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RESEARCH ARTICLE

New Records of Five *Cortinarius* Species from South Korea: Morphological and Phylogenetic Evidence

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ABSTRACT

We investigated *Cortinarius* specimens collected from major Pung-hyeol-ji sites and Mt. Odaesan in Gangwon-do, Korea, in 2024, and identified them using internal transcribed spacer (ITS)-based phylogenetic analyses and morphological observations. Phylogenetic analyses based on ITS sequences produced congruent tree topologies using maximum likelihood and Bayesian inference methods. The specimens were assigned to *Cortinarius alpinus*, *C. falsosus*, *C. fulvopaludosus*, *C. lepidopus*, and *C. scotoides*, all of which have recently emerged in South Korea. Morphological findings generally agreed with the characteristics of each species, and minor differences were interpreted as intraspecific variation. Four of the five *Cortinarius* species were collected from Pung-hyeol-ji habitats, suggesting a preference for the cool, humid microclimate of wind-hole ecosystems. This study expands the established distribution of *Cortinarius* species in South Korea and highlights the ecological significance of Pung-hyeol-ji habitats as potential microrefugia for ectomycorrhizal fungi.

Keywords: *Cortinarius alpinus*, *Cortinarius falsosus*, *Cortinarius fulvopaludosus*, *Cortinarius lepidopus*, *Cortinarius scotoides*, Pung-hyeol-ji

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INTRODUCTION

The genus *Cortinarius* (Cortinariaceae, Agaricales) is one of the most species-rich groups of ectomycorrhizal fungi worldwide [1,2]. Species of this genus form symbiotic associations with a wide range of woody plants and play essential roles in nutrient cycling and forest ecosystem functioning [2,3]. Despite their ecological importance, species delimitation within *Cortinarius* remains challenging due to considerable morphological variability and similarity among closely related taxa [4].

Recent advances in molecular phylogenetics, particularly analyses based on internal transcribed spacer (ITS) sequences, have significantly improved the resolution of species boundaries in *Cortinarius* [5,6]. Morphologically similar taxa often have distinct phylogenetic lineages, which highlights the importance of integrating molecular and morphological data for accurate identification [4,6].

Knowledge of *Cortinarius* diversity in South Korea is limited, and many species are likely under-documented [7]. Recent integrative taxonomic approaches of morphological observations in combination with molecular phylogenetic analyses have uncovered undocumented fungal taxa in Korea, such as ectomycorrhizal, and other macrofungal groups [8,9]. These findings suggest that fungal diversity in Korea is insufficiently documented, particularly in specialized or poorly investigated habitats.

Pung-hyeol-ji (wind-hole areas) are characterized by summer temperatures that are 2–5°C lower and humidity that is 10–20% higher than surrounding environments [10]. These habitats function as microrefugia that support the persistence of cold-adapted organisms [11]. However, their ecological significance for fungal communities remains poorly understood.

Several *Cortinarius* specimens were collected when major Pung-hyeol-ji areas and Mt. Odaesan (Gangwon-do) were surveyed during 2024. Preliminary findings suggested that some specimens have not been documented in South Korea.

We aimed to identify these specimens using morphological and molecular phylogenetic approaches and to document new *Cortinarius* species in South Korea. We also discuss the ecological significance of Pung-hyeol-ji habitats for ectomycorrhizal fungi.

MATERIALS AND METHODS

Specimens and morphological observations

Table 1 shows the specimens assessed herein. Dried specimens were deposited in the herbarium of the Korea National Arboretum (KH), South Korea. Macromorphological characteristics were derived from field notes and photographs of fresh basidiomata. The specimens were sectioned, hydrated and rehydrated, then mounted in 3% KOH to examine micromorphological structures using light microscopy. We measured the sizes of at least 30 mature spores

PCR amplification and sequencing

Genomic DNA was extracted from dried basidiomata using a modification of the cetyltrimethylammonium bromide (CTAB) method as described [12]. The ITS region was amplified by PCR using 0.5 pmol each of ITS1F [13] and ITS4 [14] primer pairs, 0.25 mM dNTPs, 10 mM Tris-HCl, 50 mM KCl, 1.5 mM $MgCl_2$, 2.5 U of Taq DNA polymerase, and ~ 15 ng of template DNA. The PCR cycling conditions comprised initial denaturation at 94°C for 4 min, followed by 34 cycles of 94°C for 40 s, 52°C for 40 s, and 72°C for 60 s, and a final extension at 72°C for 8 min. We purified and directly sequenced the amplicons using ExoSAP kits (USB Corp., Cleveland, OH, USA) and BigDye Terminator Cycle Sequencing Kits (Applied Biosystems, Foster City, CA, USA) and capillary electrophoresis using an ABI Prism 310 Genetic Analyzer (Applied Biosystems). The sequences were edited using Phydit 3.2 [15].

Phylogenetic analyses

The ITS sequences were aligned using ClustalX 1.8 [16] and manually adjusted. Maximum likelihood (ML) analysis was applied using RAxML v8.2.12 [17] under the GTRGAMMA model with 1,000 bootstrap replicates. Bayesian inference (BI) was analyzed using MrBayes v3.2.7 [18] under the GTR+I+G substitution model with two independent runs of four Markov chains per 5 million generations. Trees were sampled every 1,000 generations, and the first 25% of trees were discarded as burn-in. Bayesian posterior probabilities were calculated from the remaining trees. *Cortinarius sanguineus* UPS SL22091940 served as the outgroup. The phylogenetic tree was visualized using TreeView v3.2 [19].

RESULTS

Phylogenetic analyses

Phylogenetics were analyzed based on ITS sequences comprising 53 taxa and 509 aligned characters. The dataset included both new, and reference sequences retrieved from GenBank (Table 1). Analyses of maximum likelihood and Bayesian inference resulted in congruent tree topologies. The phylogenetic tree revealed that all the examined specimens were distributed among several clades that corresponded to known *Cortinarius* species (Fig. 1).

Specimens KA24-1145 and KA24-1375 were grouped within the *C. alpinus* clade with strong support (100/1.0). Specimen KA24-1195 was placed in the *C. falsosus* clade (97/1.0), and KA24-0850 was assigned to the *C. fulvopaludosus* clade (87/0.98) along with the type-derived sequence H6033460 (NR_154868), despite moderate internal node support (68/0.97). Specimen KA24-1135 formed a distinct lineage within the *C. lepidopus* clade (88/1.0), and was clearly separated from closely related taxa within the *C. anomalus* complex. Specimen KA24-0830 was clearly supported within the *C. scotoides* clade (99/1.0) and was distinguishable from the closely related *C. subscotoides*.

Overall, none of the examined specimens formed independent lineages, indicating that all specimens corresponded to known species. Combined molecular and morphological evidence supports their recognition as recently documented taxa in South Korea.

Table 1. List of *Cortinarius* specimens used in the phylogenetic analyses with their GenBank accession numbers

Species	Voucher / Strain	Country	GenBank No.
Cortinarius scotoides	CFP542	Sweden	MT935420
Cortinarius scotoides	G:13312/166a (HT)	Switzerland	MT935421
Cortinarius scotoides	BR:AdH19019	Belgium	PX221224
Cortinarius scotoides	HMAS291464	China	MW555551
Cortinarius scotoides	PC 604	France	NR_171116
Cortinarius scotoides	**KA24-0830**	**South Korea**	**PZ251246**
Cortinarius subscotoides	TN12-015 (HT)	Finland	MK211176
Cortinarius badioflavidus	WTU:J.F. Ammirati 13668 (HT)	USA	KU041723
Cortinarius badioflavidus	WTU:M.Beug 02MWB043009	USA	KU041732
Cortinarius hinnuleus	TUB 011512	Germany	AY669665
Cortinarius fulvopaludosus	ND98059	Netherlands	PX221420
Cortinarius fulvopaludosus	H6033460 (HT)	Finland	NR_154868
Cortinarius fulvopaludosus	**KA24-0850**	**South Korea**	**PZ251247**
Cortinarius falsosus	T. Niskanen 02-866	Finland	MT935041
Cortinarius falsosus	PC:3886 (HT)	France	MT935040
Cortinarius falsosus	**KA24-1195**	**South Korea**	**PZ251250**
Cortinarius decipiens	ND21123	Netherlands	PX221594
Cortinarius castaneus	FK10M	Italy	PZ016049
Cortinarius miwok	DBB43810 (HT)	USA	JQ906753
Cortinarius hemitrichus	TUB 011509	Germany	AY669680
Cortinarius paleaceus	CFP662	Sweden	MT935265
Cortinarius flexipes	TUB 011903	Germany	AY669683
Cortinarius uraceus	IK01-002	Finland	KJ206526
Cortinarius bivelus	TUB 011897	Germany	AY669682
Cortinarius saturninus	CFP514	Sweden	KX964584
Cortinarius torvus	TUB 011515	Germany	AY669668
Cortinarius armeniacus	CFP809	Sweden	DQ117925
Cortinarius tortuosus	Niskanen 05-00	Finland	KX964408
Cortinarius brunneus	IK00-012 (HT)	Finland	EU266642
Cortinarius evernius	Niskanen 05-238	Norway	KX964351
Cortinarius bovinaster	CFP1656	Sweden	JX407266
Cortinarius bovinus	TUB 011898	Germany	AY669691
Cortinarius alpinus	**KA24-1375**	**South Korea**	**PZ251251**
Cortinarius alpinus	**KA24-1145**	**South Korea**	**PZ251249**
Cortinarius alpinus	OF146214	Norway	KX239916
Cortinarius mucosus	TUB 011837	Germany	AY669591
Cortinarius collinitus	TUB 011832	Germany	AY669588
Cortinarius violaceus	S Moser 74/208 (HT)	Sweden	NR_173726
Cortinarius salor	TUB 011838	Germany	AY669592
Cortinarius lepidopus	**KA24-1135**	**South Korea**	**PZ251248**
Cortinarius lepidopus	LE315536	Russia	MN308207
Cortinarius lepidopus	DB6253	Hungary	MZ663794
Cortinarius lepidopus	HMJAU48640	China	ON254480
Cortinarius modestus	NYS:F001966 (HT)	USA	MZ580446
Cortinarius modestus	Niskanen 10-035	Canada	MZ580447
Cortinarius anomalovelatus	JFA13109 (HT)	USA	FJ717605
Cortinarius caninus	H:7022441	Sweden	KX302251
Cortinarius barlowensis	JFA13140 (HT)	USA	FJ717554
Cortinarius anomalus	Lindstrom 00.230	Switzerland	KX302231
Cortinarius suecicolor	PDD:74698 (HT)	New Zealand	JX000360
Cortinarius illuminus	ND18030	Sweden	PX220941
Cortinarius obtusus	ND19045	Norway	PX220965
Cortinarius tubarius	TUB 011821	Germany	AY669581
Cortinarius sanguineus	SL22091940 (NT, outgroup)	Sweden	NR_119967

Recently documented sequences are shown in bold. HT, holotype; NT, neotype.

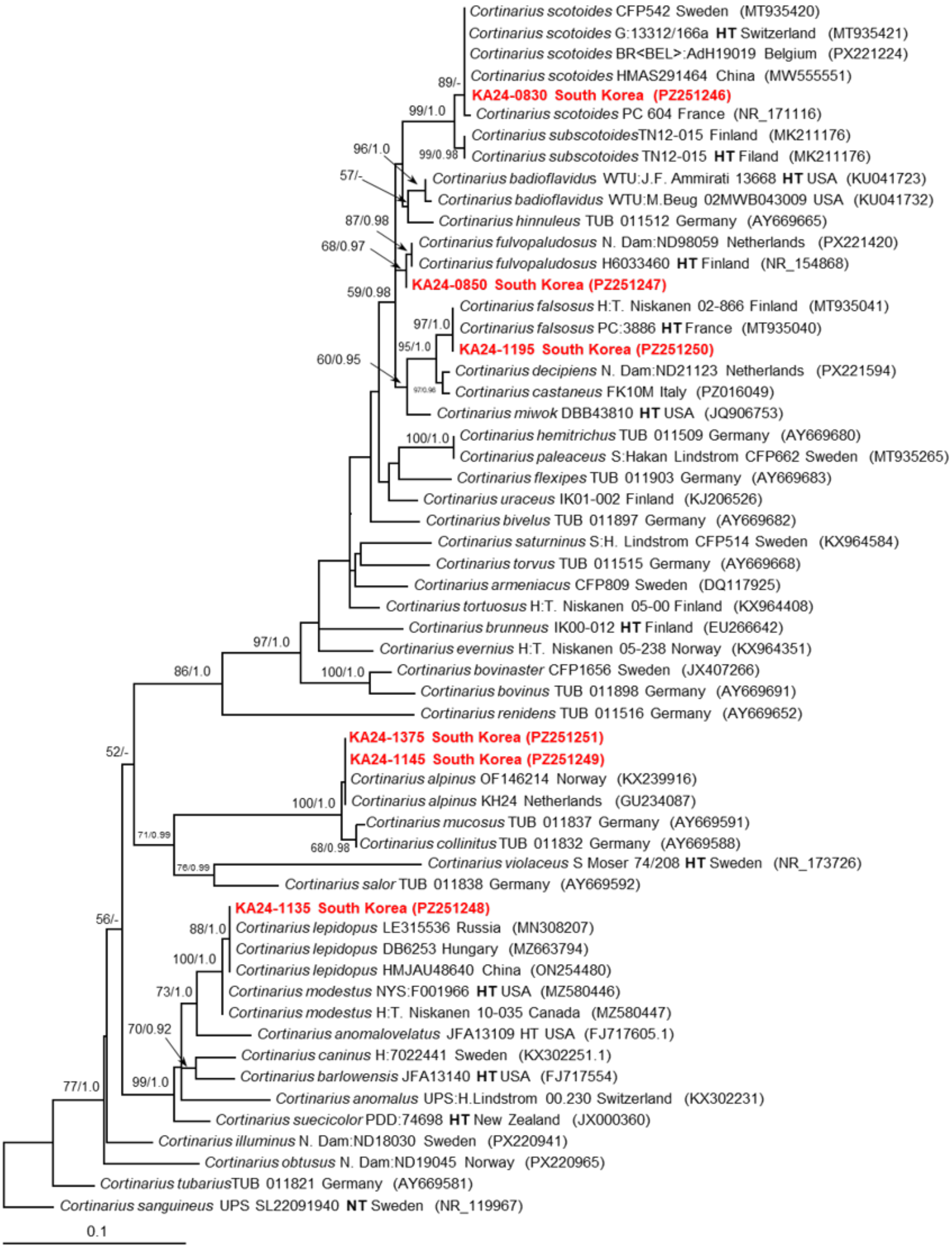

Fig. 1. Phylogenetic tree of *Cortinarius* species inferred from internal transcribed spacer (ITS) sequence data. The tree was constructed using maximum likelihood (RAxML) and Bayesian inferences (BI) methods. Bootstrap support values (≥ 50%) from RAxML and posterior probabilities (≥ 0.90) from Bayesian analysis are indicated at nodes as ML/BI. New sequences determined are shown in bold red. *Cortinarius sanguineus* UPS SL22091940 served as the outgroup. HT and NT, sequences derived from holotype and neotype specimens, respectively. Scale bar indicates the number of substitutions per site.

Taxonomic treatment

Cortinarius alpinus **Boud.**, *Bull. Soc. Mycol. Fr.* 11:27, tab. 11 (1895). Fig. 2.

Korean name: Gosan-kkeunjeock-beoseot (고산끈적버섯), the name refers to its alpine habitat ("*alpinus*").

Description: Basidiomata medium-sized. Pileus diameter, 20–50 mm; convex to plano-convex, smooth surface, weakly viscid to nearly dry, brown to orange-brown, often slightly darker at the center. Lamellae adnate to slightly emarginate, moderately spaced, pale brown to brown. Stipe 50–70 × 3–15 mm, cylindrical to slightly clavate, surface fibrillose, pale yellowish to brownish, with remnants of Cortina in young basidiomata. Basidiospores ellipsoid to subamygdaliform, verrucose, (7.8–)8.2–9.8(–10.5) × (4.5–)4.8–5.8(–6.3) μm, Q = (1.40–)1.50–1.85(–1.95); Qm = 1.67. Basidia clavate, 4-spored, 28–35 × 7–9 μm. Cheilocystidia and pleurocystidia were not found. Pileipellis has a weakly hyaline to pale brown color, a gelatinized cutis consisted of repent, cylindrical hyphae, and is smooth-walled.

Habitat: Typically found in alpine or subalpine environments, often associated with dwarf shrubs or conifers.

Specimens examined: South Korea, Gangwon-do, Pyeongchang-gun, Jinbu-myeon, Singi-ri, Bakjigol Pung-hyeol-ji, 37°35′0.3″N, 128°35′21.10″E, elev. 894 m, 24 Sep 2024, KA24-1145 (KH); Pyeongchang-gun, Daegwallyeong-myeon, Byeongnae-ri, Mt. Odaesan, 37°44′33″N, 128°38′14″E, elev. 853 m, 27 Oct 2024, KA24-1375 (KH).

Notes: *Cortinarius alpinus* formed a strongly supported clade (100/1.0) including the KA24-1375 and KA24-1145 specimens that belonged to *Cortinarius* subgenus Myxacium section Myxacium. It is known mainly to thrive in arctic, alpine, and subalpine habitats, often in association with dwarf willows such as *Salix retusa*, *S. reticulata*, *S. herbacea*, *S. polaris*, *S. rotundifolia*, and *Dryas* spp. [20]. Peintner [20] treated *C. favrei* as a synonym of *C. alpinus* and identified highly variable basidiospore sizes in this taxon. Although Boudier originally described *C. alpinus* as having basidiospores of 16–20 × 7–9 μm [21], Peintner [20] re-evaluated these sizes and corrected the measure values to 14–18 × 6–8 μm. Based on 992 spores from 32 collections, Peintner [20] reported a broad spore range of 9.6–17.5 × 5.6–9.7 μm, with a mean of 12.6 ± 1.2 × 7.4 ± 0.7 μm. The Korean specimens examined herein had somewhat smaller basidiospores, (7.8–)8.2–9.8(–10.5) × (4.5–)4.8–5.8(–6.3) μm, overlapping only with the lower end of the variation reported for *C. alpinus*. However, the sizes of *C. alpinus* spores vary considerably and are sufficient alone to delimit taxa within the *C. alpinus* complex. Thus, the Korean specimens were identified as *C. alpinus* based primarily on their ITS phylogenetic placement, together with their overall morphological agreement, including brown to orange-brown basidiomata, a weakly viscid pileus, and their presence in cool montane or wind-hole habitats. The smaller spores in the Korean collections are therefore interpreted as intraspecific variations within *C. alpinus*.

Fig. 2. *Cortinarius alpinus*. A, B: mature basidiomata (KA24-1375). C: immature basidioma (KA24-1145). D: basidia mounted in KOH. E, F: basidiospores mounted in KOH. Scale bars: A–C, 3 cm; D, E, 20 µm; F, 10 µm.

Cortinarius falsosus **Moënne-Locc. & Reumaux,** in Bidaud, Moënne-Loccoz, Reumaux, Carteret & Eyssartier, *Atlas des Cortinaires (Meyzieu)* 11:572 (2001). Fig. 3.

Korean name: Yusa-kkeunjeok-beoseot (유사끈적버섯), the name is derived from the species epithet "*falsosus*", meaning "false" or "resembling another," indicating its morphological similarity to closely related species within the genus.

Description: Basidiomata are small and slender. Pileus 15–20 mm in diameter, conical to convex, hygrophanous, dark brown when moist, pales upon drying, finely fibrillose surface. Lamellae are moderately spaced, brown. Stipes are 45–50 × 2.5–3 mm, long and slender, cylindrical, pale to brownish, and a surface that is smooth to finely fibrillose. Basidiospores ellipsoid to amygdaliform, verrucose, (6.5–)6.8–8.5(–9.0) × (3.8–)4.2–5.0(–5.5) µm, Q = (1.45–)1.55–1.90(–2.05), Qm = 1.70. Basidia clavate, 4-spored, 25–32 × 6–8 µm. Cheilocystidia and pleurocystidia were not evident. The pileipellis consists of a repent cutis, cylindrical hyphae, thin-walled, hyaline to pale brown, without evident gelatinization.

Habitat: On soil in forest habitats, frequently associated with deciduous trees.

Specimens examined: South Korea, Gangwon-do, Hwacheon-gun, Sangseo-myeon, Bongo-ri, Bongo-ri Pung-hyeol-ji, 38°12′25.60″N, 127°35′44.80″E, elev. 357 m, 27 Sep 2024, KA24-1195 (KH).

Notes: *Cortinarius falsosus* was placed within a supported clade (97/1.0) together with reference sequences. It is phylogenetically distinct from closely related taxa such as *C. decipiens* and *C. castaneus*, which occur in adjacent lineages. Species boundaries among small brown *Cortinarius* species are often difficult to delimit based solely on morphology, and DNA-based approaches are essential for accurate identification [6]. The phylogenetic placement of the specimen KA24-1195 within the *C. falsosus* clade supports its assignment to this species. Morphologically, *C. falsosus* can be distinguished from *C. decipiens* by differences in pileus coloration and basidiospore ornamentation, and from *C. castaneus* by its smaller basidiomata and spore dimensions. The examined specimen is consistent with described characteristics of *C. falsosus*.

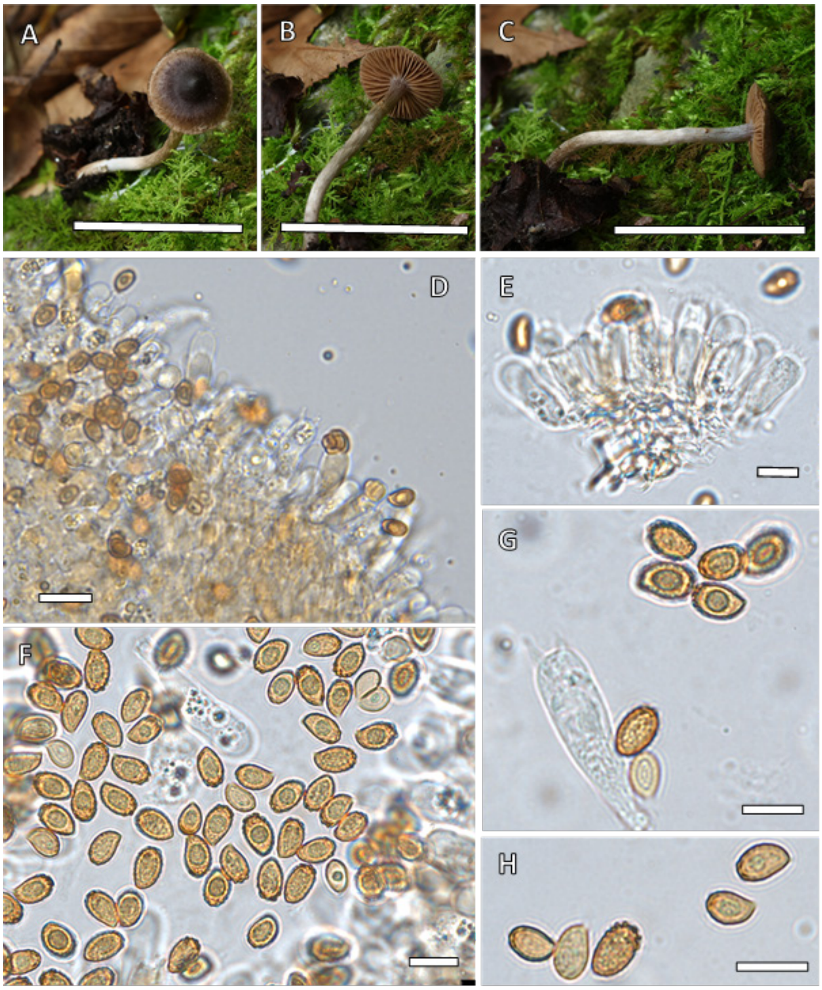

Fig. 3. *Cortinarius falsosus.* A–C: mature basidioma (KA24-1195). D, E: basidia mounted in KOH. F–H: basidiospores mounted in KOH. Scale bars: A–C, 3 cm; D, E, 20 µm; F–H, 10 µm.

***Cortinarius fulvopaludosus* Kytöv., Niskanen & Liimat.**, in Liimatainen, *Index Fungorum* 344:1 (2017). Fig. 4

Korean name: Hwanggalseupji-kkeunjeok-beoseot (황갈습지끈적버섯), the name is based on its yellowish-brown color and wetland habitat ("*fulvo*" + "*paludosus*").

Description: Small medium basidiomata. Pileus *ca.* 15–20 mm in diameter, convex, distinctly hygrophanous, fulvous to reddish-brown, surface smooth and slightly viscid when moist. Lamellae are moderately spaced and pale brown to cinnamon-brown. Stipe *ca.* 40–70 × 4–5 mm, slender, elongated, often slightly curved, pale brown to orange-brown, surface smooth. Basidiospores ellipsoid to slightly amygdaliform, verrucose, (6.8–)7.2–8.8(–9.5) × (4.0–)4.3–5.2(–5.8) μm, Q = (1.40–)1.50–1.75(–1.90), Qm = 1.63. Basidia clavate, 4-spored, 25–35 × 6–9 μm. Cheilocystidia and pleurocystidia not observed. Pileipellis a weakly to moderately gelatinized cutis, composed of repent hyphae embedded in a gelatinous matrix, hyaline to pale brown.

Habitat: Typically moist or wet forest environments, often associated with broadleaf trees.

Specimens examined: South Korea, Gangwon-do, Hwacheon-gun, Sangseo-myeon, Bongo-ri, Bongo-ri Pung-hyeol-ji, 38°12′32.82″N, 127°35′42.84″E, elev. 373 m, 23 Aug 2024, KA24-0850 (KH).

Notes: *Cortinarius fulvopaludosus* was recovered within the corresponding clade (87/0.98), although internal node support was moderate (68/0.97). The ITS sequence of KA24-0850 was 99.4% similar to the closest reference sequences of *C. fulvopaludosus* H6033460 (NR_154868), differing only by 3 nucleotide positions among 509 aligned sites. It is phylogenetically related to taxa such as *C. hinnuleus* and allied species within the Telamonia group. The resolution of ITS-based phylogenies might be limited in certain *Cortinarius* lineages, particularly among closely related, brown-spored taxa [6]. Therefore, moderate support values at internal nodes are common in this group. Morphologically, *C. fulvopaludosus* can be distinguished from *C. hinnuleus* by its more hygrophanous pileus, finer fibrillose surface, and different basidiospore size and ornamentation. Despite moderate internal support, the position of KA24-0850 within the *C. fulvopaludosus* clade, together with its morphological agreement, supports its identification.

Fig. 4. *Cortinarius fulvopaludosus*. A, B: mature basidioma (KA24-0850). C–E: basidia and F, H: basidiospores mounted in KOH. Scale bars: A, B, 3 cm; C–E, 20 µm; F, H, 10 µm.

***Cortinarius lepidopus* Cooke**, *Grevillea* 16(no. 78): 43 (1887), Fig. 5.

Korean name: Inpyeon-kkeunjeok-beoseot (인편끈적버섯), the name refers to its scaly or fibrillose pileus surface ("*lepidopus*").

Description: Medium-sized basidiomata. Pileus diameter, 40–50 mm, convex to plano-convex, pale brown to grayish-brown, surface dry, smooth to finely fibrillose. Lamellae adnate to slightly emarginate, pale brown. Stipe *ca.* 60–75 × 3–8 mm, long and slender, cylindrical, whitish to pale brown, surface smooth to finely fibrillose. Basidiospores broadly ellipsoid to sub amygdaliform, verrucose, (6.8–)7.2–8.6(–9.2) × (5.2–)5.5–6.8(–7.5) µm, Q = (1.10–)1.20–1.50(–1.65), Qm = 1.32. Basidia clavate, 4-spored, 30–40 × 7–10 µm. Cheilocystidia and pleurocystidia were not evident. The pileipellis cutis is composed of parallel, repent hyphae, smooth-walled, pale brown, lacking gelatinization.

Habitat: In forest soils, often associated with trees in temperate regions.

Specimens examined: South Korea, Gangwon-do, Pyeongchang-gun, Jinbu-myeon, Singi-ri, Bakjigol Pung-hyeol-ji, 37°35′0.30″N, 128°35′21.10″E, elev. 894 m, 24 Sep 2024, KA24-1135 (KH).

Notes: *Cortinarius lepidopus* was recovered as a distinct lineage (88/1.0) and is closely associated with members of the *C. anomalus* complex, including *C. anomalus*, *C. modestus*, and *C. anomalovelatus*. Recent phylogenomic studies have demonstrated that Cortinariaceae comprises multiple distinct evolutionary lineages and that species boundaries within the Telamonia clade remain difficult to resolve due to high morphological variability and limited resolution of ITS sequences alone [4,6]. Index Fungorum and Species Fungorum treat *C. lepidopus* in synonym with *C. anomalus*, whereas MycoBank maintains *C. lepidopus* as a separate taxon. This discrepancy reflects ongoing taxonomic uncertainty about the *C. anomalus* complex. However, our phylogenetic analysis showed that *C. lepidopus* formed a supported and independent lineage, indicating that it is a distinct taxon. Morphologically, it is characterized by a fibrillose to squamulose pileus surface and moderately verrucose basidiospores, distinguishing it from related taxa. The examined specimen (KA24-1135) agrees well with the known characteristics of this species. Therefore, we retained the name *C. lepidopus* in this study based on both phylogenetic evidence and morphological consistency.

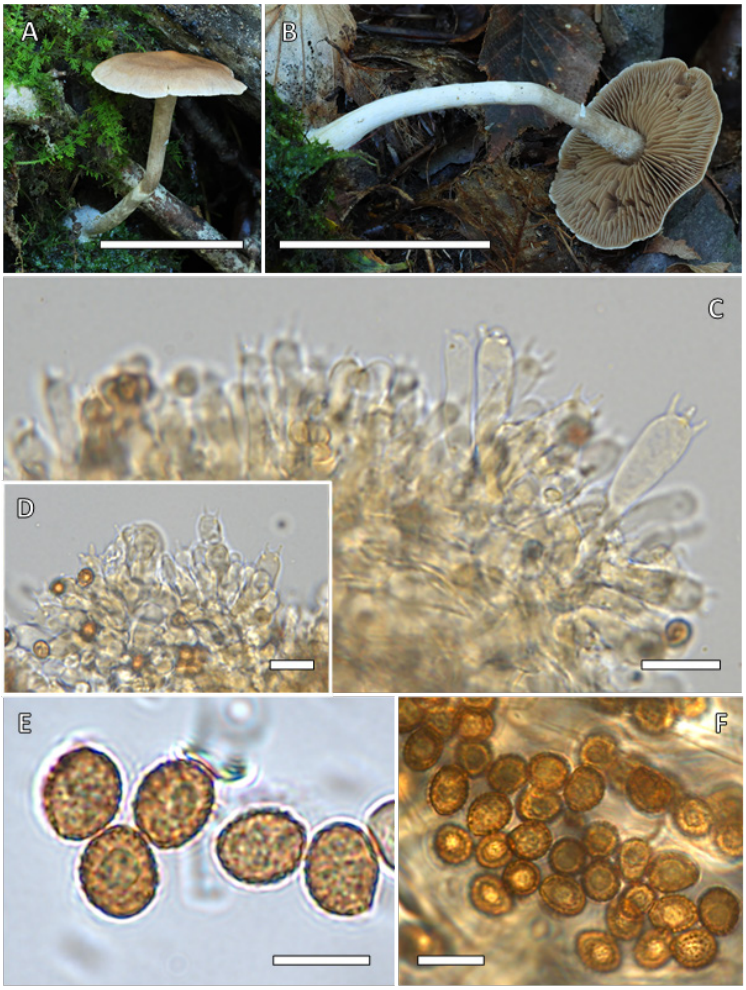

Fig. 5. *Cortinarius lepidopus.* A, B: mature basidioma (KA24-1135). C, D: basidia and E, F: basidiospores mounted in KOH. Scale bars: A, B, 3 cm; C, D, 20 µm; E, F, 10 µm.

***Cortinarius scotoides* J. Favre**, *Ergebn. Wiss. Unters. Schweiz. NatnParks* 5(no. 33): 146, 204 (1955), Fig. 6.

Korean name: Heukgal kkeunjeok beoseot (흑갈끈적버섯), the name reflects its dark brown coloration (“*scotoides*”).

Description: Basidiomata are small, with a pileus with 15–30 mm-diameter, convex, brown to dark brown, distinctly hygrophanous, surface smooth. Lamellae moderately spaced, brown. Stipe *ca*. 40–50

× 2–4 mm, slender, cylindrical, pale brown, surface finely fibrillose. Basidiospores ellipsoid to slightly amygdaliform, finely verrucose, (6.5–)6.8–8.2(–8.8) × (3.8–)4.0–4.8(–5.2) µm, Q = (1.45–)1.55–1.85(–1.95), Qm = 1.68. Basidia clavate, 4-spored, 25–32 × 6–8 µm. Cheilocystidia and pleurocystidia were not evident. Pileipellis a cutis to weakly gelatinized cutis, composed of slender, repent hyphae, hyaline to pale brown.

Habitat: Soil in forested habitats, often associated with deciduous or mixed forests.

Specimens examined: South Korea, Gangwon-do, Jeongseon-gun, Bukpyeong-myeon, Jangyeol-ri, Jangyeol-ri Pung-hyeol-ji, 37°27′06.60″N, 128°41′05.34″E, elev. 353 m, 21 Aug 2024, KA24-0830 (KH).

Notes: *Cortinarius scotoides* was supported within its clade (99/1.0) and was clearly separated from the closely related *C. subscotoides*, which forms a sister lineage in the phylogenetic tree. Morphologically similar taxa within *Cortinarius* might represent distinct evolutionary lineages, highlighting the importance of molecular data in species delimitation [4,6]. The clear separation between *C. scotoides* and *C. subscotoides* in our analysis supports their recognition as independent species. Morphologically, *C. scotoides* can be distinguished from *C. subscotoides* by slightly smaller basidiospores and differences in pileus texture and coloration. We therefore assigned specimen (KA24-0830) to *C. scotoides,* based on the phylogenetic placement and the morphological agreement.

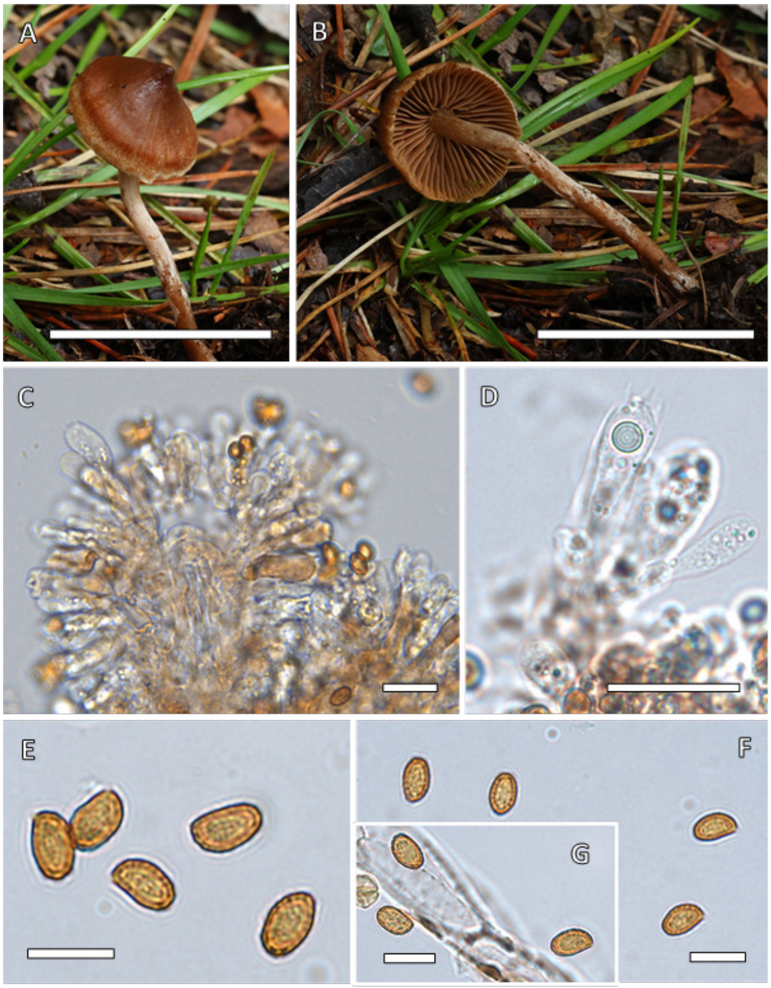

Fig. 6. *Cortinarius scotoides.* A, B: mature basidioma (KA24-0830). C, D: basidia and E–G: basidiospores mounted in KOH. Scale bars: A, B, 3 cm; C, D, 20 µm; E–G, 10 µm.

Key to five *Cortinarius* species described herein

A diagnostic key based on combined macromorphological and micromorphological characteristics is provided below.

1. Pileus distinctly hygrophanous or viscid when moist 2
1’. Pileus dry or only weakly hygrophanous 3
2. Basidiospores moderately elongated (Qm ~1.6); pileus fulvous to reddish-brown........*C. fulvopaludosus*
2’. Basidiospores more elongated (Qm ≥1.7); pileus dark brown..*C. falsosus*
3. Basidiospores relatively broad (Qm ~1.3) ....*C. lepidopus*
3’. Basidiospores more elongated (Qm >1.5) 4
4. Basidiospores relatively small (mostly <8.5 μm) ....*C. scotoides*
4’. Basidiospores larger (often >9 μm) ....*C. alpinus*

DISCUSSION

This study confirmed five *Cortinarius* species, *C. alpinus*, *C. falsosus*, *C. fulvopaludosus*, *C. lepidopus*, and *C. scotoides*, as newly recorded in South Korea based on integrated morphological and molecular evidence. All examined specimens were placed within clades corresponding to known described species, indicating that they represent previously unknown components of the Korean mycobiota rather than novel taxa.

Species identification within *Cortinarius* remains challenging because many taxa have overlapping macromorphological characters and substantial phenotypic variability [4,6]. We used diagnostic morphological characteristics such as pileus texture and hygrophany, basidiospore size and shape, and pileipellis structure to identify each species. *Cortinarius alpinus* was characterized by brown to orange-brown basidiomata, a weakly viscid pileus, and a position within a supported *C. alpinus* clade, although the Korean specimens had somewhat smaller basidiospores than those generally reported for the species [20]. *Cortinarius scotoides* was distinguished from the closely related *C. subscotoides* by its smaller basidiospores and dark hygrophanous basidiomata. *Cortinarius falsosus* and *C. fulvopaludosus* belong to morphologically similar, brown-spored lineages, in which reliable identification based solely on macromorphology is difficult. Therefore, ITS phylogenetic evidence was essential for confirming species boundaries.

Similar integrative taxonomic studies have recently discovered hitherto unknown fungal taxa in Korea, including ectomycorrhizal [8] and other macrofungal groups [9]. The present and previous findings indicate that the diversity of Korean macrofungi is underestimated and that combined morphological and molecular approaches are essential for reliable species identification.

Most species described herein were collected from Pung-hyeol-ji habitats. These sites are cooler and more humid than surrounding forests and are established as microrefugia for cold-adapted organisms [10,11]. Among the species described herein, *C. alpinus*, *C. falsosus*, *C. fulvopaludosus*, and *C. scotoides*, are primarily associated with boreal, subalpine, alpine, or *Salix*-dominated habitats in the Northern Hemisphere.

Their presence in Korean Pung-hyeol-ji habitats suggests that these environments function as local climatic refugia for ectomycorrhizal fungi with northern affinities. Similar ecological functions have been proposed for wind-hole ecosystems supporting relict plants and other cold-adapted organisms.

Overall, our findings expand the known distribution of *Cortinarius* species in South Korea and highlight the ecological significance of Pung-hyeol-ji habitats as potential refugial environments for ectomycorrhizal fungi under ongoing climate change.

CONFLICT OF INTEREST

The authors declare that they have no potential conflict of interest.

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REFERENCES

1. Kirk PM, Cannon PF, Minter DW, Stalpers JA. Dictionary of the fungi. 10th ed. Wallingford: CABI; 2008.
2. Tedersoo L, Bahram M, Põlme S, Kõljalg U, Yorou NS, Wijesundera R, Ruiz LV, Vasco-Palacios AM, Thu PQ, Suija A, et al. Global diversity and geography of soil fungi. Science 2014;346:1256688. https://doi.org/10.1126/science.1256688
3. Smith SE, Read DJ. Mycorrhizal symbiosis. 3rd ed. London: Academic Press; 2008. https://doi.org/10.1016/B978-0-12-370526-6.X5001-6
4. Liimatainen K, Kim JT, Pokorny L, Kirk PM, Dentinger B, Niskanen T. Taming the beast: A revised classification of Cortinariaceae based on genomic data. Fungal Divers 2022;112:89–170. https://doi.org/10.1007/s13225-022-00499-9
5. Garnica S, Weiß M, Oertel B, Oberwinkler F. A framework for a phylogenetic classification in the genus *Cortinarius* (Basidiomycota, Agaricales) derived from morphological and molecular data. Can J Bot 2005;83:1457–77. https://doi.org/10.1139/b05-107
6. Liimatainen K, Niskanen T, Dima B, Kytövuori I, Ammirati JF, Frøslev TG. The largest type study of Agaricales species to date: Bringing identification and nomenclature of *Phlegmecium* (*Cortinarius*) into the DNA era. Persoonia 2014;33:98–140. https://doi.org/10.3767/003158514X684681
7. National Institute of Biological Resources. National list of species of Korea [Internet]. Incheon: NIBR; 2025 [cited 2026 Apr 26]. Available from https://www.kbr.go.kr/content/view.do?menuKey=799&contentKey=174
8. Cho SE, Kwag YN, Han SK, Lee DH, Kim CS. Two new records of *Scleroderma* species (Sclerodermataceae, Boletales) in South Korea. Kor J Mycol 2022;50(2):115–23. https://doi.org/10.4489/KJM.20220011

9. Kim DH, Kwag YN, Kim HS, Kim CS, Lee JK. First Korean records of *Scutellinia sinosetosa* and *S. subhirtella* (Pezizales, Pyronemataceae) based on integrative taxonomy. Kor J Mycol 2025;53(4):363–71. http://doi.org/10.4489/kjm.2025.53.4.13
10. Kim KR, Lee SY, Lee DH, Shin HT, Kim CS, An JB. A study on the environmental and microclimatic characteristics for supporting conservation of wind-holes. Korean J Environ Ecol 2025;39(6):597–610. https://doi.org/10.13047/KJEE.2025.39.6.597
11. Hampe A, Jump AS. Climate relicts: Past, present, future. Annu Rev Ecol Evol Syst 2011;42:313–33. https://doi.org/10.1146/annurev-ecolsys-102710-145015
12. Doyle JJ, Doyle JL. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull 1987;19:11–5.
13. Gardes M, Bruns TD. ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. Mol Ecol 1993;2:113–8. https://doi.org/10.1111/j.1365-294x.1993.tb00005.x
14. White TJ, Bruns TD, Lee SB, Taylor JW. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ, editors. PCR protocols: A guide to methods and applications. San Diego: Academic Press; 1990. p. 315–22. https://doi.org/10.1016/B978-0-12-372180-8.50042-1
15. Chun J. Computer-assisted classification and identification of actinomycetes [dissertation]. Seoul: Seoul National University; 1995.
16. Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. The CLUSTAL_X windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 1997;25:4876–82. https://doi.org/10.1093/nar/25.24.4876
17. Stamatakis A. RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 2014;30:1312–3. https://doi.org/10.1093/bioinformatics/btu033
18. Ronquist F, Huelsenbeck JP. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 2003;19:1572–4. https://doi.org/10.1093/bioinformatics/btg180
19. Page RD. TreeView: An application to display phylogenetic trees on personal computers. Comput Appl Biosci 1996;12:357–8. https://doi.org/10.1093/bioinformatics/12.4.357
20. Peintner U. *Cortinarius alpinus* as an example for morphological and phylogenetic species concepts in ectomycorrhizal fungi. Sommerfeltia 2008;31:161–77. https://doi.org/10.2478/v10208-011-0009-1
21. Boudier E. Description de quelques nouvelles espèces de champignons récoltées dans les régions élevées des Alpes du Valais, en août 1894. Bull Soc Mycol Fr 1895;11:27–30.