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Re-assessment of Taxonomy and Host Range of *Colletotrichum* from Korea: Focus on the *C. boninense*, *C. spaethianum* Species Complexes, and Related Taxa

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***Colletotrichum* species are commonly known as important phytopathogens causing anthracnose in Korea and worldwide, with a diverse range of host plants. *Colletotrichum* isolates preserved in the Korean Agricultural Culture Collection (KACC) are important resources for scientific research as well as anthracnose disease management strategies in Korea. Many *Colletotrichum* isolates in KACC had been identified using morphological characteristics and their host plants by depositors, this could lead to inaccurate species names. In this study, 38 KACC isolates were, therefore, re-identified as 13 known species (*C. boninense*, *C. caudasporum*, *C. coccodes*, *C. echinochloae*, *C. karsti*, *C. liriopes*, *C. nigrum*, *C. sansevieriae*, *C. spaethianum*, *C. sublineola*, *C. sydowii*, *C. truncatum*, and *C. zhaoqingense*) and a new species candidate, based on multi-locus sequence analyses of the nuclear ribosomal internal transcribed spacers, glyceraldehyde-3-phosphate dehydrogenase (*gapdh*), chitin synthase 1 (*chs-1*), histone-3 (*his3*), actin (*act*), beta-tubulin 2 (*tub2*), and manganese-superoxide dismutase (*sod2*). Of these, *C. caudasporum*, *C. echinochloae*, and *C. zhaoqingense* are unrecorded species in Korea. The results also revealed 16 new host-fungus combinations in Korea, including 13 new combinations worldwide. However, the pathogenicity of the fungal species in this work on their hosts was not confirmed.**

Keywords : anthracnose, *Colletotrichum karsti*, multi-locus sequence analysis

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The genus *Colletotrichum* is one of the most important phytopathogenic genera worldwide (Dean et al., 2012). Many *Colletotrichum* species also exhibit endophytic or saprobic associations with plants (Jayawardena et al., 2021). To date, a large number of species in the genus *Colletotrichum* have been reported with a wide range of hosts including crops and wild plants, while many others have a narrow host range or host specificity (Jayawardena et al., 2021; Talhinhas and Baroncelli, 2023). Many studies were conducted in the genus *Colletotrichum*, but the host range of *Colletotrichum* species is still poorly understood. For instance, *C. higginsianum* was primarily known to be specific to *Brassicaceae* as mentioned by Damm et al. (2014), this species was later reported from *Polygonaceae* (*Rumex acetosa*) (Zhang et al., 2018), *Campanulaceae* (*Campanula* sp.) (Khodaei et al., 2019) and *Araliaceae* (*Panax ginseng*) (Thao et al., 2024b). Of the relevant elements, accurate identification of *Colletotrichum* species is crucial for un-

derstanding fungal diversity and their host range, leading to effective disease management, especially in biological control. For example, it helps avoid the use of crops that are infected by the same *Colletotrichum* species in intercropping systems.

The nuclear ribosomal internal transcribed spacer (ITS) region has been widely used as a primary barcode marker for fungal species identification and it could separate major clades in the *Colletotrichum* genus, but is insufficient to resolve at the species level (Cannon et al., 2012). Recently, a multi-locus phylogenetic analysis of ITS, glyceraldehyde-3-phosphate dehydrogenase (*gapdh*), chitin synthase 1 (*chs-1*), histone-3 (*his3*), actin (*act*), and beta-tubulin 2 (*tub2*) was used to differentiate many species in the genus *Colletotrichum* (Liu et al., 2022; Zhang et al., 2023). Meanwhile, other makers such as calmodulin (*cal*) and glutamine synthase (*gs*) were additionally used for species delimitation in the *C. boninense* and the *C. orbiculare* complex, respectively (Damm et al., 2012, 2013). A dataset of ITS; the 5′ end of the DNA lyase gene (*apn2*); the 3′ end of *apn2* and the 5′ end of the mating type gene *Mat1-2* (Mat1/Apn2); and manganese-superoxide dismutase (*sod2*) was used for the *C. caudatum* and *C. graminicola* complexes (Crouch, 2014; Crouch et al., 2009).

In our previous studies (Thao et al., 2023, 2024a, 2024b, 2024c), 194 *Colletotrichum* isolates preserved in KACC were re-identified into 37 known species, one newly described species, and four new species candidates, based on multi-locus sequence analyses. There are 12 species and three new species candidates in the *C. gloeosporioides* species complex, six species and one new species candidate in the *C. acutatum* complex, eight species with the neotypification of *C. panacicola* and one new species (*C. kummerowiae*) in the *C. destructivum* complex, four species in the *C. orchidearum* complex, three species in the *C. dematium* complex, two species in the *C. magnum* complex, and two species in the *C. orbiculare* complex. Of these, 101 isolates were renamed from primary names, and 30 isolates (*Colletotrichum* sp.) were identified at the species level. Thirty-eight other isolates of *Colletotrichum* preserved in KACC were collected in Korea since the 1990s. They were originally identified based on host plants and morphological features, or only ITS region by depositors. This could lead to inaccurate or unreliable species names. Therefore, the aim of this study is to (1) re-identify the 38 isolates in KACC that belong to the *C. boninense*, *C. spaethianum* species complexes and related groups based on phylogenetic analyses of multiple loci; (2) re-arrange the host plants of identified fungal species in Korea.

Materials and Methods

Fungal isolates. Thirty-eight *Colletotrichum* isolates in KACC that originated from crops and wild plants in Korea were selected in this study based on the ITS sequence analysis. These isolates have been preserved in liquid nitrogen and were retrieved on potato dextrose agar (PDA; Difco Laboratories, Detroit, MI, USA) for DNA extraction. Details of the fungal isolates (host plants, locations, collection years, and deposited names) are listed in Table 1.

DNA extraction, polymerase chain reaction amplification, and sequencing. Total genomic DNAs of fungal isolates were extracted from 5-day-old cultures grown on the PDA medium by the DNeasy plant mini kit (Qiagen, Hilden, Germany), following the manufacturer's instructions.

The ITS region, *gapdh*, *chs-1*, *act*, *his3*, *tub2*, and *sod2* genes were amplified and sequenced using the primer pairs ITS1/ITS4 (White et al., 1990), GDF1/GDR1 (Guerber et al., 2003), CHS-79F/CHS-345R, ACT-512F/ACT-783R (Carbone and Kohn, 1999), CYLH3F/CYLH3R (Crous et al., 2004), T1/Bt2b (Glass and Donaldson, 1995; O'Donnell and Cigelnik, 1997), and SOD625F/SOD625R (Crouch et al., 2006), respectively. The polymerase chain reaction (PCR) amplification was performed in a total volume of 25 μL, using an AllInOneCycler Thermal Block (Bioneer, Daejeon, Korea). The PCR mixture contained 8.5 μL nuclease-free water, 12.5 μL PCR Master Mix (2×), 1 μL (4.5 pMol) of each primer, and 2 μL genomic DNA (100 ng/μL). Conditions for amplification of *sod2* were an initial denaturation step at 94°C for 5 min, followed by 35 cycles of 94°C for 30 s, 55°C for 30 s, 72°C for 1 min, and final extension at 72°C for 10 min. PCR conditions of the other loci were set up as described by Thao et al. (2023). The PCR amplicons were visualized by gel electrophoresis, then purified and sequenced by the Macrogen Company (Seoul, Korea).

Phylogenetic analysis. The DNA sequences obtained from forward and reverse primers were paired and assembled in MEGA version 11 (Tamura et al., 2021). The sequences generated in our study were deposited to RDA-GeneBank (http://genebank.rda.go.kr) with accession numbers in Table 1. For each locus, the sequences in this study, related sequences and the outgroup from GenBank (Supplementary Table 1) were aligned using MAFFT v. 7 (http://mafft.cbrc.jp/alignment/server/index.html) with the G-INS-i option.

Table 1. KACC isolates of *Colletotrichum* spp. used in this study with collection details and RDA-GeneBank accession numbers

Re-identified species	Culture	Location	Collection year	Host	Host-fungus relationship	Scientific name by depositor	RDA-GeneBank accession no.					
							ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. boninense	KACC 42615	Namyangju	2006	*Euonymus japonicus*	Not confirmed	*Colletotrichum* sp.	RDA0061882	RDA0061884	RDA0069649	RDA0069688	RDA0069738	-
C. caudasporum	KACC 41028	Namwon	2002	*Imperata cylindrica*	Not confirmed	*C. caudatum*	RDA0062048	RDA0062374	RDA0069638	RDA0069667	RDA0069709	RDA0062170
C. coccodes	KACC 40802	Jangseong	1996	*Solanum lycopersicum*	Not confirmed	*C. coccodes*	RDA0062037	RDA0062357	RDA0069640	RDA0069684	RDA0069725	RDA0062149
	KACC 40227	Yeoju	1996	*Solanum melongena*	Not confirmed	*C. coccodes*	RDA0060930	RDA0062343	RDA0069642	RDA0069685	RDA0069728	RDA0062135
	KACC 40803	Jeju	1998	*Solanum tuberosum*	Not confirmed	*C. coccodes*	RDA0062038	RDA0062358	RDA0069639	RDA0069682	RDA0069726	RDA0062150
	KACC 47697	Pyeongchang	2012	*Solanum tuberosum*	Not confirmed	*C. coccodes*	RDA0062086	RDA0062463	RDA0069641	RDA0069683	RDA0069727	RDA0062269
C. echinochloae	KACC 46949[a]	Yangpyeong	2012	*Echinochloa crus-galli*	Not confirmed	*Colletotrichum* sp.	RDA0061825	RDA0061827	RDA0069624	RDA0069666	RDA0069710	RDA0061826
C. karsti	KACC 48238	Jeju	2015	*Actinidia chinensis* var. *deliciosa*	Not confirmed	*C. boninense*	RDA0061891	RDA0061893	RDA0069653	RDA0069691	RDA0069740	RDA0061892
	KACC 48657	Wando	2018	*Idesia polycarpa*	Not confirmed	*C. boninense*	RDA0062100	RDA0062485	RDA0069655	RDA0069695	RDA0069742	RDA0062291
	KACC 48894	Yeosu	Unknown	*Lilium lancifolium*	Not confirmed	*C. boninense*	RDA0062112	-	RDA0069656	-	RDA0069743	-
	KACC 40893	Jeju	Unknown	*Mammillaria* sp.	Not confirmed	*C. boninense*	RDA0061879	RDA0061881	RDA0069650	RDA0069690	RDA0069739	RDA0061880
	KACC 48304	Jeju	2017	*Passiflora edulis*	Not confirmed	*C. boninense*	RDA0062094	-	RDA0069654	RDA0069692	RDA0069741	RDA0062282
	KACC 43015	Daejeon	2006	*Pinus densiflora*	Not confirmed	*C. gloeosporioides*	RDA0061888	RDA0061890	RDA0069652	RDA0069694	RDA0069745	RDA0061889
	KACC 43013	Daejeon	2006	*Pinus strobus*	Not confirmed	*C. gloeosporioides*	RDA0061885	RDA0061887	RDA0069651	RDA0069693	RDA0069744	RDA0061886
C. liriopes	KACC 48099	Jeju	2015	*Liriope muscari*	Not confirmed	*Colletotrichum* sp.	RDA0061727	RDA0061765	RDA0069637	RDA0069681	RDA0069724	RDA0061752
C. nigrum	KACC 40010	Daejeon	Unknown	*Capsicum annuum*	Not confirmed	*C. coccodes*	RDA0060927	RDA0062337	RDA0069643	RDA0069686	RDA0069729	RDA0062129
	KACC 40006	Yeoju	1996	*Capsicum annuum*	Not confirmed	*Colletotrichum* sp.	RDA0062021	RDA0062333	RDA0069644	RDA0069687	RDA0069731	-
	KACC 40009	Pyeongchang	Unknown	*Capsicum annuum*	Not confirmed	*C. coccodes*	RDA0062022	RDA0062336	-	-	RDA0069730	RDA0062128
C. sansevieriae	KACC 46835	Hwaseong	2012	*Dracaena trifasciata*	Pathogen (Park et al., 2013)	*C. sansevieriae*	RDA0061818	-	RDA0069657	RDA0069696	RDA0069752	RDA0061817
C. spaethianum	KACC 48154	Anseong	2016	*Disporum smilacinum*	Not confirmed	*C. spaethianum*	RDA0061729	RDA0061763	RDA0069630	RDA0069679	RDA0069722	RDA0061750
	KACC 47788	Gangneung	2014	*Hosta capitata*	Not confirmed	*C. spaethianum*	RDA0061732	RDA0061760	RDA0069628	RDA0069676	RDA0069719	RDA0061747

(Continued)

Table 1. Continued

Re-identified species	Culture	Location	Collection year	Host	Host-fungus relationship	Scientific name by depositor	RDA-GeneBank accession no.					
							ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. spaethianum	KACC 47783	Seoul	2014	*Hosta longipes*	Not confirmed	*C. spaethianum*	RDA0061734	RDA0061758	RDA0069627	RDA0069674	RDA0069717	RDA0061745
	KACC 46409	Osan	2011	*Hosta longipes*	Not confirmed	*Colletotrichum* sp.	RDA0061736	-	RDA0069633	RDA0069672	RDA0069715	RDA0061743
	KACC 47786	Jeju	2014	*Hosta plantaginea*	Not confirmed	*C. spaethianum*	RDA0061733	RDA0061759	RDA0069634	RDA0069675	RDA0069718	RDA0061746
	KACC 47791	Jinju	2014	*Hosta plantaginea*	Not confirmed	*C. spaethianum*	RDA0061731	RDA0061761	RDA0069629	RDA0069677	RDA0069720	RDA0061748
	KACC 46633	Daejeon	2001	*Hosta plantaginea*	Not confirmed	*C. spaethianum*	RDA0061735	RDA0061757	RDA0069626	RDA0069673	RDA0069716	RDA0061744
	KACC 45503	Chuncheon	2010	*Lilium longiflorum*	Not confirmed	*Colletotrichum* sp.	RDA0061738	RDA0061754	RDA0069631	RDA0069670	RDA0069714	RDA0061741
	KACC 45504	Chuncheon	2010	*Lilium longiflorum*	Not confirmed	*Colletotrichum* sp.	RDA0061737	-	RDA0069632	RDA0069671	RDA0069723	RDA0061742
	KACC 48068	Suwon	2014	*Muscari armeniacum*	Not confirmed	*C. spaethianum*	RDA0061730	RDA0061762	RDA0069635	RDA0069678	RDA0069721	RDA0061749
C. sublineola	KACC 40229	Korea	Unknown	*Poaceae*	Not confirmed	*Glomerella tucumanensis*	RDA0061824	RDA0061822	RDA0072624	RDA0072625	RDA0069711	RDA0061823
C. sydowii	KACC 48697	Jeju	2018	*Boehmeria japonica* var. *japonica*	Not confirmed	*C. sydowii*	RDA0062107	RDA0062497	RDA0069665	RDA0069703	RDA0069753	RDA0062303
C. truncatum	KACC 40013	Daejeon	Unknown	*Capsicum annuum*	Not confirmed	*C. dematium*	RDA0060932	RDA0062339	RDA0069664	RDA0069702	RDA0069751	-
	KACC 40005	Yeoju	1996	*Capsicum annuum*	Not confirmed	*Colletotrichum* sp.	RDA0062020	RDA0062332	RDA0069663	RDA0069701	RDA0069749	RDA0062125
	KACC 40041	Korea	Unknown	*Capsicum annuum*	Not confirmed	*C. dematium*	RDA0060928	RDA0062341	RDA0069661	RDA0069699	RDA0069748	RDA0062133
	KACC 47164	Korea	2012	*Glycine max*	Not confirmed	*Colletotrichum* sp.	RDA0062081	RDA0062453	RDA0069662	RDA0069700	RDA0069750	RDA0062248
	KACC 40811	Hongcheon	1998	*Vigna angularis*	Not confirmed	*Colletotrichum* sp.	RDA0062040	RDA0062363	RDA0069659	RDA0069697	RDA0069746	RDA0062161
C. zhaoqingense	KACC 48895	Munkyeong	Unknown	*Pueraria montana* var. *lobata*	Not confirmed	*C. crassipes*	RDA0061819	RDA0061821	RDA0069658	RDA0069680	RDA0069737	RDA0061820
Colletotrichum sp.	KACC 42402	Hongcheon	2014	*Vicia venosa* subsp. *cuspidata*	Not confirmed	*Colletotrichum* sp.	RDA0061739	RDA0061753	RDA0069636	RDA0069668	RDA0069712	RDA0061740

KACC, Korean Agricultural Culture Collection; RDA, Rural Development Administration; ITS, internal transcribed spacer; *gapdh*, glyceraldehyde-3-phosphate dehydrogenase; *chs-1*, chitin synthase 1; *his3*, histone-3; *act*, actin; *tub2*, beta-tubulin 2.

[a]RDA-GeneBank accession number of *sod2* gene of isolate KACC 46949 is RDA0069758.

The alignments were manually edited and then concatenated afterwards in MEGA version 11.

Maximum likelihood (ML) phylogenetic analyses of each locus and concatenated sequence datasets were implemented using IQ-TREE Web Server (http://iqtree.cibiv.univie.ac.at/) with 10,000 ultrafast bootstrap replicates. The phylogenetic trees were viewed in MEGA version 11. The Bayesian inference analyses were performed using BEAST (version 2.7.5) package (Bouckaert et al., 2019). The running parameters were 10,000,000 Markov chain Monte Carlo (MCMC) generations and sampling every 1,000th generation. The first 10% of MCMC generations were discarded as burn-in and the tree was visualized using FigTree v1.4.4.

Re-arrangement of host-fungus associations in Korea. Host-fungus associations in this study were confirmed whether they have been previously reported in Korea or elsewhere, and other hosts reported in Korea were investigated based on literature sources obtained from The List of Plant Diseases in Korea (6.2 Edition, 2024) (https://genebank.rda.go.kr/english/plntDissInfo.do), National List of Species of Korea, 2024 (https://kbr.go.kr/content/view.do?menuKey=799&contentKey=174), USDA Fungal Databases (https://fungi.ars.usda.gov/) and other public databases.

Results

Multi-locus phylogenetic analyses. The individual trees (not shown) did not show conflicts among clades at the ML bootstrap support value ≥ 70% and the Bayesian posterior probability value ≥ 0.9 which allowed the combination of the loci. The concatenated sequence alignment of six loci (ITS, *gapdh*, *chs-1*, *his3*, *act*, and *tub2*) included 38 isolates in this study, 78 closely related taxa and an outgroup (*C. dematium* isolate CBS 125.25) from GenBank. The concatenated alignment contained 2,364 characters, including gaps (gene boundaries of ITS: 1–562; *gapdh*: 563–897; *chs-1*: 898–1,148; *his3*: 1,149–1,534; *act*: 1,535–1,827; and *tub2*: 1,828–2,364), of which 991 characters were parsimony-informative, 1,150 variable and 1,144 constant. The topologies of the phylogenetic trees generated by ML and Bayesian analysis were congruent.

The six-locus tree (Fig. 1) showed that 38 KACC isolates were divided into 14 clades, including 12 known species (*C. boninense*, *C. caudasporum*, *C. coccodes*, *C. karsti*, *C. liriopes*, *C. nigrum*, *C. sansevieriae*, *C. spaethianum*, *C. sublineola*, *C. sydowii*, *C. truncatum*, and *C. zhaoqingense*) with high bootstrap support and Bayesian posterior probability values, a novel isolate KACC 42402, and an unidentified isolate KACC 46949. The isolate KACC 46949 was grouped in a clade with *C. echinochloae* and *C. jacksonii* in the six-locus tree and was finally identified as *C. echinochloae* based on an additional locus (*sod2*) (Supplementary Fig. 1). The isolate KACC 42402 was significantly distinct from all known taxa and was considered as a new species candidate. It was closely related to *C. spaethianum* CBS 167.49, *C. lilii* CBS 109214, *C. guizhouense* CGMCC 3.15112, and *C. bicoloratum* NN055229, but genetically distinct from these species at ITS (98.12%, 97.69%, 97.84%, and 97.89%, respectively), *gapdh* (90.08%, 91.67%, 89.6%, and 86.6%), *chs-1* (97.21%, 96.81%, 96.81%, and 95.89%), *his3* (93.60%, 93.83%, 93.82%, and 91.74%), *act* (97.90%, 98.32%, 95.67%, and 93.15%), and *tub2* (94.32%, 93.31%, 93.12%, and 90.55%).

Host-fungus associations in this study. A total of 29 host-fungus combinations were found in this study. Of these, 13 combinations (*C. caudasporum* on *Imperata cylindrica*; *C. karsti* on *Actinidia chinensis*, *Idesia polycarpa*, *Lilium lancifolium*, *Mammillaria* sp., *Pinus densiflora*, *Pinus strobus*; *C. spaethianum* on *Disporum smilacinum*, *Hosta capitata*, *Lilium longiflorum*, *Muscari armeniacum*; *C. sydowii* on *Boehmeria japonica*; *C. zhaoqingense* on *Pueraria montana*) are first recorded in the world, and three combinations (*C. echinochloae* on *Echinochloa crus-galli*, *C. karsti* on *Passiflora edulis*, *C. truncatum* on *Vigna angularis*) were previously reported worldwide, but represent new records in Korea (Table 2).

Discussion

A total of 38 isolates in this research were re-identified as 13 known species and one new species candidate, belonging to the *C. boninense*, *C. spaethianum* species complexes and related taxa based on multi-locus sequence analyses. The species names of 14 isolates, originally assigned by depositors, were changed, and 10 isolates (deposited as *Colletotrichum* sp.) were identified at the species level. The results revealed three previously unrecorded species in Korea, including *C. caudasporum, C. echinochloae,* and *C. zhaoqingense*. This study, along with our earlier studies (Thao et al., 2023, 2024a, 2024b, 2024c) reclassified a comprehensive dataset of 232 *Colletotrichum* isolates collected from various host plants and geographic regions in Korea since the 1990s into 51 species and five new species candidates. Previously, *Colletotrichum* species reported more than two decades ago in Korea were identified based only on host species and morphological features (The Ko-

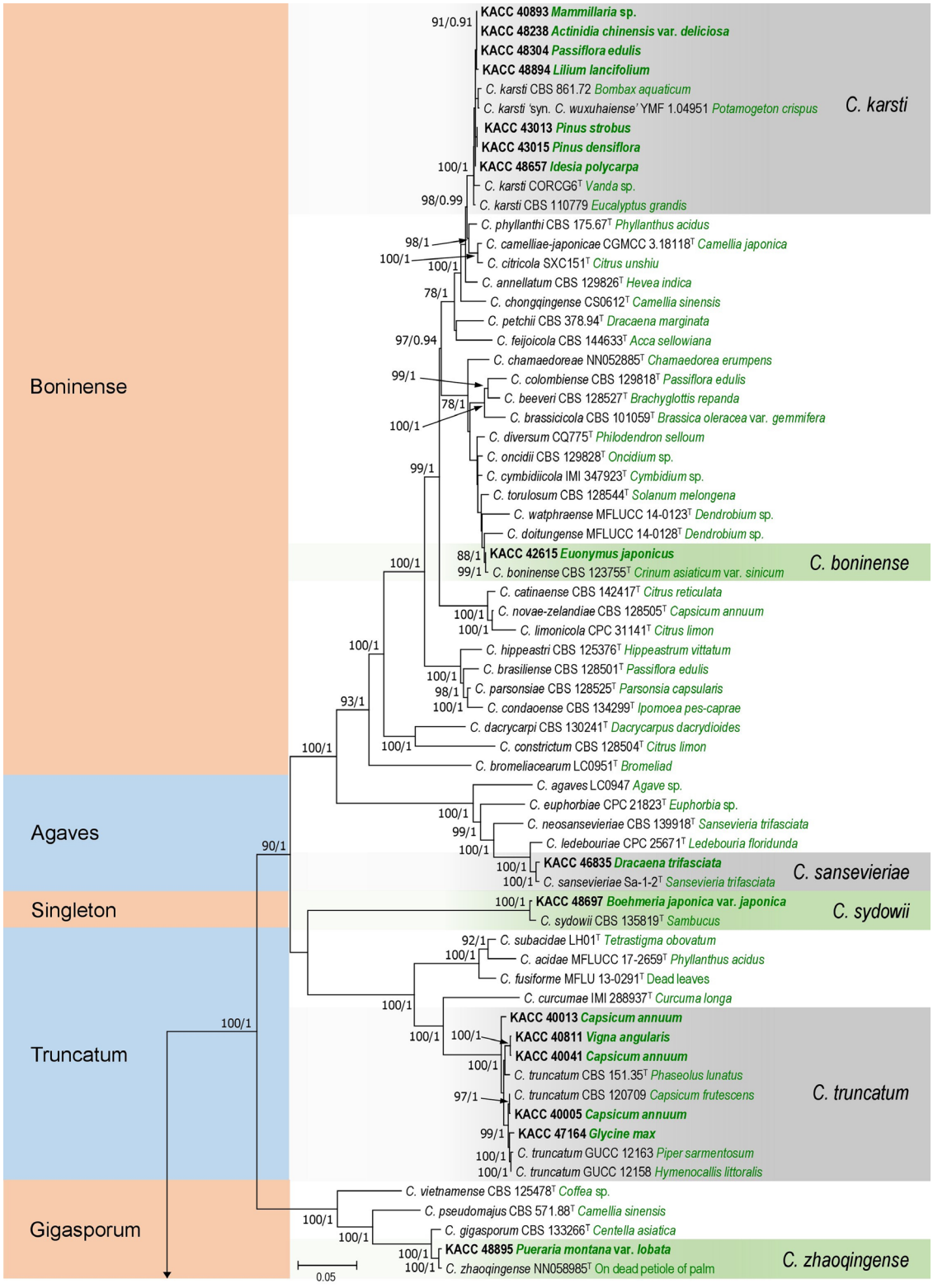

Fig. 1. Maximum likelihood tree of *Colletotrichum* isolates based on multi-locus sequences of ITS, *gapdh*, *chs-1*, *his3*, *act*, and *tub2*. Species names are followed by isolate numbers and hosts (green). Isolates from this study are in bold and the respective species are in right-coloured boxes. Singleton species and names of the species complexes are listed in the left-coloured boxes. Bootstrap support values ≥ 70% and Bayesian posterior probability values ≥ 0.9 are shown at the nodes. Ex-type strains are emphasized by the superscript "T" after isolate labels. *Colletotrichum dematium* (CBS 125.25) was used as the outgroup. (Continued)

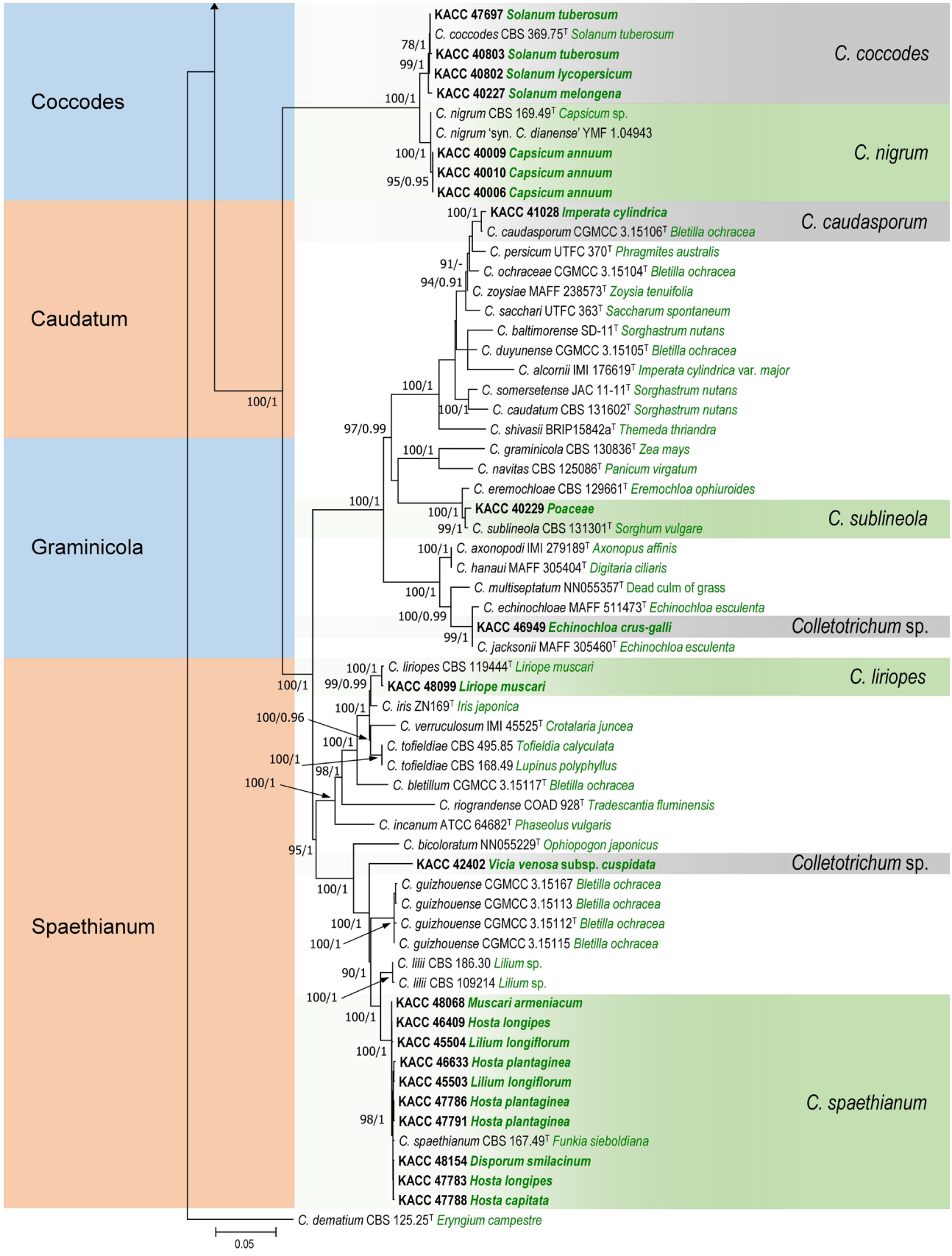

Fig. 1. (Continued).

Table 2. Comparison of host-fungus combinations between this study and previous reports

Species	Host			
	This study	Previous studies		
		Korea	Worldwide	References
Colletotrichum boninense	*Euonymus japonicus*[nc]	*Euonymus japonicus*[p]	*Euonymus japonicus*[p]	Lee et al. (2005)
C. caudasporum	*Imperata cylindrica*[nc]	-	-	-
C. coccodes	*Solanum lycopersicum*[nc]	*Solanum lycopersicum*[p]	*Solanum lycopersicum*[p]	Kim et al. (1998)
	Solanum melongena[nc]	*Solanum melongena*[p]	*Solanum melongena*[p]	Kim and Cho (1997)
	Solanum tuberosum[nc]	*Solanum tuberosum*[p]	*Solanum tuberosum*[p]	Kim (1998)
	-	*Capsicum annuum*[p]	*Capsicum annuum*[p]	Park and Kim (1992)
	-	*Rubus coreanus*[p]	*Rubus coreanus*[p]	Kim et al. (2012)
C. echinochloae	*Echinochloa crus-galli*[nc]	-	*Echinochloa crus-galli*[p]	Gu et al. (2023)
C. karsti	*Actinidia chinensis*[nc]	-	-	-
	Idesia polycarpa[nc]	-	-	-
	Lilium lancifolium[nc]	-	-	-
	Mammillaria sp.[nc]	-	-	-
	Passiflora edulis[nc]	-	*Passiflora edulis*[p]	Damm et al. (2012), Tozze et al. (2010)
	Pinus densiflora[nc]	-	-	-
	Pinus strobus[nc]	-	-	-
	-	*Juglans mandshurica*[p]	*Juglans mandshurica*[p]	Cho et al. (2024)
C. liriopes	*Liriope muscari*[nc]	*Liriope muscari*[p]	*Liriope muscari*[p]	Oo and Oh (2017)
	-	*Rohdea japonica*[p]	*Rohdea japonica*[p]	Kwon and Kim (2013)
C. nigrum	*Capsicum annuum*[nc]	*Capsicum annuum*[p]	*Capsicum annuum*[p]	The Korean Society of Plant Pathology (2024)
C. sansevieriae	*Dracaena trifasciata* (syn. *Sansevieria trifasciata*)[p]	*Sansevieria trifasciata*[p]	*Sansevieria trifasciata*[p]	Park et al. (2013)
C. spaethianum	*Disporum smilacinum*[nc]	-	-	-
	Hosta capitata[nc]	-	-	-
	Hosta longipes[nc]	*Hosta longipes*[p]	*Hosta longipes*[p]	Choi et al. (2024a)
	Hosta plantaginea[nc]	*Hosta plantaginea*[p]	*Hosta plantaginea*[p]	Cheon and Jeon (2016)
	Lilium longiflorum[nc]	-	-	-
	Muscari armeniacum[nc]	-	-	-
	-	*Convallaria keiskei*[nc]	*Convallaria keiskei*[nc]	Ahn et al. (2017)
C. sublineola	*Poaceae* (syn. *Gramineae*)[nc]	*Sorghum bicolor*[p]	*Sorghum bicolor*[p]	Choi et al. (2021)
C. sydowii	*Boehmeria japonica*[nc]	-	-	-
	-	*Albizia julibrissin*[e]	*Albizia julibrissin*[e]	Cha et al. (2023)
C. truncatum	*Capsicum annuum*[nc]	*Capsicum annuum*[p]	*Capsicum annuum*[p]	Oo and Oh (2020)
	Glycine max[nc]	*Glycine max*[p]	*Glycine max*[p]	Kim et al. (2002)
	Vigna angularis[nc]	-	*Vigna angularis*[p]	Sharma and Kaushal (1999)
	-	*Carica papaya*[p]	*Carica papaya*[p]	Aktaruzzaman et al. (2018)
	-	*Raphanus raphanistrum* subsp. *sativus*[p]	*Raphanus raphanistrum* subsp. *sativus*[p]	Choi et al. (2019)
	-	*Vigna radiata*[p]	*Vigna radiata*[p]	Han and Lee (1995)
C. zhaoqingense	*Pueraria montana*[nc]	-	-	-
Colletotrichum sp. (New species candidate)	*Vicia venosa*[nc]	-	-	-

"nc" The pathogenicity on the host was not confirmed; The fungus on the host was confirmed as a pathogen "p" or an endophyte "e".

rean Society of Plant Pathology, 2024). Therefore, data from this study contributes to a broader understanding of the taxonomic status and host range of *Colletotrichum* species in Korea.

Colletotrichum boninense s. str. was first described from *Crinum asiaticum* var. *sinicum* and other plants (*Cattleya* sp., *Clivia miniata*, *Cucumis melo*, *Cymbidium* sp., *Dendrobium kingianum*, *Passiflora edulis*, and *Prunus mume*) in Japan by Moriwaki et al. (2003). This species was later recorded as a pathogen or endophyte with a wide range of hosts worldwide (Damm et al., 2012; Liu et al., 2022). In Korea, *C. boninense* s. str. was reported as an anthracnose disease on spindle tree (*Euonymus japonicus*) based on its morphological characteristics and ITS sequence by Lee et al. (2005). This combination was re-confirmed in this study using multi-locus sequence analysis.

Colletotrichum caudasporum (syn. *C. caudisporum*) was originally introduced as an endophyte of *Bletilla ochracea* (*Orchidaceae*) in China (Tao et al., 2013), and then reported as a pathogen in the *Poaceae* family (unknown species) in this country (Liu et al., 2022). In our study, *C. caudasporum* was newly found on *Imperata cylindrica* (*Poaceae*). However, the host range of this fungal species is, to date, poorly understood.

Colletotrichum coccodes and *C. nigrum* have been reported from many different plant species and frequently from the *Solanaceae* family (Farr and Rossman, 2024). *C. coccodes* is morphologically indistinguishable from *C. nigrum* and these two species are genetically closely related (Liu et al., 2011, 2013). *C. coccodes* was reported as a causal agent of diseases on *Capsicum annunm*, *Rubus coreanus*, *Solanum lycopersicum*, *S. melongena* and *S. tuberosum*, and *C. nigrum* was from *Capsicum annunm* in Korea, but these two species were not confirmed using molecular data (Kim, 1998; Kim and Cho, 1997; Kim et al., 1998, 2012; Park and Kim, 1992; The Korean Society of Plant Pathology, 2024). Here, *C. coccodes* on *Solanum lycopersicum*, *S. melongena* and *S. tuberosum*, and *C. nigrum* on *Capsicum annuum* were well distinguished based on a combined analysis of 6 loci.

Colletotrichum echinochloae was originally described as a pathogen on *E. crus-galli* subsp. *utilis* (syn. *Echinochloa utilis*) in Japan (Moriwaki and Tsukiboshi, 2009). Later, this fungal species was found on *E. crus-galli* in China and was considered as a potential bioherbicide agent to control this grass (Gu et al., 2023). *C. echinochloae* from *E. crus-galli* identified here is a new record in Korea. To date, this fungal species is restricted to the host genus *Echinochloa*.

Colletotrichum karsti has been known as an endophyte or a pathogen with a wide host range and global distribution (Farr and Rossman, 2024; Liu et al., 2022). There were high variabilities in morphology and DNA sequences in the population of *C. karsti* (Damm et al., 2012). *C. karsti* was first reported in Korea in 2024, causing anthracnose on *Juglans mandshurica* (Cho et al., 2024). The present study revealed that *C. karsti* appeared on six unrecorded host plants (worldwide) and one new host plant in Korea, including economically important crops such as kiwi (*Actinidia chinensis*) and passion fruit plant (*Passiflora edulis*). However, the pathogenicity of the fungal species was not confirmed. This species could become an important fungus in Korea.

Colletotrichum liriopes was introduced from *Liriope muscari*, and then recorded from many different host species (Damm et al., 2009; Farr and Rossman, 2024). In Korea, *C. liriopes* was previously identified on *Rohdea japonica* and *Liriope muscari* using ITS sequence analysis and a combination of *act*, *gapdh*, and ITS (Kwon and Kim, 2013; Oo and Oh, 2017). This fungus was genetically closely related to a recently introduced species, *C. iris* (Liu et al., 2022). The isolate on *Liriope muscari* was here identified as *C. liriopes* and differentiated from *C. iris* based on a six-locus phylogenetic analysis.

Colletotrichum sansevieriae was only reported from the host genus *Dracaena* (syn. *Sansevieria*) in many countries, including Korea (Farr and Rossman, 2024). The isolate KACC 46835 from *Dracaena trifasciata* was previously identified as *C. sansevieriae* based on ITS sequence and morphological characteristics (Park et al., 2013). This isolate was re-confirmed herein using a combined analysis of ITS, *chs-1*, *his3*, *act*, and *tub2*.

Colletotrichum spaethianum s. str. has been frequently reported from the host genus *Hosta* (syn. *Funkia*), *Hymenocallis* and *Lilium* (Farr and Rossman, 2024). In Korea, *C. spaethianum* was earlier found on *Lilium* sp. (Damm et al., 2009), *Hosta plantaginea* (Cheon and Jeon, 2016), *Convallaria keiskei* (Ahn et al., 2017), *Hosta longipes* (Choi et al., 2024a), and *Polygonatum odoratum* var. *pluriflorum* (Choi et al., 2024b). In KACC, *C. spaethianum* was re-identified from *Hosta longipes*, *H. plantaginea*, and four new host plants, including *Disporum smilacinum*, *Hosta capitata*, *Lilium longiflorum*, and *Muscari armeniacum.* This indicates that *C. spaethianum* is a common *Colletotrichum* species occurring in Korea, especially in the *Asparagaceae* family.

Colletotrichum sublineola is known as one of the most important pathogens of sorghum (*Sorghum bicolor*) in many countries in the world (Abreha et al., 2021; Farr and Rossman, 2024). The fungus infected approximately 20% of sorghum leaves observed in two fields in Korea in 2014

(Choi et al., 2021). The isolate identified as *C. sublineola* in this work is from *Poaceae* (unknown species) and it was deposited in KACC in 1997 (unknown collection date). The occurrence of this pathogen on *Sorghum bicolor* as well as in the *Poaceae* family in Korea should be investigated for early control of the pathogen.

Colletotrichum sydowii was reported from *Sambucus* sp. in Taiwan (Marin-Felix et al., 2017), *Saraca dives* and monocotyledon plant in China (Liu et al., 2022), and leaf of *Albizia julibrissin* in Korea (Cha et al., 2023). *C. sydowii* was significantly distinct from all known species in the phylogeny and did not belong to any *Colletotrichum* species complexes. In this study, the fungus is, as far as we know, the first report on *Boehmeria japonica* (eudicot plant).

Colletotrichum truncatum s. str. was an important pathogen causing anthracnose of numerous plant species with a wide distribution (Damm et al., 2009; Jayawardena et al., 2016). This fungus was reported as a pathogen on important crops in Korea, including *Capsicum annuum*, *Carica papaya*, *Glycine max*, *Raphanus raphanistrum* subsp. *sativus* (syn. *Raphanus sativus*), and *Vigna radiata* (Aktaruzzaman et al., 2018; Choi et al., 2019; Han and Lee, 1995; Kim et al., 2002; Oo and Oh, 2020). Of which, *C. truncatum* was previously identified from *Capsicum max* and *Vigna radiata* based on only morphological characteristics. The isolates of *C. truncatum* from *Glycine max* and a new host *Vigna angularis* in Korea were re-identified herein using a sequence analysis of 6 loci.

Colletotrichum zhaoqingense was first described by Liu et al. (2022) on palm (*Arecaceae*), *Carica papaya* and *Musa* sp. in China, then recorded on *Camellia* spp. and *Cinnamomum camphora* in the country (Sui et al., 2024). The fungal species was newly found in Korea on a common weed *Pueraria montana*. This data supports that *C. zhaoqingense* could have a wide range of hosts and the impact of this fungus is still poorly understood.

The isolate KACC 42402 isolated from *Vicia venosa* was considered as a new species candidate based on molecular data. This taxon is genetically closely related to *C. guizhouense*, *C. lilii*, *C. spaethianum*, and *C. bicoloratum*. To confirm the taxonomic delimitation, more isolates of this taxon need to be collected.

Multi-locus sequence analyses of fungal species conducted in this study confirmed some previously reported confusing combinations, where fungal species were identified using only morphological characteristics such as *C. boninense* on *Euonymus japonicus*; *C. coccodes* on *Solanum lycopersicum*, *S. melongena* and *S. tuberosum*; *C. nigrum* on *Capsicum annuum*; *C. truncatum* on *Capsicum annuum*, *Glycine max*, and *Vigna angularis* (Kim, 1998; Kim and Cho, 1997; Kim et al., 1998, 2002; Lee et al., 2005; Oo and Oh, 2020; Sharma and Kaushal, 1999; The Korean Society of Plant Pathology, 2024). The pathogenicity of most fungal isolates in the current study was not confirmed, except for KACC 46835 (*C. sansevieriae*), which was earlier tested as a pathogen of *Dracaena trifasciata* (Park et al., 2013). They could be pathogens, endophytes or saprobes. However, all accepted fungal species in Table 2 were previously known as plant pathogens, including *C. caudasporum*, *C. sydowii*, and *C. zhaoqingense* (Liu et al., 2022). Some of them were also known as endophytes (*C. boninense*, *C. caudasporum*, *C. liriopes*, and *C. sydowii*) and saprobes (*C. liriopes* and *C. zhaoqingense*) (Jayawardena et al., 2021; Liu et al., 2022; Yang et al., 2011). Endophytic and saprobic lifecycles could play important roles in the ecological adaptation of phytopathogenic fungi to different host plants (Jayawardena et al., 2021; Peres et al., 2005). Some species could switch their lifestyle from endophytic to pathogenic within the same host plants (Photita et al., 2001, 2004). Therefore, the identification of *Colletotrichum* species associated with their host plants is important in biodiversity research and agricultural farming practices, especially in the biological control of anthracnose pathogens. For instance, understanding the diversity of fungal species on a host plant is crucial for resistance breeding programs, and the host range of fungal species will help optimize crop arrangements in intercropping systems to reduce disease infection among crops.

Conflicts of Interest

No potential conflict of interest relevant to this work was reported.

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Electronic Supplementary Material

Supplementary materials are available at The Plant Pathology Journal website (http://www.ppjonline.org/).

Correction

This article was corrected on July 7, 2025, to address a typographical error in the Materials and Methods section and a revision to the Figure 1 legend.

References

Abreha, K. B., Ortiz, R., Carlsson, A. S. and Geleta, M. 2021. Understanding the sorghum: *Colletotrichum sublineola* interactions for enhanced host resistance. *Front. Plant Sci*. 12:641969.

Ahn, G. R., Choi, M. A., Kim, J. E., Seo, E. J., Kim, J. Y. and Kim, S. H. 2017. A report of eighteen unrecorded fungal species in Korea. *Korean J. Mycol.* 45:292-303 (in Korean).

Aktaruzzaman, M., Afroz, T., Lee, Y.-G. and Kim, B.-S. 2018. Post-harvest anthracnose of papaya caused by *Colletotrichum truncatum* in Korea. *Eur. J. Plant Pathol.* 150:259-265.

Bouckaert, R., Vaughan, T. G., Barido-Sottani, J., Duchêne, S., Fourment, M., Gavryushkina, A., Heled, J., Jones, G., Kühnert, D., De Maio, N., Matschiner, M., Mendes, F. K., Müller, N. F., Ogilvie, H. A., du Plessis, L., Popinga, A., Rambaut, A., Rasmussen, D., Siveroni, I., Suchard, M. A., Wu, C.-H., Xie, D., Zhang, C., Stadler, T. and Drummond, A. J. 2019. BEAST 2.5: an advanced software platform for Bayesian evolutionary analysis. *PLoS Comput. Biol*. 15:e1006650.

Cannon, P. F., Damm, U., Johnston, P. R. and Weir, B. S. 2012. *Colletotrichum*: current status and future directions. *Stud. Mycol.* 73:181-213.

Carbone, I. and Kohn, L. M. 1999. A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia* 91:553-556.

Cha, J.-E., Kim, E.-J., Kim, Y.-J. and Eom, A.-H. 2023. Five unrecorded endophytic fungal species in Sordariomycetes from Korea. *Korean J. Mycol.* 51:335-347 (in Korean).

Cheon, W. and Jeon, Y. 2016. First report of anthracnose caused by *Colletotrichum spaethianum* on fragrant plantain lily in Korea. *Plant Dis.* 100:1498.

Cho, S.-E., Lee, D.-H., Kim, C.-W. and Seo, S.-T. 2024. First report of anthracnose on *Juglans mandshurica* caused by *Colletotrichum karsti* in Korea. *J. Plant Pathol*. 106:285-286.

Choi, H.-W., Hong, S. K., Lee, Y. H. and Yoon, Y. N. 2021. First report of *Colletotrichum sublineola* causing anthracnose on *Sorghum bicolor* in South Korea. *Plant Dis*.105:1559.

Choi, H.-W., Kim, J., Hong, S. K. and Lee, Y. K. 2019. Identification and pathogenicity of *Colletotrichum* species causing anthracnose of Korean radish (*Rhaphanus sativus*) in Korea. *Korean J. Mycol*. 47:393-406 (in Korean).

Choi, J.-H., Shin, H.-D. and Choi, Y.-J. 2024a. First report of anthracnose caused by *Colletotrichum spaethianum* on *Hosta longipes* in Korea. *Plant Dis*. 108:1895.

Choi, J.-H., Shin, H.-D. and Choi, Y.-J. 2024b. Anthracnose caused by *Colletotrichum spaethianum* on *Polygonatum odoratum* var. *pluriflorum* in Korea. *Plant Dis*. 108:3656.

Crouch, J. A. 2014. *Colletotrichum caudatum s.l.* is a species complex. *IMA Fungus* 5:17-30.

Crouch, J. A., Clarke, B. B. and Hillman, B. I. 2006. Unraveling evolutionary relationships among the divergent lineages of *Colletotrichum* causing anthracnose disease in turfgrass and corn. *Phytopathology* 96:46-60.

Crouch, J. A., Clarke, B. B., White, J. F. Jr. and Hillman, B. I. 2009. Systematic analysis of the falcate-spored graminicolous *Colletotrichum* and a description of six new species from warm-season grasses. *Mycologia* 101:717-732.

Crous, P. W., Groenewald, J. Z., Risède, J.-M., Simoneau, P. and Hywel-Jones, N. L. 2004. *Calonectria* species and their *Cylindrocladium* anamorphs: species with sphaeropedunculate vesicles. *Stud. Mycol.* 50:415-430.

Damm, U., Cannon, P. F., Liu, F., Barreto, R. W., Guatimosim, E. and Crous, P. W. 2013. The *Colletotrichum orbiculare* species complex: important pathogens of field crops and weeds. *Fungal Divers*. 61:29-59.

Damm, U., Cannon, P. F., Woudenberg, J. H. C., Johnston, P. R., Weir, B. S., Tan, Y. P., Shivas, R. G. and Crous, P. W. 2012. The *Colletotrichum boninense* species complex. *Stud. Mycol.* 73:1-36.

Damm, U., O'Connell, R. J., Groenewald, J. Z. and Crous, P. W. 2014. The *Colletotrichum destructivum* species complex: hemibiotrophic pathogens of forage and field crops. *Stud. Mycol*. 79:49-84.

Damm, U., Woudenberg, J. H. C., Cannon, P. F. and Crous, P. W. 2009. *Colletotrichum* species with curved conidia from herbaceous hosts. *Fungal Divers.* 39:45-87.

Dean, R., Van Kan, J. A. L., Pretorius, Z. A., Hammond-Kosack, K. E., Di Pietro, A., Spanu, P. D., Rudd, J. J., Dickman, M., Kahmann, R., Ellis, J. and Foster, G. D. 2012. The Top 10 fungal pathogens in molecular plant pathology. *Mol. Plant Pathol*. 13:414-430.

Farr, D. F. and Rossman, A. Y. 2024. Fungal Databases, Systematic Mycology and Microbiology Laboratory, ARS, USDA. URL https://fungi.ars.usda.gov/ [8 November 2024].

Glass, N. L. and Donaldson, G. C. 1995. Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Appl. Environ. Microbiol.* 61:1323-1330.

Gu, Q., Chu, S., Huang, Q., Chen, A., Li, L. and Li, R. 2023. *Colletotrichum echinochloae*: a potential bioherbicide agent for control of barnyardgrass (*Echinochloa crus-galli* (L.) Beauv.). *Plants* 12:421.

Guerber, J. C., Liu, B., Correll, J. C. and Johnston, P. R. 2003. Characterization of diversity in *Colletotrichum acutatum sensu lato* by sequence analysis of two gene introns, mtDNA and intron RFLPs, and mating compatibility. *Mycologia* 95:872-895.

Han, K.-S. and Lee, D.-H. 1995. Identification and etiological chracteristics of anthracnose fungi isolated from soybean,

small red bean and green bean. *Korean J. Plant Pathol*. 11:30-38 (in Korean).

Jayawardena, R. S., Bhunjun, C. S., Hyde, K. D., Gentekaki, E. and Itthayakorn, P. 2021. *Colletotrichum*: lifestyles, biology, morpho-species, species complexes and accepted species. *Mycosphere* 12:519-669.

Jayawardena, R. S., Hyde, K. D., Damm, U., Cai, L., Liu, M., Li, X. H., Zhang, W., Zhao, W. S. and Yan, J. Y. 2016. Notes on currently accepted species of *Colletotrichum*. *Mycosphere* 7:1192-1260.

Khodaei, S., Arzanlou, M., Torbati, M. and Eghbali, S. 2019. Novel hosts in the genus *Colletotrichum* and first report of *C. higginsianum* from Iran. *Nova Hedwigia* 108:449-463.

Kim, B. S. 1998. Anthracnose of potato caused by *Colletotrichum coccodes*. *Korean J. Plant Pathol*. 14:543-544.

Kim, J.-H., Jeong, U.-S., Cheong, S.-S., Lee, K.-K., Lee, H.-K. and Lee, W.-H. 2012. Anthracnose of black raspberry caused by *Colletotrichum gloeosporioides*, *C. coccodes*, and *C. acutatum* in Korea. *Res. Plant Dis.* 18:62-64 (in Korean).

Kim, W.-G. and Cho, W.-D. 1997. Black dot root rot of eggplant caused by *Colletotrichum coccodes*. *Korean J. Mycol.* 25:6-9.

Kim, W. G., Jee, H. J. and Cho, W. D. 1998. Black dot root rot of tomato caused by *Colletotrichum coccodes*. *Korean J. Plant Pathol*. 14:209-211.

Kim, Y.-K., Ryu, J.-K., Ryu, J.-D., Lee, S.-Y. and Lee, S.-D. 2002. Soybean sprout rot caused by *Colletotrichum* species. *Res. Plant Dis*. 8:175-178 (in Korean).

Kwon, J.-H. and Kim, J. 2013. First report of anthracnose on *Rohdea japonica* caused by *Colletotrichum liriopes* in Korea. *Plant Dis.* 97:559.

Lee, H. B., Park, J. Y. and Jung, H. S. 2005. Identification, growth and pathogenicity of *Colletotrichum boninense* causing leaf anthracnose on Japanese spindle tree. *Plant Pathol. J*. 21:27-32.

Liu, F., Cai, L., Crous, P. W. and Damm, U. 2013. Circumscription of the anthracnose pathogens *Colletotrichum lindemuthianum* and *C. nigrum*. *Mycologia* 105:844-860.

Liu, F., Hyde, K. D. and Cai, L. 2011. Neotypification of *Colletotrichum coccodes*, the causal agent of potato black dot disease and tomato anthracnose. *Mycology* 2:248-254.

Liu, F., Ma, Z. Y., Hou, L. W., Diao, Y. Z., Wu, W. P., Damm, U., Song, S. and Cai, L. 2022. Updating species diversity of *Colletotrichum*, with a phylogenomic overview. *Stud. Mycol.* 101:1-56.

Marin-Felix, Y., Groenewald, J. Z., Cai, L., Chen, Q., Marincowitz, S., Barnes, I., Bensch, K., Braun, U., Camporesi, E., Damm, U., de Beer, Z. W., Dissanayake, A., Edwards, J., Giraldo, A., Hernández-Restrepo, M., Hyde, K. D., Jayawardena, R. S., Lombard, L., Luangsa-Ard, J., McTaggart, A. R., Rossman, A. Y., Sandoval-Denis, M., Shen, M., Shivas, R. G., Tan, Y. P., van der Linde, E. J., Wingfield, M. J., Wood, A. R., Zhang, J. Q., Zhang, Y. and Crous, P. W. 2017. Genera of phytopathogenic fungi: GOPHY 1. *Stud. Mycol.* 86:99-216.

Moriwaki, J. and Tsukiboshi, T. 2009. *Colletotrichum echinochloae*, a new species on Japanese barnyard millet (*Echinochloa utilis*). *Mycoscience* 50:273-280.

Moriwaki, J., Sato, T. and Tsukiboshi, T. 2003. Morphological and molecular characterization of *Colletotrichum boninense* sp. nov. from Japan. *Mycoscience* 44:47-53.

O'Donnell, K. and Cigelnik, E. 1997. Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. *Mol. Phylogenet. Evol.* 7:103-116.

Oo, M. M. and Oh, S.-K. 2017. New record of anthracnose caused by *Colletotrichum liriopes* on broadleaf liriope in Korea. *Korean J. Mycol.* 45:68-73.

Oo, M. M. and Oh, S.-K. 2020. First report of anthracnose of chili pepper fruit caused by *Colletotrichum truncatum* in Korea. *Plant Dis*. 104:564.

Park, J. H., Han, K. S., Kim, J. Y. and Shin, H. D. 2013. First report of anthracnose caused by *Colletotrichum sansevieriae* on sansevieria in Korea. *Plant Dis*. 97:1510.

Park, K. S. and Kim, C. H. 1992. Identification, distribution and etiological characteristics of anthracnose fungi of red pepper in Korea. *Korean J. Plant Pathol*. 8:61-69.

Peres, N. A., Timmer, L. W., Adaskaveg, J. E. and Correll, J. C. 2005. Lifestyles of *Colletotrichum acutatum*. *Plant Dis.* 89:784-796.

Photita, W., Lumyong, S., Lumyong, P. and Hyde, K. D. 2001. Endophytic fungi of wild banana (*Musa acuminata*) at Doi Suthep Pui National Park, Thailand. *Mycol. Res.* 105:1508-1513.

Photita, W., Lumyong, S., Lumyong, P., McKenzie, E. H. C. and Hyde, K. D. 2004. Are some endophytes of *Musa acuminata* latent pathogens? *Fungal Divers.* 16:131-140.

Sharma, R. and Kaushal, R. P. 1999. Characterization of pathogenic variability in *Colletotrichum truncatum* in Himachal Pradesh. *Indian Phytopathol*. 52:389-392.

Sui, X. N., Guo, M. J., Wang, Q. T., Wang, H. Q., Zhou, H., Huang, X. B., Yu, Z. F. and Hou, C. L. 2024. Taxonomy and phylogeny of *Colletotrichum* on important forest plants in China. *Mycosphere* 15:4569-4743.

Talhinhas, P. and Baroncelli, R. 2023. Hosts of *Colletotrichum*. *Mycosphere* 14:158-261.

Tamura, K., Stecher, G. and Kumar, S. 2021. MEGA11: molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* 38:3022-3027.

Tao, G., Liu, Z.-Y., Liu, F., Gao, Y.-H. and Cai, L. 2013. Endophytic *Colletotrichum* species from *Bletilla ochracea* (Orchidaceae), with descriptions of seven new speices. *Fungal Divers*. 61:139-164.

Thao, L. D., Choi, H., Choi, Y., Mageswari, A., Lee, D. and Hong, S.-B. 2023. Re-identification of *Colletotrichum acutatum* species complex in Korea and their host plants. *Plant Pathol. J.* 39:384-396.

Thao, L. D., Choi, H., Choi, Y., Mageswari, A., Lee, D., Kim, D.-H., Lee, S.-H., Shin, H.-D., Damm, U. and Hong, S.-B. 2024a. The *Colletotrichum destructivum* species complex in

Korea, description of *C. kummerowiae* sp. nov. and neotypification of *C. panacicola*. *Mycol. Prog.* 23:43.

Thao, L. D., Choi, H., Choi, Y., Mageswari, A., Lee, D., Kim, D.-H., Shin, H.-D., Choi, H., Ju, H.-J. and Hong, S.-B. 2024b. Re-identification of *Colletotrichum gloeosporioides* species complex isolates in Korea and their host plants. *Plant Pathol. J.* 40:16-29.

Thao, L. D., Choi, H., Kang, D., Mageswari, A., Lee, D., Kim, D.-H., Choi, I.-Y., Shin, H.-D. and Hong, S.-B. 2024c. Re-identification of Korean isolates in the *Colletotrichum dematium*, *C. magnum*, *C. orchidearum*, and *C. orbiculare* species complexes. *Plant Pathol. J.* 40:425-437.

The Korean Society of Plant Pathology. 2024. List of plant diseases in Korea. 6.2th ed. Korean Society of Plant Pathology, Seoul, Korea.

Tozze, H. J. Jr., Fischer, I. H., Camara, M. P. S. and Massola, N. S. Jr. 2010. First report of *Colletotrichum boninense* infecting yellow passion fruit (*Passiflora edulis* f. *flavicarpa*) in Brazil. *Australas. Plant Dis. Notes* 5:70-72.

White, T. J, Bruns, T., Lee, S. and Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: *PCR protocols: a guide to methods and applications*, eds. by M. A. Innis, D. H. Gelfand, J. J. Sninsky and T. J. White, pp. 315-322. Academic Press, New York, USA.

Yang, Y., Cai, L., Yu, Z., Liu, Z. and Hyde, K. D. 2011. *Colletotrichum* species on *Orchidaceae* in southwest China. *Cryptogam. Mycol.* 32:229-253.

Zhang, Q., Nizamani, M. M., Feng, Y., Yang, Y. Q., Jayawardena, R. S., Hyde, K. D., Wang, Y. and Li, C. 2023. Genome-scale and multi-gene phylogenetic analyses of *Colletotrichum* spp. host preference and associated with medicinal plants. *Mycosphere* 14:1-106.

Zhang, Y. W., Xue, L. H. and Li, C. J. 2018. First report of anthracnose caused by *Colletotrichum higginsianum* on *Rumex acetosa* in China. *Plant Dis*. 102:1174.