RESEARCH ARTICLE

First Report of *Paecilomyces niveus* Isolated from Soil in Palgongsan, Korea

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ABSTRACT

A fungal isolate, designated KNUF-21-026, was isolated from a soil sample collected in Palgongsan, Gunwi-gun, Gyeongbuk Province, Korea. Morphological observations revealed abundant, thick-walled chlamydospores (8–9 µm), phialides with a cylindrical base tapering into a slender neck (11.4–22.6 × 2.3–4.1 µm), and globose to broadly ellipsoid conidia with a flattened base, measuring 3.0–4.6 × 2.5–3.6 µm. These features closely matched those of *Paecilomyces niveus* CBS 100.11^T and clearly differed from *Paecilomyces fulvus*. A multilocus sequence analysis based on concatenated sequences of the internal transcribed spacer regions, β-tubulin and calmodulin genes further confirmed the identification of strain KNUF-21-026 as *P. niveus*. This study represents the first confirmed record of *P. niveus* in Korea, expanding the known diversity of indigenous *Paecilomyces* species in the country.

Keywords: Morphology, *Paecilomyces*, Phylogenetic analyses, Soil

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INTRODUCTION

The genus *Paecilomyces* was first described by Bainier in 1907 to include *P. variotii*, and it has a long and complex taxonomic history [1]. Early classifications, based primarily on morphological characteristics, included a diverse range of thermotolerant and entomopathogenic species, often associated with teleomorphic genera such as *Byssochlamys*, *Talaromyces*, and *Thermoascus* [2,3]. However, molecular phylogenetic studies later revealed *Paecilomyces* to be polyphyletic, with species distributed across several fungal orders, including Eurotiales, Hypocreales, and Sordariales [4,5]. This led to major taxonomic revisions, and many insect-associated species were transferred to other genera, including *Purpureocillium*, *Isaria*, and *Phialemonium* [6,7]. In line with the "One Fungus = One Name" principle and with advancements in multilocus and genome-scale phylogenetic analyses, the genus *Paecilomyces* was redefined and restricted to a monophyletic clade within the order Eurotiales and the family Thermoascaceae [8–10]. This taxonomic placement is currently reflected in the MycoBank database (https://www.mycobank.org), which recognizes *Paecilomyces* as a member of Thermoascaceae. However, it is worth noting that Index Fungorum (https://www.indexfungorum.org) still lists *Paecilomyces* under the family Aspergillaceae, likely due to its historically complex and polyphyletic classification, which has only recently been resolved through phylogenomic studies. Recent phylogenomic analyses further support the monophyly of the refined genus [11], which currently comprises 15 accepted species, including newly described taxa, such as *P. paravariotii* [12], *P. clematidis*, *P. penicilliformis*, and *P. lignorum* [11], as well as reinstated species like *P. lecythidis* and *P. maximus*. Although substantially larger numbers of species are listed under *Paecilomyces* in the Index Fungorum and Mycobank databases, only these 15, confirmed through multilocus and phylogenomic analyses by Urquhart & Idnurm [12] and Visagie et al. [11], are considered phylogenetically validated members and collectively support its monophyly.

Multilocus sequence analysis (MLSA) has proven particularly effective in resolving species boundaries within morphologically similar *Paecilomyces* taxa. Commonly used markers include the internal transcribed spacer (ITS) region (including the ITS1 region, 5.8S rDNA, and ITS2 region) and the β-tubulin (*tub2*) and calmodulin (*CaM*) genes. This multilocus approach has been successfully applied in several taxonomic studies, including the revision of the genus *Paecilomyces* by Samson et al. [6] and, more recently, the establishment of *P. clematidis* as a novel species by Spetik et al. [9].

Among currently accepted *Paecilomyces* species, *P. niveus* is one of the earliest described. It was originally described as *Byssochlamys nivea* by Westling in 1909, based on an isolate from a *Geaster* specimen preserved in alcohol [13]. In 1957, Brown and Smith [2] demonstrated that the asexual state of *B. nivea* aligned with the genus *Paecilomyces*, and the name *Paecilomyces niveus* was formally adopted during Samson and Stolk's revision in 1971 [14]. Despite the significant taxonomic redefinition of the genus in the years since, *P. niveus* has consistently been recognized as a member of *Paecilomyces* in recent phylogenetic studies [8,11,12].

Morphologically, *P. niveus* is characterized by the production of abundant, thick-walled chlamydospores that are globose to pyriform, smooth to slightly roughened, and typically occur singly or in short chains. Its phialides possess a swollen, cylindrical base that narrows abruptly into a long, slender neck. Conidiophores are generally rare, smooth, and septate, usually bearing 2–3 phialides. The conidia are globose to broadly ellipsoid, often with a flattened base, and are arranged in dry, divergent chains [14]. Together, these traits are key to distinguishing *P. niveus* from other members of the genus.

This study reports the first identification of *P. niveus* in Korea. The fungus was isolated from a soil sample collected in Palgongsan, Gunwi-gun, Gyeongbuk Province, as part of an ongoing research initiative focused on documenting indigenous fungal diversity in Korea. The isolate, designated KNUF-21-026, was identified based on morphological characteristics and MLSA, confirming its taxonomic placement within the genus *Paecilomyces*.

MATERIALS AND METHODS

Collection and isolation of the fungal strain

Soil samples were obtained from Palgongsan in Gunwi-gun, Gyeongbuk Province, Korea

(35°59'33.9"N 128°41'12.7"E) and transported to the laboratory for futher analysis. Fungi were isolated using a conventional dilution and plating technique. Each soil sample was suspended in 10 mL of sterile distilled water, vortexed and then serially diluted. Aliquots (50–100 μL) of each suspension was spread onto potato dextrose agar plates (PDA; Difco, Detroit, MI, USA) and incubated at 30℃ for one week [15]. Several fungal strains were isolated and initially identified by sequencing the ITS regions. Among them, strain KNUF-21-026 was identified for further molecular phylogenetic analysis and morphological characterization. Stock culture of the strain KNUF-21-026 (NIBRFGC000509189) was deposited in the National Institute of Biological Resources as a metabolically inactive cultures.

Cultural and morphological characterization

To examine its cultural and morphological characteristics, the fungal strain KNUF-21-026 was cultured on malt extract agar (MEA; Difco, Detroit, MI, USA) and Czapek yeast extract agar (CYA; MBcell, Seoul, Korea) at 30℃. Cultures were incubated for 7 days, and macromorphological characteristics, such as the colony size and color of the mycelium, as well as micromorphological features, such as chlamydospores, phialides, conidiophores, and conidia, were observed. Additionally, microscopic fungal characteristics were observed using a BX-50 microscope (Olympus, Tokyo, Japan).

DNA extraction, PCR amplification, and sequencing

Total genomic DNA was extracted from fungal mycelia of strain KNUF-21-026 using the HiGene Genomic DNA Prep Kit (Biofact, Daejeon, Korea) according to the manufacturer's instructions. The ITS region and portions of the *tub*2 and *CaM* genes were amplified using the ITS1F/ITS4, Bt2a/Bt2b, and cmd5/cmd6 primer pairs, respectively [9]. Successfully amplified products were purified using ExoSAP-IT (Thermo Fisher Scientific, Waltham, MA, USA) and sequenced by Macrogen sequencing service (Macrogen, Seoul, Korea). The resulting ITS, *tub*2, and *CaM* sequences were deposited in the National Center for Biotechnology Information (NCBI) GenBank database under accession numbers LC874603, LC874604, and LC874605, respectively.

Molecular phylogenetic analysis

The sequences of *Paecilomyces* species were obtained from the GenBank database are listed in Table 1. Multiple sequence alignments were performed using Clustal X 2.0 within the MEGA 7 software package (https://www.megasoftware.net/) [16], and a dataset comprising the concatenated ITS region, partial *tub*2, and partial *CaM* alignments was created and used for phylogenetic analyses. Phylogenetic trees were constructed using maximum likelihood (ML), neighbor-joining (NJ), and maximum parsimony (MP) methods based on the Kimura 2-parameter model [17], with 1,000 bootstrap resamples, as implemented in MEGA 7.

Table 1. List of species used in phylogenetic analysis along with their GenBank accession numbers

Species	Strain	GenBank accession no.		
		ITS	*tub2*	*CaM*
Paecilomyces brunneolus	CBS 370.70^T	EU037050	EU037068	EU037033
Paecilomyces clematidis	MEND-F-0561	MZ923761	MZ927741	MZ927739
Paecilomyces dactylethromorphus	CBS 251.55^T	FJ389951	FJ390002	FJ389960
Paecilomyces divaricatus	CBS 284.48^T	FJ389931	FJ389992	FJ389953
Paecilomyces formosus	CBS 990.73B^T	FJ389929	FJ389993	FJ389978
Paecilomyces fulvus	CBS 135.62	FJ389943	FJ389989	FJ389976
Paecilomyces fulvus	CBS 132.33^T	FJ389939	FJ389988	FJ389957
Paecilomyces laguncularíae	CBS 373.70^T	FJ389944	FJ389995	FJ389965
Paecilomyces niveus	**KNUF-21-026**	**LC874603**	**LC874604**	**LC874605**
Paecilomyces niveus	CBS 100.11^T	FJ389934	FJ389999	FJ389956
Paecilomyces niveus	CBS 133.37	FJ389935	FJ390000	FJ389958
Paecilomyces tabacinus	CBS 141098^T	LT548280	MN969434	LT548288
Paecilomyces variotii	CBS 338.51	FJ389930	FJ390007	FJ389955
Paecilomyces zollerniae	CBS 374.70^T	FJ389933	FJ390008	FJ389966
Paecilomyces lecythidis	CMW 18170	PP191151	PP197739	PP197770
Paecilomyces maximus	CBS 124309^T	PP191153	PP197741	PP197772
Paecilomyces lignorum	CMW 18171	PP191152	PP197740	PP197771
Paecilomyces paravariotii	FRR 5287^T	JANCMN01	JANCMN01	JANCMN01
Rasamsonia emersonii	CBS 393.64^T	JF417478	JF417463	JF417510

ITS: internal transcribed spacer regions; *tub*2: β-tubulin; *CaM*: calmodulin.
^{T}Type strain. The strain isolated in this study is indicated in boldface.

RESULTS

Cultural and morphological characteristics

The morphological characteristics of strain KNUF-21-026 closely corresponded to those of the reference strain *P. niveus* CBS 100.11^T (Table 2). Both strains formed cream-colored colonies, close to cartridge buff, on MEA, with pale brown to yellow reverses (Fig. 1A). On both MEA and CYA media, KNUF-21-026 colonies reached diameters of 70–90 mm after 7 days at 30°C (Fig. 1A, B), consistent with the reported growth range for *P. niveus* on MEA. Phialides in KNUF-21-026 exhibited a cylindrical base tapering abruptly into a long, slender neck, measuring 11.4–22.6 × 2.3–4.1 μm overall (Fig. 1C), which is comparable to those of the reference strain (12.5–20.0 × 2.0–3.5 μm). Conidia, arranged in dry, divergent chains, were globose to broadly ellipsoid with a flattened base, measuring 3.0–4.6 × 2.5–3.6 μm (Fig. 1D), which closely matched the size range for *P. niveus* conidia (3.0–5.7 × 2.2–4.0 μm) [14]. Strain KNUF-21-026 also produced abundant, thick-walled chlamydospores that were globose to pyriform, smooth to slightly roughened, and 8–9 μm in diameter, consistent with the chlamydospore size reported for *P. niveus* (Fig. 1E). Conidiophores were rare, smooth, and septate, typically bearing 2–3 phialides, with diameters of 3.3–3.9 μm (Fig. 1F), making them slightly larger than those observed in CBS 100.11^T (2.0–3.0 μm). Hyphae were hyaline, mostly thick-walled, and 1.56–4.71 μm in diameter (Fig. 1F), again generally matching values reported for the reference strain CBS 100.11^T (0.5–4.5 μm) (Table 2). These consistent characteristics morphologically identify strain KNUF-21-026 as *P. niveus*.

Strain KNUF-21-026 differs from *Paecilomyces fulvus* 132.33^{T}, the type strain for the closest known relative of *P. niveus*, in several key morphological features (Table 2). Most notably, chlamydospores are absent in *P. fulvus*. Its conidia are generally larger (4.0–8.7 × 1.5–5.0 μm) and typically cylindrical, with both ends flattened. The conidiophores of *P. fulvus* are relatively short, measuring approximately 150 μm in length, and characteristically bear phialides in compact groups on short metulae arising directly from aerial hyphae. In contrast, the conidiophores of strain KNUF-21-026 are significantly longer, reaching up to 289.1 μm, and usually carry only 2–3 phialides. Additionally, the phialides of *P. fulvus* (12.7–17.0 × 2.5–3.5 μm) have a thickened apex, which is absent in strain KNUF-21-026. Colonies of *P. fulvus* also differ in pigmentation, exhibiting fulvous to olive buff colorations. These combined differences clearly distinguish KNUF-21-026 from *P. fulvus*, which supports its identification as *P. niveus*.

Table 2. Comparison of cultural and morphological characteristics of strain KNUF-21-026 with reference *Paecilomyces* species

Characteristics		*Paecilomyces niveus*[a] KNUF-21-026	*Paecilomyces niveus*[b] CBS 100.11^{T}	*Paecilomyces fulvus*[c] CBS 132.33^{T}
Colony	Color	MEA: Creamish color near cartridge buff; pale brown to yellow shades in reverse	MA: Creamish color near cartridge buff; pale brown to yellow shades in reverse	MA: Fulvous near olive buff; pale brown to yellow shades in reverse
	Size (diam.)	MEA: 70–90mm in 7 days at 30°C CYA: 70–90mm in 7 days at 30°C	MA: 90mm in 7 to 14 days at 30°C; CYA: (30–)45–55mm in 7 days at 30°C	MA: 90mm in 7 to 14 days at 30°C
	Shape	MEA: Spreading broadly; composed of a basal felt with white ascomata occasionally in localized sectors; no exudate	MA: Spreading broadly; composed of a basal felt with white ascomata occasionally in localized sectors; obscured by a floccose to funiculose overgrowth; no exudate	MA: Spreading broadly; composed of a basal felt with white ascomata occasionally in localized sectors; obscured by the velvety; occasionally floccose overgrowth of the conidial state; odor slight; sweet aromatic; no exudate
Chlamydospores	Size (μm)	8–9 in diameter	Up to 10 in diameter	Absent
	Shape	Globose; ovoid to pyriform; smooth to slightly roughened; thick-walled; usually abundantly produced; singly or in short chains	Globose; ovoid to pyriform; smooth to slightly roughened; thick-walled; usually abundantly produced; singly or in short chains	Absent
	Color	Yellow to brown	Yellow brown to brown	Absent
Phialides	Size (μm)	11.4–22.6 × 2.3–4.1	12.5–20.0 × 2.0–3.5 (total); 2.5–7.5 × 0.7–1.5 (neck)	12.5–17.0 × 2.5–3.5 (total); 3.0–8.5 (length); 1.0–1.2 (diam)
	Shape	Cylindrical base; tapering; abruptly to a long thin neck; smooth	Cylindrical base; tapering; abruptly to a long thin neck; smooth	Cylindrical basal portion; tapering abruptly to a long thin neck; with the apex thickened; smooth
Conidiophores	Size (μm)	289.1 (length); 3.3–3.9 (thickness)	300 (length); 2–3 (thickness)	Up to 150 (length)
	Shape	Rare; septate; smooth; bearing 2–3 phialides	Rare; septate; smooth; bearing 2–3 phialides	Septate; smooth; with the phialides borne in groups of two or three on short metulae; borne directly on the aerial hyphae
Conidia	Size (μm)	3.0–4.6 × 2.5–3.6	3.0–4.7 × 2.3–4.0	4.0–8.7 × 1.5–5.0
	Shape	Globose to ellipsoid with flattened base	Globose to ellipsoid with flattened base	Usually cylindrical with both ends flattened
	Color	Hyaline to pale yellowish	Hyaline to pale yellowish	Yellowish
Hyphae	Color	Hyaline	Hyaline	N/A
	Size(μm)	1.56–4.71 in diameter; up to 9.3	0.5–4.5 in diameter; up to 8.0	0.5–5.0 in diameter; up to 10.0
	Shape	Mostly thick-walled	Mostly thick-walled	Usually thick-walled

MA, malt agar; MEA, malt extract agar; CYA, Czapek yeast extract agar; diam., diameter.
[a]Fungal strain used in this study; [b]Source of description [6,14]; [c]Source of description [14].

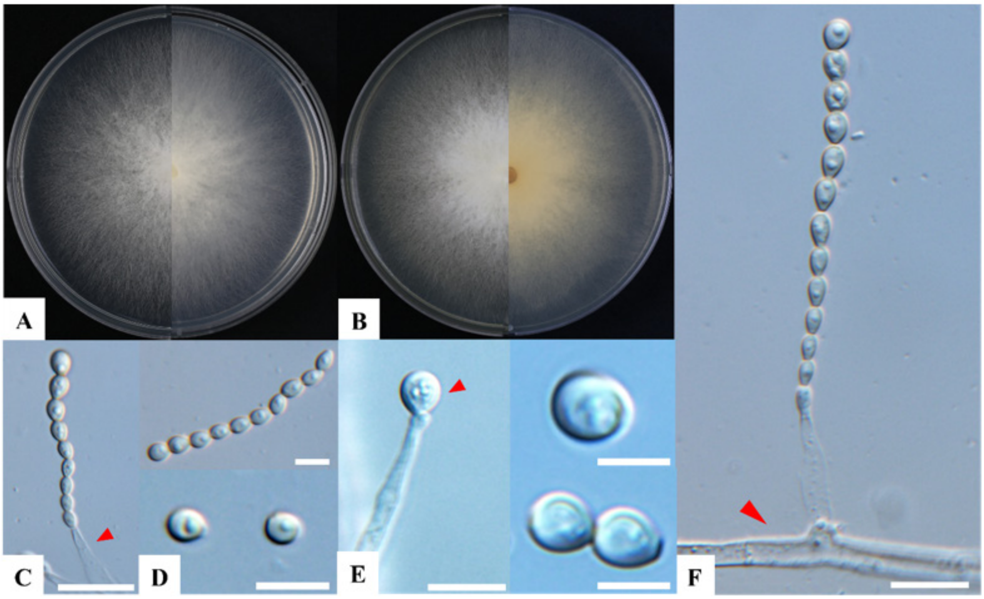

Fig. 1. Cultural and morphological characteristics of *Paecilomyces niveus* KNUF-21-026. A: Colony on malt extract agar (MEA) after 7 days at 30°C; B: Colony on Czapek yeast extract agar (CYA) after 7 days at 30°C; C: Phialides (indicated by arrowhead); D: Conidia; E: Chlamydospore (indicated by arrowhead); F: Conidiophore, hyphae (indicated by arrowhead). Scale bars = 10 µm.

Molecular and phylogenetic relationships

For the molecular identification of the isolated strain KNUF-21-026, total genomic DNA was amplified to obtain the ITS region, *tub2*, and *CaM* sequences, yielding lengths of 603, 490, and 531 bp, respectively. BLAST searches of the GenBank database using the ITS sequence as the query revealed 99.82% identities with several *P. niveus* strains, including CBS 100.11^T (NR_144910), CBS 133.37 (MH855854), NRRL 32565 (DQ322219), and CBS 608.71 (MH860287). Based on ITS similarity, the second closest species was *P. fulvus*, with strains CBS 605.71 (MH860283), IMI 40021 (OM258256), and CBS 146.48 (NR_103603) showing slightly lower identities of 99.12–99.17%. Other species with lower but notable similarities included *P. penicilliformis* CCF 5755^T (98.34%; NR_191058), *P. dactylethromorphus* CBS 251.55^T (98.06%; NR_149330), and *P. laguncularіae* CBS 373.70^T (98.06%; NR_145144). BLAST searches using KNUF-21-026's *tub2* sequence also produced *P. niveus* strains as the closest matches, with 100% identities to strains CBS 133.37 (AY753355) and NRRL 32565 (EU021671), and 99.59% similarity to CBS 100.11^T (FJ389999). In contrast, *P. fulvus* strains, CBS 135.62 (FJ389989) and CBS 132.33 (FJ389988), showed significantly lower similarities of 92.05% and 92.92%, respectively. Similarly, the *CaM* sequence of KNUF-21-026 showed 100% identity with *P. niveus* strains CBS 100.11^T (FJ389956), CBS 606.71 (FJ389968), and NRRL 32565 (EU021688), while significantly lower similarities were observed with the closest-matching type strains of other species, including *P. fulvus* CBS 132.33^T (95.1%, FJ389957), *P. tabacinus* CCF 5290^T (93.2%, LT548288), *P. laguncularіae* CBS 373.70^T (92.48%, FJ389965), *P. clematidis* MEND-F-0560^T (92.21%, MZ927738), and *P. zollerniae* CBS 374.70^T (92.09%, FJ389966). Taken together, all three molecular markers strongly support a close association between strain KNUF-21-026 and *P. niveus* strains, suggesting conspecificity. However, the ITS sequence also showed high similarities with several other *Paecilomyces* species, so species-level identification based on the single-locus data should not be considered definitive.

To unambiguously identify strain KNUF-21-026, an MLSA using concatenated ITS, *tub*2, and *CaM* sequences was performed. This approach, previously applied in the delineation of novel *Paecilomyces* species and reclassification of known taxa [6,9], provided robust phylogenetic resolution. The ML phylogenetic tree (Fig. 2) unequivocally placed strain KNUF-21-026 within the *P. niveus* clade, where it clustered tightly with the reference strains CBS 100.11^T and CBS 133.37. Among the other analyzed species, the tree topology also showed that *P. fulvus* is the closest neighbor species to the *P. niveus* clade; therefore, it was included in the morphological comparison alongside *P. niveus* (Table 2). These phylogenetic results, in combination with morphological evidence, confirm that strain KNUF-21-026 should be identified as *P. niveus*. To the best of our knowledge, this is the first report of this species in Korea.

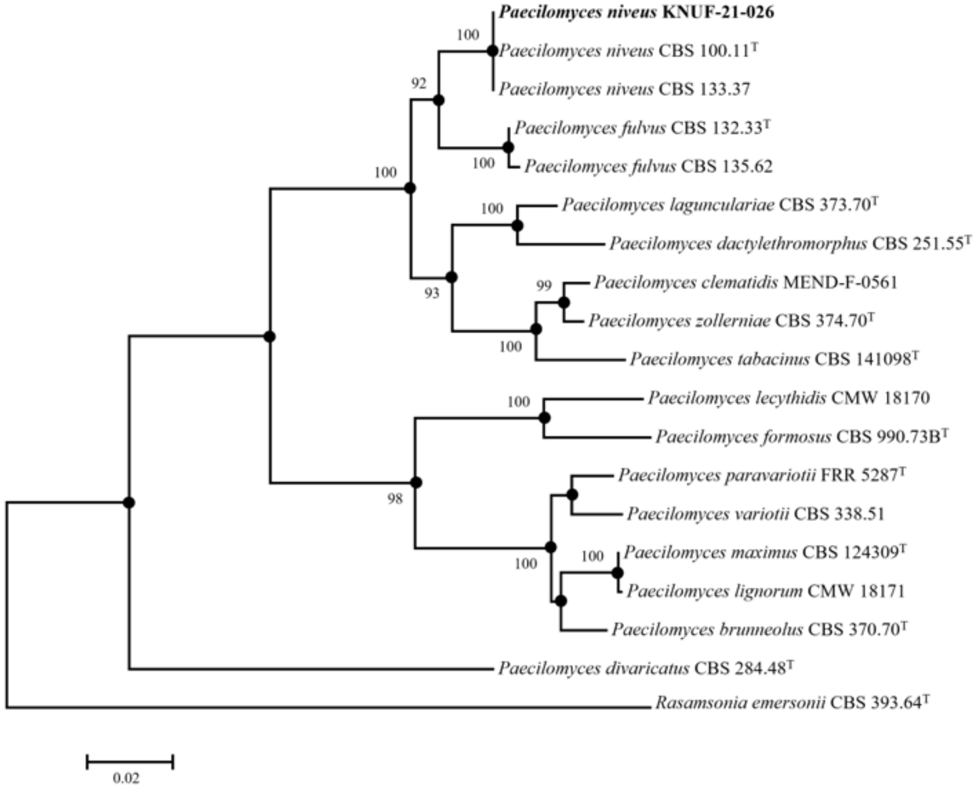

Fig. 2. Maximum-likelihood phylogenetic tree based on the combined sequences of internal transcribed (ITS) regions, β-tubulin (*tub2*) and Calmodulin (*CaM*) genes showing the phylogenetic position of strain KNUF-21-026 among *Paecilomyces* species. Bootstrap values greater than 90% (based on 1,000 replications) are shown at branch points. The filled circles indicate that the corresponding nodes were also recovered in trees generated using the neighbor-joining and maximum-parsimony algorithms. The isolated strain is indicated in bold. *Rasamsonia emersonii* CBS 393.64^T was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

DISCUSSION

In this study, the fungal isolate KNUF-21-026, recovered from a soil sample collected in Palgongsan, was identified as *P. niveus* based on a polyphasic approach integrating morphological and molecular evidence. Its colony morphology and microscopic characteristics closely matched those of the type strain CBS 100.11^T [14]. An MLSA using concatenated ITS, *tub*2, and *CaM* sequences confirmed its affiliation with *P. niveus*. The ITS region showed high similarities to several *Paecilomyces* species in addition to *P. niveus*, such as *P. fulvus*, and thus, only the concatenated dataset unambiguously identified strain KNUF-21-026 to species, underscoring the importance of MLSA in delineating closely related taxa.

Several *Paecilomyces* species have been identified in South Korea, reflecting their ecological diversity. Among them, *P. variotii* is the most frequently recorded, and it has been isolated from diverse substrates, including rat dung in Gwangju [18], creosote-treated railroad crossties in Gwangmyeong [19], jellyfish (*Nemopilema nomurai*) along Korea's southern coast [20], and traditional fermentation starters (nuruk) from various regions across the country [21]. Other species, such as *Paecilomyces inflatus*, identified as an endophyte in healthy chili pepper tissues [22]; *Paecilomyces lilacinus*, isolated from the roots of *Justicia adhatoda*, with a demonstrated potential to alleviate heavy metal stress [23]; and *Paecilomyces purpureus*, recovered from the hyposphere soil of a wrinkled mushroom on Jeju Island [24], have also been reported. However, according to recent phylogenetic revisions, *P. variotii* is the only species among these currently recognized as a valid member of the redefined genus *Paecilomyces*, which includes only 15 phylogenetically supported species [11,12]. Thus, the discovery of *P. niveus* in Korean soil is significant not only as the first confirmed record of this species in Korea but also as an expansion of the country's recognized indigenous *Paecilomyces* diversity. Thus, this finding highlights the value of continued biodiversity surveys using integrative taxonomic approaches.

Paecilomyces niveus is a thermotolerant filamentous fungus known for its broad environmental adaptability and distribution. It has been isolated from a variety of substrates, including soil, decaying plant matter, barley and oat grains, fruit surfaces, wooden materials, and heat-processed foods [8,14,25,26]. It is particularly well known for its ability to spoil fruit juices, especially apple-based beverages, due to its production of heat-resistant ascospores that can survive commercial pasteurization [26]. In this context, *P. niveus* has been recovered from fruit-processing environments, agricultural soils, and storage facilities, where its spores persist under suboptimal conditions. In addition to its well-documented occurrence in the United States, where it is recognized as a major spoilage agent and patulin producer [27,28], *P. niveus* has been reported from Belgium, China, Japan, and Switzerland, often associated, again, with fruit and fruit product contamination [6,11,29]. More recently, it was isolated from wooden utility poles in South Africa [11], further demonstrating its ecological adaptability.

Beyond its role in spoilage, *P. niveus* has emerged as a postharvest plant pathogen. It causes fruit rot in apples, peaches, and citrus fruits, gaining access through mechanical injuries, and can persist during cold storage [25,28,30]. This dual identity, as both a spoilage agent and a plant pathogen, makes it an emerging concern for both the fresh produce and processed fruit industries. *Paecilomyces niveus* is also notable for its ability to produce several biologically active secondary metabolites. Chief among these is patulin, a mycotoxin of significant public health concern due to its immunotoxic, neurotoxic, and genotoxic effects [31]. Other notable secondary metabolites include mycophenolic acid, a known immunosuppressive compound, and byssochlamysol, isolated from its teleomorph *Byssochlamys nivea*, which has demonstrated antitumor activity against IGF-1-dependent cancer cells [32,33]. The biosynthetic potential of *P. niveus,* therefore, not only contributes to its spoilage risk but also highlights a possible role as a source of pharmacologically interesting natural products.

CONCLUSION

The discovery of *Paecilomyces niveus* in Korean soil represents the first confirmed report of this species in the country, extending the known geographic distribution of phylogenetically validated *Paecilomyces* species in East Asia. Its resilience under harsh environmental conditions, potential to produce toxic and bioactive secondary metabolites, and role as a postharvest pathogen highlight its importance from both ecological and economic perspectives. This finding enhances our understanding of indigenous fungal diversity in Korea and reinforces the need for continuous environmental monitoring to assess the distributions, functional roles, and risks associated with emerging fungal taxa.

CONFLICTS OF INTERESTS

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

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