Journal of Species Research 13(2):111-126, 2024

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First report of seven unrecorded bambusicolous fungi in Korea

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Korean bamboo forests encompass 22,067 hectares and are dominated by *Phyllostachys* species. These forests serve as vital ecosystems, providing nourishment and habitat for diverse flora, fauna, and microorganisms. Among these inhabitants, various fungal species have been documented worldwide, displaying ecological roles as saprobes, parasites, and symbionts within or outside the bamboo host. However, a comprehensive study of bambusicolous fungi within the Korean bamboo ecosystem remains a critical gap in our knowledge. In this study, we conducted an extensive survey of bamboo materials collected from various bamboo forests and subsequently undertook fungal isolation. Primary identification of bambusicolous fungi was achieved through analysis of the internal transcribed spacer (ITS) region. As a result, we identified seven previously unrecorded bambusicolous fungal species (*Fusarium bambusarum*, *Fusicolla violacea*, *Macroconia gigas*, *Neopestalotiopsis camelliae-oleiferae*, *Neopestalotiopsis iberica*, *Neopestalotiopsis longiappendiculata*, and *Thyridium punctulatum*). Phylogenetic analysis using protein-coding genes appropriate for each taxon and morphological observation were conducted to ensure accurate identification. This study contributes to our understanding of fungal diversity within bamboo forests in Korea.

Keywords: bambusicolous fungi, morphological study, phylogeny, seven unrecorded species

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DOI:10.12651/JSR.2024.13.2.111

Introduction

Bamboo belongs to the family *Poaceae*, and has a significant impact on the environment and human life (Khalil, 2018; Paudyal *et al*., 2022). Recently, bamboo has gained recognition as a prominent plant for addressing the climate crisis due to its rapid growth and high carbon sequestration capacity (Lobovikov *et al*., 2007; Yuen *et al*., 2017; Paudyal *et al*., 2022). Bamboo is primarily distributed in tropical, subtropical, and temperate southern regions, with over 1,680 species found worldwide (Kellogg, 2016; Soreng *et al*., 2017). In South Korea, bamboo is mainly found in the southern regions, with the most abundant bamboo species being *Phyllostachys bambusoides*, *P. pubescens*, and *P. nigra* var. *henonis* (Yoo *et al*., 2017).

The term "bambusicolous fungi" is used to refer to all fungi that live on or in bamboo (Hino, 1938; Hyde *et al*., 2002). People have been interested in bamboo fungi since 1840, and now around 1,300 bambusicolous fungi have been reported worldwide (Dai *et al*., 2018). Among them, 88% belong to *Ascomycota* and the remaining 12% are in *Basidiomycota*. They have various roles in nature as saprobe, parasite, and symbiont. Studying the classification, phylogeny, and ecological traits of bambusicolous fungi is of considerable economic significance. This is primarily since more than 190 bamboo species spanning 33 genera are susceptible to diseases such as culm rust, top blight, and culm base rot, which are caused by pathogens. In the Asian region alone, there are documented cases of 580 fungal species linked to bamboo diseases, resulting in a decline in bamboo production (Dey *et al*., 2023).

Most of the research on this topic has been done in Asia, while there has been limited research in Korea (Lobovikov *et al*., 2007). Thus, we have discovered and identified bambusicolous fungi using advanced techniques. Among them, seven unrecorded species were confirmed. Detailed descriptions and genetic information about these newly discovered fungi are provided here.

Materials and Methods

Strains

Bamboo materials were collected from bamboo forests in Korea from 2018–2021. Fungal isolation was conducted with 2% malt extract agar medium containing 0.01% streptomycin. Small pieces of bamboo culm and leaf were placed on the medium, and growing fungal hyphae were obtained and transferred to new medium. The pure isolates were stocked in 10% glycerol stock and stored at −20°C in the Korea University Culture Collection (KUC), Seoul, Korea. The strains were deposited at the National Institute of Biological Resources, Incheon, Korea (NIBR).

Table 1. Information of strains included in the phylogenetic analyses.

Identification	Strain no.	Country	Host/Substrate[1]	GenBank accession no.[2]			
				ITS	*TEF1-α*	*TUB*	*RPB2*
Fusarium anguioides	LC7151	China	Bamboo	–	MW580438	–	MW474384
	LC7178	China	Bamboo	–	MW580439	–	MW474385
F. austroafricanum	NRRL 66741	South Africa	Kikuyu grass	–	MH742687	–	MH742616
	NRRL 53441	South Africa	Plant debris in soil	–	MH742686	–	MH742615
F. bambusarum	LC7180*	China	Bamboo	–	MW580443	–	MW474389
	LC7187	China	Bamboo	–	MW580444	–	MW474390
	KUC21851	**South Korea**	**Culm of *Ph. pubescens***	**OR654962**	**OR693481**	–	**OR693490**
	KUC21852	**South Korea**	**Culm of bamboo**	**OR654963**	**OR693482**	–	**OR693491**
	KUC21853	**South Korea**	**Culm of bamboo**	**OR654964**	**OR693483**	–	–
F. concolor	NRRL 13994*	Uruguay	Barley	–	MH742650	–	MH742569
	NRRL 53452	South Africa	Soil	–	MH742660	–	MH742580
F. flocciferum	NRRL 45999	U.S.A	Human scalp	–	OL772882	–	MH582362
	NRRL 25473	Germany	Common wheat	–	OL772878	–	MH582356
F. torulosum	NRRL 22748	Netherlands	Box wood	–	OL772877	–	MH582376
	NRRL 52772	Norway	*Galleria mellonella* larva	–	OL772887	–	MH582377
Fusicolla aquaeductuum	CBS 837.85*	Germany	Plug in water tap	–	–	–	HQ897744
Fc. betae	BBA 64317*	Germany	On young *Triticum aestivum*	–	–	–	HQ897781
Fc. epistroma	BBA 62201*	Germany	On old stromata of *Diatrypella favacea* on branches of *Betula*	–	–	–	HQ897765
Fc. matuoi	CBS 581.78*	Japan	*Albizia julibrissin*	–	–	–	HQ897720
Fc. meniscoidea	CBS 110189*	Australia	Soil	–	–	–	MW834010
Fc. ossicola	CBS 140161*	Belgium	Bone of wild boar	–	–	–	MW834011
Fc. sporellula	CBS 110191*	South Africa	Soil	–	–	–	MW834012
Fc. violacea	CBS 634.76*	Iran	*Quadrapidiotus perniciosus*	–	–	–	HQ897696
	KUC21850	**South Korea**	**Dead culm of *Ph. bambusoides***	**OR654961**	–	–	**OR693489**
Microcera larvarum	CBS 738.79/ AR 4580	Iran	*Quadrapidiotus perniciosus*	–	–	–	KM232387
Corallomycetella repens	NHRC-FC042	Russia	Human blood	AJ558114	–	–	–
	NRRL 20420	–	–	AJ557830	–	–	–
Cosmospora viridescens	R.V. olrim161	Sweden	Old stump of *Picea abies*	AY618257	–	–	–
Macroconia cupularis	HMAS 97514	China	On fruitbodies of a black ascomycete (*Stylodothis* sp.) on twigs of an unidentified tree	AY618257	–	–	–
M. gigas	HMAS 173239*	Taiwan	On rotten stem of bamboo	EF121863	–	–	–
	KUC21846	**South Korea**	**Dead culm of *Ph. bambusoides***	**OR654959**	–	–	–
	KUC21848	**South Korea**	**Dead culm of *Ph. bambusoides***	**OR654960**	–	–	–

Table 1. Continued.

Identification	Strain no.	Country	Host/Substrate[1]	GenBank accession no.[2]			
				ITS	*TEF1-α*	*TUB*	*RPB2*
Nectria cinnabarina	NBRC 30679	–	–	AB237663	–	–	–
Nc. pseudotrichia	HMAS 97518	–	–	EF121865	–	–	–
Sarcopodium flavolanatum	HMAS 76869	–	–	EF121862	–	–	–
S. flocculentum	HMAS 76873	–	–	EF121858	–	–	–
	HMAS 97517	–	–	EF121868	–	–	–
Neopestalotiopsis australis	CBS 114159*	Australia	*Telopea* sp.	KM199332	KM199475	KM199383	–
N. camelliae-oleiferae	CSUFTCC81*	China	*C. oleifera*	OK493585	OK507955	OK562360	–
	CSUFTCC82	China	*C. oleifera*	OK493586	OK507956	OK562361	–
	KUC21857	**South Korea**	**Dead leaf of *Ph. bambusoides***	**OR654966**	**OR693485**	**OR693495**	–
	KUC21858	**South Korea**	**Leaf of *Ph. bambusoides***	**OR654967**	**OR693486**	**OR693494**	–
N. chiangmaiensis	MFLUCC 18-0113*	Thailand	Dead leaves	–	MH388404	MH412725	–
N. cubana	CBS 600.96*	Cuba	Leaf litter	KM199347	KM199521	KM199438	–
N. dendrobii	MFLUCC 14-0106*	Thailand	*D. cariniferum*	MK993571	MK975829	MK975835	–
	MFLUCC 14-0099	Thailand	*D. cariniferum*	MK993570	MK975828	MK975834	–
N. egyptiaca	CBS 140162*	Egypt	*Mangifera indica*	KP943747	KP943748	KP943746	–
N. eucalypticola	CBS 264.37*	–	*E. globulus*	KM199376	KM199551	KM199431	–
N. hadrolaeliae	COAD 2637*	Brazil	*Hadrolaelia jongheana*	MK454709	MK465122	MK465120	–
N. hydeana	MFLUCC 20-0132*	Thailand	*Artocarpus heterophyllus*	MW266069	MW251129	MW251119	–
N. honoluluana	CBS 114495*	USA	*Telopea* sp.	KM199364	KM199548	KM199457	–
	CBS 111535	USA	*Telopea* sp.	KM199363	KM199546	KM199461	–
N. iberica	CBS 147688*	Portugal	*E. globulus*	MW794111	MW805402	MW802844	–
	CSUFTCC91	China	*C. oleifera*	OK493587	OK507957	OK562362	–
	CSUFTCC92	China	*C. oleifera*	OK493588	OK507958	OK562363	–
	KUC21856	**South Korea**	**Culm of *Ph. bambusoides***	**OR654965**	**OR693484**	**OR693492**	–
N. javaensis	CBS 257.31*	Indonesia	*Cocos nucifera*	KM199357	KM199543	KM199437	–
N. longiappendiculata	CBS 147690*	Portugal	*E. globulus*	MW794112	MW805404	MW802845	–
	KUC21859	**South Korea**	**Dead leaf of *Ph. bambusoides***	**OR654968**	**OR693487**	**OR693493**	–
N. pandanicola	KUMCC 17-0175*	China	*Pandanus* sp.	–	MH388389	MH412720	–
N. saprophytica	MFLUCC 12-0282*	China	*Magnolia* sp.	JX398982	JX399048	JX399017	–
N. vacciniicola	MUM 21.35*	Portugal	*Vaccinium corymbosum*	MW969751	MW959103	MW934614	–
N. vitis	MFLUCC 15-1265*	China	*V. vinifera*	KU140694	KU140676	KU140685	–
	MFLUCC 15-1270	China	*V. vinifera*	KU140699	KU140681	KU140690	–
Pestalotiopsis colombiensis	CBS 118553*	Colombia	*E. grandis* × *E. urophylla*	KM199307	KM199488	KM199421	–
Ascitendus austriascus	CBS 131685	–	–	–	–	–	JQ429257
Thyridium flavostromatum	KT 3891*	Japan	Dead twigs of *Ph. pubescens*	–	–	–	LC655967
T. pluriloculosum	KT 3803*	Japan	Dead wood of *B. maximowicziana*	–	–	–	LC655968
T. punctulatum	KT 1015	Japan	Dead culms of *Ph. pubescens*	–	–	–	LC655969
	KT 3905*	Japan	Dead twigs of *Ph. nigra* var. *henonis*	–	–	–	LC655970
	KUC21845	**South Korea**	**Dead culm of *Ph. bambusoides***	**OR654958**	–	**–**	**OR693488**
T. vestitum	CBS 113027	Austria	*Acer pseudoplatanaus*	–	–	–	DQ470890

[1]The genus names of host plant were abbreviated: *A*., *Albizia*; *B*., *Betula*; *C*., *Camellia*; *D*., *Dendrobium*; *E*., *Eucalyptus*; *Ph*., *Phyllostachys*; and *V*., *Vitis*.
[2]The sequences generated in this study are shown in bold.
*Indicate the type materials

DNA Extraction, Polymerase Chain Reaction (PCR), and Sequencing

According to a modified manufacturer's protocol, genomic DNA was extracted from bambusicolous fungal strains using an AccuPrep Genomic DNA extraction kit (Bioneer, Daejeon, Korea). PCR was conducted with an AccuPower® PCR PreMix Kit (Bioneer). For the Internal transcribed spacer (ITS) region amplification, ITS1F (or ITS1 or ITS5)/ ITS4 primer sets were used (White *et al*., 1990; Gardes and Bruns, 1993). The PCR conditions followed a previous study (Hong *et al*., 2015). DNA sequencing was conducted at Cosmogenetech (Seoul, Korea). The generated sequences were proofread and edited using Geneious Prime 2022.1.1 (Biomatter, Ltd., Auckland, New Zealand). The molecular identification was initially conducted using the sequence similarity in BLAST using the NCBI database (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Identification was assigned over 98% sequence similarity. Protein coding genes, were additionally amplified for accurate identification, such as RNA polymerase II subunit (*RPB2*) for *Fusarium*, *Fusicolla*, and *Thyridium*, translation elongation factor 1-α (*TEF1-α*) for *Fusarium* and *Neopestalotiopsis*, and beta-tubulin (*TUB*) for *Neopestalotiopsis*. Primer *RPB2*-5F2/ *RPB2*-7cr or *RPB2*-7cf/ *RPB2*-11aR was used as the *RPB2* primer sets (Liu *et al*., 1999; Sung *et al*., 2007). *TEF1-α*-EF1 (or *TEF1-α*-728F)/ *TEF1-α*-EF2 (or *TEF1-α*-1567R) for *TEF1-α* region and T1/ bt2b for *TUB* region were used as the primer sets (Glass and Donaldson, 1995; O'Donnell and Cigelnik, 1997; O'Donnell *et al*., 1998a; 1998b; Carbone and Kohn, 1999; Rehner and Buckley, 2005). All new sequences were deposited in GenBank.

Phylogenetic analysis

Sequences were assembled, proofread, and edited using Geneious Prime 2023.2.1 (Biomatter, Ltd., Auckland, New Zealand). Sequence alignment were conducted using MAFFT v7 and ambiguous alignments were manually adjusted (Katoh and Standley, 2013). Phylogenetic trees were constructed using the Maximum likelihood (ML) method using RAxML-HPC2 on XSEDE (8.2.12) with a GTR + GAMMA model and 1,000 bootstrap replicates (Stamatakis, 2014). All phylogenetic analyses were conducted on the CIPRES web portal (Miller *et al*., 2010). Phylogenetic tree morphology was edited using FigTree v1.4.3 and Adobe Illustrator CS6 (Adobe Systems, Inc., San Jose, CA, USA).

Morphological analysis

Detailed morphological characteristics were investigated for accurate identification. Cultural- and microscopic features were noted from those strains of unrecorded species. Morphological studies were performed by culturing strains on CMD, MEA, OA, PDA, and SNA (Table 2). A Munsell color chart was used to apply a standard color code (Color, 2021). Fungal colonies were mounted in distilled water or 5% KOH or 85% lactic acid with an Olympus BX51 light microscope (Olympus, Tokyo, Japan) with a DP20 microscope camera (Olympus). Some fungal colonies were mounted using lactophenol cotton blue stain for the microscopic examination of spore morphology. Values for each examined morphological character were based on at least 30 independent measurements.

Table 2. Seven bambusicolous fungi examined in this study.

Name	Strain no.	Culture media[1]	Sequences used for phylogenetic analysis
Fusarium bambusarum	KUC21851	OA, PDA, SNA	*TEF1-α, RPB2*
	KUC21852	OA, PDA, SNA	*TEF1-α, RPB2*
	KUC21853	OA, PDA, SNA	*TEF1-α*
Fusicolla violacea	KUC21850	PDA	*RPB2*
Macroconia gigas	KUC21846	CMD, PDA	ITS
	KUC21848	CMD, PDA	ITS
Neopestalotiopsis camelliae-oleiferae	KUC21857	PDA	ITS, *TEF1-α*, *TUB*
	KUC21858	PDA	ITS, *TEF1-α*, *TUB*
Neopestalotiopsis iberica	KUC21856	PDA	ITS, *TEF1-α*, *TUB*
Neopestalotiopsis longiappendiculata	KUC21859	PDA	ITS, *TEF1-α*, *TUB*
Thyridium punctulatum	KUC21845	MEA, OA, PDA	*RPB2*

[1]CMD, corn meal dextrose agar medium; MEA, malt extract agar medium; OA, oatmeal agar medium; PDA, potato dextrose agar medium; and SNA, synthetic low nutrient agar medium.

Results

Phylogenetic Identification

Eleven bambusicolous fungal strains were isolated from bamboo materials. Based on the ITS sequence similarity in BLAST searching in the NCBI database, they were tentatively identified as seven unrecorded candidate species in Korea (*Fusarium bambusarum*, *Fusicolla violacea*, *Macroconia gigas*, *Neopestalotiopsis iberica*, *N. camelliae-oleiferae*, *N. longiappendicula*, and *Thyridium punctulatum*) (Table 2). Based on the sequence similarity results, phylogenetic analyses were conducted. Phylogenetic analysis revealed that two strains (KUC21846 and KUC21848) were identified as *M. gigas* with 100% bootstrap values in the ITS tree (Fig 3). Meanwhile, other strains need additional protein-coding genes for accurate identification. As a result, three strains (KUC21851, KUC21852, and KUC21853) were identified as *F. bambusarum* with 100% bootstrap values in the *TEF1-α* + *RPB2* concatenated tree (Fig. 1). A strain (KUC21850) was identified to *Fc. violacea*, with high bootstrap values in the *RPB2* tree (Fig. 2). Four strains were identified as *Neopestalotiopsis* species in the ITS + *TEF1-α* + *TUB* concatenated tree: *N. iberica* (KUC21856), *N. camelliae-oleiferae* (KUC21857 and KUC21858), and *N. longiappendicula* (KUC21859) (Fig. 4). At last, one strain (KUC21845) was identified to *T. punctulatum* with a high bootstrap value in the *RPB2* tree (Fig. 5).

Taxonomy

***Fusarium bambusarum* M.M. Wang & L. Cai, *Persoonia* 48: 25(2022) (Figs. 1, 6)**

MycoBank. MB 842152

On PDA, colonies circular form, margin erose to entire, aerial mycelia dense, mycelia white, pigment absent in medium. On OA, colonies circular form, margin entire, aerial mycelia dense, mycelia white, pigment absent in medium. On SNA, colonies circular form, margin erose to entire, aerial mycelia scant, mycelia white, pigment absent in medium. **Conidiophores** borne on aerial mycelia, branched, hyaline, thin-walled, bearing terminal a group of 2−5 phialides. **Phialides** subulate to subcylindrical, hyaline, (11−)13−21(−26) × 2.5−3.0(−4.0) µm. **Microconidia** oval, hyaline, thin-walled, aseptate, (6.0−)8.0−11.0(−13.5) × (1.8−)2.0−3.0(−3.5) µm. **Macroconidia** not observed. **Chlamydospores** terminal, globose, rough, thick-walled, 6.0−8.0 µm diam.

Distribution. China; and Republic of Korea.

Habitat. bamboo, culm of unidentified bamboo and *Phyllostachys pubescens*.

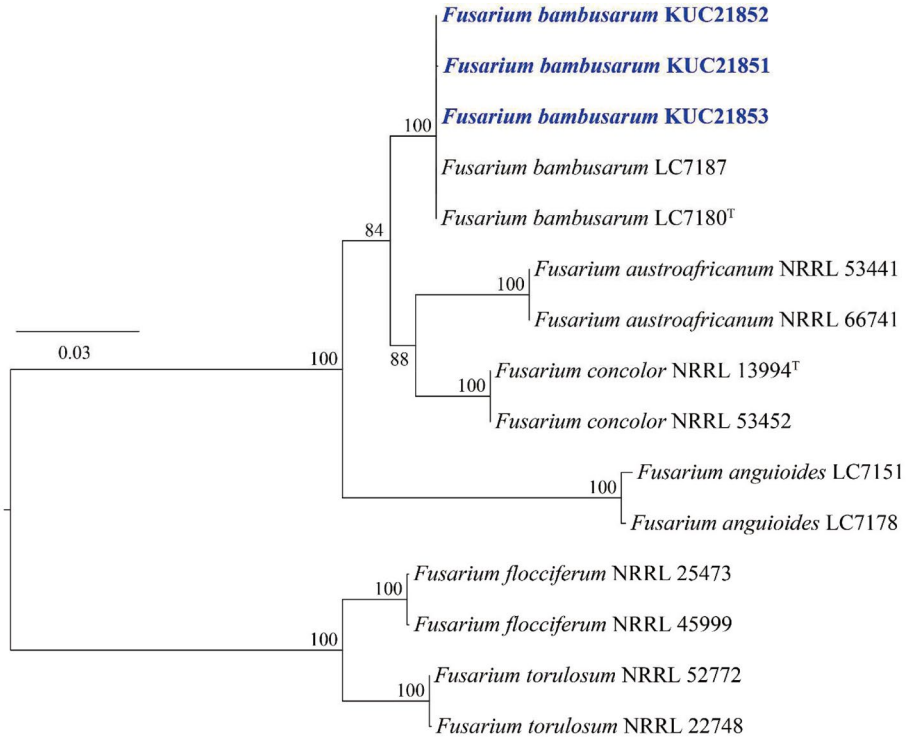

Fig. 1. Maximum Likelihood tree for genus *Fusarium* with *TEF-1α* + *RPB2* combined dataset. Node numbers indicate bootstrap value above 70%. Blue colored names indicate the strains isolated in this study. Type strains are indicated by "T".

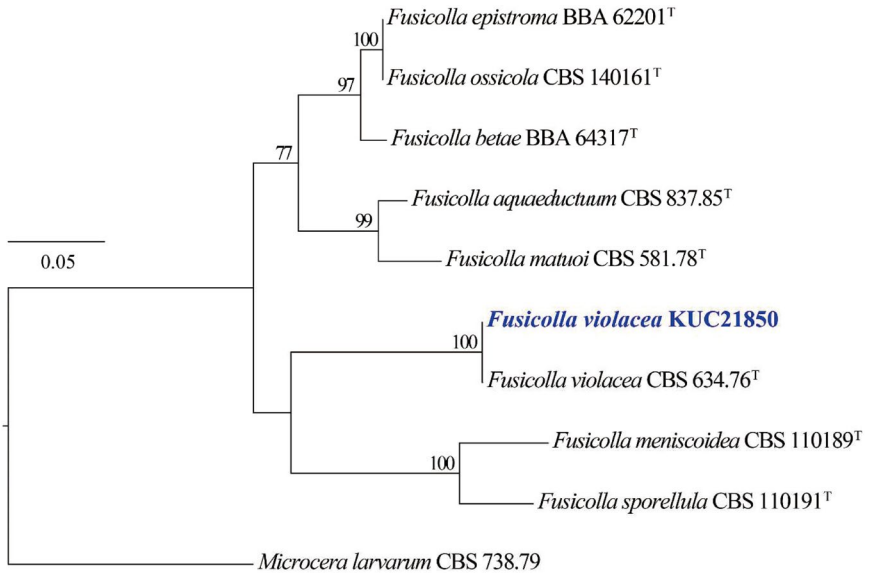

Fig. 2. Maximum Likelihood tree for genus *Fusicolla* with *RPB2* dataset. Node numbers indicate bootstrap value above 70%. Blue colored name indicates the strains isolated in this study. Type strains are indicated by "T".

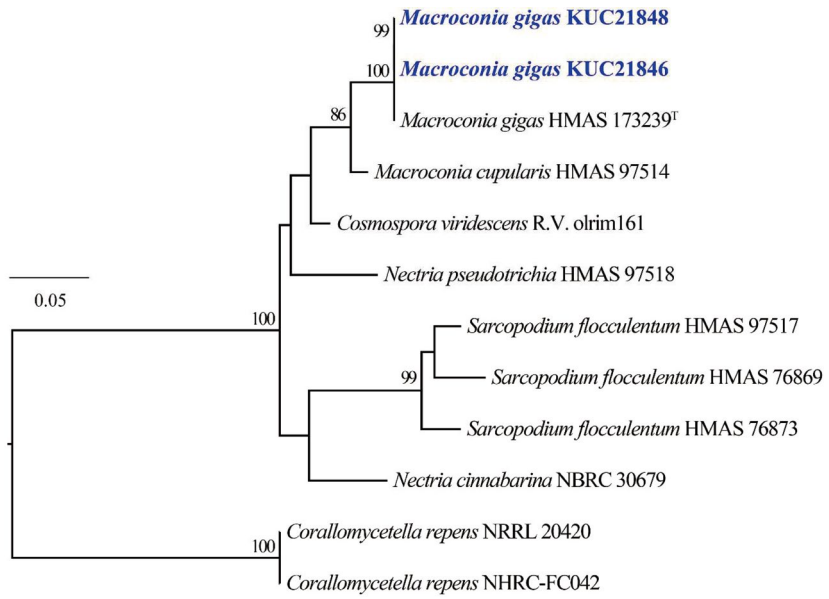

Fig. 3. Maximum Likelihood tree for genus *Macroconia* with ITS dataset. Node numbers indicate bootstrap value above 70%. Blue colored names indicate the strains isolated in this study. Type strains are indicated by "T".

Specimen examined. KOREA, Jeollabuk-do, Gochang, Gochangeupseong, 35.4303N, 126.7031E, isolated from a culm of *Phyllostachys pubescens*, 18 Mar 2021, Sun Lul Kwon, KUC21851 (=NIBRFGC000510466); KOREA, Jeollanam-do, Gwangju, Mudeungsan National Park, 35.1267N, 126.9685E, isolated from a culm of bamboo, 23 Sep 2020, Sun Lul Kwon, KUC21852 (=NIBRFGC 000510467); KOREA, Jeollanam-do, Gwangju, Mudeungsan National Park, 35.1267N, 126.9685E, isolated from a culm of bamboo, 23 Sep 2020, Sun Lul Kwon, KUC21853 (=NIBRFGC000510468).

Notes. The size of the aerial phialides of *F. bambusarum* KUC21851 (13−21 μm long) is shorter than that of *F. bambusarum* LC7180 (ex-type) (23−30 μm long) (Wang *et al*., 2022a). However, other morphological features and habitats are comparable (both strains are found from bamboo species).

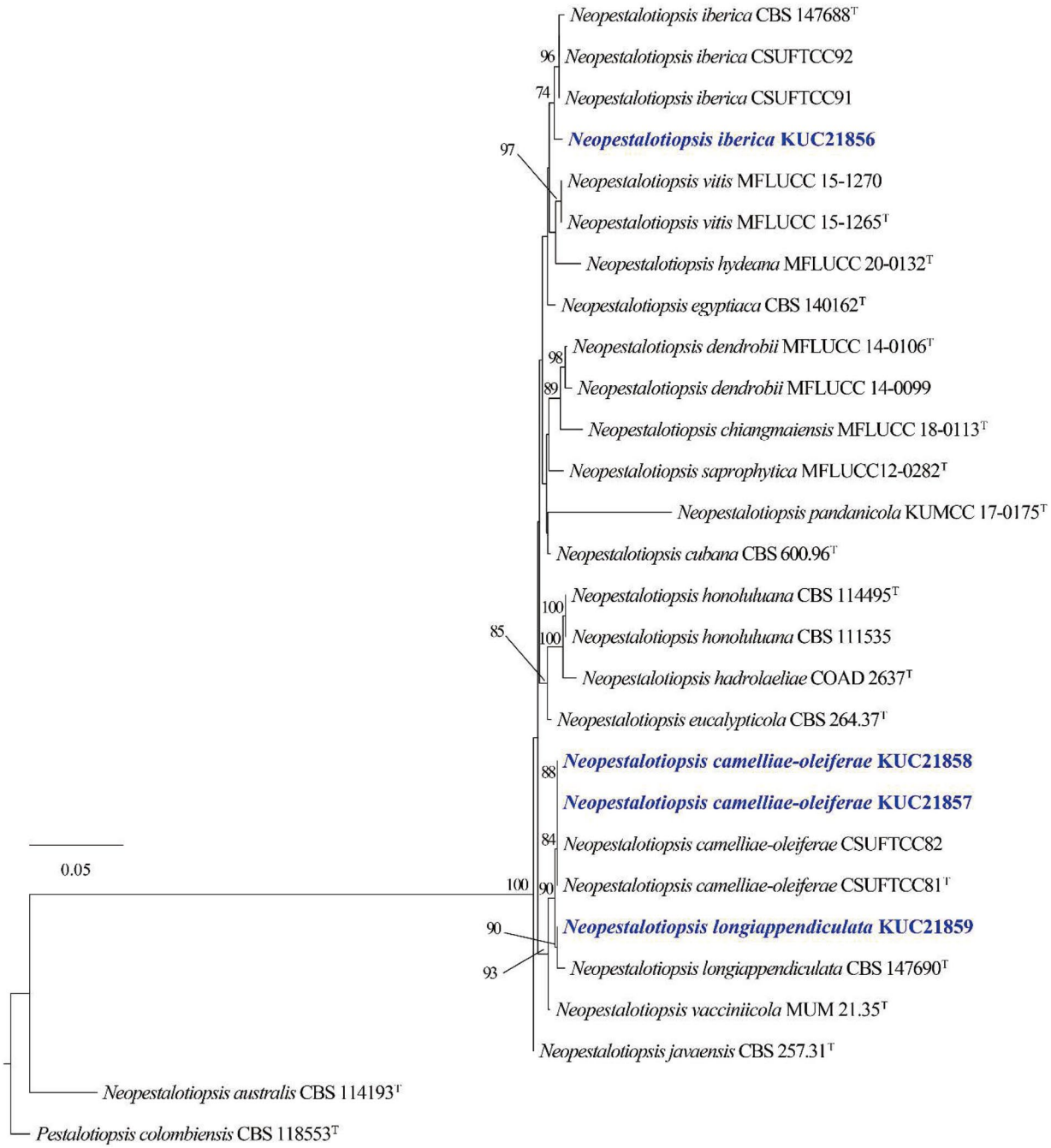

Fig. 4. Maximum Likelihood tree for genus *Neopestalotiopsis* with ITS + *TEF1-α* + *TUB* dataset. Node numbers indicate bootstrap value above 70%. Blue colored names indicate the strains isolated in this study. Type strains are indicated by "T".

***Fusicolla violacea* Gräfenhan & Seifert, Stud. Mycol. 68: 101(2011) (Figs. 2, 7)**

MycoBank. MB 519439

On PDA, colonies circular to irregular form, margin entire, mycelia brownish to brownish red, becoming partially purple after ten days. pigment absent in medium. Colony diameters (in mm after ten days in dark): 25°C, 3 mm diam. **Mono- and poly-phialides**, subulate to subcylindrical, hyaline, (18−)19−25 × 2.5−3.5 µm. **Macroconidia** mostly 3-septate, falcate to subfalcate, hyaline, smooth, thin-walled, (40−)45−55(−57) × (3.0−)3.5−4.5(−5.0) µm. **Chlamydospores** not observed.

Distribution. Iran, China, and Republic of Korea.

Habitat. On *Quadraspidiotus perniciosus* on dying twig of *Prunus domestica*, *Actinidia cinensis*, and dead culm of

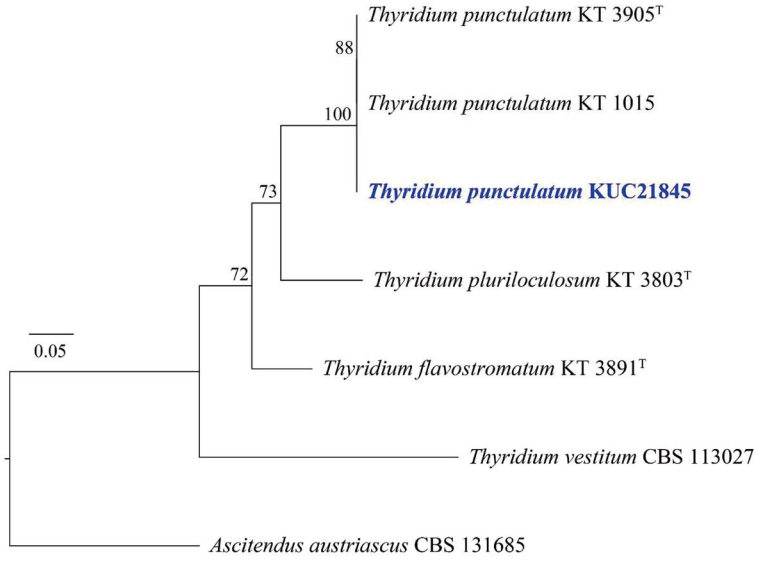

Fig. 5. Maximum Likelihood tree for genus *Thyridium* with *RPB2* dataset. Node numbers indicate bootstrap value above 70%. Blue colored names indicate the strains isolated in this study. Type strains are indicated by "T".

Phyllostachys bambusoides.
Specimen examined. KOREA, Jeollanam-do, Damyang, Juknokwon, 35.3284N, 126.9855E, isolated from a dead culm of *Phyllostachys bambusoides*, 20 Dec 2021, Sun Lul Kwon, KUC21850 (=NIBRFGC000510469).
Notes. The morphological information of *Fc. violacea* is poor in the original description (Gerlach, 1977). However, following the study of Zeng and Zhuang (2023), the purple pigment of *Fc. violacea* is the taxonomical key factor, and it was also found in our strain after 10 days of culture. Thus, our strain KUC21850 was identified as *Fc. violacea* by the cultural characteristics. The phylogeny and microscopic features (conidia size and shape) also supported the identification. A prior investigation has revealed that *Fc. violacea* J-1 possesses antifungal properties effective against *Alternaria alternata*, the pathogen responsible for causing soft rot disease in kiwifruit (Li *et al*., 2021b). Consequently, this fungus exhibits potential as a viable biocontrol agent.

Macroconia gigas (J. Luo & W.Y. Zhuang) Gräfenhan & Seifert, Stud. Mycol., 68: 102(2011) (Figs. 3, 8)

MycoBank. MB 519444
On PDA, colonies circular to irregular form, margin entire, aerial mycelia dense, mycelia white. Pigment absent in medium. On CMD, colonies circular, margin erose to entire, aerial mycelia scant, mycelia white to yellow (10YR 8/8). Pigment absent in medium. **Conidiophores** unbranched, erect, septate, (18.5−)30−55(−70) × (3.0−)4.0−5.0(−5.5) μm. **Conidia** curved, (40−)50−65 (−70) × (4.0−)4.5−5.5 (−7.0) μm.
Distribution. Taiwan; and Republic of Korea.
Habitat. On rotten culm of bamboo and dead culm of *Phyllostachys bambusoides*.
Specimen examined. KOREA, Jeollanam-do, Damyang, Juknokwon, 35.3284N, 126.9855E, isolated from a dead culm of *Phyllostachys bambusoides*, 20 Dec 2021, Sun Lul Kwon, KUC21846 (=NIBRFGC000510470); KOREA, Jeollanam-do, Damyang, Juknokwon, 35.3284N, 126.9855E, isolated from a dead culm of *Phyllostachys bambusoides*, 20 Dec 2021, Sun Lul Kwon, KUC21848 (=NIBRFGC000510471).
Notes. The morphology of conidia and conidiophores of our strains (KUC21846 and KUC21848) closely resembles those found in the original description, born from the sporodochia (Luo and Zhuang, 2008). While the morphological characteristics alone do not provide sufficient evidence to definitively identify our strain as *M. gigas*, the combination of molecular data and ecological traits is able to identify it *M. gigas*.

Neopestalotiopsis camelliae-oleiferae Qin Yang & He Li, Journal of Fungi 7(12, no. 1080): 16(2021) (Figs. 4, 9)

MycoBank. MB 841476
On PDA, colonies thick, circular form, margin entire, aerial mycelia dense, mycelia white to very pale yellow (2.5Y 3/2). Very pale yellow (2.5Y 3/2) pigment diffused in media. **Conidiomata** pycnidial, black. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** ampulliform, hyaline, thin-walled, smooth, (9.0−)12−

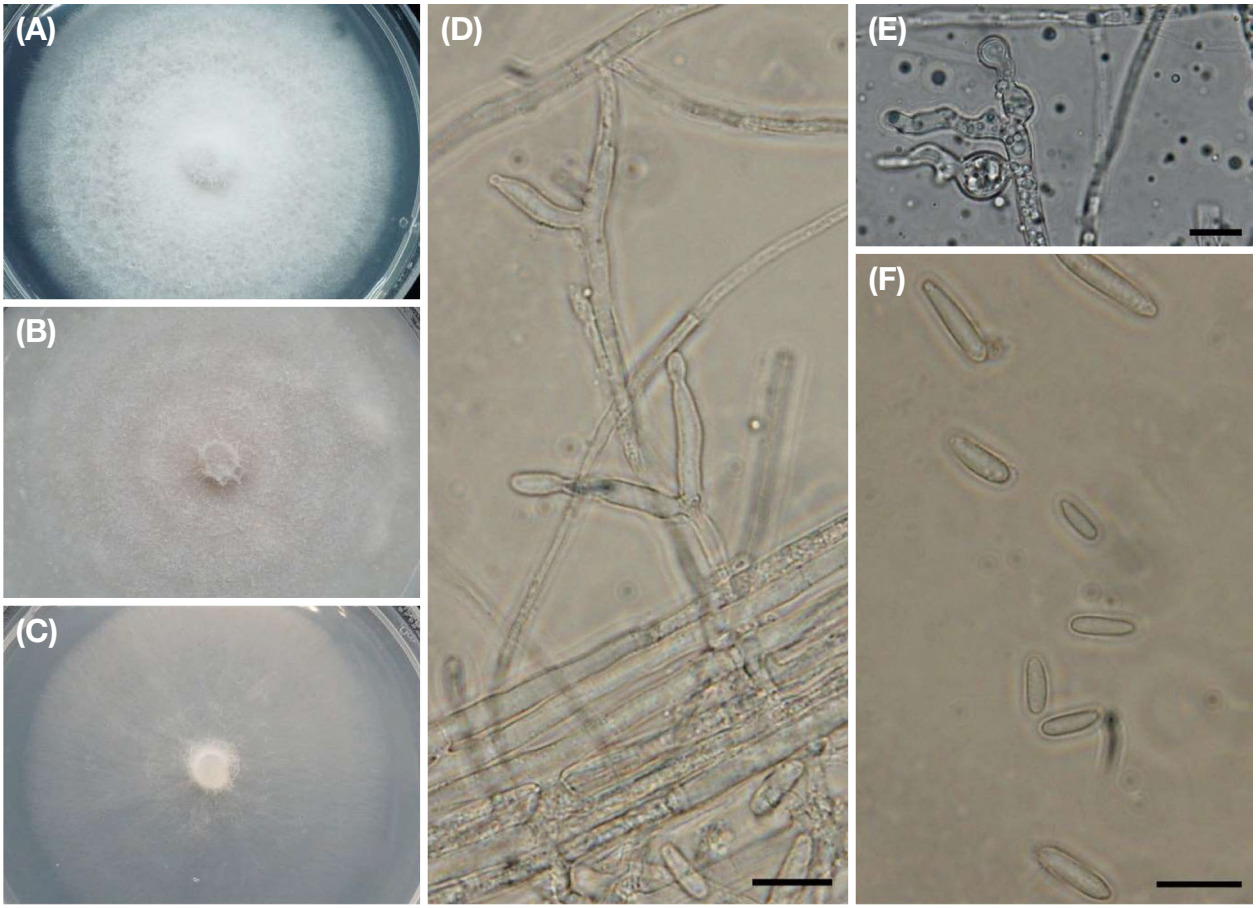

Fig. 6. Morphology of *Fusarium bambusarum* (KUC21851). (A) colony on PDA; (B) colony on OA; (C) colony on SNA; (D) conidiophore bearing phialides; (E) chlamydospores; (F) microspores. Scale bars: 10 μm (D–F).

17(–18.5) × (4.0–)5.0–5.5(–8.0) μm. **Conidia** fusiform to clavate, straight, 4-septate, (19–)20–23.5(–26.5) × (6.0–)6.5–7.5(–8.0) μm; **basal cell** obconic, (2.5–)3.5–5.0(–6.5) μm long, with a single filiform appendage, hyaline, thin-walled, (1.5–)3.0–4.5(–5.5) μm long; **apical cell** conical, (2.5–)3.0–5.5(–6.5) μm long, with 2–3 filiform apical appendage, hyaline, flexuous, thin-walled, (16–)19–25 (–30) μm long; **three median cells** doliiform, (10–)12–15(–18.5) μm long, third septa from the base darker than rest cell (second cell from base pale brown, (3.5–)4.0–5.5(–7.0) μm long; third cell from dark brown, (3.5–)4.0–5.0 μm long; fourth cell from base medium brown, 4.0–5.5 μm long).

Distribution. China and Republic of Korea.

Habitat. On leaves of *Camellia oleifera*, and dead leaf of *Phyllostachys bambusoides*.

Specimen examined. KOREA, Jeju-do, Pyoseon-myeon, Maeoreum, 33.3179N, 126.8132E, isolated from a dead leaf of *Phyllostachys bambusoides*, 15 Apr 2021, Jae-Jin Kim, KUC21857 (= NIBRFGC000510472). KOREA, Jeju-do, Pyoseon-myeon, Maeoreum, 33.3179N, 126.8132E, isolated from a leaf of *Phyllostachys bambusoides*, 15 Apr 2021, Jae-Jin Kim, KUC21858 (= NIBRFGC000510473).

Notes. The morphological features of KUC21857 and KUC21858 were slightly different by narrow conidia, short basal cell length, short appendage attached basal cell, and long length of appendage of apical cell from the original description (Li *et al*., 2021a). However, other morphological features and phylogeny result were congruent to the type species (Fig. 4, Fig. 9). Thus, KUC21857 and KUC21858 were identified as *N. camelliae-oleiferae*. *Neopestalotiopsis camelliae-oleiferae* CSUFT081 (type species) was isolated from leaves of symptomatic *Camellia oleiferae* in China (Li *et al*., 2021a). Pathogenicity tests have shown that this species infects wounded leaves of plants, causing lesions, but the lesions are not large (Li *et al*., 2021a).

Neopestalotiopsis iberica

E. Diogo, M.H. Bragança & A.J.L. Phillips, Mycol. Progr. 20(11): 1449(2021) (Figs. 4, 10)

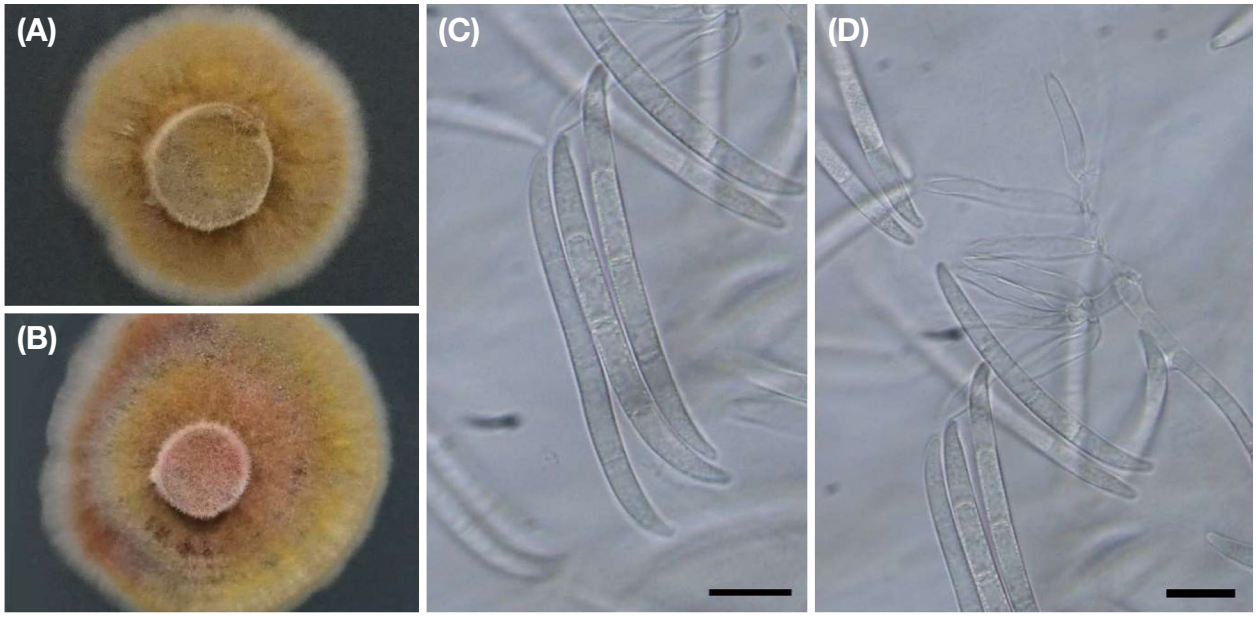

Fig. 7. Morphology of *Fusicolla violacea* (KUC21850). (A) colony on PDA after five days; (B) colony on PDA after ten days; (C) conidia; (D) phialides. Scale bars: 10 μm (C, D).

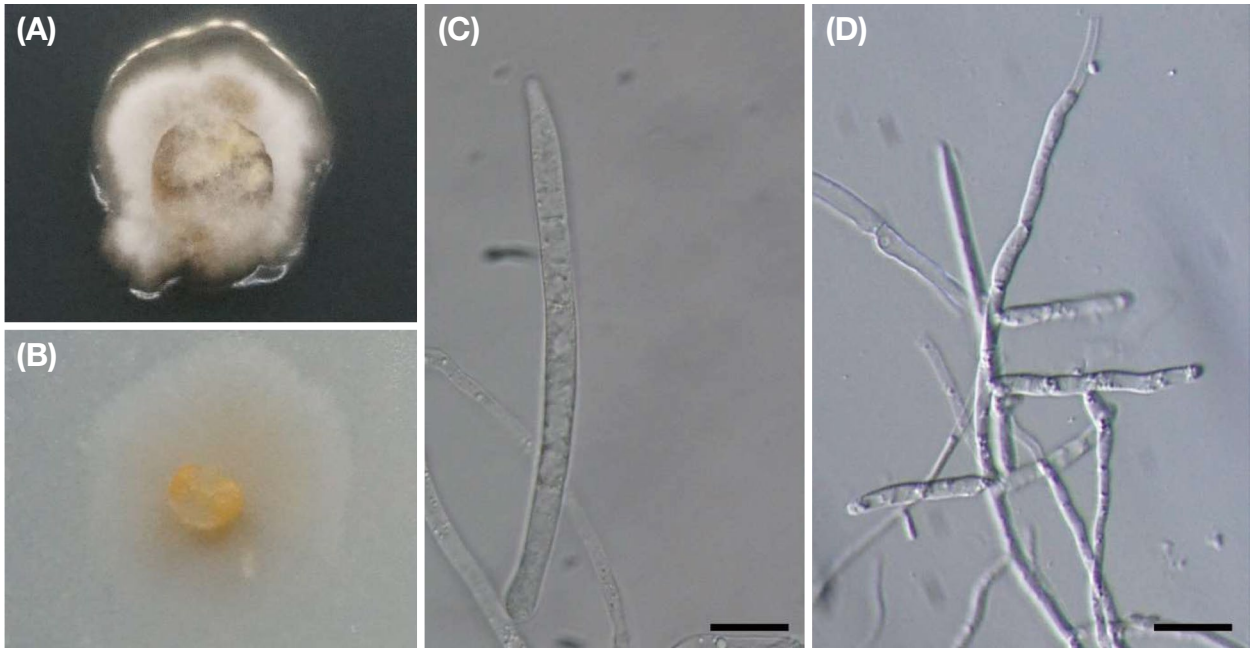

Fig. 8. Morphology of *Macroconia gigas* (KUC21846). (A) colony on PDA; (B) colony on CMD; (C) conidia from aerial mycelia; (D) conidiophores from aerial mycelium. Scale bars: 10 μm (C); 20 μm (D).

MycoBank. MB 839459

On PDA, colonies thick, circular form, margin curled to undulate, aerial mycelia fluffy, abundant, mycelia white. Yellow (10YR 8/6) pigment diffused in media. Conidiomata abundant. **Conidiomata** pycnidial, black, abundant. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** ampulliform to lageniform, hyaline, thin-walled, smooth, (7.0−)9.0−11.5(−14.5) × (3.0−)4.0−5.0 (−6.5) μm. **Conidia** ellipsoidal, straight, 4-septate, (18.5−) 20−24.5(−27.5) × (5.5−)6.0−6.5(−7.0) μm; **basal cell**

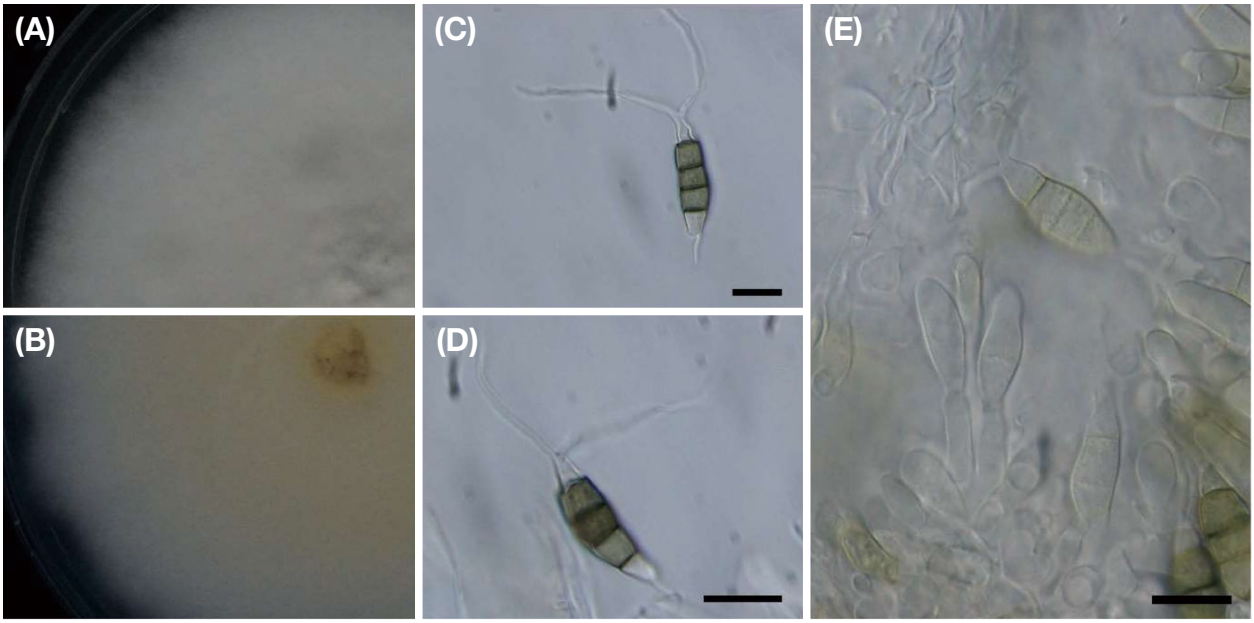

Fig. 9. Morphology of *Neopestalotiopsis camelliae-oleiferae* (KUC21857). (A, B) colony on PDA (above and reverse); (C, D) conidia; (E) conidiogenous cells. Scale bars: 10 μm (C–E).

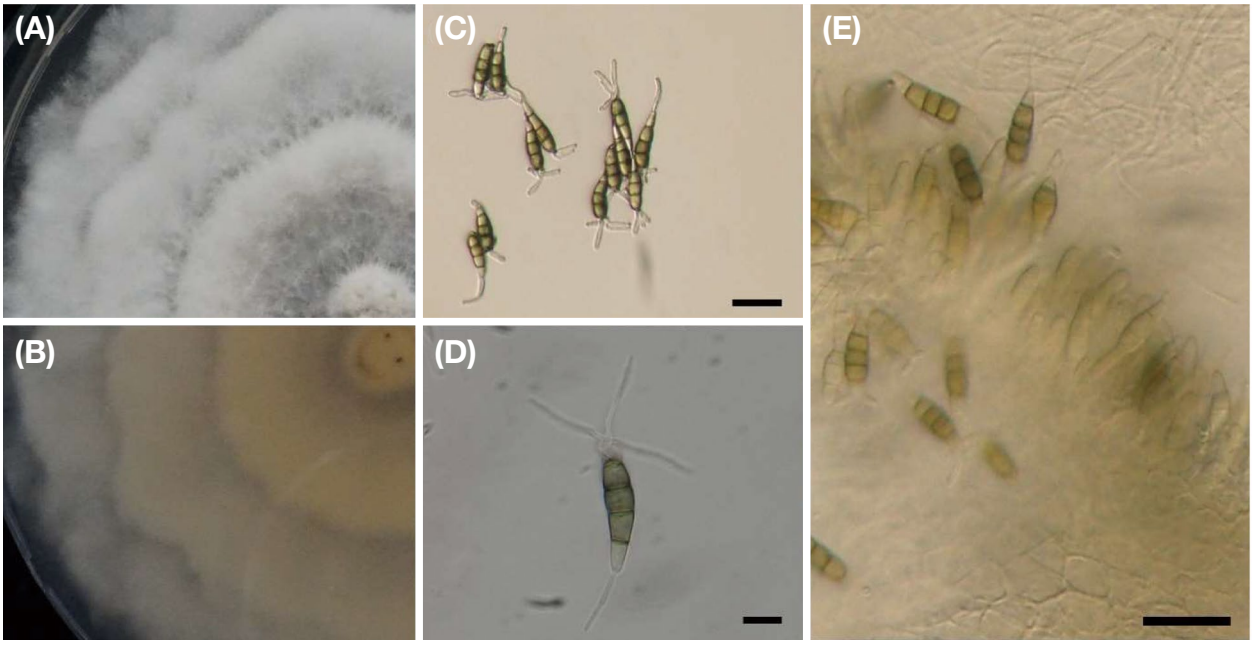

Fig. 10. Morphology of *Neopestalotiopsis iberica* (KUC21856). (A, B) colony on PDA (above and reverse); (C, D) conidia; (E) conidiogenous cells. Scale bars: 20 μm (C, E); 10 μm (D).

obconic to subcylindrical, (4.0−)4.5−6.0(−7.0) μm long, with a single filiform appendage, hyaline, thin-walled, (2.5−)6.5−10(−15) μm long; **apical cell** subcylindrical to conical, (2.5−)3.5−5.5(−6.0) μm long, with 2−3 filiform apical appendage, hyaline, flexuous, thin-walled, (8.5−)9.5−17(−19.5) μm long; **three median cells** doliiform, (11−)12.5−15(−16) μm long, third septa from the base darker than rest cell (second cell from base pale brown, 4.0−5.5(−5.8) μm long; third cell from dark brown, (3.0−)4.0−5.0 μm long; fourth cell from base brown, (3.5−)4.0−5.5(−6.0) μm long).

Distribution. Portugal, Spain, and Republic of Korea.

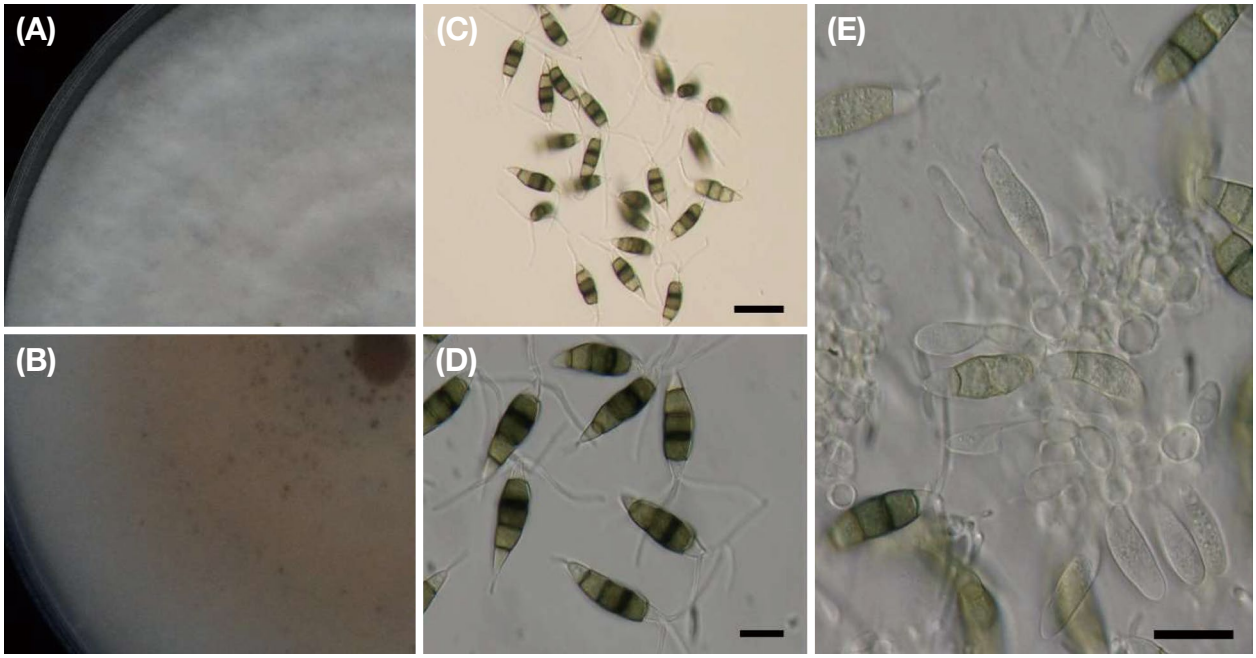

Fig. 11. Morphology of *Neopestalotiopsis longiappendiculata* (KUC21859). (A, B) colony on PDA (above and reverse); (C, D) conidia; (E) conidiogenous cells. Scale bars: 10 μm (C–E).

Habitat. On leaves and stems of *Eucalyptus globulus*, leaves of symptomatic *Camellia oleifera*, and culm of *Phyllostachys bambusoides*.
Specimen examined. KOREA, Jeju-do, Pyoseon-myeon, Maeoreum, 33.3179N, 126.8132E, isolated from a culm of *Phyllostachys bambusoides*, 15 Apr 2021, Jae-Jin Kim, KUC21856 (=NIBRFGC000510474).
Notes. The morphological features of KUC21856 were slightly different by narrow conidia, long basal cells, long basal cell attached appendages, and short apical attached appendages from the original description (Diogo *et al*., 2021). However, other features (e.g., culture characteristics and conidiogenous cells) and phylogeny indicated that the strain KUC21856 is *N. iberica*. This is the first report of *N. iberica* species living on the culm of *P. bambusoides*.

Neopestalotiopsis longiappendiculata
E. Diogo, M.H. Bragança & A.J.L. Phillips, Mycol. Progr. 20(11): 1450(2021) (Figs. 4, 11)

MycoBank. MB 839460
On PDA, colonies thick, circular form, margin entire, aerial mycelia abundant, mycelia white. Yellow (10YR 7/6) pigment diffused in media. **Conidiomata** pycnidia, black, rare. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** ampulliform to subcylindrical, hyaline, thin-walled, smooth, (8.0−)10−12.5 (−16) × (3.5−) 4.5−6.0(−7.0) μm. **Conidia** fusiform to ellipsoidal, straight or slightly curved, 4-septate, (16.0−)19−23(−25) × (6.0−) 6.5−7.5(−8.0) μm; **basal cell** obconic to subcylindrical, (2.5−)3.5−5.0 μm long, with a single filiform appendage, hyaline, thin-walled, 3.0−7.0(−9.0) μm long; **apical cell** conical, (3.0−)3.5−4.5(−5.0) μm long, with 2−4 filiform apical appendage, hyaline, flexuous, thin-walled, (19−) 20−27(−30) μm long; **three median cells** doliiform, (12.5−)13−14.5(−15.5) μm long, third septa from the base darker than rest cell (second cell from base pale brown, (3.5−)4.0−5.0 μm long; third cell from brown to dark brown, (3.0−)4.0−5.5(−6.5) μm long; fourth cell from base brown, 4.0−6.0(−6.5) μm long).
Distribution. Portugal and Republic of Korea.
Habitat. On leaves and stems of *Eucalyptus globulus* and *E. nitens*, and dead leaf of *Phyllostachys bambusoides*.
Specimen examined. KOREA, Jeju-do, Pyoseon-myeon, Maeoreum, 33.3179N, 126.8132E, isolated from a dead leaf of *Phyllostachys bambusoides*, 15 Apr 2021, Jae-Jin Kim, KUC21859 (=NIBRFGC000510475).
Notes. The morphological features of KUC21859 are well-matched with the original description (Diogo *et al*., 2021). Therefore, the bambusicolous fungi KUC21859 was successfully identified as *N. longiappendiculata* by integrating both the morphology and phylogenetic results. This is the first report of *N. longiappendiculata* species living on the dead bamboo leaf. This species was reported as a plant pathogen causing grey blight disease in tea plants and *Camellia* species (Wang *et al*., 2022b).

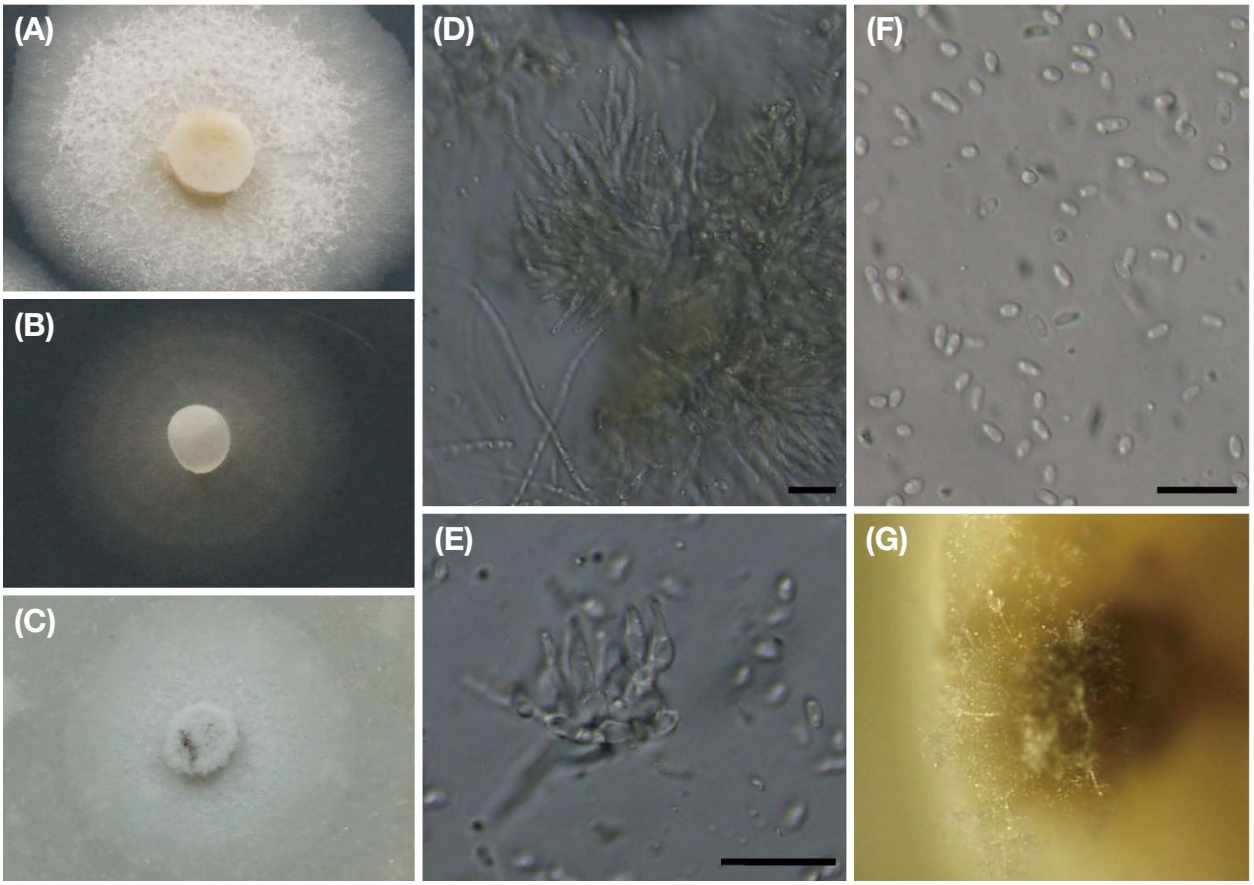

Fig. 12. Morphology of *Thyridium punctulatum* (KUC21845). (A) colony on PDA; (B) colony on MEA; (C) colony on OA; (D, E) conidiophores; (F) conidia; (G) conidiomata on PDA. Scale bars: 10 μm (D–G).

Thyridium punctulatum **(I. Hino & Katum.) R. Sugita & Kaz. Tanaka, MycoKeys 86: 162(2022) (Figs. 5, 12)**

MycoBank. MB 841919

On PDA, colonies low, flat, circular form, margin erose to entire, aerial mycelia dense, mycelia white, pigment absent in medium. On MEA, colonies circular form, margin filamentous to entire, aerial mycelia scant, mycelia hyaline to white, pigment absent. On OA, colonies circular form, margin entire, aerial mycelia little, mycelia white, pigment absent in medium. **Coelomycetous asexual morph**, **Conidiomata** pycnidia, single to grouped. **Conidiophores** branched, hyaline, thin-walled, bearing terminal a group of 2–5 phialides. **Phialides** lageniform, hyaline, (9.0–) 9.5–15(–16) × 2.0–3.0(–4.5) μm. **Conidia** ellipsoidal to obovoid, slightly apiculate base, hyaline, smooth, 3.0–4.0(–4.5) × 1.5–2.0 μm. **Chlamydospores** not observed.

Distribution. Japan and Republic of Korea.

Habitat. On dead twigs or culms of *Phyllostachys nigra* var. *henonis*, *P. pubescens*, and *P. bambusoides*.

Specimen examined. KOREA, Jeollanam-do, Damyang, Juknokwon, 35.3284N, 126.9855E, isolated from a dead culm of *Phyllostachys bambusoides*, 20 Dec 2021, Sun Lul Kwon, KUC21845 (= NIBRFGC000510476).

Notes. The size of the conidia of *T. punctulatum* KUC 21845 (3–4 μm long) is slightly longer than that of *T. punctulatum* KT 3905 (epitype) (2–3.5 μm long) (Sugita and Tanaka, 2022). However, other morphological features are comparable. The holotype and epitype strains were isolated from bamboo (dead twigs of *Phyllostachys nigra* var. *henonis*) in Japan (Sugita and Tanaka, 2022). Moreover, another specimen examined in the study was also isolated from bamboo (dead culm of *Phyllostachys pubescens*). This suggests that *T. punctulatum* species prefer to have a habitat on the dead *Phyllostachys* species. Previous research has demonstrated that the *Thyridium* genus possesses enzymes and pathways responsible for the degradation of diesel fuel (Deng *et al*., 2023). Consequently, it is postulated that this genus could be harnessed for the remediation of oil pollutants.

Discussion

In this study, seven unrecorded fungi were isolated from bamboo materials. They all belong to Sordariomycetes, which possess variability in morphology, growth form, and habitat (Lundqvist, 1972; Berbee and Taylor, 1992). They can occur in soil, dung, and leaf litter as decomposers, as well as plant pathogen (Alexopoulos *et al*., 1996; Samuels and Blackwell, 2001; Zhang and Wang, 2015). Among the unrecorded species, *Fusarium*, *Fusicolla*, and *Macroconia* are known nectriaceous fungi (Gräfenhan *et al*., 2011; Forin *et al*., 2020). Member of these are typically reported as parasites of plants, occurring on hardwood trees and shrubs in tropical, subtropical, or temperate regions. Although nectriaceous fungi are typically recognized to plant pathogens, however, *Fu. violacea* has been reported to have the capacity to produce an effective antifungal agent against *Alternaria alternata*, the pathogen infecting kiwifruit (Li *et al*., 2021b). This implies that *Fu. violacea* holds promise as a valuable biological control agent. Pestalotioid fungi including *Pestalotiopsis*, *Neopestalotiopsis*, and *Pseudopestalotiopsis* are distributed in tropical and temperate regions, where they exhibit versatile ecological roles such as plant pathogens, endophytes, and saprobes (Maharachchikumbura *et al*., 2011; 2014). *Neopestalotiopsis* species can be distinguished from other Pestalotioid fungi due to their distinctive versicolorous median cells (Maharachchikumbura *et al*., 2014). Notably, three *Neopestalotiopsis* species, *N. camellia-olefera*, *N. iberica*, and *N. longiappendiculata*, have been identified as causing leaf lesions on *Camellia olefera*. However, in the current study, no lesions were observed on bamboo living leaves. Previous research has reported that *Neopestalotiopsis* species produce antibacterial, antifungal, and cytotoxic agents (Halecker *et al*., 2014; Zhao *et al*., 2015). A new compound related to estrogenic activity has also been identified in *N. clavispora* (Kwon *et al*., 2022). These findings suggest that *Neopestalotiopsis* species hold the potential for producing valuable extracts. On the other hand, the genus *Thyridium* has a long history of observation but is relatively less explored in terms of scientific study.

In this study, seven unrecorded species were isolated from bamboo and subsequently described their characteristics in morphology and phylogeny. As only limited biological research has been conducted on these newly isolated species, further research must be done to explore the potential applications and significance.

Conflicts of Interest

The author of this paper has no affiliation with any interests and is solely responsible for the paper.

Acknowledgements

This research was supported by the project of the National Institute of Biological Resources [NIBR202304104] under the Ministry of Environment, Korea; National Research Foundation of Korea (NRF) grants funded by the Korean government (MSIT) [2021R1A2C1011894]. This study was also supported by the Korea University Grant.

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Submitted: October 30, 2023
Revised: November 7, 2023
Accepted: November 15, 2023