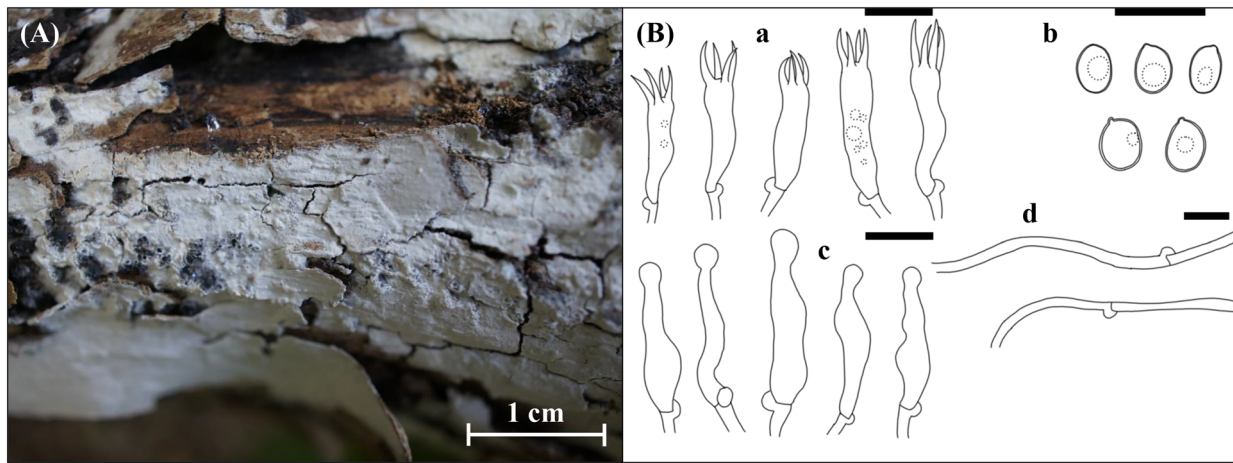


Figure 10. Morphological features of *Lyomyces orientalis* KUC20190620-29. (A) Basidiome; (B) Microscopic features, a. basidia; b. basidiospores; c. cystidia; d. hyphae (Scale bars: A = 1 cm, B = 10 μ m).

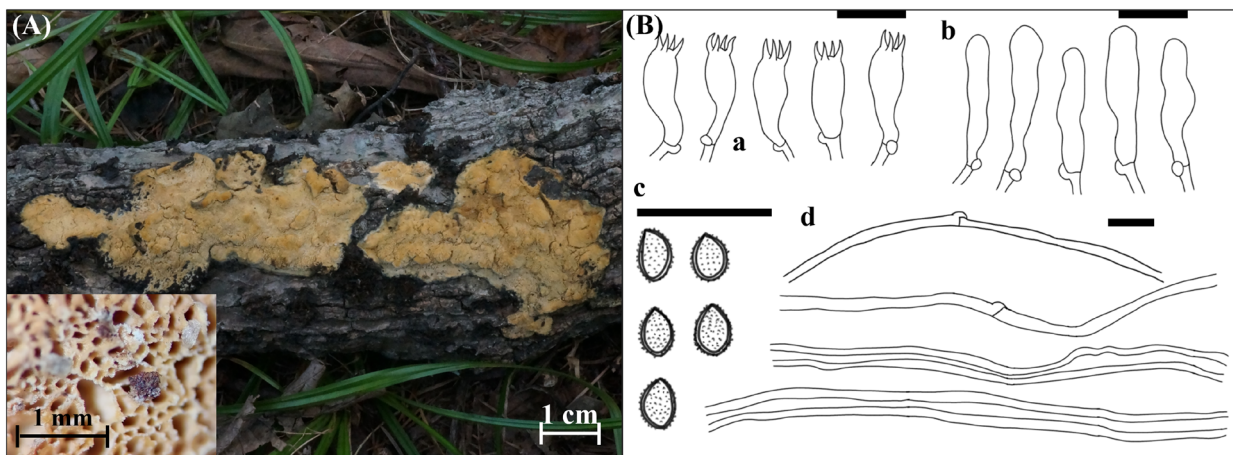


Figure 11. Morphological features of *Pseudowrightoporia crassihypha* KUC20191011-08B and KUC20191011-17B. (A) Basidiome; (B) Microscopic features, a. basidia; b. cystidia; c. basidiospores; d. hyphae (Scale bars: A = 1 cm for basidiome, 1 mm for pores, B = 10 μ m).

hyphal system, and asperulate basidiospores [37]. Our specimens had morphological characteristics similar to those in the original description [37] and diverged well in the phylogenetic tree. Most of the *Pseudowrightoporia* specimens are distributed in the subtropical and tropical regions [37,38]. In addition, the holotype and paratypes of *P. crassihypha* (Yuan 6247, Yuan 5884, and Cui 9073) were collected from a subtropical region [37]. Therefore, KUC20191011-08B and KUC20191011-17B are the first reports of *P. crassihypha* in temperate regions and a rare case of the genus *Pseudowrightoporia*. Morphologically, *P. japonica* has corky basidiome with pores (6–8 per mm) [39,40], resembling *P. crassihypha*. However, *P. japonica* has fewer cystidia and narrower skeletal hyphae (2.4–5.3 μ m) than *P. crassihypha* [39,40].

5. Discussion

In this study, we discovered five unrecorded wood-decaying polyporoid and corticioid species in Juwangsan National Park using morphological and molecular analyses. Among the five species, the polyporoid species was *P. crassihypha*, and the other four were *E. sinensis*, *Hym. anomala*, *Hyp. subsetigerum*, and *L. orientalis*, which were corticioid species. A previous study conducted in Juwangsan focused on unrecorded cap-forming saprobic fungi [14]; therefore, this is the first study on wood-decaying polyporoid or corticioid fungi in Juwangsan. Studies on polyporoid and corticioid fungi in Korea are relatively scarce, although globally, wood-decaying fungi have been studied intensively for a decade [41–47]. Therefore, further research is required to determine the diversity of macrofungi in Juwangsan National Park, as well as the diversity of polyporoid and corticioid fungi in Korea.

Eichleriella Bres. is characterized by a leathery-to-ceraceous basidiome, two- or four-celled basidia, and cylindrical to narrow cylindrical basidiospores [48,49]. Currently, 17 species are listed in the genus *Eichleriella* [24,48,50], and this is the first report of *Eichleriella* at the species level in Korea. According to a previous phylogenetic analysis, *Eichleriella* clusters with the genera *Auricularia*, *Exidia*, *Exidiopsis*, and *Heterochaete* in the nLSU region [51]. However, these genera possess different basidia forms [51]. Therefore, molecular analysis using the ITS region was performed, and consequently, *Eichleriella* was grouped with *Amphistereum* and *Auricularia* [48]. In addition, four species of *Exidiopsis* and *Heterochaete* were reclassified as *Eichleriella* [48]. *Eichleriella* is distinguished from *Amphistereum* by its hyphal structure, whereas the other morphological characteristics are similar [48]. Therefore, accurate morphological observations and molecular approaches are required to clearly identify *Eichleriella* species.

Hymenochaete Lév is a white-rot fungi, and is characterized by brown effused basidiome, abundant yellowish to brownish hymenial setae, and simple septate hyphae [27,52–55]. Previously, species with poroid and smooth hymenial surfaces were classified as *Hymenochaete* [53–55] but currently, species with effused-reflexed and pileate basidiomes (*H. odontoides*, *H. rubiginosa*, *H. subporioides*, and *H. xerantica*) are also classified as *Hymenochaete*. Owing to their morphological variability, many *Hymenochaete* species were included in other genera, including *Cerrenella*, *Cyclomyces*, *Cycloporellus*, *Dichochoete*, *Hydnochaete*, *Hymenochaetella*, and *Stiptochaete* are currently considered illegitimate names [52]. More than 120 species were considered *Hymenochaete* in 2012 [27] and 13 of them were listed in Korea according to the NIBR database. This must be revised following the phylogenetic reclassification and delimitation studies of *Hymenochaete*.

Hyphoderma Wallr. is characterized by resupinate to effused-reflexed basidiome with membranaceous, smooth to tuberculate hymenial surface, and monomitic hyphal system with clamp connections [41,56]. Although approximately 100 species are accepted as *Hyphoderma* worldwide [57,58], only 11 species have been reported in Korea. Previously, six *Hyphoderma* species were clustered with *Hypochnicium*, *Physisporinus*, and *Rigidoporus* species [59,60]. These species are currently classified as Hyphodermataceae and not as Meripilaceae (*Physisporinus* and *Rigidoporus*) and Podoscyphaceae (*Hypochnicium*) [58]. *Hyphoderma* species have long been studied in Europe [41,56,61] and recently in China [31,57,58,62].

Thus, most *Hyphoderma* species are distributed in Europe, and some have been reported in southern China and Japan [58]. In addition, most *Hyphoderma* species occur in hardwood, whereas a few occur in softwood [58]. Therefore, additional studies are required to determine the diversity of Asian *Hyphoderma* species and identify the relationships between *Hyphoderma* and its host trees.

Lyomyces P. Karst. has 23 species worldwide and is new to Korea at the species level [35,36,63,64]. *Lyomyces* is a genus in the family Schizoporaceae, which is characterized by an effused basidiome with a smooth to odontoid hymenial surface, a monomitic hyphal system with abundant clamp connections, and thin- to thick-walled basidiospores [35,36,65,66]. They usually occur on dead hardwood branches and stems and sometimes on softwood [35,36]. The genus *Lyomyces* was first introduced by Karsten as *Lyomices* [65] and was previously recognized as *Hyphodontia* owing to a lack of molecular data [67]. Based on the molecular and phylogenetic analyses, *Lyomyces* was reintroduced by dividing *Hyphodontia* s.l. to *Hyphodontia*, *Kneiffiella*, *Lagarobasidium*, *Lyomyces*, *Palifer*, *Rogersella*, and *Xylodon* [63,64]. Currently, *Rogersella* is considered synonymous to *Lyomyces* [35]. In addition, *Xylodon* encompasses *Lagarobasidium*, *Palifer*, and other genera (*Odontiopsis* and *Schizopora*) along with some mislabeled species of *Hyphodontia* (family Hyphodontiaceae) and *Kneiffiella* (family Chaetoporellaceae) [64,68–71]. *Lyomyces* is now considered the second largest genus in the family Schizoporaceae, followed by *Xylodon*. Therefore, accurate identification is required, following the recent taxonomic revision studies [70,71].

Pseudowrightoporia Y.C. Dai, Jia J. Chen, and B.K. Cui is a small genus with 11 species that is new to Korea [37,38]. *Pseudowrightoporia* are characterized by a corky basidiome, pores on the hymenial surface, a dimittic hyphal system, and asperulate basidiospores [37,38]. *Pseudowrightoporia* is a newly introduced genus that diverged from *Wrightoporia* s.l. due to the polyphyly of *Wrightoporia* [37]. In addition to *Pseudowrightoporia*, some *Wrightoporia* species have been reclassified as *Amylonotus*, *Amyloporus*, and two new genera, *Larssoniporia* and *Wrightoporiopsis* [37]. Thus, *W. africana*, *W. aurantipora*, *W. cylindrospora* (generic type), *W. gillesii*, *W. japonica*, *W. solomonensis*, and *W. straminea* were transferred to *Pseudowrightoporia* based on morphological and phylogenetic analyses [37,38]. Most *Pseudowrightoporia* species have been reported in tropical and subtropical regions [38], and few have been reported in temperate regions. Further studies are required to determine the global diversity of *Pseudowrightoporia* species.

Wood-decaying fungi are diverse and taxonomically complex. Many of its species have been misclassified because of morphological similarities between distinct groups. Currently, species delimitation and reclassification of wood-decaying fungi are being conducted owing to the development of DNA-based identification [37,52,60,70,72,73]. Consequently, many species have been reclassified into other genera and families. However, their scientific names have not yet been completely updated in online databases, such as GenBank, which confuses mycologists and the public. In conclusion, further studies are needed to resolve the confusion regarding accepted species names and for the species delimitation and reclassification of phylogenetically complex groups.

Acknowledgements

The authors thank Editage (www.editage.co.kr) for English language editing.

Disclosure statement

The authors declare that the research was conducted in the absence of any commercial or financial relationship that could be construed as a potential conflict of interest.

Funding

This research was supported by the project of the National Institute of Biological Resources [NIBR202304104] under the Ministry of Environment, Republic of Korea. This study was also supported by the Korea University Grant.

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