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Article

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Endophytic *Fusarium* and allied fungi from *Rosa roxburghii* in China

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Abstract

Fusarium usually implies plant pathogens. However, endophytic *Fusarium* and allied fungi, the non-pathogenic species, share equal importance due to their excellent biosynthetic capacity and wide range of biological activities. *Rosa roxburghii* is an economically important source of medicine and food. We have previously reported on the diversity and antimicrobial activity of endophytic fungi from this plant. Finding several *Fusarium* species that may represent new taxa requires further confirmation using multi-locus phylogenetic analyses combined with morphology. In this study, 60 related isolates were obtained and identified from healthy *R. roxburghii*. Eleven novel species and four new combinations are described and illustrated based on multi-gene phylogenetic analyses of *Fusarium* and thirteen allied genera and morphological comparisons. The new species described herein are *Albonectria guizhouensis*, *Fusarium arbusti*, *F. caulendophyticum*, *F. caulicola*, *F. cili*, *F. qiannanense*, *F. radicigenum*, *F. rosae-roxburghii*, *F. rosendophyticum*, *F. rosiradicicola*, and *Neocosmospora liupanshuiensis*, whereas *N. gannanensis*, *N. passiflorae*, *N. populicola*, and *N. tumidisperma* were introduced as new combinations. In addition, pathogenic and endophytic *Fusarium* and allied fungi associated with Rosaceae are summarized. The results of this study have important implications for accurately identifying *Fusarium*-linked fungi and developing potential applications for these endophytic fungi.

Keywords – Multi-gene phylogeny – Morphology – New taxa – Rosaceae-associated fungi – Taxonomy

Introduction

Fusarium was introduced by Link (1809) with distinctive canoe- or banana-shaped conidia. Since then, the taxonomic framework of the genus has been controversial. In particular, Gräfenhan et al. (2011) and Schroers et al. (2011) provided compelling phylogenetic evidence and introduced several genera in the basal *Fusarium* clade in Nectriaceae. However, Geiser et al. (2013) made opposite arguments for a broader definition of *Fusarium* to avoid introducing additional genera and excluding many agriculturally and medically relevant species. A few years later, O'Donnell et al. (2020) and Geiser et al. (2021) re-supported the broad *Fusarium* concept based on phylogenetic analyses of 19 genes. Subsequently, Crous et al. (2021) re-examined the fusarioid taxa of Nectriaceae based on multi-gene phylogenetic analyses and showed that the Wollenweber concept of *Fusarium* presently accounts for 20 segregated genera. It is also supposed that a broad circumscription of *Fusarium* is vague, without obvious synapomorphies, and does not include all genera in Nectriaceae with fusarium-like macroconidia (Crous et al. 2021). Recent studies have

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shown that the genus *Fusarium* includes 18 recognized species complexes and one undefined species complex, *F. nurragi* (Wang et al. 2019, Crous et al. 2021, Han et al. 2023).

Fusarium and allied fungi, a ubiquitous and cosmopolitan group, are known to be destructive, threatening plants, animals, human health, and food security (Schroers et al. 2011, O'Donnell et al. 2013, Jian et al. 2022, Wang et al. 2022). However, just as every coin has two sides, endophytic *Fusarium* and allied fungi have been extensively used in a wide range of agriculture and medicine for strong bioactivities. Various endophytic *Fusarium* and allied fungi are used to develop bioactive compounds, such as *F. equiseti*, *F. oxysporum*, *F. lateritium*, *F. proliferatum*, *F. redolens* (Toghueo et al. 2020), *Neocosmospora solani* and *Neocosmospora* sp. (Chowdhury et al. 2017, Toghueo et al. 2020, Klomchit et al. 2021), *Albonectria rigidiuscula* (Liu et al. 2016), *Neonectria ramulariae* (Shiono et al. 2012), *Ilyonectria robusta* (Ye et al. 2022), and *Fusicolla violacea* (Li et al. 2021). These bioactive natural products include anticancer agents vinblastine and vincristine (Kumar et al. 2013), taxol (Elavarasi et al. 2012), rohitukine (Kumara et al. 2012); antimicrobial agents fusarithioamide A (Ibrahim et al. 2016), angularly prenylated indole alkaloids (Zhang et al. 2019), beauvericin (Zhang et al. 2016), and antioxidant agents exopolysaccharide (Mahapatra & Banerjee 2013). In addition, endophytic *Fusarium* and allied fungi also exhibit antiviral, antiparasitic, immunosuppressant, immunomodulatory, antithrombotic, and biocontrol properties against nematodes (Toghueo et al. 2020).

Rosa (Rosaceae) is a group of economically important horticultural plants, comprising about 200 species, often used for ornamental, food, and medicine (Yan et al. 2018, Shameh et al. 2019). Several *Rosa* species have been demonstrated to be rich in endophytic fungi. Endophytic communities on *R. multiflora* and *R. multiflora* var. *carnea* investigated with high-throughput sequencing resulted in four fungal phyla, 17 classes, 43 orders, 86 families, 157 genera, and 208 species (Zhao et al. 2018). *Rosa hybrida* colonized at least 24 genera with 30 possible endophytic culturable species (Heinz et al. 2018). Endophytic *Fusarium* and allied fungi from *Rosa* mainly reported *Fusarium*, *Ilyonectria*, and *Thelonectria* (Li et al. 2012, Menkis et al. 2014, Dasari et al. 2015, Heinz et al. 2018, Grunewaldt-Stöcker et al. 2020, Zhang et al. 2021). In these reports, however, almost only molecular phylogeny was used for species identification. Moreover, some *Fusarium* and allied genera have not been identified at the species level, suggesting that many new taxa of *Fusarium* and allied fungi may occur in *Rosa*.

In our previous studies, about 300 strains belonging to more than 100 species were isolated from *R. roxburghii*, an economically important source of medicine and food (Zhang et al. 2021, Zhang et al. 2022a). These findings suggest that several new endophytic *Fusarium* and allied species may be present in *R. roxburghii* and may have moderate to intense antimicrobial activity (Zhang et al. 2021). Therefore, this study aims to further isolate endophytic *Fusarium* and allied fungi from *R. roxburghii* and to combine phylogeny and morphology for identification. The results of this study will lay the foundation for developing bioactive natural products of endophytic *Fusarium* and allied fungi.

Materials & Methods

Sample collection and endophytic fungal isolation

Healthy tissues of *R. roxburghii*, including the roots, stems, leaves, flowers, fruits, and seeds, were collected from three areas in Guizhou Province, China: Guiyang City (27°4′50″ N, 106°29′50″ E), which is a natural environment; Liupanshui City (25°52′52″ N, 104°33′59″ E), and Qiannan District (26°47′4″ N, 107°8′37″ E), which are plantations. The collection dates were April 22, 2020; August 4, 2020; and August 17, 2021, respectively.

Endophytic fungi were isolated from *R. roxburghii* using a previously described method (Kumar et al. 2013). The tissues were rinsed thoroughly with running tap water, followed by washing with double-distilled water, air-drying, fragmenting into small pieces (5–10 mm diam.), and transferring them to a clean bench. The tissue segments were surface sterilized using 75% ethanol for 1 min. Next, the segments were rinsed three times with sterile water. The tissues were then immersed in 1% (w/v) aqueous sodium hypochlorite (NaOCl) for 1–3 minutes, depending on the tissue type (roots 2 min, stems and seeds 3 min, and leaves, fruits, and flowers 1 min), after which they were washed three times with sterile distilled water. Finally, the tissue pieces were blotted dry on sterile filter paper, and the margins were trimmed. Fungal isolation was carried out using six different media: potato dextrose agar (PDA), oatmeal agar (OA), malt extract agar (MEA), Czapek Dox agar (CDA), water agar (WA), and synthetic low nutrient agar (SNA), all supplemented with streptomycin sulfate (0.5 g/L) to prevent bacterial contamination. All plates containing fungi were incubated in the dark at 28 °C for 3 to 7 days. Subsequently, the single hyphal tip was picked and subcultured on PDA plates until pure cultures were obtained. Surface sterilization was monitored using three previously described methods (Zhang et al. 2022a).

The holotype specimens were deposited in the Herbarium of the Department of Plant Pathology, Agricultural College, Guizhou University (HGUP). Ex-type cultures were conserved in the Culture Collection of the Department of Plant Pathology, College of Agriculture, Guizhou University, China (GUCC), and the China General Microbiological Culture Collection Center (CGMCC).

Morphological observations

Cultures were incubated on PDA, OA, and SNA in the dark at 28 ℃. After several days, colony diameters were measured, and colony characteristics were observed and recorded. Macroscopic morphology was examined under a digital microscope (VHX-7000, Keyence). After sporulation, micromorphological features were observed in 25% lactic acid under a Zeiss Axiolab 5 light microscope equipped with an Axiocam 208 camera.

DNA extraction, PCR amplification, and sequencing

DNA of endophytic strains was extracted using the Fungal gDNA Isolation Kit (BW-GD2416, Biomiga, China), following the manufacturer’s instructions, and the products were stored at -20 °C. Primers for polymerase chain reaction (PCR) were provided in Table 1. Generally, annealing at 55 °C for 35 cycles is sufficient for successful amplification. The conditions of *rpb1* need attention: 94 °C 90 s; 5 cycles of 94 °C 45 s, 58 °C 45 s, 72 °C 2 min; 5 cycles of 94 °C 45 s, 57 °C 45 s, 72 °C 2 min; 35 cycles of 94 °C 45 s, 56 °C 45s, 72 °C 2 min; 72 °C 10 min; 10 °C soak (O’Donnell et al. 2010). Amplification products were sequenced by Sangon Biotech (Shanghai, China).

Phylogenetic analyses

All forward and reverse sequences were converted into consensus sequences using BioEdit v. 7.0.9.0 (Hall 1999). All sequences generated in this study were submitted to GenBank. BLASTn searches were performed with ITS sequences to retrieve the closest matches from GenBank. *Fusarium* and allied genera were screened for further study. Recently published sequences have been included in phylogenetic analyses (Supplementary Tables 1, 2). For each locus, sequences were aligned using MAFFT (Katoh & Standley 2013), selecting the “auto” strategy and normal alignment mode, and alignments were manually adjusted where necessary in BioEdit and concatenated in PhyloSuite v. 1.2.2 (Zhang et al. 2020a). Phylogenetic analyses were inferred using Maximum likelihood (ML) and Bayesian inference (BI) methods. The best-fit substitution models under the Bayesian Information Criteria (BIC) for ML analyses and the Akaike Information Criterion (AIC) for BI analyses were selected using ModelFinder (Kalyaanamoorthy et al. 2017). The ML analyses were inferred using IQ-TREE (Nguyen et al. 2014) under the edge-linked partition model for 100,000 ultrafast bootstraps (Minh et al. 2013). The BI analyses were done using MrBayes 3.2.6 (Ronquist et al. 2012) under a partition model (2 parallel runs, 10,000,000 generations), in which the preliminary 25% of the sampled data were discarded as burn-in. MAFFT, ModelFinder, IQ-TREE, and MrBayes were integrated into PhyloSuite (Zhang et al. 2020a). Trees were visualized with FigTree v.1.4.3 (Rambaut 2014). ML bootstrap support values

(BS) over 50% and Bayesian posterior probabilities (PP) over 0.90 (BS/PP) were displayed near the branches in Adobe Illustrator CC 2019.

Table 1 Primers information of PCR amplification of *Fusarium* and allied fungi.

Genes	Primers (Direction)	Sequence (5′–3′)	References
ACT*	TRIACT1 (F)	TGGCACCACACCTTCTACAATGA	Samuels et al. (2006)
	TRIACT2 (R)	TCTCCTTCTGCATACGGTCGGA	
ITS	ITS5 (F[1])	GGAAGTAAAAGTCGTAACAAGG	White et al. (1990)
	ITS4 (R[2])	TCCTCCGCTTATTGATATGC	
LSU	LR0R (F)	ACCCGCTGAACTTAAGC	Vilgalys & Sun (1994)
	LR5 (R)	ATCCTGAGGGAAACTTC	Vilgalys & Hester (1990)
SSU	NS1 (F)*	GTAGTCATATGCTTGTCTC	Gargas & Taylor (1992)
	SR7 (R)*	GTTCAACTACGAGCTTTTTAA	
acl1	230up (F)	AGCCCGATCAGCTCATCAAG	Gräfenhan et al. (2011)
	1220low (R)	CCTGGCAGCAAGATCVAGGAAGT	
CaM	CAL-228f (F)	GAGTTCAAGGAGGCCTTCTCCC	Carbone & Kohn (1999)
	CAL-2Rd (R)	TGRTCNGCCTCDCGGATCATCTC	Quaedvlieg et al. (2011)
rpb1	Fa (F)	CAYAARGARTCYATGATGGGWC	O’Donnell et al. (2010)
	G2R (R)	GTCATYTGDGTDGCDGGYTCDCC	
	RPB1a (F)*	CAYCCWGGYTTYATCAAGAA	Castlebury et al. (2004)
	RPB1c (R)*	CCNGCDATNTCRTTRTCCATRTA	
rpb2	RPB2-5f2 (F)	GGGGWGAYCAGAAGAAGGC	Reeb et al. (2004)
	fRPB2-7cr (R)	CCCATRGCTTGYTTRCCCAT	Liu et al. (1999)
	RPB2-7cf (F)	ATGGGYAARCAAGCYATGGG	
	RPB2-11aR (R)	GCRTGGATCTTRTCRTCSACC	
tef1	EF-1 (F)	ATGGGTAAGGARGACAAGAC	O’Donnell et al. (1998)
	EF-2 (R)	GGARGTACCAGTSATCATG	
	EF-728 (F)*	CATCGAGAAGTTCGAGAAGG	Carbone & Kohn (1999)
	EF-1567 (R)*	ACHGTRCCRATACCACCRAT	
tub2	T1 (F)	AACATGCGTGAGATTGTAAGT	O’Donnell & Cigelnik (1997)
	TUB4RD (R)	CCRGAYTGRCCRAARACRAAGTTGTC	Woudenberg et al. (2009)
	T2 (R)*	TAGTGACCCTTGGCCCAGTTG	O’Donnell & Cigelnik (1997)

[1]F: Forward, [2]R: Reverse; *only for *Thelonectria* in this study.

Genealogical concordance phylogenetic species recognition analyses

Fungal species that are phylogenetically related but ambiguous are often analyzed by performing a pairwise homoplasy index (PHI) test with the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) model (Quaedvlieg et al. 2014, Sun et al. 2023). The PHI test was conducted in SplitsTree4 (v. 4.19.0) using LogDet transformation and split decomposition options to determine recombination level (Huson & Bryant 2006, Quaedvlieg et al. 2014). If PHI is above the 0.05 threshold ($p > 0.05$), it indicates that no significant recombination is present in the dataset.

Results

Molecular phylogeny

The genus-level phylogeny of *Fusarium* and allied fungi was investigated based on a combined dataset of ITS, LSU, *rpb1*, *rpb2*, and *tef1* gene region, which consisted of 572 bp for ITS, 840 bp for LSU, 1581 bp for *rpb1*, 897 bp for *rpb2*, and 819 bp for *tef1*. A total of 235 isolates were used for ML and BI analyses, and the resulting tree was rooted with *Nectria cinnabarina* (CBS 125165). For ML analysis, the best-fit models for ITS, LSU, *rpb1*, *rpb2*, and *tef1* were GTR+F+I+G4, TIM2e+I+G4, TIM3e+R5, TIM3e+R5, and TIM3+F+R4, respectively. For BI analysis, the corresponding best-fit models were GTR+F+I+G4, GTR+F+I+G4, SYM+I+G4, SYM+I+G4, and GTR+F+I+G4, respectively. The topology is consistent with the phylogeny proposed by Crous et al. (2021). The phylogeny showed that 60 isolates were distributed over seven *Fusarium* species complexes and four allied genera (*Albonectria*, *Luteonectria*, *Neocosmospora*, and *Thelonectria*) (Fig. 1).

Phylogenetic analyses of several *Fusarium* species complexes and allied genera were conducted respectively using different datasets. The phylogenetic tree of the *F. incarnatum-equiseti* species complex was constructed by combining ITS, *tef1*, *CaM*, *rpb1*, and *rpb2* sequence data from 108 strains (Fig. 7), and the tree topology is similar to those in previous studies (Wang et al. 2022, Han et al. 2023). Following the description of Wang et al. (2022), a phylogenetic tree of the *F. oxysporum* species complex was generated in this study by combining *CaM*, *rpb1*, *rpb2*, *tef1*, and *tub2* sequence data from 124 strains (Fig. 11), and similar phylogenetic results were observed. Also, the phylogenetic tree of the *F. tricinctum* species complex was obtained in this study by combining ITS, *rpb1*, *rpb2*, *tef1*, and *tub2* sequence data from 59 strains (Fig. 17), and the topology of ML and BI trees was similar to that of Han et al. (2023). For the species-rich *Neocosmospora*, a phylogenetic tree was generated in this study combining *acl1*, *CaM*, ITS, LSU, *rpb1*, *rpb2*, and *tef1* sequence data from 196 strains as previously described (Crous et al. 2021), and a similar topology was obtained (Fig. 21). Finally, a phylogenetic tree of *Thelonectria* was generated based on the previously described (Salgado-Salazar et al. 2016), combining ACT, ITS, LSU, *rpb1*, *rpb2*, SSU, *tef1*, and *tub2* sequence data from 130 strains, which was topologically consistent with the previous ones (Fig. 27).

As a result of phylogenetic analyses and morphological features, the 60 selected isolates were identified into 25 species, including 14 known species and 11 new species. *Fusarium* comprised the majority with 15 species, while *Albonectria*, *Luteonectria*, *Neocosmospora*, and *Thelonectria* had one or two species present. Notably, additional analyses revealed four new *Neocosmospora* combinations.

Taxonomy

Albonectria Rossman & Samuels

Albonectria was described by Rossman et al. (1999), with *A. rigidiuscula* designated as the type species. The genus encompasses species with white to pale yellow ascomata that are associated with *Fusarium* anamorph (Lombard et al. 2015). According to Index Fungorum (2023), *Albonectria* currently comprises four species, namely *A. albida*, *A. albosuccinea*, *A. rigidiuscula*, and *A. verrucosa*, where *A. albida* was transferred to *Luteonectria* (Crous et al. 2021). *Albonectria rigidiuscula* can cause a variety of plant diseases such as cocoa green point gall (Vicente et al. 2012), *Magnolia denudata* cancer (Wang et al. 2015), and apple rot (Lee et al. 2017), while endophytic *A. rigidiuscula* exhibited antimicrobial activity against *Bacillus subtilis*, *Sclerotinia sclerotiorum*, and *Staphylococcus aureus* (Liu et al. 2016). Two strains of endophytic *Albonectria* were isolated from *R. roxburghii* in this study (Fig. 1).

Albonectria guizhouensis H. Zhang & Y.L. Jiang, sp. nov. Fig. 2

Index Fungorum number: IF900485; Facesoffungi numbers: FoF 14969

Etymology – Name refers to the location where the fungus was collected, Guizhou, China.

Endophytic in roots of *R. roxburghii* in China. Sexual morph: not observed. Asexual morph: *Sporodochia* yellow, formed on SNA. *Sporodochial conidiophores* often reduced to single phialides. *Sporodochial conidiogenous cells* monophialidic or polyphialidic, cylindrical to subcylindrical, hyaline, smooth, thick-walled, straight to slightly curved, tapering towards the apex, periclinal thickening and collarette inconspicuous, 17–71.5 × 5–7 µm (av. = 51.5 × 6.1 µm, n = 10). *Sporodochial macroconidia* curved with parallel walls, apical cell curved to blunt; basal cell papillate, poorly developed to well-developed, foot-shaped, 5–7-septate (mostly 7-septate), hyaline, smooth, thin-walled: 5-septate macroconidia 68.5–77.5 × 5.5–7 µm (av. = 73.6 × 6.2 µm, n = 30); 6-septate macroconidia 68–82 × 5.5–7.5 µm (av. = 76 × 6.3 µm, n = 30); 7-septate macroconidia

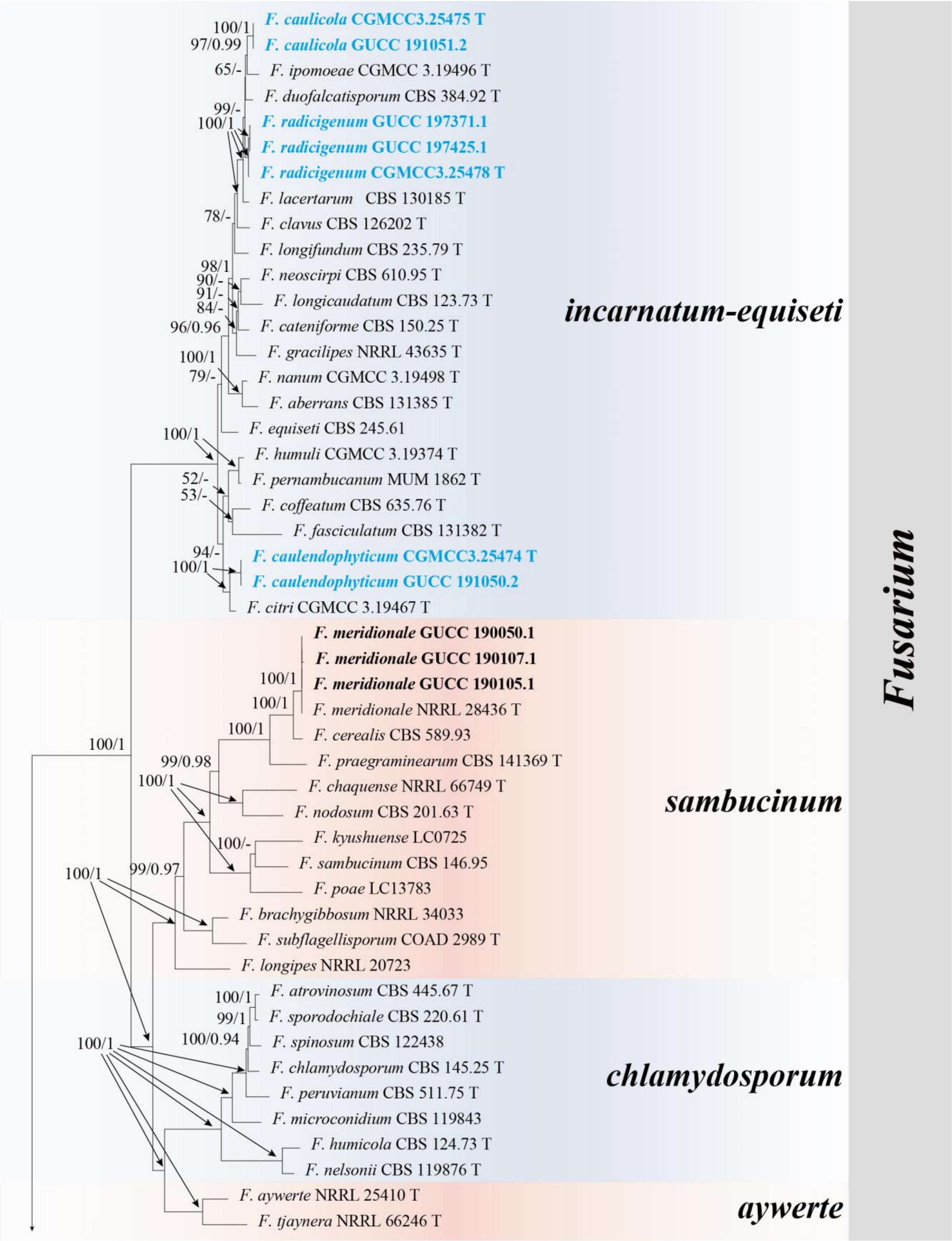
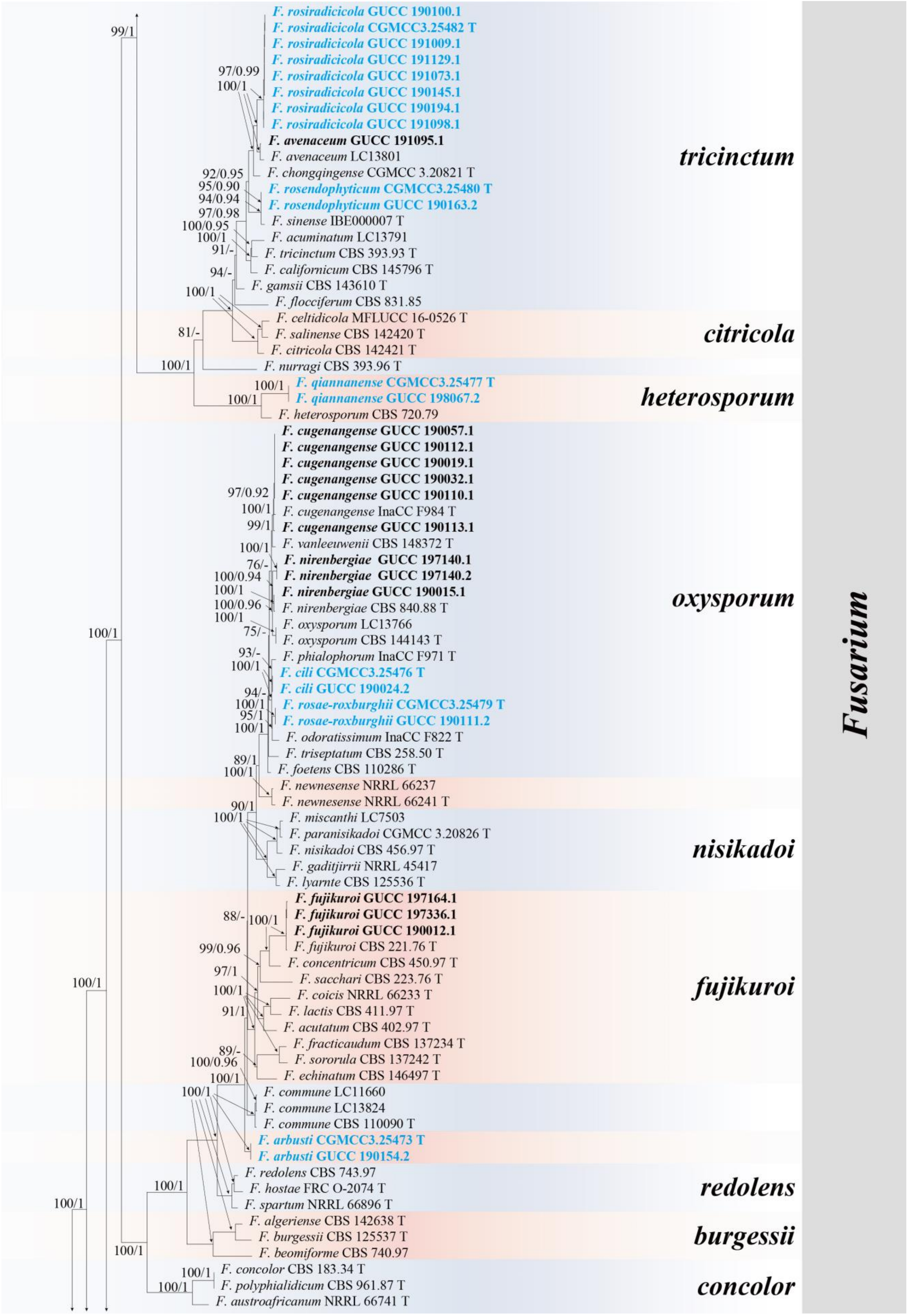


Figure 1 – Phylogenetic relationships of several species complexes in *Fusarium* and allied fungi. The phylogenetic tree was generated using the maximum likelihood (ML) method by combining ITS, LSU, *rpb1*, *rpb2*, and *tef1* sequence data from 235 strains. The tree is rooted with *Nectria cinnabarina* (CBS 125165). ML bootstrap support values > 50% (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near nodes (BS/PP). Strains isolated in this study are **bold**. New species and combinations are shown in bold blue and blue, respectively. **T** holotype or ex-type.



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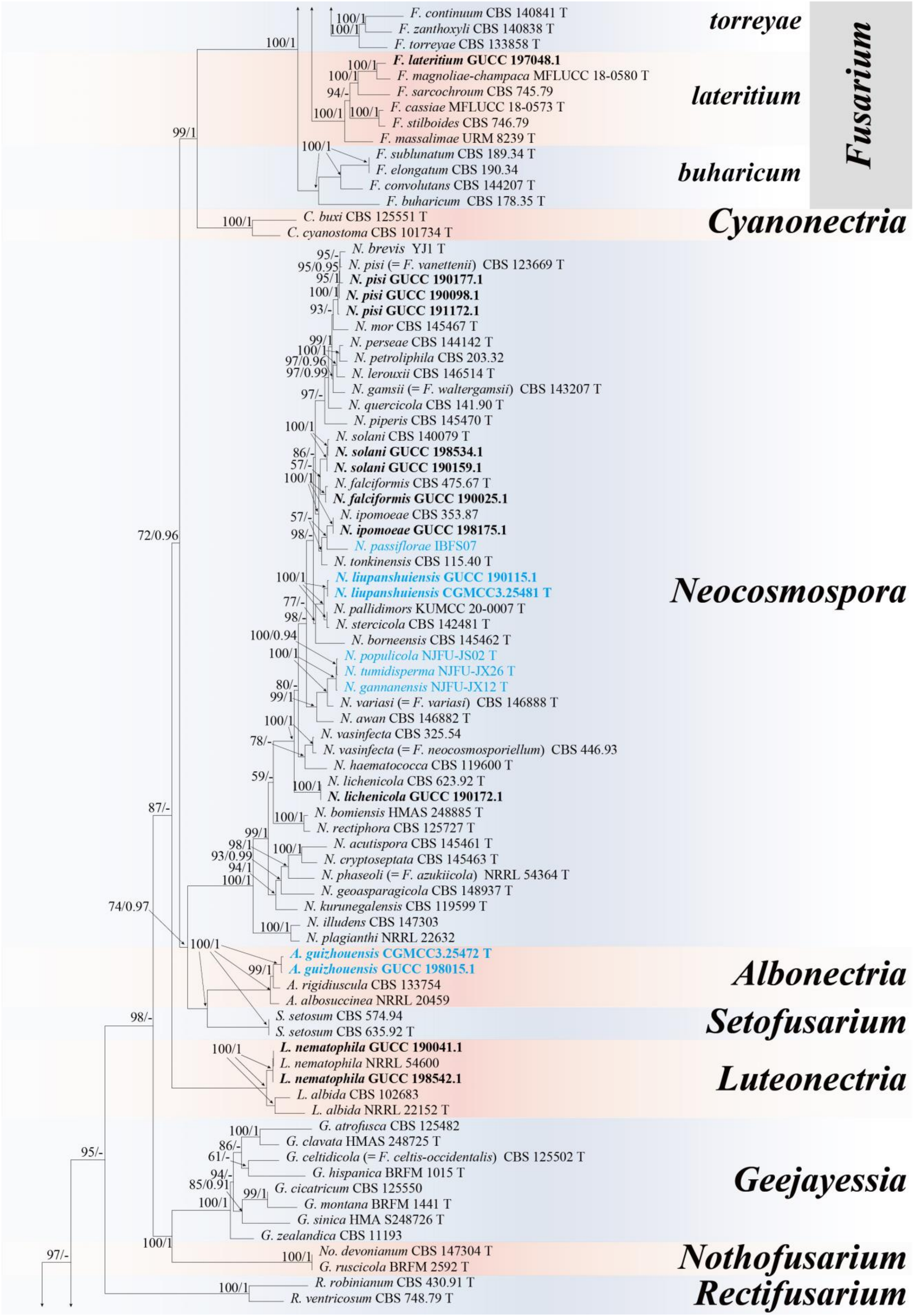

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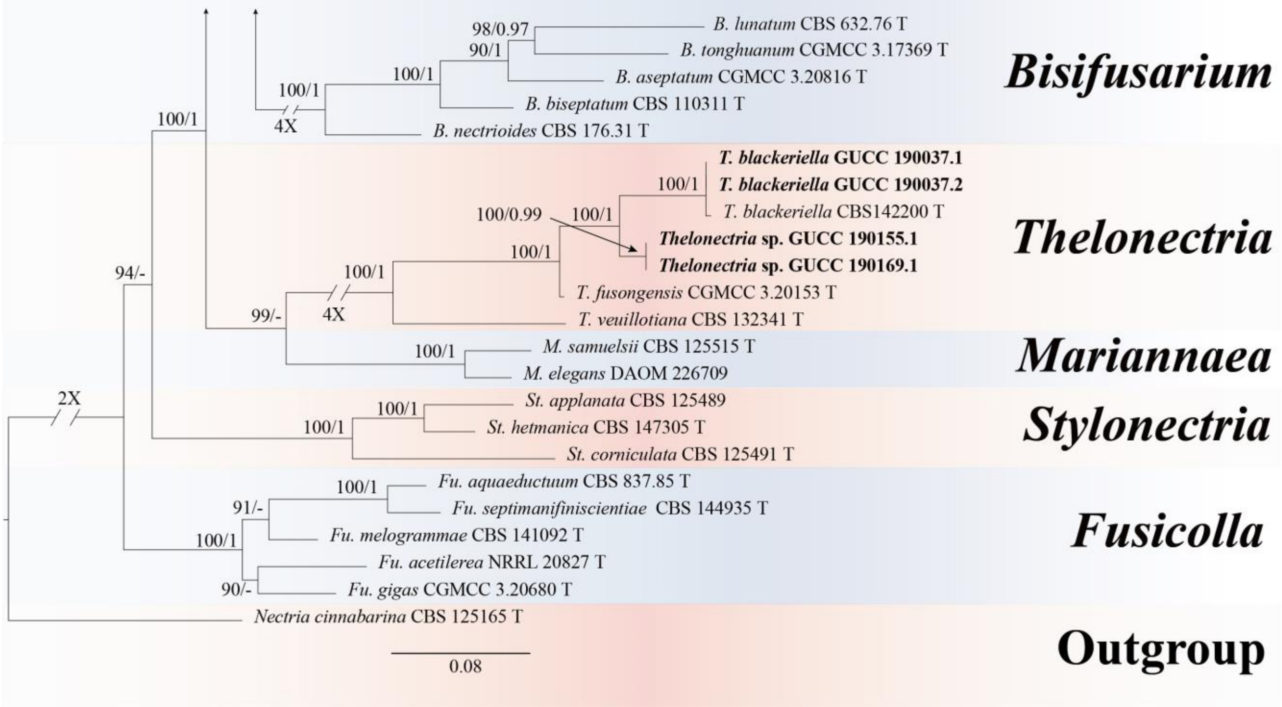

Figure 1 – Continued.

61.5–89.5 × 5.5–7.5 µm (av. = 80.1 × 6.4 µm, n = 30). *Conidiophores* on aerial mycelium unbranched, often reduced to single phialides. *Aerial conidiogenous cells* monophialidic, straight or slightly curved, cylindrical, 4–34 × 1.5–3.5 µm (av. = 17 × 2.2 µm, n = 10), hyaline, smooth- and thin-walled, periclinal thickening and collarette inconspicuous. *Aerial microconidia* forming small false heads on tips of phialides, hyaline, slightly rough-walled, thin-walled, straight, oblong, apex obtuse, base truncate, aseptate, 5–13.5 × 2–4 µm (av. = 8.4 × 2.8 µm, n = 30). *Chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 52 mm diam. after 12 days in the dark at 28 ℃, flat, dense, light brown in the center, white toward the margin, aerial mycelium floccose, round, with irregular edge, aerial mycelia abundant, and reverse light brown. On OA attaining 52 mm diam. after 12 days, buff to yellow, flat, margin entire, with concentric rings, abundant aerial mycelium, and reverse concolorous. On SNA attaining 52 mm diam. after 12 days, hyaline to pale grey, with sparse aerial mycelium, slightly reddish in the center, and reverse same color. Pigment and odor absent.

Material examined – China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang (HGUP198014, holotype), ex-type living culture: GUCC 198014.1 = CGMCC3.25472; other living culture: GUCC 198015.1.

Notes – Two strains (CGMCC3.25472 and GUCC 198015.1) isolated from *R. roxburghii* in this study, *A. rigidiuscula* (CBS 133754), and *A. albosuccinea* (NRRL 20459) clustered as a distinct clade (Fig. 1). Our collections are phylogenetically closer to *A. rigidiuscula* with high statistical support (BS = 99%, PP = 1.00), sharing 98.13% (471/480, no gaps) sequence similarity on ITS, 98.84% (425/430, no gaps) on LSU, 98.19% (761/775, one gap) on *rpb1*, 97.51% (783/803, no gaps) on *rpb2*, and 98.29% (518/527, one gap) on *tef1*. Other genes are missing for *A. rigidiuscula*. Morphologically, the two species differ in the shape of aerial conidiophores (unbranched in *A. guizhouensis* vs. branched in *A. rigidiuscula*), the number of septa and macroconidial dimensions (5–7-septate, 5-septate 68.5–77.5 × 5.5–7 µm, 6-septate 68–82 × 5.5–7.5 µm, 7-septate 61.5–89.5 × 5.5–7.5 µm in *A. guizhouensis* vs. 7–10-septate, 55–130 × 6–10 µm in *A. rigidiuscula*), the size of aerial conidiogenous cells (4–34 × 1.5–3.5 µm, av. = 17 × 2.2 µm in *A. guizhouensis* vs. 28–36 × 4–5 µm in *A. rigidiuscula*), the aerial microconidial organization (microconidia arranged in false heads in *A. guizhouensis* vs. microconidia formed in chains in *A. rigidiuscula*), and the number of microconidial septa (aseptate in *A. guizhouensis* vs. 0–1-septate in *A. rigidiuscula*) (Rossman et al. 1999, Crous et al. 2021). Furthermore, the PHI test showed that there is no significant recombination (p = 1.0 > 0.05) between *A. guizhouensis* and its closely related taxa (Fig. 3). Thus, *A. guizhouensis* is introduced as a new species.

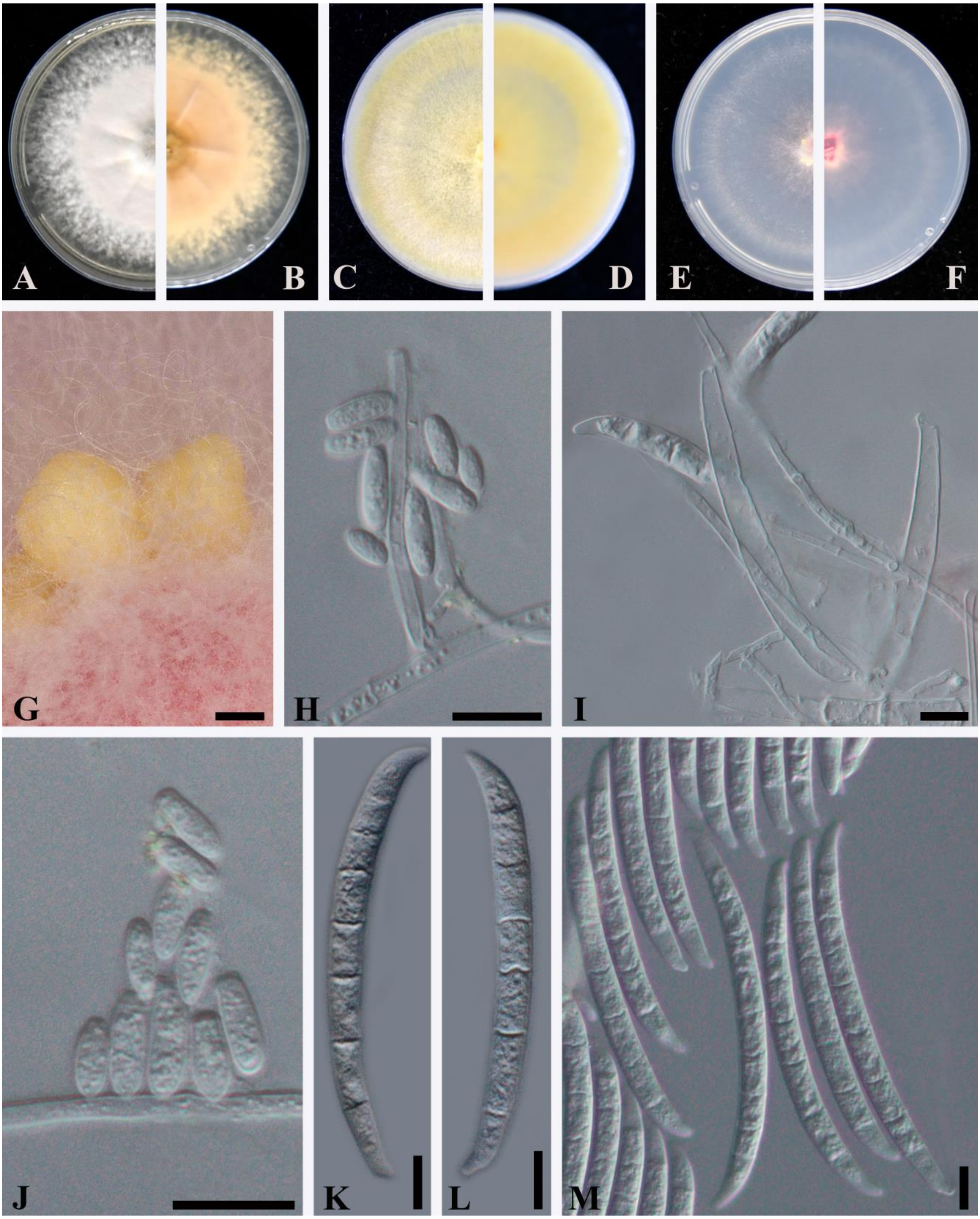

Figure 2 – *Albonectria guizhouensis* (ex-type culture CGMCC3.25472). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–I Aerial and

sporodochial conidiophores and conidiogenous cells. J Microconidia. K–M Macroconidia. Scale bars: G = 500 µm, H–M = 10 µm.

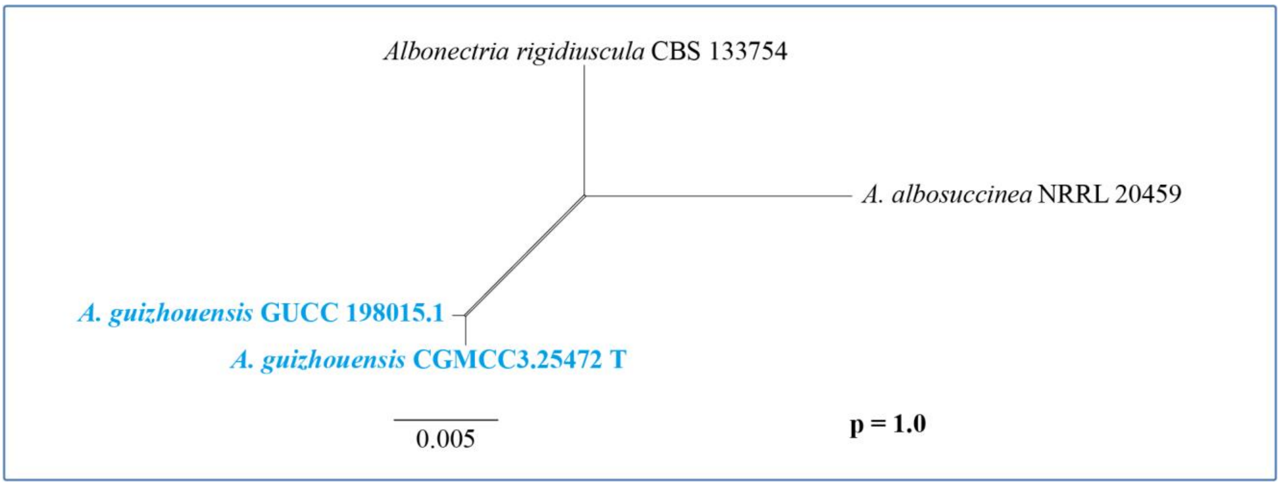

Figure 3 – Results of the pairwise homoplasy index (PHI) test of new *Albonectria* species and their closely related species. New taxa are printed in bold blue.

Fusarium Link

Fusarium, typified by *F. sambucinum*, is diagnostically characterized as dark blue to black perithecia that produce clavate asci; asci bears ellipsoidal to cylindrical 1- to multiseptate ascospores; asexual morphs, conidiophores arising from aerial hyphae, mono- and/or polyphialides; conidiogenous cells produce micro- and macroconidia, sometimes mesoconidia or only macroconidia are produced in sporodochia, and chlamydospores form in hyphae (Crous et al. 2021). Index Fungorum (2023) lists 1757 species names in *Fusarium*, while many species have been transferred to other genera. Many *Fusarium* species are responsible for causing disease in economically important plants, with about 80% of cultivated crops suffering from one or more *Fusarium* diseases (Wingfield et al. 2018). However, some endophytic *Fusarium* strains may benefit certain hosts (Hill et al. 2022). In the present study, 42 strains of endophytic *Fusarium* were isolated from *R. roxburghii* and identified as 15 species based on multigene phylogenetic analyses (Fig. 1).

Fusarium arbusti H. Zhang & Y.L. Jiang, sp. nov. Fig. 4

Index Fungorum number: IF900494; Facesoffungi numbers: FoF 14970

Etymology – Name refers to the plantation from which the species was isolated.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, arising from aerial hyphae, solitary, unbranched, often reduced into conidiogenous cells. *Conidiogenous cells* monophialidic, hyaline, lateral, subcylindrical, tapering towards the apex, straight or slightly curved, smooth to rough, thin-walled, collarette and periclinal thickening inconspicuous, 1–23.5 × 1–3 µm (av. = 10.4 × 2.3 µm, n = 10). *Microconidia* solitary or forming false heads on tips of monophialides, sometimes produced directly on mycelium, hyaline, aseptate, oval to subcylindrical, straight to curved, ends obtuse, guttulate, 4.5–15 × 1.5–3 µm (av. = 7.7 × 2.4 µm, n = 30); *Macroconidia* slender with no significant curvature to slightly curved, slightly narrowing towards each end, apical cell blunt; basal cell obtuse, not foot-shaped, 0–2-septate (mostly aseptate), hyaline, guttulate, thin- to thick-walled; aseptate macroconidia 16–31.5 × 2–4.5 µm (av. = 20.9 × 3.1 µm, n = 30); 1-septate macroconidia 17.5–26 × 3–4.5 µm (av. = 23.3 × 3.7 µm, n = 30); 2-septate macroconidia 25–37.5 × 2.5–4.5 µm (av. = 28.1 × 3.2 µm, n = 30). *Chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 55 mm diam. after 14 days in the dark at 28 °C, white, round, raised, fluffy, cottony, irregular margin, colonies fertile, with abundant aerial hyphae, and reverse white to pale pink. On OA attaining 50 mm diam. after 14 days, whitish to light pink, cottony, dense, margin irregular, aerial mycelia abundant, and reverse concolorous. On SNA attaining 50 mm diam. after 14 days, greyish white, flat, aerial mycelia sparse, margin entire, and reverse concolorous. Pigment and odor absent.

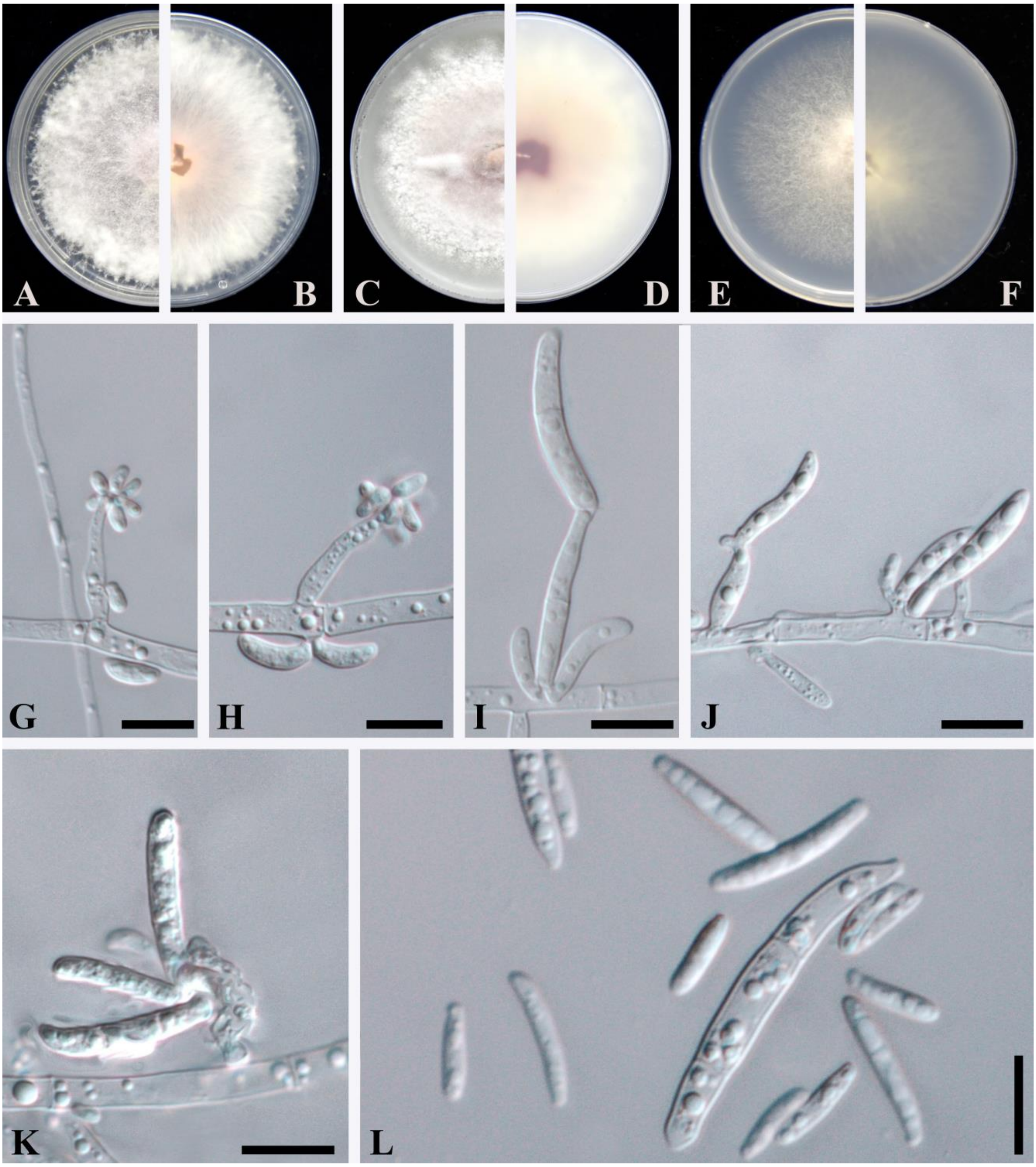

Figure 4 – *Fusarium arbusti* (ex-type culture CGMCC3.25473). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–K Aerial conidiophores and conidiogenous cells. L Aerial microconidia and macroconidia. Scale bars: G–L = 10 µm.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August

2020, H. Zhang (HGUP190154, holotype), ex-type living culture: GUCC 190154.1 = CGMCC3.25473; other living culture: GUCC 190154.2.

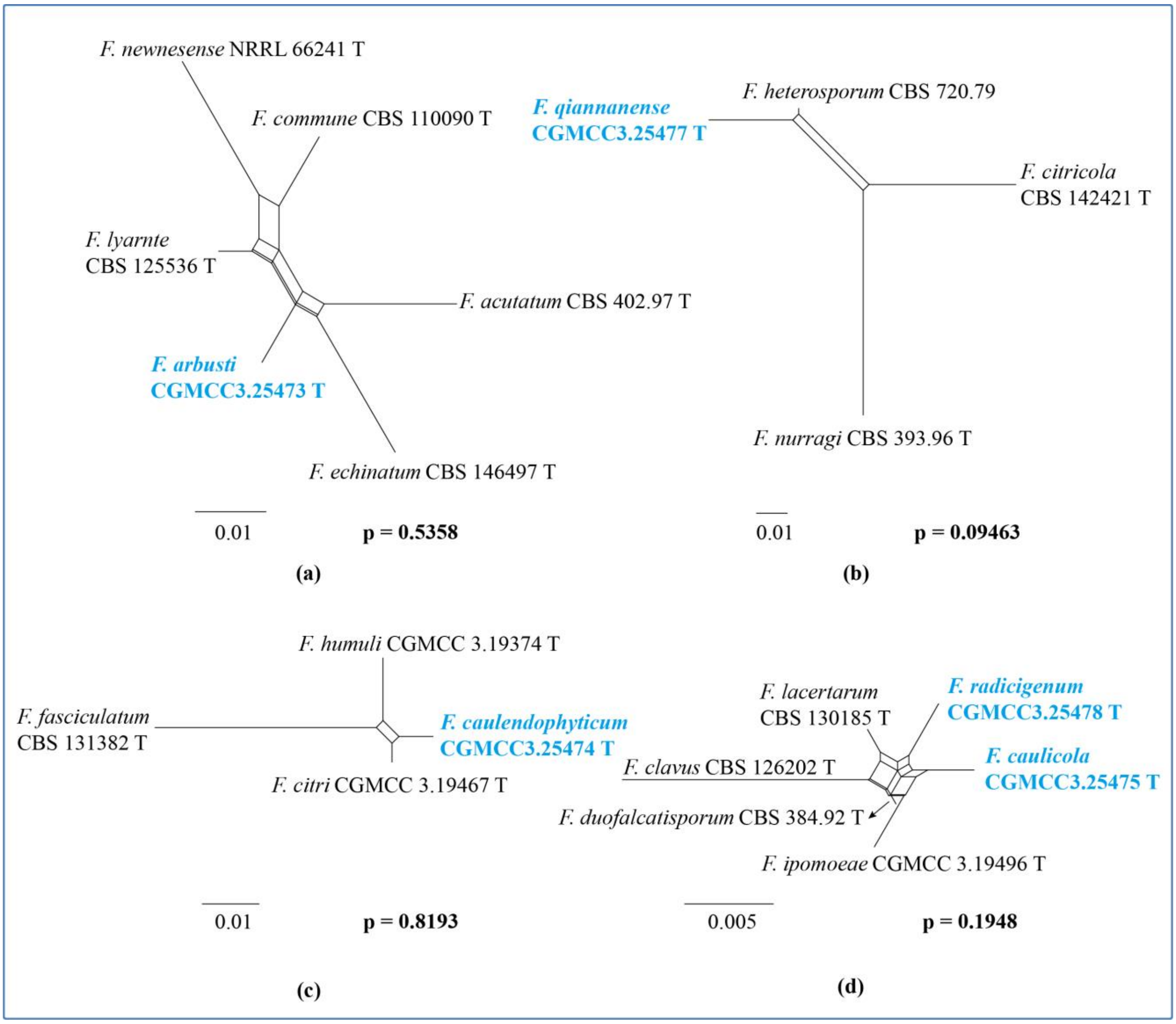

Figure 5 – Results of the pairwise homoplasy index (PHI) test of new *Fusarium* species and their closely related species. New taxa are printed in bold blue.

Notes – Phylogenetic analyses revealed that *F. arbusti* is located in a distinct clade with high statistical support (BS = 100%, PP = 1.00) but is closely related to *F. commune* (Fig. 1). The *tef1* sequence of *F. arbusti* shares 95.64% (504/527, 3 gaps) similarity to *F. commune* (ITS, LSU, *rpb1*, and *rpb2* are missing for the ex-type *F. commune*). Morphologically, *F. arbusti* differs from *F. commune* in having different shapes of conidiogenous cells (monophialidic and subcylindrical in *F. arbusti* vs. mono- to polyphialidic and sub-fusiform in *F. commune*), microconidial organization (microconidia solitary, forming false heads, or produced directly on the mycelium in *F. arbusti* vs. solitary or 2–3 microconidia arising from simple polyphialide in *F. commune*), shorter monophialides (up to 23.5 µm long in *F. arbusti* vs. up to 60 µm long in *F. commune*), macroconidial formations (from hyphae in *F. arbusti* vs. borne in sporodochia in *F. commune*), and macroconidial shapes (0–2-septate, mostly aseptate in *F. arbusti* vs. 3-septate or 5-septate in *F. commune*; guttulate in *F. arbusti* vs. smooth in *F. commune*; slender with no significant curvature to slightly curved, apical cell blunt, basal cell obtuse, not foot-shaped in *F. arbusti* vs. typically fusiform with a slightly curved apical cell and a foot-shaped basal cell in *F. commune*). In addition, chlamydospores were not observed in *F. arbusti*, but are commonly observed in

F. commune (Skovgaard et al. 2003). As shown in Fig. 5a, the result of PHI test also showed that there is no obvious recombination (p = 0.5358 > 0.05) between *F. arbusti* and its closely related taxa. Therefore, we introduce *F. arbusti* as a new species.

Fusarium heterosporum species complex

Fusarium qiannanense H. Zhang & Y.L. Jiang, sp. nov. Fig. 6

Index Fungorum number: IF900486; Facesoffungi numbers: FoF 14971

Etymology – Name refers to the location where the fungus was collected, Qiannan Districts, Guizhou Province, China.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* light yellow, formed abundantly on SNA. *Sporodochial conidiophores* 2–3 branched, bearing terminal whorls of 2–4 monophialides. *Sporodochial conidiogenous cells* polyphialidic, cylindrical to subcylindrical, hyaline, smooth, thin-walled, straight to slightly curved, periclinal thickening inconspicuous, with slightly flared collarette, 14.5–21 × 2–3 μm (av. = 17.4 × 2.3 μm, n = 10). *Sporodochial macroconidia* moderately curved, sometimes with no significant curvature, slender, tapering towards the basal part, apical cell curved, elongated, and tapered; basal cell poorly developed to well-developed, foot-shaped, 0–5-septate (mostly 3–4-septate), hyaline, verrucae, thin-walled: aseptate macroconidia 15–21.5 × 2–3 μm (av. = 18.1 × 2.4 μm, n = 30); 1-septate macroconidia 21–37 × 2–3 μm (av. = 27.7 × 2.5 μm, n = 30); 2-septate macroconidia 27–41.5 × 2–3 μm (av. = 37.1 × 2.7 μm, n = 30); 3-septate macroconidia 37–48 × 2–3 μm (av. = 42.9 × 2.5 μm, n = 30); 4-septate macroconidia 39–49.5 × 2–3 μm (av. = 45.5 × 2.5 μm, n = 30); 5-septate macroconidia 47–55 × 2–3 μm (av. = 51 × 2.6 μm, n = 30). *Conidiophores* on aerial mycelium unbranched, often reduced to conidiogenous cells. *Aerial conidiogenous cells* monophialidic, 5.5–18 × 1.5–3 μm (av. = 11.3 × 2.4 μm, n = 10), hyaline, smooth- and thin-walled, with conspicuous periclinal thickening and inconspicuous collarettes. *Aerial macroconidia* straight to slightly curved, tapering towards the basal part, apical cell blunt to inconspicuously papillate, basal cell obtuse to poorly developed, foot-shaped, 1–3-septate, hyaline, thin-walled, verrucae; 1-septate macroconidia 12.5–22.5 × 1.5–3 μm (av. = 17.4 × 2.1 μm, n = 30); 2-septate macroconidia 19.5–22 × 1.5–2.5 μm (av. = 20.1 × 2.1 μm, n = 30); 3-septate macroconidia 17.5–31 × 1.5–3 μm (av. = 25.7 × 2.3 μm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 52 mm diam. after 12 days in the dark at 28℃, off-white, raised, flocculent, round, with irregular edge, aerial mycelia abundant, and reverse off-white. On OA attaining 55 mm diam. after 12 days, grey, flat, margin entire, moderate aerial mycelium, and reverse grey. On SNA attaining 50 mm diam. after 12 days, white, with sparse to moderate aerial mycelium, slightly raised center, and reverse same color. Pigment and odor absent.

Material examined – China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang (HGUP198067, holotype), ex-type living culture: GUCC 198067.1 = CGMCC3.25477; other living culture: GUCC 198067.2.

Notes – Phylogenetically, *F. qiannanense* forms a sister clade to *F. heterosporum* with high statistical support (BS = 100%, PP = 1.00), belonging to a separate clade (Fig. 1). *Fusarium qiannanense* differs from *F. heterosporum* by having 97.66% (501/513, 3 gaps) similarity in ITS, 96.11% (1506/1567, no gaps) similarity in *rpb1*, and 96.67% (872/902, no gaps) similarity in *rpb2* sequences. Other genes are missing for *F. heterosporum* except LSU. Morphologically, the two species are distinguished based on sporodochial conidiogenous cells (polyphialidic of *F. qiannanense* vs. monophialidic of *F. heterosporum*), the number of septa in sporodochial macroconidia (0–5 septa of *F. qiannanense* vs. 3–5 septa of *F. heterosporum*), and the length of 3-septate sporodochial macroconidia (37–48 μm, av. = 42.9 μm of *F. qiannanense* vs. 20–30 μm of *F. heterosporum*). Additionally, distinct morphology was observed in the aerial macroconidia of *F. qiannanense* compared to its sporodochial macroconidia, while no significant differences were found in *F. heterosporum* (Leslie & Summerell 2006, Crous et al. 2021). Moreover, the PHI test on

F. *qiannanense* showed no significant recombination (p = 0.09463 > 0.05) between *F*. *qiannanense* and its closely related taxa as shown in Fig. 5b. Thus, *F*. *qiannanense* is introduced as a new species.

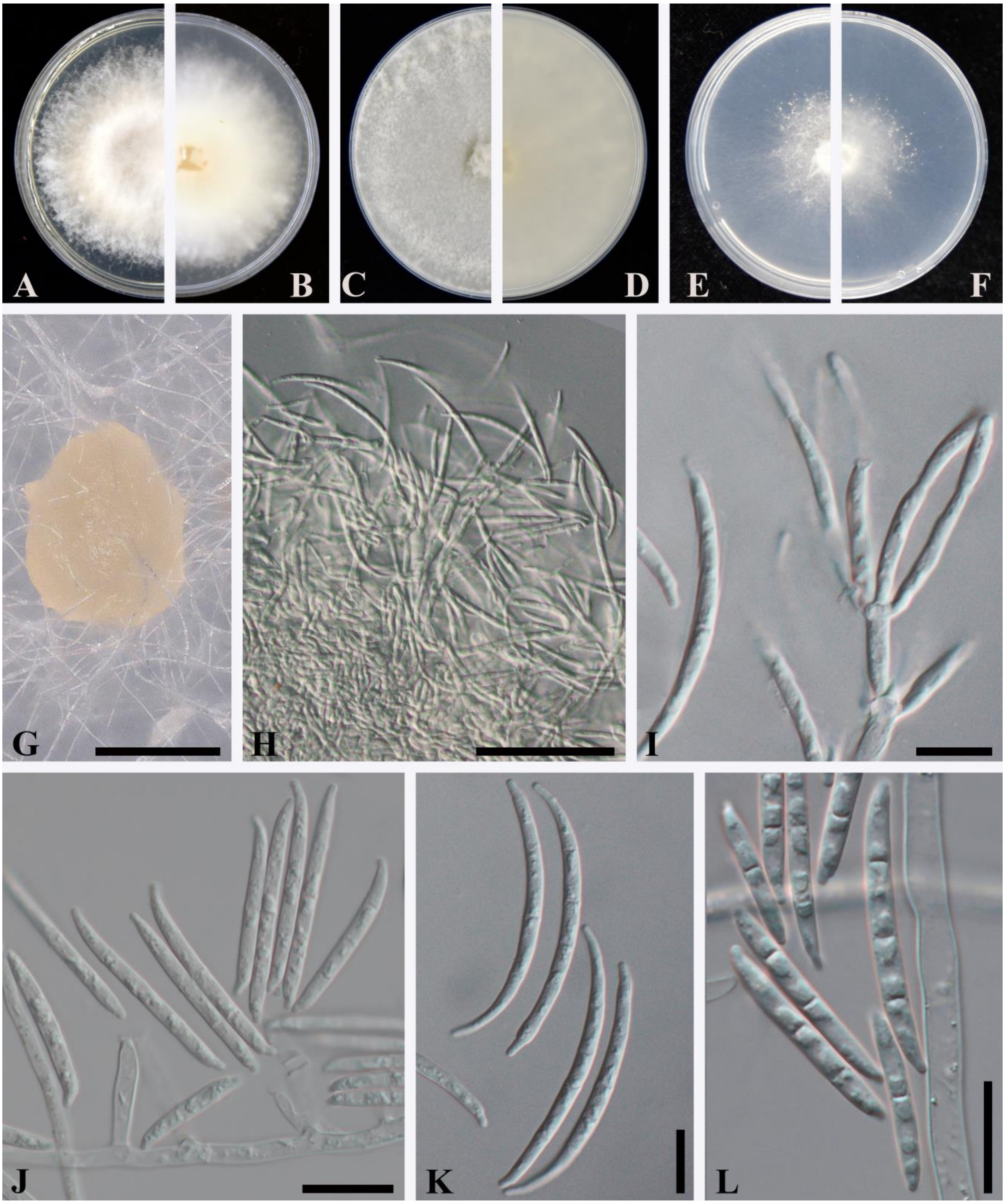

Figure 6 – *Fusarium qiannanense* (ex-type culture CGMCC3.25477). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–I Sporodochial conidiophores and conidiogenous cells. J Aerial conidiophores and conidiogenous cells. K Sporodochial macroconidia. L Aerial macroconidia. Scale bars: G = 200 μm, H = 50 μm, I–L = 10 μm.

Fusarium incarnatum-equiseti **species complex**

Fusarium caulendophyticum H. Zhang & Y.L. Jiang, sp. nov. Fig. 8

Index Fungorum number: IF900487; Facesoffungi numbers: FoF 14972

Etymology – Name refers to endophytic fungi isolated from the stems.

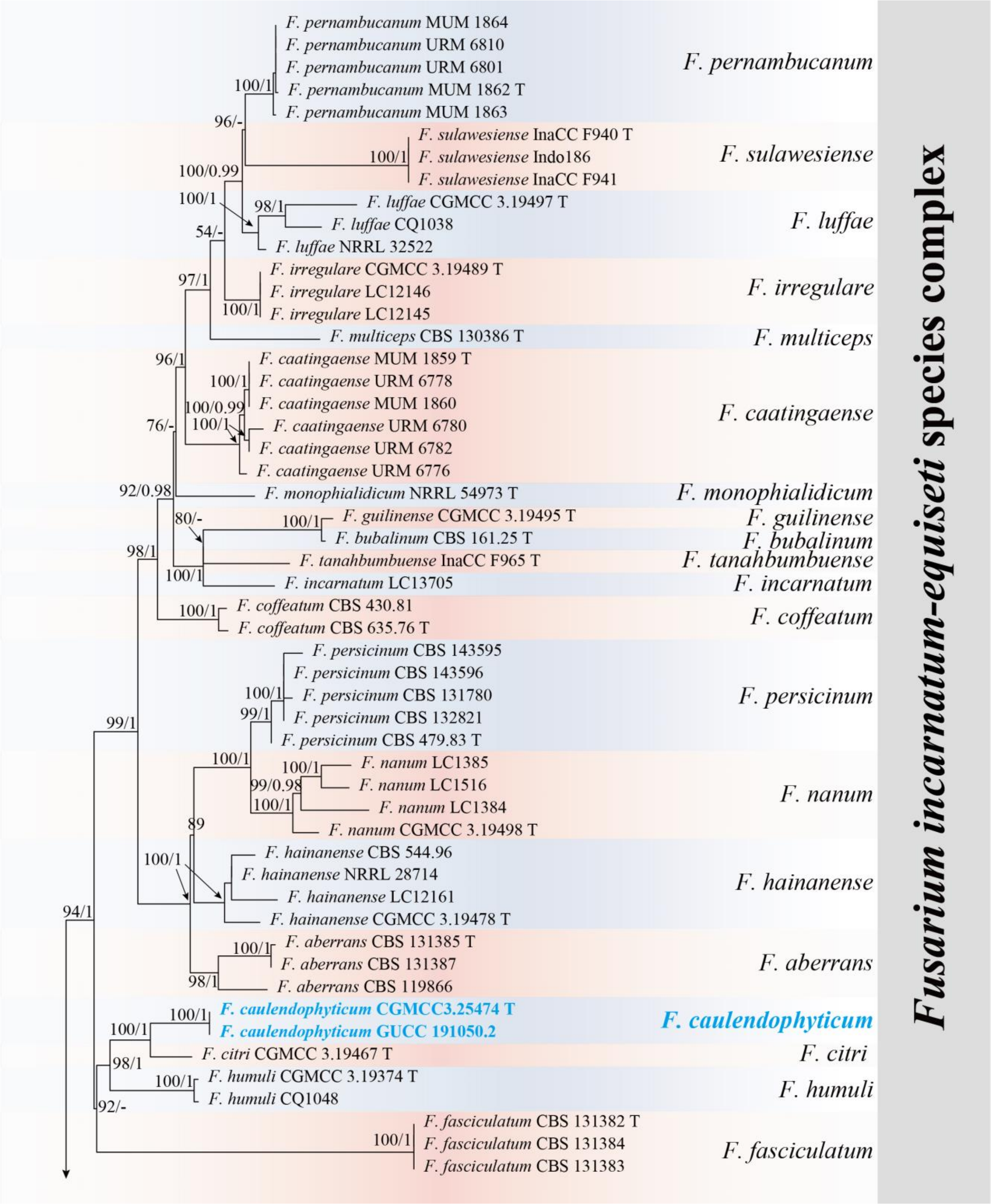

Figure 7 – Phylogenetic relationships of *Fusarium incarnatum-equiseti* species complex. The phylogenetic tree was generated using the maximum likelihood (ML) method by combining ITS, *tef1*, *CaM*, *rpb1*, and *rpb2* sequence data from 108 strains. The tree is rooted with *F. tjaynera*

(NRRL 66246) and *F. aywerte* (NRRL 25410). The ML bootstrap support values > 50% (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near nodes (BS/PP). Strains isolated in this study are indicated in **bold**. The new species are in bold blue. **T** holotype or ex-type.

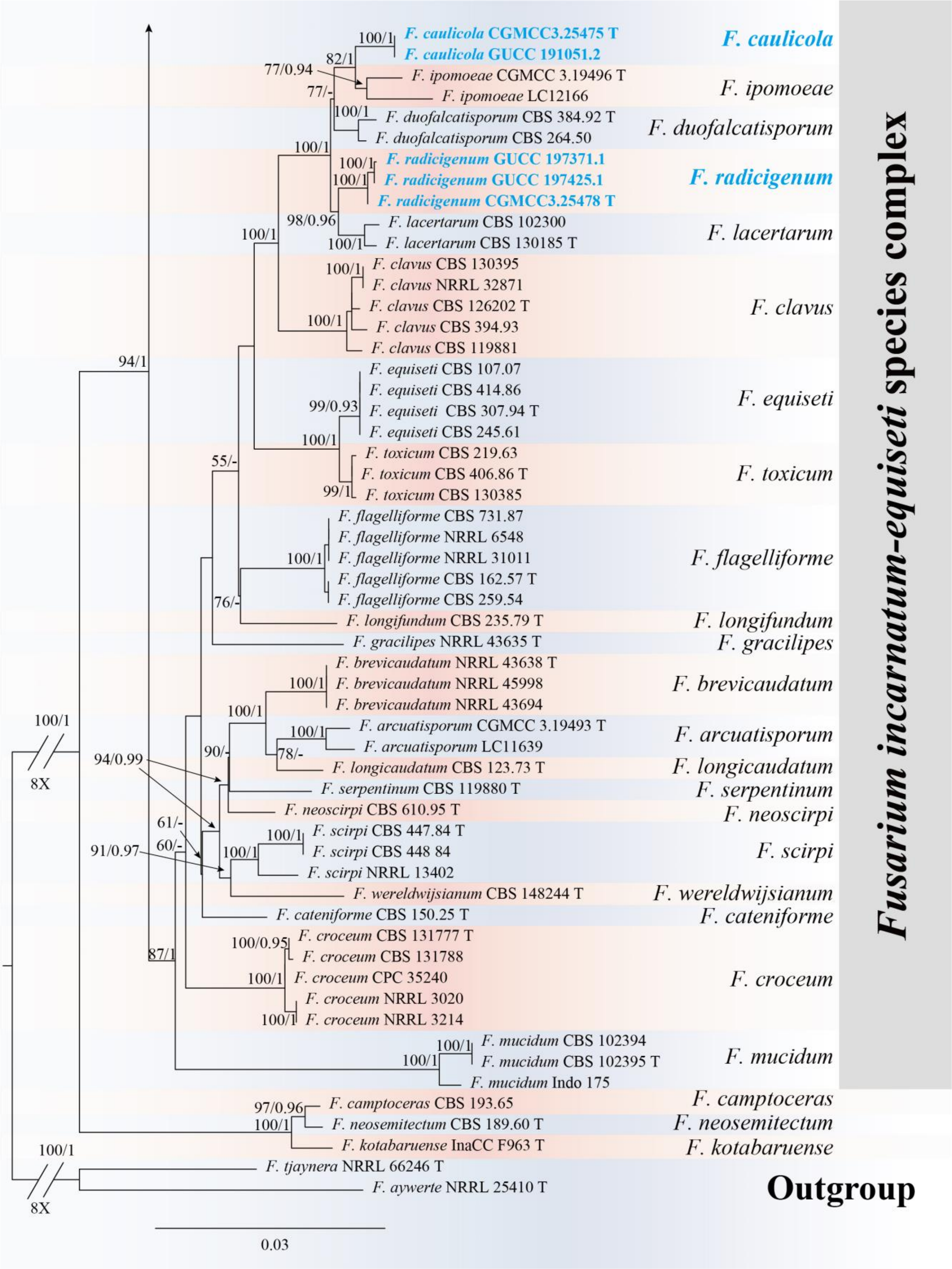

Figure 7 – Continued.

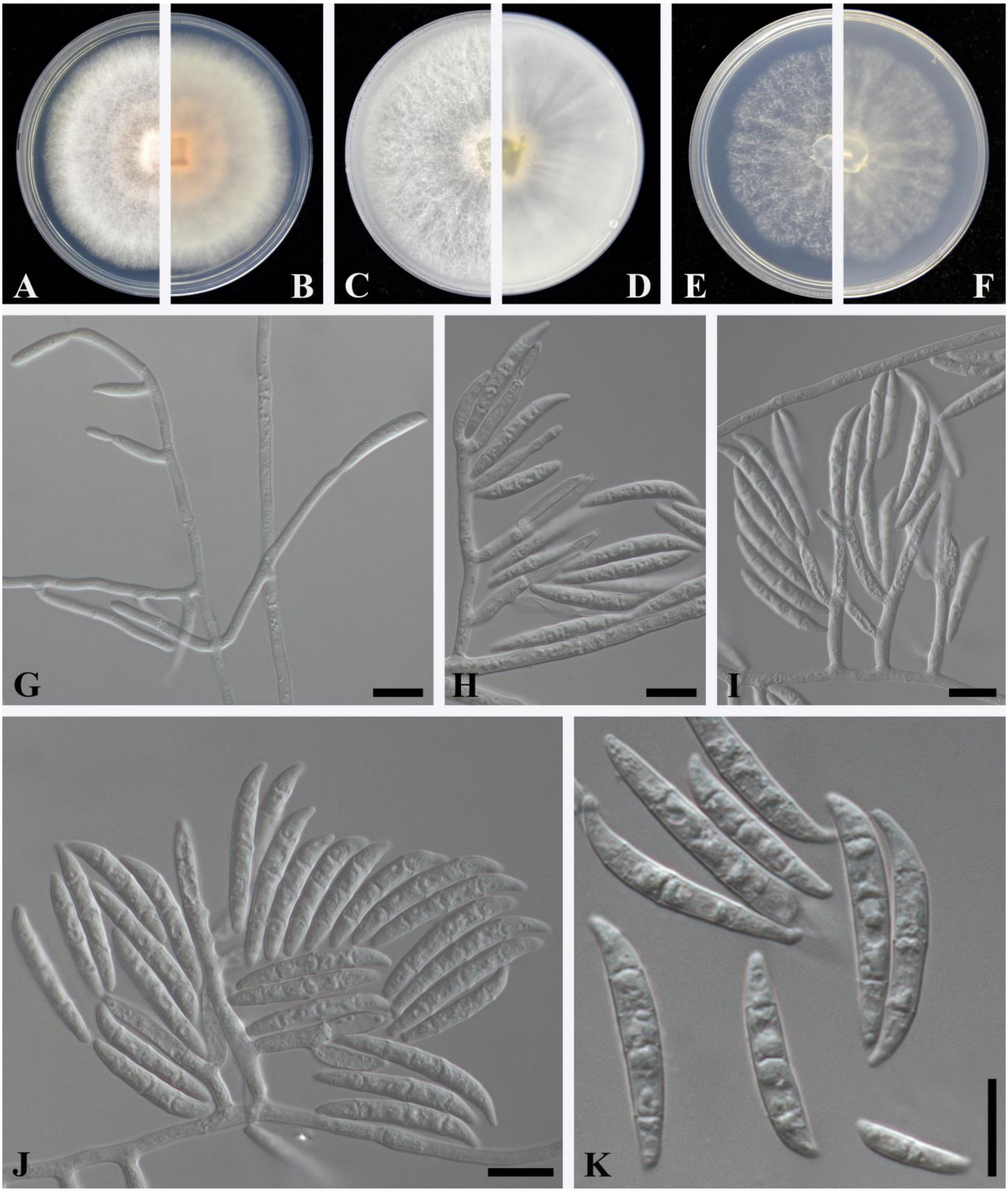

Figure 8 – *Fusarium caulendophyticum* (ex-type culture CGMCC3.25474). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G–J Aerial conidiophores and conidiogenous cells. K Macroconidia. Scale bars: G–K = 10 µm.

Endophytic in stems of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, irregularly laterally branched, bearing lateral and terminal monophialide or simple polyphialide. *Conidiogenous cells* monophialidic or polyphialidic, subcylindrical, straight or slightly curved, smooth or swollen and rough due to abundant conidiogenous loci, thin-walled, periclinal thickening and collarettes inconspicuous, 10–24 × 2–3 µm (av. = 14.3 × 2.6 µm, n = 10). *Macroconidia* slender with no significant curvature to curved with parallel walls, tapering towards the basal part, apical cell pointed to blunt; basal cell obtuse to papillate, not foot-shaped, 1–5-septate (mostly 3-septate), hyaline, granular to guttulate, thin-walled; 1-septate macroconidia 10–15.5 × 2–3 µm (av. = 13.1 × 2.6 µm, n = 30); 2-septate macroconidia 13–20.5 × 2–3.5 µm (av. = 15.5 × 2.7 µm, n = 30); 3-septate macroconidia 16–27 × 2.5–4 µm (av. = 22.1 × 3.3 µm, n = 30); 4-septate macroconidia 21.5–33.5 × 2.5–4.5 µm (av. = 28.5 × 3.7 µm, n = 30); 5-septate macroconidia 28–47 × 3.5–4.5 µm (av. = 33.4 × 4 µm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 50 mm diam. after 5 days in the dark at 28 °C, whitish to light pink, round, raised, margin regular, with abundant aerial hyphae, and reverse whitish to light pink. On OA attaining 52 mm diam. after 5 days, white, cottony, margin regular, moderate aerial mycelium, and reverse concolorous. On SNA attaining 45 mm diam. after 5 days, greyish white, aerial mycelia sparse, undulate margin, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy stems of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang (HGUP191050, holotype), ex-type living culture: GUCC 191050.1 = CGMCC3.25474; other living culture: GUCC 191050.2.

Notes – Our collections (CGMCC3.25474 and GUCC 191050.2), *F. citri*, *F. humuli*, and *F. fasciculatum* form a distinct clade in the phylogeny, and *F. caulendophyticum* is sister to *F. citri* (ex-type CGMCC 3.19467) with high statistical support (BS = 100%, PP = 1.00) (Fig. 7). *Fusarium caulendophyticum* shows 98.88% (528/534, no gaps) *CaM* sequence similarity with *F. citri*, 99.56% (457/459, 2 gaps) on ITS, 99.36% (1560/1570, 2 gaps) on *rpb1*, 98.57% (825/837, no gaps) on *rpb2*, and 96.70% (615/636, 2 gaps) on *tef1*. Other genes are missing for *F. citri*. Morphologically, both species produce only macroconidia. However, *F. caulendophyticum* is distinct from *F. citri*. Macroconidia of *F. caulendophyticum* were borne on aerial conidiogenous cells but borne on sporodochial conidiogenous cells in *F. citri*. In addition, they have different conidiophores (irregularly laterally branched, bearing lateral and terminal monophialide or simple polyphialide in *F. caulendophyticum* vs. verticillately branched and densely packed, mostly bearing apical whorls of three monophialides in *F. citri*), conidiogenous cells (smooth or swollen and rough due to abundant conidiogenous loci, 10–24 × 2–3 µm in *F. caulendophyticum* vs. smooth, 7.5–11.5 × 2–4 µm in *F. citri*), apical cell (pointed to blunt in *F. caulendophyticum* vs. papillate to hooked in *F. citri*), basal cell (obtuse to papillate, not foot-shaped in *F. caulendophyticum* vs. foot-shaped in *F. citri*), number of macroconidial septa (1–5 septa, mostly 3 septa in *F. caulendophyticum* vs. 3–5 septa in *F. citri*), and 3-septate macroconidial sizes (16–27 × 2.5–4 µm, av. = 22.1 × 3.3 µm in *F. caulendophyticum* vs. 25–31 × 3.5–5 µm, av. 28.9 × 4 µm in *F. citri*) (Wang et al. 2019). Furthermore, the PHI test on *F. caulendophyticum* indicated that there is no significant recombination (p = 0.8193 > 0.05) between *F. caulendophyticum* and its closely related taxa as defined in Fig. 5c. Thus, we introduce *F. caulendophyticum* as a new species.

Fusarium caulicola H. Zhang & Y.L. Jiang, sp. nov. Fig. 9

Index Fungorum number: IF900488; Facesoffungi numbers: FoF 14973

Etymology – Name refers to stems, from which this fungus was isolated.

Endophytic in stems of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, arising from aerial hyphae, solitary, unbranched or sparsely branched, bearing lateral and terminal monophialide or polyphialides. *Conidiogenous cells* monophialidic or polyphialidic, hyaline, terminal and lateral, subcylindrical to fusiform or tapering towards the apex and base, straight or slightly curved, smooth to rough, thin-walled, without noticeable periclinal thickening, a minute apical collarette can be present, 6–13 × 2.5–4 µm (av. = 9 × 3.2 µm, n = 10). *Macroconidia* slender with no significant curvature to curved with widest at the middle portion, narrowing towards each end, apical cell often pointed, sometimes blunt; basal cell obtuse to papillate, not foot-shaped or poorly developed, foot-shaped, 1–4-septate (mostly 3-septate), hyaline, smooth, thin-walled; 1-septate macroconidia 14–24.5 × 2–3.5 µm (av. =

18.7 × 2.7 µm, n = 30); 2-septate macroconidia 16.5–27 × 2–3.5 µm (av. = 21 × 3 µm, n = 30); 3-septate macroconidia 20–39.5 × 2.5–4 µm (av. = 30.1 × 3.2 µm, n = 30); 4-septate macroconidia 28.5–40.5 × 3–5 µm (av. = 34.6 × 4.1 µm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 45–50 mm diam. after 5 days in the dark at 28 °C, white, round, raised, fringed edge, with abundant aerial hyphae, and reverse buff. On OA attaining 55 mm diam. after 5 days, grey, flocculent, margin regular, moderate aerial mycelium, and reverse grey. On SNA attaining 47 mm diam. after 5 days, greyish white, moderate aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy stems of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang (HGUP191051, holotype), ex-type living culture: GUCC 191051.1 = CGMCC3.25475; other living culture: GUCC 191051.2.

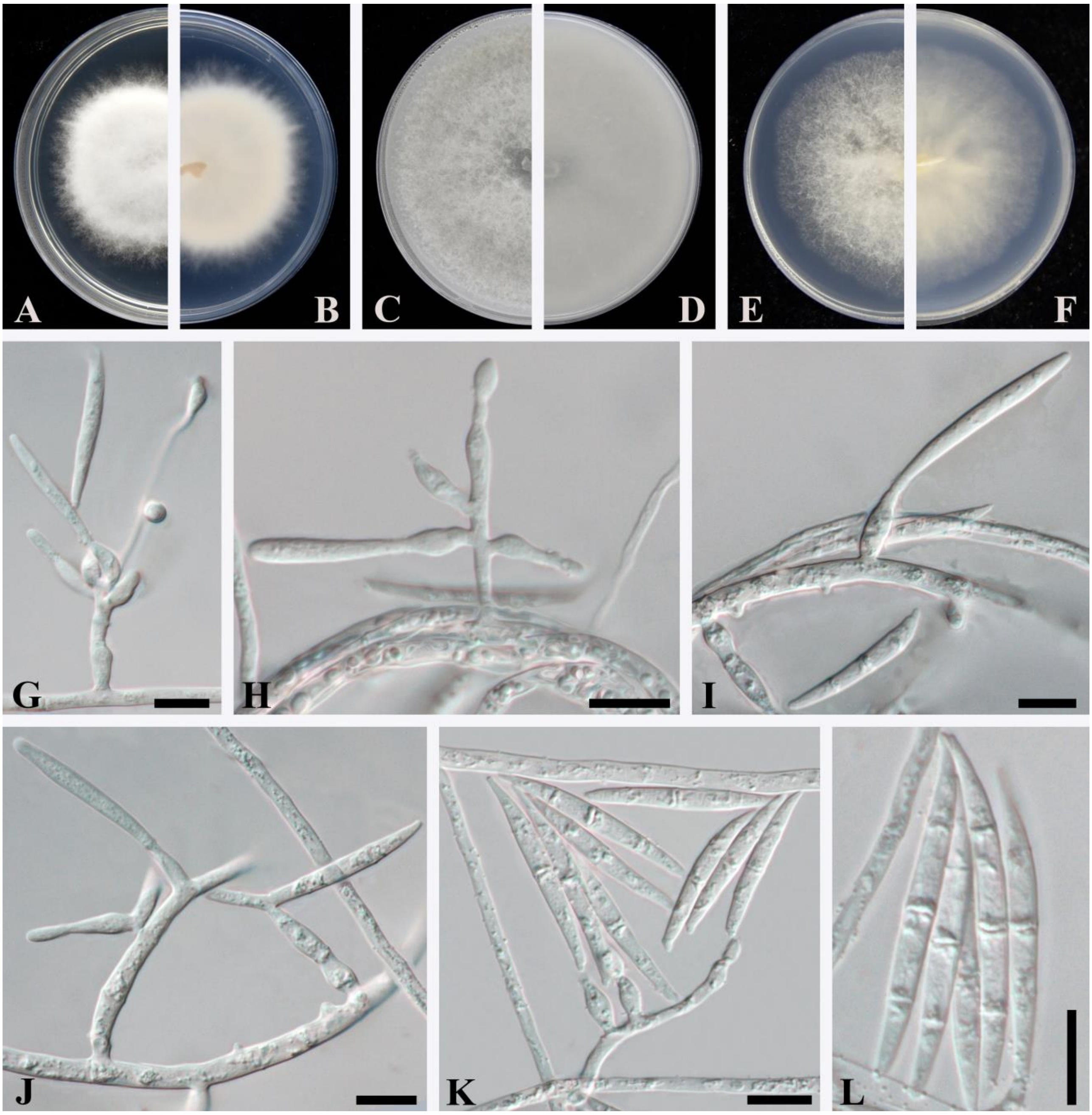

Figure 9 – *Fusarium caulicola* (ex-type culture CGMCC3.25475). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–K Aerial conidiophores and conidiogenous cells. L Macroconidia. Scale bars: G–L = 10 µm.

Notes – *Fusarium caulicola* (CGMCC3.25475 and GUCC 191051.2) is closely related to *F. ipomoeae* (ex-type CGMCC 3.19496) in the phylogenetic tree (Fig. 7), with high statistical support (BS = 82%, PP = 1.00), sharing 99.55% (439/441, 2 gaps) sequence similarity on ITS, 97.83% (1535/1569, one gap) on *rpb1*, and 98.58% (624/633, no gaps) on *tef1*. Although both species produce only macroconidia, *F. caulicola* is morphologically distinct from *F. ipomoeae* based on the different macroconidial formations (borne on aerial conidiogenous cells in *F. caulicola* vs. from sporodochial conidiogenous cells in *F. ipomoeae*), conidiophores (solitary, unbranched or sparsely branched, bearing lateral and terminal monophialide or polyphialides in *F. caulicola* vs. verticillately branched and densely packed, bearing apical whorls of 3–5 monophialides in *F. ipomoeae*), conidiogenous cells (subcylindrical to fusiform or tapering towards the apex and base, smooth to rough in *F. caulicola* vs. subulate to subcylindrical, smooth in *F. ipomoeae*), number of septa in macroconidia (*F. caulicola* 1–4 septa, while 3–5 septa in *F. ipomoeae*), macroconidial shapes (*F. caulicola* is straighter than *F. ipomoeae*), apical cell (often pointed, sometimes blunt in *F. caulicola* vs. hooked to tapering in *F. ipomoeae*), and basal cell (obtuse to papillate, not foot-shaped or poorly developed, foot-shaped in *F. caulicola* vs. foot-shaped in *F. ipomoeae*) (Wang et al. 2019). Additionally, the PHI test showed that there is no significant recombination ($p = 0.1948 > 0.05$) between *F. caulicola* and its closely related taxa as shown in Fig. 5d. Therefore, we introduced *F. caulicola* as a novel species.

Fusarium radicigenum H. Zhang & Y.L. Jiang, sp. nov. Fig. 10

Index Fungorum number: IF900489; Facesoffungi numbers: FoF 14974

Etymology – Name refers to endophytic fungi isolated from the roots.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* borne on aerial mycelia, unbranched, often reduced to conidiogenous cells. *Aerial conidiogenous cells* monophialidic, subulate to subcylindrical, straight to slightly curved, tapering towards both ends, smooth- and thin-walled, apex with inconspicuous periclinal thickening and minute collarette, 8.5–11 × 2.5–3.5 μm (av. = 9.4 × 3 μm, n = 10). *Aerial microconidia* sparse, hyaline, oblong with a truncate base, apex obtuse, smooth- and thin-walled, 0–1-septate, aseptate microconidia 10–14 × 2–3 μm (av. = 11.3 × 2.4 μm, n = 30); 1-septate microconidia 7.5–18 × 2–3.5 μm (av. = 12.7 × 2.6 μm, n = 30). *Aerial macroconidia* slightly curved to distinctly curved, 1–5-septate, predominantly 3-septate, hyaline, smooth- and thick-walled, narrowing towards each end, apical cell blunt to hooked, elongated; basal cell papillate to well-developed, foot-shaped, 1-septate macroconidia 12.5–23.5 × 2–3.5 μm (av. = 17.9 × 2.4 μm, n = 30); 2-septate macroconidia 16.5–23.5 × 2–3.5 μm (av. = 20.3 × 2.7 μm, n = 30); 3-septate macroconidia 17–35 × 2–3.5 μm (av. = 26.2 × 2.9 μm, n = 30); 4-septate macroconidia 26.5–38 × 2.5–4 μm (av. = 32.2 × 3.3 μm, n = 30); 5-septate macroconidia 28.5–44.5 × 2.5–4 μm (av. = 36.6 × 3.2 μm, n = 30). *Chlamydospores* spherical, subspherical to ellipsoid, lateral or intercalary, in pairs, chains, sometimes solitary, thick-walled, guttulate, 6.5–14 μm (av. = 10.1 μm, n = 30) diam.

Culture characteristics – Colonies on PDA attaining 48 mm diam. after 5 days in the dark at 28℃, cottony, white, round, raised, margin irregular, with abundant aerial hyphae, colonies fertile, and reverse light orange. On OA attaining 46 mm diam. after 5 days, cottony, white, raised, dense, margin irregular, abundant aerial mycelium, and reverse light yellow. On SNA attaining 47–52 mm diam. after 5 days, white, margin irregular, abundant aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang (HGUP197221, holotype), ex-type living culture: GUCC 7221.1 = CGMCC3.25478; other living cultures: GUCC 197371.1 and GUCC 197425.1.

Notes – *Fusarium radicigenum* is phylogenetically closely related to *F. lacertarum* with high statistical support (BS = 98%, PP = 0.96) (Fig. 7), sharing 98.46% (576/585, no gaps) sequence similarity on *CaM*, 99.23% (1555/1567, no gaps) on *rpb1*, and 98.80% (494/500, no gaps) on *tef1*. The ITS is missing in *F. lacertarum* and *rpb2* is missing in *F. radicigenum*. Morphologically, *F. radicigenum* can be distinguished from *F. lacertarum* by different conidiophores (*F. radicigenum* unbranched, while branched or unbranched in *F. lacertarum*), longer conidiogenous cells (monophialidic, subulate to subcylindrical, 8.5–11 × 2.5–3.5 µm, av. = 9.4 × 3 µm in *F. radicigenum* vs. rarely present, 2.5–4.0 × 1.0–1.5 µm or without short stalk in *F. lacertarum*), number of septa in conidia (1–5 septa in *F. radicigenum* vs. 2–4 septa in *F. lacertarum*), conidial shape (*F. radicigenum* is curvier than *F. lacertarum*), apical cell

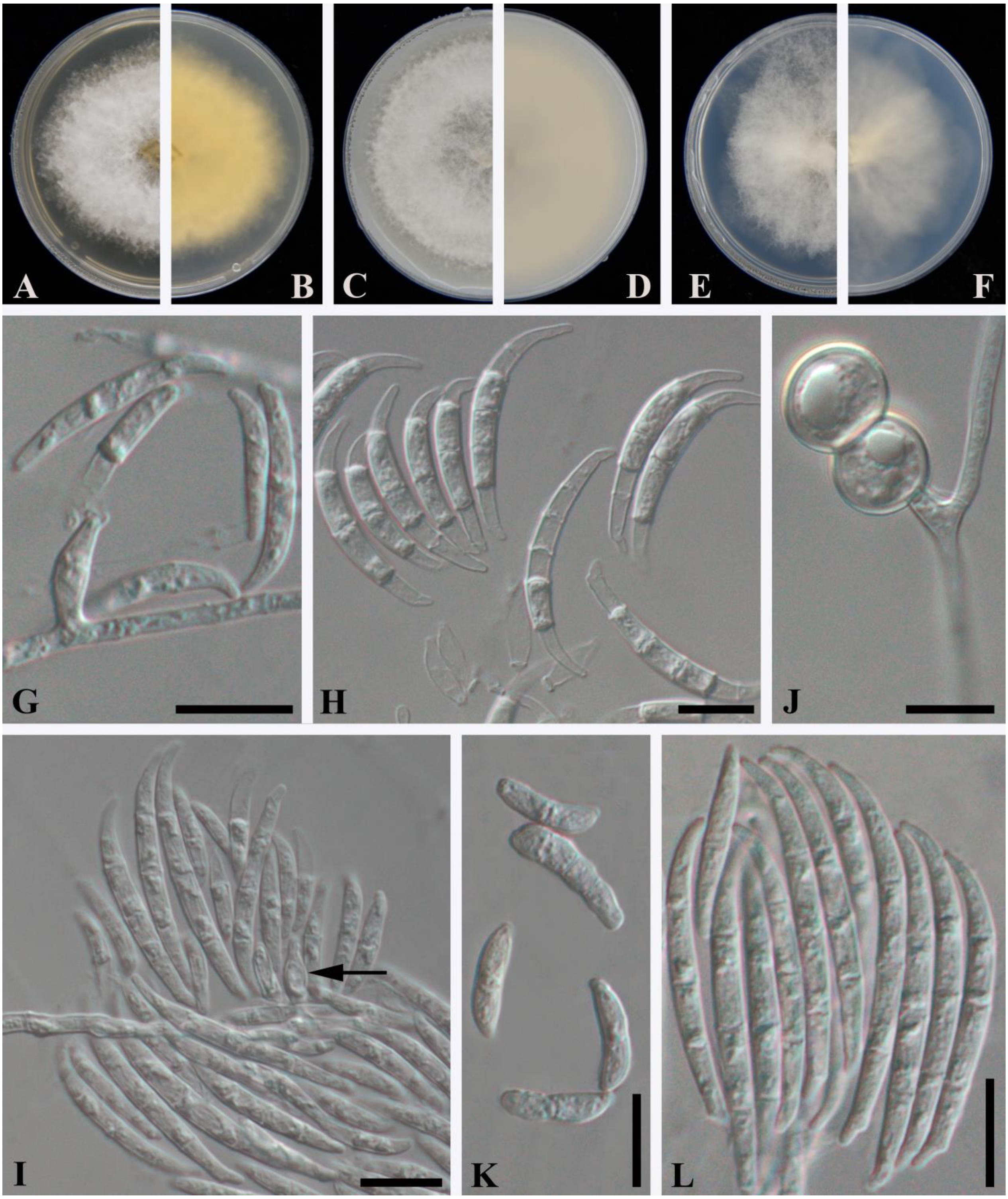

Figure 10 – *Fusarium radicigenum* (ex-type culture CGMCC3.25478). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G–I Aerial conidiophores and conidiogenous cells. J Chlamydospores. K Aerial microconidia. L Aerial macroconidia. Scale bars: G–L = 10 µm.

(blunt to hooked, elongated in *F. radicigenum* vs. pointed or slightly beaked in *F. lacertarum*), and conidial organization (conidia densely aggregated in *F. radicigenum* vs. conidia single or produced in groups of 3–4 in *F. lacertarum*). Since Subrahmanyam (1983) did not distinguish between macro- and microconidia, it was not conducive to comparing conidia size. However, the longest conidia in *F. radicigenum* are significantly longer than those of *F. lacertarum* (up to 44.5 µm long in *F. radicigenum* vs. up to 30.8 µm long in *F. lacertarum*) (Subrahmanyam 1983). Moreover, the PHI test on *F. radicigenum* indicated that there is no significant recombination ($p = 0.1948 > 0.05$) between *F. radicigenum* and its closely related taxa as shown in Fig. 5d. Thus, we introduce *F. radicigenum* as a new species.

Fusarium oxysporum **species complex**

Fusarium cili H. Zhang & Y.L. Jiang, sp. nov. Fig. 12

Index Fungorum number: IF900490; Facesoffungi numbers: FoF 14975

Etymology – Name refers to the Chinese name "Ci Li" of host plant, *R. roxburghii*.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, borne on aerial mycelia, hyaline, cylindrical to subcylindrical, straight, unbranched, short, often reduced to single conidiogenous cells. *Conidiogenous cells* monophialidic, formed directly from hyphae or terminal on conidiophores, cylindrical to subcylindrical, straight or slightly curved, smooth- and thin-walled, slightly tapering towards the apex and the base, with a distinct collarette and periclinal thickening; small phialides (produce microconidia) 5.5–45 × 1.5–2.5 µm (av. = 20.8 × 2.4 µm, n = 10); large phialides (produce mesoconidia) 13–17 × 3–4 µm (av. = 15.8 × 3.4 µm, n = 10). *Microconidia* single or forming false heads on tips of monophialides, obovoid to reniform conidia: hyaline, aseptate, smooth- and thin-walled, 4.5–10 × 2–3 µm (av. = 6.7 × 2.5 µm, n = 30), l: w = 1.9–4.2 (av. = 2.7, n = 30); oval to oblong with obtuse ends conidia: 6–13 × 4.5–6 µm (av. = 9 × 5 µm, n = 30), l: w = 1.2–2.9 (av. = 1.8, n = 30), minutely verruculose or irregularly rough-walled, thick-walled, 0–1-septate (mostly aseptate). *Mesoconidia* single, 1-septate, hyaline, oblong with obtuse ends, straight or slightly curved, basal cell not foot-shaped, minutely verruculose or slightly rough-walled, thick-walled, 10–22.5 × 3–5 µm (av. = 15.7 × 3.5 µm, n = 30), l: w = 3.5–5.6 (av. = 4.6, n = 30). *Chlamydospores* solitary, terminal or intercalary, mostly subglobose, verruculose, hyaline, rough- and thick-walled, aseptate, 4–14 µm diam. (av. = 8.6 µm, n = 30). *Macroconidia* not observed.

Culture characteristics – Colonies on PDA attaining 50 mm diam. after 5 days in the dark at 28 °C, pink, round, fringed edge, aerial mycelia abundant, and reverse with a pale pink center. On OA attaining 50 mm diam. after 5 days, white to light pink, cottony, margin entire, and reverse light pink. On SNA attaining 52 mm diam. after 5 days, light grey, with sparse aerial mycelium, and reverse light grey. Pigment and odor absent.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy roots of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang (HGUP190024, holotype), ex-type living culture: GUCC 190024.1 = CGMCC3.25476; other living culture: GUCC 190024.2.

Notes – Our collections (CGMCC3.25476 and GUCC 190024.2) are phylogenetically close to *F. phialophorum* (holotype InaCC F971), *F. rosae-roxburghii* (ex-type CGMCC3.25479, in this study), and *F. odoratissimum* (holotype InaCC F822). Evolutionarily, *F. cili* is significantly more closely related to *F. phialophorum* and *F. rosae-roxburghii*, forming a distinct clade, with moderate ML statistical support (BS = 77%) (Fig. 11). *Fusarium cili* is phylogenetically closest to *F. phialophorum*, sharing 98.96% (1429/1444, no gaps) sequence similarity on *rpb1*. *Fusarium cili* is morphologically quite distinct from *F. phialophorum* by having different macroconidial formations (borne on aerial conidiophores in *F. cili* vs. formed on sporodochia and on aerial conidiophores in *F. phialophorum*), conidial types (*F. cili* produces 1-septate mesoconidia, oblong with obtuse ends, straight or slightly curved, basal cell not foot-shaped, 10–22.5 × 3–5 µm, av. =

15.7 × 3.5 µm; while 2–5-septate macroconidia, apical cells papillate, basal cells foot-shaped, 54–60 × 4–5 µm in *F. phialophorum*), and microconidial shapes and sizes (obovoid to reniform microconidia, 4.5–10 × 2–3 µm, av. = 6.7 × 2.5 µm, and oval to oblong with obtuse ends microconidia, 6–13 × 4.5–6 µm,

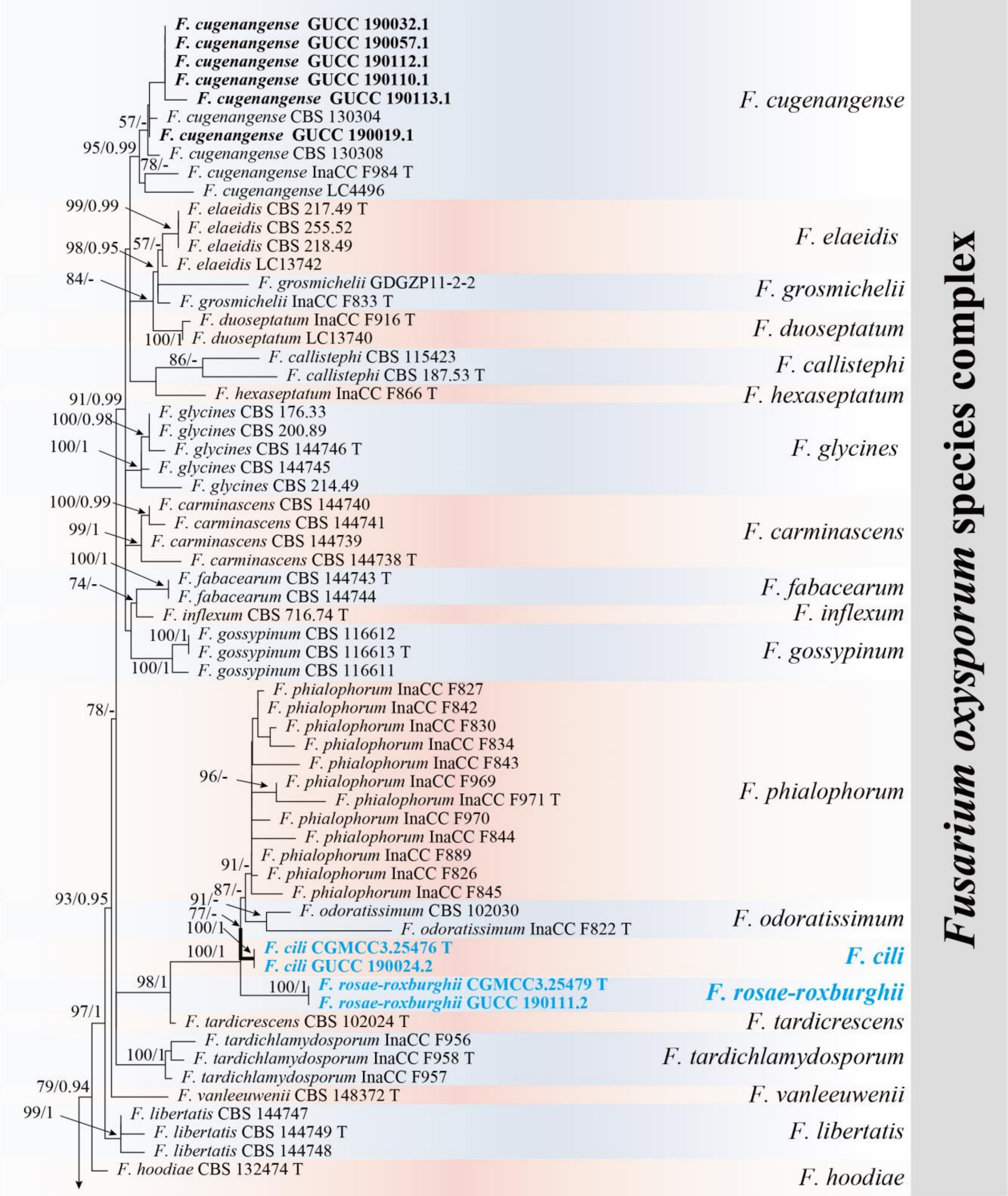

Figure 11 – Phylogenetic relationships of *Fusarium oxysporum* species complex. The phylogenetic tree was generated using the maximum likelihood (ML) method by combining *CaM*, *rpb1*, *rpb2*, *tef1*, and *tub2* sequence data from 124 strains. The tree is rooted with *F. miscanthi* (LC7503) and *F. paranisikadoi* (CGMCC 3.20826). The ML bootstrap support values > 50% (BS) and Bayesian

posterior probabilities > 0.90 (PP) are given near nodes (BS/PP). Strains isolated in this study are indicated in **bold**. The new species are in bold blue. **T** holotype or ex-type.

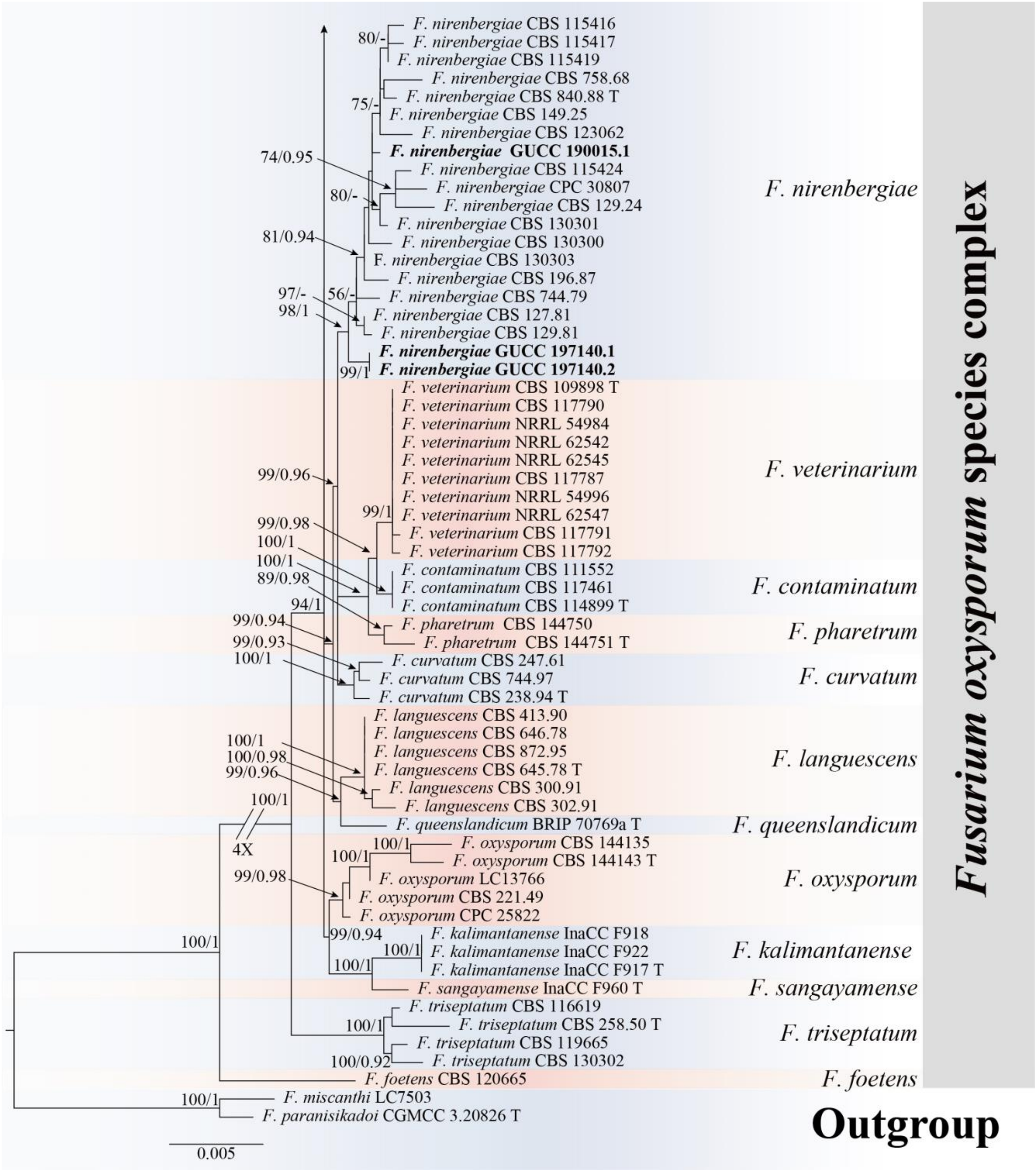

Figure 11 – Continued.

av. = 9 × 5 µm in *F. cili* vs. ovoid to ellipsoid, 6–24 × 3–6 µm, av. = 12 × 5 µm in *F. phialophorum*) (Maryani et al. 2019). *Fusarium cili* is also phylogenetically close to *F. rosae-roxburghii*, having 98.98% (1752/1770, 4 gaps) sequence similarity on *rpb1*. Morphologically, *F. cili* is also completely distinct from *F. rosae-roxburghii* by having different conidiogenous cells (distinct collarette and periclinal thickening in *F. cili* vs. minute periclinal thickening and inconspicuous collarettes in *F. rosae-roxburghii*), conidial types (*F. cili* produces 1-septate mesoconidia, oblong with obtuse ends, basal cell not foot-shaped, 10–22.5 × 3–5 µm, av. = 15.7 ×

3.5 μm; while 1–3-septate macroconidia, with a blunt apical cell, basal cell obtuse to papillate, 1-

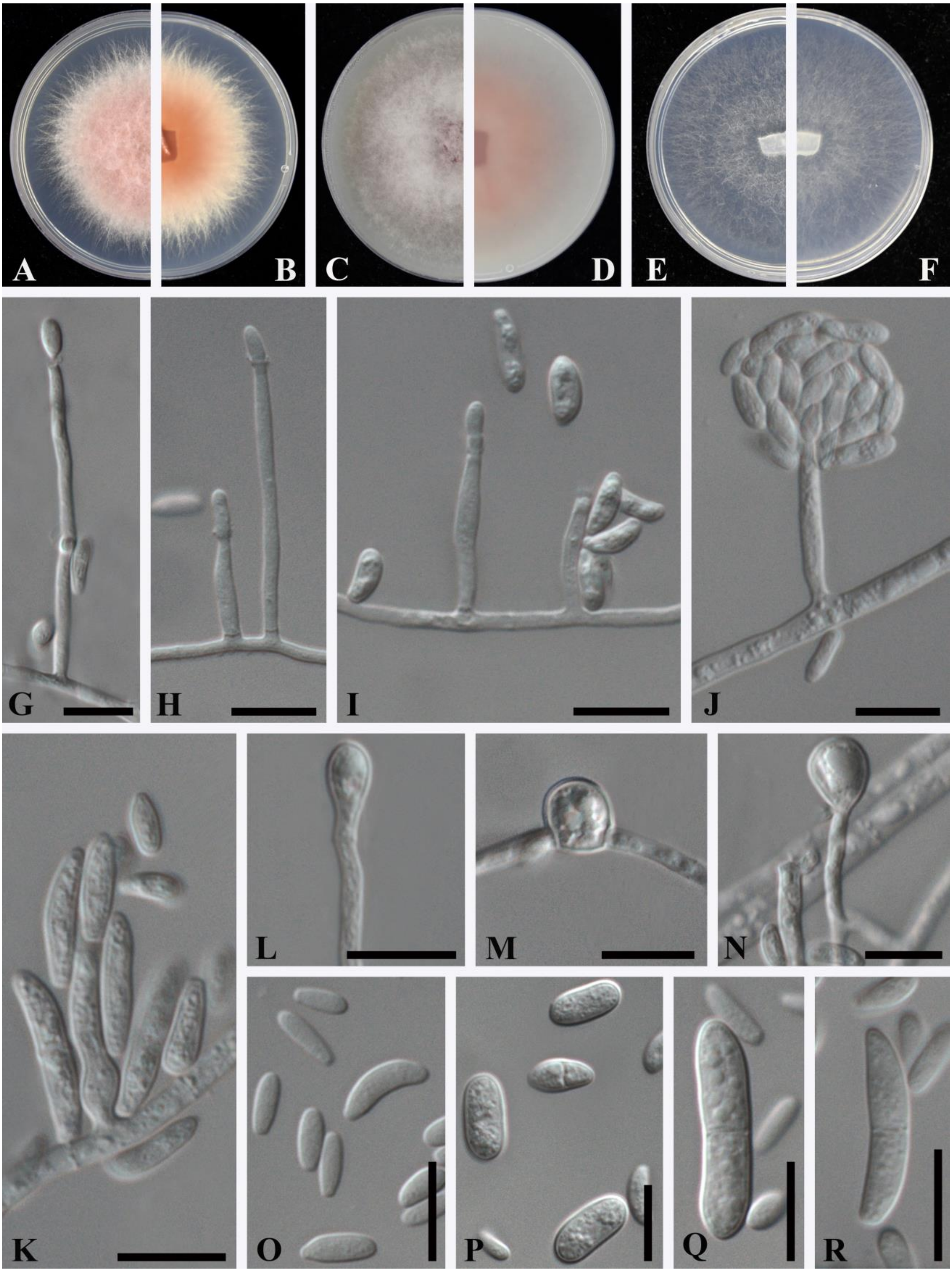

Figure 12 – *Fusarium cili* (ex-type culture CGMCC3.25476). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–K Aerial conidiophores and conidiogenous cells. L–N Chlamydospores. O–P Microconidia. Q–R Mesoconidia. Scale bars: G–R = 10 μm.

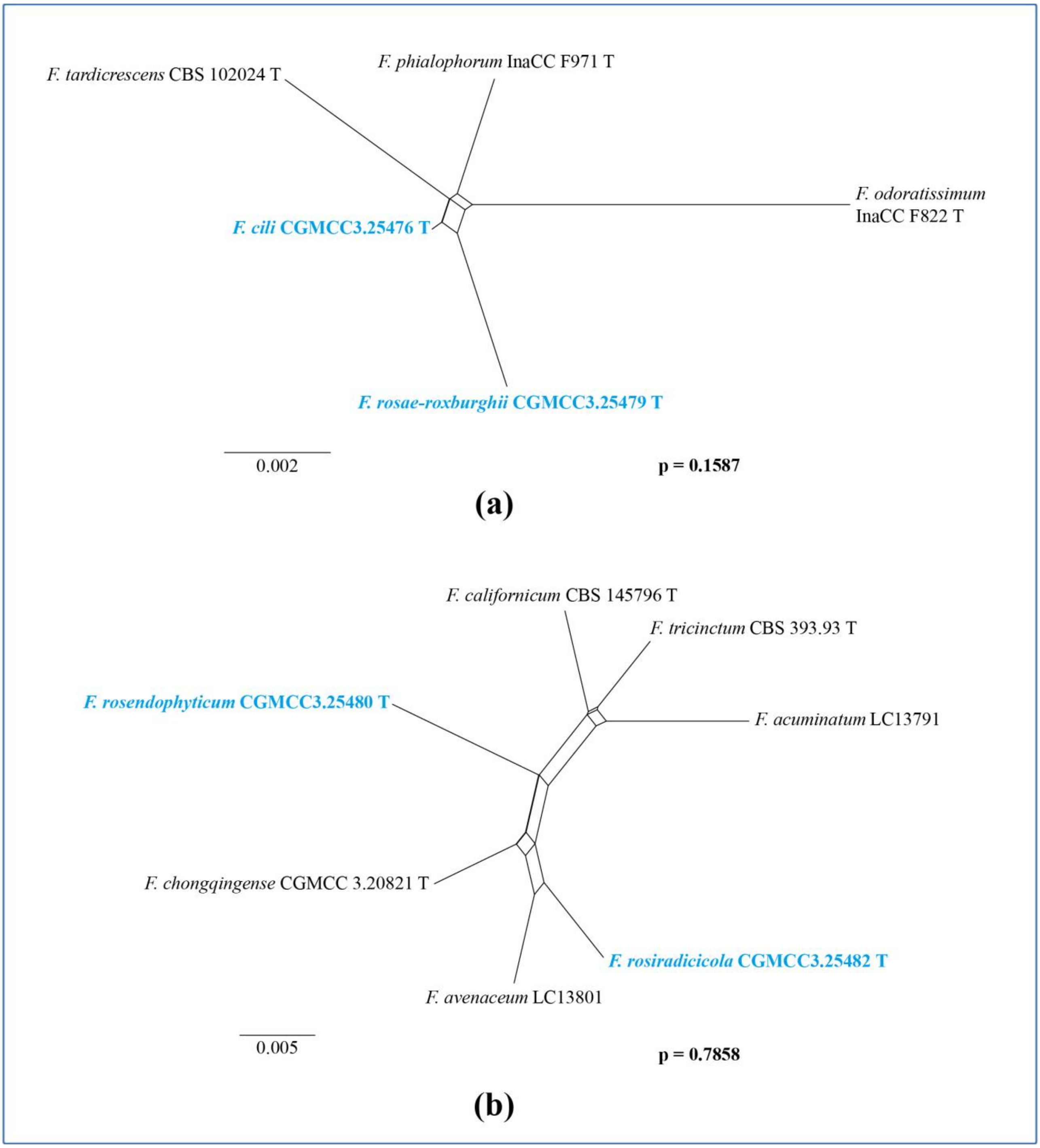

Figure 13 – Results of the pairwise homoplasy index (PHI) test of new *Fusarium* species and their closely related species. New taxa are printed in bold blue.

septate macroconidia 11.5–19 × 2–3 µm, 2-septate macroconidia 14–22.5 × 2–3 µm, 3-septate macroconidia 18.5–26 × 2–3 µm in *F. rosae-roxburghii*), microconidial formations (single or forming false heads in *F. cili* vs. single, forming false heads or borne in dry chains in *F. rosae-roxburghii*), and microconidial shapes and sizes (obovoid to reniform microconidia, 4.5–10 × 2–3 µm, av. = 6.7 × 2.5 µm, and oval to oblong with obtuse ends microconidia, 6–13 × 4.5–6 µm, av. = 9 × 5 µm, minutely verruculose or irregularly rough-walled, thick-walled in *F. cili*; while oblong with a truncate base, smooth- and thin-walled, 0–1-septate, aseptate microconidia 4–21 × 2–3.5 µm, 1-septate microconidia 10–15 × 2–3 µm in *F. rosae-roxburghii*). Overall, *F. cili*, *F. phialophorum*, and *F. rosae-roxburghii* are significantly different morphologically. As shown in Fig. 13a, the PHI test on *F*. *cili* also showed that there is no significant recombination (p = 0.1587 > 0.05) between *F*. *cili* and its closely related taxa. Therefore, we introduce *F*. *cili* as a new species.

Fusarium nirenbergiae L. Lombard & Crous, Persoonia 43: 29 (2018) Fig. 14

Index Fungorum number: IF826845

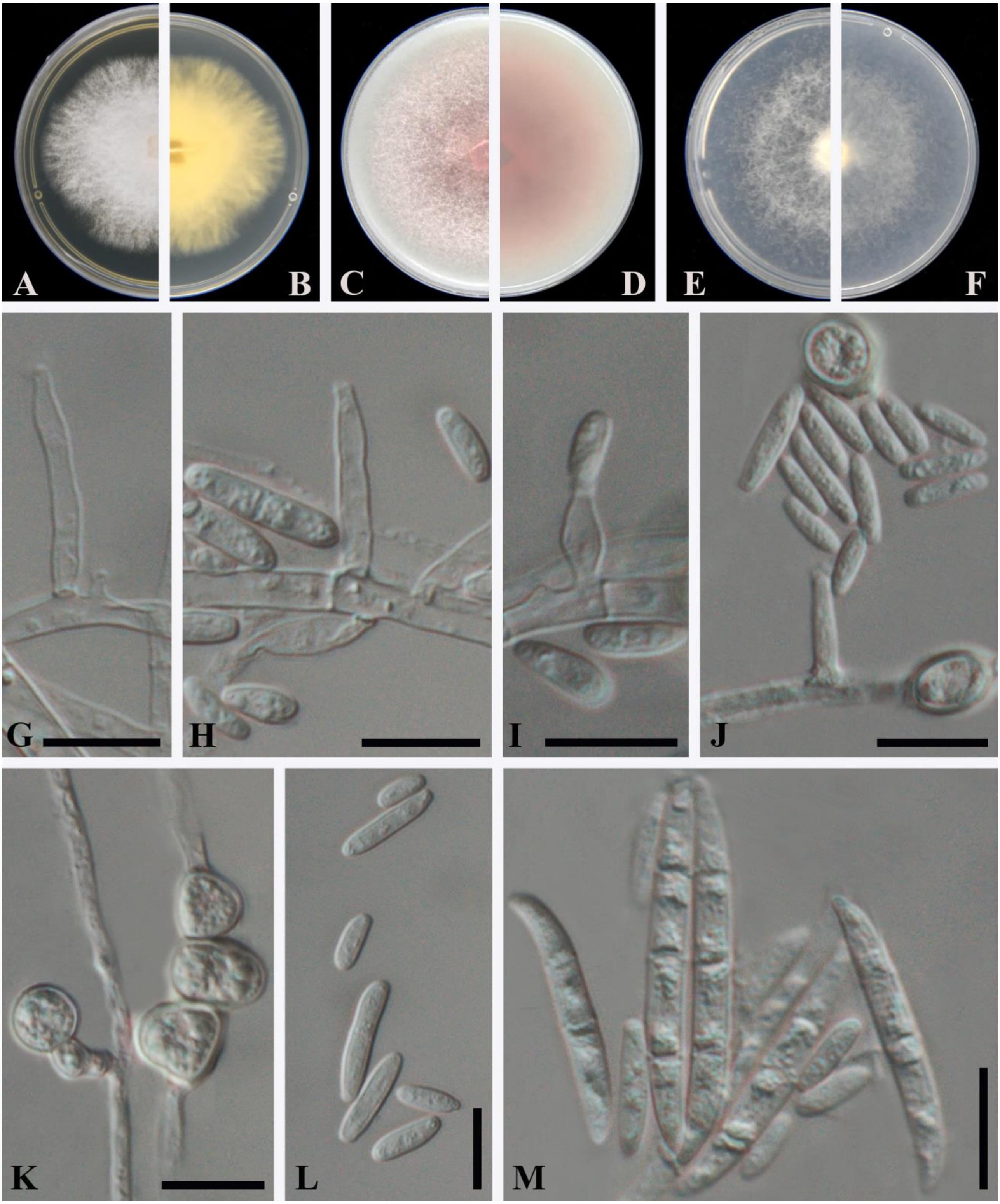

Figure 14 – *Fusarium nirenbergiae* (GUCC 197140.1). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G–J Aerial conidiophores and conidiogenous cells. K Chlamydospores. L Aerial microconidia. M Aerial macroconidia. Scale bars: G–M = 10 µm.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* borne on aerial mycelia, unbranched, often reduced to conidiogenous cells. *Aerial* conidiogenous cells monophialidic, subulate, cylindrical, subcylindrical, straight to slightly curved, tapering slightly towards the apex, smooth- and thin-walled, with inconspicuous periclinal thickening and collarettes, 2.5–19.5 × 1.5–3 µm (av. = 11 × 2.6 µm, n = 10). *Aerial microconidia* forming small false heads on tips of monophialides, hyaline, oblong with a truncate base, smooth- and thin-walled, 0–1-septate (mostly aseptate), aseptate microconidia 5.5–11 × 1.5–2.5 µm (av. = 7.4 × 2.2 µm, n = 30); 1-septate microconidia 11.5–20 × 2–3.5 µm (av. = 15.7 × 2.9 µm, n = 30). *Aerial macroconidia* borne on tips of conidiogenous cells on aerial conidiophores, almost straight or slightly curved, 2–3-septate, predominantly 3-septate, hyaline, smooth- and thick-walled, with a blunt apical cell; basal cell obtuse to papillate, not foot-shaped, 2-septate macroconidia 18–23 × 2.5–3.5 µm (av. = 21.1 × 2.9 µm, n = 30); 3-septate macroconidia 21–36.5 × 2.5–4 µm (av. = 28.9 × 3.1 µm, n = 30). *Chlamydospores* subglobose to ellipsoidal, lateral, terminal, or intercalary, solitary or in chains, thick-walled, guttulate, 5–12.5 µm (av. = 7.6 µm, n = 30) diam.

Culture characteristics – Colonies on PDA attaining 40–45 mm diam. after 5 days in the dark at 28°C, white, raised, cottony, with irregular edge, aerial mycelia abundant, and reverse light orange. On OA attaining 48 mm diam. after 5 days, light pink, flat, flocculent, margin entire, moderate aerial mycelium, and reverse light pink. On SNA attaining 52 mm diam. after 5 days, off-white, raised in center, with sparse to moderate aerial mycelium, and reverse grey. Pigment and odor absent.

Material examined – China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang, living cultures: GUCC 197140.1 and GUCC 197140.2. China, Guizhou Province, Guiyang City, natural environment, healthy roots of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang, living culture: GUCC 190015.1.

Notes – In phylogeny, our collections, GUCC 197140.1, GUCC 197140.2, and GUCC 190015.1, clustered with *F. nirenbergiae* (ex-type CBS 840.88), with high statistical support (BS = 98%, PP = 1.00) (Fig. 11). The strain GUCC 197140.1 shares 99.54% (871/875, no gaps) *rpb2* sequence similarity with the ex-type of *F. nirenbergiae*, 99.78% (447/448, no gaps) on *tef1*, and 100% (602/602) on *CaM*. The *tub2* is missing in the strain GUCC 197140.1 and other genes are missing for ex-type. Minor differences can be seen in base pairs between our strains and the ex-type. Morphologically, Our collections and the ex-type *F. nirenbergiae* exhibited similar conidiophores (borne on aerial mycelia, unbranched, bearing terminal monophialides, often reduced to single phialides), similar aerial conidiogenous cells (monophialide, subulate to subcylindrical, smooth- and thin-walled, periclinal thickening inconspicuous or absent), and similar aerial microconidia (forming small false heads on tips of monophialides, smooth- and thin-walled, 0–1-septate; aseptate microconidia 5.5–11 × 1.5–2.5 µm, av. = 7.4 × 2.2 µm in GUCC 197140.1 vs. 5–11 × 2–4 µm, av. = 8 × 3 µm in CBS 840.88; 1-septate microconidia 11.5–20 × 2–3.5 µm, av. = 15.7 × 2.9 µm in GUCC 197140.1 vs. 9–15 × 2–4 µm, av. = 12 × 3 µm in the ex-type) (Lombard et al. 2019). Therefore, we report our collections as new host records of *F. nirenbergiae* isolated from the roots of *R. roxburghii*.

Fusarium rosae-roxburghii H. Zhang & Y.L. Jiang, sp. nov. Fig. 15

Index Fungorum number: IF900491; Facesoffungi numbers: FoF 14976

Etymology – Name refers to cultivated *R. roxburghii*, from which this fungus was isolated.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* borne on aerial mycelia, unbranched or sparsely branched, often reduced to conidiogenous cells. *Aerial conidiogenous cells* monophialidic, cylindrical to subcylindrical, straight, tapering towards the apex, smooth- and thin-walled, with minute periclinal thickening and inconspicuous collarettes, 3.5–23.5 × 1.5–2.5 µm (av. = 10.5 × 2 µm, n = 10). *Aerial microconidia* forming small false heads on tips of monophialides or borne in dry chains, hyaline, oblong with a truncate base, smooth- and thin-walled, 0–1-septate (mostly aseptate), aseptate microconidia 4–21 × 2–3.5 µm (av. = 8.3 × 2.6 µm, n = 30); 1-septate microconidia 10–15 × 2–3 µm (av. = 11.9 × 2.3 µm, n = 30). *Aerial macroconidia* borne on tips of conidiogenous cells on aerial conidiophores, straight or slightly curved, 1–3-septate, hyaline, rough,

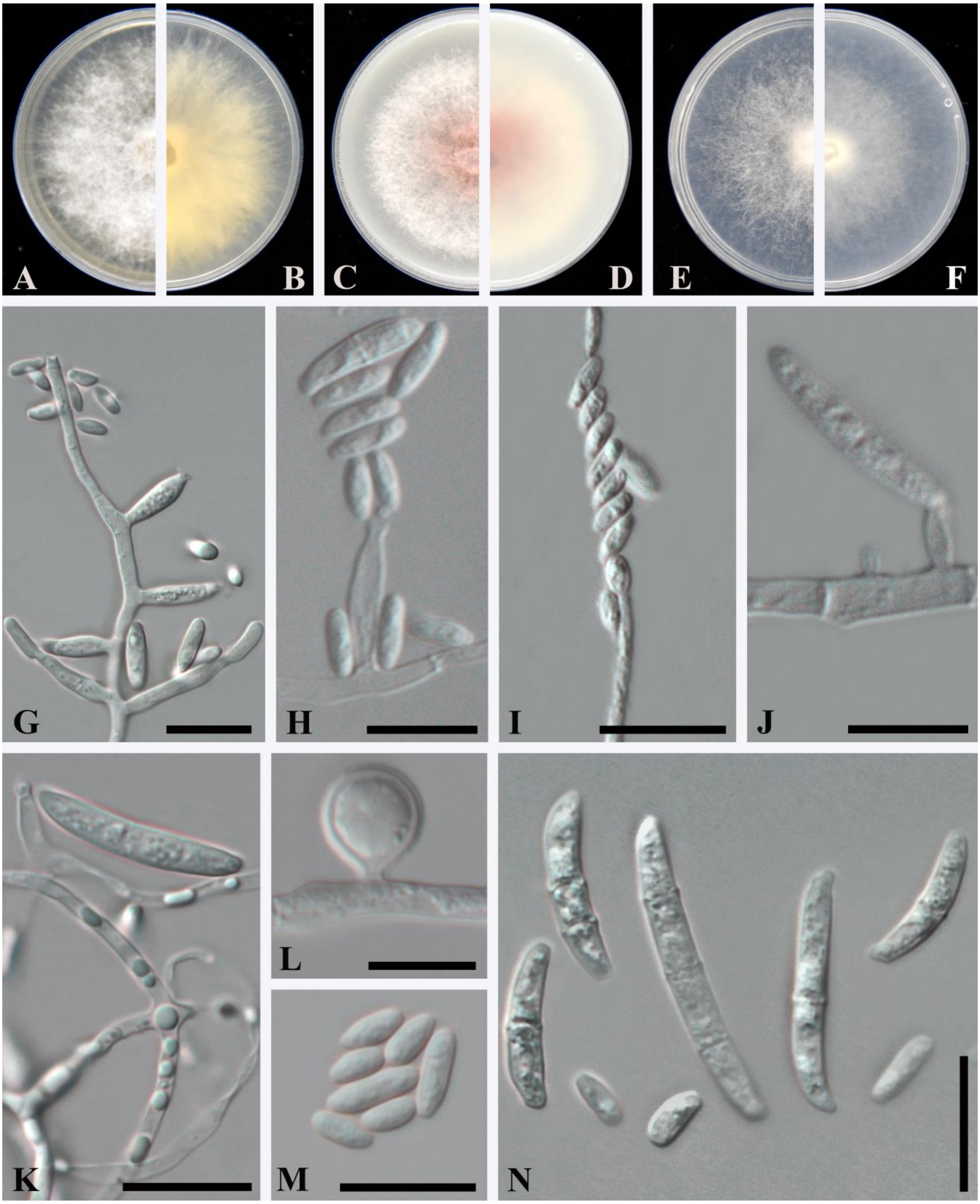

Figure 15 – *Fusarium rosae-roxburghii* (ex-type culture CGMCC3.25479). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–K Aerial conidiophores and conidiogenous cells. L Chlamydospores. M Aerial microconidia. N Aerial macroconidia. Scale bars: G–N = 10 µm.

thick-walled, with a blunt apical cell; basal cell obtuse to papillate, not foot-shaped, 1-septate macroconidia 11.5–19 × 2–3 µm (av. = 15.9 × 2.7 µm, n = 30); 2-septate macroconidia 14–22.5 × 2–3 µm (av. = 18 × 2.7 µm, n = 30); 3-septate macroconidia 18.5–26 × 2–3 µm (av. = 21.5 × 2.9 µm, n = 30). *Chlamydospores* spherical to subspherical, lateral, terminal, or intercalary, solitary, occasionally in chains, thick-walled, 5.5–14.5 µm (av. = 9 µm, n = 30) diam.

Culture characteristics – Colonies on PDA attaining 52 mm diam. after 5 days in the dark at 28°C, colonies fertile, white, raised, cottony, round, with irregular edges, aerial mycelia abundant, and reverse light orange. On OA attaining 48 mm diam. after 5 days, light pink at center and white edges, raised, cottony, round, margin entire, abundant aerial mycelium, and reverse similar. On SNA attaining 52 mm diam. after 5 days, off-white, raised in center, with sparse to moderate aerial mycelium, and reverse similar. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang (HGUP190111, holotype), ex-type living culture: GUCC 190111.1 = CGMCC3.25479; other living culture: GUCC 190111.2.

Notes – In the phylogenetic tree, our collections (CGMCC3.25479 and GUCC 190111.2) are close to *F. cili* (ex-type CGMCC3.25476, in this study), *F. phialophorum* (holotype InaCC F971), and *F. odoratissimum* (holotype InaCC F822), forming an independent clade with high statistical support (BS = 100%, PP = 1.00) (Fig. 11). *Fusarium rosae-roxburghii* is phylogenetically closer to *F. cili*. Sequence similarities and morphological differences between *F. rosae-roxburghii* and *F. cili* are described in the notes of *F. cili* in this study. As shown in Fig. 13a, the PHI test on *F. rosae-roxburghii* also indicated that there is no significant recombination ($p = 0.1587 > 0.05$) between *F. rosae-roxburghii* and its closely related taxa. Therefore, we introduce *F. rosae-roxburghii* as a new species.

Fusarium sambucinum species complex

Fusarium meridionale T. Aoki, Kistler, Geiser & O'Donnell, Fungal Genet. Biol. 41 (6): 618 (2004) Fig. 16

Index Fungorum number: IF843474

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* borne on aerial mycelia, macronematous, irregularly branched. *Aerial conidiogenous cells* polyphialidic, cylindrical, tapering towards the apex or flask-shaped, straight or slightly curved, smooth- and thin-walled, periclinal thickening and collarettes inconspicuous, 8–19 × 2–3.5 µm (av. = 11.7 × 2.8 µm, n = 10). *Macroconidia* gradually curved, sometimes straight, tapering towards the basal part, apical cell blunt, widest at the middle portion; basal cell obtuse, not foot-shaped, 1–5-septate (predominantly 3–4-septate), hyaline, smooth to slightly rough, granular to guttulate; 1-septate macroconidia 9.5–19 × 2.5–3.5 µm (av. = 13.7 × 3 µm, n = 30); 2-septate macroconidia 10–18.5 × 2.5–4 µm (av. = 16.3 × 3.2 µm, n = 30); 3-septate macroconidia 18.5–32.5 × 2.5–4 µm (av. = 24.3 × 3.5 µm, n = 30); 4-septate macroconidia 24.5–29.5 × 3–4 µm (av. = 27 × 3.6 µm, n = 30); 5-septate macroconidia 26.5–40.5 × 3.5–4.5 µm (av. = 32 × 3.7 µm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 55 mm diam. after 5 days in the dark at 28 °C, olivaceous beige, round, margin regular, with abundant aerial hyphae, and reverse concolorous. On OA attaining 50 mm diam. after 5 days, center pale olive-buff, periphery white, flat, margin regular, moderate aerial mycelium, and reverse concolorous. On SNA attaining 50 mm diam. after 5 days, greyish to greyish white, abundant aerial mycelia in center, raised, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang, living cultures: GUCC 190050.1, GUCC 190105.1, and GUCC 190107.1.

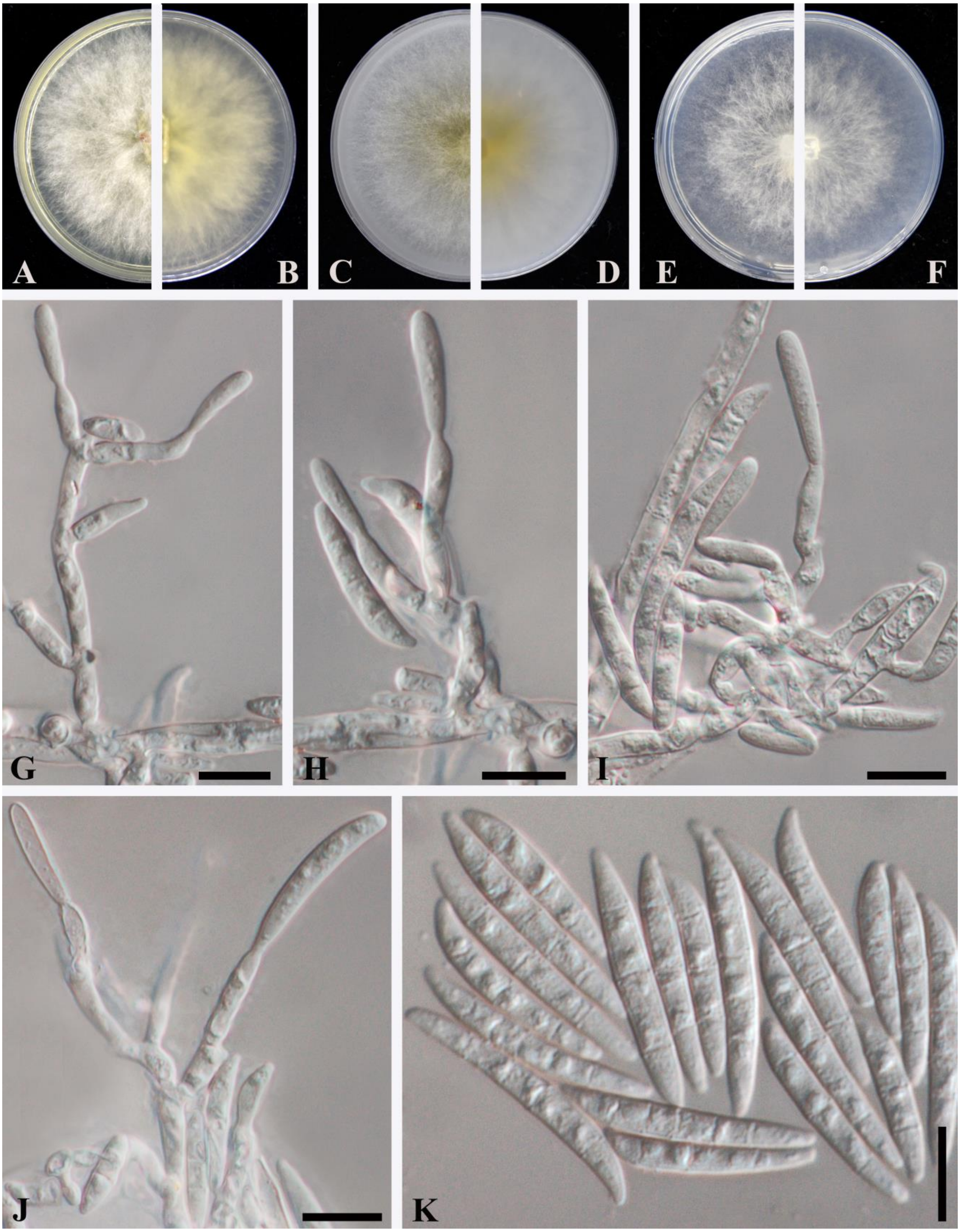

Figure 16 – *Fusarium meridionale* (GUCC 190050.1). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–J Aerial conidiophores and conidiogenous cells. K Macroconidia. Scale bars: G–K = 10 µm.

Notes – Phylogenetic analyses revealed that our collections, GUCC 190050.1, GUCC 190105.1, and GUCC 190107.1, clustered with *F. meridionale* (ex-holotype NRRL 28436) in a clade with high statistical support of 100% BS and 1.00 PP (Fig. 1). The strain GUCC 190050.1

has 99.94% (1766/1767, no gaps) *rpb1* sequence similarity with ex-holotype *F. meridionale*, 99.83% (585/586, one gap) on *tef1*, and 100% (911/911) on *rpb2*. Other genes are missing for ex-holotype NRRL 28436. Our collection is morphologically similar to the ex-holotype *F. meridionale* in having 5-septate macroconidia (average width: 3.7 µm in GUCC 190050.1 vs. < 4.5 µm in NRRL 28436) and gradually curved conidia. Additionally, the widest area of the conidia is in the middle, and the upper and lower half of the conidia are mostly symmetric (O'Donnell et al. 2004). Hence, we introduce our collections as a new host record of *F. meridionale* isolated from the healthy roots of *R. roxburghii*.

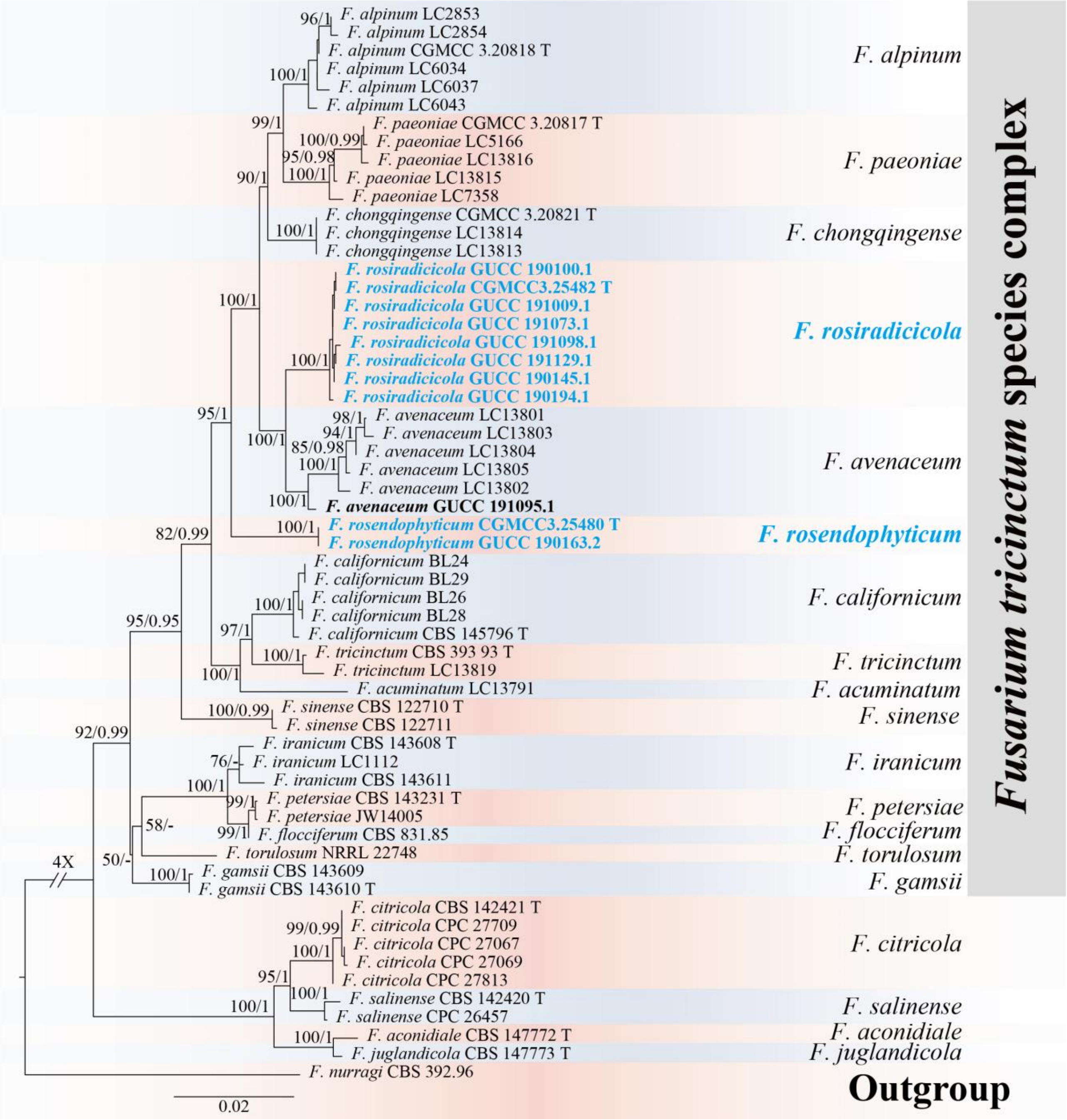

Figure 17 – Phylogenetic relationships of *Fusarium tricinctum* species complex. The phylogenetic tree was generated using the maximum likelihood (ML) method by combining ITS, *rpb1*, *rpb2*, *tef1*, and *tub2* sequence data from 59 strains. The tree is rooted with *F. nurragi* (CBS 392.96). The ML bootstrap support values > 50 % (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near nodes (BS/PP). Strains isolated in this study are indicated in **bold**. New species are in bold blue. **T** holotype or ex-type.

Fusarium tricinctum species complex

Fusarium rosiradicicola H. Zhang & Y.L. Jiang, sp. nov. Fig. 18

Index Fungorum number: IF900492; Facesoffungi numbers: FoF 14977

Etymology – Name refers to the roots of *R. roxburghii*, from which the holotype of this fungus was isolated.

Endophytic in roots and stems of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, arising from aerial hyphae, unbranched or sparsely branched, often reduced into conidiogenous cells. *Aerial conidiogenous cells* monophialidic or polyphialidic, sometimes enteroblastic, hyaline, arising laterally from hyphae, subcylindrical to bottle-shaped, straight to slightly curved, smooth- and thick-walled, apical collarettes and periclinal thickening inconspicuous or absent, 1.5–35 × 1.5–3.5 µm (av. = 15.2 × 2.5 µm, n = 10). *Aerial microconidia* forming small false heads on tips of phialides, hyaline, smooth, thin-walled, 0–1-septate, oblong, apex obtuse, base truncate, straight, aseptate microconidia 5.5–18 × 2–4 µm (av. = 10.8 × 2.8 µm, n = 30); 1-septate microconidia 14.5–24 × 2–4 µm (av. = 19 × 3 µm, n = 30). *Aerial macroconidia* borne on tips of conidiogenous cells on aerial conidiophores, straight, sometimes distinctly curved, 2–5-septate, predominantly 3-septate, hyaline, smooth- and thick-walled, narrowing towards each end, apical cell blunt; basal cell obtuse, not foot-shaped, 2-septate macroconidia 16.5–22.5 × 2–3 µm (av. = 19.9 × 2.7 µm, n = 30); 3-septate macroconidia 22–34.5 × 2.5–4.5 µm (av. = 28.7 × 3.6 µm, n = 30); 4-septate macroconidia 28.5–41.5 × 3–4.5 µm (av. = 35.1 × 3.9 µm, n = 30); 5-septate macroconidia 33.5–44 × 3.5–4.5 µm (av. = 37.1 × 4.1 µm, n = 30). *Chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 22–28 mm diam. after 5 days in the dark at 28 °C, white, somewhat pale pink center, raised, cottony, irregular margin, with abundant aerial hyphae, and reverse light yellow. On OA attaining 50 mm diam. after 5 days, white, light yellow near the center, floccose, raised with entire edge, aerial mycelium moderate, and reverse concolorous. On SNA attaining 28–32 mm diam. after 5 days, buff, raised, aerial mycelia sparse, with an irregular or slightly wavy margin, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots and stems of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang (HGUP 190168, holotype), ex-type living culture: GUCC 190168.1 = CGMCC3.25482; other living cultures: GUCC 190100.1, GUCC 191129.1, GUCC 190145.1, GUCC 191098.1, and GUCC 190194.1. China, Guizhou Province, Guiyang City, natural environment, healthy stems of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang, living cultures: GUCC 191009.1 and GUCC 191073.1.

Notes – Although we are unable to find molecular data for the type species of *F. avenaceum*, we selected several strains of this species from Wang et al. (2022) for phylogenetic analyses in this study. *Fusarium rosiradicola* is phylogenetically sister to *F. avenaceum* with high statistical support (BS = 100%, PP = 1.00) (Fig. 17). *Fusarium rosiradicola* and *F. avenaceum* have similar conidiophores and conidiogenous cells (monophialides or polyphialides) (Crous et al. 2021). However, *F. rosiradicola* is distinct from *F. avenaceum* in having different macroconidial formations (from hyphae in *F. rosiradicola* vs. borne in sporodochia in *F. avenaceum*), macroconidial shapes (straight, sometimes distinctly curved, thick-walled, narrowing towards each end, apical cell blunt, basal cell obtuse, not foot-shaped in *F. rosiradicola* vs. straight to slightly curved, thin-walled, apical cell long and tapering to a point, may be bent, basal cell usually notched, sometimes foot-shaped in *F. avenaceum*), number of macroconidial septa (2–5-septate, predominantly 3-septate in *F. rosiradicola* vs. usually 5-septate, but 3- and 4-septate may be observed in *F. avenaceum*), macroconidial sizes (3-septate macroconidia 22–34.5 µm long in *F. rosiradicola* vs. 37–50 µm long in *F. avenaceum*; 4-septate macroconidia 28.5–41.5 µm long in *F. rosiradicola* vs. 51–58 µm long in *F. avenaceum*; 5-septate macroconidia 33.5–44 µm long in *F. rosiradicola* vs. 54–63 µm long in *F. avenaceum*), and number of microconidial septa (0–1-septate in *F. rosiradicola* vs. 1–2-septate in *F. avenaceum*) and their shapes (oblong in

F. rosiradicola vs. fusoid in *F. avenaceum*) (Wollenweber & Reinking 1935, Leslie & Summerell 2006). In addition, the PHI test on *F. rosiradicola* indicated that there is no significant recombination (p = 0.7858 > 0.05) between *F. rosiradicola* and its closely related taxa as shown in Fig. 13b. Thus, we introduce *F. rosiradicola* as a new species.

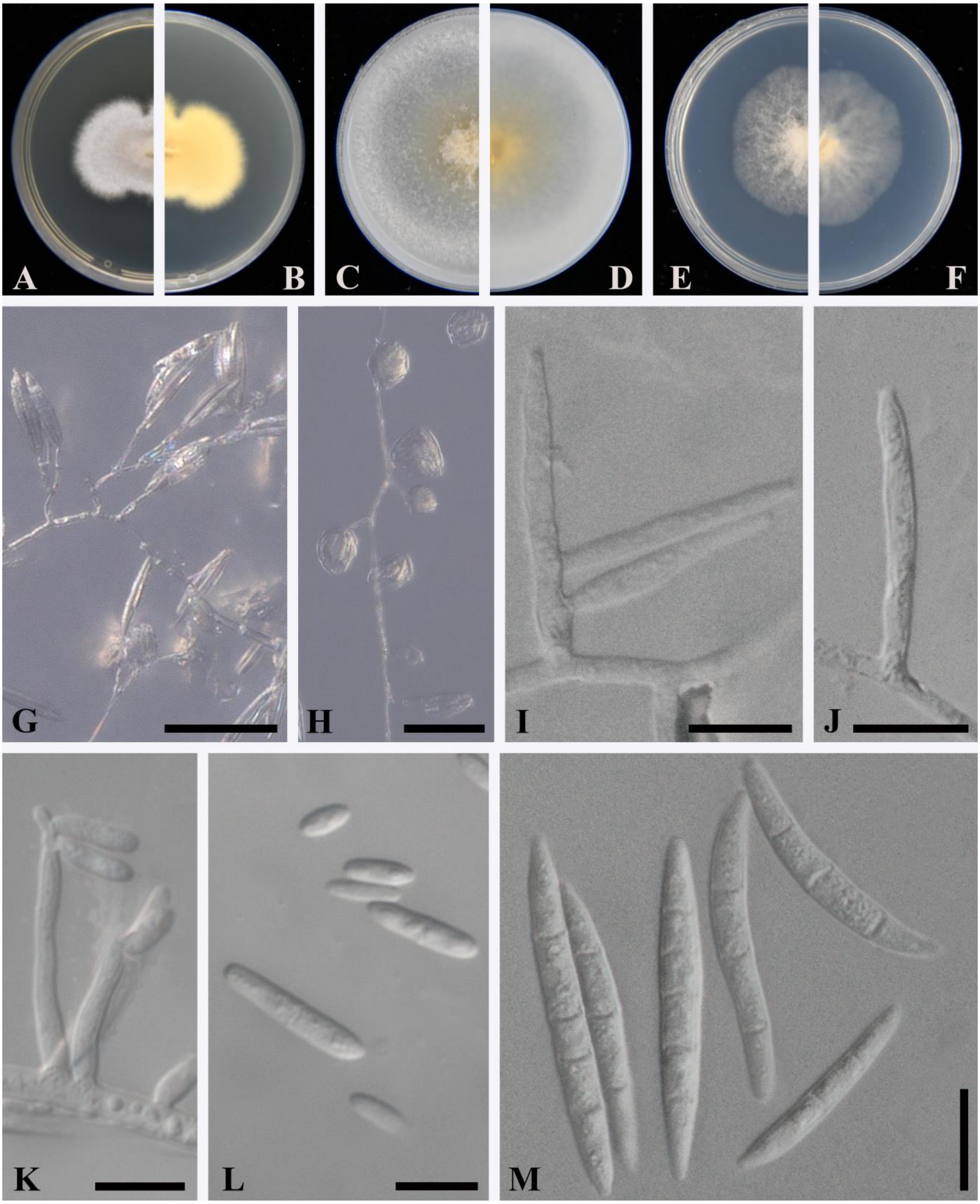

Figure 18 – *Fusarium rosiradicicola* (ex-type culture CGMCC3.25482). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–K Aerial conidiophores and conidiogenous cells. L Aerial microconidia. M Aerial macroconidia. Scale bars: G–H = 50 μm, I–M = 10 μm

Fusarium rosendophyticum H. Zhang & Y.L. Jiang, sp. nov. Fig. 19

Index Fungorum number: IF900493; Facesoffungi numbers: FoF 14978

Etymology – Name refers to endophytic fungi isolated from the *R. roxburghii*.

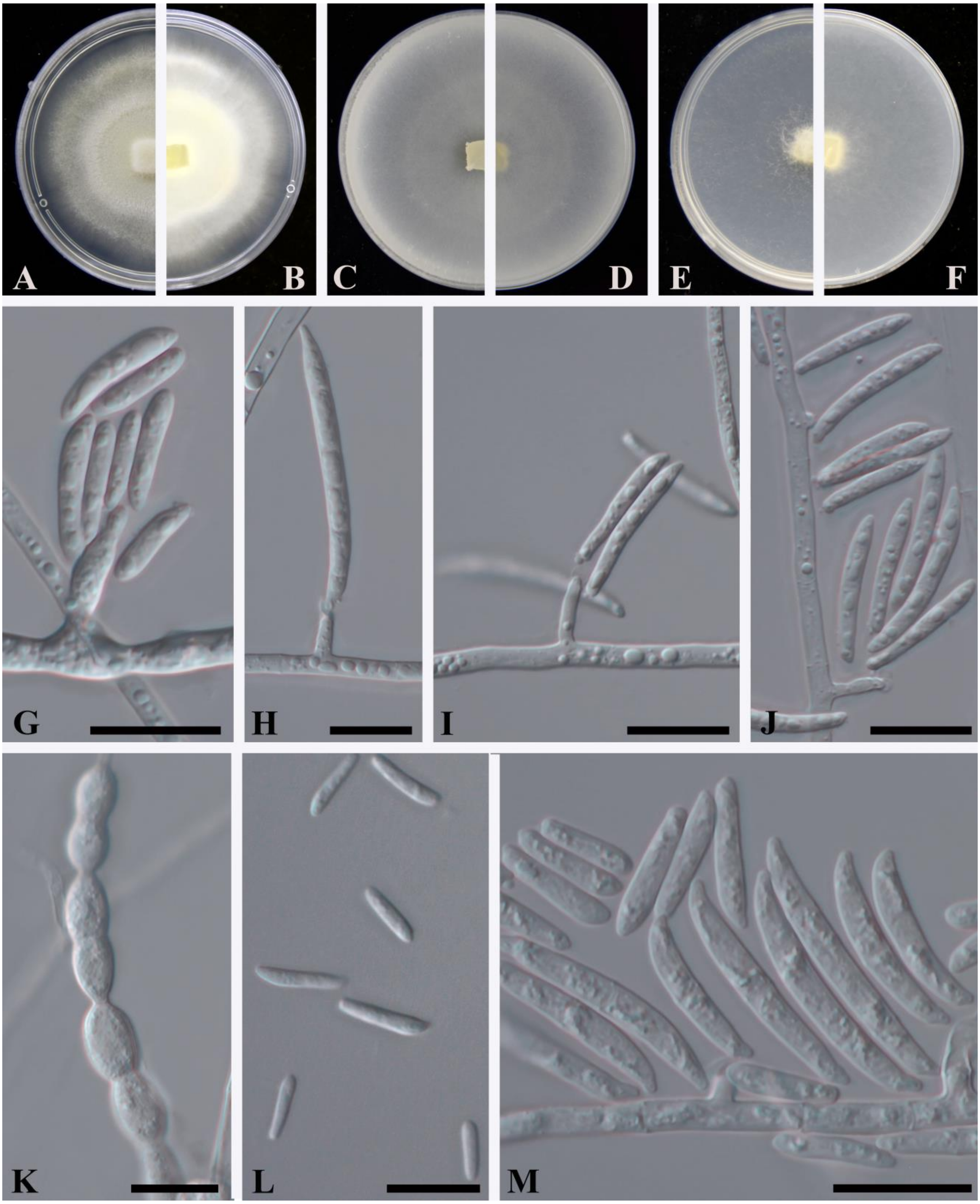

Figure 19 – *Fusarium rosendophyticum* (ex-type culture CGMCC3.25480). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G–J Aerial conidiophores and conidiogenous cells. K Chlamydospores. L–M Aerial microconidia and macroconidia. Scale bars: G–M = 10 μm.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* borne on aerial mycelia, unbranched or sparingly branched, often reduced to conidiogenous cells. *Aerial conidiogenous cells* monophialidic, cylindrical to subcylindrical, or as short lateral pegs, straight to slightly curved, tapering slightly towards the apex, smooth- and thin-walled, periclinal thickenings inconspicuous, collarettes absent to prominent, 1–14.5 × 1–3 µm (av. = 4.4 × 1.6 µm, n = 10). *Aerial microconidia* forming small false heads on tips of monophialides, hyaline, clavate to obclavate, apex obtuse, base truncate, straight, smooth- and thin-walled, aseptate, 4–11.5 × 1–2.5 µm (av. = 7.9 × 1.8 µm, n = 30). *Aerial macroconidia* borne on tips of conidiogenous cells on aerial conidiophores, slender with no significant curvature to curved with parallel walls, 1–5-septate, predominantly 1–3-septate, hyaline, smooth- and thin-walled, apical cell curved to blunt; basal cell papillate to poorly developed, foot-shaped, 1-septate macroconidia 11–22.5 × 1.5–2.5 µm (av. = 15.4 × 2.2 µm, n = 30); 2-septate macroconidia 19–33 × 2–3 µm (av. = 22.2 × 2.3 µm, n = 30); 3-septate macroconidia 23–29.5 × 2–3.5 µm (av. = 25.9 × 2.4 µm, n = 30); 4-septate macroconidia 34–36 × 2–3 µm (av. = 35.3 × 2.7 µm, n = 30); 5-septate macroconidia 34–36 × 2–3 µm (av. = 34.9 × 2.8 µm, n = 30). *Chlamydospores* spherical, ellipsoidal to cylindrical, mostly in long chains, lateral, terminal, or intercalary, rough or smooth, thick-walled, 5.5–11.5 × 23.5–8 µm (av. = 7.4 × 5.1 µm, n = 30), l: w = 1–3 (av. = 1.5, n = 30).

Culture characteristics – Colonies on PDA attaining 50 mm diam. after 5 days in the dark at 28 °C, beige, flat, appressed, cottony, irregular concentric circles, undulate margin, moderate aerial mycelia, and reverse concolorous. On OA attaining 60 mm diam. after 5 days, grey, smooth, flat, round, margin entire, with sparse aerial hyphae, and reverse concolorous. On SNA attaining 50 mm diam. after 5 days, transparent, smooth, flat, round, with sparse aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang (HGUP 190163, holotype), ex-type living culture: GUCC 190163.1 = CGMCC3.25480; other living culture: GUCC 190163.2.

Notes – Phylogenetically, *F. rosendophyticum* belongs to the *F. tricinctum* species complex, and forms a separate branch with BS = 95% and PP = 1.00 statistical support (Fig. 17). This species is phylogenetically close to *F. rosiradicicola* (ex-type CGMCC3.25482 in this study), sharing 99.62% (523/525, one gap) sequence similarity on ITS, 96.81% (1702/1758, no gaps) on *rpb1*, 96.74% (919/950, no gaps) on *rpb2*, and 97.16% (513/528, no gaps) on *tub2*. The *tef1* is missing in ex-type CGMCC3.25482. Morphologically, *F. rosendophyticum* differs from the latter in having different aerial conidiogenous cells (cylindrical to subcylindrical, or as short lateral pegs, thin-walled, 1–14.5 × 1–3 µm, av. = 4.4 × 1.6 µm of *F. rosendophyticum* vs. subcylindrical to bottle-shaped, thick-walled, 1.5–35 × 1.5–3.5 µm, av. = 15.2 × 2.5 µm of *F. rosiradicicola*), aerial microconidia (aseptate, 4–11.5 × 1–2.5 µm, av. = 7.9 × 1.8 µm of *F. rosendophyticum* vs. 0–1-septate, aseptate microconidia 5.5–18 × 2–4 µm, av. = 10.8 × 2.8 µm; 1-septate microconidia 14.5–24 × 2–4 µm, av. = 19 × 3 µm of *F. rosiradicicola*), and aerial macroconidia (slender with no significant curvature to curved with parallel walls, 1–5-septate, predominantly 1–3-septate, thin-walled, basal cell papillate to poorly developed, foot-shaped of *F. rosendophyticum* vs. straight, sometimes distinctly curved, 2–5-septate, predominantly 3-septate, thick-walled, basal cell obtuse, not foot-shaped of *F. rosiradicicola*). The PHI test on *F. rosendophyticum* also showed no significant recombination ($p = 0.7858 > 0.05$) between *F. rosendophyticum* and its closely related taxa as shown in Fig. 13b. Thus, *F. rosendophyticum* is introduced as a new species.

Luteonectria Sand.-Den., L. Lombard, Schroers & Rossman

Luteonectria was introduced by Crous et al. (2021), with *L. albida* as the type species. Diagnostic morphological features of the genus are off-white to pale luteous perithecia that do not change color on KOH or lactic acid, formed on the well-developed stroma, asci clavate, ascospores fusiform, 3-septate, finely striate; asexual morphologies, conidiophores arising from aerial mycelium, monophialides producing fusoid and multiseptate macroconidia, lacking micro- and mesoconidia, and chlamydospores. To date, only two species have been listed in Index Fungorum (2023), *L. albida* and *L. nematophila*. In this study, two strains of endophytic *Luteonectria* were isolated from *R. roxburghii* (Fig. 1).

Luteonectria nematophila (Nirenberg & Hagedorn) Sand.-Den. & L. Lombard, Stud. Mycol. 98: 60 (2021) Fig. 20

Index Fungorum number: IF838666

Basionym: *Fusarium nematophilum* Nirenberg & Hagedorn, Nachrichtenbl. Deutsch. Pflanzenschutzdienstes 60: 214. 2008.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* not observed. *Conidiophores* macronematous, borne on aerial mycelia, hyaline, unbranched or sparingly branched, bearing lateral and terminal phialides, often reduced to conidiogenous cells. *Aerial conidiogenous cells* mono- to polyphialidic, formed directly from hyphae, hyaline, smooth, straight or slightly curved, cylindrical, with single or abundant conidiogenous loci, 10–56 × 3–4.5 µm (av. = 26.4 × 3.9 µm, n = 10). *Aerial macroconidia* straight to moderately curved, tapering towards the basal part, apical cell blunt and smaller than the adjacent cell; basal cell papillate to poorly developed, foot-shaped, 3-septate, hyaline, thin- and smooth-walled, 32–48.5 × 4–6 µm (av. = 41.9 × 5.4 µm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 35–38 mm diam. after 7 days in the dark at 28°C, light yellow, round, slightly raised, margin regular, with abundant aerial mycelium, and reverse yellow. On OA attaining 38 mm diam. after 7 days, light olive, round, flat, appressed, flocculent, margin entire, with sparse aerial mycelium, and reverse light olive. On SNA attaining 34 mm diam. after 7 days, white, raised with abundant aerial mycelium in center, flat with an entire edge, with sparse aerial mycelium, and reverse white. Pigment and odor absent.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy roots of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang, living culture: GUCC 190041.1. China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang, living culture: GUCC 198542.1.

Notes – Our collections, GUCC 190041.1 and GUCC 198542.1, were phylogenetically similar to *L. nematophila* (ex-type NRRL 54600) as they clustered together with high statistical support (BS = 99%, PP = 1.00) (Fig. 1), sharing 100% (844/844) similarity for *rpb1* and 100% (837/837) similarity for *rpb2*. Other genes are missing for the ex-type NRRL 54600. Our collections resemble the ex-type of *L. nematophila* (NRRL 54600) in having conidiophores (borne on aerial mycelia, simple, unbranched or sparingly branched, bearing lateral and terminal phialides), conidiogenous cells (mono- to polyphialidic, cylindrical; 10–56 × 3–4.5 µm in GUCC 190041.1 vs. 8.9–36 × 3.5–4 µm in NRRL 54600), and macroconidia (fusiform, straight to moderately curved, tapering towards both ends; 3-septate, 32–48.5 × 4–6 µm in GUCC 190041.1 vs. 29–43 × 6.1–8.2 µm in NRRL 54600) of similar morphologies. This study revealed that the morphology and phylogenetic identity of this isolate overlaps with *L. nematophila*; we therefore report our collections as a new host record isolated from the roots of *R. roxburghii* (Nirenberg & Hagedorn 2008).

Neocosmospora E.F. Sm.

Neocosmospora, typified by *N. vasinfecta*, is diagnostically characterized as asci saccate, clavate to cylindrical; ascospores globose to ellipsoidal, 0-1–septate, longitudinally striate, cerebriform or spinulose; asexual morphs producing micro- and macroconidia on aerial conidiophores with monophialides or only macroconidia in sporodochia (Crous et al. 2021). According to Index Fungorum (2023), a total of 141 epithets have been placed in *Neocosmospora* and more than 80 species have been accepted (Wijayawardene et al. 2022). *Neocosmospora* is widely distributed, frequently found in soil, plant debris, living plant material, air, and water, and contains saprophytes, endophytes, pathogens, and opportunistic animal pathogens (Sandoval-Denis et al. 2019). In this study, ten *Neocosmospora* strains, including six species, were isolated from *R. roxburghii* (Fig. 21).

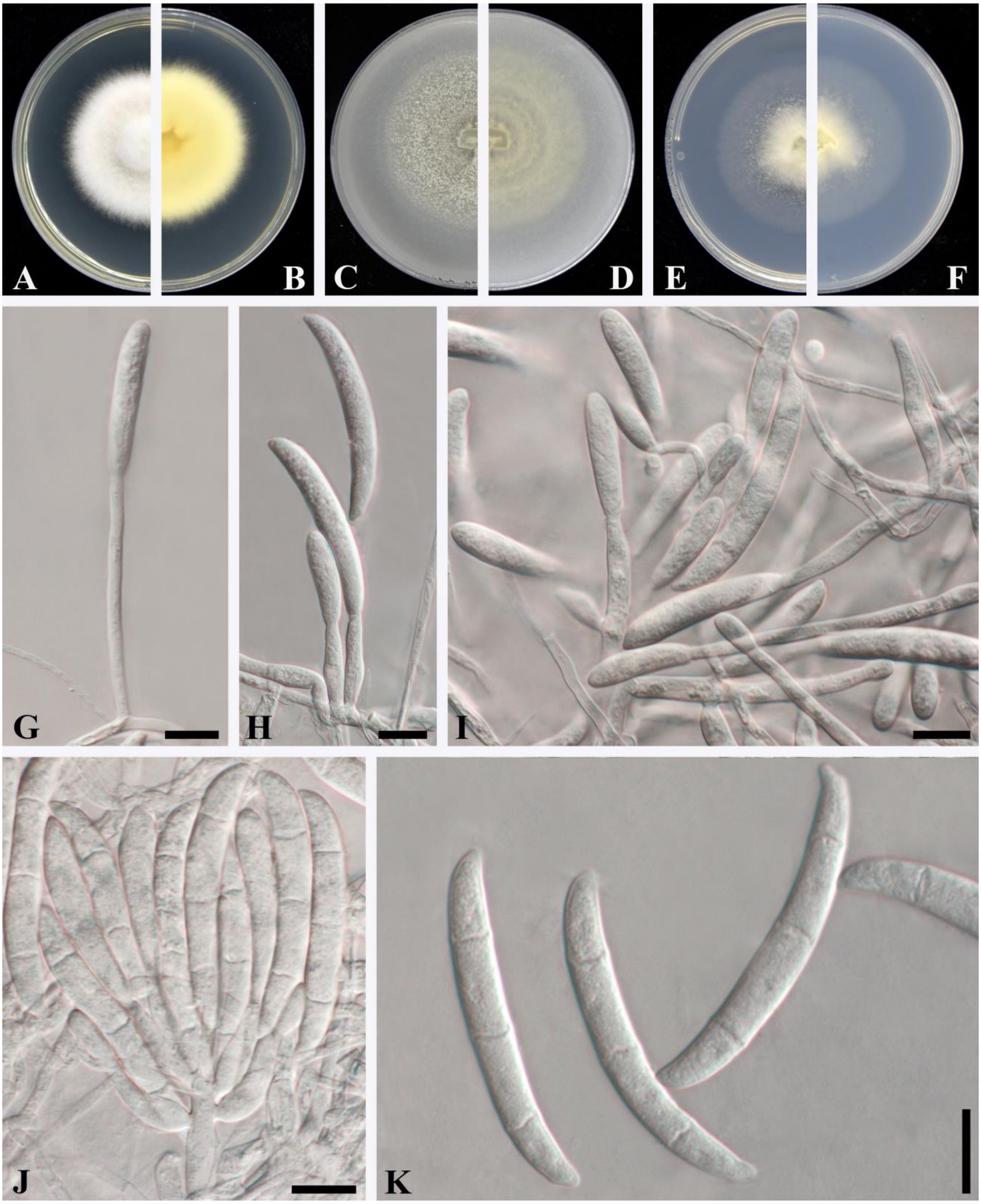

Figure 20 – *Luteonectria nematophila* (GUCC 190041.1). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G–J Aerial conidiophores and conidiogenous cells. K Macroconidia. Scale bars: G–K = 10 µm.

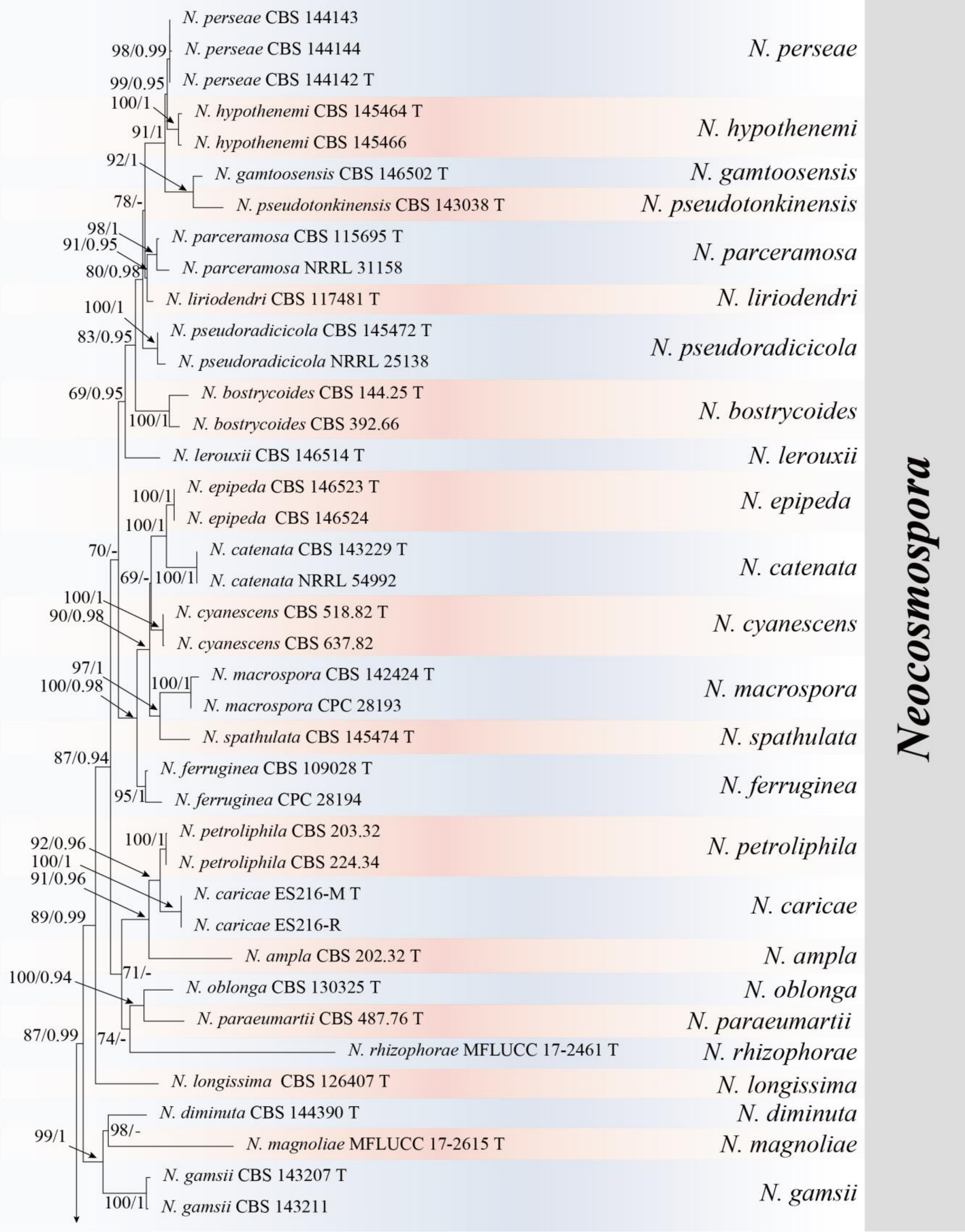

Figure 21 – Phylogenetic relationships of *Neocosmospora*. The phylogenetic tree was generated using the maximum likelihood (ML) method by combining *acl1*, *CaM*, ITS, LSU, *rpb1*, *rpb2*, and *tef1* sequence data from 196 strains. The tree is rooted with *Geejayessia cicatricum* (CBS 125552) and *G. atrofusca* (NRRL 22316). The ML bootstrap support values > 50 % (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near nodes (BS/PP). Strains isolated in this study are indicated in **bold**. New species and combinations are shown in bold blue and blue, respectively. **T** holotype or ex-type.

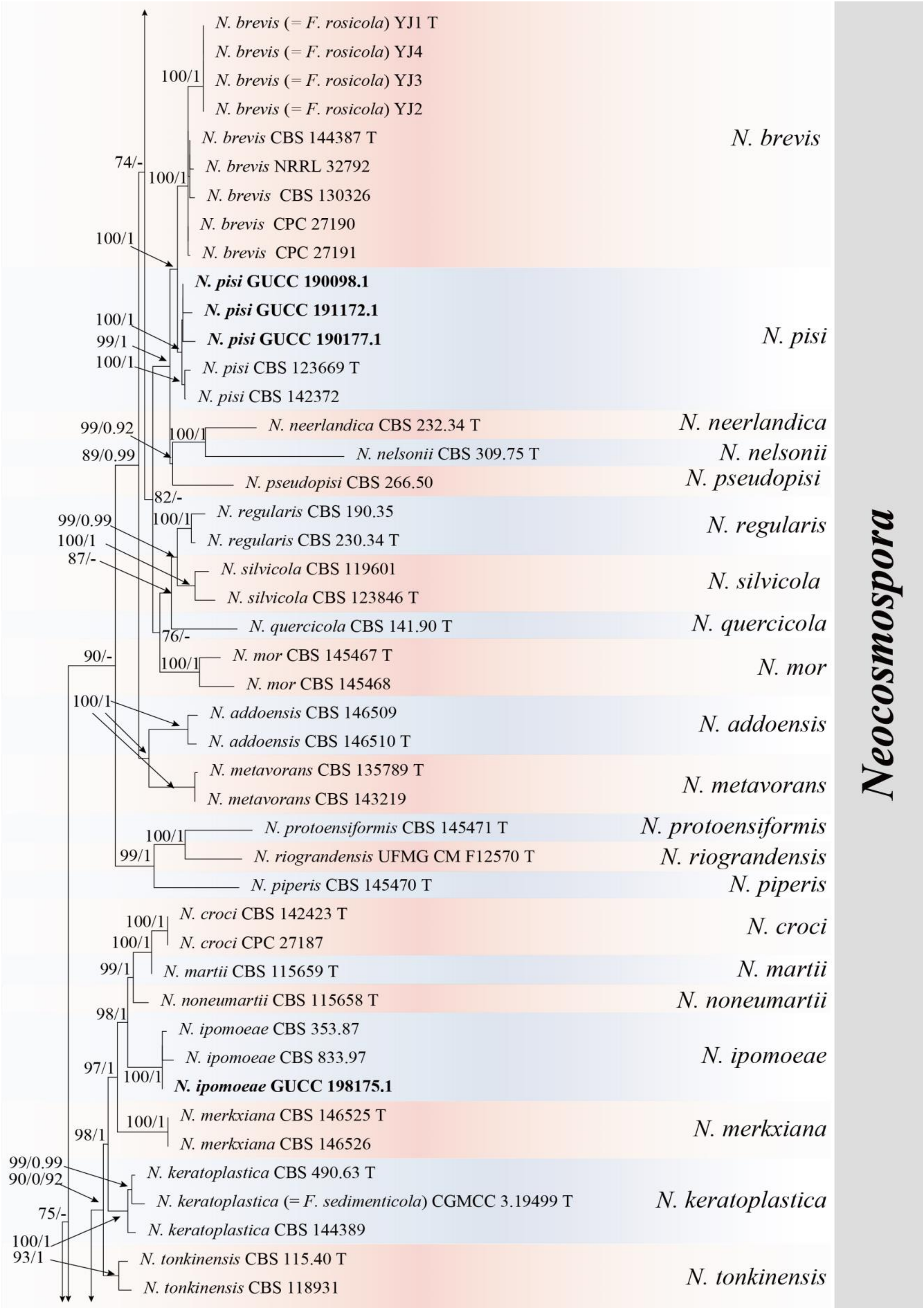

Figure 21 – Continued.

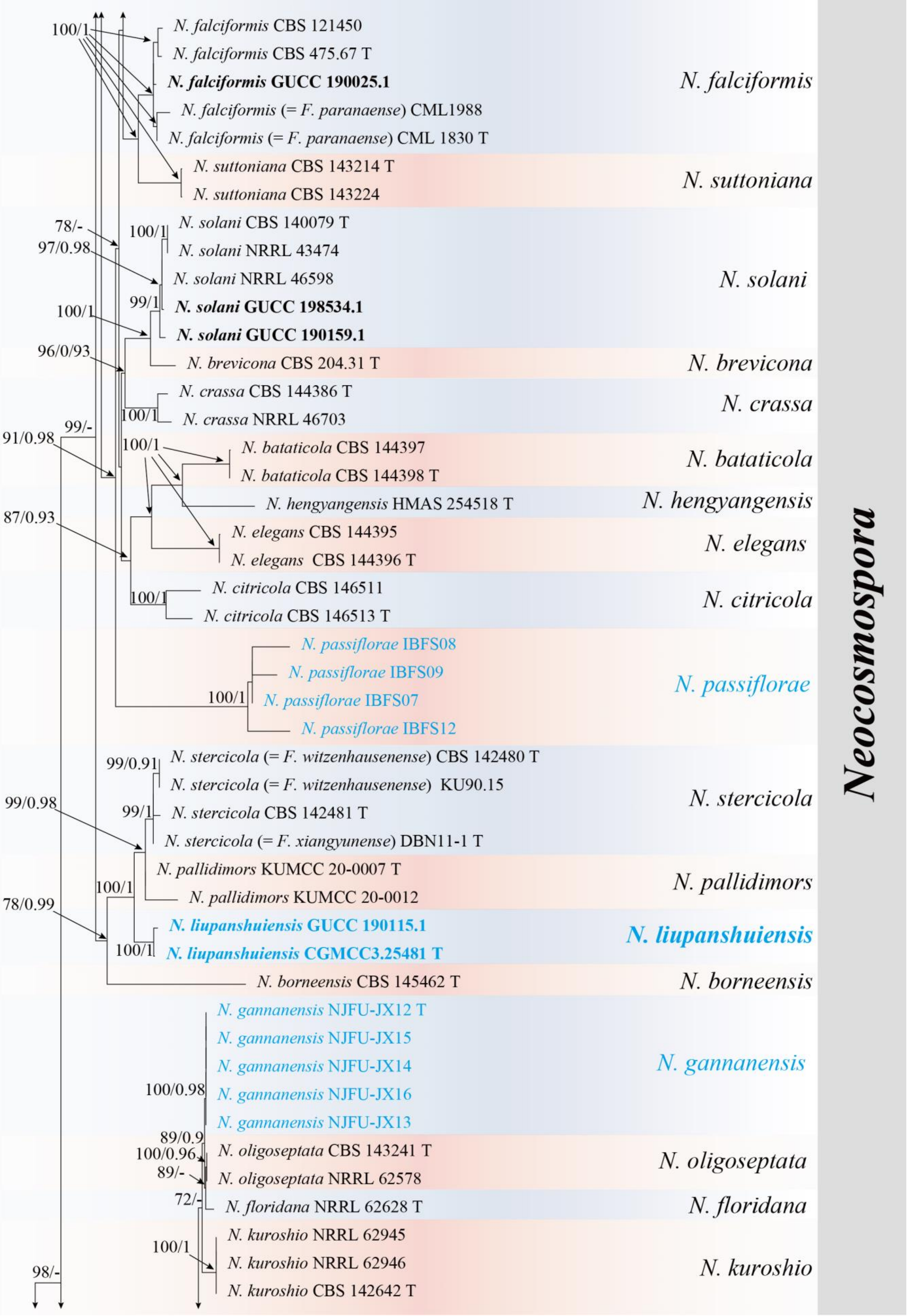

Figure 21 – Continued.

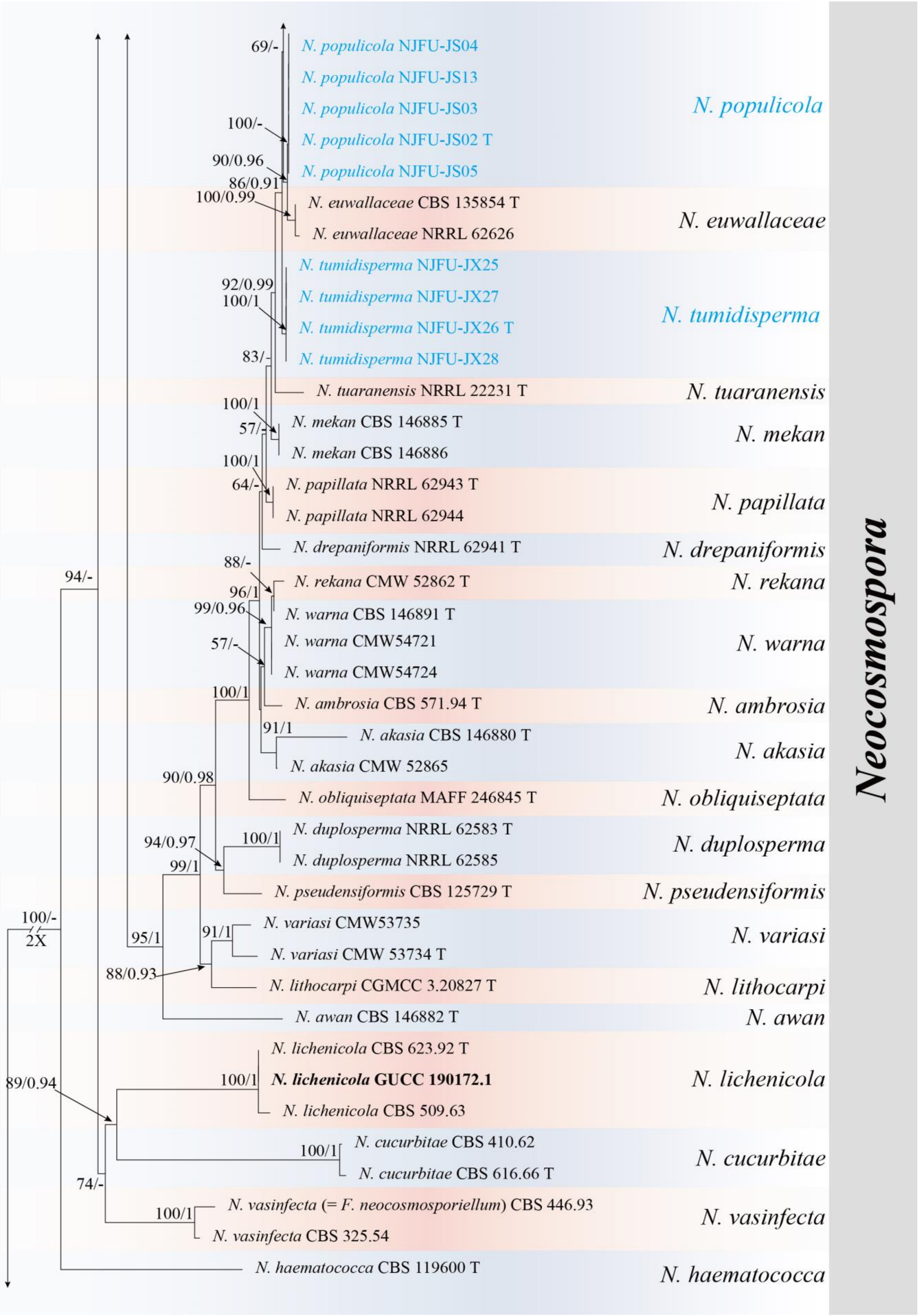

Figure 21 – Continued.

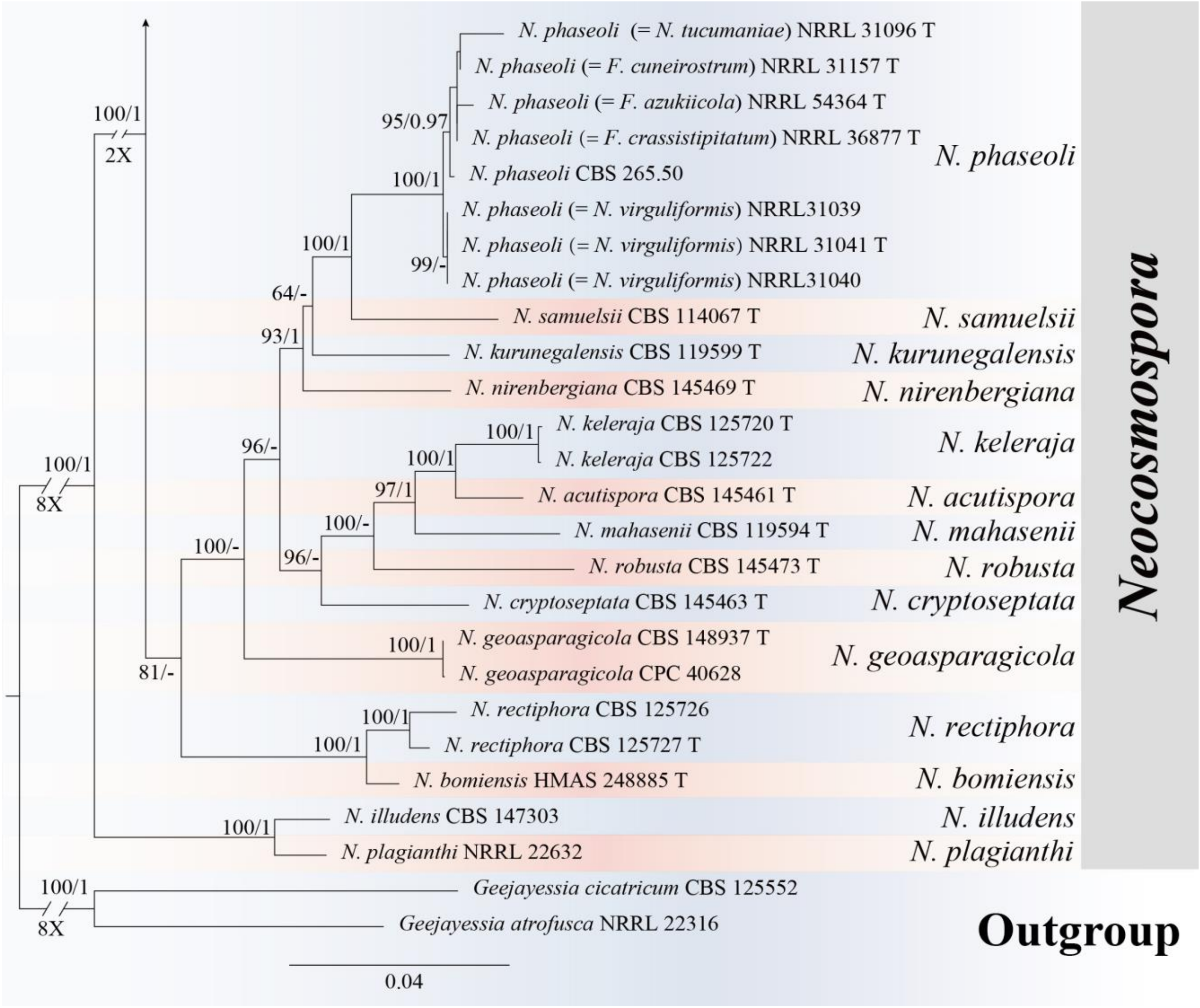

Figure 21 – Continued.

Neocosmospora falciformis (Carrión) L. Lombard & Crous, Stud. Mycol. 80: 227 (2015) Fig. 22

Index Fungorum number: IF810958

Basionym: *Cephalosporium falciforme* Carrion, Mycologia 43: 523 (1951).

Synonyms: *Acremonium falciforme* (Carrion) W. Gams, Cephalosporium-artige Schimmelpilze: 139 (1971).

Fusarium falciforme (Carrión) Summerb. & Schroers, Journal of Clinical Microbiology 40 (8): 2872 (2002)

Fusarium paranaense S.S. Costa et al., Fungal Biology 120 (1): 55 (2015).

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* light yellow, formed on PDA. *Sporodochial conidiophores* macronematous, borne on agar substrate, hyaline, solitary to densely aggregated, irregularly branched, bearing terminal or intercalary mono- and polyphialides. *Sporodochial conidiogenous cells* mono- and polyphialidic, hyaline, smooth- and thin-walled, straight or slightly curved, subcylindrical to bottle-shaped, flared apical collarettes and periclinal thickening present, 12–32.5 × 2.5–4 μm (av. = 20.1 × 3.2 μm, n = 10). *Microconidia* oblong with obtuse ends, aseptate, hyaline, smooth- and thin-walled, straight to slightly curved, 7–15 × 2.5–4.5 μm (av. = 12.2 × 3.6 μm, n = 30). *Macroconidia* fusiform to falcate, hyaline, smooth- and thin-walled, straight to slightly curved, with a blunt apical cell, basal cell obtuse, not foot-shaped, 1–3-septate; 1-septate macroconidia 15.5–26.5 × 3–5 μm (av. = 19.6 × 4.1

µm, n = 30); 2-septate macroconidia 21–26 × 4–5 µm (av. = 23.8 × 4.5 µm, n = 30); 3-septate macroconidia 24–30.5 × 4–5 µm (av. = 27.5 × 4.6 µm, n = 30). *Chlamydospores* not observed.

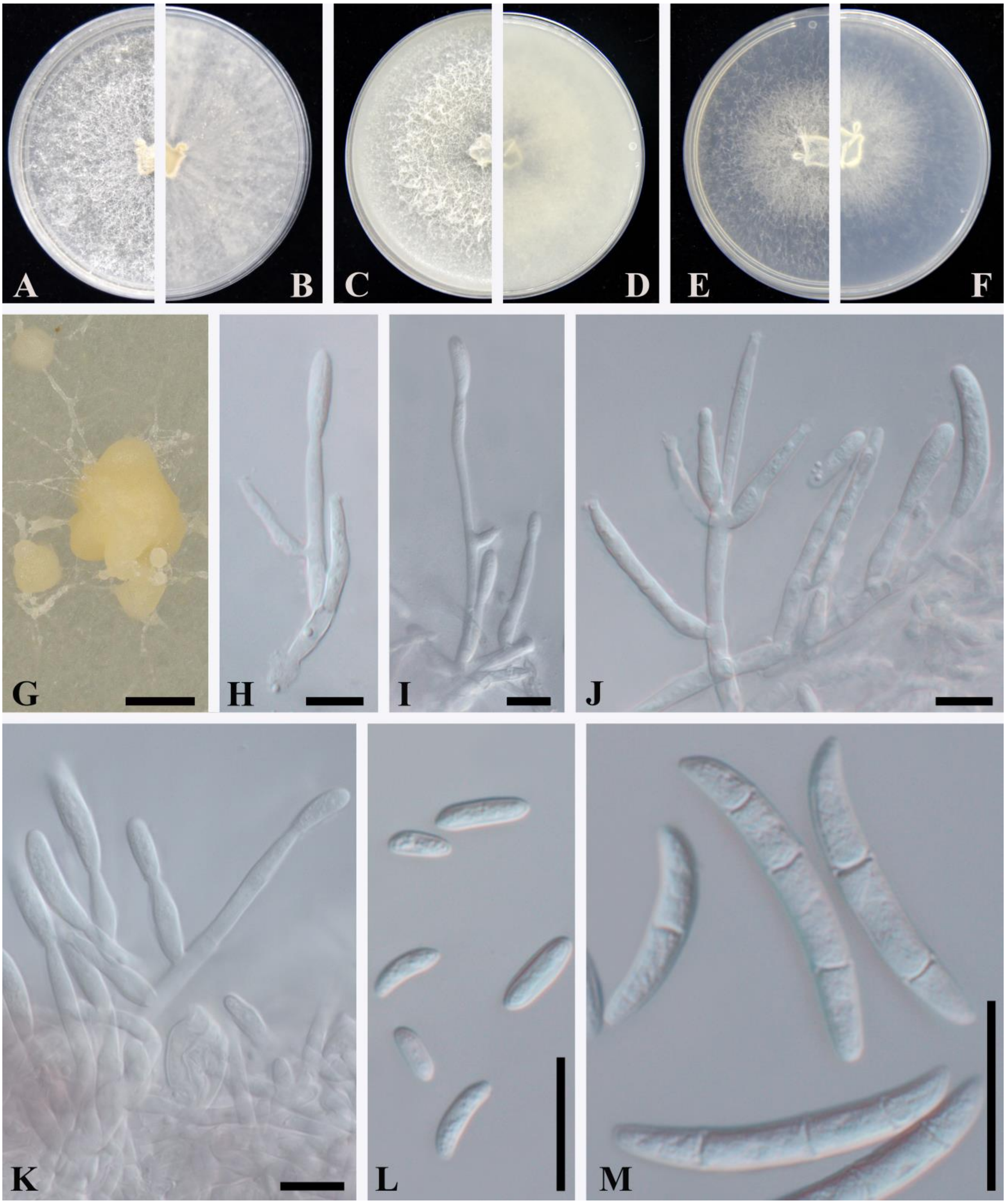

Figure 22 – *Neocosmospora falciformis* (GUCC 190025.1). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–K Sporodochial conidiophores and conidiogenous cells. L Microconidia. M Macroconidia. Scale bars: G = 500 µm, H–M = 10 µm.

Culture characteristics – Colonies on PDA attaining 60 mm diam. after 5 days in the dark at 28 °C, white, round, flocculent, entire margin, moderate aerial mycelium, and reverse off-white. On

OA attaining 50 mm diam. after 5 days, grey, round, flocculent, moderate aerial mycelium, and reverse concolorous. On SNA attaining 55 mm diam. after 5 days, pale grey, flocculent, with sparse aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy roots of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang, living culture: GUCC 190025.1.

Notes – *Fusarium paranaense* was first described by Costa et al. (2016), and ex-holotype strain is CML 1830. Sandoval-Denis et al. (2019) and Crous et al. (2021) treated *F. paranaense* as a synonym of *N. falciformis*. *Neocosmospora falciformis* is a combination species established by Lombard et al. (2015) with a designated ex-type culture of CBS 475.67. In this work, phylogenetic analyses revealed that our collection GUCC 190025.1 clustered with CBS 475.67 and CML 1830 in a clade with statistical support of 100% BS and 1.00 PP (Fig. 21). Compared to CBS 475.67, our sequences share 99.83% (590/591, no gaps), 99.82% (560/561, no gaps), 100% (486/486), 99.88% (832/833, no gaps), 99.63% (1333/1338, 2 gaps), 99.88% (828/829, 1 gap), and 98.81% (579/586, 3 gaps) similarities between the two isolates for *acl1*, *CaM*, ITS, LSU, *rpb1*, *rpb2*, and *tef1* gene regions, respectively. Morphologically, our collection is similar to the ex-type, with similar sporodochial conidiophores (solitary to densely aggregated, verticillately branched or rarely unbranched, forming apical monophialides), sporodochial macroconidia (cylindrical, fusiform to falcate; 1-septate macroconidia 15.5–26.5 × 3–5 µm, av. = 19.6 × 4.1 µm in GUCC 190025.1 vs. 12–27.5 × 2.5–4 µm in the ex-type; 3-septate macroconidia 24–30.5 × 4–5 µm, av. = 27.5 × 4.6 µm in GUCC 190025.1 vs. 22–37.5 × 2.5–5 µm in the ex-type), and microconidial morphology (oblong with obtuse ends) (Costa et al. 2016, Sandoval-Denis et al. 2018). Therefore, we introduce our collection as a new host record of *N. falciformis* isolated from the healthy roots of *R. roxburghii*.

Neocosmospora gannanensis (S.C. Lai, L.L. Dai & D.J. Hao) H. Zhang & Y.L. Jiang, comb. nov.

Index Fungorum number – IF900495

Basionym – *Fusarium gannanense* S.C. Lai, L.L. Dai & D.J. Hao, Mycological Progress 21: 70 (2022).

Description and illustration – See Lai et al. (2022).

Material examined – China, Jiangxi, Ganzhou, Xunwu, Xiangshan Town, from the oral mycetangium of a *Euwallacea interjectus* infesting a trunk of a live *Triadica cochinchinensis* Loureiro, 17 July 2021, Shengchang Lai; holotype: CFCC 57491, dried specimen: NJFU-JX12; ex-type: NJFU-JX12; ITS-28S rDNA: LC702041, *tef1*: LC701609, *rpb1*: LC701945, *rpb2*: LC701981, LC702017.

Notes – Based on the phylogenetic analyses, *F. gannanense* belongs to the genus *Neocosmospora*, with BS = 100% and BI = 0.98 statistical support. *Fusarium gannanense* is phylogenetically close to *N. oligoseptata* (ex-type CBS 143241) (Fig. 21). Morphologically, *F. gannanense* and *N. oligoseptata* have similar aerial conidiophores (erect, unbranched or sometimes sparsely branched, thin-walled, forming monophialides often integrated at the apex), aerial phialides (subcylindrical to subulate), aerial conidia (possesses two different shapes), sporodochial conidiophores (shorter than aerial conidiophores), sporodochial phialides (simple and subcylindrical), and sporodochial conidia (possesses two distinct shapes). However, *F. gannanense* and *N. oligoseptata* also have a significant difference based on aerial conidiophores (up to 280 µm long in *F. gannanense* vs. up to 130 µm long in *N. oligoseptata*), aerial conidia (first shape 0–3-septate in *F. gannanense* vs. 0–2-septate in *N. oligoseptata*; the second shape 1–5-septate in *F. gannanense* vs. 1–3-septate in *N. oligoseptata*), sporodochial conidiophores (often branched in *F. gannanense* vs. unbranched or sometimes sparsely branched in *N. oligoseptata*), sporodochial phialides (collarette inconspicuous in *F. gannanense* vs. conspicuous in *N. oligoseptata*), and sporodochial conidia (first shape 0–6-septate in *F. gannanense* vs. 0–5-septate in *N. oligoseptata*) (Aoki et al. 2018, Sandoval-Denis et al. 2019). These two species share similar morphological features but also possess unique microstructures. Therefore, we transferred *F. gannanense* to *Neocosmospora* as a new combination and named it *N. gannanensis*.

Neocosmospora liupanshuiensis H. Zhang & Y.L. Jiang, sp. nov. Fig. 23

Index Fungorum number: IF900500; Facesoffungi numbers: FoF 14979

Etymology – Name refers to the location where the fungus was collected, Liupanshui City, Guizhou, China.

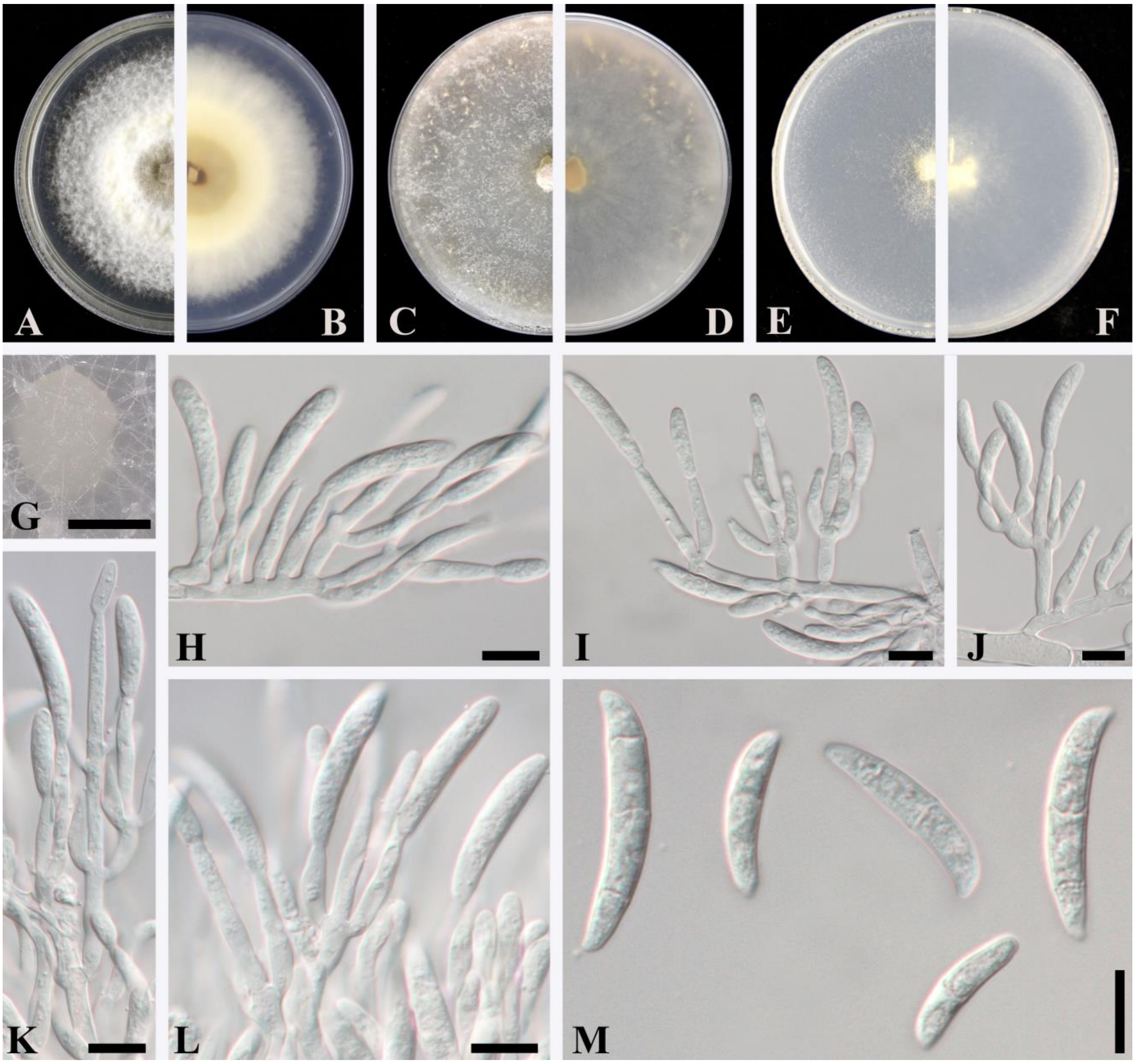

Figure 23 – *Neocosmospora liupanshuiensis* (ex-type culture CGMCC3.25481). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–L Sporodochial conidiophores and conidiogenous cells. M Macroconidia. Scale bars: G = 200 µm, H–M = 10 µm.

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* grey to pale luteous colored, formed on SNA or PDA. *Sporodochial conidiophores* macronematous, hyaline, irregularly or verticillately branched, often richly branched, bearing terminal or lateral polyphialides. *Sporodochial conidiogenous cells* polyphialidic, hyaline, smooth, straight or slightly curved, subulate to subcylindrical, thin-walled, with minute periclinal thickenings, collarette absent or indistinct, 9–31 × 2.5–4 µm (av. = 17.1 × 3.1 µm, n = 10). *Sporodochial macroconidia* tapering towards both ends, straight to curved with parallel walls, tapering towards the basal part, apical cell blunt and smaller than the adjacent cell; basal cell obtuse to papillate, not foot-shaped, 1–3-septate, hyaline, thin- and smooth-walled; 1-septate macroconidia

14–25 × 3.5–5.5 µm (av. = 19.5 × 4.1 µm, n = 30); 2-septate macroconidia 21.5–30 × 3.5–5.5 µm (av. = 25.6 × 4.5 µm, n = 30); 3-septate macroconidia 23–36 × 4–5.5 µm (av. = 30 × 4.7 µm, n = 30); overall 14–36 × 3.5–5.5 µm (av. = 25 × 4.4 µm, n = 30). *Microconidia* and *chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 50 mm diam. after 7 days in the dark at 28 °C, white, cottony, circular, raised, margin regular, aerial mycelium abundant, and reverse light yellow. On OA attaining 55 mm diam. after 7 days, light yellow to white, flat, flocculent, aerial mycelia sparse, and reverse concolorous. On SNA attaining 55 mm diam. after 7 days, light grey, with sparse aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang (HGUP 190201, holotype), ex-type living culture: GUCC 190201.1 = CGMCC3.25481; other living culture: GUCC 190115.1.

Notes – In the phylogenetic tree, *N. borneensis*, *N. liupanshuiensis*, *N. pallidimors*, and *N. stercicola* were clustered in a moderately supported clade (BS = 78%, PP = 0.99). *Neocosmospora liupanshuiensis* (CGMCC3.25481 and GUCC 1900115.1) forms an independent branch with high statistical support (BS = 100%, PP = 1.00) (Fig. 21). *Neocosmospora liupanshuiensis* is phylogenetically close to *N. pallidimors*, sharing 98.28% (457/465, 3 gaps), 99.75% (804/806 no gaps), and 99.34% (450/453, one gap) similarities for ITS, LSU, and *tef1*, respectively. Morphologically, *N. liupanshuiensis* differs from *N. pallidimors* in having sporodochia (grey to pale luteous of *N. liupanshuiensis* vs. black of *N. pallidimors*), sporodochial conidiophores (irregularly or verticillately branched, often richly branched, bearing terminal or lateral polyphialides in *N. liupanshuiensis* vs. simple or branched, more rarely irregularly or sympodially, bearing terminal and lateral, single monophialides in *N. pallidimors*), sporodochial conidiogenous cells (with minute periclinal thickenings in *N. liupanshuiensis* vs. with rather inconspicuous periclinal thickening in *N. pallidimors*), and macroconidia (thin- and smooth-walled, overall 14–36 × 3.5–5.5 µm, av. = 25 × 4.4 µm in *N. liupanshuiensis* vs. granulate, thick-walled, 30–40 × 4–7 µm, av. = 35.2 × 5.7 µm in *N. pallidimors*). In addition, microconidia and chlamydospores not observed in *N. liupanshuiensis*, while observed in *N. pallidimors* (Karunarathna et al. 2020). Moreover, the PHI test on *N. liupanshuiensis* indicated that there is no significant recombination (p = 1.0 > 0.05) between *N. liupanshuiensis* and its closely related taxa as shown in Fig. 24. Thus, we introduce *N. liupanshuiensis* as a new species.

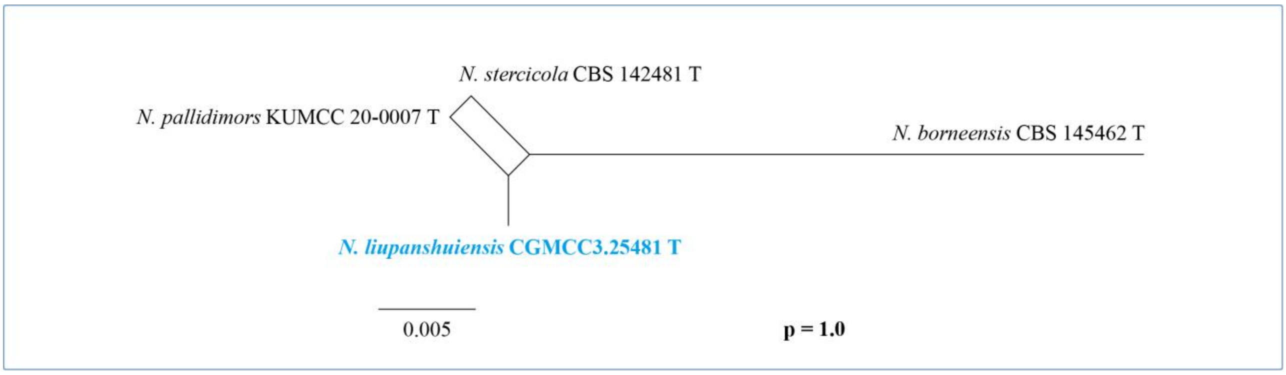

Figure 24 – Results of the pairwise homoplasy index (PHI) test of *Neocosmospora liupanshuiensis* and their closely related species. New taxa are printed in bold blue.

Neocosmospora passiflorae (C.J. Bueno, I.H. Fischer, D.D. Rosa, A.C. Firmino, Harakava, C.M.G. Oliveira & E.L. Furtado) H. Zhang & Y.L. Jiang, comb. nov.

Index Fungorum number: IF900496

Basionym – *Fusarium solani* f. sp. *passiflorae* C.J. Bueno, I.H. Fischer, D.D. Rosa, A.C. Firmino, Harakava, C.M.G. Oliveira & E.L. Furtado, Plant Pathology 63 (2): 382–389 (2014).

Description and illustration – See Bueno et al. (2014).

Material examined – Pederneira, SP, João Ulisses GonÇalves (Fazenda Ribeirão Grande), 2007, IBFS07 and IBFS09; Bauru, SP, Salvador Cabella Filho (Fazenda Barreirinha), 2007, IBFS08; Jaú, SP, ETEC 'Prof. Urias Ferreira' (Escola AgrÍcola) de Jaú, 2007, IBFS11; Pederneiras, SP, Márcio Pereira (Sitio Água da Capivara), 2007, IBFS12 and IBFS18; Borborema, SP, Nilton Tarallo (Estância Santa Ana), 2007, IBFSE; Campos dos Goytacazes, RJ, Sérgio Inácio Rocha (SÍtio Santo Eduardo), 2007, IBFSRJ. Additional information unknown. ITS: FJ200220–FJ200224, FJ200226–FJ200228, *tef1*: FX524768–FX524775. The holotype or ex-type not specified.

Notes –Phylogenetic trees constructed with ITS and *tef1* single gene regions by Bueno et al. (2014) have shown that *F. solani* f. sp. *passiflorae* is phylogenetically close to *F. solani* (= *N. solani*). The multi-gene phylogenetic analyses combining *acl1*, *CaM*, ITS, LSU, *rpb1*, *rpb2* and *tef1* sequence data in this study indicated that *F. solani* f. sp. *passiflorae* belongs to *Neocosmospora*, forming a separate clade with high statistical support (BS = 91%, BI = 0.98) (Fig. 21). Therefore, we transferred *F. solani* f.sp. *passiflorae* into *Neocosmospora* as a new combination and named *N. passiflorae*.

Neocosmospora pisi (F.R. Jones) Sand.-Den. & Crous, Persoonia 43: 154 (2019) Fig. 25

Index Fungorum number: IF831196

Basionym – *Fusarium martii* var. *pisi* F.R. Jones, J. Agric. Res. 26: 459 (1923).

Synonyms – *Fusarium solani* f. *pisi* (F.R. Jones) W.C. Snyder & H.N. Hansen, Amer. J. Bot. 28: 740 (1941).

Endophytic in roots and stems of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* pale luteous to orange, formed abundantly on OA. *Sporodochial conidiophores* macronematous, hyaline, solitary or loosely aggregated, unbranched or sparsely branched, bearing terminal or lateral mono- and polyphialides. *Sporodochial conidiogenous cells* mono- and polyphialidic, hyaline, smooth, thin-walled, straight or slightly curved, subcylindrical, with inconspicuous collarettes and periclinal thickening, 15–53 × 1.5–3 μm (av. = 28.8 × 2.3 μm, n = 10). *Microconidia* allantoid to oblong with obtuse ends, truncate base, aseptate, hyaline, smooth- and thin-walled, straight to slightly curved, 6–17 × 1.5–4 μm (av. = 8.8 × 2.6 μm, n = 30). *Macroconidia* falcate, straight to curved, tapering toward the apex, apical cell blunt, basal cell obtuse to papillate, not foot-shaped, 1–3-septate, hyaline, thin- and smooth-walled; 1-septate macroconidia 16–23.5 × 2.5–4.5 μm (av. = 20.4 × 3.4 μm, n = 30); 2-septate macroconidia 19.5–36 × 2.5–4 μm (av. = 29.8 × 3.6 μm, n = 30); 3-septate macroconidia 32–48 × 3–5 μm (av. = 38.8 × 4.1 μm, n = 30). *Chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining 60 mm diam. after 14 days in the dark at 28 °C, raised at center, white, outer area of colony light orange, round, cottony, margin regular, aerial mycelium abundant, and reverse pale-yellow to orange-yellow, with concentric rings. On OA attaining 60 mm diam. after 14 days, light salmon, round, flat, abundant sporodochia visible, moderate aerial mycelium, and reverse concolorous. On SNA attaining 60 mm diam. after 14 days, pale grey, with sparse aerial mycelium, and reverse concolorous. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots and stems of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang, living cultures: GUCC 190098.1, GUCC 190177.1, and GUCC 191172.1.

Notes – Molecular analyses in this study showed that our collections (GUCC 190098.1, GUCC 190177.1, and GUCC 191172.1) clustered together with *N. pisi* (ex-epitype CBS 123669) with high statistical support (BS = 100%, PP = 1.00) (Fig. 21), and the sequence similarity between GUCC 191172.1 and CBS 123669 for *acl1*, *CaM*, ITS, LSU, *rpb2*, and *tef1* is high at 97.98% (582/594, 11 gaps), 100% (553/553), 99.78% (448/449, no gaps), 100% (473/473), 99.33% (739/744, no gaps), and 99.00% (594/600, one gap), respectively. The *rpb1* is missing for GUCC 191172.1. These strains are morphologically similar in having sporodochial conidiogenous cells with mono- and polyphialides, inconspicuous preclinical thickening, collarette not fared;

macroconidia slightly curved or arcuate, apical cell blunt, basal cell obtuse; microconidia aseptate, with a rounded apex and truncate base (6–17 × 1.5–4 µm, av. = 8.8 × 2.6 µm in GUCC 191172.1 vs. 2.5–12.7 × 1.5–2.1 µm in ex-epitype); and chlamydospores absent (Jones 1923, Šišić et al. 2018). This study revealed that the morphology and phylogenetic identity of this isolate overlaps with *N. pisi*; therefore, we report our collections as a new host record isolated from *R. roxburghii*.

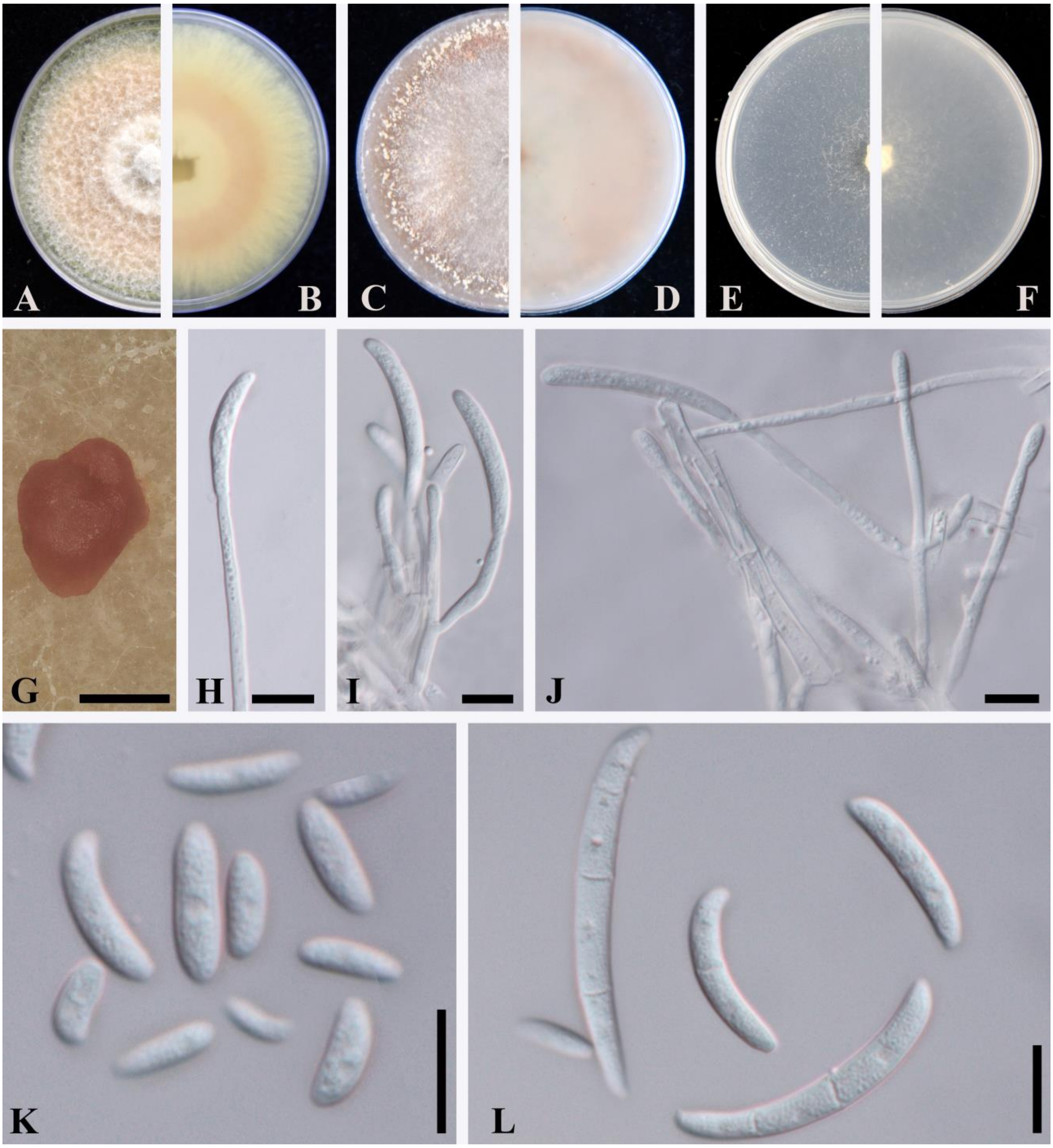

Figure 25 – *Neocosmospora pisi* (GUCC 191172.1). A–F Colony on PDA, OA, and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–J Sporodochial conidiophores and conidiogenous cells. K Microconidia. L. Macroconidia. Scale bars: G = 500 µm, H–L = 10 µm.

Neocosmospora populicola (S.C. Lai, L.L. Dai & D.J. Hao) H. Zhang & Y.L. Jiang, comb. nov.
Index Fungorum number: IF900497

Basionym: *Fusarium populicola* S.C. Lai, L.L. Dai & D.J. Hao, Mycological Progress 21: 70 (2022).

Description and illustration: See Lai et al. (2022).

Material examined – China, Jiangsu, Yancheng, Dongtai, Huanghai Forest, poplar plantation, from the oral mycetangium of *Euwallacea interjectus* infesting a live poplar (*Populus* × *canadensis* 'I-214'), 20 May 2021, Shengchang Lai, Chen Zhao, Lulu Dai; holotype: CFCC 57490, dried specimen: NJFU-JS02; ex-type: NJFU-JS02; ITS-28S rDNA: LC702061; *tef1*: LC701601; *rpb1*: LC701929; *rpb2*: LC701965, LC702001.

Notes – Based on the phylogenetic analyses, *F. populicola* belongs to the genus *Neocosmospora*, with high statistical support (BS = 90%, PP = 0.96). *Fusarium populicola* is phylogenetically close to *N. euwallaceae* (ex-type CBS 135854) (Fig. 21), forming two sister clades. Morphologically, *F. populicola* and *N. euwallaceae* have similar aerial conidiophores (erect, tall and narrow, unbranched, rarely branched sparsely, thin-walled, forming monophialides integrated at the apex), aerial phialides (simple, subcylindrical to subulate), aerial conidia (with two distinct shapes), sporodochial conidiophores (branched irregularly or unbranched, forming apical monophialides), sporodochial phialides (simple, subcylindrical), and sporodochial conidia (with two distinct shapes). However, *F. populicola* is distinguished from *N. euwallaceae* by the aerial conidiophores (up to 344 μm long in *F. populicola* vs. up to 290 mm long in *N. euwallaceae*), aerial phialides (with a minute collarette in *F. populicola* vs. with a conspicuous collarette in *N. euwallaceae*), aerial conidia (first shape 0–1-septate in *F. populicola* vs. 0–2-septate in *N. euwallaceae*; second shape 1–5-septate in *F. populicola* vs. 1–4-septate in *N. euwallaceae*), sporodochial phialides (collarette inconspicuous in *F. populicola* vs. conspicuous in *N. euwallaceae*), and sporodochial conidia (first shape almost straight, not curved in *F. populicola* vs. straight or curved in *N. euwallaceae*; second shape 0–6-septate, with a distinct or indistinct foot-shaped or tapering basal cell in *F. populicola* vs. 0–7-septate, with a distinct foot-like basal cell in *N. euwallaceae*) (Freeman et al. 2013, Lai et al. 2022). *Fusarium populicola* and *N. euwallaceae* have similar morphological characteristics but are also distinct from each other. Therefore, we transferred *F. populicola* to *Neocosmospora* as a new combination and named it *N. populicola*.

Neocosmospora solani (Mart.) L. Lombard & Crous, Stud. Mycol. 80: 228 (2015) Fig. 26

Index Fungorum number: IF810964

Basionym: *Fusisporium solani* Mart., Die Kartoffel-Epidemie der letzten Jahre oder die Stockfäule und Räude der Kartoffeln: 20 (1842).

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Sporodochia* orange, formed on SNA. *Sporodochial conidiophores* macronematous, irregularly branched, bearing terminal solitary or whorls of 2–3 phialides. *Sporodochial conidiogenous cells* polyphialidic, doliiform to subcylindrical, smooth- and thin-walled, 11–24.5 × 2.5–4.5 μm (av. = 17 × 3.8 μm, n = 10). *Sporodochial macroconidia* moderately curved, tapering towards the basal part, apical cell blunt and smaller than the adjacent cell; basal cell obtuse to papillate, not foot-shaped, 3–5-septate, hyaline, thin- and smooth-walled; 3-septate macroconidia 23–41 × 4–5.5 μm (av. = 32.7 × 4.6 μm, n = 30); 4-septate macroconidia 31.5–45 × 4.5–5.5 μm (av. = 38.5 × 5 μm, n = 30); 5-septate macroconidia 37–47.5 × 4.5–6 μm (av. = 40.9 × 4.9 μm, n = 30). *Aerial conidiophores* occasionally septate, simple, unbranched, sometimes reduced to single conidiogenous cells, borne laterally or terminally on hyphae. *Aerial conidiogenous cells* monophialidic, hyaline, smooth, straight or slightly curved, cylindrical to subcylindrical, tapering towards the apex, collarettes and periclinal thickening conspicuous, 39–69.5 × 2–4.5 μm (av. = 50.9 × 3.6 μm, n = 10). *Aerial microconidia* solitary or forming small false heads, obovoid to allantoid, 0–1-septate, hyaline, thin-walled, smooth to minutely verruculose or irregularly rough-walled; aseptate microconidia 7.5–13.5 × 2.5–4 μm (av. = 10.1 × 3 μm, n = 30); 1-septate microconidia 13.5–21 × 3–5.5 μm (av. = 16.6 × 4.3 μm, n = 30). *Chlamydospores* single or in chains, terminal or intercalary, mostly subglobose, smooth or verrucose, hyaline, thick-walled, 7–10.5 μm (av. = 8.4 μm, n = 30) diam.

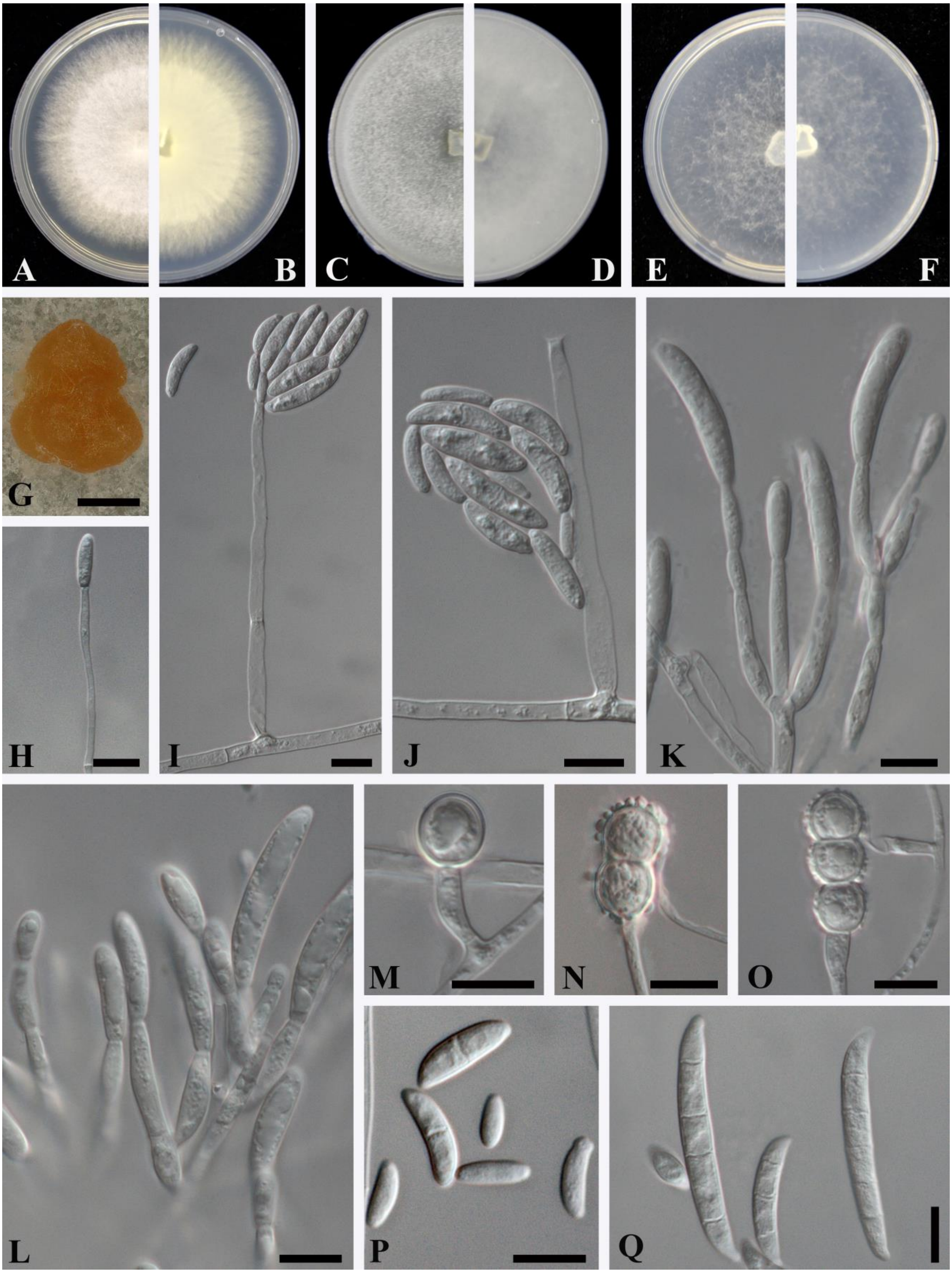

Figure 26 – *Neocosmospora solani* (GUCC 190159.1). A–F Colony on PDA, OA and SNA (A, C, and E from above; B, D, and F from below). G Sporodochia. H–J Aerial conidiophores and conidiogenous cells. K–L Sporodochial conidiophores and conidiogenous cells. M–O Chlamydospores. P Microconidia. Q Macroconidia. Scale bars: G = 500 µm, H–Q = 10 µm.

Culture characteristics – Colonies on PDA attaining 48 mm diam. after 5 days in the dark at 28 °C, white to light yellow, with white fluffy mycelia in the center, round, margin regular, aerial mycelium abundant, and reverse light yellow. On OA attaining 50 mm diam. after 5 days, greyish white, round, flat, flocculent, margin entire, and reverse greyish white. On SNA attaining 55 mm diam. after 5 days, pale grey, with sparse aerial mycelium, and reverse pale grey. Pigment and odor absent.

Material examined – China, Guizhou Province, Liupanshui City, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 25°52′52″ N, 104°33′59″ E, alt. 2047 m, 4 August 2020, H. Zhang, living cultures: GUCC 190159.1. China, Guizhou Province, Qiannan Districts, *R. roxburghii* Plantation, from healthy roots of *R. roxburghii* (Rosaceae), 26°47′4″ N, 107°8′37″ E, alt. 1322 m, 17 August 2021, H. Zhang, living culture: GUCC 198534.1.

Notes – Phylogenetically, our collections (GUCC 190159.1 and GUCC 198534.1) clustered with *N. solani* (ex-epitype CBS 140079) with high statistical support (BS = 99%, PP = 1.00) (Fig. 21), and the sequence similarities between GUCC 190159.1 and CBS 140079 for *acl1*, *CaM*, ITS, LSU, *rpb1*, *rpb2*, and *tef1* are 100% (558/558), 99.28% (550/554, one gap), 99.81% (522/523, no gaps), 100% (558/558), 99.54% (1306/1312, one gap), 99.52% (837/841), and 99.56% (681/684, one gap), respectively. Morphologically, they have similar sporodochial conidiophores (repeatedly branched), sporodochial conidiogenous cells (polyphialidic, subcylindrical, straight or slightly curved), sporodochial macroconidia (falcate, moderately curved; 3-septate macroconidia 23–41 × 4–5.5 μm in GUCC 190159.1 vs. 36–44 × 4.5–6 μm in ex-epitype; 4-septate macroconidia 31.5–45 × 4.5–5.5 μm in GUCC 190159.1 vs. 42–48 × 4.5–6 μm in ex-epitype; 5-septate macroconidia 37–47.5 × 4.5–6 μm in GUCC 190159.1 vs. 45–51 × 4.5–6 μm in ex-epitype), aerial conidiophores (sometimes unbranched, thin-walled, smooth, terminating in a single phialide), aerial microconidia (aseptate microconidia 7.5–13.5 × 2.5–4 μm in GUCC 190159.1 vs. 8.5–13.5 × 2.5–4.5 μm in ex-epitype; 1-septate microconidia 13.5–21 × 3–5.5 μm in GUCC 190159.1 vs. 17–24 × 3.5–5.5 μm in ex-epitype), and chlamydospores (rough; 7–10.5 μm diam. in GUCC 190159.1 vs. 6.5–8.5 μm diam. in ex-epitype) (Schroers et al. 2016, Sandoval-Denis et al. 2019). The present study suggested that the morphological and phylogenetic characteristics of these isolates overlapped with *N. solani*. Therefore, we report our collections as a new host record isolated from the roots of *R. roxburghii*.

Neocosmospora tumidisperma (S.C. Lai, L.L. Dai & D.J. Hao) H. Zhang & Y.L. Jiang, comb. nov.

Index Fungorum number: IF900499

Basionym – *Fusarium tumidispermum* S.C. Lai, L.L. Dai & D.J. Hao, Mycological Progress 21: 70 (2022).

Description and illustration – see Lai et al. (2022).

Material examined – China, Jiangxi, Nanchang, Jiangxi Agricultural University, from a *Euwallacea interjectus* infesting in trunks of live *Elaeocarpus decipiens* Hemsl., 19 July 2021, Shengchang Lai, Yang Zhou; holotype: CFCC 57492; ex-type strain NJFU-JX26; ITS-28S rDNA: LC702053; *tef1*: LC701621; *rpb1*: LC701957; *rpb2*: LC701993, LC702029.

Notes – *Fusarium tumidispermum* formed a separate clade in the phylogenetic analyses with moderate statistical support (BS = 86%, PP = 0.91) (Fig. 21), belonging to the genus *Neocosmospora*. *Fusarium tumidispermum* is phylogenetically close to *N. populicola*. *Fusarium tumidispermus* is morphologically similar to *N. populicola* in that it forms sporodochial conidiophores (cylindrical and thick, straight or some crooked, forming apical monophialides), sporodochial phialides (simple, subcylindrical, sometimes ampulliform), sporodochial conidia (with two distinct shapes), aerial conidiophores (erect, often tall and narrow, unbranched or sparsely branched, forming monophialides), aerial phialides (simple, subcylindrical to subulate), aerial conidia (with two different shapes). However, *F. tumidispermum* is distinguished from *N. populicola* by the sporodochial conidia (first shape swollen in their upper parts with a rounded or a blunt apex in *F. tumidispermum* vs. not swollen apically, with a rounded or a protruding apex in *N. populicola*; second shape mostly 1–4-septate in *F. tumidispermum* vs. predominantly 3–5-

septate in *N. populicola*), aerial conidiophores (up to 271 μm long in *F. tumidispermum* vs. up to 344 μm long in *N. populicola*), aerial conidia (first shape with distinct swollen upper part in *F. tumidispermum* vs. not swollen in *N. populicola*; second shape swollen upper parts, mostly 2–4-septate in *F. tumidispermum* vs. not swollen, predominantly 3–4-septate in *N. populicola*) (Lai et al. 2022). *Fusarium tumidispermum* and *N. populicola* have similar morphological characteristics but are also distinct from each other. Therefore, we transferred *F. tumidispermum* to *Neocosmospora* and named the species *N. tumidisperma*.

Thelonectria P. Chaverri & C.G. Salgado

Thelonectria was established by Chaverri et al. (2011) to accommodate fungi with asci cylindrical to narrowly clavate; ascospores ellipsoidal to fusoid, 1-septate; and cylindrocarpon-like asexual morphs, with *T. discophora* as the type species. To date, 56 species have been listed in Index Fungorum (2023). *Thelonectria* is a cosmopolitan genus that commonly occurs as saprobes on the bark of recently dead or dying trees, roots, and soil (Salgado-Salazar et al. 2016), as well as root-endophytic fungi (Manici et al. 2013, Lee et al. 2016b), and occasionally causes plant diseases (Guan et al. 2020). In this study, four endophytic *Thelonectria* strains were isolated from *R. roxburghii* roots, and multi-gene phylogenetic analyses indicated that they belonged to two species (Fig. 27).

Thelonectria blackeriella M.L. Raimondo & A. Carlucci, Phytopathol. Medit. 56 (1): 30 (2017) Fig. 28

Index Fungorum number: IF834916

Endophytic in roots of *R. roxburghii* in China. Sexual morph not observed. Asexual morph: *Mycelia* not visible on the host. *Sporodochia* absent under laboratory conditions. *Aerial conidiophores* sparsely branched, hyaline, smooth, septate, straight or slightly curved, each ending in a single terminal phialide, frequently bearing one or two lateral phialides next to the terminal phialide, 14.5–32 × 1.5–3 μm (av. = 24.3 × 2.4 μm, n = 10). *Aerial conidiogenous cells* borne apically on irregularly branching clusters of cells or directly from hyphae, cylindrical or slightly swollen, with inconspicuous periclinal thickening and collarette, 4.5–31 × 1.5–3 μm (av. = 15.6 × 2.7 μm, n = 10). *Aerial macroconidia* hyphae, cylindrical or slightly fusiform, curved with rounded ends, with small guttules, 1–5-septate, slightly constricted at septa: 1-septate macroconidia 16–34.5 × 3.5–7.5 μm (av. = 29.6 × 5.8 μm, n = 30), 2-septate macroconidia 34–50 × 5–7.5 μm (av. = 42.9 × 6.6 μm, n = 30), 3-septate macroconidia 40–74.5 × 6–8.5 μm (av. = 54.8 × 6.8 μm, n = 30), 4-septate macroconidia 60.5–78.5 × 5.5–8 μm (av. = 70.6 × 6.8 μm, n = 30), 5-septate macroconidia 73.5–78 × 6.5–7.5 μm (av. = 75.6 × 6.9 μm, n = 30). *Aerial microconidia* produced in culture, hyaline, aseptate, round to oblong or ellipsoidal with abscission scar, 4.5–14 × 3–4.5 μm (av. = 7.8 × 3.6 μm, n = 30), with small guttules. *Chlamydospores* globose to subglobose, thick-walled, being terminal or intercalary within hyphae, mostly occurring in chains, 5.5–15.5 × 5.5–14 μm (av. = 11.2 × 10.1 μm, n = 30).

Culture characteristics – Colonies on PDA, OA, and MEA attaining 50, 50, and 37 mm diam. after 14 days at 28 °C in the dark, respectively. On PDA grey, round, raised, with abundant aerial mycelium, margin regular, and reverse grey to pale yellow. On OA grey, round, aerial mycelia flattened, with concentric rings, margin irregular, crenate, dense, and reverse concolorous, with concentric rings. On MEA white, round, slightly raised, with slightly sparse central mycelium, and reverse buff to orange.

Material examined – China, Guizhou Province, Guiyang City, natural environment, healthy roots of *R. roxburghii* (Rosaceae), 27°4′50″ N, 106°29′50″ E, alt. 1184 m, 22 April 2020, H. Zhang, living cultures: GUCC 190037.1 and GUCC 190037.2.

Notes – In the phylogenetic analyses based on eight loci, our collections are close to *T. blackeriella* with high statistical support (BS = 100%, PP = 1.00) (Fig. 27), sharing 99.83% (574/575, no gaps), 99.81% (518/519, no gaps), 99.26% (535/539, no gaps), 100% (670/670), and 99.81% (537/538, no gaps) similarities for ACT, ITS, LSU, *rpb1*, and *tub2*, respectively. The *rpb2*, SSU, and *tef1* are missing for *T. blackeriella* (ex-type CBS 142200). They are morphologically similar based on their conidiophores (septate, each ending in a single terminal phialide, frequently bearing one or two lateral phialides next to the terminal phialide; 14.5–32 × 1.5–3 µm, av. = 24.3 × 2.4 µm in our collections vs. 19.58–34.76 × 2.27–3.47 µm, av. = 27.17 × 2.87 µm in the ex-type),

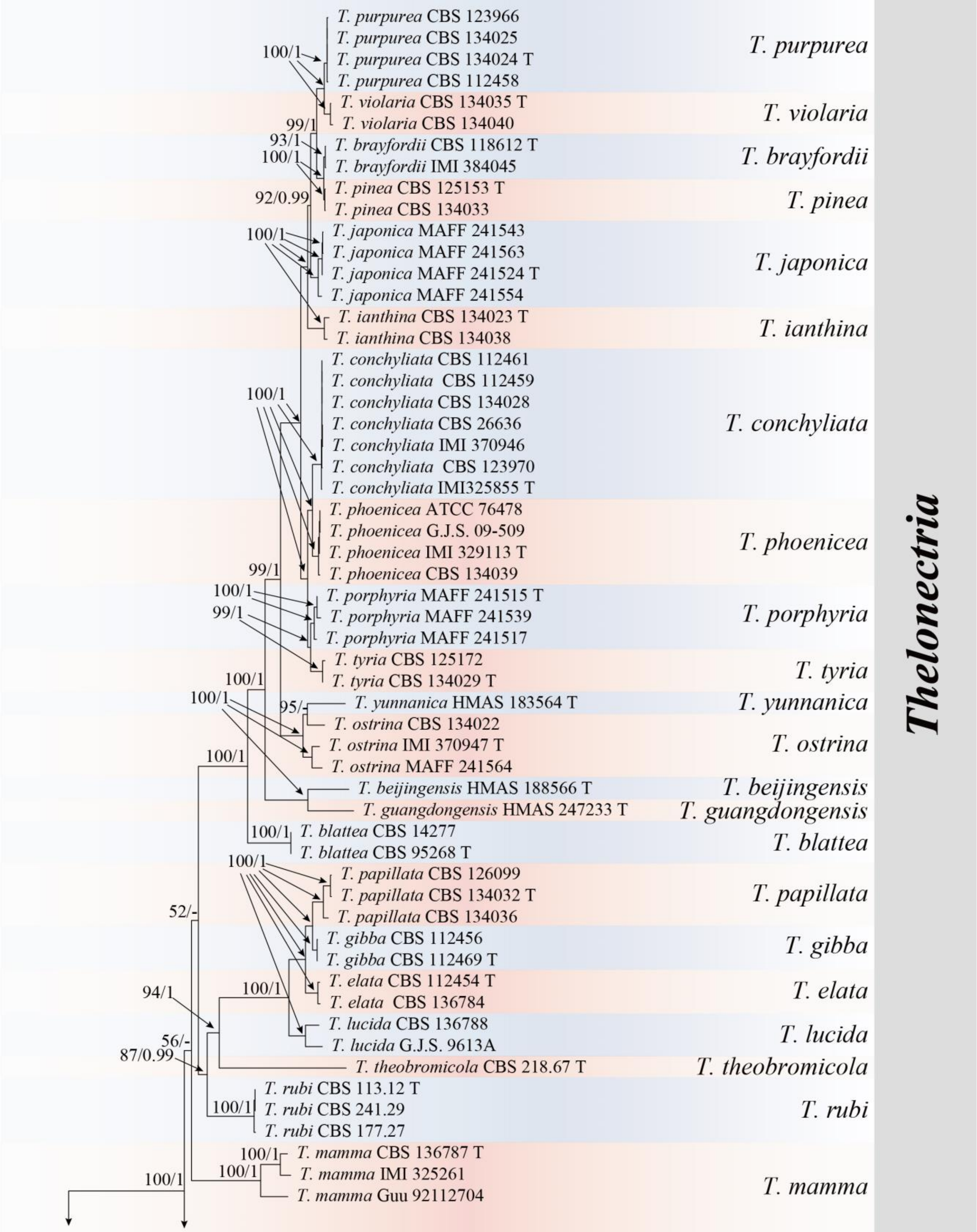

Figure 27 – Phylogenetic relationships of *Thelonectria*. Phylogenetic tree was generated using the maximum likelihood (ML) method by combining the ACT, ITS, LSU, *rpb1*, *rpb2*, SSU, *tef1*, and

tub2 sequence data of 130 strains. The tree is rooted with *Cinnamomeonectria cinnamomea* (IMI 325248). The ML bootstrap support values > 50% (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near the nodes (BS/PP). Strains isolated in this study are indicated in **bold**. **T** holotype or ex-type.

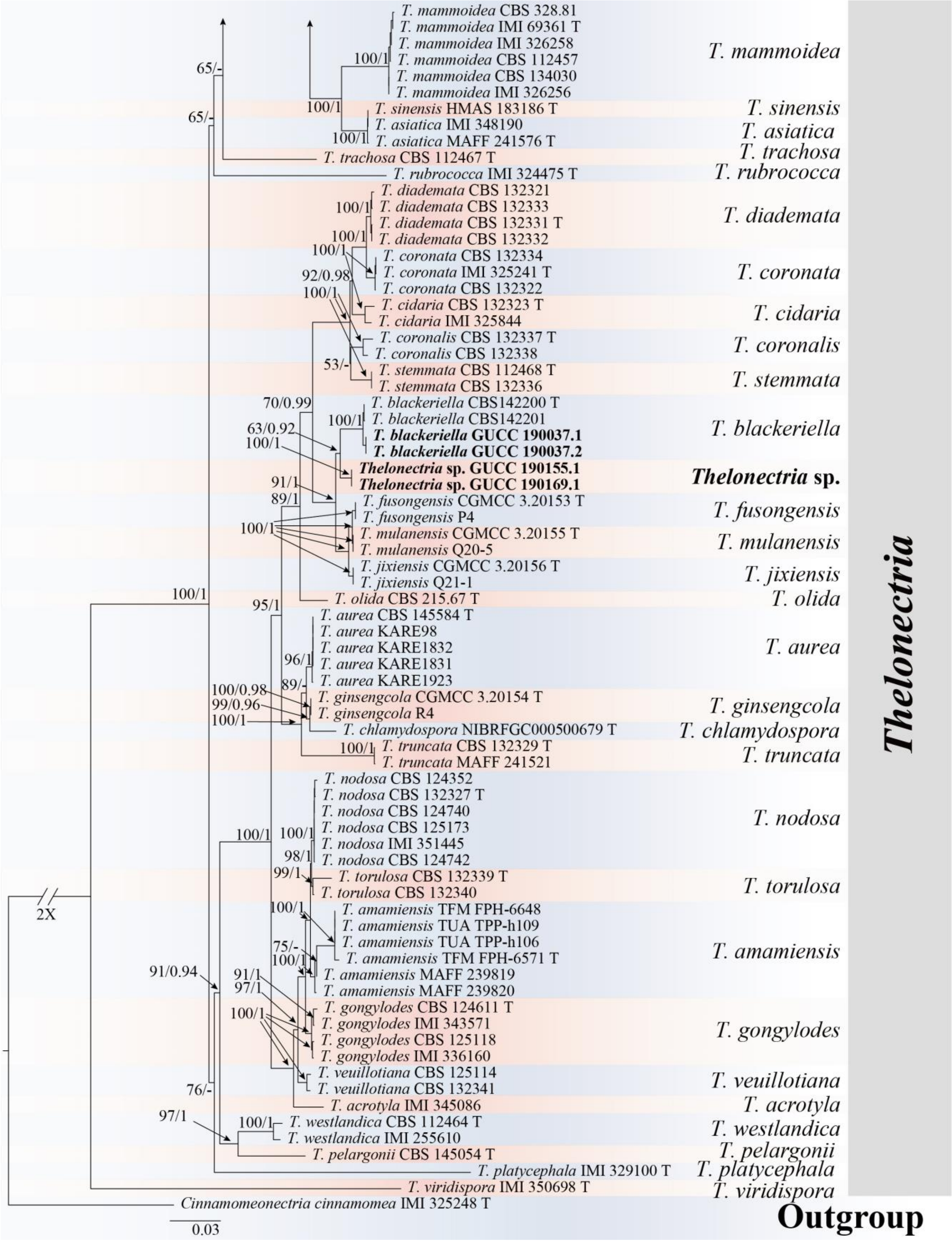

Figure 27 – Continued.

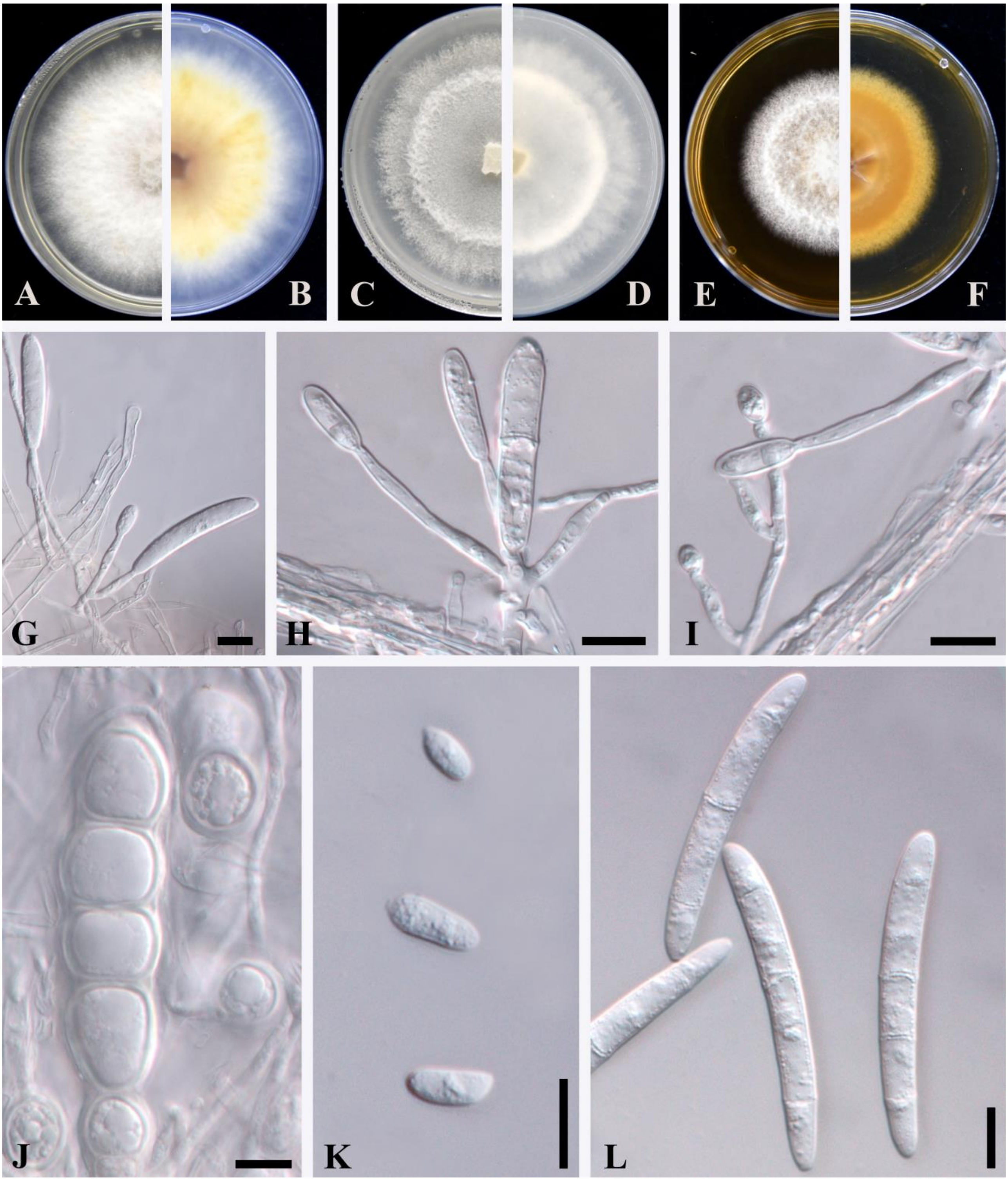

Figure 28 – *Thelonectria blackeriella* (GUCC 190037.1). A–F Colony on PDA, OA, and MEA (A, C, and E from above; B, D, and F from below). G–I Aerial conidiophores and conidiogenous cells. J Chlamydospores. K Microconidia. L Macroconidia. Scale bars: G–L = 10 µm.

conidiogenous cells (borne apically on irregularly branching clusters of cells or directly from hyphae, cylindrical or slightly swollen; 4.5–31 × 1.5–3 µm, av. = 15.6 × 2.7 µm in our collections vs. 8.16–13.39 × 1.52–5.85 µm, av. = 10.78 × 3.69 µm in the ex-type), macroconidia (cylindrical or slightly fusiform, curved with rounded ends; 1-septate macroconidia 16–34.5 × 3.5–7.5 µm, av. = 29.6 × 5.8 µm in GUCC 190037.1 vs. 21.97–28.22 × 2.44–4.66 µm, av. = 24.35 × 4.15 µm in the ex-type), and chlamydospores (globose to subglobose; 5.5–15.5 × 5.5–14 µm, av. = 11.2 × 10.1 µm in GUCC 190037.1 vs. av. = 8.62 × 4.69 µm in the ex-type) (Carlucci et al. 2017). This study revealed that the morphology and phylogenetic identity of this isolate overlaps with *T. blackeriella*. Therefore, we report our collections as a new host record isolated from the roots of *R. roxburghii*.

Discussion

Pathogenic and endophytic *Fusarium* and allied fungi in Rosaceae

Fusarium and allied genera are typically known as plant pathogens. However, endophytes of these genera also hold significant importance for their diverse biological activities. Endophytic *F. verticillioides* can interfere with the early infection process of the pathogen *Ustilago maydis* on maize, thereby limiting disease development and promoting plant growth (Lee et al. 2009). Endophytic *Fusarium* sp. CBRF44 from roots, which is resistant to metals and could produce indole-3-acetic acid (IAA) and siderophore, significantly increased rape biomass and improved the phytoremediation efficacy of host plants (Shi et al. 2017). Moreover, endophytic *Fusarium* and allied fungi can synthesize structurally diverse secondary metabolites (Toghueo 2020), including over one hundred compounds with unique chemical structures and more than three hundred compounds of different classes (Ahmed et al. 2023). These compounds exhibit incredible biological activities (Toghueo 2020, Ahmed et al. 2023). In a previous study, we also found that endophytic *F. rosendophyticum* (CGMCC3.25480) from *R. roxburghii* showed a broad-spectrum of antimicrobial activities against *Botryosphaeria dothidea*, *Lasiodiplodia theobromae*, and *Pyricularia oryzae* (Zhang et al. 2021).

In this study, 60 related fungal strains were isolated from healthy roots and stems of *R. roxburghii*, belonging to 25 species across five genera (*Albonectria*, *Fusarium*, *Luteonectria*, *Neocosmospora*, and *Thelonectria*). Of these, 11 species were described as new taxa, while *Thelonectria* sp. (GUCC 190155.1 and GUCC 190169.1) may represent new species, and unfortunately, multiple attempts to promote sporulation have failed. Furthermore, we summarised the records of pathogenic and endophytic *Fusarium* and allied fungi associated with Rosaceae worldwide (Table 2). As shown in Table 2, *F. acuminatum*, *F. avenaceum*, *F. equiseti*, *F. oxysporum*, *F. proliferatum*, and *N. solani* are the most significant pathogens of Rosaceae, causing different diseases in a wide range of host plants. Of which, *F. acuminatum*, *F. avenaceum*, *F. oxysporum*, and *N. solani* are also common endophytic fungi in the plants of this family. Endophytic *F. avenaceum*, *F. cugenangense*, *F. fujikuroi*, *F. lateritium*, and *N. solani* isolated in this study have been reported as Rosaceae pathogens, suggesting that they may be potentially harmful to *R. roxburghii* when host conditions become unfavorable (McGrann et al. 2015). Except for the present study, there are fewer reports of endophytic *Fusarium* associated with Rosaceae. In future research, it can be tried in *R. roxburghii* production practices to promote growth and improve disease resistance by these endophytic *Fusarium* and allied fungi and exploit their bioactive secondary metabolites as well. Additionally, it is notable to investigate possible *Fusarium* diseases in agriculture due to their abundant colonization on *R. roxburghii*.

Table 2 Pathogenic and endophytic *Fusarium* and allied fungi in Rosaceae.

Current name	Reported name	Host (Rosaceae)	Pathogenic/ Endophytic	Diseases	Bioactivity	References
Albonectria guizhouensis	***Albonectria guizhouensis***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
A. rigidiuscula	*F. decemcellulare*	Apple (*Malus pumila* Mill.)	Pathogen	Fruit rot	–	Lee et al. (2017)
Fusarium acuminatum	*F. acuminatum*	Apple	Pathogen	Apple replant disease	–	Zou et al. (2014)
		Strawberry	Pathogen	Fruit diseases	–	Ayoubi & Soleimani (2016)

Table 2 Continued.

Current name	Reported name	Host (Rosaceae)	Pathogenic/ Endophytic	Diseases	Bioactivity	References
		Almond trees (*Prunus dulcis*)	Pathogen	Canker disease	–	Stack et al. (2020)
		Geum macrophyllum	Endophyte	–	Antimicrobial activity	Clark et al. (2018)
		Apple (*Malus* sp.)	Endophyte	–	Antifungal activity	Ebrahimi et al. (2022)
F. arbusti	***F. arbusti***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. avenaceum	*F. avenaceum*	Raspberry (*Rubus idaeus* L.)	Pathogen	Fruit rot	–	Wang et al. (2017)
		Almond trees (*Prunus dulcis*)	Pathogen	Canker disease	–	Stack et al. (2020)
		Peach (*Prunus persica* L.)	Pathogen	Fruit Rot	–	Heo et al. (2020)
		Pear (*Pyrus communis*)	Pathogen	Branch canker	–	Polat et al. (2022)
		Raspberry	Pathogen	Raspberry cane blight	–	Weber & Entrop (2008)
		Apple	Pathogen	Apple rot	–	Petreš et al. (2023)
		Rosa roxburghii	**Endophyte**	–	**Antimicrobial activity**	**In this study, Zhang et al. (2021)**
F. brachygibbosum	*F. brachygibbosum*	Almond trees (*Prunus dulcis*)	Pathogen	Canker disease	–	Stack et al. (2020)
F. californicum	*F. californicum*	Almond trees (*Prunus dulcis*)	Pathogen	Canker disease	–	Stack et al. (2020)
F. caulendophyticum	***F. caulendophyticum***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. caulicola	***F. caulicola***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. cili	***F. cili***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. citri	*F. citri*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. clavum	*F. clavum*	Roses (*Rosa* spp.)	Pathogen	Petal brown spot disease	–	Manganiello et al. (2021)
F. commune	*F. commune*	Strawberry (*Fragaria* × *ananassa*)	Pathogen	Root rot	–	He et al. (2022)
F. compactum	*F. compactum*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. culmorum	*F. culmorum*	*Rosa rugosa*	Endophyte	–	–	Menkis et al. (2014)
F. cugenangense	*F. cugenangense*	Korean blackberry (*Rubus coreanus*)	Pathogen	Fusarium wilt	–	Kim et al. (2021)
		Rosa roxburghii	**Endophyte**	–	–	**In this study**
F. curvatum	*F. curvatum*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. equiseti	*F. equiseti*	Strawberry	Pathogen	Fruit diseases	–	Ayoubi & Soleimani (2016)
		Apple	Pathogen	Apple replant disease	–	Zou et al. (2014)
		Peach (*Prunus persica*)	Pathogen	Fruit rot	–	Zhang et al. (2020b)
		Chinese cherry (*Cerasus pseudocerasus*)	Pathogen	Postharvest rot	–	Wang et al. (2021)
F. fujikuroi	*F. fujikuroi*	Plum	Pathogen	Fruit blotch	–	Long et al. (2021)

Table 2 Continued.

Current name	Reported name	Host (Rosaceae)	Pathogenic/ Endophytic	Diseases	Bioactivity	References
		Apple (*Malus* sp.)	Endophyte	–	Slight antifungal activity	Ebrahimi et al. (2022)
		Rosa roxburghii	**Endophyte**	–	–	**In this study**
F. graminearum	*F. graminearum*	*Prunus mandshurica*	Endophyte	–	–	Nekrasov et al. (2022)
		Apple	Pathogen	Apple rot	–	Petreš et al. (2023)
F. incarnatum	*F. incarnatum*	Strawberry	Pathogen	Fruit diseases	–	Ayoubi & Soleimani (2016)
		Apple (*Malus* sp.)	Endophyte	–	Slight antifungal activity	Ebrahimi et al. (2022)
F. ipomoeae	*F. ipomoeae*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. lateritium	*F. lateritium*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
		Apple (*Malus* sp.)	Endophyte	–	Antifungal activity	Ebrahimi et al. (2022)
		Rosa roxburghii	**Endophyte**	–	–	**In this study**
F. luffae	*F. luffae*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. meridionale	***F. meridionale***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. nirenbergiae	***F. nirenbergiae***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. nygamai	*F. nygamai*	Sweet cherry (*Prunus avium* L.)	Pathogen	Leaf spot	–	Zhou et al. (2022)
F. oxysporum	*F. oxysporum*	Apple	Pathogen	Apple replant disease	–	Zou et al. (2014)
		Prunus mandshurica	Endophyte		–	Nekrasov et al. (2022)
		Strawberry	Pathogen	Fruit diseases	–	Ayoubi & Soleimani (2016)
		Strawberry	Pathogen	Root rot	–	Ning et al. (2017)
		Firethorn (*Pyracantha* sp.)	Pathogen	Wilt	–	McRitchie (1973)
		Prunus amygdalus	Pathogen	Stem rot	–	Chehri et al. (2010)
		Apricot (*Prunus armeniaca*)	Pathogen	Fruit rot	–	Wu et al. (2022)
		Sweet cherry (*Prunus avium*)	Pathogen	Root and crown rot	–	Úrbez-Torres et al. (2016)
		Blackberry	Pathogen	Wilt	–	Gordon et al. (2016)
		Photinia × *fraseri*	Pathogen	Crown and root rot	–	Chen et al. (2022)
		Rose (*Rosa* spp.)	Pathogen	Dry rot	–	Barguil et al. (2009)
		Rosa rugosa	Endophyte		–	Menkis et al. (2014)
F. oxysporum f.sp. *fragariae*	*F. oxysporum* f.sp. *fragariae*	Strawberry	Pathogen	Strawberry fusarium wilt.	–	Chen et al. (2014)
F. oxysporum f.sp. *mori*	*F. oxysporum* f.sp. *mori*	Blackberry	Pathogen	Fusarium wilt	–	Pastrana et al. (2017)

Table 2 Continued.

Current name	Reported name	Host (Rosaceae)	Pathogenic/ Endophytic	Diseases	Bioactivity	References
F. pernambucanum	*F. pernambucanum*	Plum (*Prunus salicina* Lindl.)	Pathogen	Leaf blight	–	Lu et al. (2022)
F. proliferatum	*F. proliferatum*	Apple	Pathogen	Apple replant disease	–	Zou et al. (2014)
		Peach (*Prunus persica* L.)	Pathogen	Fruit rot	–	Xie et al. (2018)
		Pear (*Pyrus pyrifolia* cv. 'Cuiguan')	Pathogen	Fruit rot	–	Zhao et al. (2020)
		Strawberry (*Fragaria* × *ananassa* Duch.)	Pathogen	Vascular Wilt	–	Borrero et al. (2019)
F. qiannanense	***F. qiannanense***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. radicigenum	***F. radicigenum***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. rosae-roxburghii	***F. rosae-roxburghii***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. rosendophyticum	***F. rosendophyticum***	***Rosa roxburghii***	**Endophyte**	–	**Antimicrobial activity**	**In this study, Zhang et al. (2021)**
F. rosiradicicola	***F. rosiradicicola***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
F. sambucinum	*F. sambucinum*	Raspberry	Pathogen	Raspberry primocane fruiting disease	–	Shternshis et al. (2015)
Fusarium sp.	*Fusarium* sp.	Eastern mountain avens (*Geum peckii*)	Endophyte	–	–	Adams et al. (2021)
		Rosa longicuspis	Endophyte	–	–	Li et al. (2012)
		Rose	Endophyte	–	–	Heinz et al. (2018)
		Rosa corymbifera	Endophyte	–	–	Grunewaldt-Stöcker et al. (2020)
		Rosa sp.	Endophyte	–	Antimicrobial activity	Dasari et al. (2015)
F. sporotrichioides	*F. sporotrichioides*	Peach (*Prunus persica*)	Pathogen	Fruit rot	–	Khan et al. (2023)
F. sulawesiense	*F. sulawesiense*	Plum (*Prunus salicina* Lindl.)	Pathogen	Leaf blight	–	Lu et al. (2022)
F. tricinctum	*F. tricinctum*	Apple tree	Pathogen	Stem vascular and woody xylem browning, wilting, and dieback	–	Zhang et al. (2022b)
		Aronia melanocarpa	Pathogen	Post-harvest fruit rot	–	Lee et al. (2016a)
Luteonectria nematophila	***L. nematophila***	***Rosa roxburghii***	**Endophyte**		–	**In this study**
Neocosmospora brevis	*F. rosicola*	*Rosa chinensis*	Pathogen	Vascular wilt	–	He et al. (2021)
N. euwallaceae	*F. euwallaceae*	Nectarine and plum	Pathogen	Fusarium dieback disease	–	de Jager & Roets (2023)

Table 2 Continued.

Current name	Reported name	Host (Rosaceae)	Pathogenic/ Endophytic	Diseases	Bioactivity	References
		Almond (*Prunus dulcis*)	Pathogen	Vascular streaking	–	Moreno et al. (2018)
N. falciformis	***N. falciformis***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
N. ipomoeae	***N. ipomoeae***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
N. lichenicola	***N. lichenicola***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
N. liupanshuiensis	***N. liupanshuiensis***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
N. parceramosa	*N. parceramosa*	Red raspberry (*Rubus idaeus* L.)	Pathogen	Cane blight	–	Guarnaccia et al. (2022)
N. pisi	***N. pisi***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
N. solani	***N. solani***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
	F. solani	Peach (*Prunus persica*)	Pathogen	Fruit rot	–	Zhu et al. (2019)
		Apple	Pathogen	Apple replant disease	–	Zou et al. (2014)
		Strawberry	Pathogen	Fruit diseases	–	Ayoubi & Soleimani (2016)
		Sweet cherry (*Prunus avium*)	Pathogen	Fusarium wilt	–	Zheng et al. (2022)
		Prunus amygdalus	Pathogen	Stem rot	–	Chehri et al. (2010)
		Pear	Pathogen	Root rot	–	Zhu et al. (2017)
		Loquat (*Eriobotrya japonica*)	Pathogen	Fruit rot	–	Abbas et al. (2017)
		Almond (*Prunus dulcis*)	Pathogen	Stem canker	–	Markakis et al. (2021)
		Photinia × *fraseri*	Pathogen	Crown and root rot	–	Zhou et al. (2023)
		Strawberry	Endophyte	–	Weak mortality on *Duponchelia fovealis*	Amatuzzi et al. (2017)
	F. eumartii	*Prunus amygdalus*	Pathogen	Stem rot	–	Chehri et al. (2010)
Neocosmospora sp.	*Fusarium solani* species complex	Loquat (*Eriobotrya japonica*)	Pathogen	Root rot	–	Wu et al. (2021)
Thelonectria blackeriella	***T. blackeriella***	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**
T. rubi	*T. rubi*	*Rubus* spp.	Pathogen	Canker disease	–	Skaltsas & Salgado-Salazar (2020)
***Thelonectria* sp.**	***Thelonectria* sp.**	***Rosa roxburghii***	**Endophyte**	–	–	**In this study**

Species identified in this study are in **bold**.

Several *Fusarium* species whose taxonomic status in the species complex is undetermined

Fusarium avenaceum subsp. *nurragi* was first described by Sangalang et al. (1995) and later combined as *F. nurragi* (Benyon et al. 2000). Recent studies by Crous et al. (2021) and Han et al. (2023) showed that *F. nurragi* remained singleton and unassigned to the species complex. *Fusarium newnesense* was introduced by Laurence et al. (2016), and phylogenetic analyses using both single-gene and multi-gene approaches have consistently shown it to be an independent clade (Laurence et al. 2016). A similar result was obtained in the phylogenetic tree constructed by Crous et al. (2021) combining *rpb1*, *rpb2,* and *tef1,* although they did not assign it to any specific species complex. Recently, Han et al. (2023) assigned *F. newnesense* to the *F. newnesense* species complex

(FnewSC), which still contains only one species and no morphological and phylogenetic comparisons of this complex with other species complexes.

In this study, multigene phylogenetic analyses showed that 42 isolates belonged to *Fusarium*, covering seven species complexes, namely *F. fujikuroi*, *F. heterosporum*, *F. incarnatum-equiseti*, *F. lateritium*, *F. oxysporum*, *F. sambucinum*, and *F. tricinctum*. A novel species, *F. arbusti*, may represent a new species complex. Combined phylogenetic analysis using ITS, LSU, *tef1*, *rpb1*, and *rpb2* or *tef1*, *rpb1*, and *rpb2* showed that *F. arbusti* (CGMCC3.25473 and GUCC 190154.2) forms an independent lineage with high statistical support (BS = 100%, PP = 1.00) (Fig. 1, Supplementary Fig. 1). Phylogenetically, the species is close to the species complex *F. fujikuroi*, *F. nisikadoi*, and *F. oxysporum*. The phylogenetic tree shows that *F. arbusti* is close to the ex-type *F. commune*. *Fusarium commune* was introduced by Skovgaard et al. (2003), forming a strongly supported clade closely related to but independent of the *F. oxysporum* and *F. fujikuroi* species complexes. Crous et al. (2021), Wang et al. (2022), and Han et al. (2023) combined *rpb1*, *rpb2*, and *tef1* for phylogenetic analyses of *Fusarium* and allied genera, and the results indicated that *F. commune* belongs to the *F. nisikadoi* species complex. However, we also observed that *F. commune* is evolutionarily distant from other species of this complex. We obtained similar results using these three genes for phylogenetic analyses (Supplementary Fig. 1). As a means of including several other species missing the *rpb1*, *rpb2*, and *tef1* genes, such as *No. ruscicola* (only ITS), in the phylogenetic analyses, we used ITS, LSU, *rpb1*, *rpb2*, and *tef1* sequence data (Fig. 1). This results in the *F. commune* being slightly far from the *F. nisikadoi* species complex and may represent a separate species complex. In most cases, the phylogenetic structure evident in multigene phylogenies is not entirely consistent in all gene trees (Weir et al. 2012). In future work, more adjacent species need to be discovered to determine the taxonomic status of *F. arbusti*, *F. commune*, *F. nurragi*, and *F. newnesense* in the species complexes.

Primer differences and applications of *Fusarium* and allied fungi

Although *Thelonectria* belongs to a related genus of *Fusarium*, primers used for the same gene in phylogenetic analyses varied significantly, such as *rpb1* using RPB1a/RPB1c instead of Fa/G2R and *tef1* using EF-728/EF-1567 instead of EF-1/EF-2 (Salgado-Salazar et al. 2015). Sequence data varied for different primer pairs. Therefore, to perform phylogenetic analyses of *Fusarium* and allied fungi (including *Thelonectria*), universal ITS and LSU primers were added in this study compared to Crous et al. (2021) (using *rpb1*, *rpb2*, and *tef1*), and the results were consistent with the topology of the previous phylogenetic tree. Wang et al. (2022) reported that *rpb1*, *rpb2*, and *tef1* are relatively effective in species recognition of *Fusarium* and related genera. Moreover, different species complexes require different gene sequences for identification, and the generally available ITS gene fails to delineate most *Fusarium* spp. (Kulik et al. 2020), making the identification process of *Fusarium* and allied fungi extremely difficult for researchers (Han et al. 2023). Due to this fact, the identification of several related fungi is insufficiently accurate, and new combinations are often reported. Therefore, more versatile and useful barcodes need to continue to be sought to facilitate rapid and accurate identification of *Fusarium* species (Han et al. 2023).

Broad and narrow concept of *Fusarium*, which one to apply?

Over the past decade, there have been two controversies about the boundaries of *Fusarium*, the broad and narrow concepts. These controversies led to the Index Fungorum (http://www.indexfungorum.org/), MycoBank (https://www.mycobank.org/), and the National Center for Biotechnology Information (NCBI) (https://www.ncbi.nlm.nih.gov/) databases to confuse the names of *Fusarium* and related genera. That causes significant difficulties for researchers, especially beginners or researchers of fungal natural products, to identify species accurately and does not facilitate the accurate transfer of biochemical information of *Fusarium* and related species. This study described four new combinations, namely *N. gannanensis*, *N. passiflorae*, *N. populicola*, and *N. tumidisperma*. Of these, *N. gannanensis* (= *F. gannanense*), *N. populicola* (= *F. populicola*), and *N. tumidisperma* (= *F. tumidispermum*) were introduced as new species of *Fusarium* by Lai et al. (2022), which was mainly due to the genus name dispute. So, which one to apply?

One view is that *Fusarium* should be retained broadly defined so that most well-known pathogens are held under the generic name *Fusarium* (O'Donnell et al. 2020, Geiser et al. 2021). However, another view suggests that the broad circumscription of *Fusarium* is blurry and without apparent synapomorphies and does not include all genera with fusarium-like macroconidia (Crous et al. 2021). In contrast, *Fusarium* is described in a narrow sense, not only as monophyletic and morphologically meaningful but also as a definable unit (Han et al. 2023). The broad *Fusarium* concept emphasizes that the "terminal *Fusarium* clade" (F1) is monophyletic, featuring the same fusarium-like macroconidia (Geiser et al. 2021). Nevertheless, besides F1, fusarium-like asexual macroconidia are also present in many other genera (Crous et al. 2021). Using a "narrow" concept, a set of synapomorphies with sexual and asexual characteristics can be used to divide the genus *Fusarium* from allied genera (Crous et al. 2021). Based on genomic datasets, phylogenomic reconstruction of *Fusarium* and allied genera showed that different codon usage biases and increased codon optimization distinguish *Fusarium s. stri*. from other fusarioid taxa (Hill et al. 2022). Moreover, Han et al. (2023) constructed a high-confidence species tree based on 1001 homologous loci from 228 genomes, further supporting the "narrow" genus concept of *Fusarium*. Therefore, in this study, a "narrow" concept was used to identify endophytic *Fusarium* and allied fungi from *R. roxburghii*.

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Supplementary Table 1 Strains used in this study and their GenBank accession numbers.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
Albonectria albosuccinea	NRRL 20459	JAADYS010000048.1	JAADYS010000048.1	–	JX171471	–	JX171585	JAADYS010002360.1	–
A. guizhouensis **sp. nov.**	**GUCC 198014.1 = CGMCC3.25472 T**	**OR034252**	**OR039360**	**OR043930**	**OR043779**	**OR043728**	**OR753368**	**OR043878**	**OR043678**
A. guizhouensis **sp. nov.**	**GUCC 198015.1**	**OR034253**	**OR039361**	**OR043931**	**OR043780**	**OR043729**	**OR043824**	**OR043879**	**OR043679**
A. rigidiuscula	CBS 133754	MW827602	MW827641	–	MW834177	–	MW833995	MW834269	–
Bisifusarium allantoides	UBOCC-A-120036 T	MW654548	MW654523	MW811102	MW811054	MW811029	MW811072	MW811087	MW810999
B. aseptatum	CGMCC 3.20816 = LC1075 T	MW016389	–	MW533716	–	MW566256	MW474375	MW580429	–
B. aseptatum	LC13607	MW016390	–	MW533717	–	MW566257	MW474376	MW580430	–
B. aseptatum	LC13608	MW016391	–	MW533718	–	MW566258	MW474377	MW580431	–
B. biseptatum	CBS 110311 T	MW654547	MW654522	MW811101	–	MW811028	MW811071	MW811086	MW810998
B. delphinoides	CBS 120718 T = CPC 13041	EU926229	KM231660	KM232056	–	KM231363	–	EU926296	KM230994
B. dimerum	CBS 108944 T = NRRL 36140	JQ434586	JQ434514	EU926400	–	KM231365	KM232363	EU926334	KM230996
B. domesticum	CBS 116517 = NRRL 29976	EU926219	JQ434512	JQ434531	–	KM231366	HQ897694	EU926286	KM230997
B. lunatum	CBS 632.76 T = BBA 63199 = NRRL 20690	HQ897819	KM231662	KM232057	–	KM231367	HQ897766	EU926291	HQ897902
B. nectrioides	CBS 176.31 T = NRRL 20689	EU926245	KM231659	KM232055	–	KM231362	HQ897721	EU926312	KM230993
B. penicilloides	UBOCC-A-120021 T	MW654542	MW654517	MW811096	–	MW811023	MW811066	MW811081	MW810993
B. penzigii	CBS 317.34 T = NRRL 22109	KM231795	KM231661	EU926390	–	KM231364	KM232362	EU926324	KM230995
B. tonghuanum	CGMCC 3.17369 T	KX790413	KX790414	KX790417	–	–	–	KX790418	–
Cyanonectria buxi	CBS 125551 T	MH863556	MH875034	–	MW834183	–	MW834001	KM231939	–
C. cyanostoma	CBS 101734 T = CBS 115512 = GJS 98-127	FJ474076	MH874353	–	MW834184	–	MW834002	HM626647	–
Fusarium aberrans	CBS 131385 T	–	–	–	–	MN170311	MN170378	MN170445	–
F. aberrans	CBS 119866 = MRC 6715	–	–	–	–	MN170310	MN170377	MN170444	–
F. aberrans	CBS 131387	–	–	–	–	MN170312	MN170379	MN170446	–
F. abutilonis	NRRL 66738 T	OM117601	–	–	OM160826	–	OM160847	OM160868	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. acaciae-mearnsii	LC13786 = FJWYS2-3	MW016630	–	MW533978	MW024658	–	MW474616	MW620091	–
F. acaciae-mearnsii	NRRL 26755 = CBS 110255 = MRC 5122	–	–	–	KM361640	–	KM361658	AF212449	–
F. aconidiale	CBS 147772 T = CPC37959	MZ064464	MZ064522	–	MZ078192	MZ078177	MZ078218	MZ078246	–
F. acuminatum	LC13791 = F034	MW016644	–	MW533990	MW024672	–	MW474630	MW620105	–
F. acutatum	CBS 402.97 T	–	–	MW402323	MW402653	MW402459	MW402768	MW402125	–
F. aethiopicum	NRRL 46726	FJ240309	–	FJ240288	MW233298	–	MW233470	MW233126	–
F. agapanthi	NRRL 54463 T	–	–	KU900635	KU900620	KU900611	KU900625	KU900630	–
F. algeriense	NRRL 66647 = CBS 142638 T = IL-79	MF120477	–	–	MF120488	–	MF120499	MF120510	–
F. alpinum	CGMCC 3.20818 = LC6045 T	MW016689	–	MW534035	MW024717	–	MW474675	MW620150	–
F. alpinum	LC2853	MW016684	–	MW534030	MW024712	–	MW474670	MW620145	–
F. alpinum	LC2854	MW016685	–	MW534031	MW024713	–	MW474671	MW620146	–
F. alpinum	LC6034	MW016686	–	MW534032	MW024714	–	MW474672	MW620147	–
F. alpinum	LC6037	MW016687	–	MW534033	MW024715	–	MW474673	MW620148	–
F. alpinum	LC6043	MW016688	–	MW534034	MW024716	–	MW474674	MW620149	–
F. ananatum	CBS 118516 T	–	–	LT996112	LT996188	LT996175	LT996137	LT996091	–
F. andiyazi	CBS 119857 T	–	–	LT996113	LT996189	LT996176	LT996138	LT996092	–
F. annulatum	CBS 258.54 T	–	–	MT011041	MT010944	MT010908	MT010983	MT010994	–
F. anthophilum	CBS 222.76 T	–	–	MW402312	MW402641	MW402451	MW402811	MW402114	–
F. aquaticum	CGMCC 3.20819 = LC7502 T	MW016408	–	MW533730	MW024439	MW566275	MW474394	MW580448	–
***F. arbusti* sp. nov.**	**GUCC 190154.1 = CGMCC3.25473 T**	**MZ724826**	**OR039375**	**OR043940**	**OR043788**	**OR043743**	**OR043837**	**OR043893**	**OR043693**
***F. arbusti* sp. nov.**	**GUCC 190154.2**	**OR034257**	**OR039376**	**OR043941**	**OR043789**	**OR043744**	**OR043838**	**OR043894**	**OR043694**
F. arcuatisporum	CGMCC 3.19493 = LC12147 = LF1502 T	MK280802	–	MW533837	MK289799	MK289697	MK289739	MK289584	–
F. arcuatisporum	LC11639	MK280840	–	–	MK289798	MK289658	MK289736	MK289586	–
F. armeniacum	LC2797	MW016608	–	MW533963	MW024636	–	MW474594	MW620069	–
F. asiaticum	NRRL 13818 T = FRCR-5469	–	–	AF212768	JX171459	–	JX171573	AF212451	–
F. asiaticum	LC13773 = CQ974	MW016607	–	MW533962	MW024635	–	MW474593	MW620068	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. atrovinosum	CBS 445.67 = BBA 10357 =NRRL 26913T	–	–	–	MN120713	MN120693	–	MN120752	–
F. austroafricanum	PPRI 10408 = PPRI 23548 = NRRL 66741 T	–	–	–	MH742537	–	MH742616	MH742687	–
F. austroamericanum	NRRL 2903 T	–	–	AF212755	–	–	–	AF212438	–
F. avenaceum	LC13801 = F010	MW016655	–	MW534001	MW024683	–	MW474641	MW620116	–
F. avenaceum	LC13802 = F038	MW016656	–	MW534002	MW024684	–	MW474642	MW620117	–
F. avenaceum	LC13803 = F039	MW016657	–	MW534003	MW024685	–	MW474643	MW620118	–
F. avenaceum	LC13804 = F071	MW016658	–	MW534004	MW024686	–	MW474644	MW620119	–
F. avenaceum	LC13805 = F403	MW016659	–	MW534005	MW024687	–	MW474645	MW620120	–
F. avenaceum	**GUCC 191095.1**	**MZ724838**	**OR039362**	**OR043932**	–	**OR043730**	**OR043825**	**OR043880**	**OR043680**
F. awaxy	LGMF 1930 T	–	–	MG839013	–	MK766940	MK766941	MG839004	–
F. aywerte	NRRL 25410 T	–	–	–	JX171513	KU171417	JX171626	–	–
F. bactridioides	CBS 100057 T	–	–	MN534112	MW402490	MN534173	MN534235	MN533993	–
F. begoniae	CBS 403.97 T	–	–	U61543	LT996191	AF158346	LT996140	AF160293	–
F. beomiforme	CBS 740.97 = BBA 65829 = DAOM 225123 = IMI 375328 = NRRL 25174	U61674	U61648	–	JX171506	–	JX171619	PVQB02000800	–
F. boothii	NRRL 26916 = CBS 316.73 T = IMI 160243	–	–	–	MW233259	–	MW233431	MW233088	–
F. brachiariae	CML 3032 T	–	–	MT901321	–	–	MT901314	MT901348	–
F. brachygibbosum	NRRL 34033	–	–	–	HM347172	GQ505388	GQ505482	GQ505418	–
F. brevicatenulatum	CBS 404.97 T	–	–	MN534063	MW402655	–	MN534295	MN533995	–
F. brevicaudatum	NRRL 43638 T = UTHSC R-3500	GQ505754	GQ505754	–	–	GQ505576	GQ505843	GQ505665	–
F. brevicaudatum	NRRL 43694	–	–	–	–	GQ505579	GQ505846	GQ505668	–
F. brevicaudatum	NRRL 45998	–	–	–	–	GQ505584	GQ505851	GQ505673	–
F. bubalinum	CBS 161.25 T = NRRL 26857 = NRRL 26918	–	–	–	–	MN170314	MN170381	MN170448	–
F. buharicum	CBS 178.35 T= DSM 62166 = NRRL 25488	–	–	–	KX302920	–	KX302928	KX302912	–
F. bulbicola	CBS 220.76 T	–	–	KF466437	KF466394	KF466327	KF466404	KF466415	–
F. burgessii	CBS 125537 T = NRRL 66654 = RBG 5315	–	–	–	–	–	HQ646393	HQ667148	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. caapi	CML 3657 T	–	–	MT901323	–	–	MT901316	MT901350	–
F. caatingaense	MUM 1859 T = URM 6779	MH668816	MH307669	–	MH668845	–	LS398495	LS398466	–
F. caatingaense	URM 6776	MH668813	MH307666	–	MH668842	–	LS398492	LS398463	–
F. caatingaense	MUM 1860 = URM 6777	MH668814	MH307667	–	MH668843	–	LS398493	LS398464	–
F. caatingaense	URM 6778	MH668815	MH307668	–	MH668844	–	LS398494	LS398465	–
F. caatingaense	URM 6780	MH668817	MH307670	–	MH668846	–	LS398496	LS398467	–
F. caatingaense	URM 6782	MH668818	MH307671	–	MH668847	–	LS398497	LS398468	–
F. californicum	CBS 145796 T = BL30	MK880138	MK878589	MK878574	MK878584	–	MK878569	MK878579	–
F. californicum	BL24	MK880134	MK878585	MK878570	MK878580	–	MK878565	MK878575	–
F. californicum	BL26	MK880135	MK878586	MK878571	MK878581	–	MK878566	MK878576	–
F. californicum	BL28	MK880136	MK878587	MK878572	MK878582	–	MK878567	MK878577	–
F. californicum	BL29	MK880137	MK878588	MK878573	MK878583	–	MK878568	MK878578	–
F. callistephi	CBS 187.53 T	–	–	MH485057	–	MH484693	MH484875	MH484966	–
F. callistephi	CBS 115423	–	–	MH485087	–	MH484723	MH484905	MH484996	–
F. camptoceras	ATCC 16065 = ATCC 24364 = BBA 9810 = CBS 193.65 = DSM 62167 = IMI 112500 = NRRL 20716 = NRRL 36344 T	–	–	–	MW928800	–	MN170383	MN170450	–
F. carminascens	CBS 144738 T = CPC 25800	–	–	MH485119	–	MH484755	MH484937	MH485028	–
F. carminascens	CBS 144739 = CPC 25792	–	–	MH485116	–	MH484752	MH484934	MH485025	–
F. carminascens	CBS 144740 = CPC 25793	–	–	MH485117	–	MH484753	MH484935	MH485026	–
F. carminascens	CBS 144741 = CPC 25795	–	–	MH485118	–	MH484754	MH484936	MH485027	–
F. casha	PPRI 21883 T = PREM 61342	–	–	MF787255	–	–	MN605059	MF787261	–
F. cassiae	LC13727 = F092	MW016554	–	MW533911	MW024582	–	MW474540	MW594307	–
F. cassiae	MFLUCC 18-0573 T	MT215495	MT215546	–	–	–	MT212197	MT212205	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. cateniforme	CBS 150.25 T = ATCC 11853	–	–	–	–	MN170317	MN170384	MN170451	–
***F. caulendophyticum* sp. nov.**	**GUCC 191050.1 = CGMCC3.25474 T**	**MZ724828**	**OR039363**	**OR043933**	**OR043781**	**OR043731**	**OR043826**	**OR043881**	**OR043681**
***F. caulendophyticum* sp. nov.**	**GUCC 191050.2**	**OR034254**	**OR039364**	**OR043934**	**OR043782**	**OR043732**	**OR043827**	**OR043882**	**OR043682**
***F. caulicola* sp. nov.**	**GUCC 191051.1 = CGMCC3.25475 T**	**MZ724827**	**OR039365**	**OR043935**	**OR043783**	**OR043733**	**OR043828**	**OR043883**	**OR043683**
***F. caulicola* sp. nov.**	**GUCC 191051.2**	**OR034255**	**OR039366**	**OR043936**	**OR043784**	**OR043734**	**OR043829**	**OR043884**	**OR043684**
F. celtidicola	MFLUCC 16-0526 T	MG873469	MG873466	MH576583	MH576579	–	MH576577	–	–
F. cerealis	NRRL 25491 = CBS 589.93	–	–	–	MG282371	–	MG282400	AF212465	–
F. chaquense	NRRL 66749 T = RC-J293	–	–	–	–	–	MK033033	MF795061	–
F. chinhoyiense	NRRL 25221 T	–	–	MN534082	MW402711	MN534196	MN534262	MN534050	–
F. chlamydosporum	CBS 145.25 T	–	–	–	MN120715	MN120695	MN120735	MN120754	–
F. chongqingense	CGMCC 3.20821 = LC4957 T	MW016677	–	MW534023	MW024705	–	MW474663	MW620138	–
F. chongqingense	LC13813	MW016675	–	MW534021	MW024703	–	MW474661	MW620136	–
F. chongqingense	LC13814	MW016676	–	MW534022	MW024704	–	MW474662	MW620137	–
F. chuoi	CBS 148464 T	OK586454	OK586452	OK626310	OK626306	OK626304	OK626302	OK626308	–
***F. cili* sp. nov.**	**GUCC 190024.1 = CGMCC3.25476 T**	**MZ724823**	**OR039367**	**OR043937**	**OR043785**	**OR043735**	**OR043830**	**OR043885**	**OR043685**
***F. cili* sp. nov.**	**GUCC 190024.2**	**OR034256**	**OR039368**	**OR043938**	**OR043786**	**OR043736**	**OR043831**	**OR043886**	**OR043686**
F. circinatum	CBS 405.97 T	U61677	–	KM232080	JX171510	KM231393	JX171623	KM231943	KM231017
F. citri	CGMCC 3.19467 T	MK280803	–	–	MK289828	MK289668	MK289771	MK289617	–
F. citricola	CBS 142421 = CPC 27805 T	LT746245	LT746245	–	LT746290	–	LT746310	LT746197	–
F. citricola	CPC 27067	LT746242	LT746242	–	LT746287	–	LT746307	LT746194	–
F. citricola	CPC 27069	LT746243	LT746243	–	–	–	LT746308	LT746195	–
F. citricola	CPC 27709	LT746244	LT746244	–	–	–	LT746309	LT746196	–
F. citricola	CPC 27813	LT746246	LT746246	–	–	–	LT746311	LT746198	–
F. clavus	CBS 394.93 = BBA 64265 = NRRL 25795	–	–	–	–	GQ505509	GQ505775	GQ505597	–
F. clavus	CBS 126202 T	–	–	–	–	MN170322	MN170389	MN170456	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. clavus	CBS 130395 = NRRL 34032 = UTHSC 98-2172	–	–	–	–	GQ505547	GQ505813	GQ505635	–
F. clavus	CBS 119881 = MRC 8412	–	–	–	–	MN170323	MN170390	MN170457	–
F. clavus	NRRL 32871 = FRC R-9561	–	–	–	–	GQ505531	GQ505797	GQ505619	–
F. coffeatum	CBS 635.76 T = BBA 62053 = NRRL 208	–	–	–	MN120717	MN120696	MN120736	MN120755	–
F. coffeatum	CBS 430.81 = NRRL 28577	–	–	–	–	MN120697	MN120737	MN120756	–
F. coicis	NRRL 66233 T	–	–	LT996115	KP083269	LT996178	KP083274	KP083251	–
F. commune	CBS 110090 T	–	–	–	–	–	–	AF362263	–
F. commune	LC11660 = HM259-R03	MW016699	–	MW534045	MW024727	–	MW474685	MW620160	–
F. commune	LC13824 = GXQZPSRDE4	MW016701	–	–	MW024729	–	MW474687	MW620162	–
F. compactum	NRRL 13829	–	–	–	JX171460	–	JX171574	–	–
F. concentricum	CBS 450.97 T	–	–	MW402334	MW402674	MW402467	JF741086	AF160282	–
F. concolor	BBA 2607 = BBA 63601 = CBS 183.34 = DAOM 225131 = DSM 62179 = IMI 112502 = NRRL 13994 T	–	–	–	MH742492	–	MH742569	MH742650	–
F. contaminatum	CBS 114899 T	–	–	MH485083	–	MH484719	MH484901	MH484992	–
F. contaminatum	CBS 111552	–	–	MH485082	–	MH484718	MH484900	MH484991	–
F. contaminatum	CBS 117461	–	–	MH485093	–	MH484729	MH484911	MH485002	–
F. continuum	F2010305 = NRRL 662865 = CBS 140841 T	KM236752	–	–	KM520387	–	KM236782	KM236722	–
F. convolutans	CBS 144207 T= CPC 33733	–	–	–	LT996193	–	LT996141	LT996094	–
F. cortaderiae	NRRL 29297 T= ICMP 5435	–	–	–	MW233270	–	MW233442	MW233098	–
F. croceum	CBS 131777 T	–	–	–	–	MN170329	MN170396	MN170463	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. croceum	CBS 131788	–	–	–	–	MN170330	MN170397	MN170464	–
F. croceum	CPC 35240	–	–	–	–	MN170331	MN170398	MN170465	–
F. croceum	NRRL 3020 = FRC R-6053 =MRC 2231	–	–	–	–	GQ505498	GQ505764	GQ505586	–
F. croceum	NRRL 3214 = FRC R-6054 =MRC 2232	–	–	–	–	GQ505499	GQ505765	GQ505587	–
F. cugenangense	CBS 130308 = NRRL 25387 = ATCC 26225	MW827607	MW827646	–	JX171512	–	JX171625	MH485011	–
F. cugenangense	InaCC F984 T	–	–	–	LS479560	–	LS479308	LS479757	–
F. cugenangense	LC4496	MW016571	–	MW533928	MW024599	–	MW474557	MW594324	–
F. cugenangense	CBS 130304 = BBA 69050 = NRRL 25433	–	–	MH485103	–	MH484739	MH484921	MH485012	–
F. cugenangense	**GUCC 190019.1**	**MZ724816**	**OR039369**	**OR043939**	–	**OR043737**	**OR043832**	**OR043887**	**OR043687**
F. cugenangense	**GUCC 190032.1**	**MZ724817**	**OR039370**	–	–	**OR043738**	**OR043833**	**OR043888**	**OR043688**
F. cugenangense	**GUCC 190110.1**	**MZ724818**	**OR039371**	–	–	**OR043739**	–	**OR043889**	**OR043689**
F. cugenangense	**GUCC 190113.1**	**MZ724819**	**OR039372**	–	–	**OR043740**	**OR043834**	**OR043890**	**OR043690**
F. cugenangense	**GUCC 190112.1**	**MZ724820**	**OR039373**	–	–	**OR043741**	**OR043835**	**OR043891**	**OR043691**
F. cugenangense	**GUCC 190057.1**	**MZ724821**	**OR039374**	–	**OR043787**	**OR043742**	**OR043836**	**OR043892**	**OR043692**
F. culmorum	NRRL 25475 = CBS 417.86 = FRC R-8504 = IMI 309344	–	–	–	JX171515	–	JX171628	AF212463	–
F. curculicola	PPRI 20458 T = PREM 61345	–	–	MF787258	–	–	MN605062	MF787266	–
F. curvatum	CBS 744.97 = IMI 375335 = NRRL 22902	–	–	U34424	LT996203	AF158365	LT575065	AF160312	–
F. curvatum	CBS 238.94 T = NRRL 26422 = PD 94/184	–	–	MH485075	–	MH484711	MH484893	MH484984	–
F. curvatum	CBS 247.61 = BBA 8398 = DSM 62308 = NRRL 22545	–	–	MH485058	–	MH484694	MH484876	MH484967	–
F. dactylidis	NRRL 29298 = CBS 119181 T = ICMP 5269	–	–	–	KM361654	–	KM361672	–	–
F. denticulatum	CBS 407.97 T	–	–	MN534068	MW402658	MN534186	MN534274	MN534000	–
F. desaboruense	InaCC F950 T	–	–	LS479435	LS479870	–	LS479852	–	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. dhileepanii	BRIP 71717 T	–	–	–	–	–	OK533536	OK509072	–
F. dlaminii	CBS 119860 T	–	–	MW402195	KU171681	MW402388	KU171701	MW401995	–
F. duofalcatisporum	CBS 384.92 T = NRRL 36448	GQ505741	GQ505741	–	–	GQ505564	GQ505830	GQ505652	–
F. duofalcatisporum	CBS 264.50 = NRRL 36401	–	–	–	–	GQ505563	GQ505829	GQ505651	–
F. duoseptatum	LC13740 = GXHCFoc1	MW016573	–	MW533930	MW024601	–	MW474559	MW594326	–
F. duoseptatum	InaCC F916 T	–	–	–	LS479495	–	LS479239	LS479688	–
F. echinatum	CBS 146497 T = CPC 30815	–	–	MW834301	MW834187	MW834110	MW834004	MW834273	–
F. elaeagni	CGMCC 3.20822 = LC13627 = CQ1053 T	MW016426	–	MW533748	MW024457	MW566293	MW474412	MW580466	–
F. elaeidis	LC13742 = M0765	MW016575	–	MW533932	MW024603	–	MW474561	MW594328	–
F. elaeidis	CBS 217.49 T = NRRL 36358	–	–	MH485052	–	MH484688	MH484870	MH484961	–
F. elaeidis	CBS 218.49 = NRRL 36359	–	–	MH485053	–	MH484689	MH484871	MH484962	–
F. elaeidis	CBS 255.52 = NRRL 36386	–	–	MH485056	–	MH484692	MH484874	MH484965	–
F. elongatum	CBS 190.34 = NRRL 20897	–	–	–	KX302927	–	KX302935	KX302919	–
F. equiseti	CBS 245.61 = NRRL 20697	MH858038	MH869603	–	JX171481	–	JX171595	–	–
F. equiseti	NRRL 26419 = CBS 307.94, BBA 68556 T	GQ505688	–	–	–	GQ505511	GQ505777	GQ505599	–
F. equiseti	NRRL 36136 = CBS 107.07, IMI 091982	GQ505733	–	–	–	GQ505556	GQ505822	GQ505644	–
F. equiseti	NRRL 36466 = CBS 414.86	GQ505742	–	–	–	GQ505565	GQ505831	GQ505653	–
F. fabacearum	CBS 144743 T = CPC 25802	–	–	MH485121	–	MH484757	MH484939	MH485030	–
F. fabacearum	CBS 144744 = CPC 25803	–	–	MH485122	–	MH484758	MH484940	MH485031	–
F. fasciculatum	CBS 131382 T	–	–	–	–	MN170339	MN170406	MN170473	–
F. fasciculatum	CBS 131383	–	–	–	–	MN170340	MN170407	MN170474	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. fasciculatum	CBS 131384	–	–	–	–	MN170341	MN170408	MN170475	–
F. ficicrescens	CBS 125178 T	–	–	KP662896	MW402546	KU603958	KT154002	KU604452	–
F. flagelliforme	CBS 162.57 T = NRRL 36269	GQ505734	GQ505734	–	–	GQ505557	GQ505823	GQ505645	–
F. flagelliforme	CBS 259.54 = NRRL 36392	–	–	–	–	GQ505562	GQ505828	GQ505650	–
F. flagelliforme	NRRL 6548 = IMI 112503	–	–	–	–	GQ505501	GQ505767	GQ505589	–
F. flagelliforme	NRRL 26921 = CBS 731.87	–	–	–	–	GQ505512	GQ505778	GQ505600	–
F. flagelliforme	NRRL 31011 = BBA 69079	–	–	–	–	GQ505518	GQ505784	GQ505606	–
F. flocciferum	CBS 831.85 = BBA 64346 = NRRL 25473	–	MW827647	–	JX171514	–	JX171627	–	–
F. foetens	CBS 110286 T = NRRL 31852 = PD 2001/7244	–	–	–	MW928808	–	MW928825	AY320087	–
F. fracticaudum	CBS 137234 T = CMW 25237	–	–	KJ541051	LT996196	LT996179	LT996144	KJ541059	–
F. fractiflexum	NRRL 28852 T	–	–	AF160315	–	AF158341	LT575064	AF160288	–
F. fredkrugeri	CBS 144209 T	–	–	LT996118	LT996199	LT996181	LT996147	LT996097	–
F. fujikuroi	CBS 221.76 T	MW827608	MW827648	MN534130	MW402640	–	KU604255	MN534010	–
F. fujikuroi	**GUCC 190012.1**	**MZ724825**	**OR039377**	**OR043942**	–	**OR043745**	**OR043839**	**OR043895**	**OR043695**
F. fujikuroi	**GUCC 197164.1**	**OR034258**	–	**OR043943**	–	–	**OR043840**	**OR043896**	–
F. fujikuroi	**GUCC 197336.1**	**OR034259**	–	**OR043944**	–	–	**OR043841**	**OR043897**	–
F. gaditjirrii	NRRL 45417	–	–	–	MN193937	–	MN193909	MN193881	–
F. gamsii	CBS 143610 T = CPC 30862 = OrSaAg4	LT970824	LT970824	–	–	–	LT970760	LT970788	–
F. gamsii	CBS 143609 = CPC 30861 = OrSaAg3	LT970823	LT970823	–	–	–	LT970759	LT970787	–
F. gerlachii	NRRL 36905 T = LRG 00-551	DQ459862	DQ459862	DQ459640	–	–	–	DQ459742	–
F. giganteum	CMM 3557 T	–	–	–	–	–	MT188557	KY490537	–
F. globosum	CBS 428.97 T	–	–	MN534124	MW402668	MN534218	KF466406	KF466417	–
F. glycines	CBS 144746 T = CPC 25808	–	–	MH485124	–	MH484760	MH484942	MH485033	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. glycines	CBS 176.33 = NRRL 36286	–	–	MH485050	–	MH484686	MH484868	MH484959	–
F. glycines	CBS 214.49 = NRRL 36356	–	–	MH485051	–	MH484687	MH484869	MH484960	–
F. glycines	CBS 200.89	–	–	MH485070	–	MH484706	MH484888	MH484979	–
F. glycines	CBS 144745 = CPC 25804	–	–	MH485123	–	MH484759	MH484941	MH485032	–
F. goolgardi	NRRL 66250 T = RBG 5411	–	–	–	KP083270	–	KP083280	–	–
F. gossypinum	CBS 116613 T	–	–	MH485091	–	MH484727	MH484909	MH485000	–
F. gossypinum	CBS 116611	–	–	MH485089	–	MH484725	MH484907	MH484998	–
F. gossypinum	CBS 116612	–	–	MH485090	–	MH484726	MH484908	MH484999	–
F. gracilipes	NRRL 43635 T	–	–	–	–	GQ505573	GQ505840	GQ505662	–
F. graminearum	CBS 123657 = NRRL 31084	DQ459823	DQ459823	–	JX171531	–	JX171644	AY452957	–
F. grosmichelii	GDGZP11-2-2	OL744448	–	OL771397	OL771373	–	OL771381	OL771389	–
F. grosmichelii	InaCC F833 T	–	–	–	LS479548	–	LS479295	LS479744	–
F. guadeloupense	NRRL 66743 T	OM117607	–	–	OM160832	–	OM160853	OM160874	–
F. guilinense	CGMCC 3.19495 = LC12160 = GXGL9-3 T	MK280837	–	MW533851	MK289831	MK289652	MK289747	MK289594	–
F. guttiforme	CBS 409.97 T	–	–	MT011048	MT010938	MT010901	MT010967	MT010999	–
F. hainanense	CGMCC 3.19478 = LC11638 = HA5-S03 T	MK280836	–	MW533852	MK289833	MK289657	MK289735	MK289581	–
F. hainanense	LC12161	MK280793	–	–	MK289832	MK289648	MK289748	MK289595	–
F. hainanense	NRRL 26417 = CBS 544.96	GQ505687	–	–	JX171522	GQ505510	GQ505776	GQ505598	–
F. hainanense	NRRL 28714 = ATCC 74289	GQ505693	–	–	–	GQ505516	GQ505782	GQ505604	–
F. hechiense	CGMCC 3.20824 = LC13644 = GXHCSWL14-E1 T	MW016454	–	MW533773	MW024482	MW566321	MW474440	MW580494	–
F. heterosporum	CBS 720.79 = NRRL 20693	MW827609	MW827649	–	JX171480	–	JX171594	–	–
F. hexaseptatum	InaCC F866 T	–	–	–	–	–	LS479359	LS479805	–
F. hoodiae	CBS 132474 T	–	–	MH485111	–	MH484747	MH484929	MH485020	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. hostae	FRC O-2074 T	–	–	AF331808	–	–	–	AF331818	–
F. humicola	CBS 124.73 T= ATCC 24372 = IMI 128101 = NRRL 25535	–	–	–	MN120718	MN120698	MN120738	MN120757	–
F. humuli	CGMCC 3.19374 = CQ1039 T	MK280845	–	MW533857	MK289840	MK289712	MK289724	MK289570	–
F. humuli	CQ1048	MK280850	–	–	MK289841	MK289713	MK289725	MK289571	–
F. incarnatum	LC13705 = LGS051	MW016532	–	MW533871	MW024560	MW574197	MW474518	MW594375	–
F. inflexum	CBS 716.74 T = ATCC 32213 = BBA 63203 = DAOM 225130 = DSM 63203 = IMI 375336 = NRRL 20433	–	–	U34435	JX171469	AF158366	JX171583	AF008479	–
F. ipomoeae	CGMCC 3.19496 = LC12165 = M0111 T	MK280832	–	MW533878	MK289859	MK289704	MK289752	MK289599	–
F. ipomoeae	LC12166	MK280791	–	–	MK289860	MK289706	MK289753	MK289600	–
F. iranicum	LC1112	MW016678	–	MW534024	MW024706	–	MW474664	MW620139	–
F. iranicum	CBS 143608 T= CPC 30860 = OrSaAg2	LT970821	LT970821	–	–	–	LT970757	LT970785	–
F. iranicum	CBS 143611 = CPC 30863 = OrSaAg5	LT970822	LT970822	–	–	–	LT970758	LT970786	–
F. irregulare	CGMCC 3.19489 = LC7188 T	MK280829	–	–	MK289863	MK289680	MK289783	MK289629	–
F. irregulare	LC12145 = WMM 0324	MK280830	–	–	MK289864	MK289681	MK289737	MK289582	–
F. irregulare	LC12146 = WMM 0325	MK280831	–	–	MK289865	MK289682	MK289738	MK289583	–
F. juglandicola	CBS 147773 T = CPC 37962 = UBOCC-A-119001	MZ064461	MZ064519	–	MZ078190	MZ078174	MZ078215	MZ078243	–
F. kalimantanense	InaCC F917 T	–	–	–	LS479497	–	LS479241	LS479690	–
F. kalimantanense	InaCC F918	–	–	–	–	–	LS479242	LS479691	–
F. kalimantanense	InaCC F922	–	–	–	–	–	LS479246	LS479695	–
F. konzum	CBS 119849 T	–	–	MN534095	MW402519	LT996182	MW402733	LT996098	–
F. kotabaruense	InaCC F963 T	LS479417	LS479890	–	LS479875	LS479429	LS479859	LS479445	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. mkyushuense	LC0725	MW016613	–	MW533967	MW024641	–	MW474599	MW620074	–
F. lacertarum	NRRL 20423 = ATCC 42771 = CBS 130185 T= IMI 300797	–	–	–	JX171467	GQ505505	JX171581	GQ505593	–
F. lacertarum	NRRL 36123 = CBS 102300, BBA 70843	GQ505732	–	–	–	GQ505555	GQ505821	GQ505643	–
F. lactis	CBS 411.97 T	–	–	MN534077	MW402659	MN534178	MN534275	MN193862	–
F. langsethiae	NRRL 53417	–	–	–	KT597713	–	HQ154460	HM744672	–
F. languescens	CBS 645.78 T = NRRL 36531	–	–	MH485062	–	MH484698	MH484880	MH484971	–
F. languescens	CBS 646.78 = NRRL 36532	–	–	MH485063	–	MH484699	MH484881	MH484972	–
F. languescens	CBS 413.90 = ATCC 66046 = NRRL 36465	–	–	MH485072	–	MH484708	MH484890	MH484981	–
F. languescens	CBS 300.91 = NRRL 36416	–	–	MH485073	–	MH484709	MH484891	MH484982	–
F. languescens	CBS 302.91 = NRRL 36419	–	–	MH485074	–	MH484710	MH484892	MH484983	–
F. languescens	CBS 872.95 = NRRL 36570	–	–	MH485077	–	MH484713	MH484895	MH484986	–
F. lateritium	NRRL 13622 = NRRL A-26433	–	–	–	JX171457	–	JX171571	AY707173	–
F. lateritium	**GUCC 197048.1**	**OR034260**	–	**OR043945**	–	–	**OR043842**	**OR043898**	–
F. libertatis	CBS 144749 T = CPC 28465	–	–	MH485126	–	MH484762	MH484944	MH485035	–
F. libertatis	CBS 144748 = CPC 25782	–	–	MH485114	–	MH484750	MH484932	MH485023	–
F. libertatis	CBS 144747 = CPC 25788	–	–	MH485115	–	MH484751	MH484933	MH485024	–
F. longicaudatum	CBS 123.73 T = ATCC 24370 = IMI 160825 = NRRL 25477	–	–	–	–	MN170347	MN170414	MN170481	–
F. longicornicola	NRRL 52706 T	–	–	MW402360	–	MW402487	JF741114	JF740788	–
F. longifundum	CBS 235.79 T= NRRL 36372	GQ505738	GQ505738	–	–	GQ505561	GQ505827	GQ505649	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*tub2*	*rpb1*	*CaM*	*rpb2*	*tef1*	*acl1*
F. longipes	NRRL 20723 = IMI 265540	–	–	–	JX171483	–	JX171596	–	–
F. louisianense	NRRL 54197 = CBS 127525	–	–	KM889628	KM361649	–	KM361667	KM889633	–
F. luffae	CGMCC 3.19497 = LC12167 T	MK280807	–	–	MK289869	MK289698	MK289754	MK289601	–
F. luffae	CQ1038	MK280852	–	–	MK289870	MK289711	MK289723	MK289569	–
F. luffae	NRRL 32522 = Loyola W-14182	GQ505701	–	–	HM347158	GQ505524	GQ505790	GQ505612	–
F. lumajangense	InaCCF872 T	–	–	LS479433	–	–	LS479850	LS479441	–
F. lunulosporum	NRRL 13393 = BBA 62459 = CBS 636.76 T = FRC R-5822 = IMI 322097	–	–	–	KM361637	–	KM361655	AF212467	–
F. lyarnte	CBS 125536 T = NRRL 54252 = RBG5331	–	–	–	JX171549	–	JX171661	EF107118	–
F. madaense	CBS 146669 T	–	–	MW402297	MW402619	MW402439	MW402764	MW402098	–
F. magnoliae-champaca	MFLUCC 18-0580 T	MT215496	MT215547	–	–	–	MT212198	–	–
F. mangiferae	CBS 120994 T	–	–	MN534128	MW402530	MN534224	MN534271	MN534017	–
F. marasasianum	CMW 25512 T	–	–	MN534113	–	MN534208	MN534249	MN534018	–
F. massalimae	URM 8239 T	MN945153	–	MN939759	–	–	MN939767	MN939763	–
F. meridionale	NRRL 28436 T	–	–	–	MW233263	–	MW233435	MW233092	–
F. meridionale	**GUCC 190050.1**	**MZ724829**	**OR039378**	**OR043946**	**OR043790**	**OR043746**	**OR043843**	**OR043899**	**OR043696**
F. meridionale	**GUCC 190105.1**	**MZ724830**	**OR039379**	**OR043947**	**OR043791**	**OR043747**	**OR043844**	**OR043900**	**OR043697**
F. meridionale	**GUCC 190107.1**	**MZ724831**	**OR039380**	**OR043948**	**OR043792**	**OR043748**	**OR043845**	**OR043901**	**OR043698**
F. mesoamericanum	NRRL 25797 = CBS 415.86 T = FRC R-8506 = IMI 309346	–	–	–	MW233254	–	MW233426	MW233083	–
F. mexicanum	NRRL 53147 T	–	–	GU737494	MG838088	–	MN724973	GU737282	–
F. microconidium	CBS 119843 = MRC 8391	–	–	–	MN120721	MN120700	–	MN120759	–
F. mirum	KSU 4735 = CML 3859 T	–	–	MK907329	–	–	MK907308	MK895725	–
F. miscanthi	LC7503	MW016565	–	MW533922	MW024593	–	MW474551	MW594318	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. monophialidicum	NRRL 54973 T = UTHSC 06-1473	–	–	–	–	MN170349	MN170416	MN170483	–
F. mucidum	CBS 102395 T	–	–	–	–	MN170351	MN170418	MN170485	–
F. mucidum	CBS 102394	–	–	–	–	MN170350	MN170417	MN170484	–
F. mucidum	Indo 175	–	–	–	–	LS479431	LS479862	LS479447	–
F. multiceps	CBS 130386 T = NRRL 43639 = UTHSC 04-135	–	–	–	–	GQ505577	GQ505844	GQ505666	–
F. mundagurra	RGB5717 T	–	–	MN534146	–	MN534214	KP083276	KP083256	–
F. musae	CBS 624.87 T	–	–	FN545368	MW402689	MW402474	MW402772	FN552086	–
F. nanum	CGMCC 3.19498 = LC12168 = GXGL14-2 T	MK280794	–	–	MK289871	MK289651	MK289755	MK289602	–
F. nanum	LC1384	MK280842	–	–	MK289872	MK289661	MK289764	MK289611	–
F. nanum	LC1385	MK280781	–	–	MK289873	MK289662	MK289765	MK289612	–
F. nanum	LC1516	MK280782	–	–	MK289874	MK289663	MK289766	MK289613	–
F. napiforme	CBS 748.97 T	–	–	MN534085	MW402701	MN534192	MN534291	MN193863	–
F. nelsonii	CBS 119876 T= FRC R-8670 = MRC 4570	–	–	–	MN120722	MN120701	MN120740	MN120760	–
F. neoscirpi	CBS 610.95 T = NRRL 26861 = NRRL 26922	GQ505755	GQ505755	–	–	GQ505513	GQ505779	GQ505601	–
F. neosemitectum	CBS 189.60 T	–	–	–	–	MN170355	MN170422	MN170489	–
F. nepalense	LC13781 = GDBYL14-E3	MW016623	–	MW533975	MW024651	–	MW474609	MW620084	–
F. newnesense	NRRL66241 T = RBG610	–	–	–	–	–	–	KP083261	–
F. newnesense	RBG5443 = NRRL66237	–	–	–	KP083271	–	KP083277	KJ397074	–
F. nirenbergiae	CBS 840.88 T	–	–	MH485069	–	MH484705	MH484887	MH484978	–
F. nirenbergiae	CBS 129.24	–	–	MH485046	–	MH484682	MH484864	MH484955	–
F. nirenbergiae	CBS 149.25 = NRRL 36261	–	–	MH485047	–	MH484683	MH484865	MH484956	–
F. nirenbergiae	CBS 758.68 = NRRL 36546	–	–	MH485059	–	MH484695	MH484877	MH484968	–
F. nirenbergiae	CBS 744.79 = BBA 62355 = NRRL 22549	–	–	MH485064	–	MH484700	MH484882	MH484973	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*tub2*	*rpb1*	*CaM*	*rpb2*	*tef1*	*acl1*
F. nirenbergiae	CBS 127.81 = BBA 63924 = NRRL 36229	–	–	MH485065	–	MH484701	MH484883	MH484974	–
F. nirenbergiae	CBS 129.81 = BBA 63926 = NRRL 22539	–	–	MH485067	–	MH484703	MH484885	MH484976	–
F. nirenbergiae	CBS 196.87 = NRRL 26219	–	–	MH485068	–	MH484704	MH484886	MH484977	–
F. nirenbergiae	CBS 115416 = CPC 5307	–	–	MH485084	–	MH484720	MH484902	MH484993	–
F. nirenbergiae	CBS 115417 = CPC 5306	–	–	MH485085	–	MH484721	MH484903	MH484994	–
F. nirenbergiae	CBS 115419 = CPC 5308	–	–	MH485086	–	MH484722	MH484904	MH484995	–
F. nirenbergiae	CBS 115424 = CPC 5312	–	–	MH485088	–	MH484724	MH484906	MH484997	–
F. nirenbergiae	CBS 123062 = GJS 91-17	–	–	MH485101	–	MH484737	MH484919	MH485010	–
F. nirenbergiae	CBS 130300 = NRRL 26368	–	–	MH485107	–	MH484743	MH484925	MH485016	–
F. nirenbergiae	CBS 130301 = NRRL 26374	–	–	MH485108	–	MH484744	MH484926	MH485017	–
F. nirenbergiae	CBS 130303	–	–	MH485105	–	MH484741	MH484923	MH485014	–
F. nirenbergiae	CPC 30807	–	–	MH485132	–	MH484768	MH484950	MH485041	–
F. nirenbergiae	**GUCC 190015.1**	**MZ724822**	**OR039381**	**OR043949**	–	**OR043749**	**OR043846**	**OR043902**	**OR043699**
F. nirenbergiae	**GUCC 197140.1**	**OR034261**	–	–	**OR043793**	**OR043750**	**OR043847**	**OR043903**	–
F. nirenbergiae	**GUCC 197140.2**	**OR034262**	–	–	**OR043794**	**OR043751**	**OR043848**	**OR043904**	–
F. nisikadoi	BBA 69015 T= CBS 456.97 = MAFF 237506 = NRRL 25205 = NRRL 25308	–	–	–	MG282391	–	MG282421	KR909358	–
F. nodosum	CBS 201.63 T	–	–	–	MN120725	MN120704	MN120743	MN120763	–
F. nurragi	CBS 393.96 T = DAR 69501 = F10108 = F11121	–	–	–	MW928814	–	MW928830	MW928840	–
F. nygamai	CBS 749.97 T	–	–	MW402352	MW402703	MW402479	EF470114	MW402151	–
F. odoratissimum	InaCC F822 T	–	–	–	LS479618	–	LS479386	LS479828	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. odoratissimum	CBS 102030	–	–	MH485080	–	MH484716	MH484898	MH484989	–
F. ophioides	CBS 118512 T	–	–	MN534118	–	MN534209	MN534303	MN534022	–
F. oxysporum	LC13766 = F065	MW016600	–	MW533955	MW024628	–	MW474586	MW594353	–
F. oxysporum	CBS 144143 T	–	–	MH485135	–	MH484771	MH484953	MH485044	–
F. oxysporum	CBS 221.49 = IHEM 4508 = NRRL 22546	–	–	MH485054	–	MH484690	MH484872	MH484963	–
F. oxysporum	CBS 144135	–	–	MH485136	–	MH484772	MH484954	MH485045	–
F. oxysporum	CPC 25822	–	–	MH485125	–	MH484761	MH484943	MH485034	–
F. paeoniae	CGMCC 3.20817 = LC13817 = YZG12-2 T	MW016681	–	MW534027	MW024709	–	MW474667	MW620142	–
F. paeoniae	LC7358	MW016683	–	MW534029	MW024711	–	MW474669	MW620144	–
F. paeoniae	LC13815 = GM56	MW016679	–	MW534025	MW024707	–	MW474665	MW620140	–
F. paeoniae	LC5166	MW016682	–	MW534028	MW024710	–	MW474668	MW620143	–
F. paeoniae	LC13816 = YZG10-2	MW016680	–	MW534026	MW024708	–	MW474666	MW620141	–
F. paeoniae	CBS 143231 T= JW14004	MG386078	MG386131	–	MG386138	–	MG386149	MG386159	–
F. paeoniae	JW14005	MG386079	MG386132	–	MG386139	–	MG386150	MG386160	–
F. palustre	NRRL 54056	–	–	–	KT597718	–	KT597731	–	–
F. panlongense	CGMCC 3.20825 = LC13656 = GXGLPLL15E2 T	MW016470	–	MW533789	MW024498	MW566337	MW474456	MW580510	–
F. paranisikadoi	CGMCC 3.20826 = LC2800 T	MW016561	–	MW533918	MW024589	–	MW474547	MW594314	–
F. parvisorum	CBS 137236 T	–	–	KJ541055	–	LT996183	LT996150	KJ541060	–
F. pernambucanum	MUM 1862 T= URM 7559	MH668840	MH307693	–	MH668869	–	LS398519	LS398489	–
F. pernambucanum	URM 6801	MH668834	MH307687	–	MH668863	–	LS398513	LS398483	–
F. pernambucanum	URM 6810	MH668836	MH307689	–	MH668865	–	LS398515	LS398485	–
F. pernambucanum	MUM 1864 = URM 7554	MH668837	MH307690	–	MH668866	–	LS398516	LS398486	–
F. pernambucanum	MUM 1863 = URM 7561	MH668841	MH307694	—	MH668870	–	LS398520	LS398490	–
F. persicinum	CBS 479.83 T	–	–	–	–	MN170361	MN170428	MN170495	–
F. persicinum	CBS 131780	–	–	–	–	MN170362	MN170429	MN170496	–
F. persicinum	CBS 132821	–	–	–	–	MN170363	MN170430	MN170497	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. persicinum	CBS 143595 = CPC 30847	–	–	–	–	LT970731	LT970750	LT970778	–
F. persicinum	CBS 143596 = CPC 30848	–	–	–	–	LT970732	LT970751	LT970779	–
F. peruvianum	CBS 511.75 T	–	–	–	MN120728	MN120707	MN120746	MN120767	–
F. petersiae	CBS 143231 T = JW14004	MG386078	MG386131	–	MG386138	–	MG386149	MG386159	–
F. pharetrum	CBS 144751 T = CPC 30824	–	–	MH485134	–	MH484770	MH484952	MH485043	–
F. pharetrum	CBS 144750 = CPC 30822	–	–	MH485133	–	MH484769	MH484951	MH485042	–
F. phialophorum	InaCC F971 T	–	–	–	LS479545	–	LS479292	LS479741	–
F. phialophorum	InaCC F826	–	–	–	LS479505	–	LS479251	LS479700	–
F. phialophorum	InaCC F827	–	–	–	LS479513	–	LS479259	LS479708	–
F. phialophorum	InaCC F830	–	–	–	LS479536	–	LS479282	LS479731	–
F. phialophorum	InaCC F834	–	–	–	LS479557	–	LS479305	LS479754	–
F. phialophorum	InaCC F842	–	–	–	LS479582	–	LS479331	LS479780	–
F. phialophorum	InaCC F843	–	–	–	LS479583	–	LS479332	LS479781	–
F. phialophorum	InaCC F844	–	–	–	LS479585	–	LS479334	LS479783	–
F. phialophorum	InaCC F845	–	–	–	LS479586	–	LS479335	LS479784	–
F. phialophorum	InaCC F889	–	–	–	LS479622	–	LS479391	LS479832	–
F. phialophorum	InaCC F969	–	–	–	LS479543	–	LS479290	LS479739	–
F. phialophorum	InaCC F970	–	–	–	LS479544	–	LS479291	LS479740	–
F. phyllophilum	CBS 216.76 T	–	–	KF466443	MW402637	KF466333	KF466410	MN193864	–
F. pilosicola	NRRL 29124 T	–	–	MN534099	–	MN534159	MN534248	MN534055	–
F. pininemorale	CMW 25243	–	–	MN534115	–	MN534211	MN534250	MN534026	–
F. poae	NRRL 13714 = FRC T-503 = MRC 2181	–	–	–	JX171458	–	JX171572	—	–
F. poae	LC13783 = F150	MW016626	–	–	MW024654	–	MW474612	MW620087	–
F. polyphialidicum	ATCC 60096 = CBS 961.87 T = DAR 52851 = FRC M-2405 = MRC 3389 = NRRL 13459.	–	–	–	JX171455	–	JX171569	MH742681	–
F. praegraminearum	ICMP 8996 = NRRL 39664 = CBS 141369 T	–	–	KX260131	KX260125	–	KX260126	KX260120	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*tub2*	*rpb1*	*CaM*	*rpb2*	*tef1*	*acl1*
F. prieskaense	CBS 146498 T = CPC 30826	–	–	MW834303	MW834190	MW834112	MW834007	MW834275	–
F. proliferatum	CBS 480.96 T	–	–	MN534129	–	MN534217	MN534272	MN534059	–
F. pseudoanthophilum	CBS 414.97 T	–	–	MW402326	MW402661	MW402463	—	MW402128	–
F. pseudocircinatum	CBS 449.97 T	–	–	MN534069	MW402673	MN534190	MN534277	AF160271	–
F. pseudograminearum	CBS 109956 T = NRRL 28062	DQ459871	DQ459871	–	JX171524	–	JX171637	AF212468	–
F. pseudonygamai	CBS 417.97 T	–	–	MN534066	MW402664	AF158316	MN534285	AF160263	–
***F. qiannanense* sp. nov.**	**GUCC 198067.1 = CGMCC3.25477 T**	**OR034263**	**OR039382**	**OR043950**	**OR043795**	–	**OR043849**	**OR043905**	–
***F. qiannanense* sp. nov.**	**GUCC 198067.2**	**OR034264**	**OR039383**	**OR043951**	**OR043796**	–	**OR043850**	**OR043906**	–
F. queenslandicum	BRIP 70769a T	–	–	MW403138	MW038832	–	MW038833	MW038834	–
***F. radicigenum* sp. nov.**	**GUCC 197371.1**	**OR034265**	–	**OR043952**	**OR043797**	**OR043752**	**OR043851**	**OR043907**	–
***F. radicigenum* sp. nov.**	**GUCC 197425.1**	**OR034266**	–	**OR043953**	**OR043798**	**OR043753**	**OR043852**	**OR043908**	–
***F. radicigenum* sp. nov.**	**GUCC 197221.1 = CGMCC3.25478 T**	**OR034267**	–	**OR043954**	**OR043799**	**OR043754**	–	**OR043909**	–
F. ramigenum	CBS 418.97 T	–	–	MN534145	MW402665	MN534187	KF466412	KF466423	–
F. ramsdenii	BRIP 62306a T	OL330776	OL330777	OL332734	–	–	OL332733	OL332732	–
F. redolens	CBS 743.97 = DAOM 225128 = IMI 375334 = NRRL 22901	U34565	U34536	–	JX171503	–	JX171616	MT409452	–
***F. rosae-roxburghii* sp. nov.**	**GUCC 190111.1 = CGMCC3.25479 T**	**MZ724824**	**OR039384**	–	**OR043800**	**OR043755**	**OR043853**	**OR043910**	**OR043700**
***F. rosae-roxburghii* sp. nov.**	**GUCC 190111.2**	**OR034268**	**OR039385**	–	**OR043801**	**OR043756**	**OR043854**	**OR043911**	**OR043701**
***F. rosendophyticum* sp. nov.**	**GUCC 190163.1 = CGMCC3.25480 T**	**MZ724841**	**OR039386**	**OR043955**	**OR043802**	**OR043757**	**OR043855**	–	**OR043702**
***F. rosendophyticum* sp. nov.**	**GUCC 190163.2**	**OR034269**	**OR039387**	**OR043956**	**OR043803**	**OR043758**	**OR043856**	–	**OR043703**
***F. rosiradicicola* sp. nov.**	**GUCC 190100.1**	**MZ724832**	**OR039388**	**OR043957**	**OR043804**	**OR043759**	**OR043857**	**OR043912**	**OR043704**

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
***F. rosiradicicola* sp. nov.**	**GUCC 190145.1**	**MZ724833**	**OR039389**	**OR043958**	**OR043805**	**OR043760**	–	**OR043913**	**OR043705**
***F. rosiradicicola* sp. nov.**	**GUCC 190168.1 = CGMCC3.25482 T**	**MZ724834**	**OR039390**	**OR043959**	**OR043806**	**OR043761**	**OR043858**	**OR043914**	**OR043706**
***F. rosiradicicola* sp. nov.**	**GUCC 191009.1**	**MZ724835**	**OR039391**	**OR043960**	**OR043807**	**OR043762**	**OR043859**	**OR043915**	**OR043707**
***F. rosiradicicola* sp. nov.**	**GUCC 191073.1**	**MZ724836**	**OR039392**	**OR043961**	–	**OR043763**	**OR043860**	**OR043916**	**OR043708**
***F. rosiradicicola* sp. nov.**	**GUCC 191129.1**	**MZ724837**	**OR039393**	**OR043962**	–	**OR043764**	**OR043861**	–	**OR043709**
***F. rosiradicicola* sp. nov.**	**GUCC 190194.1**	**MZ724839**	**OR039394**	**OR043963**	**OR043808**	**OR043765**	**OR043862**	**OR043917**	**OR043710**
***F. rosiradicicola* sp. nov.**	**GUCC 191098.1**	**MZ724840**	**OR039395**	**OR043964**	**OR043809**	**OR043766**	**OR043863**	**OR043918**	**OR043711**
F. sacchari	CBS 223.76 T	–	–	MW402313	JX171466	AF158331	JX171580	MW402115	–
F. salinense	CPC 26457	LT746240	LT746240	–	LT746285	–	LT746305	LT746192	–
F. salinense	CPC 26973 = CBS 142420 T	LT746241	–	–	LT746286	–	LT746306	LT746193	–
F. sambucinum	CBS 146.95 = BBA 64226 = NRRL 22187 = NRRL 20727	–	–	–	JX171493	–	JX171606	MW834277	–
F. sangayamense	InaCC F960 T	–	–	–	LS479537	–	LS479283	LS479732	–
F. sarcochroum	CBS 745.79 = BBA 63714 = NRRL 20472	MW827611	MW827651	–	JX171472	–	JX171586	MW834278	–
F. scirpi	NRRL 13402	GQ505681	GQ505681	–	JX171452	–	JX171566	GQ505592	–
F. scirpi	CBS 447.84 = FRC R-6252 =NRRL 36478 T	GQ505743	–	–	–	GQ505566	GQ505832	GQ505654	–
F. scirpi	NRRL 29134 = CBS 448.84	GQ505694	–	–	–	GQ505517	GQ505783	GQ505605	–
F. secorum	NRRL 62593 T	–	–	–	–	KJ189235	–	KJ189225	–
F. serpentinum	CBS 119880 T = BBA62209 = MRC 1813	–	–	–	–	MN170365	MN170432	MN170499	–
F. sibiricum	NRRL 53430	–	–	–	–	–	HQ154472	HM744684	–
F. siculi	CBS 142222 T	–	–	LT746346	–	LT746189	LT746327	LT746214	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. sinense	IBE000007 = CBS 122710 T	EF531229	–	EF531241	–	–	–	EF531235	–
F. sinense	IBE000008 = CBS 122711	EF531230	–	EF531242	–	–	–	EF531238	–
F. sororula	CMW 40578 = CBS 137242 T	–	–	KJ541057	LT996206	LT996184	LT996153	KJ541067	–
F. spartum	NRRL 66896 T = TN243	MT435070	MT435070	–	MT409439	–	MT409449	MT409459	–
F. spinosum	CBS 122438	–	–	–	MN120729	MN120708	MN120747	MN120768	–
F. sporodochiale	CBS 220.61 T= ATCC 14167 = MUCL 8047 = NRRL 20	–	–	–	MN120731	MN120710	MN120749	MN120770	–
F. sporotrichioides	CBS 462.94	–	–	–	MN120732	MN120711	MN120750	MN120771	–
F. sterilihyphosum	NRRL 25623 T	–	–	AF160316	MW402713	AF158353	MN193897	MN193869	–
F. stilboides	BBA 63887 = CBS 746.79 = ICMP 10624 = NRRL 25485.	–	–	–	MW928817	–	MW928832	MW928843	–
F. subflagellisporum	COAD 2989 T	–	–	–	–	–	MZ970426	MT774486	–
F. subglutinans	CBS 747.97 T	–	–	MW402351	MW402700	MW402478	MW402773	MW402150	–
F. sublunatum	CBS 189.34 T = BBA 62431 = DSM 62431 = NRRL 20840 = NRRL 13384	HQ897830	KM231680	KM232076	JX171451	KM231389	JX171565	–	HQ897916
F. subtropicale	NRRL 66764 = CBS 144706 T	–	–	MH706968	MH706972	–	MH706973	MH706974	–
F. succisae	CBS 219.76 T	–	–	U34419	MW402639	AF158344	MW402766	AF160291	–
F. sudanense	CBS 454.97 T	–	–	MN534073	MW402677	MN534179	MN534278	MN534037	–
F. sulawesiense	InaCC F940 T	LS479410	LS479883	–	–	LS479422	LS479855	LS479443	–
F. sulawesiense	InaCC F941	LS479411	LS479884	–	–	LS479423	LS479856	LS479444	–
F. sulawesiense	Indo186	LS479414	LS479887	–	LS479878	LS479426	LS479864	LS479449	–
F. tanahbumbuense	InaCC F965 T	LS479420	LS479893	–	LS479877	LS479432	LS479863	LS479448	–
F. tardichlamydosporum	InaCC F958 T	–	–	–	LS479534	–	LS479280	LS479729	–
F. tardichlamydosporum	InaCC F956	–	–	–	LS479532	–	LS479278	LS479727	–
F. tardichlamydosporum	InaCC F957	–	–	–	LS479533	–	LS479279	LS479728	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. tardicrescens	CBS 102024 T = NRRL 36113	–	–	–	LS479474	–	LS479217	LS479665	–
F. temperatum	MUCL 52463 T	–	–	MW402359	–	MW402486	MW402776	–	–
F. terricola	CBS 483.94 T	–	–	MN534076	MW402680	MN534189	LT996156	MN534042	–
F. thapsinum	CBS 119850 T	–	–	MN534075	MW402520	MN534180	MN534280	MN534041	–
F. tjaetaba	CBS 144400 T = NRRL 66243 = RBG 5361	–	–	–	KP083267	LT996187	KP083275	KP083263	–
F. tjaynera	NRRL 66246 T = RBG5367	–	–	–	KP083268	–	KP083279	KP083266	–
F. torreyae	CBS 133858 T = NRRL 54151	HM068344	MW827652	–	JX171548	–	JX171660	HM068337	–
F. torulosum	NRRL 22748	–	–	–	JX171502	–	JX171615	–	–
F. toxicum	CBS 406.86 T = FRC R-8507 = IMI 309347 = NRRL 25796	–	–	–	–	MN170374	MN170441	MN170508	–
F. toxicum	CBS 219.63	–	–	–	–	MN170373	MN170440	MN170507	–
F. toxicum	CBS 130385	–	–	–	–	MN170375	MN170442	MN170509	–
F. trachichlamydosporum	CBS 102028 = NRRL 36117	–	–	MH485079	–	MH484715	MH484897	MH484988	–
F. transvaalense	LC13784 = F157	MW016628	–	–	MW024656	–	MW474614	MW620089	–
F. tricinctum	CBS 393.93 T = BBA 64485 = NRRL 25481	HM068317	HM068317	–	JX171516	–	JX171629	AB674263	–
F. tricinctum	LC13819 = F020	MW016693	–	MW534039	MW024721	–	MW474679	MW620154	–
F. triseptatum	CBS 258.50 T = NRRL 36389	–	–	MH485055	–	MH484691	MH484873	MH484964	–
F. triseptatum	CBS 116619	–	–	MH485092	–	MH484728	MH484910	MH485001	–
F. triseptatum	CBS 119665	–	–	MH485098	–	MH484734	MH484916	MH485007	–
F. triseptatum	CBS 130302 = NRRL 26360 = FRC 755	–	–	MH485106	–	MH484742	MH484924	MH485015	–
F. tupiense	NRRL 53984 T	–	–	GU737296	LR792583	GU737377	LR792619	GU737404	–
F. udum	NRRL 25199 T	–	–	KY498892	–	–	KY498875	KY498862	–
F. ussurianum	LC13790 = LJM 1343	MW016634	–	–	MW024662	–	MW474620	MW620095	–
F. vanleeuwenii	CBS 148372 T = JW 10008	–	MZ890401	–	MZ921669	MZ921585	MZ921765	MZ921896	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
F. vanleeuwenii	CBS 109898 T= NRRL 36153	–	–	MH485081	–	MH484717	MH484899	MH484990	–
F. vanleeuwenii	CBS 117787	–	–	MH485094	–	MH484730	MH484912	MH485003	–
F. vanleeuwenii	CBS 117790	–	–	MH485095	–	MH484731	MH484913	MH485004	–
F. vanleeuwenii	CBS 117791	–	–	MH485096	–	MH484732	MH484914	MH485005	–
F. vanleeuwenii	CBS 117792	–	–	MH485097	–	MH484733	MH484915	MH485006	–
F. vanleeuwenii	NRRL 54984	–	–	MH485127	–	MH484763	MH484945	MH485036	–
F. vanleeuwenii	NRRL 54996	–	–	MH485128	–	MH484764	MH484946	MH485037	–
F. vanleeuwenii	NRRL 62542	–	–	MH485129	–	MH484765	MH484947	MH485038	–
F. vanleeuwenii	NRRL 62545	–	–	MH485130	–	MH484766	MH484948	MH485039	–
F. vanleeuwenii	NRRL 62547	–	–	MH485131	–	MH484767	MH484949	MH485040	–
F. venenatum	NRRL 22196 = BBA 65031	–	–	–	JX171494	–	JX171607	–	–
F. verticillioides	CBS 218.76 T	–	–	MW402311	MW402638	MW402449	–	MW402113	–
F. verticilloides	InaCC F991	–	–	LS479438	LS479881	LS479421	LS479867	LS479452	–
F. veterinarium	CBS 109898 T = NRRL 36153	–	–	MH485081	–	MH484717	MH484899	MH484990	–
F. volatile	CBS 143874 T	–	–	LR596008	–	MK984595	LR596006	LR596007	–
F. vorosii	NRRL 37605 T = TO´ TH FgHF012	DQ459865	DQ459865	DQ459643	–	–	–	–	–
F. wereldwijsianum	CBS 148244 T = NL19-94009	MZ890507	MZ890363	–	MZ921636	MZ921538	MZ921718	MZ921850	–
F. werrikimbe	CBS 125535 T = F19350 = RBG 5332	–	–	MN534104	MW928821	MN534203	MN534304	MW928846	–
F. xylarioides	CBS 258.52 T	–	–	AY707118	MW402646	MW402455	HM068355	MN193874	–
F. xyrophilum	NRRL 62721 T	–	–	–	MW402721	–	MN193905	MN193877	–
F. zanthoxyli	F201311 5 = NRRL 66285 5= CBS 140838 T	OM117610	–	–	OM160837	–	OM160858	OM160879	–
Fusicolla acetilerea	BBA 63789 T = IMI 181488 = NRRL 20827	HQ897790	U88108	–	–	–	HQ897701	–	–
Fu. aquaeductuum	CBS 837.85 T =BBA 64559 = NRRL 20865 = NRRL 37595	KM231823	KM231699	KM232094	–	–	–	–	–
Fu. betae	BBA 64317 T	MH855265	MH866717	–	–	–	HQ897781	–	HQ897917

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
Fu. bharatavarshae	NFCCI 4423 T	MK152510	MK152511	MK376462	–	–	MK157022	–	–
Fu. cassiae-fistulae	MFLUCC 19-0318 T	MT215497	MT215549	–	–	–	–	–	–
Fu. epistroma	BBA 62201 T = ATCC 24369 = IMI 85601 = NRRL 20439 = NRRL 20461	–	AF228352	–	–	–	HQ897765	–	HQ897901
Fu. gigantispora	MFLU 161206 T	MN047105	MN017876	–	–	–	–	–	–
Fu. gigas	CGMCC 3.20680 T	OK465362	OK465449	–	–	–	–	–	–
Fu. guangxiensis	CGMCC 3.20679 T	OK465363	OK465450	–	–	–	–	–	–
Fu. matuoi	CBS 581.78= ATCC 18694=NRRL 20427	KM231822	KM231698	KM232093	MW834194	–	HQ897720	KM231954	HQ897858
Fu. melogrammae	CBS 141092 T	KX897140	KY092489	MW834305	–	–	–	–	–
Fu. meniscoidea	CBS 110189 = FRC E-0086	MW827613	MW827654	MW834306	–	–	MW834010	MW834279	MW834043
Fu. merismoides	CBS 186.34 = BBA 1867a = NRRL 20895	MH855482	MH866963	–	–	–	–	–	–
Fu. ossicola	CBS 140161 T	MF628022	MF628021	MW834307	–	–	MW834011	MW834280	–
Fu. quarantenae	URM 8367 T = CBS 141541	MW553789	MW553788	MW556624	–	–	MW556626	MW556625	–
Fu. septimanifiniscientiae	CBS 144935 T	MK069422	MK069418	MK069408	–	–	–	MK077808	–
Fu. siamensis	MFLUCC 17-2577 T	MT215498	MT215550	–	–	–	–	–	–
Fu. sporellula	CBS 110191 = FRC E-0139	MW827614	MW827655	MW834308	–	–	MW834012	MW834281	MW834044
Fu. violacea	CBS 634.76 T = BBA 62461 = NRRL 20896	KM231824	U88112	KM232095	MW834195	–	HQ897696	KM231956	–
Geejayessia atrofusca	CBS 125505	HM626659	–	–	–	–	HM626682	–	HM626628
G. atrofusca	CBS 125482 = DAOM 238117	MH863592	MH875066	–	MW834196	–	HQ897775	MW834282	–
G. atrofusca	NRRL 22316	AF178423	AF178392	–	JX171496	–	EU329502	AF178361	–
G. celtidicola (= *F. celtis-occidentalis*)	CBS 125502 T = TG 2008-32	HM626657	HM626669	KM232074	MW834197	–	MW834013	HM626638	HM626625
G. cicatricum	CBS 125550	HM626654	HM626666	–	MW834198	–	HQ897697	HM626642	–
G. cicatricum	CBS 125552	HQ728145	MH875038	–	–	–	HQ728153	HM626644	HQ728171
G. clavata	HMAS 248725 T	KY873307	–	–	–	–	KY873309	–	KY873305
G. hispanica	BRFM 1015 T	JX082350	–	–	–	–	–	–	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
G. montana	BRFM 1441 T	MF611653	–	–	–	–	–	–	–
G. ruscicola	BRFM 2592 T	MZ509541	–	–	–	–	–	–	–
G. sinica	HMA S248726 T	KY873308	–	–	–	–	KY873310	–	KY873306
G. zealandica	CBS 11193	HM626658	–	–	–	–	HM626684	–	HM626626
Luteonectria albida	CBS 102683 = GJS 99-73 = GJS 8522A	MW827615	MH874402	–	MW834200	–	MW834016	MW834283	–
L. albida	NRRL 22152 T = NRRL 13950	–	–	–	JX171492	–	JX171605	–	–
L. nematophila	NRRL 54600	–	–	–	JX171552	–	JX171664	–	–
L. nematophila	**GUCC 190041.1**	**MZ724842**	**OR039396**	**OR043965**	**OR043810**	**OR043767**	**OR043864**	**OR043919**	**OR043712**
L. nematophila	**GUCC 198542.1**	**OR034270**	**OR039397**	**OR043966**	–	**OR043768**	**OR043865**	**OR043920**	**OR043713**
Mariannaea elegans	DAOM 226709	–	HQ843768	–	–	–	HQ897747	–	–
M. samuelsii	CBS 125515T = DAOM 235814	NR_137767	NG_060269	–	–	–	HQ897752	–	–
Nectria cinnabarina	CBS 125165 T	HM484548	HM484562	–	–	–	KM232402	HM484527	KM231074
Neocosmospora acutispora	CBS 145461 T = NRRL 22574 = BBA 62213	LR583700	LR583908	–	MW834210	MW834122	LR583814	LR583593	MW834050
N. addoensis	CBS 146510 T = CPC 37128	MW173042	MW173033	–	MW218098	MW218052	MW446575	MW248741	MW218005
N. addoensis	CBS 146509 = VG279 = CPC 37127	MW173041	MW173032	–	MW218097	MW218051	MW446574	MW248740	MW218004
N. akasia (= *F. akasia*)	CMW 54735 = PPRI 27978 = CBS 146880 T	MN954357	MN954357	–	–	–	MT009931	MT009971	–
N. akasia (= *F. akasia*)	CMW52865	MN954330	MN954330	–	–	–	MT009904	MT009943	–
N. ambrosia	CBS 571.94 T = NRRL 22346 = BBA 65390 = MAFF 246287	EU329669	EU329669	–	MW834211	–	EU329503	FJ240350	–
N. ampla	CBS 202.32 T = BBA 4170	LR583701	LR583909	–	MW834212	MW834123	LR583815	LR583594	MW834051
N. awan	CMW 54719 = PPRI 27973 = CBS 146882 T	MN954345	MN954345	–	–	–	MT009919	MT009959	–
N. bataticola	CBS 144398 T = NRRL 22402 = BBA 64954 = FRC S-0567	AF178408	AF178377	–	MW218100	MW218054	FJ240381	AF178344	MW218007

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. bataticola	CBS 144397 = NRRL 22400 = BBA 64683	AF178407	AF178376	–	MW218099	MW218053	EU329509	AF178343	MW218006
N. bomiensis	HMAS 248885 T	KY829447	–	–	–	–	–	KY829449	–
N. borneensis	CBS 145462 T = NRRL 22579 = BBA 65095 = GJS 85-197	AF178415	AF178384	–	MW834213	MW834124	EU329515	AF178352	MW834052
N. bostrycoides	CBS 144.25 T	LR583704	LR583912	–	MW218101	MW218055	LR583818	LR583597	MW218008
N. bostrycoides	CBS 392.66 = NRRL 25325 = BBA 69595	LR583705	LR583913	–	MW218102	MW218056	LR583819	LR583598	MW218009
N. brevicona	CBS 204.31 T = NRRL 22659 = BBA 2123	LR583707	LR583915	–	MW218103	MW218057	LR583821	LR583600	MW218010
N. brevis (= *F. breve*)	CBS 130326 = NRRL 28009 = CDC B-5543	DQ094351	DQ236393	–	MW834214	MW834125	EF470136	DQ246869	MW834053
N. brevis (= *F. breve*)	CBS 144387 T = MUCL 16108	LR583708	LR583916	–	–	–	LR583822	LR583601	–
N. brevis (= *F. breve*)	CPC 27190	LT746247	LT746247	–	–	–	LT746312	LT746199	–
N. brevis (= *F. breve*)	CPC 27191	LT746248	LT746248	–	–	–	LT746313	LT746200	–
N. brevis (= *F. breve*)	NRRL 32792 = FRC S-1143	DQ094561	DQ236603	–	–	–	EU329621	DQ247101	–
N. caricae	ES216-M T	OK422518	–	–	–	–	OK415859	OK539518	–
N. caricae	ES216-R	OK422519	–	–	–	–	OK415860	OK539519	–
N. catenata	CBS 143229 T = NRRL 54993 = UTHSC 09-1009	KC808256	KC808256	–	MW218105	MW218059	KC808355	KC808214	MW218012
N. catenata	NRRL 54992	KC808255	MG189913	–	–	–	KC808354	KC808213	–
N. citricola	CBS 146513 T = CPC 37131	MW173048	MW173036	–	MW218108	MW218062	MW446581	MW248747	MW218015
N. citricola	CBS 146511 = VG302 =CPC 37129	MW173046	MW173034	–	MW218106	MW218060	MW446579	MW248745	MW218013
N. crassa	CBS 144386 T = MUCL 11420	LR583709	LR583917	–	MW218109	MW218063	LR583823	LR583604	MW218016
N. crassa	NRRL 46703 = FMR 8281	EU329712	EU329712	–	–	–	EU329661	HM347126	–
N. croci	CPC 27186 = CBS 142423 T	LT746264	LT746264	–	–	–	LT746329	LT746216	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. croci	CPC 27187	LT746265	LT746265	–	–	–	LT746330	LT746217	–
N. cryptoseptata	CBS 145463 T = NRRL 22412 = BBA 65024	AF178414	AF178383	–	MW834215	MW834126	EU329510	AF178351	MW834054
N. cucurbitae	CBS 616.66 T = NRRL 22399 = BBA 64411	LR583711	LR583919	–	MW834217	MW834128	LR583825	DQ247592	MW834056
N. cucurbitae	CBS 410.62 = NRRL 22658 = CECT 2864	LR583710	LR583918	–	MW834216	MW834127	LR583824	DQ247640	MW834055
N. cyanescens	CBS 518.82 T	AB190389	LR583920	–	MW218110	MW218064	LR583826	LR583605	MW218017
N. cyanescens	CBS 637.82	LR583712	LR583921	–	MW218111	MW218065	LR583827	LR583606	MW218018
N. diminuta	CBS 144390 T = MUCL 18798	LR583713	LR583922	–	MW834218	MW834129	LR583828	LR583607	MW834057
N. drepaniformis	NRRL 62941 T	KM406633	KM406633	–	KM406640	–	KM406647	KM406626	–
N. duplosperma	NRRL 62583 T= MAFF 247220	KC691581	KC691581	–	KC691611	–	KC691642	KC691553	–
N. duplosperma	NRRL 62585	KC691577	KC691577	–	KC691607	–	KC691638	KC691549	–
N. elegans (= *F. yamamotoi*)	CBS 144396 T = NRRL 22277 = MAFF 238541 = ATCC 42366	AF178401	AF178370	–	MW218113	MW218067	FJ240380	AF178336	MW218020
N. elegans (= *F. yamamotoi*)	CBS 144395 = NRRL 22163 = MAFF 238540 = ATCC 18690	AF178394	AF178363	–	MW218112	MW218066	EU329496	AF178328	MW218019
N. epipeda	CBS 146523 T = CPC 38310	MW827624	MW827665	–	MW834219	MW834130	MW834022	MW834285	MW834058
N. epipeda	CBS 146524 = CPC 38311	MW827625	MW827666	–	MW834220	MW834131	MW834023	MW834286	MW834059
N. euwallaceae	CBS 135854 T = NRRL 54722	JQ038014	JQ038014	–	JQ038021	–	JQ038028	JQ038007	–
N. euwallaceae	NRRL 62626	KC691560	KC691560	–	–	–	KU171702	KC691532	–
N. falciformis	CBS 475.67 T = IMI 268681	MG189935	MG189915	–	MW218114	MW218068	LT960558	LT906669	MW218021
N. falciformis	CBS 121450	JX435211	JX435211	–	MW218115	MW218069	JX435261	JX435161	MW218022
N. falciformis	**GUCC 190025.1**	**MZ724848**	**OR039398**	**OR043967**	**OR043811**	**OR043769**	**OR043866**	**OR043921**	**OR043714**
N. falciformis (= *F. paranaense*)	CML 1830 T	–	–	–	–	–	KF680011	KF597797	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. falciformis (= *F. paranaense*)	CML1988	–	–	–	–	–	KF680013	KF597819	–
N. ferruginea	CBS 109028 T = NRRL 32437	DQ094446	DQ236488	–	MW834221	MW834132	EU329581	DQ246979	MW834060
N. ferruginea	CPC 28194	LT746276	LT746276	–	MW834222	MW834133	LT746341	LR583602	MW834061
N. floridana	NRRL 62628 T = MAFF 246849	KC691563	KC691563	–	KC691593	–	KC691624	KC691535	–
N. gamsii (= *F. waltergamsii*)	CBS 143207 T = NRRL 32323 = UTHSC 99-205	DQ094420	DQ236462	–	MW834223	MW834134	EU329622	DQ247103	MW834062
N. gamsii (= *F. waltergamsii*)	CBS 143211 = NRRL 32794 = FRC S-1152	DQ094563	DQ236605	–	MW834224	MW834135	EU329576	DQ246951	MW834063
N. gamtoosensis	CBS 146502 T = VG16 = CPC 37120	MW173063	MW173038	–	MW218116	MW218070	MW446611	MW248762	MW218023
***N. gannanensis* comb. nov.**	**NJFU-JX12 T**	**LC702041**	**LC702041**	–	**LC701945**	–	**LC701981**	**LC701609**	–
***N. gannanensis* comb. nov.**	**NJFU-JX13**	**LC702042**	**LC702042**	–	**LC701946**	–	**LC701982**	**LC701610**	–
***N. gannanensis* comb. nov.**	**NJFU-JX14**	**LC702043**	**LC702043**	–	**LC701947**	–	**LC701983**	**LC701611**	–
***N. gannanensis* comb. nov.**	**NJFU-JX15**	**LC702044**	**LC702044**	–	**LC701948**	–	**LC701984**	**LC701612**	–
***N. gannanensis* comb. nov.**	**NJFU-JX16**	**LC702045**	**LC702045**	–	**LC701949**	–	**LC701985**	**LC701613**	–
N. geoasparagicola	CBS 148937 T	ON763207	–	–	ON759290	–	ON759301	ON745622	–
N. geoasparagicola	CPC 40628	ON763212	–	–	ON759295	–	ON759306	ON745627	–
N. haematococca	CBS 119600 T = FRC S-1832	KM231797	KM231664	–	–	MW834136	LT960561	DQ247510	MW834064
N. hengyangensis	HMAS 254518 T	KY829446	–	–	–	–	–	KY829448	–
N. hypothenemi	CBS 145464T = NRRL 52782 = ARSEF 5878	LR583715	LR583923	–	MW218117	–	JF741176	JF740850	MW218024
N. hypothenemi	CBS 145466 = NRRL 52783 = ARSEF 5879	MW827626	MW827667	–	MW218118	MW218071	MW834024	MW834287	MW218025
N. illudens	CBS 147303 = NRRL 22090 = BBA 67606 = GJS 82-98	AF178393	AF178362	–	JX171488	MW834137	JX171601	AF178326	MW834065

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. ipomoeae	CBS 353.87 = NRRL 22657	LR583717	LR583925	–	MW218119	MW218072	LR583831	DQ247639	MW218026
N. ipomoeae	CBS 833.97	LR583719	LR583927	–	MW218120	MW218073	LR583833	LR583611	MW218027
N. ipomoeae	**GUCC 198175.1**	**OR034271**	–	–	**OR043812**	**OR043770**	**OR043867**	**OR043922**	**OR043715**
N. keleraja	CBS 125720 T = FRC S-1837 = GJS 02-114	LR583720	LR583928	–	MW834225	MW834138	LR583834	LR583612	MW834066
N. keleraja	CBS 125722 = FRC S-1836	JF433039	JF433039	–	MW834226	MW834139	LR583835	DQ247515	MW834067
N. keratoplastica	CBS 490.63 T= NRRL 22661	LR583721	LR583929	–	MW218121	MW218074	LT960562	LT906670	MW218028
N. keratoplastica	CBS 144389 = MUCL 18301	LR583722	LR583930	–	MW218122	MW218075	LR583836	LR583613	MW218029
N. keratoplastica (= *F. sedimenticola*)	CGMCC 3.19499 T = LC12845	MK207059	–	–	–	–	MK190729	MK190727	–
N. kuroshio	CBS 142642 T	LR583723	LR583931	–	MW834227	MW834140	LR583837	KX262216	MW834068
N. kuroshio	NRRL 62945	KM406636	KM406636	–	–	–	KM406649	KM406629	–
N. kuroshio	NRRL 62946	KM406637	KM406637	–	–	–	KM406650	KM406630	–
N. kurunegalensis	CBS 119599 T = GJS 02-94	JF433036	JF433036	–	MW834228	MW834141	LR583838	DQ247511	MW834069
N. lerouxii	CBS 146514 T = CPC 37132	MW173069	MW173039	–	MW218123	MW218076	MW446617	MW248768	MW218030
N. lichenicola	CBS 623.92 T	LR583730	LR583938	–	–	MW834143	LR583845	LR583620	MW834071
N. lichenicola	CBS 509.63 = MUCL 8050 = IMUR 410	LR583728	LR583936	–	MW834229	MW834142	LR583843	LR583618	MW834070
N. lichenicola	**GUCC 190172.1**	**MZ724847**	**OR039399**	**OR043968**	**OR043813**	**OR043771**	**OR043868**	–	**OR043716**
N. liriodendri	CBS 117481 T = NRRL 22389 = BBA 67587 = GJS 91-148	AF178404	AF178373	–	MW218124	MW218077	EU329506	AF178340	MW218031
N. lithocarpi	CGMCC 3.20827 = LC1113 T	MW016711	–	MW534051	MW024739	–	MW474697	MW620172	–
***N. liupanshuiensis* sp. nov.**	**GUCC 190115.1**	**MZ724849**	**OR039400**	**OR043969**	**OR043814**	**OR043772**	**OR043869**	**OR043923**	**OR043717**
***N. liupanshuiensis* sp. nov.**	**GUCC 190201.1 = CGMCC3.25481 T**	**MZ724850**	**OR039401**	**OR043970**	**OR043815**	**OR043773**	–	**OR043924**	**OR043718**

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. longissima (= *F. ngaiotongaense*)	CBS 126407 T = GJS 85-72	LR583731	LR583939	–	MW834230	MW834144	LR583846	LR583621	MW834072
N. macrospora	CBS 142424 T = CPC 28191	LT746266	LT746281	–	MW218125	MW218078	LT746331	LT746218	MW218032
N. macrospora	CPC 28193	LT746268	LT746283	–	MW218126	MW218079	LT746333	LT746220	MW218033
N. magnoliae	MFLUCC 17-2615 T	MT215508	MT215557	–	–	–	MT212200	MT212207	–
N. mahasenii	CBS 119594 T	JF433045	JF433045	–	MW834231	MW834145	LT960563	DQ247513	MW834073
N. martii	CBS 115659 T = FRC S-0679 = MRC 2198	JX435206	JX435206	–	MW834232	MW834146	JX435256	JX435156	MW834074
N. mekan	CMW 54714 = PPRI 27971 = CBS 146885 T	MN954342	MN954342	–	–	–	MT009916	MT009964	–
N. mekan	CBS 146886	MN954335	MN954335	–	–	–	MT009909	MT009962	–
N. merkxiana	CBS 146525 T	MW827627	MW827668	–	MW834233	MW834147	MW834025	MW834288	MW834075
N. merkxiana	CBS 146526	MW827628	MW827669	–	MW834234	MW834148	MW834026	MW834289	MW834076
N. metavorans	CBS 135789 T	LR583738	LR583946	–	MW218127	MW218080	LR583849	LR583627	MW218034
N. metavorans	CBS 143219 = NRRL 46708 = FMR 8634	LR583744	LR583948	–	MW218128	MW218081	LR583851	LR583629	MW218035
N. mor	CBS 145467 T = NRRL 22230 = MAFF 238539	DQ094305	DQ236347	–	MW834235	MW834149	EU329499	AF178358	MW834077
N. mor	CBS 145468 = NRRL 22157 = MAFF 238538	DQ094306	DQ236348	–	MW834236	MW834150	EU329493	AF178359	MW834078
N. neerlandica	CBS 232.34 T	MW827629	MW827670	–	MW834237	MW834151	MW847903	MW847906	MW834079
N. nelsonii	CBS 309.75 T	MW827630	MW827671	–	MW834238	MW834152	MW847904	MW847907	MW834080
N. nirenbergiana	CBS 145469 T = NRRL 22387 = BBA 65023 = GJS 87-127	AF178403	AF178372	–	–	MW834153	EU329505	AF178339	MW834081
N. noneumartii	CBS 115658 T = FRC S-0661	LR583745	LR583949	–	MW218129	MW218082	MW446618	LR583630	MW218036
N. obliquiseptata	MAFF 246845 T = NRRL 62611	KC691576	KC691576	–	KC691606	–	KC691637	KC691548	–
N. oblonga	CBS 130325 T = NRRL 28008 = CDC B-4701	LR583746	LR583950	–	MW834239	MW834154	LR583853	LR583631	MW834082
N. oligoseptata	CBS 143241 T = NRRL 62579 = FRCS-2581 = MAFF 246283	KC691566	KC691566	–	KC691596	MW834155	LR583854	KC691538	MW834083

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. oligoseptata	NRRL 62578 = FRC S-2576	KC691565	KC691565	–	–	–	KC691626	KC691537	–
N. pallidimors	KUMCC20-0007 T	MT031915	MT032140	–	–	–	–	MT024983	–
N. pallidimors	KUMCC 20-0012	MT031916	MT032141	–	–	–	–	MT024984	–
N. papillata	NRRL 62943 T= KOD 796 = MAFF 247228	KM406635	KM406635	–	KM406642	–	KM406648	KM406628	–
N. papillata	NRRL 62944	KM406634	KM406634	–	KM406641	–	KM406648	KM406627	–
N. paraeumartii	CBS 487.76 T = NRRL 13997 = BBA 62215	LR583747	LR583951	–	MW834240	MW834156	LR583855	DQ247549	MW834084
N. parceramosa	CBS 115695 T	JX435199	JX435199	–	–	MW218083	JX435249	JX435149	MW218037
N. parceramosa	NRRL 31158	DQ094389	DQ236431	–	–	–	EU329559	DQ246916	–
***N. passiflorae* comb. nov.**	**IBFS07**	**FJ200220**	–	–	–	–	–	**JX524768**	–
***N. passiflorae* comb. nov.**	**IBFS09**	**FJ200222**	–	–	–	–	–	**FX524770**	–
***N. passiflorae* comb. nov.**	**IBFS08**	**FJ200221**	–	–	–	–	–	**FX524769**	–
***N. passiflorae* comb. nov.**	**IBFS12**	**FJ200224**	–	–	–	–	–	**FX524772**	–
N. perseae	CBS 144142 T = CPC 26829	LT991940	LT991947	–	MW218130	MW218084	LT991909	LT991902	MW218038
N. perseae	CBS 144143 = CPC 26830	LT991941	LT991948	–	–	–	LT991910	LT991903	–
N. perseae	CBS 144144 = CPC 26831	LT991942	LT991949	–	–	–	LT991911	LT991904	–
N. petroliphila	CBS 203.32 = NRRL 13952	DQ094320	DQ236362	–	MW218131	MW218085	LR583857	DQ246835	MW218039
N. petroliphila	CBS 224.34 = NRRL 28579	DQ094383	DQ236425	–	MW218132	MW218086	LR583858	DQ246910	MW218040
N. phaseoli	CBS 265.50	LR583750	LR583954	–	–	MW834157	KJ511278	FJ919464	MW834085
N. phaseoli (= *F. azukiicola*)	NRRL 54364 T= MAFF 242371= F. Tanaka 97UA3	–	–	–	KJ511276	–	KJ511287	JQ670137	–
N. phaseoli (= *F. crassistipitatum*)	NRRL 36877 T	–	FJ240376	–	–	–	FJ240405	FJ240351	–

Supplementary Table 1 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. phaseoli (= *F. cuneirostrum*)	NRRL 31157 T = MAFF 239038 = FRC S-1551 = Michigan State Univ. FS12	AY320196	–	–	KJ511271	–	KJ511282	–	–
N. phaseoli (= *N. tucumaniae*)	NRRL 31096 T = MAFF 238418 = MJ-172	EF408523	–	EF408453	–	EF408383	–	EF408418	–
N. piperis	CBS 145470T = NRRL 22570 = GJS 89-14 = CML 1888	AF178422	AF178391	–	MW834241	MW834158	EU329513	AF178360	MW834086
N. pisi	**GUCC 190098.1**	**MZ724843**	**OR039402**	**OR043971**	–	**OR043774**	**OR043870**	**OR043925**	**OR043719**
N. pisi	**GUCC 190177.1**	**MZ724844**	**OR039403**	**OR043972**	**OR043816**	**OR043775**	**OR043871**	**OR043926**	**OR043720**
N. pisi	**GUCC 191172.1**	**MZ724845**	**OR039404**	**OR043973**	–	**OR043776**	**OR043872**	**OR043927**	**OR043721**
N. pisi (= *F. vanettenii*)	CBS 123669 T = NRRL 45880 = ATCC MYA-4622	LR583753	LR583957	–	MW834242	MW834159	LR583862	LR583636	MW834087
N. pisi (= *F. vanettenii*)	CBS 142372	LR583755	LR583959	–	MW834243	MW834160	LR583864	KY556454	MW834088
N. plagianthi	NRRL 22632 = GJS 83-146	AF178417	AF178386	–	JX171501	–	JX171614	AF178354	–
***N. populicola* comb. nov.**	**NJFU-JS02 T**	**LC702061**	**LC702061**	–	**LC701929**	–	**LC701965**	**LC701601**	–
***N. populicola* comb. nov.**	**NJFU-JS03**	**LC702062**	**LC702062**	–	**LC701930**	–	**LC701966**	**LC701602**	–
***N. populicola* comb. nov.**	**NJFU-JS04**	**LC702063**	**LC702063**	–	**LC701931**	–	**LC701967**	**LC701603**	–
***N. populicola* comb. nov.**	**NJFU-JS05**	**LC702064**	**LC702064**	–	**LC701932**	–	**LC701968**	**LC701604**	–
***N. populicola* comb. nov.**	**NJFU-JS13**	**LC702065**	**LC702065**	–	**LC701933**	–	**LC701969**	**LC701605**	–
N. protoensiformis	CBS 145471 T = NRRL 22178 = GJS 90-168	AF178399	AF178368	–	MW834244	MW834161	EU329498	AF178334	MW834089
N. pseudensiformis	FRCS-1834 = CBS 125729 T	JF433037	JF433037	–	–	–	–	DQ247512	–
N. pseudopisi	CBS 266.50	MW827631	MW827672	–	MW834246	MW834163	MW834027	MW834290	MW834091
N. pseudoradicicola	CBS 145472 T = NRRL 25137 = ARSEF 2313	JF740899	JF740899	–	MW218133	MW218087	JF741084	JF740757	MW218041
N. pseudoradicicola	NRRL 25138 = ARSEF 2314	JF740900	JF740900	–	–	–	JF741085	JF740758	–
N. pseudotonkinensis	CBS 143038 T	LR583758	LR583962	–	–	–	LR583867	LR583640	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. quercicola	CBS 141.90 T = NRRL 22652	LR583760	LR583964	–	MW834247	MW834164	LR583869	DQ247634	MW834092
N. rectiphora	CBS 125727 T = GJS 02-89 = FRC S-1831	JF433034	JF433034	–	MW834249	MW834166	LR583871	DQ247509	MW834094
N. rectiphora	CBS 125726 = FRC S-1842	JF433043	JF433043	–	MW834248	MW834165	MW834028	JF433026	MW834093
N. regularis	CBS 230.34 T	LR583763	LR583967	–	–	MW834168	MW834029	LR583643	MW834096
N. regularis	CBS 190.35	LR583762	LR583966	–	MW834250	MW834167	LR583872	LR583642	MW834095
N. rekana	CMW 52862 T	MN249094	—	–	–	–	MN249137	MN249151	–
N. rhizophorae	MFLUCC 17-2461 T	MN047109	MN017872	–	–	–	–	–	–
N. riograndensis	UFMG CMF12570 T	KT186366	KX534001	–	–	–	KX534003	KX534002	–
N. robusta (= *F. venezuelense*)	CBS 145473 T = NRRL 22395 = BBA 65682	AF178405	LR583968	–	MW834251	MW834169	EU329507	AF178341	–
N. brevis (*F. rosicola*)	YJ1 T	MW724816	—	–	–	–	MW795356	MW795357	–
N. brevis (*F. rosicola*)	YJ2	MW724818	—	–	–	–	MW795358	MW795359	–
N. brevis (*F. rosicola*)	YJ3	MW724817	—	–	–	–	MW795360	MW795361	–
N. brevis (*F. rosicola*)	YJ4	MW724819	—	–	–	–	MW795362	MW795363	–
N. samuelsii	CBS 114067 T = GJS 89-70	LR583764	LR583969	–	MW834252	MW834170	LR583874	LR583644	MW834097
N. silvicola	CBS 123846 T = GJS 04-147	LR583766	LR583971	–	MW834254	MW834172	LR583876	LR583646	MW834099
N. silvicola	CBS 119601 = GJS 98-135	LR583765	LR583970	–	MW834253	MW834171	LR583875	LR583645	MW834098
N. solani	CBS 140079 T = NRRL 66304 = GJS 09-1466 = FRC S-2364	KT313633	KT313633	–	MW218134	MW218088	KT313623	KT313611	MW218042
N. solani	NRRL 43474	EF453097	EF453097	–	–	–	EF469984	EF452945	–
N. solani	NRRL 46598	GU170648	GU170648	–	–	–	GU170593	GU170628	–
N. solani	**GUCC 190159.1**	**MZ724846**	**OR039405**	**OR043974**	**OR043817**	**OR043777**	**OR043873**	**OR043928**	**OR043722**
N. solani	**GUCC 198534.1**	**OR034272**	–	–	**OR043818**	**OR043778**	**OR043874**	**OR043929**	**OR043723**
N. spathulata	CBS 145474 T = NRRL 28541 = UTHSC 98-1305	EU329674	EU329674	–	MW218137	MW218091	EU329542	DQ246882	MW218045
N. stercicola	CBS 142481 T = DSM 106211	LR583779	LR583984	–	MW834255	MW834173	LR583887	LR583658	MW834100

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***tub2***	***rpb1***	***CaM***	***rpb2***	***tef1***	***acl1***
N. stercicola (= *F. witzenhausenense*)	CBS 142480 T= DSM 106212	MG250477	–	–	–	–	KY556553	KY556525	–
N. stercicola (= *F. witzenhausenense*)	KU90.15	–	–	–	–	–	MG237866	MG237868	–
N. stercicola (= *F. xiangyunense*)	DBN11-1 T	MH780923	–	–	MH999281	–	–	MH992629	–
N. suttoniana	CBS 143214 T = NRRL 32858	DQ094617	DQ236659	–	MW218138	MW218092	EU329630	DQ247163	MW218046
N. suttoniana	CBS 143224 = NRRL 54972	MG189940	MG189925	–	MW218139	MW218093	KC808336	KC808197	MW218047
N. tenuicristata	IMI 277708 T= NHL 2911	LR583782	LR583986	–	–	–	–	–	–
N. tonkinensis	CBS 115.40 T = NRRL 53586 = IMI 113868	MG189941	MG189926	–	MW218140	MW218094	LT960564	LT906672	MW218048
N. tonkinensis	CBS 118931	LR583784	LR583989	–	MW218141	MW218095	LR583891	LR583662	MW218049
N. tuaranensis	NRRL 22231 T = ATCC 16563 = MAFF 246842	KC691570	KC691570	–	KC691600	–	KC691631	KC691542	–
***N. tumidisperma* comb. nov.**	**NJFU-JX26 T**	**LC702053**	**LC702053**	–	**LC701957**	–	**LC701993**	**LC701621**	–
***N. tumidisperma* comb. nov.**	**NJFU-JX27**	**LC702054**	**LC702054**	–	**LC701958**	–	**LC701994**	**LC701622**	–
***N. tumidisperma* comb. nov.**	**NJFU-JX28**	**LC702055**	**LC702055**	–	**LC701959**	–	**LC701995**	**LC701623**	–
***N. tumidisperma* comb. nov.**	**NJFU-JX25**	**LC702052**	**LC702052**	–	**LC701956**	–	**LC701992**	**LC701620**	–
N. variasi (= *F. variasi*)	CMW 53734 = PPRI 27958 = CBS 146888 T	MN954356	MN954356	–	–	–	MT009913	MT009953	–
N. variasi (= *F. variasi*)	CMW53735	MN954340	MN954340	–	–	–	MT009914	MT009968	–
N. vasinfecta	CBS 325.54 = ATCC 16238 = IFO 7591 = IMI 251386 = NRRL 22436	AF178412	AF178381	–	JX171497	–	JX171610	AF178348	–
N. vasinfecta (= *F. neocosmosporiellum*)	CBS 446.93 = IMI 316967 = NHL 2919	LR583791	LR583996	–	MW834257	MW834175	LR583898	LR583670	MW834102
N. virguliformis	NRRL 31041 T = MAFF 238553	AY220239	AY220169	–	–	–	–	AY220193	–

Supplementary Table 1 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*tub2*	*rpb1*	*CaM*	*rpb2*	*tef1*	*acl1*
N. virguliformis	NRRL31040	AY220238	AY220168	–	–	–	–	AY220192	–
N. virguliformis	NRRL31039	AY220237	AY220167	–	–	–	–	AY220191	–
N. warna (= *F. warna*)	CMW 54720 = PPRI 27974 = CBS 146891 T	MN954346	MN954346	–	–	–	MT009920	MT009960	–
N. warna (= *F. warna*)	CMW54721	MN954347	MN954347	–	–	–	MT009921	MT009956	–
N. warna (= *F. warna*)	CMW54724	MN954350	MN954350	–	–	–	MT009924	MT009957	–
Nothofusarium devonianum	CBS 147304 T = NRRL 22134	MW827632	MW827673	–	JX171490	–	JX171603	MW834291	–
Rectifusarium robinianum	CBS 430.91 T = NRRL 25729	KM231794	NG_058096	–	JX171520	–	JX171633	KM231923	–
R. ventricosum	CBS 748.79 T = BBA 62452 = NRRL 20846 = NRRL 22113	HQ897816	KM231658	–	JX171484	–	JX171597	KM231924	–
Setofusarium setosum	CBS 574.94 = BBA 65063	MW827633	MW827674	–	MW834262	–	MW834033	MW834293	–
Se. setosum	CBS 635.92 T = GJS 88-12 = NRRL 36526	MW827634	MW827675	–	JX171539	–	JX171651	MW834294	–
Stylonectria applanata	CBS 125489	HQ897805	KM231689	–	–	–	HQ897739	KM231944	HQ897875
St. corniculata	CBS 125491 T	HQ897829	KM231691	–	–	–	HQ897779	KM231946	HQ897915
St. hetmanica	CBS 147305 T = CPC 38725	MW827637	–	–	–	–	MW834036	–	MW834104

Supplementary Table 2 Strains used for phylogenetic analysis of *Thelonectria* in this study and their GenBank accession numbers.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*rpb1*	*rpb2*	SSU	*tef1*	*tub2*	ACT
Cinnamomeonectria cinnamomea	G.J.S 86–117 = IMI 325248 T	KJ022010	KJ022072	KJ022451	KJ022584	KJ022206	KJ022393	KJ022341	KJ022286
Thelonectria acrotyla	IMI 345086	KJ021971	KJ022026	KJ022407	KJ022590	KJ022211	KJ022347	KJ022293	KJ022238
T. amamiensis	MAFF 239820	JQ403338	JQ403376	JQ403413	KJ022595	KJ022216	KJ022349	JQ394728	JQ365055
T. amamiensis	MAFF 239819	JQ403337	JQ403375	KJ022408	KJ022594	KJ022215	KJ022348	JQ394727	JQ365054
T. amamiensis	TFM FPH-6571 T	–	–	–	–	–	–	AB237472	–
T. amamiensis	TFM FPH-6648	–	–	–	–	–	–	AB237473	–

Supplementary Table 2 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*rpb1*	*rpb2*	SSU	*tef1*	*tub2*	ACT
T. amamiensis	TUA TPP-h106	–	–	–	–	–	–	AB237470	–
T. amamiensis	TUA TPP-h109	–	–	–	–	–	–	AB237469	–
T. asiatica	G.J.S. 88-84 = IMI 348190	KC153741	KC121467	KC153934	KJ022549	KJ022171	KC153870	KC153806	KC121403
T. asiatica	MAFF 241576 T	KC153774	KC121500	KC153967	KJ022613	KJ022234	KC153903	KC153839	KC121436
T. aurea	KARE1830 = CBS 145584 T	MK400285	–	–	–	–	MK409929	MK409852	–
T. aurea	KARE1923	MK400297	–	–	–	–	MK409941	MK409864	–
T. aurea	KARE98	MK400286	–	–	–	–	MK409930	MK409853	–
T. aurea	KARE1831	MK400287	–	–	–	–	MK409931	MK409854	–
T. aurea	KARE1832	MK400288	–	–	–	–	MK409932	MK409855	–
T. beijingensis	HMAS 188566 T	JQ836656	MF669054	–	–	–	–	JQ836658	MF669047
T. blackeriella	BF142 = CBS142200 T	KX778711	KX778690	KX778693	–	–	–	KX778702	KX778687
T. blackeriella	BF133 = CBS142201	KX778712	KX778691	KX778694	–	–	–	KX778703	KX778688
T. blackeriella	**GUCC 190037.1**	**MZ724813**	**MZ724956**	**OR043819**	**OR043875**	**OR029400**	–	**OR043975**	**OR043724**
T. blackeriella	**GUCC 190037.2**	**OR034273**	**OR039406**	**OR043820**	**OR043876**	**OR029401**	–	**OR043976**	**OR043725**
T. blattea	CBS 14277	KC153720	KC121446	KC153913	KJ022489	KJ022110	KC153849	KC153785	KC121382
T. blattea	CBS 95268 T	KC153725	KC121451	KC153918	KJ022501	KJ022123	KC153854	KC153790	KC121387
T. brayfordii	CBS 118612 T	KC153719	KC121445	KC153912	KJ022483	KJ022104	KC153848	KC153784	KC121381
T. brayfordii	IMI 384045	KC153762	KC121488	KC153955	KJ022592	KJ022213	KC153891	KC153827	KC121424
T. chlamydospora	NIBRFGC00050 0679 T	LC509450	LC509452	–	–	–	LC519559	–	LC519560
T. cidaria	G.J.S. 10–135 = CBS 132323 T	JQ403316	JQ403356	JQ403393	KJ022530	KJ022152	KJ022350	JQ394714	JQ365036
T. cidaria	CTR71-79 = IMI 325844	JQ403315	JQ403355	JQ403392	KJ022508	KJ022130	JQ394741	JQ394707	JQ365035
T. conchyliata	CBS 26636	KC153723	KC121449	KC153916	KJ022496	KJ022118	KC153852	KC153788	KC121385
T. conchyliata	G.J.S. 87–45 = IMI325855 T	KC153739	KC121465	KC153932	KJ022547	KJ022169	KC153868	KC153804	KC121401
T. conchyliata	G.J.S.87–49 = CBS 112461	KC153740	KC121466	KC153933	KJ022548	KJ022170	KC153869	KC153805	KC121402
T. conchyliata	G.J.S. 89–57 = CBS 112459	KC153742	KC121468	KC153935	KJ022551	KJ022173	KC153871	KC153807	KC121404
T. conchyliata	G.J.S.89–65 = CBS 123970	KC153744	KC121470	KC153937	KJ022553	KJ022175	KC153873	KC153809	KC121406

Supplementary Table 2 Continued.

Genus and species	Strain no.	GenBank accession no.							
		ITS	LSU	*rpb1*	*rpb2*	SSU	*tef1*	*tub2*	ACT
T. conchyliata	G.J.S. 96–22 = IMI 370946	KC153755	KC121481	KC153948	KJ022573	KJ022195	KC153884	KC153820	KC121417
T. conchyliata	G.J.S.90–212 = CBS 134028	KC153750	KC121476	KC153943	KJ022561	KJ022183	KC153879	KC153815	KC121412
T. coronalis	J.-R. Guu 93082102 = CBS 132337 T	JQ403343	JQ403380	JQ403418	KJ022459	KJ022080	JQ394761	JQ394732	KJ022240
T. coronalis	J.-R Guu 94043006 = CBS 132338	JQ403344	JQ403381	JQ403419	KJ022462	KJ022083	KJ022352	JQ394733	KJ022241
T. coronata	G.J.S. 85-207 = IMI325241 T	JQ403326	JQ403365	JQ403404	KJ022542	KJ022164	JQ394749	JQ394717	JQ365044
T. coronata	Guu 92100902 = CBS 132334	JQ403342	–	JQ403417	KJ022456	KJ022077	JQ394760	JQ394731	JQ365059
T. coronata	G.J.S.10–108 = CBS 132322	JQ403320	JQ403360	JQ403397	KJ022521	KJ022143	JQ394746	JQ394711	JQ365040
T. diademata	A.R. 4765 = CBS 132331 T	JQ403308	JQ403348	JQ403384	KJ022474	KJ022095	JQ394736	JQ394700	JQ365029
T. diademata	A.R. 4787 = CBS 132332	JQ403311	JQ403351	JQ403387	KJ022478	KJ022099	JQ394738	JQ394703	JQ365032
T. diademata	G.J.S. 10–137 = CBS 132321	JQ403325	JQ403364	JQ403403	KJ022532	KJ022154	JQ394748	JQ394716	KJ022243
T. diademata	C.T.R. 71–52 = CBS 132333	JQ403314	JQ403354	JQ403391	KJ022507	KJ022129	JQ394740	JQ394706	KJ022242
T. elata	C.T.R. 71–241 = CBS 112454 T	KJ021999	KJ022051	KJ022431	KJ022504	KJ022126	KJ022377	KJ022315	KJ022265
T. elata	G.J.S. 10–122 = CBS 136784	KJ022003	KJ022054	KJ022434	KJ022524	KJ022146	KJ022380	KJ022318	KJ022268
T. fusongensis	CGMCC 3.20153 T =R1-8	MT742972	MT742982	MT792240	MT792248	MT742998	MT792272	MT792256	MT792264
T. fusongensis	P4	MT742973	MT742983	MT792241	MT792249	MT742999	MT792273	MT792257	MT792265
T. gibba	G.J.S. 96–10 = IMI 370944 = CBS 112469 T	KC153754	KC121480	KC153947	KJ022572	KJ022194	KC153883	KC153819	KC121416
T. gibba	G.J.S. 96–35 = CBS 112456	KC153757	KC121483	KC153950	KJ022575	KJ022197	KC153886	KC153822	KC121419

Supplementary Table 2 Continued.

Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***rpb1***	***rpb2***	**SSU**	***tef1***	***tub2***	**ACT**
T. ginsengcola	CGMCC 3.20154 T = R9	MT742968	MT742978	MT792236	MT792244	MT742994	MT792268	MT792252	MT792260
T. ginsengcola	R4	MT742969	MT742979	MT792237	MT792245	MT742995	MT792269	MT792253	MT792261
T. gongylodes	CBS 124611	JQ403318	JQ403358	JQ403395	KJ022514	KJ022136	JQ394744	JQ394710	JQ365038
T. gongylodes	IMI 343571 = G.J.S.90-50	JQ403331	JQ403370	JQ403408	KJ022564	KJ022186	JQ394752	JQ394721	JQ365048
T. gongylodes	G.J.S. 89–131 = IMI 336160	JQ403336	JQ403374	JQ403412	KJ022550	KJ022172	JQ394756	JQ394726	JQ365053
T. gongylodes	G.J.S. 90–48 = CBS 125118	JQ403330	JQ403369	HM364338	KJ022563	KJ022185	HM364357	HM352870	HM352888
T. guangdongensis	HMAS 247233 T	MF669051	MF669053	MF669057	–	–	–	–	MF669045
T. ianthina	G.J.S. 10–118 = CBS 134023 T	KC153731	KC121457	KC153924	KJ022523	KJ022145	KC153860	KC153796	KC121393
T. ianthina	Guu 92122107 = CBS 134038	KC153711	KC121437	KC153904	KJ022458	KJ022079	KC153840	KC153775	KC121373
T. japonica	MAFF 241524 T	KC153766	KC121492	KC153959	KJ022602	KJ022223	KC153895	KC153831	KC121428
T. japonica	MAFF 241543	KC153769	KC121495	KC153962	KJ022606	KJ022227	KC153898	KC153834	KC121431
T. japonica	MAFF 241554	KC153770	KC121496	KC153963	KJ022609	KJ022230	KC153899	KC153835	KC121432
T. japonica	MAFF 241563	KC153771	KC121497	KC153964	KJ022610	KJ022231	KC153900	KC153836	KC121433
T. jixiensis	CGMCC 3.20156 T = Q21-5	MT742974	MT742984	MT792242	MT792250	MT743000	MT792274	MT792258	MT792266
T. jixiensis	Q21-1	MT742975	MT742985	MT792243	MT792251	MT743001	MT792275	MT792259	MT792267
T. lucida	GJS 9613A = G.J.S. 08–232	KJ022002	KJ022053	KJ022433	KJ022516	KJ022138	KJ022379	KJ022317	KJ022267
T. lucida	G.J.S. 10–146 = CBS 136788	KJ021989	KJ022055	KJ022435	KJ022534	KJ022156	KJ022381	KJ022319	KJ022269
T. mamma	Guu 94043002 = CBS 136787 T	KF569839	KF569848	KF569876	KJ022461	KJ022082	KF569857	KF569866	KF569829
T. mamma	Guu 92112704	KF569838	KF569847	KF569875	KJ022457	KJ022078	KF569856	KF569865	KF569828
T. mamma	G.J.S. 86–249 = IMI 325261	KF569840	KF569849	KF569877	KJ022546	KJ022168	KF569858	KF569867	KF569830
T. mammoidea	CBS 328.81	KF569836	KF569845	KF569873	KJ022499	KJ022121	KF569854	KF569863	KF569826
T. mammoidea	IMI 69361 T	KC153763	KC121489	KC153956	KJ022593	KJ022214	KC153892	KC153828	KC121425
T. mammoidea	G.J.S. 85–27 = CBS 112457	KC153738	KC121464	KC153931	KJ022543	KJ022165	KC153867	KC153803	KC121400

Supplementary Table 2 Continued.

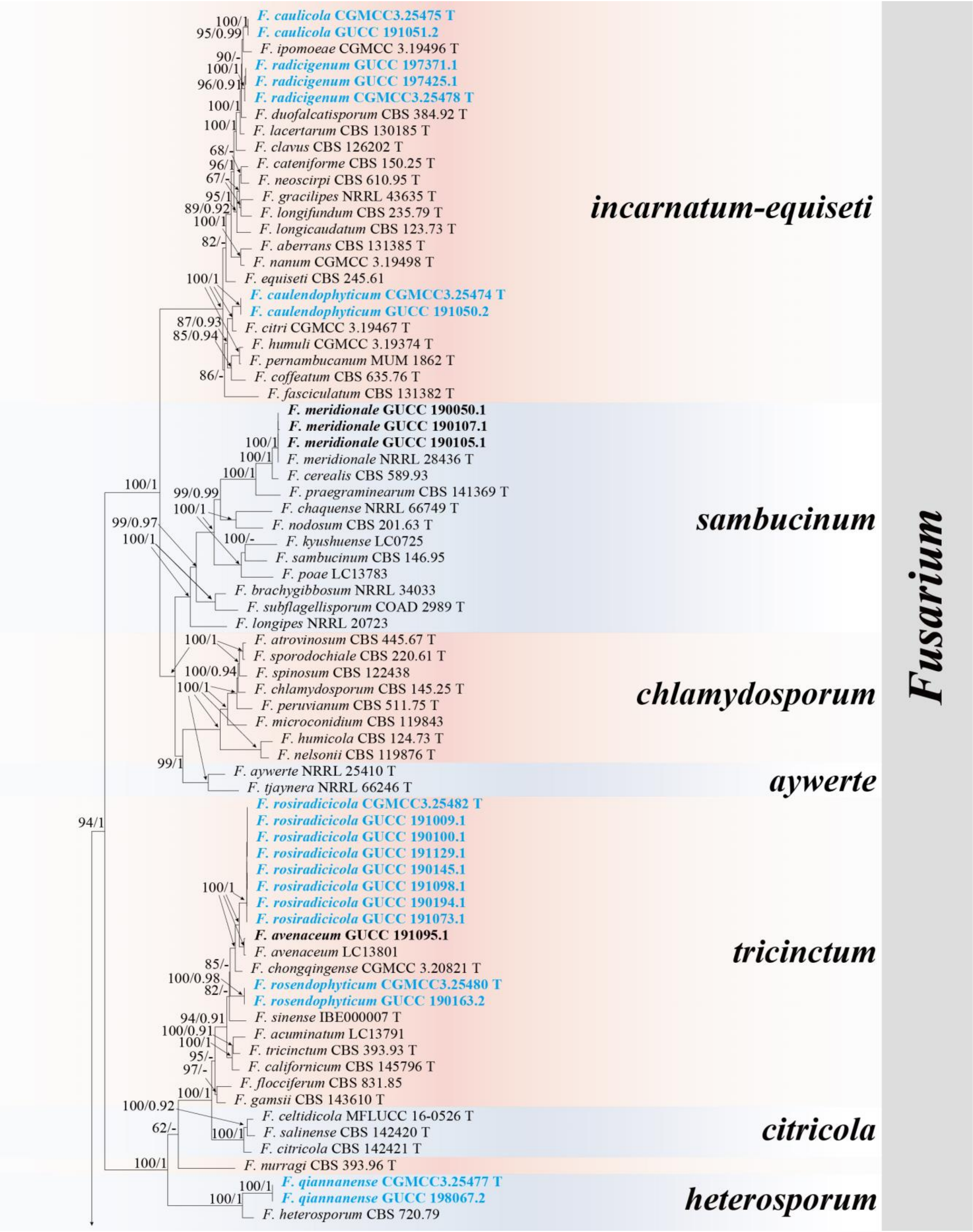
Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***rpb1***	***rpb2***	**SSU**	***tef1***	***tub2***	**ACT**
T. mammoidea	G.J.S. 83–188 = IMI 326256	KC153734	KC121460	KC153927	KJ022538	KJ022160	KC153863	KC153799	KC121396
T. mammoidea	G.J.S.83–206 = IMI 326258	KC153735	KC121461	KC153928	KJ022539	KJ022161	KC153864	KC153800	KC121397
T. mammoidea	G.J.S. 92–34 = CBS 134030	KC153752	KC121478	KC153945	KJ022569	KJ022191	KC153881	KC153817	KC121414
T. mulanensis	CGMCC 3.20155 T = Q20-8	MT742970	MT742980	MT792238	MT792246	MT742996	MT792270	MT792254	MT792262
T. mulanensis	Q20-5	MT742971	MT742981	MT792239	MT792247	MT742997	MT792271	MT792255	MT792263
T. nodosa	G.J.S. 04–155 = CBS 132327 T	JQ403317	JQ403357	JQ403394	KJ022513	KJ022135	JQ394743	JQ394709	JQ365037
T. nodosa	A.R. 4500 = CBS 124742	JQ403306	JQ403346	JQ403383	KJ022469	KJ022090	JQ394735	JQ394699	JQ365028
T. nodosa	A.R.4505 = CBS 125173	JQ403307	JQ403347	HM364328	KJ022470	KJ022091	HM364348	HM352862	HM352878
T. nodosa	G.J.S. 90–66 = CBS124352	JQ403332	JQ403371	JQ403409	KJ022565	KJ022187	JQ394753	JQ394722	JQ365049
T. nodosa	G.J.S. 91–116 = CBS 124740	JQ403334	JQ403373	JQ403411	KJ022567	KJ022189	–	JQ394724	JQ365051
T. nodosa	G.J.S. 91–105 = IMI 351445	JQ403333	JQ403372	JQ403410	KJ022566	KJ022188	JQ394754	JQ394723	JQ365050
T. olida	CBS 215.67 T	KJ021982	KJ022058	HM364334	–	–	–	–	HM352884
T. ostrina	G.J.S. 96–23 = IMI 370947 T	KC153756	KC121482	KC153949	KJ022574	KJ022196	KC153885	KC153821	KC121418
T. ostrina	MAFF 241564	KC153772	KC121498	KC153965	KJ022611	KJ022232	KC153901	KC153837	KC121434
T. ostrina	G.J.S. 09–1327 = CBS 134022	KC153729	KC121455	KC153922	KJ022517	KJ022139	KC153858	KC153794	KC121391
T. papillata	G.J.S. 90–146 = CBS 134032 T	KC153746	KC121472	KC153939	KJ022556	KJ022178	KC153875	KC153811	KC121408
T. papillata	A.R. 4781 = CBS 134036	KC153716	KC121442	KC153909	KJ022477	KJ022098	KC153845	KC153781	KC121378
T. papillata	G.J.S. 90–166 = CBS 126099	KC153748	KC121474	KC153941	KJ022558	KJ022180	KC153877	KC153813	KC121410
T. pelargonii	CBS 145 054 T	MK047426	MK047477	–	–	–	–	MK047578	–

Supplementary Table 2 Continued.

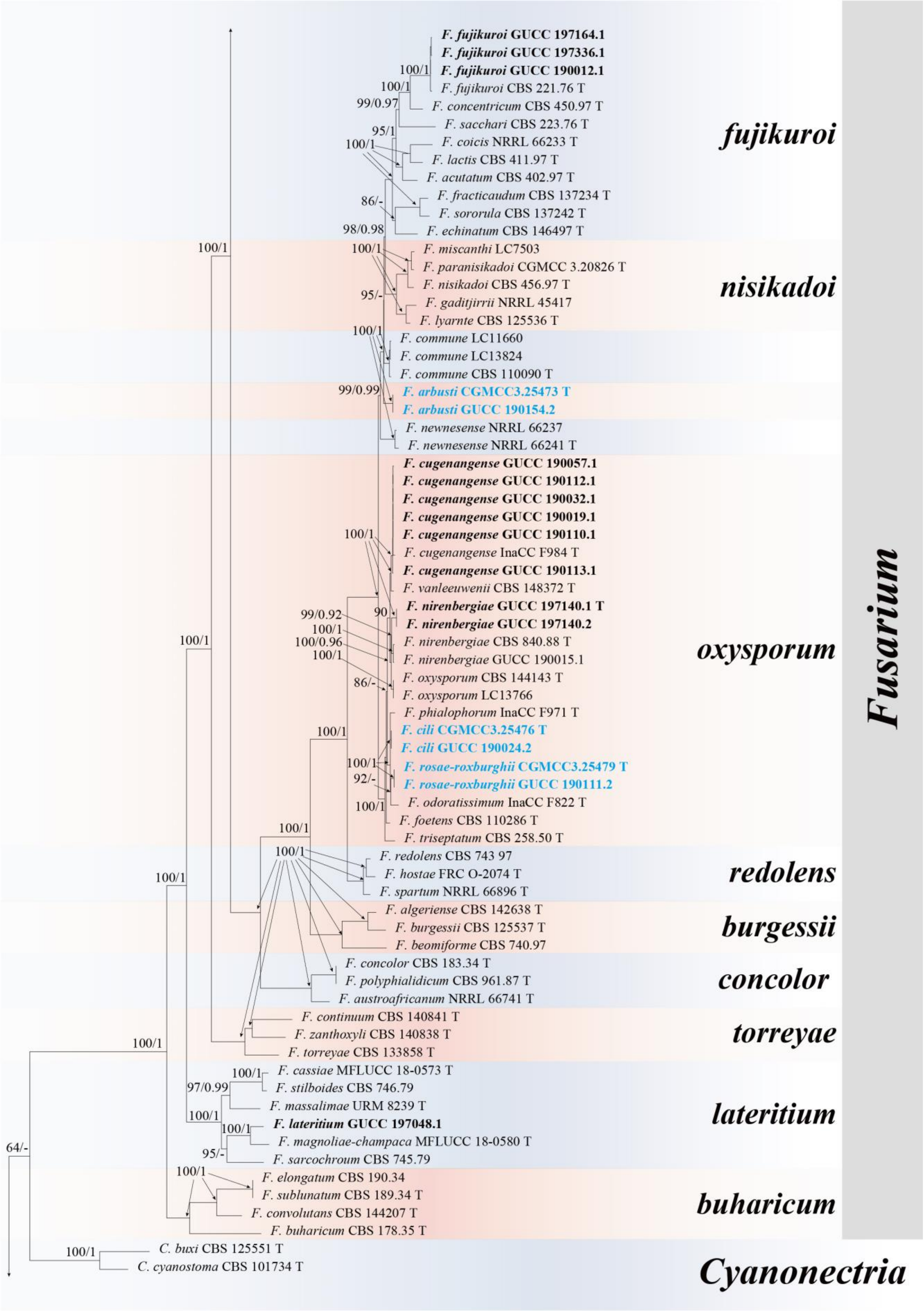
Genus and species	**Strain no.**	**GenBank accession no.**							
		ITS	**LSU**	***rpb1***	***rpb*2**	**SSU**	***tef1***	***tub2***	**ACT**
T. phoenicea	G.J.S. 85–179 = IMI 329113 T	KC153736	KC121462	KC153929	KJ022540	KJ022162	KC153865	KC153801	KC121398
T. phoenicea	G.J.S. 09–509	KC153730	KC121456	KC153923	KJ022520	KJ022142	KC153859	KC153795	KC121392
T. phoenicea	G.J.S. 85–187 = ATCC 76478	KC153737	KC121463	KC153930	KJ022541	KJ022163	KC153866	KC153802	KC121399
T. phoenicea	Guu 94031007 = CBS 134039	KC153712	KC121438	KC153905	KJ022460	KJ022081	KC153841	KC153776	KC121374
T. pinea	A.R. 4324 = CBS 125153 T	HM364294	HM364307	HM364326	KJ022467	KJ022088	HM364345	HM352860	HM352875
T. pinea	A.R. 4321 = CBS 134033	KC153713	KC121439	KC153906	KJ022466	KJ022087	KC153842	KC153777	KC121375
T. platycephala	IMI 329100 T	KJ022015	KJ022064	KJ022442	KJ022588	–	KJ022398	KJ022332	–
T. porphyria	MAFF 241515 T	KC153764	KC121490	KC153957	KJ022599	KJ022220	KC153893	KC153829	KC121426
T. porphyria	MAFF 241517	KC153765	KC121491	KC153958	KJ022600	KJ022221	KC153894	KC153830	KC121427
T. porphyria	MAFF 241539	KC153768	KC121494	KC153961	KJ022605	KJ022226	KC153897	KC153833	KC121430
T. purpurea	G.J.S. 10–131 = CBS 134024 T	KC153732	KC121458	KC153925	KJ022529	KJ022151	KC153861	KC153797	KC121394
T. purpurea	G.J.S. 10–145 = CBS 134025	KC153733	KC121459	KC153926	KJ022533	KJ022155	KC153862	KC153798	KC121395
T. purpurea	C.T.R. 71–281 = CBS 112458	KC153726	KC121452	KC153919	KJ022506	KJ022128	KC153855	KC153791	KC121388
T. purpurea	G.J.S. 90–155 = CBS 123966	KC153747	KC121473	KC153940	KJ022557	KJ022179	KC153876	KC153812	KC121409
T. rubi	CBS 113.12 = IMI 113918 T	KC153718	KC121444	KC153911	KJ022482	KJ022103	KC153847	KC153783	KC121380
T. rubi	CBS 241.29 = IMI 113919	KC153722	KC121448	KC153915	KJ022495	KJ022117	KC153851	KC153787	KC121384
T. rubi	CBS 177.27 = IMI 113917	KC153721	KC121447	KC153914	KJ022491	KJ022113	KC153850	KC153786	KC121383
T. rubrococca	G.J.S. 86–330 = IMI 324475 T	KJ022008	KJ022061	KJ022439	KJ022582	KJ022204	KJ022391	KJ022329	KJ022275
T. sinensis	HMAS 183 186	FJ560441	FJ560436	–	–	–	–	–	–
***Thelonectria* sp.**	**GUCC 190155.1**	**MZ724814**	**MZ724957**	**OR043821**	**—**	**OR029402**	–	**OR043977**	**OR043726**
***Thelonectria* sp.**	**GUCC 190169.1**	**MZ724815**	**MZ724958**	**OR043822**	**OR043877**	**OR029403**	–	**OR043978**	**OR043727**

Supplementary Table 2 Continued.

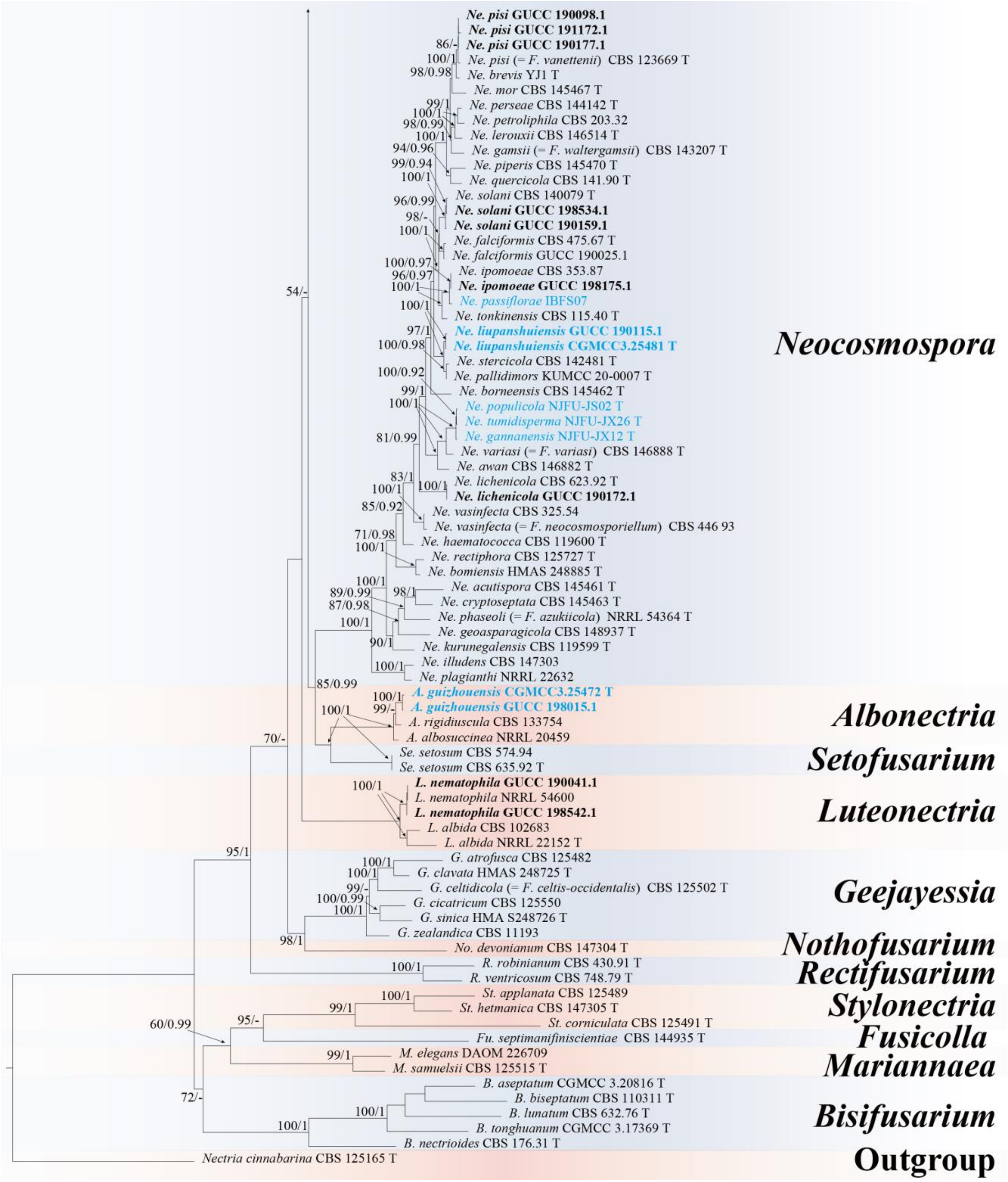
Genus and species	Strain no.	GenBank accession no.							
		ITS	**LSU**	***rpb1***	***rpb*2**	**SSU**	***tef1***	***tub2***	**ACT**
T. stemmata	C.T.R. 71.19 = CBS 112468T	JQ403312	JQ403352	JQ403388	KJ022502	KJ022124	JQ394739	JQ394704	JQ365033
T. stemmata	CBS 132336 C.T.R.71.21	JQ403313	JQ403353	JQ403389	KJ022503	KJ022125	KJ022384	JQ394705	JQ365034
T. theobromicola	CBS 218.67 = IMI 112161a T	KJ021983	KJ022059	KJ022444	KJ022494	KJ022116	KJ022362	KJ022334	KJ022279
T. torulosa	CBS 132339 = AR4764 T	JQ403309	JQ403349	JQ403385	KJ022473	KJ022094	KJ022389	JQ394701	JQ365030
T. torulosa	CBS 132340 T = AR4768A	JQ403310	JQ403350	JQ403386	KJ022476	KJ022097	JQ394737	JQ394702	JQ365031
T. trachosa	G.J.S. 92-45 = CBS 112467 T	KF569842	KF569851	KF569879	KJ022570	KJ022192	KF569860	KF569869	KF569832
T. truncata	MAFF 241521	JQ403339	JQ403377	JQ403414	KJ022601	KJ022222	JQ394757	KJ022325	JQ365056
T. truncata	CBS 132329 T = GJS04-357	JQ403319	JQ403359	JQ403396	KJ022515	KJ022137	JQ394745	KJ022324	JQ365039
T. tyria	G.J.S. 90–46 = CBS 134029 T	KC153751	KC121477	KC153944	KJ022562	KJ022184	KC153880	KC153816	KC121413
T. tyria	A.R. 4499 = CBS 125172	HM364296	HM364309	HM364327	KJ022468	KJ022089	HM364347	KC153778	HM352877
T. veuillotiana	CBS 132341 = AR1751	JQ403305	JQ403345	JQ403382	KJ022465	KJ022086	JQ394734	JQ394698	KJ022273
T. veuillotiana	G.J.S. 92–24 = CBS 125114	JQ403335	GQ506005	GQ506034	KJ022568	KJ022190	JQ394755	JQ394725	GQ505980
T. violaria	A.R. 4766 = CBS 134035 T	KC153715	KC121441	KC153908	KJ022475	KJ022096	KC153844	KC153780	KC121377
T. violaria	C.T.R. 72–188 = CBS 134040	KC153727	KC121453	KC153920	KJ022510	KJ022132	KC153856	KC153792	KC121389
T. viridispora	IMI 350 698 T	KJ022025	KJ022075	KJ022454	KJ022591	KJ022212	KJ022405	–	KJ022292
T. westlandica	IMI 255610	KF569843	KF569852	KF569880	KJ022577	KJ022199	KF569861	KF569870	KF569833
T. westlandica	G.J.S. 83-156 = CBS 112464 T	HM484559	HM364321	HM364337	KJ022537	KJ022159	HM484533	HM484610	HM352887
T. yunnanica	HMAS 183 564 T	FJ560438	–	–	–	–	–	JQ836660	–



Supplementary Figure 1 – Phylogenetic relationships of several species complexes in *Fusarium* and allied fungi. Phylogenetic tree was generated using the maximum likelihood (ML) method by combining the *rpb1*, *rpb2*, and *tef1* sequence data of 225 strains. The tree is rooted with *Nectria cinnabarina* (CBS 125165). The ML bootstrap support values > 50 % (BS) and Bayesian posterior probabilities > 0.90 (PP) are given near the nodes (BS/PP). Strains isolated in this study are indicated in **bold**. New species and combinations are shown in bold blue and blue, respectively. **T** holotype or ex-type.



Supplementary Figure 1 – Continued.



Supplementary Figure 1 – Continued.