RESEARCH ARTICLE

Trichoderma panacis and *T. brevicompactum*: Morphological and Phylogenetic Analyses of Two Previously Unreported *Trichoderma* Species in Korea

Ji-Eon Kim[1], Seong-Keun Lim[1], Hae-Dam Kim[1], So-Yeon An[1], Christophe Nteziryayo[2], Seung-Yeol Lee[1,3*], and Hee-Young Jung[1,3]

[1]Department of Plant Medicine, Kyungpook National University, Daegu 41566, Korea
[2]Community Engagement for Food and Agriculture Development in Rwanda, Kigali, Rwanda
[3]Institute of Plant Medicine, Kyungpook National University, Daegu 41566, Korea

*Corresponding author: leesy1123@knu.ac.kr

ABSTRACT

This study reports the discovery of two previously unreported fungal strains belonging to Hypocreales, designated KNUF-20-085 and KNUF-20-NI014, from soil samples in Korea. Phylogenetic analyses based on the concatenated nucleotide sequences of the internal transcribed spacer regions and partial sequences of the translation elongation factor 1-alpha and second-largest subunit of RNA polymerase II genes placed the strains within the genus of *Trichoderma*. We investigated the strains cultural features on potato dextrose agar, malt extract agar, corn meal agar, and synthetic nutrient-poor agar, and their morphological characteristics through microscopic observation. For strain KNUF-20-085, cultural and morphological characteristics showed a high similarity with those of *Trichoderma panacis* SYPF 8050^{T}. For strain KNUF-20-NI014, cultural and morphological characteristics were similar to those previously reported for *T. brevicompactum* CBS 109720^{T}. The phylogenetic analysis supported these affiliations, with strains KNUF-20-085 and KNUF-20-NI014 clustering with *T. panacis* and *T. brevicompactum*, respectively. This study represents the first documentation of *T. panacis* and *T. brevicompactum* in Korea.

Keywords: Morphology, Phylogeny, *Trichoderma brevicompactum*, *Trichoderma panacis*

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INTRODUCTION

Hypocreales is an order within the phylum Ascomycota and the class Sordariomycetes. Members of this order are typically recognized by their bright, lightly pigmented fruiting bodies [1]. Hypocreales comprises 15 families, including Hypocreaceae, Bionectriaceae, Nectriaceae, and Clavicipitaceae [2]. Within Hypocreaceae, 17 genera have been identified, among which *Trichoderma* is prominent [2,3]. *Trichoderma* was first proposed as a genus by C. H. Persoon in 1794 based on material collected in Germany [4]. Due to changes in the International Code of Nomenclature, the genus *Trichoderma* has been proposed for conservation over its teleomorph, *Hypocrea*. Thus, all species bearing both the names *Hypocrea* and

Trichoderma, as well as those described solely under *Hypocrea*, have been officially transferred to the genus *Trichoderma* [5], which now includes more than 400 species, including the type species *T. fuliginoides* [2]. The genus *Trichoderma* is commonly found in and isolated from a diverse range of habitats, such as soils, moist wood, tropical forest trees, mushrooms, bracket fungi in forests, and even water-damaged buildings [5,6]. Species in this genus are typically characterized by rapid growth, the production of bright green masses of conidia, a repetitively branched conidiophore structure, and their role as plant symbionts [7,8]. Another well-known characteristic of many *Trichoderma* species is their antifungal or plant-growth-stimulating activities, along with the production of unique enzymes and secondary metabolites [3]. These features have made them exploitable as biological control agents against fungal phytopathogens, with some isolates currently used in commercially available applications [9–11]. Due to their enzymatic versatility and secondary metabolite production, species of *Trichoderma* also play critical roles in ecological nutrient cycling, decomposition, and plant–microbe interactions [3], and they are increasingly valued in sustainable agriculture, particularly as eco-friendly alternatives to chemical fungicides [3]. Traditionally, taxonomic studies of *Trichoderma* species were based on morphological and physiological characteristics [12]. However, as the number of described species has grown, distinguishing them solely through morphological observation has become difficult due to high degrees of similarity among many species. As a result, DNA sequence analysis has become the new standard in fungal phylogenetics and systematics. Phylogenetic analyses combining the sequences of the internal transcribed spacer (ITS) regions and the translation elongation factor 1-alpha (*TEF1*) and second-largest subunit of RNA polymerase II (*RPB2*) genes are now widely used to study phylogenetic relationships within *Trichoderma* and to reveal taxonomic diversity [13]. Although the genus *Trichoderma* has been widely studied worldwide, only 33 species have been reported from environmental samples in Korea [14–19]. Therefore, the two *Trichoderma* species isolated for the first time from Korean soil in this study contribute to expanding our current understanding of fungal diversity in the region. In this paper, we document and describe the morphological and phylogenetic characteristics of these strains.

MATERIALS AND METHODS

Sample collection and fungal strain isolation

Fungal strains were isolated using the plate dilution method from soil samples collected in Pohang-si (36°11'05.8"N 129°23'03.4"E) and Dokdo (37°14'28.9"N, 131°51'54.5"E), Gyeongbuk province in Korea. Strains KNUF-20-085 and KNUF-20-NI014 were selected from numerous fungal strains for further morphological and molecular phylogenetic analysis. Stock cultures of strains KNUF-20-085 and KNUF-20-NI014 were deposited in the National Institute of Biological Resources (NIBR) as metabolically inactive cultures under accession numbers NIBRFGC000507845 and NIBRFGC000507835, respectively.

Cultural and morphological characteristics

Cultural and micromorphological characteristics were studied using different cultural media for each strain. Cultural characteristics, including colony texture, color, size, and shape, were examined using potato dextrose agar (PDA; Difco, Detroit, MI, USA) and corn meal agar (CMA; Difco, Detroit, MI, USA) for both strains, while malt extract agar (MEA; Difco) was used exclusively for strain KNUF-20-085 and synthetic nutrient-poor agar (SNA; MBcell, Seoul, Korea) was used exclusively for strain KNUF-20-NI014, with an incubation temperature of 20℃ for all cultures [20,21]. Micromorphological features were observed under a light microscope (BX-50; Olympus, Tokyo, Japan).

Genomic DNA extraction, polymerase chain reaction amplification, and sequencing

Total genomic DNA was extracted from fungal mycelia cultured on PDA using a HiGene™ Genomic DNA Prep Kit (BIOFACT, Daejeon, Korea) according to the manufacturer's instructions. Molecular identification was conducted by analyzing the ITS regions with partial *RPB2* and partial *TEF1* gene sequences, which were amplified using the primer pairs ITS1F/ITS4, fRPB2-5f/fRPB2-7cr, and EF1-728F/TEF1LLErev, respectively [22–25]. The amplified PCR products were purified using the EXOSAP-IT PCR Product Cleanup Reagent (Thermo Fisher Scientific, Waltham, MA, USA) and sequenced by SolGent (Daejeon, South Korea). The obtained sequences of strains KNUF-20-085 and KNUF-20-NI014 were deposited in the National Center for Biotechnology Information (NCBI) GenBank database (Table 1).

Table 1. GenBank accession numbers of sequences used for the phylogenetic analyses in this study

Species	Strain	GenBank accession number		
		ITS	*TEF1*	*RPB2*
Protocrea pallida	CBS 299.78^{T}	EU703925	EU703900	EU703948
Trichoderma arundinaceum	GJS 05-184	EU330933	EU338280	EU338308
Trichoderma arundinaceum	NRRL 3199	EU330932	EU338279	EU338307
Trichoderma atroviride	CBS 119499	FJ860726	FJ860611	FJ860518
Trichoderma atroviride	CBS 142.95	MH862505	AY376051	EU341801
Trichoderma brasiliensis	14F5R-AM	MK713497	MT300486	MT300488
Trichoderma brasiliensis	17F5R-AM	MK713499	MT300492	MT300489
Trichoderma brevicompactum	**KNUF-20-NI014**	**PV766722**	**PV786242**	**PV786243**
Trichoderma brevicompactum	HBT7-10	OQ734626	OQ791321	OQ791318
Trichoderma dorotheae	GJS 99-202^{T}	NR_166014	DQ307536	EU248602
Trichoderma erinaceum	CEN1421	MK714901	MK696659	MK696820
Trichoderma erinaceum	CEN1420	MK714900	MK696658	MK696819
Trichoderma erinaceum	DAOM 230019^{T}	DQ083009	AY750880	KJ842151
Trichoderma hamatum	Th23	MW797032	OL439486	OL412667
Trichoderma intricatum	G.J.S. 02-78	EU264002	EU248630	EU241505
Trichoderma koningii	7723^{T}	KJ783285	KJ634753	KJ634720
Trichoderma koningiopsis	GJS 93-20^{T}	DQ313140	DQ284966	EU241506
Trichoderma panacis	**KNUF-20-085**	**PV766723**	**PV786245**	**PV786244**
Trichoderma panacis	SYPF 8050^{T}	MF565524	MF565523	MF565525

Table 1. GenBank accession numbers of sequences used for the phylogenetic analyses in this study

Species	Strain	GenBank accession number		
		ITS	*TEF1*	*RPB2*
Trichoderma protrudens	DIS 119F	EU330946	EU338289	EU338322
Trichoderma rodmanii	GJS 91-88^{T}	EU330948	EU338286	EU338324
Trichoderma rogersonii	CBS 119503	FJ860826	FJ860690	FJ860583
Trichoderma songyi	SFC20130926-S001	MG491505	KJ636525	KJ636518
Trichoderma turrialbense	CBS 112445^{T}	EU330945	EU338284	EU338321
Trichoderma turrialbense	BBA 72294	EU330944	EU338282	EU338320
Trichoderma viride	GJS 04-372	DQ677655	DQ672615	EU711362

ITS: internal transcribed spacer regions; *TEF1*: translation elongation factor 1-alpha; *RPB2*: RNA polymerase II subunit.
^{T}Type strain.
The newly generated sequences are indicated in bold.

Phylogenetic analysis

The ITS regions, *TEF1*, and *RPB2* gene sequences of strains KNUF-20-085 and KNUF-20-NI014 were aligned with reference sequences retrieved from the NCBI GenBank database. Ambiguous regions were deleted from the alignments, and evolutionary distance matrices for the neighbor-joining (NJ) algorithm were calculated using the Kimura two-parameter model [26,27]. Phylogenetic relationships were inferred via the topology of trees generated using the NJ method in MEGA11 software with 1,000 bootstrap replications [28].

RESULTS

Taxonomy

Trichoderma panacis **S.Y. Liu, T. Yuan Zhang, Ying Yu & Yi X. Zhang, Int J Syst Evol Microbiol 70 (5): 3165 (2020) [MB#824197]**

Specimen collection: Cheongha-myeon, Pohang-si, Gyeongbuk province, Korea (36°11'05.8"N, 129°23'03.4"E), isolated from soil.

Description: Colonies on PDA reached 32–36 mm in diameter after 72 h of culturing at 20℃. Mycelia were hyaline and whitish, with aerial hyphae, wavy margins, and downy to finely floccose surfaces (Fig. 1A). A coconut-like odor was detected, with no diffusing pigment observed. On MEA, colonies reached 15–22 mm in diameter after 72 h of culturing at 20℃. Colonies were dense and whitish, with well-defined margins, aerial hyphae, and downy to floccose surfaces (Fig. 1B). A coconut-like odor was detected, with no diffusing pigment observed. On CMA, colonies reached 14–18 mm in diameter after 72 h of culturing at 20℃. Colonies were hyaline and thin, with aerial hyphae, and slightly wavy margins (Fig. 1C). *Hyphae* were aerial, radial, and sometimes inconspicuous. C*onidiophores* were Verticillium-like, substituted by phialides singly or in whorls (Fig. 1D). *Phialides* were produced in a terminal cluster (Fig. 1E and F). *Conidia* were ellipsoidal, smooth, yellowish green to green, and 4–5 × 2.3–3.2 µm (n = 40) (Fig. 1G). *Chlamydospores* were not observed.

Notes: Comparing the strains *T. panacis* KNUF-20-085 and SYPF 8050^{T}, both strains exhibit similar cultural characteristics on PDA, MEA, and CMA media, and share morphological traits such as smooth, ellipsoidal conidia formed at the ends of Verticillium-like conidiophores (Table 2) [20].

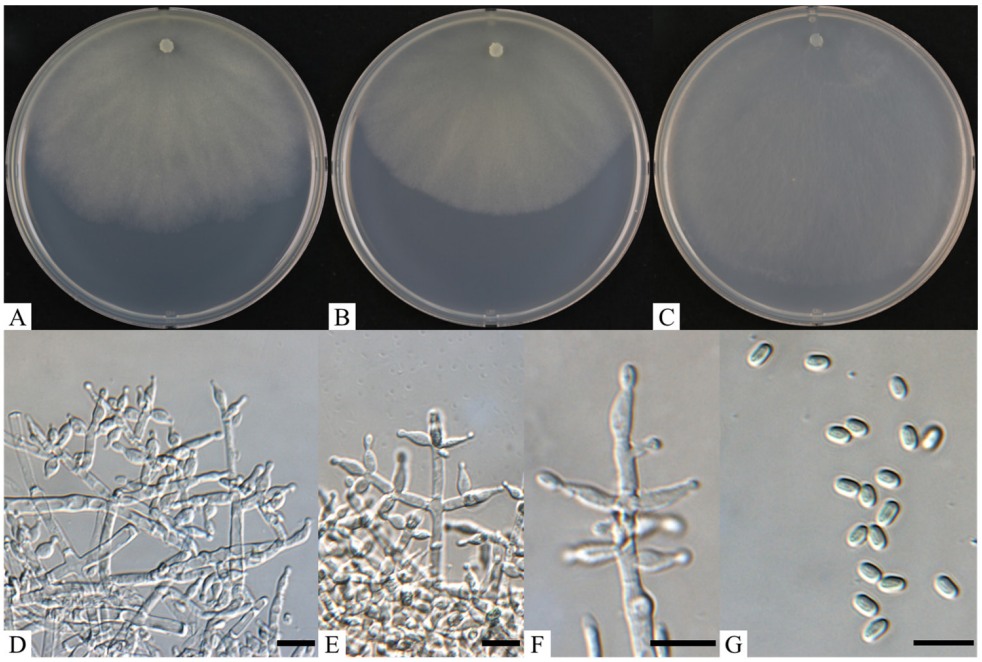

Fig. 1. Cultural and morphological characteristics of *Trichoderma panacis* KNUF-20-085. A–C: Front views of colonies after 7 d at 20℃ on potato dextrose agar, malt extract agar, and corn meal agar, respectively; D: conidiophores and phialides with hyphae; E: phialides at the ends of branched hyphae; F: phialides; G: conidia. Scale bars = 10 μm.

Table 2. Cultural and morphological comparison of *Trichoderma panacis* KNUF-20-085 with closely related *Trichoderma* strains

	Trichoderma panacis KN UF-20-085[a]	*Trichoderma panacis* SYPF 8050[Tb]	*Trichoderma songyi* SFC20130 926-S001[Tc]	*Trichoderma erinaceum* DAOM 230019[Td]
Colony characteristics	PDA: 32–36mm; whitish, wavy margin, downy to fine floccose; coconut-like odor MEA: 15.0–22.0 mm; dense, whitish, defined margin; coconut-like odor CMA: 14–18mm; hyaline, thin, slightly wavy margin, aerial hyphae; coconut-like odor	PDA: 30 .4–32.8mm; coarse wavy margin, thick, downy floccose; coconut-like odor MEA: 13.0–19.0 mm; dense, whitish, defined margin; coconut-like odor CMA: 12 .0–12.4mm; hyaline, thin, aerial hyphae, wavy margin; coconut-like odor	PDA: 41–53mm; white, aerial mycelium, sterile; coconut-like odor MEA: N/A CMA: 45–47mm; deep to yellowish green, cottony pustules; coconut-like odor	PDA: 46.0–63.0 mm, whi te, arachnoi d, appressed myce lium, yellow patches, reverse white to greyish MEA: N/A CMA:N/A
Conidiophore	Vertic illium-like, solitary or whorled phialides	Vertic illium-like, solitary or whorled phialides	Verti cillium-like	Vertic illium-like, spiny sterile extensions
Phialides	5.1–10.4 × 2–4 μm, narrow lageniform, straight	N/A	8.0–14.9 × 2.6–3.4 μm, narrow lageniform, swollen in the middle, straight	3.6–7.4 × 2.8–3.6 μm, terminal, ampullifor m-lageniform
Conidia	4 –5×2.3–3.2 μm, yellowish green to green, smooth, ellipsoidal	3.5– 4.9×2.7–3.6 μm, white to yellowish green, smooth, broadly ellipsoidal	3–3.7 × 2.5–3 μm, yellowish to deep green, smooth, broadly ellipsoidal	3.3–4.8 × 2.4–3.3 μm, dark-blue green, ellipsoidal to obovoidal, smooth

PDA: potato dextrose agar; MEA: malt extract agar; CMA: corn meal agar.
[T]Type strain; [a]Fungal strain studied in this research; [b]Source of descriptions [20]; [c]Source of description [36]; [d]Source of description [37].

Phylogenetic relationships of strain KNUF-20-085

Amplification of the ITS regions, *RPB2*, and *TEF1* gene of strain KNUF-20-085 yielded 573, 922, and 892 bp fragments, respectively. The ITS regions of strain KNUF-20-085 showed a 99.3% similarity with that of *Trichoderma panacis* SYPF 8050^{T}, a 99.1% similarity with those of *T. erinaceum* strains CEN1420 and CEN1421, and a 99.0% similarity with that of *T. koningii* APSAC 01. For the partial *TEF1* gene sequence, strain KNUF-20-085 showed a 98.8% similarity with *T. panacis* SYPF 8050^{T}, 98.6% similarities with *T. erinaceum* strains DUCC15708 and CEN1558, and a 96.0% similarity with *T. atroviride* HNG4-3. In the case of the partial *RPB2* gene sequence, strain KNUF-20-085 showed 100% similarity with *T. erinaceum* DUCC15708, a 99.8% similarity with *T. panacis* SYPF 8050^{T}, and a 97.0% similarity with *T. songyi* SFC20130926-S001 (Fig. 2). In the NJ phylogenetic tree generated using the concatenated ITS regions, *RPB2*, and *TEF1* gene sequences, strain KNUF-20-085 clustered together with *T. panacis* SYPF 8050^{T}. Thus, based on the morphological and phylogenetic analyses, strain KNUF-20-085 was identified as *T. panacis*.

***Trichoderma brevicompactum* G.F. Kraus, C.P. Kubicek & W. Gams, Mycol. 96 (5): 1063 (2004) [MB#487780]**

Specimen collection: Dokdo, Ulleung-gun, Gyeongbuk province, Korea (37°14'28.9"N, 131°51'54.5"E), isolated from soil.

Description: Colonies on PDA reached 44–50 mm in diameter after 72 h of culturing at 20℃. Mycelia were filamentous, white, and broad, with concentric rings, entire margins, and yellowish green to green conidia (Fig. 3A). On CMA, colonies reached 42–47 mm in diameter after 72 h of culturing at 20℃. Mycelia were white, with scant arial hyphae, forming yellowish green conidia (Fig. 3B). On SNA, colonies reached 33–36 mm in diameter after 72 h of culturing at 20℃. Mycelia were white, with scant arial hyphae and yellowish green conidia (Fig. 3C). *Hyphae* were white, terminal, verticillate, and fertile, with the distal parts of some hyphae forming conidiogenous hyphal cells commonly with one to three conidiogenous loci (Fig. 3D). *Conidiophore* branches arose from the surface and were verticillate, fertile, and terminal, with phialides (Fig. 3E). *Phialides* were produced in a dense terminal cluster, ampulliform, and slightly enlarged in the middle (Fig. 3F). *Conidia* were subglobose, yellowish green to green, smooth, and 3.0–4.2 × 2.5–3.3 μm (n = 40) (Fig. 3G). *Chlamydospores* developed in older cultures and were subglobose and intercalary or terminal (Fig. 3H).

Notes: Comparing the *T. brevicompactum* KNUF-20-NI014 and MA 3296^{T}, both strains exhibit similar cultural characteristics on PDA, SNA, and CMA media, and share morphological traits such as subglobose, smooth, green conidia formed at the ends of verticillate conidiophores (Table 3) [21].

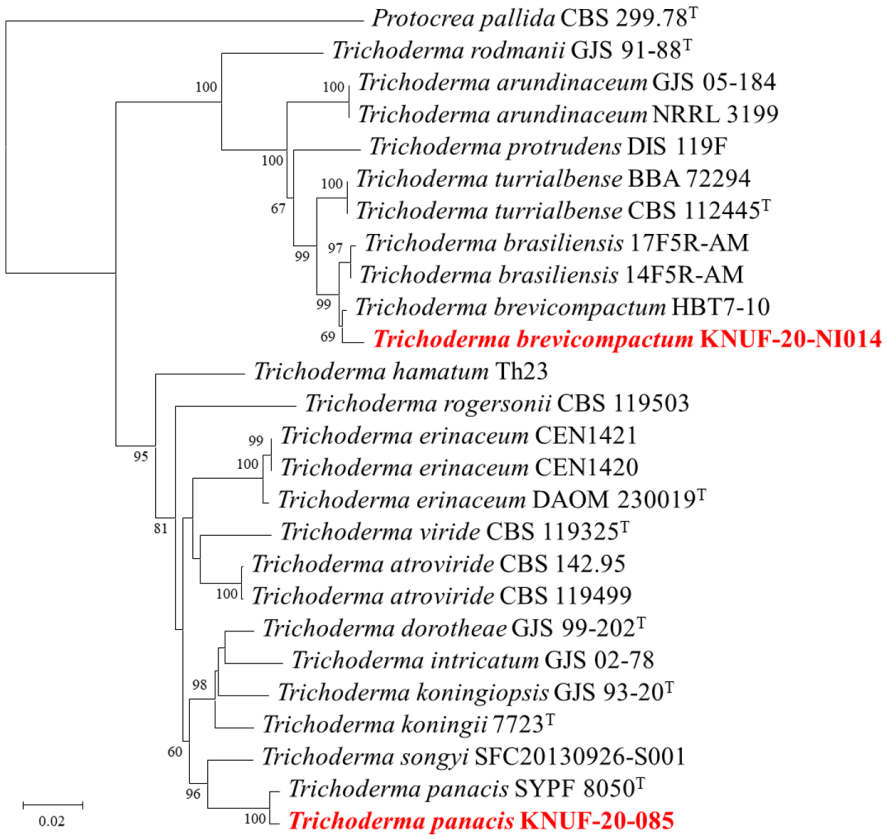

Fig. 2. Neighbor-joining phylogenetic tree based on the concatenated sequences of internal transcribed spacer (ITS) regions, RNA polymerase II subunit B (*RPB2*) and translation elongation factor 1-alpha (*TEF1*) gene showing the phylogenetic position of strains KNUF-20-085 and KNUF-20-NI014 among *Trichoderma* species. Bootstrap values greater than 60% (percentage of 1,000 replications) are shown at branching points. The strain isolated in this study is in bold and red. The tree was rooted using *Protocrea pallida* CBS 299.78^{T} as an out-group. Bar, 0.02 substitutions per nucleotide position.

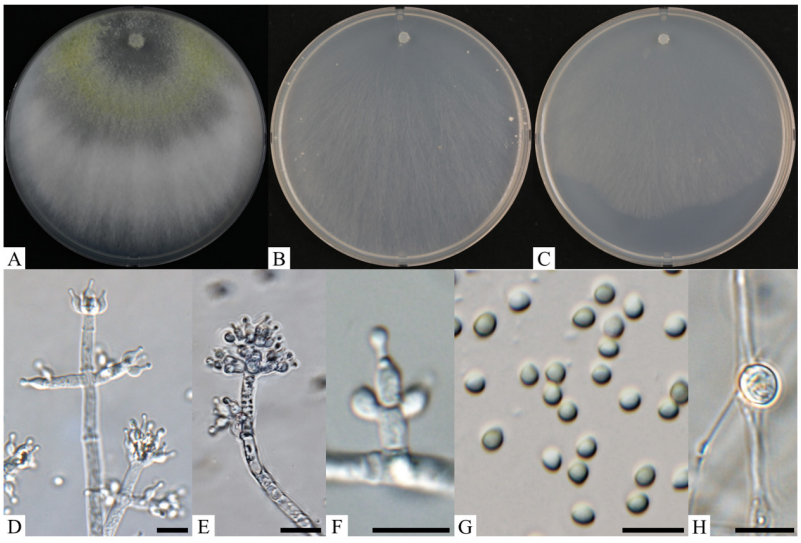

Fig. 3. Cultural and morphological characteristics of *Trichoderma brevicompactum* KNUF-20-NI014. A–C: Front views of colonies after 7 d at 20℃ on potato dextrose agar, corn meal agar, and synthetic nutrient-poor agar, respectively; D: conidiophores and phialides with conidia; E: conidiophores and phialides; F: phialides; G: conidia; H: chlamydospore. Scale bars = 10 μm.

Table 3. Cultural and morphological comparison of *Trichoderma brevicompactum* KNUF-20-NI014 with closely related *Trichoderma* strains

	Trichoderma brevicompactum KNUF-20-NI014[a]	*Trichoderma brevicompactum* MA 3296[Tb]	*Trichiderma brasiliensis* COAD2324[c]	*Trichoderma turrialbense* CBS 112445[b]
Colony characteristics	PDA: 44–50 mm; concentric rings, white, entire margin, no distinctive odor CMA: 42–47 mm; white, entire margin, aerial hyphae, no distinctive odor SNA: 33–36 mm; white, entire margin, aerial hyphae, no distinctive odor	PDA: 27–33 mm; concentric rings, white, entire margin, no distinctive odor CMA: 27–32 mm; concentric rings, white, entire margin, no distinctive odor SNA: 22–26 mm; concentric rings, white, entire margin, no distinctive odor	PDA: 64.5–66.5 mm; dense, hairy CMA: 59.5–61.5 mm; white, flat, downy surface SNA: 46.5–50.5 mm; white, thin	PDA: 21–36 mm; yellowish green, margin, no distinctive odor CMA: 21–35 mm; flat, yellow green SNA: 20–35 mm; flat, yellow green
Conidiophore	Terminal, verticillate, fertile	Single, terminal, verticillate	Pyramidal, verticillate, pachybasium-type	Wide base, verticillate
Phialides (μm)	5.1–7.9 × 2.0–3.4, ampulliform, clustered	5.6–5.9 × 3.3–3.4, slightly enlarged, lageniform-ampulliform, clustered	5–16 × 2–4, ampulliform to flask-shaped	5.3–5.9 × 3.1–3.3, ampulliform, short, flared collarette
Conidia (μm)	3.0–4.2 × 2.5–3.3, subglobose, green, smooth	2.7–3 × 2.2–2.7, subglobose, smooth, green	2–4 × 2–4, globose-subglobose, green	2.5–3.0 × 2.2–2.7, subglobose, green, wet heads
Chlamydospores	Subglobose, intercalary/terminal	Terminal	Gloobose, terminal, thick-walled, pale brown	N/A

PDA: potato dextrose agar; CMA: corn meal agar; SNA: synthetic nutrient-poor agar.
[T]Type strain; [a]Fungal strain studied in this research; [b]Source of descriptions [21]; [c]Source of descriptions [35].

Phylogenetic relationships of strain KNUF-20-NI014

Amplification of ITS regions, *RPB2*, and *TEF1* gene of strain KNUF-20-NI014 yielded 559, 980, and 527 bp fragments, respectively. The ITS regions of strain KNUF-20-NI014 showed 100% similarities with those of various strains of *T. brevicompactum*, including strain CEN510, CEN1071, 100% similarity with that of *T. turrialbense* CBS 112445, and 100% similarity with that of *T. brasiliensis* 14F5R-AM. The partial *TEF1* gene sequence of strain KNUF-20-NI014 showed 98.1–98.6% similarities with those of various *T. brevicompactum* strains, including strains DAOM 233362, 27RCS, GJS 04-381, and CBS 112444, 95.0% similarities with those of *T. brasiliensis* strains 14F5R-AM and 17F5R-AM, and a 92.7% similarity with that of *T. turrialbense* BBA 72294. For the partial *RPB2* gene sequence, strain KNUF-20-NI014 showed 100% similarities with various *T. brevicompactum* strains, including strains BF06, HZA7, and HBG1-1, a 99.7% similarity with *T. brasiliensis* 17F5R-AM, and a 98.2% similarity with *T. turrialbense* BBA 72294. A phylogenetic tree was constructed using the NJ method based on the concatenated ITS regions, *RPB2*, and *TEF1* gene sequences (Fig. 2). In this phylogenetic tree, strain KNUF-20-NI014 clustered closely with *T. brevicompactum* HBT7-10. For the phylogenetic analysis, the type strain MA 3296[T] was not used due to the lack of an RPB2 gene sequence, and thus, another *T. brevicompactum* strain was used. Overall, the cultural, morphological, and phylogenetic analyses collectively identified strain KNUF-20-NI014 as *T. brevicompactum*.

DISCUSSION

Since the genus was first established in 1794 [4], *Trichoderma* species have been isolated from a wide range of sources [5,6]. In this study, strains KNUF-20-085 and KNUF-20-NI014, both isolated from soil samples in Korea, were identified as *T. panacis* and *T. brevicompactum*, respectively. As there are no previous records of *T. panacis* and *T. brevicompactum* from Korea, this study represents the first official report of these species in the country. Various *Trichoderma* species are well-recognized for their roles as biocontrol agents due to their production of bioactive secondary metabolites and enzymes, as well as their ability to suppress mycotoxin production [29]. To date, a number of studies have addressed the usage of the secondary metabolites of the *T. brevicompactum* complex as antibiotics [30]. The term "complex" here refers to a group of closely related species within *Trichoderma* that are morphologically similar to *T. brevicompactum* but genetically distinct from each other and often difficult to distinguish using traditional identification methods. *Trichoderma brevicompactum* is reported to produce trichothecene (trichodermin), which exhibits inhibitory activity against fungal pathogens like *Rhizoctonia solani* and *Botrytis cinerea* [31]. In addition, a study of the antagonistic effects of *T. brevicompactum* against fungal plant pathogens revealed significant inhibition of *Fusarium oxysporum* growth and development with disruption of physiological structures and spore formation [32]. Therefore, the antibiotics and metabolites of strain KNUF-20-NI014 warrant further research, as they may have potential future applications as commercially viable bioprotective agents against fungal diseases. In the case of *T. panacis*, there are no reports of antibiotic activities at the time of this study. However, some closely related species, such as *T. erinaceum* and *T. atroviride*, are known to produce secondary metabolites exhibiting antifungal activity [33–35]. Therefore, further investigation of *T. panacis* is warranted to determine whether it possesses similar biosynthetic pathways for the production of secondary metabolites and antibiotics that may contribute to its use as a biological control agent.

The discovery of the newly reported species isolated in this study, *T. brevicompactum* and *T. panacis*, contributes to our understanding of domestic biodiversity and its conservation. Their descriptions may benefit future research in ecology and the development of human-related and industrial applications of fungus-derived products. As *Trichoderma* is noteworthy for its species' important roles in biocontrol and abilities to persist in soils through crop rotations and in intercropping systems, conducting systematic studies in this genus will be essential for informing future scientific applications.

CONFLICT OF INTEREST

No potential conflict of interest was reported by the authors.

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