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ARTICLE

Identification and characterization of *Albonectria*, *Fusarium*, and *Neocosmospora* species associated with ornamental plants in Southern China

Zhang YX[1±*], Chen C[1,2±], Nie LT[1±], Maharachchikumbura SSN[3], Crous PW[4], Hyde KD[1,5,6], Xiang MM[1], Al-Otibi F[6] and Manawasinghe IS[1*]

[1] *Innovative Institute for Plant Health / Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, Guangdong, P.R. China*
[2] *Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand*
[3] *School of Life Science and Technology, Center for Informational Biology, University of Electronic Science and Technology, Chengdu, P.R. China*
[4] *Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands*
[5] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[6] *Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 22452, 11495 Riyadh, Saudi Arabia*

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Abstract

Species belonging to *Albonectria*, *Fusarium*, and *Neocosmospora* are well-known destructive phytopathogens and are widely distributed worldwide. Although these genera have been well studied in recent years, fewer studies have focused on understanding the relationship between these fungi and ornamental plants in China, the largest producer of ornamental plants. The present study collected ornamental plant samples with disease symptoms from South China. In total, 77 fusarioid isolates were obtained from 25 ornamental plants representing 24 genera. These isolates were further identified using six gene regions: the internal transcribed spacer regions (ITS), calmodulin (*CaM*), the RNA polymerase largest subunit (*rpb1*), the RNA polymerase second largest subunit (*rpb2*), the translation elongation factor 1-alpha (*tef1-α*) and β-tubulin (*tub2*). Based on multi-gene phylogeny and morphology, 25 species were identified, including eight new species belonging to three genera, *Albonectria*, *Fusarium*, and *Neocosmospora* were identified. Among these, 19 species belonged to four *Fusarium* species complexes, viz., *F. fujikuroi* species complex, *F. nisikadoi* species complex, *F. oxysporum* species complex, and the *F. tricinctum* species complex. Here, we described five new *Fusarium* species, namely, *F. anoectochili*, *F. cymbidii*, *F. dendrobii*, *F. dendranthematis*, *F. guangdongense*, and one undefined species. In addition, five *Neocosmospora* species were identified, and two species *N. guangdongensis* and *N. paphiopedili*, were described as new. In addition, we described a new *Albonectria* species, *A. schimae*. Further, taxonomic updates in this study showed that *Fusarium rosae-roxburghii* should be reduced to synonymy with *F. odoratissimum* based on phylogenetic placements and morphological similarities. Our study also provides 23 new fungal-host associations from 15 fusarioid species. This study indicates a rich diversity of fusarium-like genera in ornamental plants in subtropical and tropical parts of China. Also, it provides a basic understanding of identifying common diseases caused by fusarioid fungi.

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***Corresponding Author:** Manawasinghe IS – e-mail – ishara9017@gmail.com,
Zhang YX – e-mail – yx_zhang08@163.com
± Authors have equally contributed to this study
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INTRODUCTION

Albonectria, *Fusarium*, and *Neocosmospora* belong to *Nectriaceae*, *Hypocreales* in *Sordariomycetes* (Maharachchikumbura et al. 2015, Wijayawardene et al. 2022, Chen et al. 2023b). They include some of the most devastating phytopathogens, comprising diverse and cosmopolitan species (Burgess 2014). Including *Fusarium*, 21 genera in *Nectriaceae* produce fusarium-like asexual morphs, commonly known as fusarioid species (Crous et al. 2021, https://www.fusarium.org/). The two largest genera, *Fusarium* and *Neocosmospora*, include numerous plant pathogens, as well as saprobes and endophytes (Crous et al. 2021). Link (1809) introduced *Fusarium* based on its morphology, but the genus has subsequently undergone several controversial taxonomic treatments (Geiser et al. 2013, Sandoval-Denis et al. 2019, O'Donnell et al. 2020, Geiser et al. 2021, Hyde et al. 2023). The most recent taxonomic update for *Fusarium* is given by Crous et al. (2021), in which fusarioid species were analysed based on multi-gene phylogenetic analyses and in-depth morphological characterisation. To date, 20 species complexes or lineages have been accepted in *Fusarium* (Crous et al. 2021, https://www.fusarium.org/), and the number of species is still increasing, with 1783 *Fusarium* epithets listed in Index Fungorum (www.indexfungorum.org). *Neocosmospora* was established by Smith (1899). Sandoval-Denis et al. (2019) suggested that the *F. solani* species complex should be redefined as *Neocosmospora*. These taxonomic changes have undergone several controversial treatments, and currently, the *F. solani* species complex is accepted as *Neocosmospora* (Crous et al. 2021). Members of *Albonectria* are associated with fusarioid asexual morphs and are characterised by white to pale yellow perithecia (Lombard et al. 2015). Four *Albonectria* species have been accepted (Zhang et al. 2023a), and only two species have DNA sequence data.

Species of *Albonectria*, *Fusarium* and *Neocosmospora* have been found in various perennial crops, such as apples (Lee et al. 2017), cashew nuts (Matos et al. 2016), cocoa trees (Vicente et al. 2012), and robusta coffee (Belan et al. 2018), causing root and stem rots, and vascular wilt on economically important crops worldwide (Navi & Yang 2016, Guarnaccia et al. 2019, Han et al. 2023, Zakaria 2023). In addition, Fusarium-wilt causes major damage to annual crops such as solanaceous and grain crops. Ornamental plants consist of cut flowers, foliage, and a wide range of potted plants including woody ornamentals (Lecomte et al. 2016). *Fusarium* and allied genera have been reported causing various diseases such as wilts, rots and blights on over 30 ornamental plants genera, including *Alocasia*, *Chrysanthemum*, *Gladiolus*, *Lilium* and *Tibouchina* worldwide. These plants play an important role in aesthetic values and economic development in many countries, and thus, the ornamental plants industry has become a significant sector of modern agriculture. However, with the increasing global trade in ornamentals and the subsequent development of industry, various diseases, especially fungal infections, have become a growing threat to ornamental plant production (Hammond et al. 2023).

Fusarioid species represent one of the major pathogen complexes on ornamental plants, leading to vascular wilt, crown and root rot (Lecomte et al. 2016, Zhang et al. 2021, 2022, Chen et al. 2023a). *Fusarium* species have been observed to thrive on various ornamental plants globally, leading to significant Fusarium wilt (Gullino et al. 2015, Srivastava et al. 2018, Chen et al. 2023a). He et al. (2021) reported that Rose (*Rosa chinensis*) vascular wilt was caused by *N. brevis* (as *F. rosicola*), stem and root rot on *Alocasia longiloba* by *F. elaeidis* (Zhang et al. 2021), and stem rot on *Aglaonema modestum* by *F. aglaonematis* and *F. elaeidis* (Zhang et al. 2022). Furthermore, Fusarium wilt on *Tibouchina seecandra* caused by *F. grosmichelii* was first reported by Chen et al. (2023a). Fusarioid species, especially *Fusarium* and *Neocosmospora* are prominent in orchid diseases worldwide (Srivastava et al. 2018). Srivastava (2014) reported that *F. circinatum* and *F. poae* are associated with *Cymbidium* and *Dendrobium*, and *F. begonia* from *Miltonia* and *Dendrobium*. In addition, *F. oxysporum*, *F. fractiflexum*, *F. proliferatum* (Chang et al. 1998, Swett & Uchida 2015), *F. subglutinans*, and *N. solani* (as *F. solani*, Lee et al. 2002, Chung et al. 2011)

have been reported from various orchid species. They have also been associated with dry and soft rot in ornamental *Cactus* (Cactaceae) and succulent species (Kamali-Sarvestani et al. (2022). Furthermore, *Fusarium* and *Neocosmospora* species have been associated with soilborne diseases on ornamental plants in Italy (Guarnaccia et al. 2019).

China is the world's leading producer of ornamental plants, with South China being a major region for decorative plant production (Darras 2020). However, compared to the other economically important crops in Southern China, fewer studies have focused on the systematics of fungal pathogens of ornamental plants. This study aims to provide insight into the diversity of fusarioid species on ornamental plants in Southern China. From 2021 to 2023, diseased samples with leaf spots, root rot, stem rot and wilt were collected from 13 cities in Southern China. Fusarioid taxa were isolated, and identifications were made based on morphology and multi-locus phylogenetic analyses. Illustrations and notes are provided for all identified species, along with taxonomic descriptions.

MATERIALS AND METHODS

Sample collection and isolation

From 2021 to 2023, diseased samples with typical symptoms of wilt, root rot, stem rot and leaf blight (Fig. 1) were collected in Southern China, including Guangdong, Yunnan, and Hunan provinces. Samples were collected and placed in Ziplock bags, photographs were taken, and relevant data (host, cultivar, and location) were recorded. Using the tissue isolation method, the putative pathogens were isolated following Senanayake et al. (2020) and Zhang et al. (2023b). Single spore and hyphal tip isolation methods were used to obtain axenic cultures. All living cultures obtained in this study were deposited in Zhongkai University of Agriculture and Engineering culture collection (ZHKUCC), and Fungarium materials (as dried cultures) were deposited in the Mycological Fungarium of Zhongkai University of Agriculture and Engineering (MHZU).

Morphological characterisation

Representative strains from each species were incubated on potato dextrose agar (PDA) for five days at 25 ℃. Mycelium plugs (7 mm diam.) were taken from the edge, then subculture on fresh PDA and oatmeal agar (OA) at 25 ℃ (Crous et al. 2021). The colony diameters were measured after five and seven days, and the growth rates were calculated. Colony characteristics were observed and recorded. In addition, carnation leaf agar (CLA) and synthetic nutrient-poor agar (SNA) were used for micro-morphological characteristics analysis (Leslie & Summerell 2006, Crous et al. 2021). Representative strains were incubated on CLA/SNA at 25 ℃ under 12 h light/12 h dark or in dark. After three or five days, the aerial microconidia and conidiogenous cells were observed and measured, and pictures were taken. After 1–2 weeks, sporodochial conidia or aerial conidia, conidiogenous cells and chlamydospores were observed and recorded. All microscopic structures were observed using a compound microscope (Nikon Eclipse 80i, Tokyo, Japan) and measured by NIS-Elements BR version 3.2. Each structure was measured with at least 30 replications. Taxonomic novelties were submitted to Index Fungorum (IF), and Facesoffungi (FoF) numbers were obtained as described by Jayasiri et al. (2015).

DNA extraction and PCR amplification

Mycelia were scrapped from five-day-old cultures grown on PDA. Genomic DNA was extracted using a DNA Extraction Kit (Aidlab Biotechnologies Co., Beijing, China). Six genomic loci, the internal transcribed spacer regions (ITS), calmodulin (*CaM*), RNA polymerase largest subunit I (*rpb1*), RNA polymerase largest subunit II (*rpb2*), translation elongation factor 1-alpha (*tef1-α*) and β-tubulin (*tub2*) were amplified for *Albonectria*, *Fusarium* and *Neocosmospora* phylogenetic analysis (Sandoval-Denis et al. 2019, Crous et al. 2021, Yilmaz et al. 2021). The primer pairs and PCR amplification procedure for each locus followed relative references (Table 1).

The PCR products were visualized using agarose gel electrophoresis after staining with ethidium bromide and sequenced (Tianyi Huiyuan Science and Technology Corporation Ltd., Guangzhou, China). All sequence data generated in this study are deposited in NCBI GenBank (Supplementary Table 1).

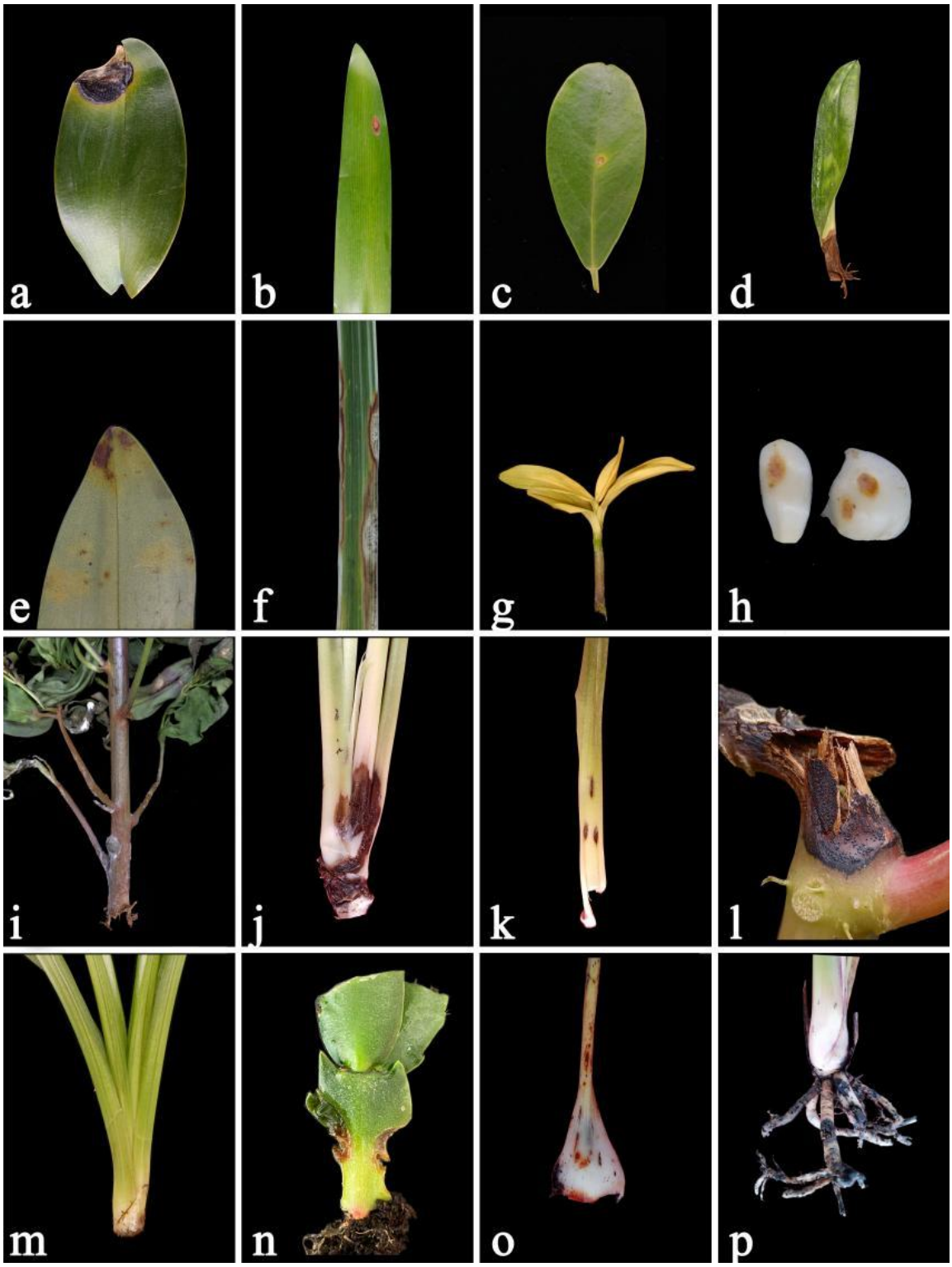

Figure 1 – Field symptoms of diseased plants in this study. a *Phalaenopsis aphrodite*. b *Hymenocallis littoralis*. c *Heptapleurum heptaphyllum*. d *Paphiopedilum* sp. e *Dendrobium nobile*. f. *Arrhenatherum elatius*. g. *Dendrobium nobile*. h *Lilium brownii*. i *Antirrhinum majus*. j, k *Spathiphyllum floribundum*. l *Chaenomeles sinensis*. m. *Cymbidium* sp. n *Zygocactus truncatus*. o–p *Strelitzia reginae*.

Table 1 The loci used for phylogenetic analyses in this study.

Locus	Primer	Annealing temperature (°C)	References
ITS	ITS4/ITS5	55	White (1990)
CaM	CL1/CL 2A	50	O'Donnell et al. (2000)
tef1-α	EF1H/EF2T	56	O'Donnell (2000)
	EF1/EF2	52	O'Donnell et al. (1998)
tub2	T1/CYLTUB1R	52	O'Donnell & Cigelnik (1997), Crous et al. (2004)
	T1/T2	55	O'Donnell & Cigelnik (1997)
rpb1	Fa/R8	59 (5 cycles) 58 (5) 57 (35)	Hofstetter et al. (2007), O'Donnell et al. (2010)
	F8/G2R		O'Donnell et al. (2010)
	Fa/G2R		Hofstetter et al. (2007), O'Donnell et al. (2010)
rpb2	5f/7cr	53	Liu et al. (1999)
	5f2/7cr	52	Reeb et al. (2004), Liu et al. (1999)
	7cf/11ar	52	Liu et al. (1999)

Abbreviations: ITS: internal transcribed spacer regions, *CaM*: calmodulin, *tef1-α*: translation elongation factor 1-alpha, *tub2*: β-tubulin, *rpb1*: RNA polymerase largest subunit I, and *rpb2*: RNA polymerase largest subunit II.

Phylogenetic analysis

BioEdit v. 7.0.9.0. (Hall 1999) was employed to assure the sequence quality by checking the chromatograms. For the preliminary identification, *tef1-α* sequences were subjected to BLASTn v. 2.15.0 searches in the NCBI database (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The BLASTn results of *tef1-α* identified our isolates belonging to *Albonectria*, *Fusarium* and *Neocosmospora*. *Fusarium* isolates were further categorised into four species complexes: The *F. fujikuroi*, *F. nisikadoi*, *F. oxysporum*, and *F. tricinctum* species complex. Required sequences were obtained from NCBI for the phylogenetic analysis by following Lombard et al. (2019), Crous et al. (2021), Sandoval-Denis et al. (2019), Yilmaz et al. (2021), Wang et al. (2022), Zeng & Zhuang (2023). MAFFT v. 7 was used to align all sequences (https://mafft.cbrc.jp/alignment/server/). The sequences were manually checked using BioEdit v. 7.0.5.2 (Hall 1999).

In the phylogenetic analyses, six data sets were used following the most recent taxonomic treatments by Crous et al. (2021). For *Albonectria*, a combined *tef1-α*, *rpb1*, *rpb2*, and *tub2* sequence data set was used (Zhang et al. 2023a). For the *Fusarium fujikuroi* species complex combined dataset of *tef1-α -rpb2-rpb1-tub2*, for *Fusarium oxysporum* species complex datasets of *tef1-α-CaM-rpb1-rpb2-tub2*, for the *Fusarium nisikadoi* species complex concatenated dataset of *rpb1-rpb2-tef1-α-tub2* and the *Fusarium tricinctum* species complex, *tef1-α-rpb1-rpb2-tub2* were employed (Lombard et al. 2019, Sandoval-Denis et al. 2019, Crous et al. 2021, Wang et al. 2022).

Phylogenetic analyses were performed on the CIPRES science gateway platform (Miller et al. 2010) using the maximum likelihood (ML) method implemented in RAxML (Stamatakis et al. 2008, Stamatakis 2014) and Bayesian posterior probability analysis (BYPP) in MrBayes v.3.2.7a (Ronquist & Huelsenbeck 2003). For the ML analysis, the nucleotide evolution model was GTR + GAMMA, and the analyses were carried out using RAxML-HPC2 on XSEDE (8.2.12) (Miller et al. 2010) with 1000 nonparametric bootstrapping replicates. Using the XSEDE tool in CIPRESS, Bayesian inference (BI) was carried out in MrBayes v.3.2.7a (Ronquist & Huelsenbeck 2003). The evolution models were selected using the jModelTest2 on XSEDE in the CIPRES Gateway (Table 2). A million generations of MrBayes analyses were performed, with a tree sample every 100 generations. Out of the 10,000 trees acquired, the initial 2000, which represented the burn-in stage, were discarded. The majority rule consensus tree's posterior probability was computed using

the remaining 8000 trees. Phylogenetic trees were edited in Adobe Illustrator and visualized using FigTree v1.4.

Table 2 The evolution models used in the phylogenetic analysis of the present study.

Gene	ITS	*CaM*	*rpb1*	*rpb2*	*tef1-α*	*tub2*
Albonectria						
Number of number of characters	–	–	1775	1720	695	401
Best Fitting Model	–	–	SYM+I	SYM+I+G	HKY+I	HKY
F. fujikuroi species complex						
Number of number of characters	–	–	1552	1669	638	562
Best Fitting Model	–	–	GTR+I+G	GTR+I+G	GTR+I+G	GTR+G
F. oxysporum species complex						
Number of number of characters	–	599	1451	861	619	538
Best Fitting Model	–	K80	SYM+G	SYM+G	HKY+G	K80+G
F. tricinctum species complex						
Number of number of characters	–	–	1603	1765	653	501
Best Fitting Model	–	–	SYM+G	GTR+I+G	GTR+G	K80+I
F. nisikadoi species complex						
Number of number of characters	–	–	1581	1762	661	482
Best Fitting Model	–	–	SYM+G	SYM+G	HKY+G	HKY
Neocosmospora						
Number of number of characters	459	–	1487	1609	646	-
Best Fitting Model	GTR+I+G	–	GTR+I+G	GTR+I+G	GTR+I+G	-

RESULTS

Seventy-seven fusarioid isolates were obtained from 25 ornamental plants. Based on the BLASTn results of *tef1-α* sequence data, 62 isolates were identified as *Fusarium* species and further classified into four *Fusarium* species complexes (*Fusarium fujikuroi*, *Fusarium nisikadoi*, *Fusarium oxysporum*, and *Fusarium tricinctum* species complexes), and 13 strains were identified as *Neocosmospora* species, while two isolates identified as *Albonectria* species.

Phylogenetic analyses

Phylogenetic analysis of *Albonectria*

The phylogenetic tree of *Albonectria* was obtained using combined sequences of *tef1-α*, *rpb1*, *rpb2*, and *tub2*. The final alignment comprised seven *Albonectria* strains, including two isolates from this study and *Setofusarium setosum* (CBS 635.92) as an outgroup. The RAxML tree of *Albonectria* was similar in topology to the Bayesian posterior probability (BYPP) analysis. The final likelihood value of the ML tree was –11040.173826 (Fig. 2). The matrix comprised 287 distinct alignment patterns and 16.56% of undetermined characters or gaps. For the final tree, the estimated base frequencies were A = 0.242381, C = 0.271703, G = 0.250832, and T = 0.236605; substitution rates AC = 1.314947, AG = 3.649965, AT = 1.072620, CG = 0.903077, CT = 8.881487, and GT = 1.000000; and gamma distribution shape parameter α = 1.396985. We have identified our two isolates as a new taxon as they diverged from existing *Albonectria* species.

Phylogenetic analysis of *Fusarium fujikuroi* species complex

Based on concatenated sequences of *tef1-α*, *rpb2*, *rpb1*, and *tub2*, the phylogenetic analyses of the *F. fujikuroi* species complex was conducted. The final alignment comprised 243 *Fusarium*

strains, including 23 isolates from the present study and *F. nirenbergiae* (CBS 744.97) as the outgroup taxon. The best-scoring RAxML tree of the *F. fujikuroi* species complex is similar in topology to the Bayesian posterior probability (BYPP) analysis (Fig. 3). The final likelihood value of the ML tree was −29401.274062 (Fig. 3). The matrix comprised 1727 distinct alignment patterns, and 25.32% of undetermined characters or gaps. For the final tree, the estimated base frequencies were A = 0.251914, C = 0.255916, G = 0.243865, and T = 0.248305; substitution rates AC = 1.370871, AG = 5.875861, AT = 1.070327, CG = 0.940005, CT = 10.641847, and GT = 1.000000; and gamma distribution shape parameter α = 0.812903. Twenty-three isolates were grouped into seven clades of the *Fusarium fujikuroi* species complex, including three new species.

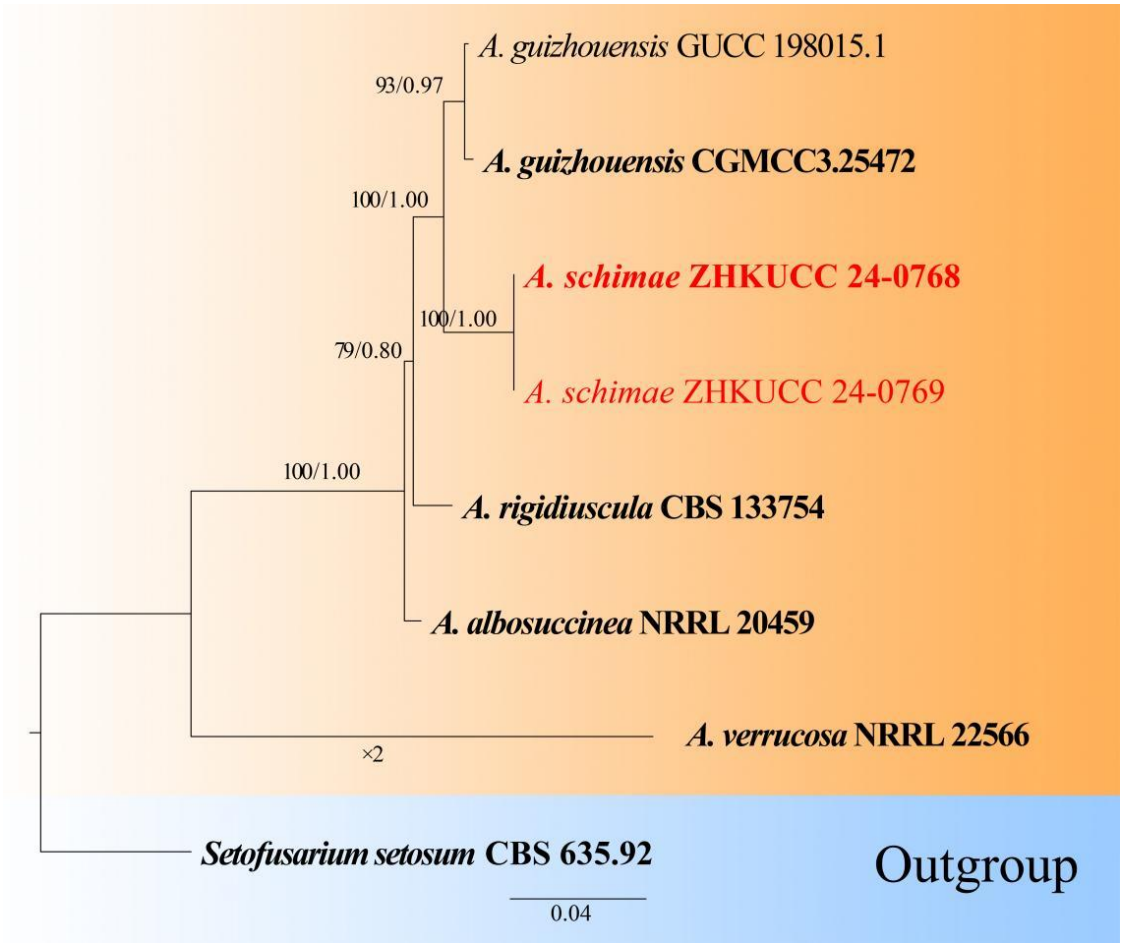

Figure 2 – Maximum likelihood tree of the *Albonectria*. The tree is rooted with *Setofusarium setosum* (CBS 635.92). The bootstrap support levels for ML and BYPP are shown at each node as ML/PP. Isolates from the current study are shown in red, and type strains are indicated in bold. The scale bar represents 0.04 nucleotide mutations per site.

Phylogenetic analysis of *Fusarium nisikadoi* species complex

Based on combined sequences of *rpb1*, *rpb*2, *tef1-α* and *tub2*, the phylogenetic analyses of *Fusarium nisikadoi* species complex was done. In total, 16 strains, including two of our isolates, and *F. falsibabinda* (LC 13610) and *F. concolor* (CBS 183.34) were used as the outgroup taxa. The best-scoring RAxML tree had a similar topology to the Bayesian posterior probability (BYPP) analysis (Fig. 4). The final likelihood value of the ML tree was −11930.897532. The matrix comprised 484 distinct alignment patterns and 13.09% of undetermined characters or gaps. For the final tree, the estimated base frequencies were A = 0.258448, C = 0.257823, G = 0.238602, and T = 0.245127; substitution rates AC = 1.243689, AG = 6.854921, AT = 1.074130, CG = 0.770855, CT = 6.284618, and GT = 1.000000; and gamma distribution shape parameter α = 5.680045. Our two isolates were identified as one new taxon of the *F. nisikadoi* species complex.

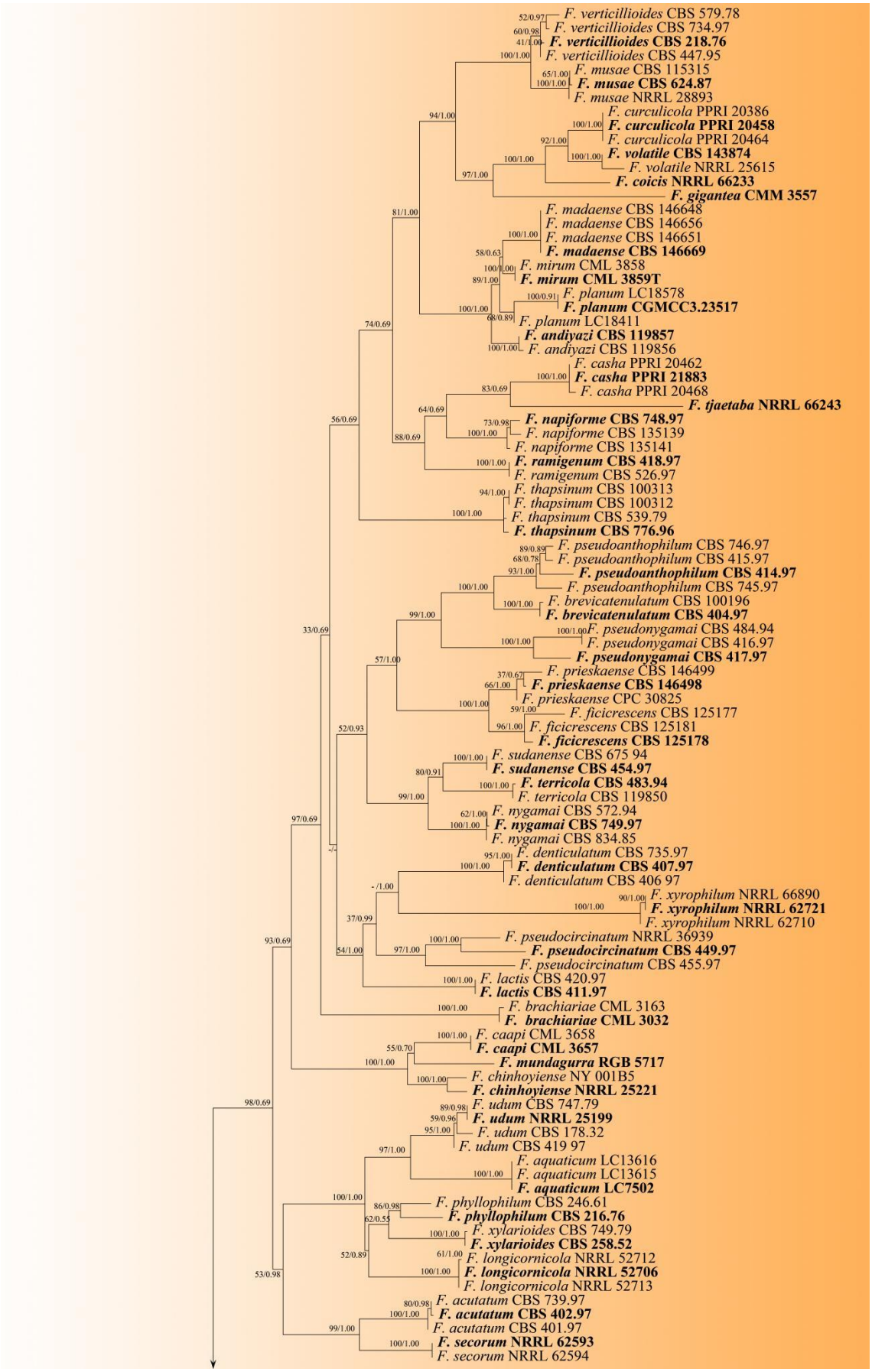

Figure 3 – Maximum likelihood tree of the *Fusarium fujikuroi* species complex. The tree is rooted with *F. nirenbergiae* (CBS 744.97). The bootstrap support levels for ML and BYPP are shown at

each node as ML/PP. Isolates from the current study are shown in red, and type strains are indicated in bold. The scale bar = 0.009 nucleotide mutations per site.

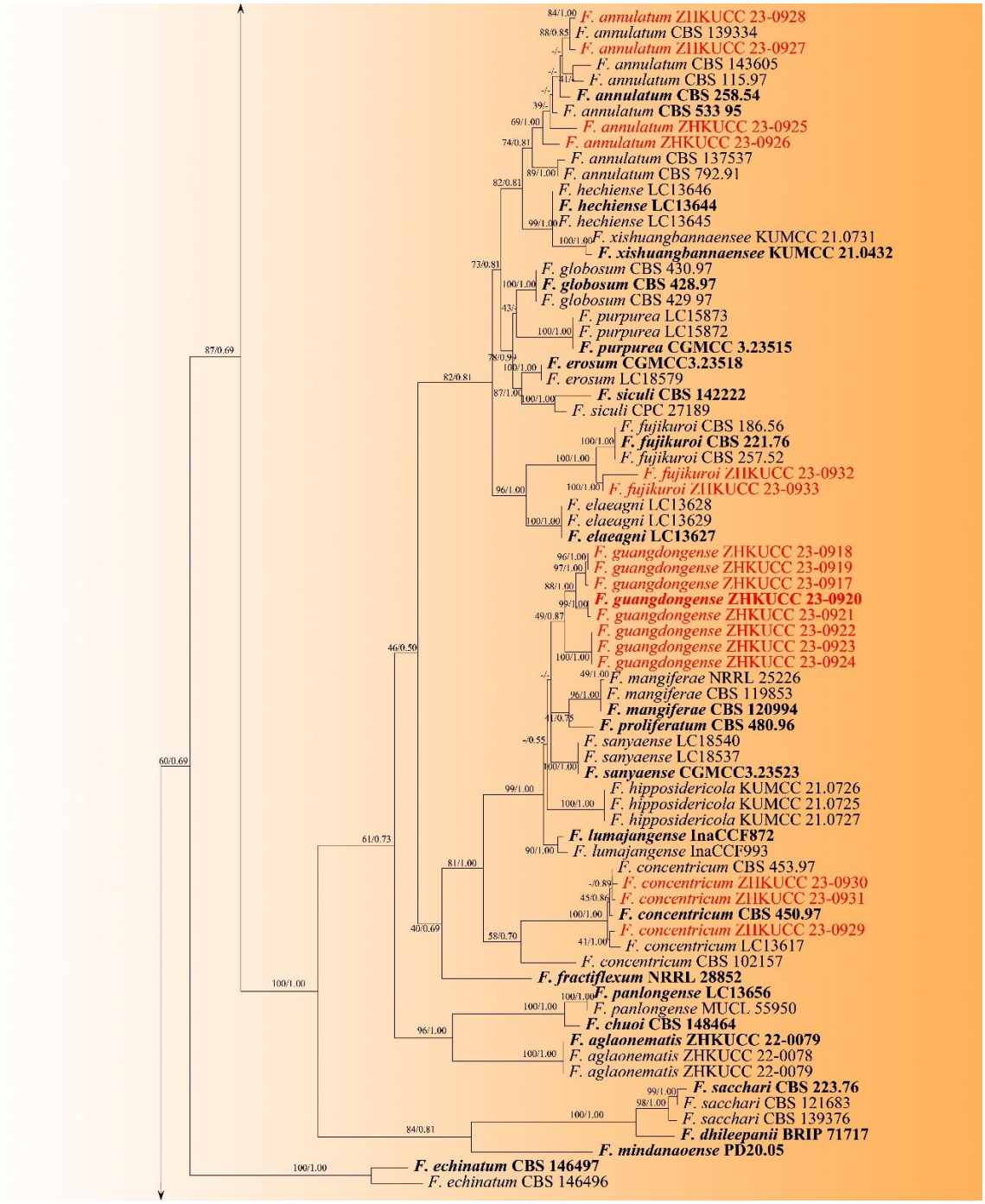

Figure 3 – Continued.

Phylogenetic analysis of *Fusarium oxysporum* species complex

Based on combined sequences of *tef1-α*, *CaM*, *rpb*1, *rpb*2, and *tub2*, the phylogenetic trees of the *Fusarium oxysporum* species complex were generated. Thirty-three isolates from this study aligned with 117 *Fusarium* strains and *F. udum* (CBS 177.31) and *F. foetens* (CBS 120665) as outgroup species. The ML tree topology resembled that of the BYPP. Fig. 5 presents the best-scoring RAxML tree, with a final probability value of -9717.185961. The matrix had 506 distinct alignment patterns, with 21.07% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252317, C = 0.260782, G = 0.238935, and T = 0.247966; substitution rates AC = 1.500955, AG = 3.255988, AT = 1.131824, CG = 0.944393, CT = 6.833629, and GT =

1.000000; and gamma distribution shape parameter α = 0.947343. Isolates from the present study clustered into nine clades in the *F. oxysporum* species complex. One clade clustered as independent lineages from other known species in the *Fusarium oxysporum* species complex. Based on the morphology and phylogenetic analyses, we identified nine species, including one undefined taxon from this *F. oxysporum* species complex.

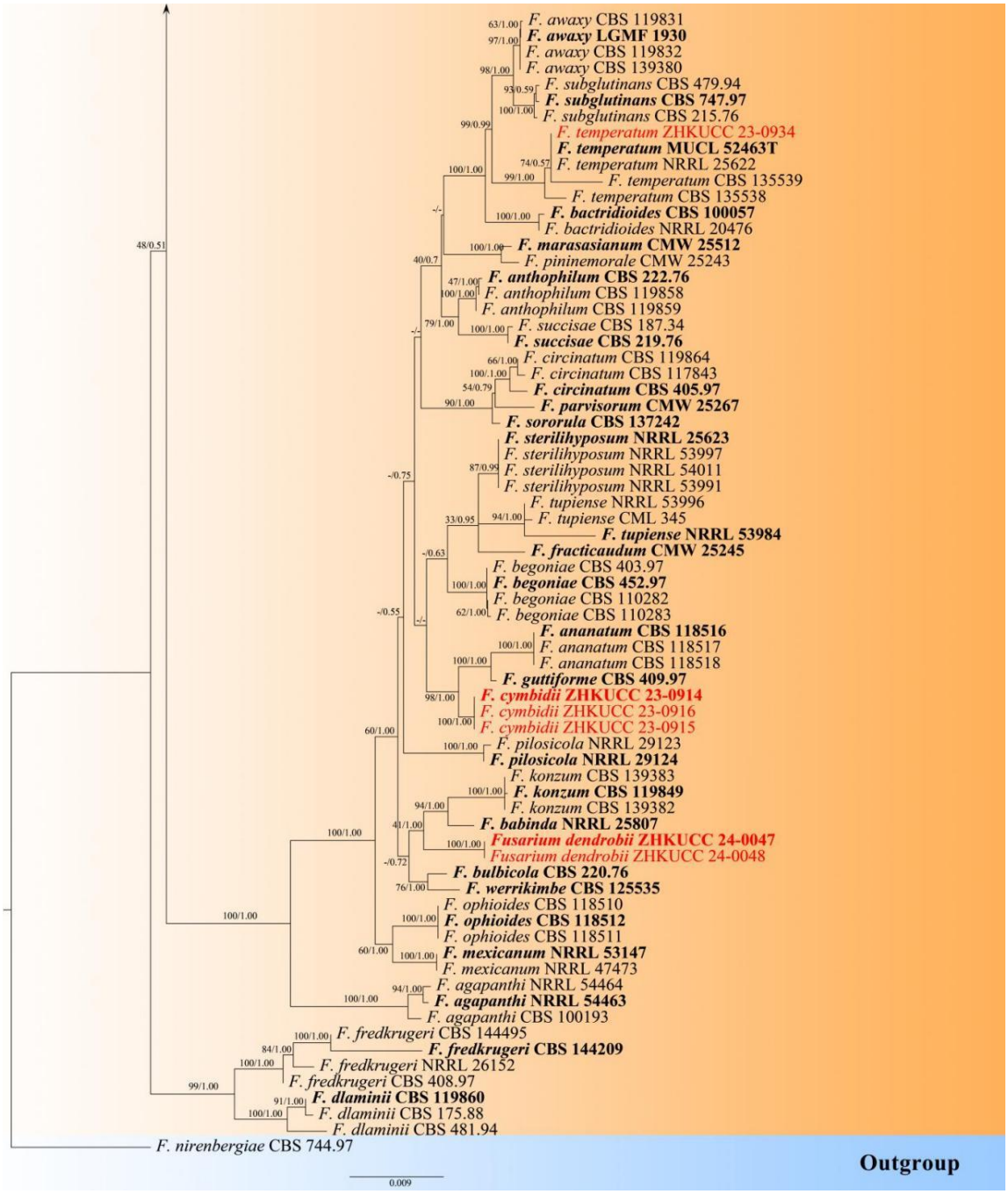

Figure 3 – Continued.

Phylogenetic analysis of *Fusarium tricinctum* species complex

Combining sequencing data sets of *tub2*, *rpb1*, *tef1-α*, and *rpb2* was used to generate the phylogenetic tree for the *Fusarium tricinctum* species complex. The final alignment comprised four isolates from the current study, with 58 *Fusarium* strains in total. As the outgroup taxon, *F. concolor* (NRRL 13994) was employed. The best-scoring RAxML tree of *F. tricinctum* species complex was similar in topology to the Bayesian posterior probability (BYPP) analysis (Fig. 6).

The final likelihood value of the ML tree was –15451.034384 (Fig. 6). The matrix comprised 1059 distinct alignment patterns, and 22.94% of undetermined characters or gaps. For the final tree, the estimated base frequencies were A = 0.249821, C = 0.253917, G = 0.247876, and T = 0.248386; substitution rates AC = 1.204128, AG = 3.825187, AT = 1.123248, CG = 0.648877, CT = 8.480231, and GT = 1.000000; and gamma distribution shape parameter α = 0.782560. Four isolates from this study were identified as two species in the *F. tricinctum* species complex.

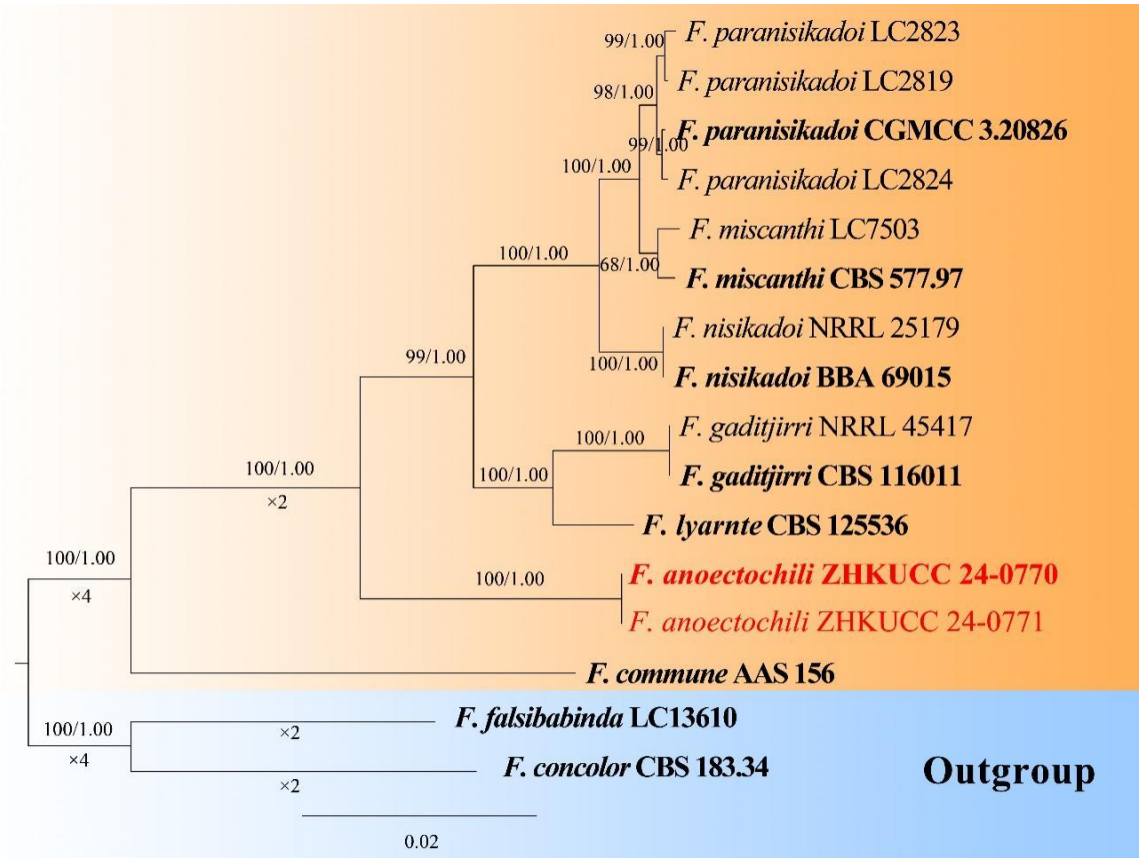

Figure 4 – Maximum likelihood tree of the *Fusarium nisikadoi* species complex. *Fusarium falsibabinda* (LC 13610) and *F. concolor* (CBS 183.34) were used as the outgroup taxa. Bootstrap support for ML and BYPP are shown at the nodes (ML/PP). Isolates of the type are bolded. The study's isolates are indicated in red. The scale bar = 0.02 nucleotide changes per site.

Phylogenetic analysis of *Neocosmospora*

Based on combined sequences of ITS, *rpb1*, *rpb2*, and *tef1-α*, the phylogenetic analyses of the *Neocosmospora* were generated. The final alignment comprised 146 *Neocosmospora* strains, including our 13 isolates and *Geejayessia atrofusca* (NRRL 22316) and *G. cicatricum* (CBS 125552) as the outgroup taxa. The best scoring RAxML tree of *Neocosmospora* is similar in topology to the BYPP analysis (Fig. 7). The final likelihood value of the ML tree is –37357.872710 (Fig. 7). The matrix comprised 1863 distinct alignment patterns, and 21.78% of undetermined characters or gaps. For the final tree, the estimated base frequencies were A = 0.239989, C = 0.281882, G = 0.255212, and T = 0.222918; substitution rates AC = 1.446812, AG = 5.122438, AT = 1.521063, CG = 1.256075, CT = 10.375131, and GT = 1.000000; and gamma distribution shape parameter α = 0.711838. Our 13 isolates clustered into five distinct clades. Based on morphology and phylogenetic analyses, two clades were identified as independent lineages from other known species of *Neocosmospora*, and three known species associated with ornamental plants from Southern China.

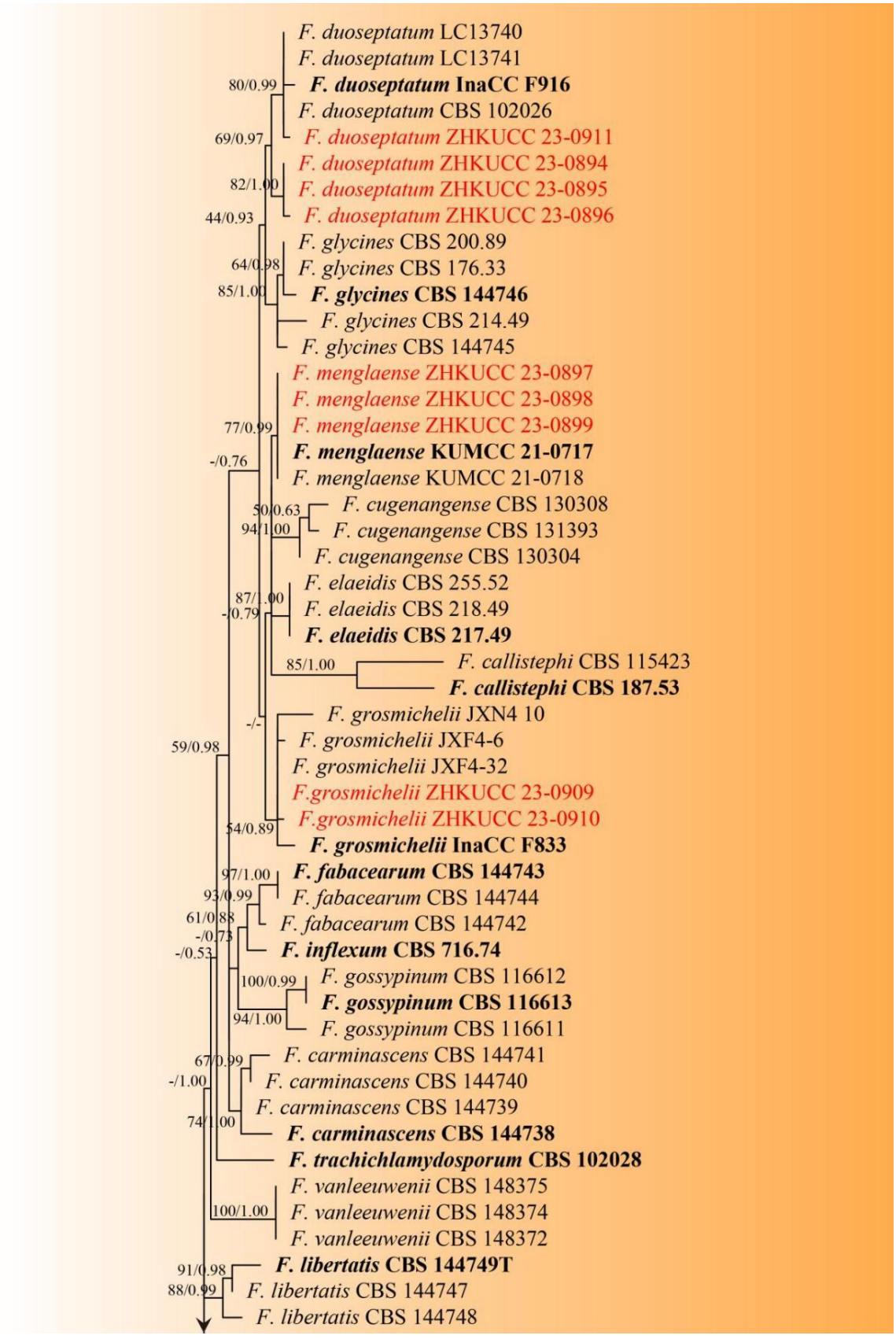

Figure 5 – Maximum likelihood tree of the *Fusarium oxysporum* species complex. *Fusarium udum* (CBS 177.31) and *F. foetens* (CBS 120665) were used as the outgroup taxa. Bootstrap supports for ML and BYPP are shown at the nodes (ML/PP). Isolates of the ex-type are bolded. The isolates from the current study are indicated in red.

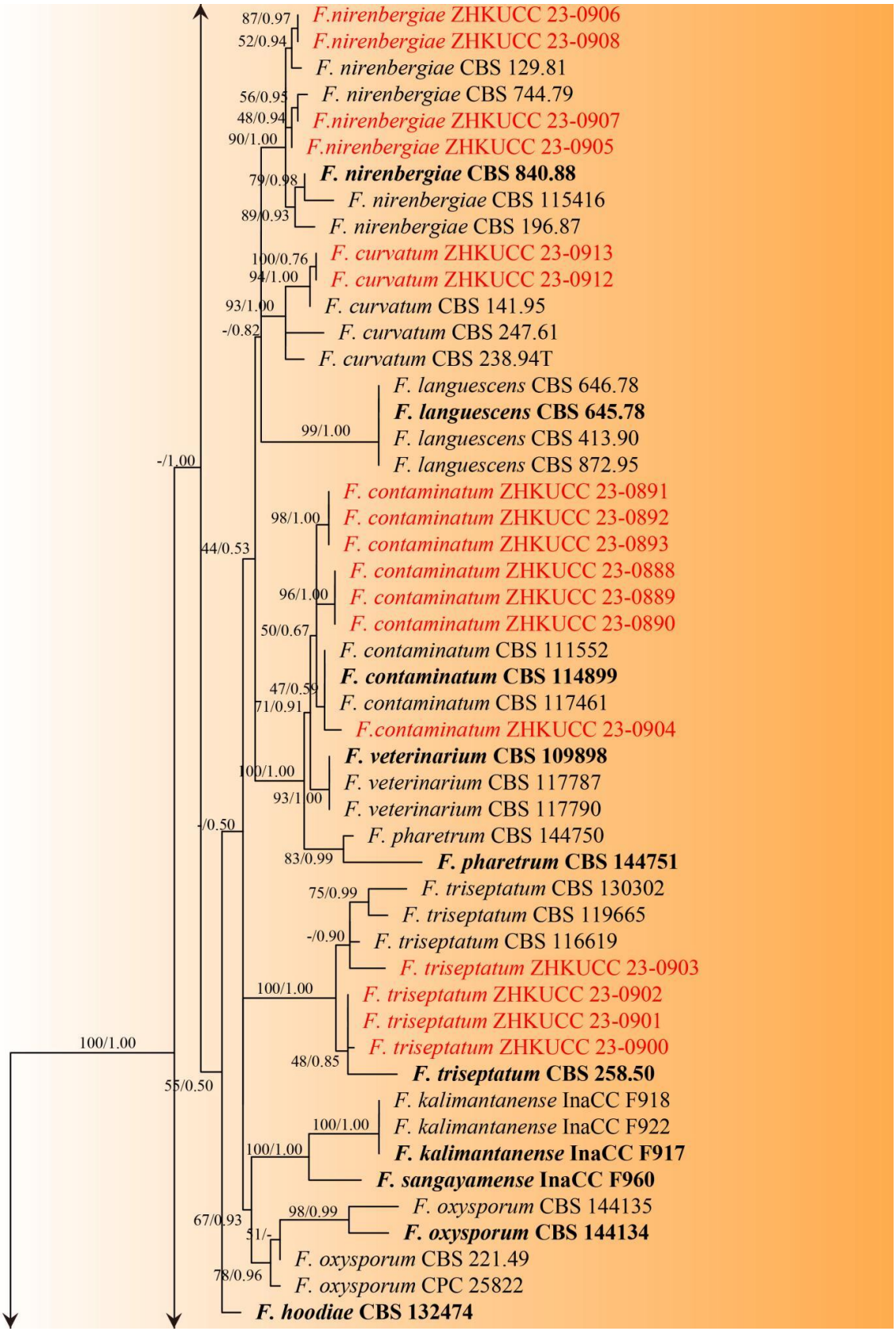

Figure 5 – Continued.

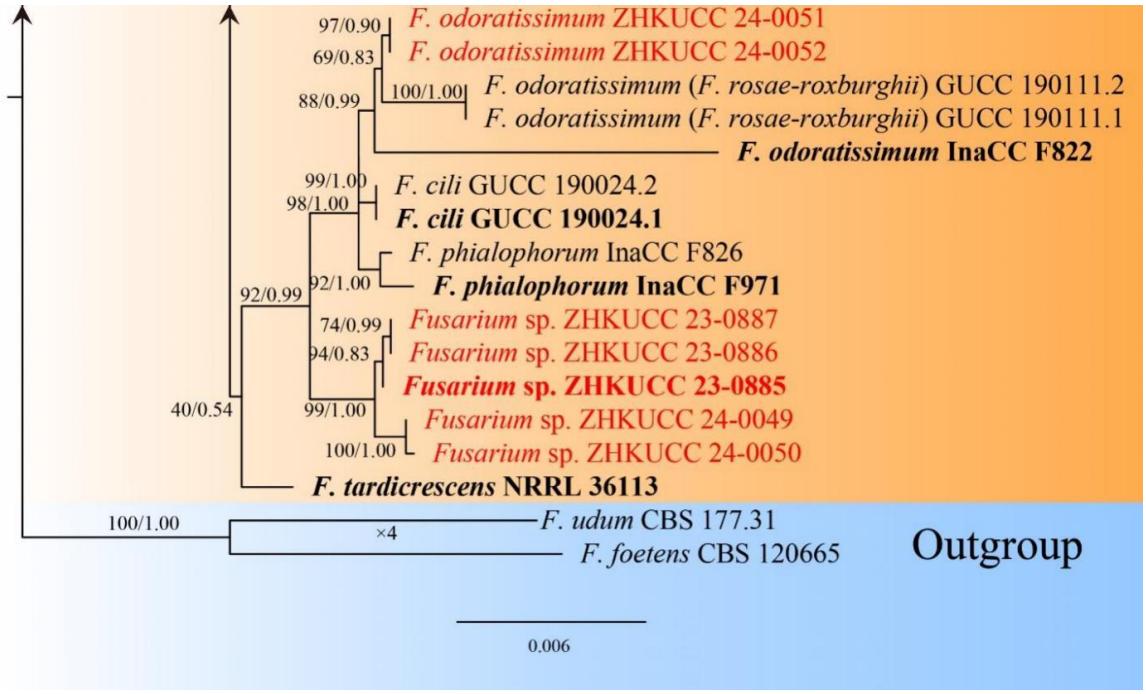

Figure 5 – Continued.

Taxonomy

Albonectria Rossman & Samuels, in Rossman, Samuels, Rogerson & Lowen, Stud. Mycol. 42: 105 (1999)

Albonectria was erected by Rossman et al. (1999) to accommodate species with white to pale yellow ascomata with fusarioid asexual morphs (Perera et al. 2023). *Albonectria rigidiuscula* (Berk. & Broome) Rossman & Samuels is the type species, and currently, four species, *A. albosuccinea*, *A. guizhouense*, *A. rigidiuscula*, and *A. verrucosa* are accepted (https://www.fusarium.org/). Herein, we introduce a novel *Albonectria* species associated with *Schima superba* from China.

Albonectria schimae Y.X. Zhang, K.D. Hyde, C. Chen & Manawas., sp. nov. Fig. 8

Index Fungorum number: IF902561; Facesoffungi number: FoF16623

Etymology – Refers to the *Schima superba*, the host plant from which this fungus was collected.

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* verticillately branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* cylindrical to subcylindrical, 15–30 × 2–5 µm ($\overline{x}$ = 21 × 3 µm, n = 50); *Sporodochial conidia* curved, apical cell curved to blunt; basal cell foot-shaped, papillate, (3–)5–10 (–16)-septate, rough thick-walled, off-white; 3-septate conidia: (36–)40–45 × 5–6 µm ($\overline{x}$ = 43 × 6 µm, n = 6); 4-septate conidia: 44–60 (–65) × 5–7 µm ($\overline{x}$ = 50 × 6 µm, n = 22); 5-septate conidia: (47–)50–80× 5–8 µm ($\overline{x}$ = 64 × 6 µm, n = 50); 6-septate conidia: 65–90 (–96) × 6–8 µm ($\overline{x}$ = 80 × 7 µm, n = 50); 7-septate conidia: 75–90 × 5–10 µm ($\overline{x}$ = 82 × 8 µm, n = 50); 8-septate conidia: 75–95× 7–10 µm ($\overline{x}$ = 86 × 8 µm, n = 50); 9-septate conidia: 80–95 × 7–9 µm ($\overline{x}$ = 88 × 8 µm, n = 50); 10-septate conidia: 90 × 8 µm (n = 1); 12-septate conidia: 87 × 8 µm (n = 1); 13-septate conidia: 95 × 8 µm (n = 1); 15-septate conidia: 95 × 10 µm (n = 1); 16-septate conidia: 100 × 9 µm (n = 1). *Aerial conidiophores* branched. *Conidiogenous cells* subcylindrical, long and slender smooth and thin-walled, monophialidic, 20–45 × 2–3 µm ($\overline{x}$ = 31 ×3 µm, n = 50). *Aerial microconidia* in chains or false heads, obovate to ovoid, with or without flattened basal cells, 0–1-septate; aseptate conidia: 5–10 × 3–4 µm ($\overline{x}$ = 7 × 3 µm, n = 50); 1-septate conidia: 11–15 × 4–5 µm ($\overline{x}$ = 13 × 4 µm, n = 8). *Chlamydospores* not observed. Sexual morph: not observed.

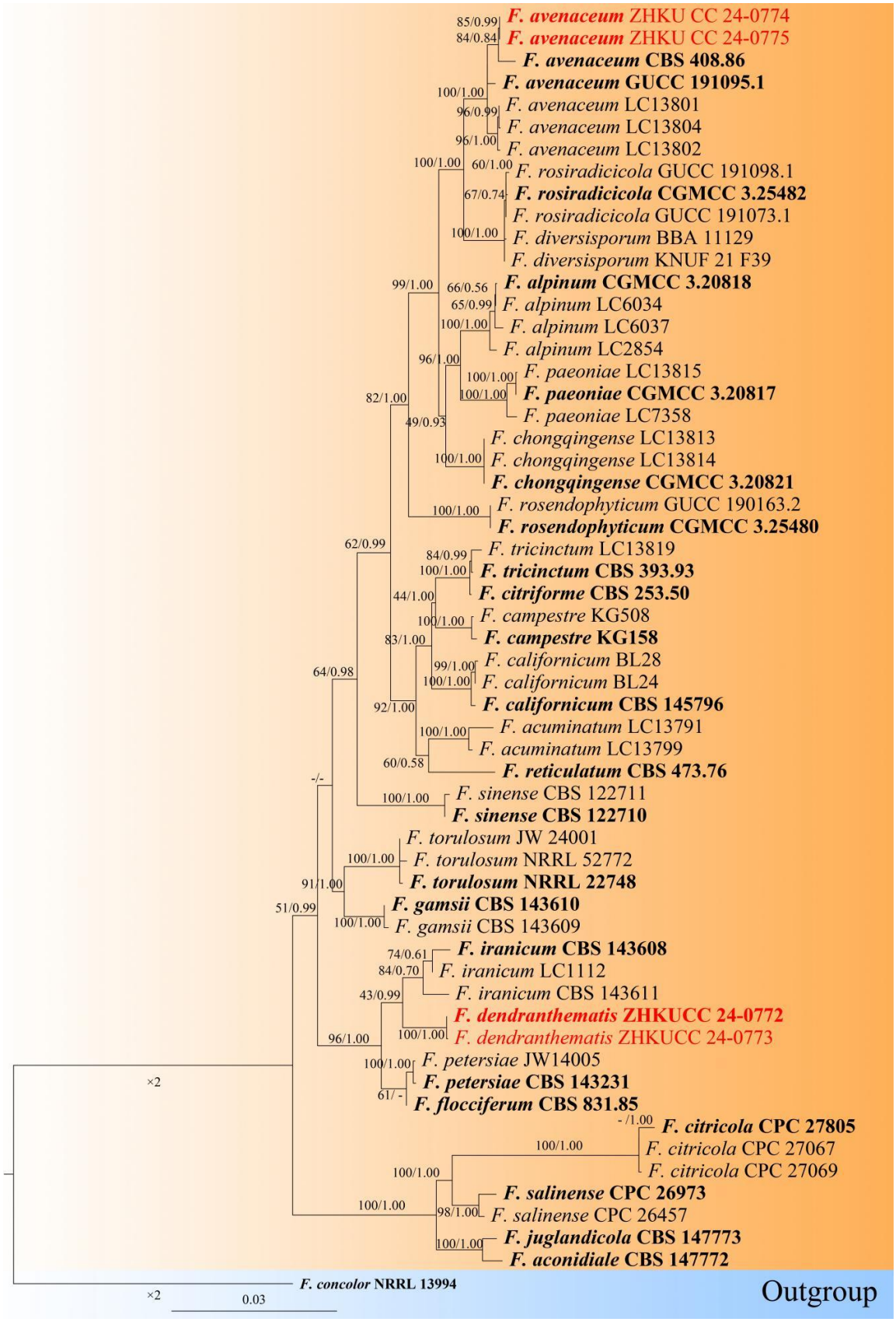

Figure 6 – The best-scoring RAxML tree of the *Fusarium tricinctum* species complex. The tree is rooted with *F. concolor* (NRRL 13994). The bootstrap support values for ML and BYPP are displayed as ML/PP at each node. Type strains are given in bold, and isolates from this study are in red.

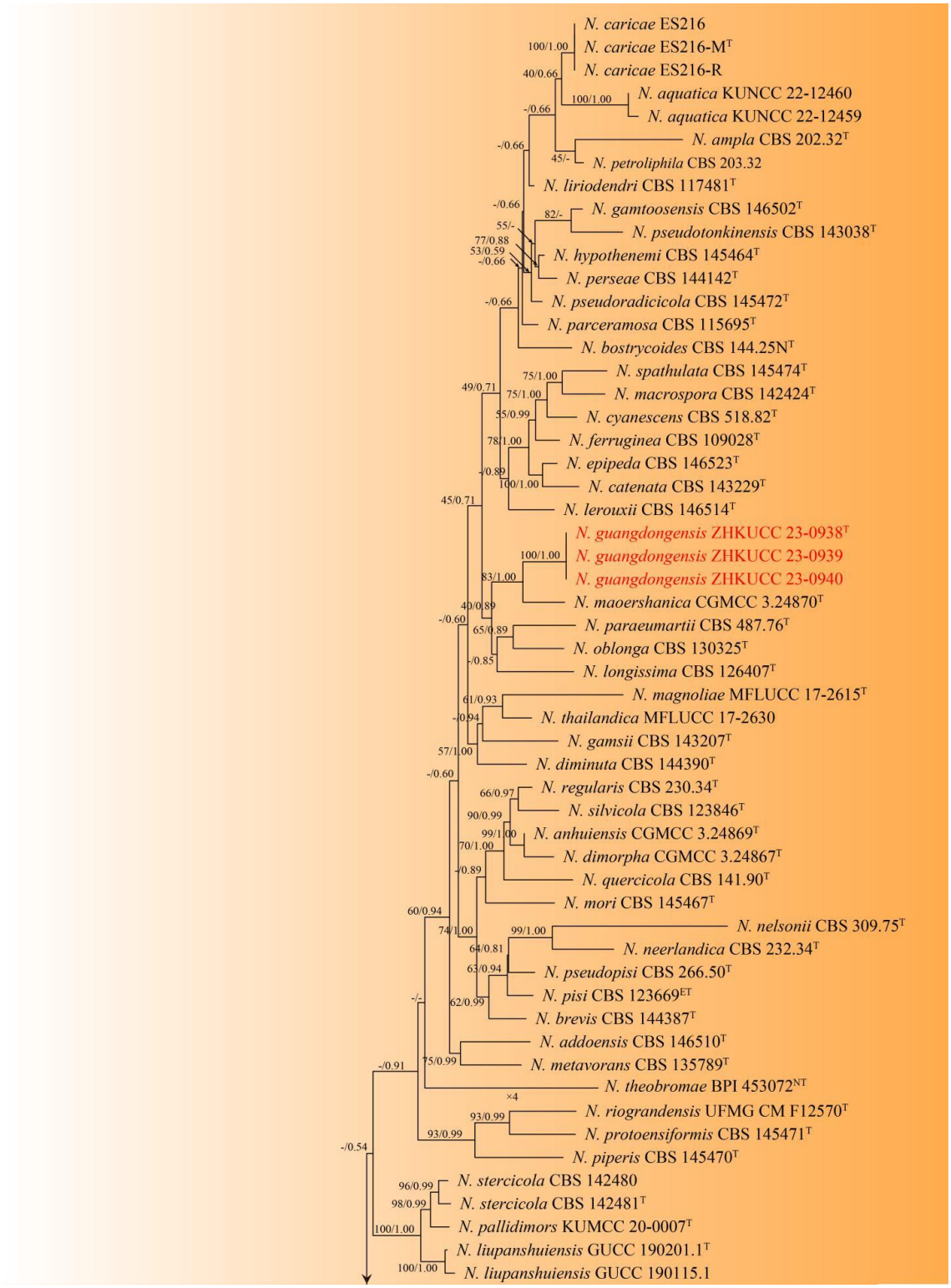

Figure 7 – The best-scoring RAxML tree of the *Neocosmospora*. *Geejayessia cicatricum* (CBS 125552) and *G. atrofusca* (NRRL 22316) are selected as outgroup taxa. The bootstrap support values for ML and BYPP are displayed as ML/PP at each node. Type isolates are marked with "T", epi-types are marked with "ET", and neotypes are marked with "NT. Isolations belonging to the current study are shown in red.

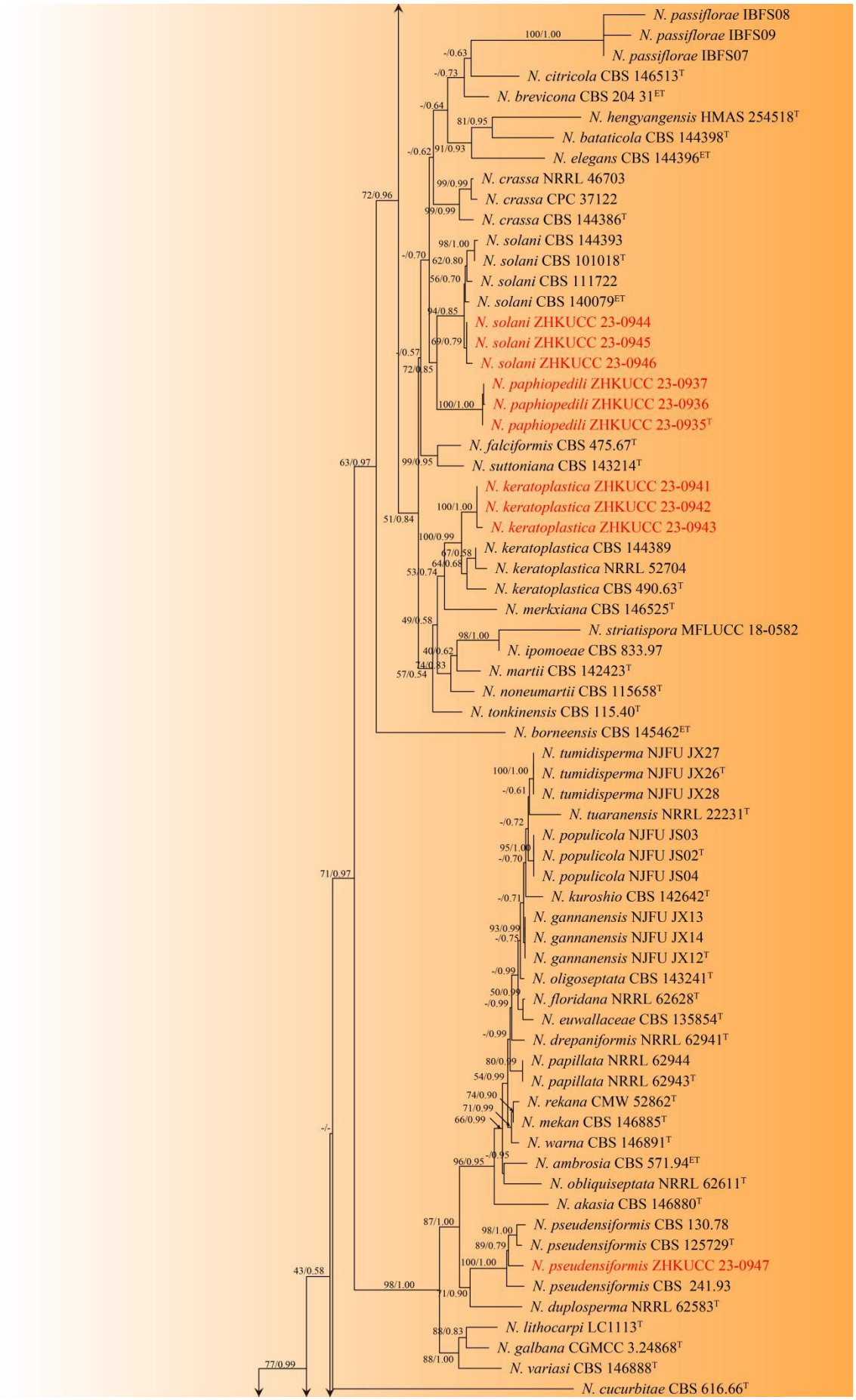

Figure 7 – Continued.

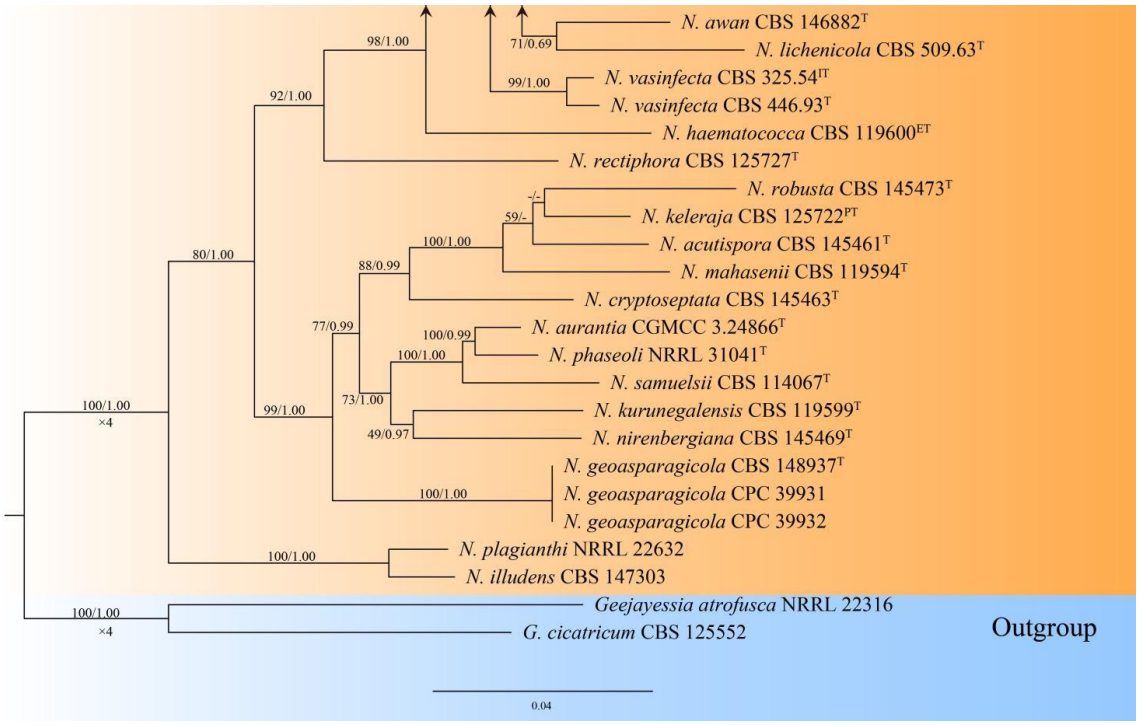

Figure 7 – Continued.

Culture characteristics – Colonial growth rate on PDA was 5 mm/d at 25 ℃. Surface view: pale pink to rose coloured, floccose, filamentous margin. In reverse; dark rose-coloured in the centre. Sporodochia produced on CLA after 5 days. Colonial growth rate on OA was 3 mm/d at 25 ℃. Colony surface yellow in the center, white at the margin, aerial mycelia flat, dense, and margin entire; reverse purple.

Material examined – China, Guangdong Province, Meizhou City, on a leaf of *Schima superba* (*Theaceae*), 5 October 2023, YX Zhang and LT Nie (MHZU 24-0440; holotype); ZHKUCC 24-0768, ex-type; living culture, ZHKUCC 24-0769.

Notes – In the phylogenetic analysis of *Albonectria* species, two strains clustered in a lineage close to *A. guizhouensis* with 99% ML bootstrap support and 1.00 BYPP values (Fig. 2). Our strains differ from *A. guizhouensis* by developing more septa and the different size of macroconidia (3–16 septa and 36–100 × 5–9 µm in *A. schimae* vs 5–7 septa, 68–90 × 5.5–7.5 µm in *A. guizhouensis*, Zhang et al. 2023a). In addition, the nucleotide of *A. schimae* (ZHKUCC 24-0768) differs from *A. guizhouensis* (CBS 635.92) by 28.18% (113/401) variations in *tub2*. When we BLAST our sequence (ZHKUCC 24-0768) in NCBI GenBank, it showed 100–98% query cover and 97.0–99.5% similarities with fusariod species. However, the blast result of *A. guizhouensis* (CBS 635.92) (Zhang et al. 2023a) is similar to *Colletotrichum bromeliacearum* (LC0951), with 29% query cover and 88.76% identity. All protein-coding gene (*tef1-α*, *rpb1*, *rpb2*, and *tub2*) data belonging to *A. guizhouensis* are not verified in NCBI GenBank. This questioned the taxonomic status of the *A. guizhouensis*. Based on this, we introduce our isolations of *A. schimae* as a new species, and we suggest that the taxonomic status of *A. guizhouensis* be evaluated.

Fusarium Link., Mag. Gesell. naturf. Freunde, Berlin 3(1–2): 10 (1809)

This genus is typified by *Fusarium sambucinum* Fuckel (Hyde et al. 2023). It encompasses diverse species belonging to 20 lineages (Crous et al. 2021, https://www.fusarium.org/). Herein, we identified 19 *Fusarium* species, which are further classified into four species complexes: *Fusarium fujikuroi* species complex, *Fusarium nisikadoi* species complex, *Fusarium oxysporum* species complex and *Fusarium tricinctum* species complex.

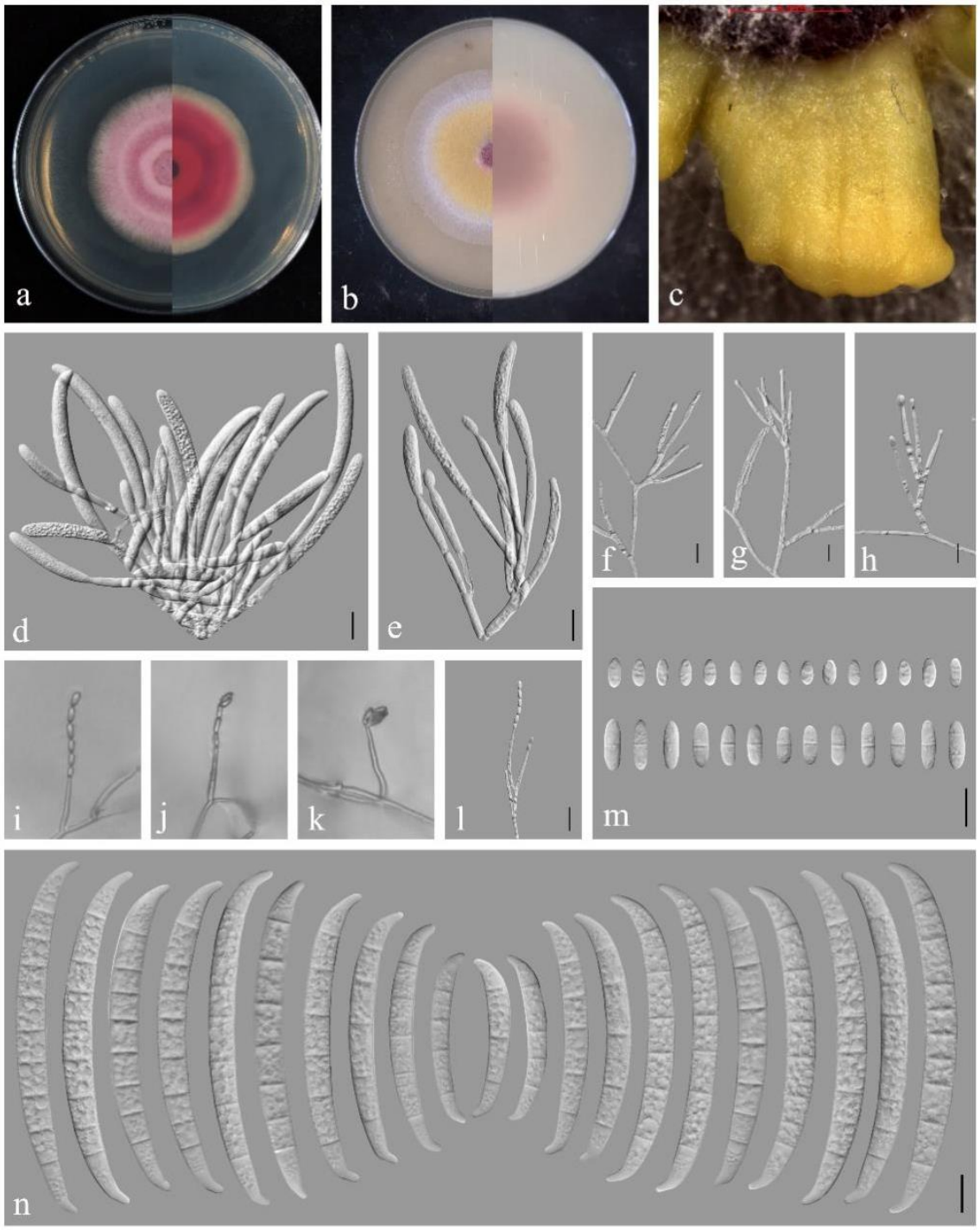

Figure 8 – *Albonectria schimae* (ZHKUCC 24-0768, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochial conidiophores, phialides. f–h Aerial conidiophores phialides. i–l Aerial conidial chains and false head. m Aerial microconidia. n Sporodochial conidia. Scale bars: 10 μm.

Fusarium annulatum Bugnic., Rev. gén. Bot. 59: 13 (1952) Fig. 9

Index Fungorum number: IF297536; Facesoffungi number: FoF16723

Asexual morph: *Sporodochia* light yellow, formed on SNA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 10–17(–20) × (2–)3–4 μm ($\bar{x}$ = 14 × 3 μm, n = 50). *Sporodochial conidia* slender, apical cell curved, basal cell foot-shaped, (1–2)3–6(–7)-septate, hyaline; 1-septate conidia: 52–61 × 4 μm ($\bar{x}$ = 57 × 4 μm, n = 2); 2-septate conidia: 59–60 × 4 μm ($\bar{x}$ = 60 × 4 μm, n = 2); 3-septate conidia: (40–)43–66(–70) × 3–4

μm ($\bar{x}$ = 57 × 4 μm, n = 50); 4-septate conidia: (42–)51–72(–75) × 3–5 μm ($\bar{x}$ = 60 × 4 μm, n = 50); 5-septate conidia: 52–74(–81) × 3–5 μm ($\bar{x}$ = 64 × 4 μm, n = 50); 6-septate conidia: 58–86 × 3–5 μm ($\bar{x}$ = 69 × 4 μm, n = 50); 7-septate conidia: 64–67 × 3–4 μm ($\bar{x}$ = 65 × 4 μm, n = 2). *Conidiogenous cells* subcylindrical, phialides or polyphialides, 6–22 × 2–4 μm ($\bar{x}$ = 15 × 3 μm, n = 50). *Aerial microconidia* in small false heads or chains, oval and obovoid, 0-septate conidia: 5–10 × 2–4 μm ($\bar{x}$ = 7 × 3 μm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 6 mm/d at 25 ℃. Surface view: white, floccose with a filamentous margin. In reverse, white. On SNA, sporodochia produced after 60 days.

Material examined – China, Guangdong Province, Zhongshan City, on the leaf of *Dendrobium nobile* (*Orchidaceae*), 17 October 2021, YX Zhang, JW Chen, C Chen, living culture, ZHKUCC 23-0925; Guangdong Province, Shaoguan City, on leaf of *Phalaenopsis aphrodite* (*Orchidaceae*), 17 July 2021, YX Zhang, living culture, ZHKUCC 23-0926; Hunan Province, Changsha City, on leaf of *Rosa chinensis* (*Rosaceae*), 7 October 2021, C. Chen, living culture, ZHKUCC 23-0927; Guangdong Province, Guangzhou City, on stem of *Paliurus hemsleyanus* (*Rhamnaceae*), 25 March 2021, YX Zhang, living culture, ZHKUCC 23-0928.

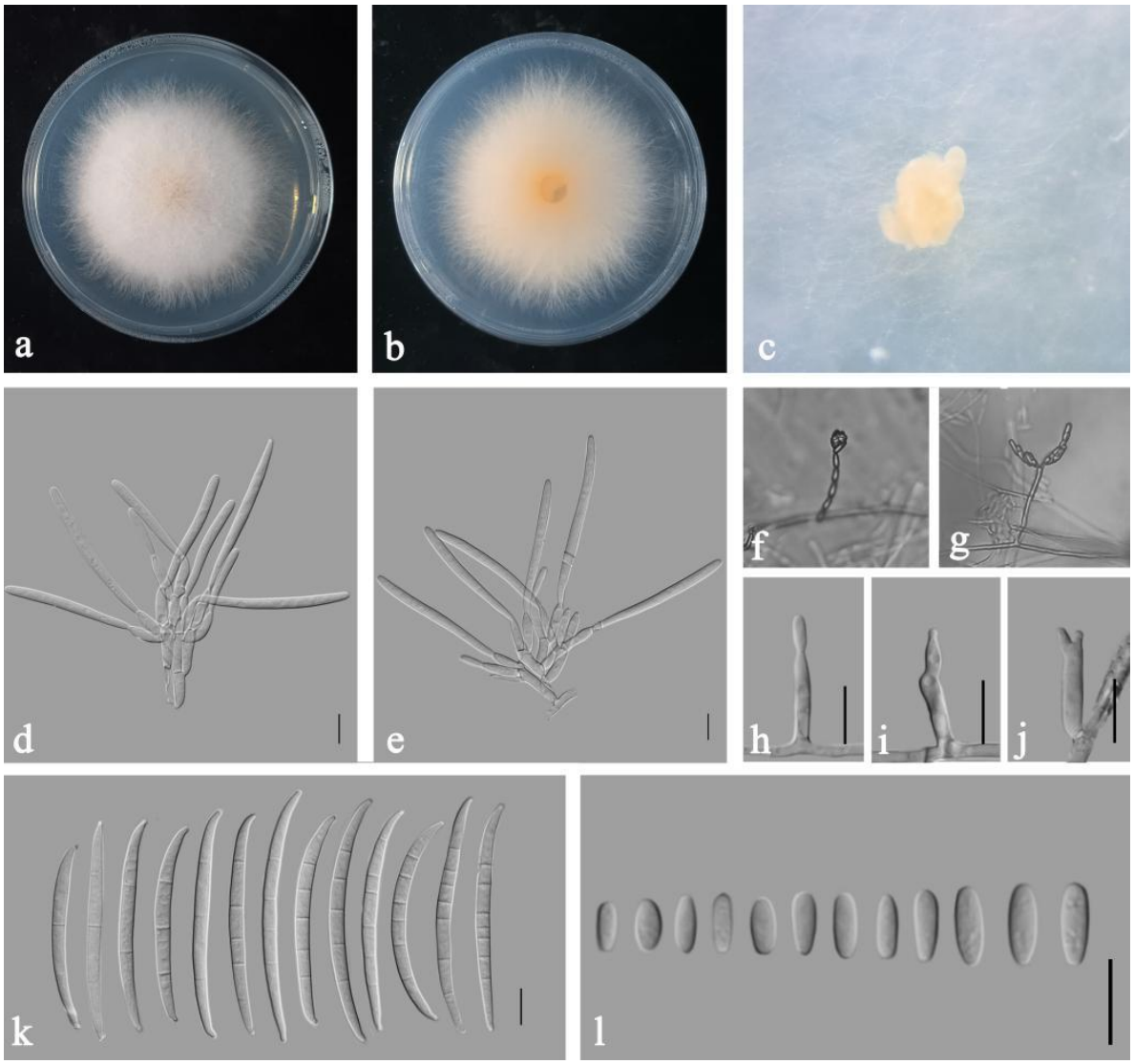

Figure 9 – *Fusarium annulatum* (ZHKUCC 23-0925). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on SNA. d–e Conidiophores and phialides on sporodochia. f–g Aerial microconidia produced in chains. h–j Aerial conidiophores phialides and polyphialides. k Sporodochial conidia. l Microconidia. Scale bars: 10 μm.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, four strains from the present study were clustered with *F. annulatum* (Fig. 3). Our strains are morphologically similar to *F. annulatum* (Bugnicourt 1952, Nelson et al. 1983, Yilmaz et al. 2021, Parra et al. 2022). Based on morphology and phylogeny, we identified these isolates as *F. annulatum*. *Fusarium annulatum* has a wide host range, including *Gossypium* sp., *Oryza sativa*, *Dianthus caryophyllus*, *Vanilla*, and *Gladiolus* (Yilmaz et al. 2021) and this species is also reported as a soil fungus (Lombard et al. 2022). To our knowledge, this is the first report of *F. annulatum* isolated from *Phalaenopsis aphrodite* and *Rosa chinensis* worldwide.

Fusarium anoectochili Y.X. Zhang, K.D. Hyde, C. Chen & Manawas., sp. nov. Fig. 10

Index Fungorum number: IF902562; Facesoffungi number: FoF16624

Etymology – Referring to the host of this fungus, *Anoectochilus roxburghii*.

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* verticillately branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* subcylindrical, 11–36 (–39) × 3–6 µm ($\overline{x}$ = 24 × 5 µm, n = 50); *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (1–)3–5 (–6)-septate-septate; 1-septate conidia: 44 × 4 µm (n = 1); 2-septate conidia: 26–39 × 3–5 µm ($\overline{x}$ = 31 × 3 µm, n = 50); 3-septate conidia: 31–45 (–48) × 4–5 µm ($\overline{x}$ = 38 × 4 µm, n = 50); 4-septate conidia: 37–53 (–56) × 4–5 µm ($\overline{x}$ = 44 × 4 µm, n = 50); 5-septate conidia: 42–57 × 4–5 µm ($\overline{x}$ = 49 × 4 µm, n = 50). 6-septate conidia: 41–52 × 4–5 µm ($\overline{x}$ = 47 × 4 µm, n = 3). *Aerial conidiophores* unbranched and often reduced to single phialides. *Conidiogenous cells* subcylindrical, molophialides, 7–21(–25) × 2–4 µm ($\overline{x}$ = 13 × 3 µm, n = 50). *Aerial microconidia* in small false heads, obovoid, fusiform and oval, 0–1-septate; 0-septate conidia: 5–12 × 2–4 µm ($\overline{x}$ = 8 × 3 µm, n = 50); 1-septate conidia: 12–19 × 3–4 µm ($\overline{x}$ = 15 × 3 µm, n = 50). *Chlamydospores* not observed. Sexual morph: Not observed.

Culture characteristics – Colonial growth rate on PDA was 7 mm/d at 25 ℃. Surface view: white, floccose, filamentous margin. In reverse, pink in the centre. Sporodochia produced on CLA after 30 days. Colonial growth rate on OA was 4 mm/d at 25 ℃. Colony surface white, aerial mycelia raised, dense; reverse light yellow.

Material examined – China, Guangdong Province, Meizhou City, on a leaf of *Anoectochilus roxburghii* (*Orchidaceae*), 2 November 2021, Y.X. Zhang, J.Y. Lin (MHZU 24-0441; holotype); ZHKUCC 24-0770, ex-type; living culture, ZHKUCC 24-0771.

Notes – In the phylogenetic analysis of the *Fusarium nisikadoi* species complex (Fig. 4), our strains formed a single lineage with 100% ML bootstrap support and 1.00 BYPP values close to *F. commune*, *F. gaditjirri* and *F. lyarnte*. Our strains (21–52 × 2–5 µm) differ from their related species by developing larger macroconidia than that of *F. commune* (24–30 × 3.8–4.1 µm) (Skovgaard et al. 2003), and smaller macroconidia than that of *F. gaditjirri* (40–70 × 3–5 µm) (Phan et al. 2004) and *F. lyarnte* (45–65 × 2–5 µm) (Walsh et al. 2010). In addition, the nucleotide of *F. anoectochili* (ZHKUCC 24-0770) differs from *F. commune* (AAS 156) by 21.3% (336/1575) variations in *rpb1*, 3.06% (54/1762) variations in *rpb2*, and 4.51% (24/532) variations in *tub2*, differs from *F. lyarnte* (CBS 125536) by 7.63% (471616) variations in *tef1-α*, 3.35% (53/1581) variations in *rpb1*, and 4.48% (79/1762) variations in *rpb2*, differs from *F. gaditjirri* (CBS 116011) by 4.76% (76/1597) variations in *rpb2*. Based on morphology, phylogeny, and sequence data, we introduce *F. anoectochili* as a new species in the *Fusarium nisikadoi* species complex.

Fusarium avenaceum (Fr.) Sacc., Syll. fung. (Abellini) 4: 713 (1886) Fig. 11

Index Fungorum number: IF161610; Facesoffungi number: FoF16731

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 11–36(–39) × 3–6 µm ($\overline{x}$ = 24 × 5 µm, n = 50); *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (1–)3–5(–6)-septate-septate, hyaline; 1-septate conidia: 44 × 4 µm (n = 1); 2-septate conidia: 26–39 × 3–5 µm ($\overline{x}$ = 31 × 3 µm, n = 50); 3-septate conidia: 31–45(–48) × 4–5 µm ($\overline{x}$ = 38 × 4 µm, n = 50); 4-septate conidia: 37–53 (–56) × 4–5 µm ($\overline{x}$ = 44 × 4 µm, n = 50); 5-septate conidia: 42–57 × 4–5 µm

($\overline{x}$ = 49 × 4 µm, n = 50). 6-septate conidia: 41–52 × 4–5 µm ($\overline{x}$ = 47 × 4 µm, n = 3). *Conidiogenous cells* subcylindrical, smooth and thin-walled, molophialides, 13–32(–34) × 2–4 µm ($\overline{x}$ = 21 × 3 µm, n = 50). *Aerial microconidia* in small false heads, obovoid, fusiform, obovoid and reniform, 0–3-septate; 0-septate conidia: 7–15(–17) × 3–5 µm ($\overline{x}$ = 12 × 3 µm, n = 50); 1-septate conidia: 14–27 × 2–4 µm ($\overline{x}$ = 19 × 3 µm, n = 50); 2-septate conidia: 19–32 × 3–4 µm ($\overline{x}$ = 26 × 4 µm, n = 50); 3-septate conidia: 24–35 × 3–4 µm ($\overline{x}$ = 29 × 4 µm, n = 20). *Chlamydospores* subglobose to globose, intercalarily or terminally, singly or in pairs, 4–15 × 4–14 µm ($\overline{x}$ = 9 × 9 µm, n = 50). Sexual morph: not observed.

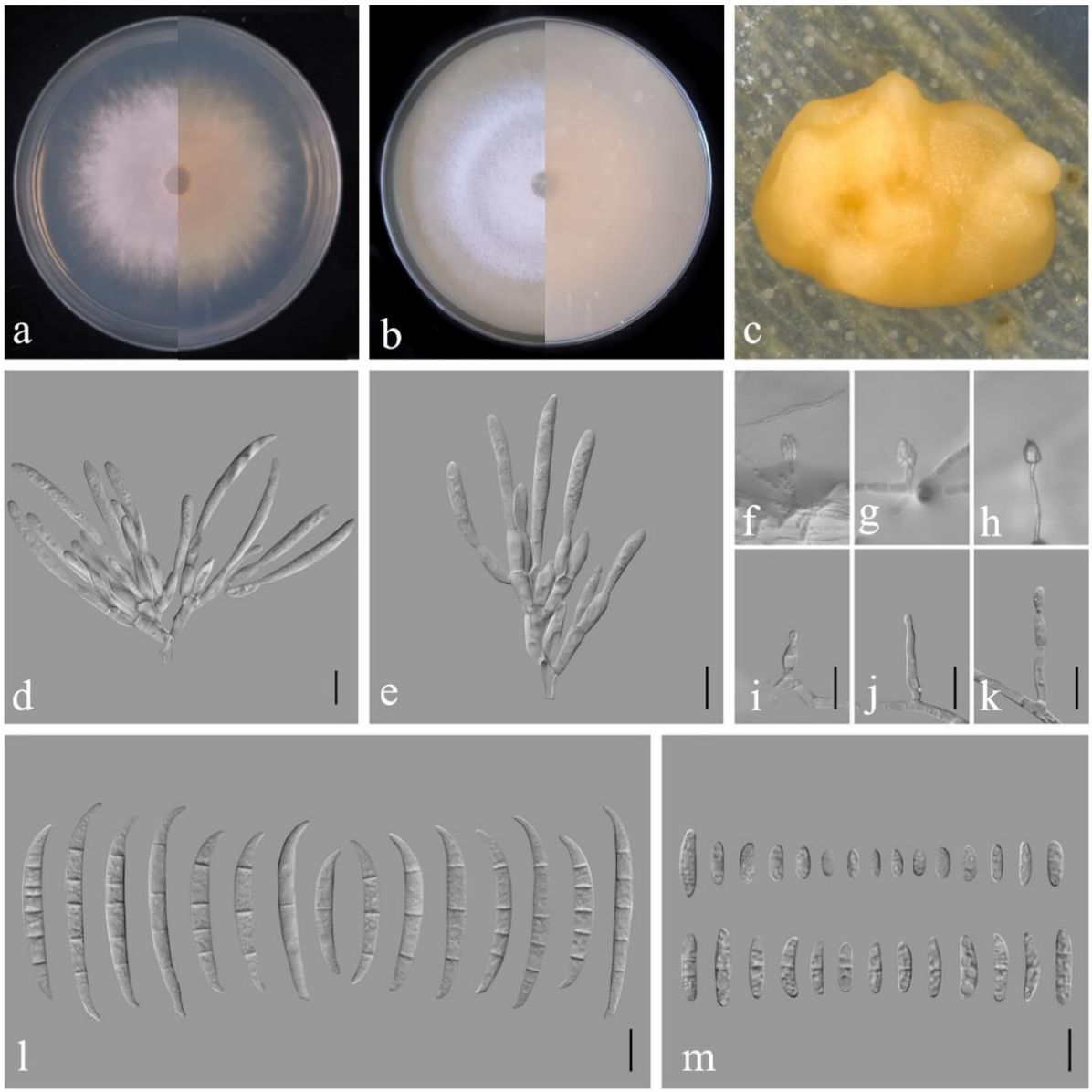

Figure 10 – *Fusarium anoectochili* (ZHKUCC 24-0770, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Sporodochia on carnation leaves. d–e Conidiophores and phialides on sporodochia. f–h Aerial conidial false heads. i–k Aerial conidiophores phialides and polyphialides. l Sporodochial macroconidia. m Aerial microconidia. Scale bars: 10 µm.

Culture characteristics – Colonial growth rate on PDA was 6 mm/d at 25 ℃. Surface view: brown with white margin, floccose. In reverse, brown in the centre. Sporodochia produced on CLA after 30 days.

Material examined – China, Guangdong Province, Meizhou City, on a leaf of *Hydrangea macrophylla* (*Hydrangeaceae*), 3 June 2023, Y.X. Zhang, and J.Y. Lin; living cultures, ZHKUCC 24-0774, and ZHKUCC 24-0775.

Notes – In the phylogenetic analysis of the *Fusarium tricinctum* species complex (Fig. 6), our strains clustered with *F. avenaceum* with 100% ML bootstrap support and 1.00 BYPP values. Morphologically, our strains share similarities to *F. avenaceum* (Leslie & Summerell 2006). Based on phylogeny and morphology, we introduce our isolates as *F. avenaceum*. *Fusarium avenaceum* is commonly recovered from soil (Leslie & Summerell 2006). This species is the causal organism of stem and stub rot of carnations and *Eustoma grandiflorum*, *Allium giganteum* bulb rot, head blight of wheat, and other diseases of broccoli, Douglas fir and lentils (Broadhurst 1990, Leslie & Summerell 2006, Zhang et al. 2016). To our knowledge, this is the first record of *F. avenaceum* isolated from *Hydrangea macrophylla*.

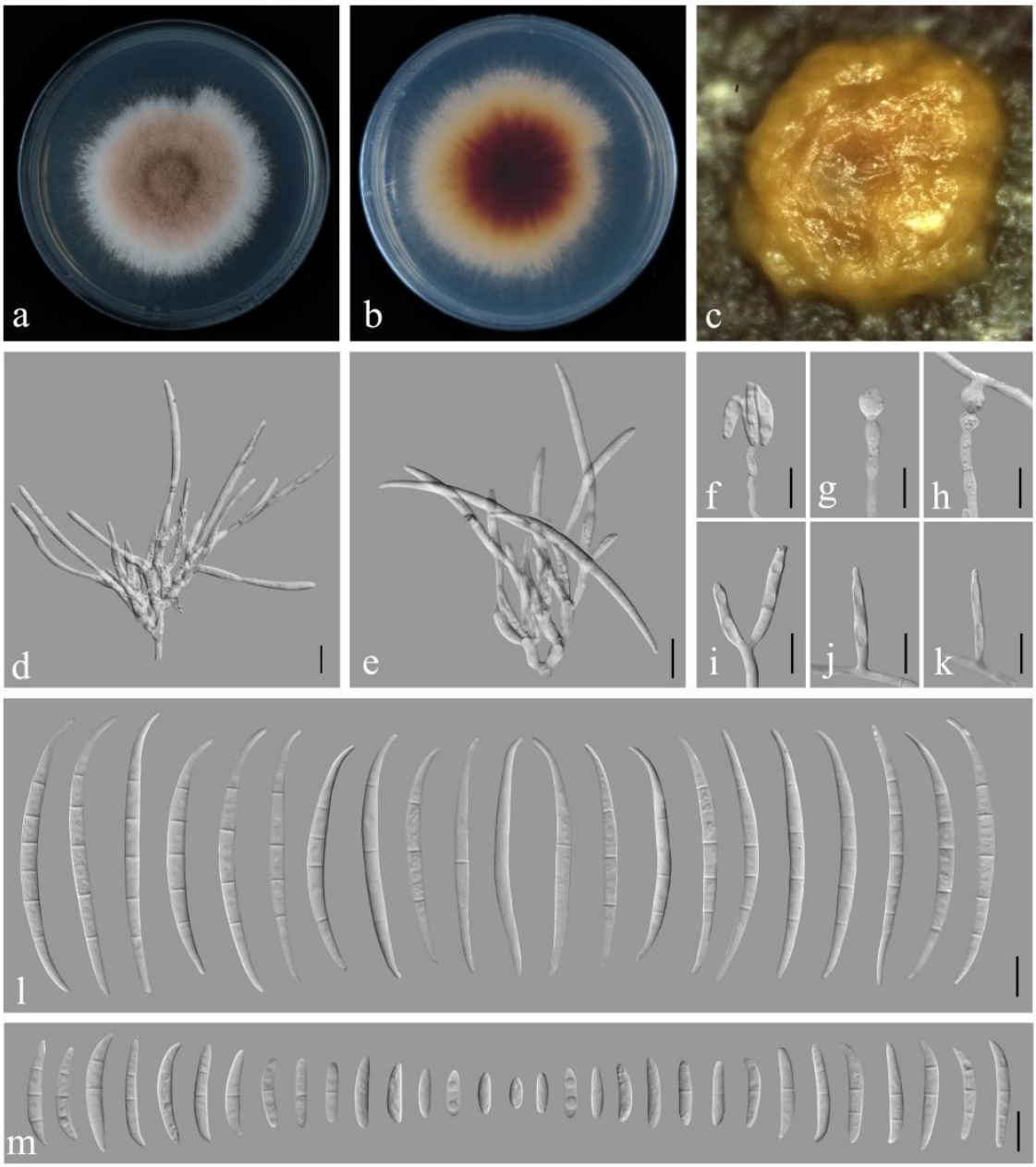

Figure 11 – *Fusarium avenaceum* (ZHKUCC 24-0774). a–b 7-day-old PDA culture (surface, reverse). c. Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Fusarium concentricum Nirenberg & O'Donnell, Mycologia 90(3): 442 (1998) Fig. 12

Index Fungorum number: IF444884; Facesoffungi number: FoF09423

Asexual morph: Sporodochia light yellow, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 11–22 × 2–4 µm ($\overline{x}$ = 16 × 3 µm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (1–2)3–5(6)-septate, 1-septate conidia: 33–62 × 3–4 µm ($\overline{x}$ = 56 × 3 µm, n = 6); 2-septate conidia: 36–58 × 3–4 µm ($\overline{x}$ = 48 × 3 µm, n = 3); 3-septate conidia: 34–57 × 3–4 µm ($\overline{x}$ = 46 × 4 µm, n = 50); 4-septate conidia: 43–66 × 3–4 µm ($\overline{x}$ = 54 × 4 µm, n = 50); 5-septate conidia: 52–71 × 3–4 µm ($\overline{x}$ = 61 × 4 µm, n = 50); 6-septate conidia: 49–65 × 4 µm ($\overline{x}$ = 57 × 4 µm, n = 3). *Conidiogenous cells* subcylindrical, molophialides and polyphialides, (6–)9–26(–28) × 2–4 µm ($\overline{x}$ = 17 × 3 µm, n = 50). *Aerial microconidia* in small false heads, fusiform and obovoid, 0–1-septate; 0-septate conidia: 6–14 × 2–4 µm ($\overline{x}$ = 10 × 3 µm, n = 50); 1-septate conidia: (12–)14–24 × 3–4 µm ($\overline{x}$ = 10 × 3 µm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 5 mm/d at 25 ℃. Upper view: light purple, floccose, filamentous margin. In reverse; white. Sporodochia produced on CLA after 15 days.

Material examined – China, Guangdong Province, Shaoguan City, on a stem of *Spathiphyllum floribundum* (*Araceae*), 17 July 2021, YX Zhang, living culture ZHKUCC 23-0929; Guangdong Province, Zhaoqing City, on a stem of *Bougainvillea glabra* (*Nyctaginacea*e), 14 November 2021, YX Zhang, living culture ZHKUCC 23-0930; Guangdong Province, Zhaoqing City, on a stem of *Philodendron tatei* (*Araceae*), 28 February 2021, C. Chen; living culture, ZHKUCC 23-0931.

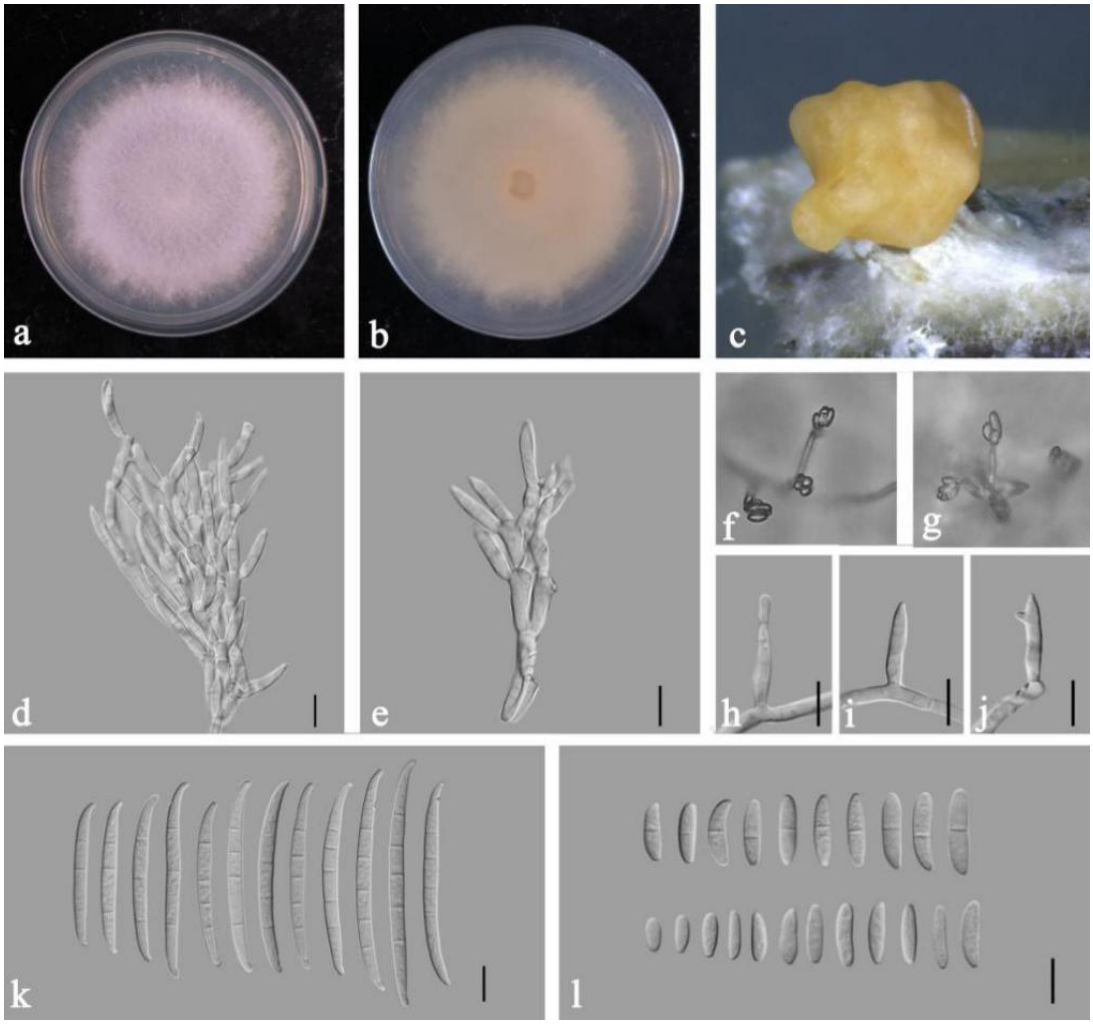

Figure 12 – *Fusarium concentricum* (ZHKUCC 23-0930). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f–g Aerial conidial

false heads. h–j Aerial conidiophores phialides and polyphialides. k Sporodochial conidia. l Aerial microconidia. Scale bars: 10 μm.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, three isolates from this study (ZHKUCC 23-0929, ZHKUCC 23-0930, ZHKUCC 23-0931) clustered with *F. concentricum* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 3). Our strains and *F. concentricum* have overlapping morphological characteristics (Nirenberg & O'Donnell 1998) thus we identified our strains as *F. concentricum*. *Fusarium concentricum* was described from *Musa sapientum* (Nirenberg & O'Donnell 1998). This species is associated with a variety of host diseases, including pepper (*Capsicum annuum*) and banana (*Musa* sp.), *Paris polyphylla*, and maize (*Hibiscus sabdariffa*) (Wang et al. 2013, Abd Murad et al. 2017, Xiao et al. 2019, Du et al. 2020, Huda-Shakirah et al. 2020). To our knowledge, this is the first report of *F. concentricum* on *Spathiphyllum floribundum*, *Bougainvillea glabra*, and *Philodendron tatei* worldwide.

Fusarium contaminatum L. Lombard & Crous, Persoonia 41: 20 (2018) Fig. 13

Index Fungorum number: IF826836; Facesoffungi number: FoF16732

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 9–17(–19) × 3–5 μm ($\overline{x}$ = 13 × 4 μm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, 3–5-septate, 3-septate conidia: 33–48 × 4–6 μm ($\overline{x}$ = 39 × 5 μm, n = 50); 4-septate conidia: 36–52(–60) × 4–5 μm ($\overline{x}$ = 44 × 4 μm, n = 50); 5-septate conidia: 40–53 × 4–6 μm ($\overline{x}$ = 46 × 5 μm, n = 50). *Conidiogenous cells* subulate to subcylindrical, molophialides, 3–21 × 2–4 μm ($\overline{x}$ = 10 × 3 μm, n = 50). *Aerial microconidia* in small false heads, oval to reniform, 0–1(–2)-septate; aseptate conidia: 5–15 × 2–4(–5) μm ($\overline{x}$ = 8 × 3 μm, n = 50); 1-septate conidia: (9–)11–19 × 3–5 μm ($\overline{x}$ = 14 × 4 μm, n = 50); 2-septate conidia: 15–21(–26)× 3–5(–6) μm ($\overline{x}$ = 18 × 5 μm, n = 16). *Chlamydospores* globose to subglobose, single or in chains, (6–)8–12 × 5–10 μm ($\overline{x}$ = 9 × 8 μm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 6 mm/d at 25 ℃. Surface view: light purple, floccose, filamentous margin. In reverse; purple and white at margin. On CLA, Orange sporodochia produced after 20 days.

Material examined – China, Guangdong Province, Guangzhou City, on the root of *Anoectochilus roxburghii* (*Orchidaceae*), 1 March 2022, ZB Zhuang, living culture ZHKUCC 23-0904. China, Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, on leaves of *Zygocactus truncatus* (Cactaceae), 2 November 2021, L. Li, and N. Mo; living cultures, ZHKUCC 23-0888, ZHKUCC 23-0889, and ZHKUCC 23-0890.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, our strains clustered with *F. contaminatum* (Fig. 5). Our strains have larger 3-septate macroconidia ($\overline{x}$ = 39 × 5 μm) than *F. contaminatum* ($\overline{x}$ = 23 × 4 μm) and 4–5-septate macroconidia as described by Lombard et al. (2019). However, considering the lack of significant morphological variations and phylogenetic placement, we identified our collection as *F. contaminatum*. *Fusarium contaminatum* was identified only from contaminated food products (Lombard et al. 2019). This is the first report of *F. contaminatum* associated with *Anoectochilus roxburghii* and *Zygocactus truncatus*.

Fusarium curvatum L. Lombard & Crous, Persoonia 41: 21 (2018) Fig. 14

Index Fungorum number: IF826837; Facesoffungi number: FoF16733

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 10–21 × 3–4 μm ($\overline{x}$ = 16 × 3 μm, n = 50). *Sporodochial conidia* apical cell blunt to curved, basal cell blunt to foot-shaped, (0–)1–5-septate, aseptate conidia: 25–39(–42)× 3–5 μm ($\overline{x}$ = 32 × 4 μm, n = 20); 1-septate conidia: 29–41 × 3–5 μm ($\overline{x}$ = 34 × 4 μm, n = 50); 2-septate conidia: 31–36 × 4–5 μm ($\overline{x}$ = 33 × 4 μm, n = 2); 3-septate conidia: 30–41 × 4–5 μm ($\overline{x}$ = 36 × 4 μm, n = 50); 4-septate conidia: 35–45 × 4–5 μm ($\overline{x}$ = 40 × 4 μm, n = 50); 5-septate conidia: (26–)34–48 × 4–6 μm ($\overline{x}$ = 41 × 4 μm, n = 50).

Conidiogenous cells subcylindrical, molophialides and polyphialides, 5–23(–25) × 2–4 µm ($\overline{x}$ = 12 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval to reniform, 0–2-septate; aseptate conidia: 5–13 × 2–4 µm ($\overline{x}$ = 8 × 3 µm, n = 50); 1-septate conidia: 11–17(–20) × 3–5 µm ($\overline{x}$ = 14 × 4 µm, n = 50); 2-septate conidia: 16–20 × 4–5 µm ($\overline{x}$ = 18 × 4 µm, n = 6). *Chlamydospores* globose to subglobose, single or in clumps, 6–11 × 6–12 µm ($\overline{x}$ = 8 × 8 µm, n = 50). Sexual morph: not observed.

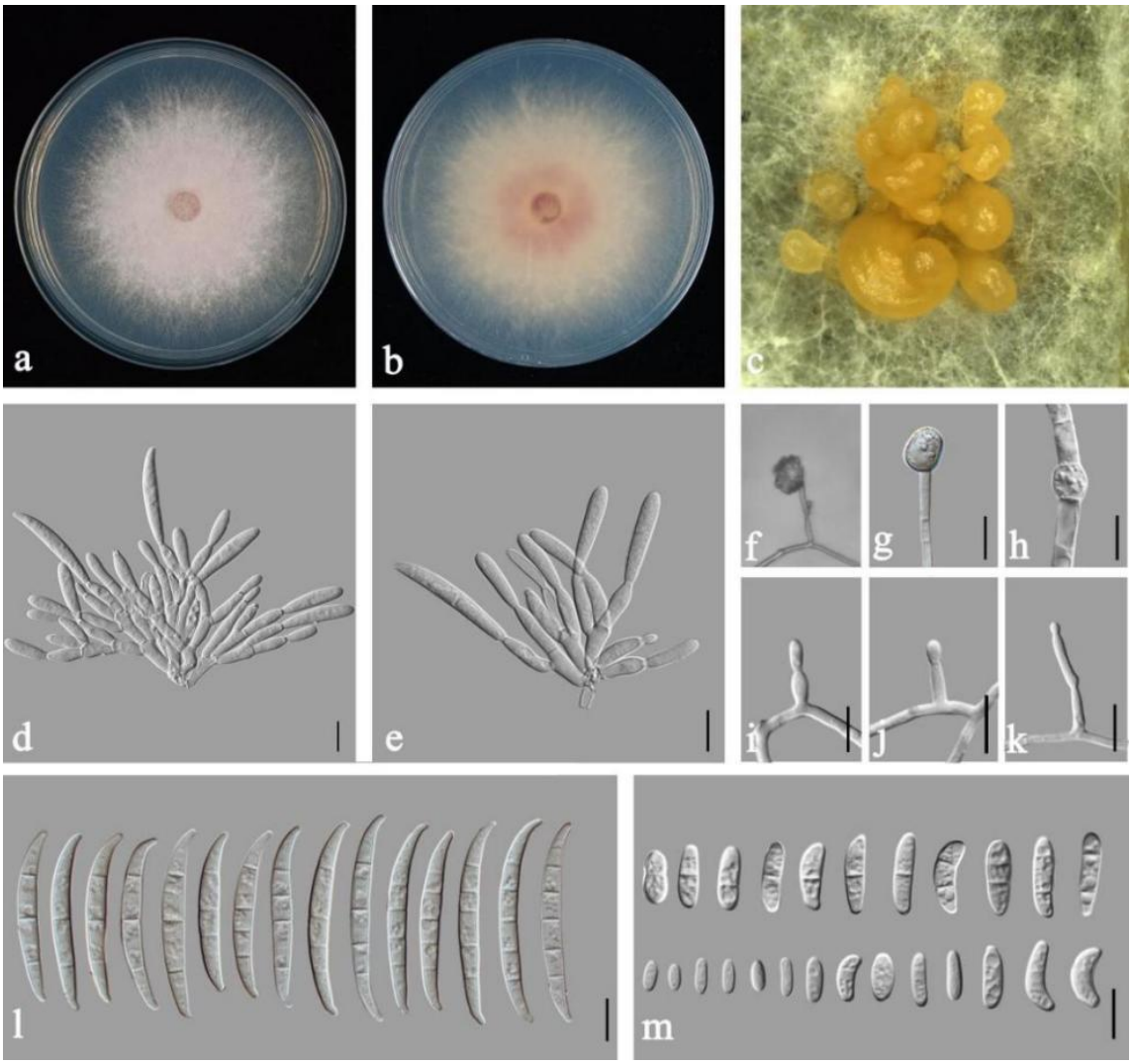

Figure 13 – *Fusarium contaminatum* (ZHKUCC 23-0904). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Conidiophores and phialides on sporodochia. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 µm.

Culture characteristics – Growth rate on PDA was 7 mm/d at 25 ℃. Surface view: white, sparse, filamentous margin. In reverse; white. Sporodochia produced on CLA after 40 days.

Material examined – China, Guangdong Province, Guangzhou City, on a leaf of *Cymbidium sinense* (*Orchidaceae*), 1 October 2021, Y.X. Zhang (living culture ZHKUCC 23-0912); Guangdong Province, Dongguan City, on a stem of *Dendrobium* sp. (*Orchidaceae*), 9 December 2021, Y.X. Zhang, J.Y. Lin, C. Chen; living culture, ZHKUCC 23-0913.

Notes – The isolates, ZHKUCC 23-0912, and ZHKUCC 23-0913 obtained in the study were preliminarily identified as belonging to the *Fusarium oxysporum* species complex. In the phylogenetic analysis, these two strains clustered with *F. curvatum* with 93% in ML and 1.00 BYPP value (Fig. 5). Morphologically, our strains differ from *F. curvatum* (Lombard et al. 2019)

by producing 0–1-septate macroconidia while other characteristics are similar. Based on these facts, our isolates were identified as *F. curvatum.* To date, this species has been reported from *Beaucarnea* sp., *Matthiola incana* and *Hedera helix* (Lombard et al. 2019). Herein we report *F. curvatum* isolated from *Dendrobium* sp. for the first time.

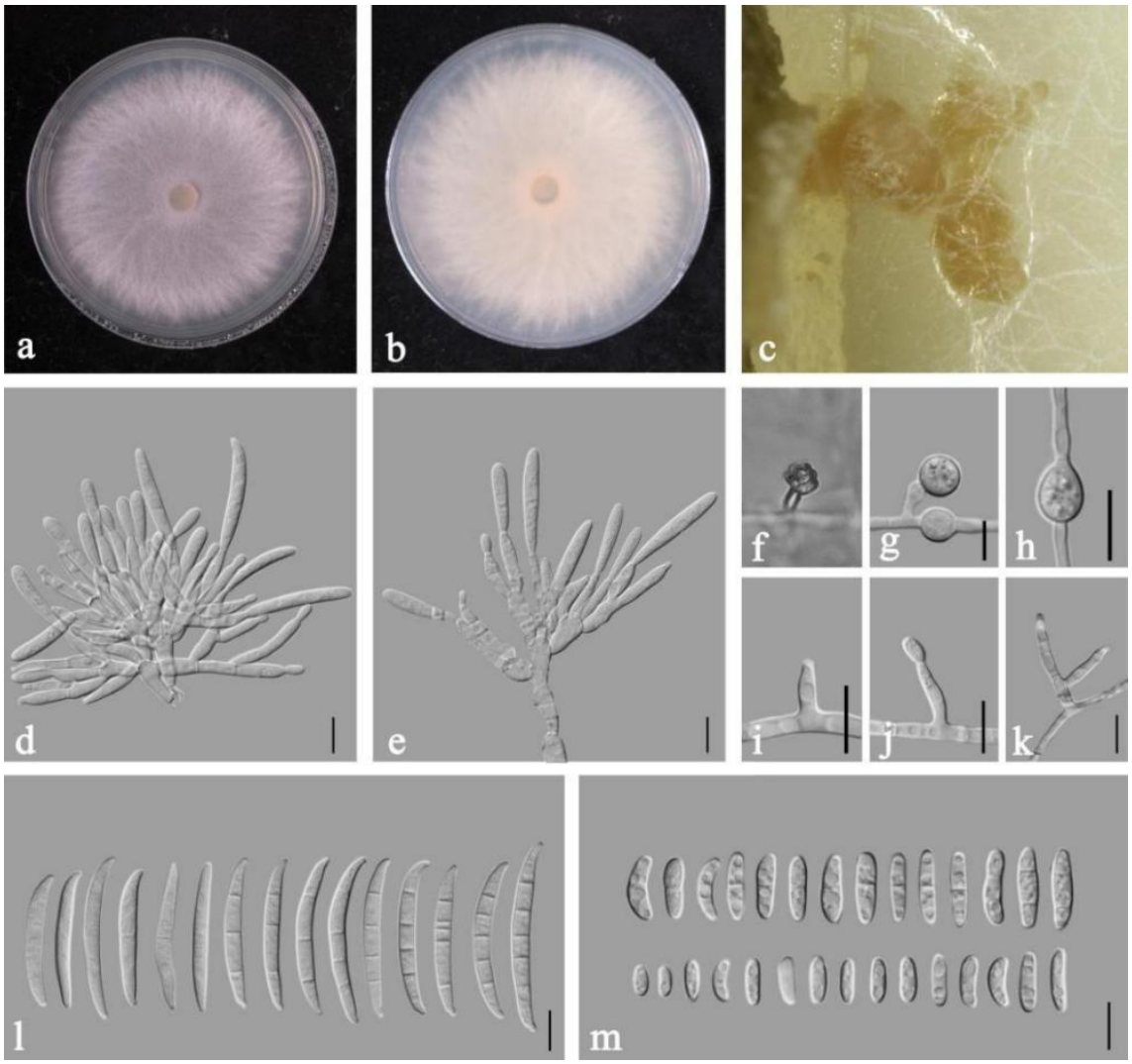

Figure 14 – *Fusarium curvatum* (ZHKUCC 23-0912). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Fusarium cymbidii Y.X. Zhang, K.D Hyde, C. Chen & Manawas., sp. nov. Fig. 15

Index Fungorum number: IF902563; Facesoffungi number: FoF16625

Etymology –Referring to the host of this fungus, *Cymbidium sinense*.

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* verticillately branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* subcylindrical, 10–16 × 2–4 μm ($\overline{x}$ = 13 × 3 μm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (0–)1–3(–5)-septate, hyaline; aseptate conidia: 30–38 × 3–4 μm ($\overline{x}$ = 34 × 3 μm, n = 2); 1-septate conidia: 21–37(–40) × 2–4 μm ($\overline{x}$ = 27 × 3 μm, n = 50); 2-septate conidia: 26–39 × 3–5 μm ($\overline{x}$ = 31 × 3 μm, n = 50); 3-septate conidia: 37–51(–53) × 4–5 μm ($\overline{x}$ = 46 × 4 μm, n = 50); 4-septate conidia: 37–42 × 4–5 μm ($\overline{x}$ = 39 × 5 μm, n = 2); 5-septate conidia: 47–57 × 4–6 μm ($\overline{x}$ = 50 × 4 μm, n = 3). Aerial conidiophores are unbranched and often reduced to single phialides. *Conidiogenous cells* subcylindrical,

monophialides and polyphialides, 3–21(–24) × 2–4 µm ($\bar{x}$ = 11 × 3 µm, n = 50). *Aerial microconidia* in small false heads, fusiform, reiform and obovoid, aseptate, (2–)5–15(–17) × 2–4 µm ($\bar{x}$ = 9 × 3 µm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Colonial growth rate on PDA was 5 mm/d at 25 ℃. Surface view: light pink, floccose, filamentous margin. In reverse; pink in the centre. Sporodochia produced on CLA after 30 days. Colonial growth rate on OA was 4 mm/d at 25 ℃. Colony surface yellow in the center, white at the margin, aerial mycelia flat, dense, and margin entire; reverse white.

Material examined – China, Guangdong Province, Meizhou City, on a leaf of *Cymbidium sinense* (*Orchidaceae*), 26 October 2021, YX Zhang, JY Lin (MHZU 23-0220; holotype); ex-type, ZHKUCC 23-0914; living cultures, ZHKUCC 23-0915 and ZHKUCC 23-0916.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, three isolates from our study formed a lineage with 100% ML bootstrap support and 1.00 BYPP values close to *F. ananatum* and *F. guttiforme* (Fig. 3). Our strain produces (0–)1–3(–5)-septate macroconidia from sporodochia, whereas *F. ananatum* only produces 1–3-septate macroconidia on aerial mycelium (Jacobs et al. 2010) and macroconidia are absent in *F. guttiforme* (Nirenberg & O'Donnell 1998). Furthermore, macroconidia of our strains are larger (21–51 × 2–5 µm) than those of *F. ananatum* (16–31 × 3–6 µm) (Jacobs et al. 2010). Based on these variations, we introduce our isolates as new species in the *Fusarium fujikuroi* species complex.

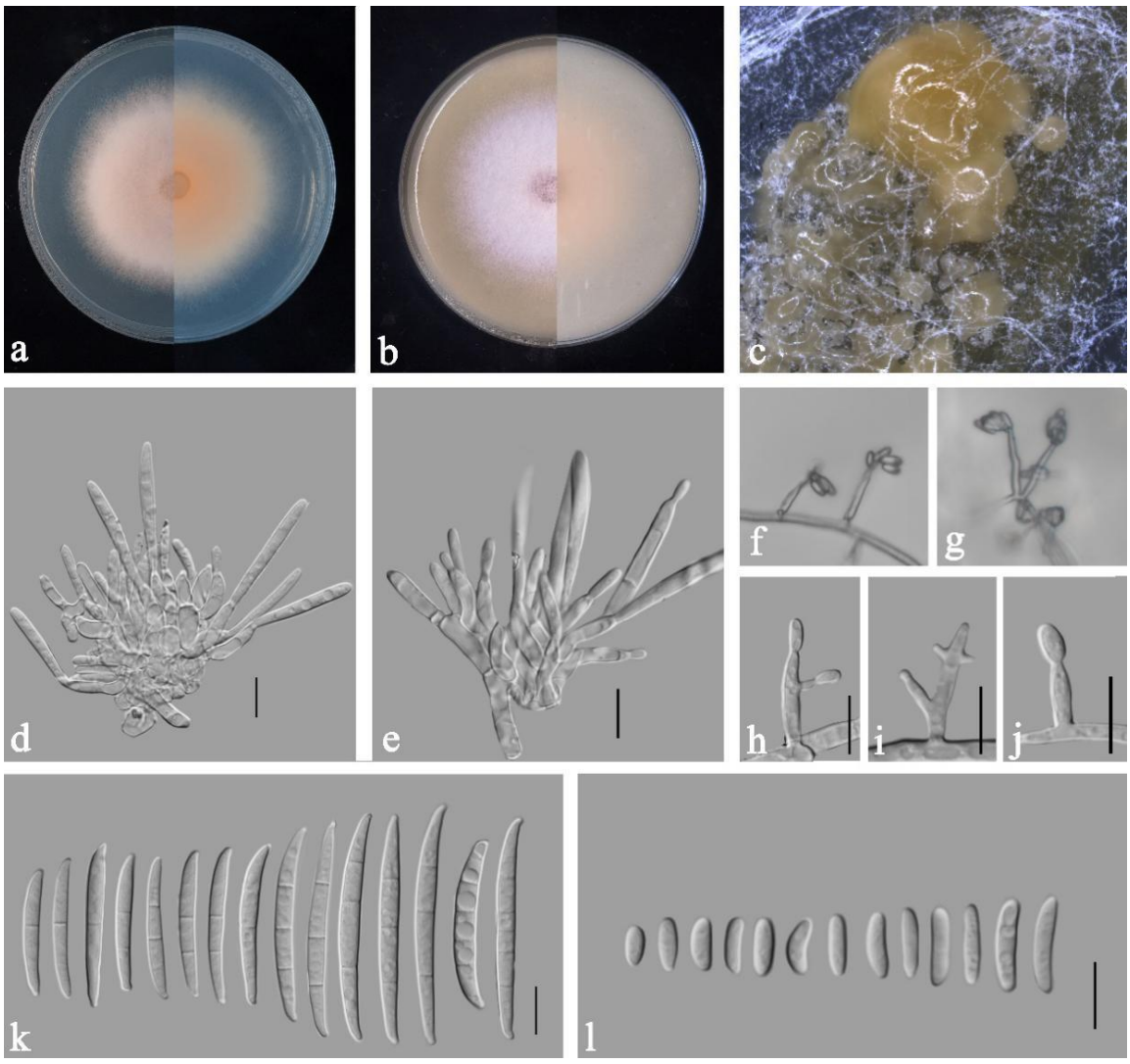

Figure 15 – *Fusarium cymbidii* (ZHKUCC 23-0914, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia

conidiophores, phialides. f–g Aerial conidial false heads. h–j Aerial conidiophores phialides and polyphialides. k Sporodochial conidia. l Microconidia. Scale bars = 10 μm.

Fusarium dendranthematis Y.X. Zhang, K.D. Hyde, C. Chen & Manawas., sp. nov.

Index Fungorum number: IF902565; Facesoffungi number: FoF16626

Etymology – Referring to the host of this fungus, *Dendranthema morifolium*.

Asexual morph: *Conidiophores*: Not observed. *Sporodochial conidiogenous cell*: Not observed. *Sporodochial conidia*: Not observed. *Aerial microconidia*: Not observed. *Chlamydospores* single or in pairs, chained or fascicled, yellowish-brown, globose to subglobose, 4–15 × 4–14 μm ($\overline{x}$ = 9 × 9 μm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 6 mm/d at 25 ℃. Surface view: white, floccose, filamentous margin. In reverse; lemon yellow in the centre. Colonial growth rate on OA was 3 mm/d at 25 ℃. Colony surface yellow in the center, white at the margin, aerial mycelia raised, dense, with an undulate margin; reverse white.

Material examined – China, Guangdong Province, Meizhou City, on a leaf of *Dendranthema morifolium* (*Asteraceae*), 15 May 2023, Y.X. Zhang, J.Y. Lin (MHZU 24-0442; holotype, dried culture); ZHKUCC 24-0772, ex-type; living culture, ZHKUCC 24-0773.

Notes – In the phylogenetic analysis of the *Fusarium tricinctum* species complex, two strains from this study were close to *F. iranicum*, *F. petersiae* and *F. flocciferum* with 100% ML bootstrap support and 1.00 BYPP values (Fig. 6). Our strains did not produce macroconidia and microconidia, which were observed in. *F. iranicum*, *F. petersiae* and *F. flocciferum* (Torbati et al. 2019, Crous et al. 2017, Gerlach & Nirenberg 1982) in any of the media which we were used in the present study. Therefore, the identification of these isolates was based on phylogenetic analyses and sequence comparisons. We compared nucleotide differences between our strains (ZHKUCC 24-0772) and *F. iranicum* (CBS 143608), which is closely related to our strain in the phylogenetic analyses, in which they differ by 1.81% (9/496) variations in *tef1-α*, differs from *F. petersiae* (CBS 143231) by 1.69% (11/650) variations in *tef1-α*, 1.47% (22/1500) variations in *rpb1*, and 5.20% (26/500) variations in *tub2*, differs from *F. flocciferum* (CBS 831.85) by 1.40% (22/1575) variations in *rpb1*. Based on phylogeny and sequence data we introduce *F. dendranthematis* as a new species in the *Fusarium tricinctum* species complex.

Fusarium dendrobii Y.X. Zhang, K.D. Hyde L.T. Nie & Manawas., sp. nov. Fig. 16

Index Fungorum number: IF902566; Facesoffungi number: FoF16627

Etymology – Referring to the host of this fungus, *Dendrboium* sp.

Asexual morph: *Sporodochia* not observed. *Aerial conidiophores* unbranched often reduced to single phialides. *Conidiogenous cells* subcylindrical, molophialides and polyphialides, 7–29 × 2–4 μm ($\overline{x}$ = 16 × 3 μm, n = 50). *Aerial microconidia* in small false heads, oval, fusiform, 0-septate conidia: 5–16 × 2–3 μm ($\overline{x}$ = 9 × 3 μm, n = 50). *Chlamydospores* not observed. Sexual morph: Not observed. Sexual morph: not observed.

Culture characteristics – Colonial growth on PDA was 6 mm/d at 25 ℃. Surface view: light purple, floccose, regular margin. In reverse; purple in the centre, white at the margin. Colonial growth rate on OA was 4 mm/d at 25 ℃. Colony surface light amaranth in the center, aerial mycelia flat, with an undulate margin. Reverse light amaranth to white.

Material examined – China, Guangdong Province, Jieyang City, on a stem of *Dendrboium* sp. (*Orchidaceae*), 30 May 2023, YX Zhang, LT Nie (MHZU 24-0010, holotype); ZHKUCC 24-0047, ex-type; living culture, ZHKUCC 24-0048.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, our isolates (ZHKUCC 24-0047 and ZHKUCC 24-0048) formed a sister clade to *F. konzum* and *F. babinda*, with 1.00 BYPP value (Fig. 3). Morphologically, *F. dendrobii* differs from its related species by the presence of sporodochia and macroconidia (absent in *F. dendrobii*) (Zeller et al. 2003, Summerell et al. 1995). In addition, *F. dendrobii* differs from *F. konzum* in the size and shape of microconidia (oval to fusiform, 5–16 × 2–3 μm in *F. dendrobii* vs oval, 7–10 × 2–5 μm; pyriform, 3–6 × 3–8;

napiform to globose, 5–6 µm in diam in *F. konzum*) (Zeller et al. 2003). Based on these variations we introduce our strains as a new species.

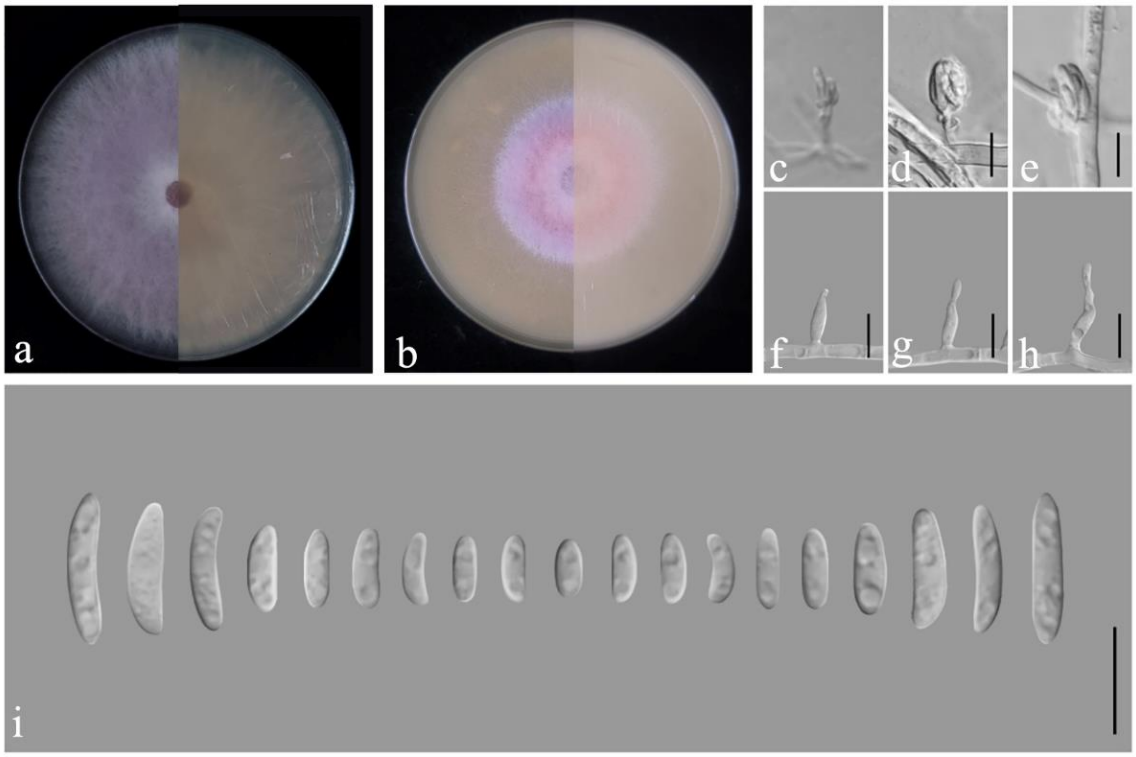

Figure 16 – *Fusarium dendrobii* (ZHKUCC 24-0047, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c–e Aerial conidial false heads. f–h Aerial conidiophores phialides. i Aerial microconidia. Scale bars = 10 µm.

Fusarium duoseptatum Maryani, L. Lombard, Kema & Crous, Stud. Mycol. 92: 181 (2018) Fig. 17

Index Fungorum number: IF826804; Facesoffungi number: FoF16734

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* doliiform to subcylindrical, 8–15 × 3–5 µm ($\overline{x}$ = 11 × 4 µm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (1–2)3–5(–6)-septate, 1-septate conidia: 32–42 × 4–5 µm ($\overline{x}$ = 36 × 4 µm, n = 7); 2-septate conidia: 33–39 × 4–5 µm ($\overline{x}$ = 37 × 5 µm, n = 6); 3-septate conidia: 32–46 × 3–5 µm ($\overline{x}$ = 38 × 4 µm, n = 50); 4-septate conidia: 36–54 × 4–5 µm ($\overline{x}$ = 44 × 4 µm, n = 50); 5-septate conidia: 36–54 × 4–5 µm ($\overline{x}$ = 44 × 4 µm, n = 50); 6-septate conidia: 37–41 × 5 µm ($\overline{x}$ = 39 × 5 µm, n = 3). *Conidiogenous cells* subulate to subcylindrical, molophialides, (3–)6–25 × 2–4(–5) µm ($\overline{x}$ = 14 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval to reniform, 0–2-septate; aseptate conidia: 7–17 × 3–4(–5) µm ($\overline{x}$ = 10 × 3 µm, n = 50); 1-septate conidia: 13–20 × 3–4(–5) µm ($\overline{x}$ = 16 × 4 µm, n = 50); 2-septate conidia: 17–29 × 4–5 µm ($\overline{x}$ = 20 × 4 µm, n = 11). *Chlamydospores* globose to subglobose, single or in pairs, 6–11 × 5–11 µm ($\overline{x}$ = 8 × 8 µm, n = 50). Sexual morph: Not observed.

Culture characteristics – Colonial growth on PDA was 6 mm/d at 25 ℃. Surface view: light purple, floccose, filamentous margin. In reverse; light pink. Sporodochia produced on CLA after 40 days.

Material examined – China, Guangdong Province, Guangzhou City, on the root of *Strelitzia reginae* (*Musaceae*), 19 April 2021, YX Zhang, C Chen, SQ Ma, living cultures, ZHKUCC 23-0911, ZHKUCC 23-0894, ZHKUCC 23-0895, and ZHKUCC 23-0896).

Notes – In the phylogenetic analysis of *Fusarium oxysporum* species complex, four isolates from this study clustered with *F. duoseptatum* with 0.97 in BYPP support (Fig. 5). Morphologically our strains are similar to *F. duoseptatum* (Maryani et al. 2019), except the of macroconidia of our

strain was smaller than *F. duoseptatum* ($\overline{x}$ = 41 × 4 µm vs $\overline{x}$ = 58 × 7 µm). Herein, we identified our strains from *Strelitzia reginae* as *F. duoseptatum*. Previously, this species has been isolated only from *Musa* sp. (Maryani et al. 2019, Wang et al. 2022). To our knowledge, this is the first report of *F. duoseptatum* from *S. reginae*.

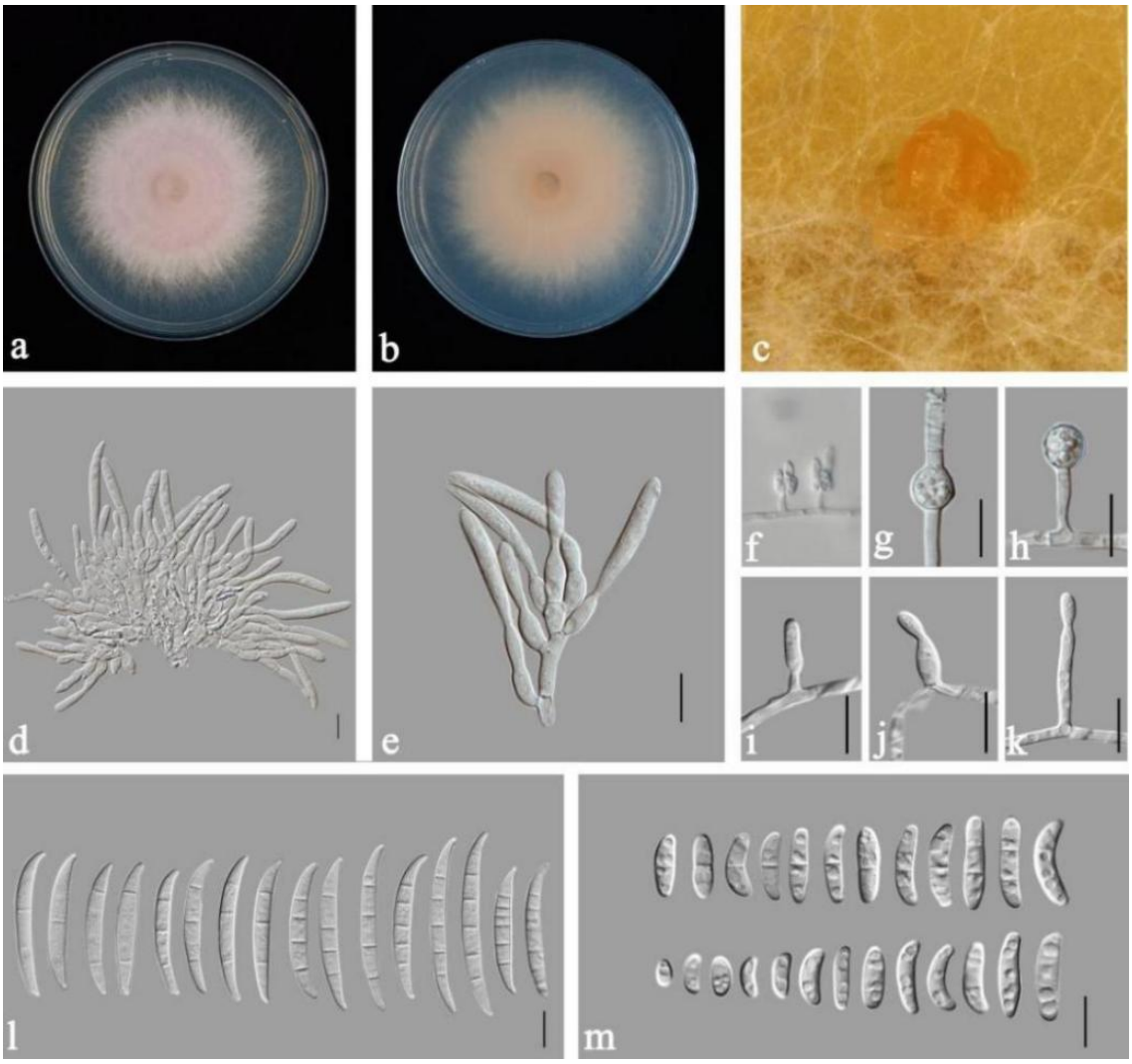

Figure 17 – *Fusarium duoseptatum* (ZHKUCC 23-0911). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 µm.

Fusarium fujikuroi Nirenberg, Mitt. Biol. BundAnst. Ld- u. Forstw. 169: 32 (1976) Fig. 18

Index Fungorum number: IF314213; Facesoffungi number: FoF16735

Asexual morph: *Sporodochia* off-white, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 10–23 × 3–4 µm ($\overline{x}$ = 14 × 3 µm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (1–2)3–5(–7)-septate, 1-septate conidia: 24–65 × 2–5 µm ($\overline{x}$ = 32 × 3 µm, n = 50); 2-septate conidia: 41–50 × 3–4 µm ($\overline{x}$ = 45 × 4 µm, n = 50); 3-septate conidia: 38–59 × 3–4 µm ($\overline{x}$ = 46 × 4 µm, n = 50); 4-septate conidia: 42–60(–63)× 3–5 µm ($\overline{x}$ = 52 × 4 µm, n = 50); 5-septate conidia: 49–66(–69)× 3–5 µm ($\overline{x}$ = 56 × 4 µm, n = 50); 6-septate conidia: 47–54 × 3–4 µm ($\overline{x}$ = 50 × 4 µm, n = 3); 7-septate conidia: 58 × 4 µm(n = 1). *Conidiogenous cells* subcylindrical, molophialides, 6–24 × 2–4 µm ($\overline{x}$ = 12 × 3 µm, n = 50). *Aerial microconidia* in small false heads or chains, oval, aseptate; aseptate

conidia: 5–19 × 2–4 µm ($\bar{x}$ = 9 × 3 µm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Colonial growth on PDA was 6 mm/d at 25 ℃. Surface view: light yellow, white at the margin, floccose, filamentous margin. In reverse; yellow. On CLA, sporodochia produced after 25 days.

Material examined – China, Guangdong Province, Zhaoqing City, on a stem of *Philodendron tatei* (*Araceae*), 28 February 2022, C Chen, living culture ZHKUCC 23-0932, ZHKUCC 23-0933.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, two isolates from this study clustered with the *F. fujikuroi* type species and other representative strains with 100% ML bootstrap support and 1.00 BYPP value (Fig. 3) while sharing overlapping morphological characteristics with *F. fujikuroi* (Yilmaz et al. 2021). Thus, our isolates are identified as *F. fujikuroi* based on both morphology and phylogenetic placement. *Fusarium fujikuroi* was introduced from *Oryza sativa* (Yilmaz et al. 2021). This species has been described from a wide range of hosts, including economically important crops including *Avena sativa*, *Bamboo* sp., *Echinochloa* sp., *Lilium* sp., and *Saccharum officinarum* (Carter et al. 2008, Maryani et al. 2019, Yilmaz et al. 2021, Wang et al. 2022). This is the first report of *F. fujikuroi* isolated from *Philodendron tatei.*

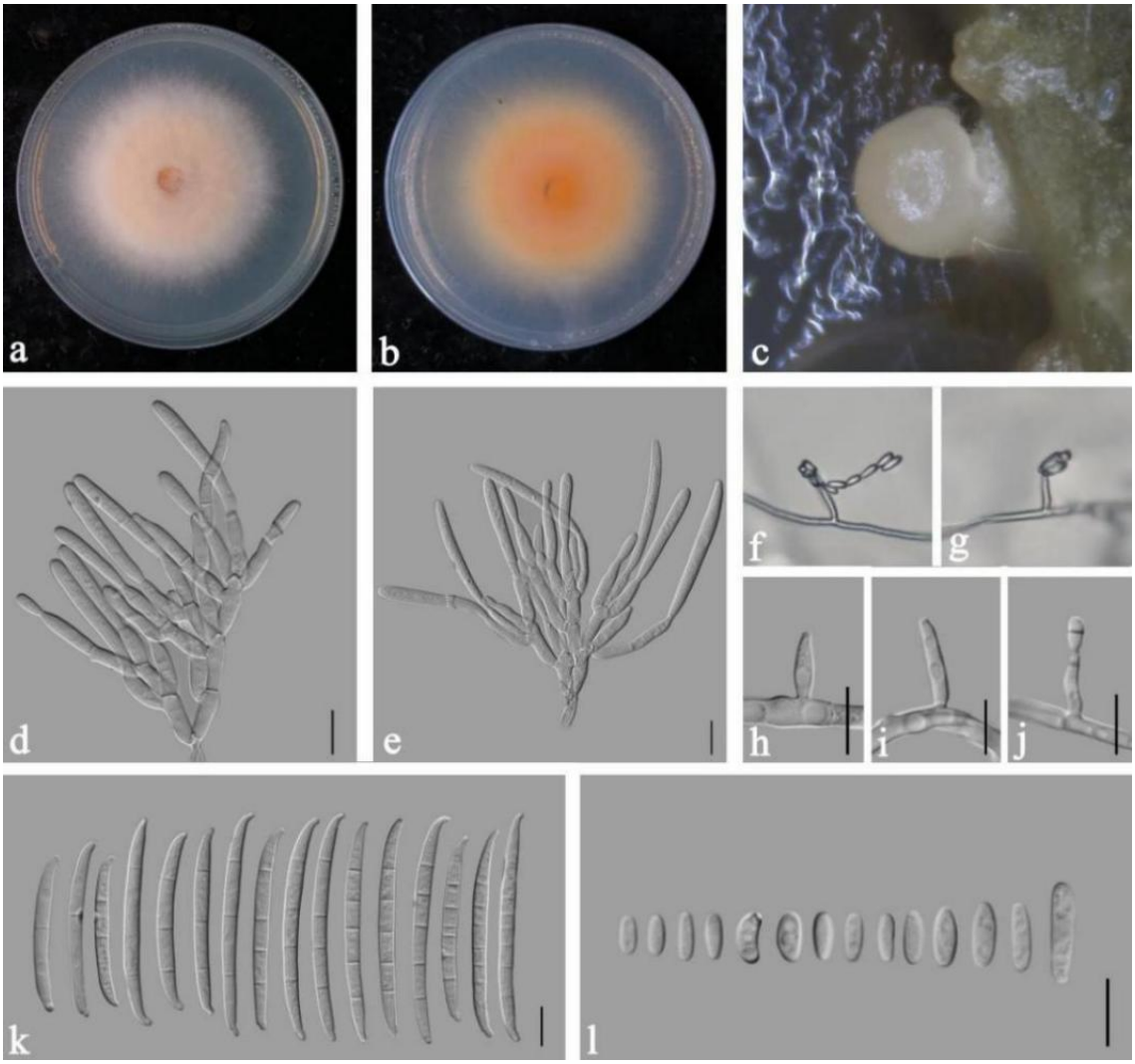

Figure 18 – *Fusarium fujikuroi* (ZHKUCC 23-0932). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Conidiophores and phialides on sporodochia. f Aerial microconidia produced in chains. g Aerial conidial chain and false head. h–j Aerial conidiophores phialides. k Macroconidia. l Microconidia. Scale bars: 10 µm.

Fusarium grosmichelii Maryani, L. Lombard, Kema & Crous, in Maryani, et al., Stud. Mycol. 92: 176 (2018) Fig. 19

Index Fungorum number: IF826803; Facesoffungi number: FoF16736

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subulate to subcylindrical, 7–15 × 3–5 µm ($\overline{x}$ = 12 × 4 µm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, 3–5-septate, 3-septate conidia: 32–47 × 3–6 µm ($\overline{x}$ = 38 × 5 µm, n = 50); 4-septate conidia: 35–51 × 4–5 µm ($\overline{x}$ = 42 × 5 µm, n = 50); 5-septate conidia: 41–59 × 4–5 µm ($\overline{x}$ = 47 × 5 µm, n = 50). *Conidiogenous cells* subcylindrical, molophialides and polyphialides, 6–20 × 2–5 µm ($\overline{x}$ = 12 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval to reniform, 0–1 septate; aseptate conidia: 5–12 × 2–4 µm ($\overline{x}$ = 8 × 3 µm, n = 50); 1-septate conidia: 9–16 × 3–5 µm ($\overline{x}$ = 12 × 4 µm, n = 50). *Chlamydospores* globose to subglobose, single or in pairs, 5–12 × 5–10 µm ($\overline{x}$ = 8 × 8 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Colonial growth on PDA was 6 mm/d at 25 ℃. Surface view: white, floccose, filamentous margin. In reverse; pink in the centre. Sporodochia produced on CLA after 23 days.

Material examined – China, Guangdong Province, Guangzhou City, on sheath of *Strelitzia reginae* (*Musaceae*), 19 April 2021, YX Zhang, C Chen, SQ Ma, living culture, ZHKUCC 23-0909); Guangdong Province, Guangzhou City, on stem of *Antirrhinum majus* (*Plantaginaceae*), 26 February 2022, JC Wang, R Li, and XD Zheng, living culture, ZHKUCC 23-0910.

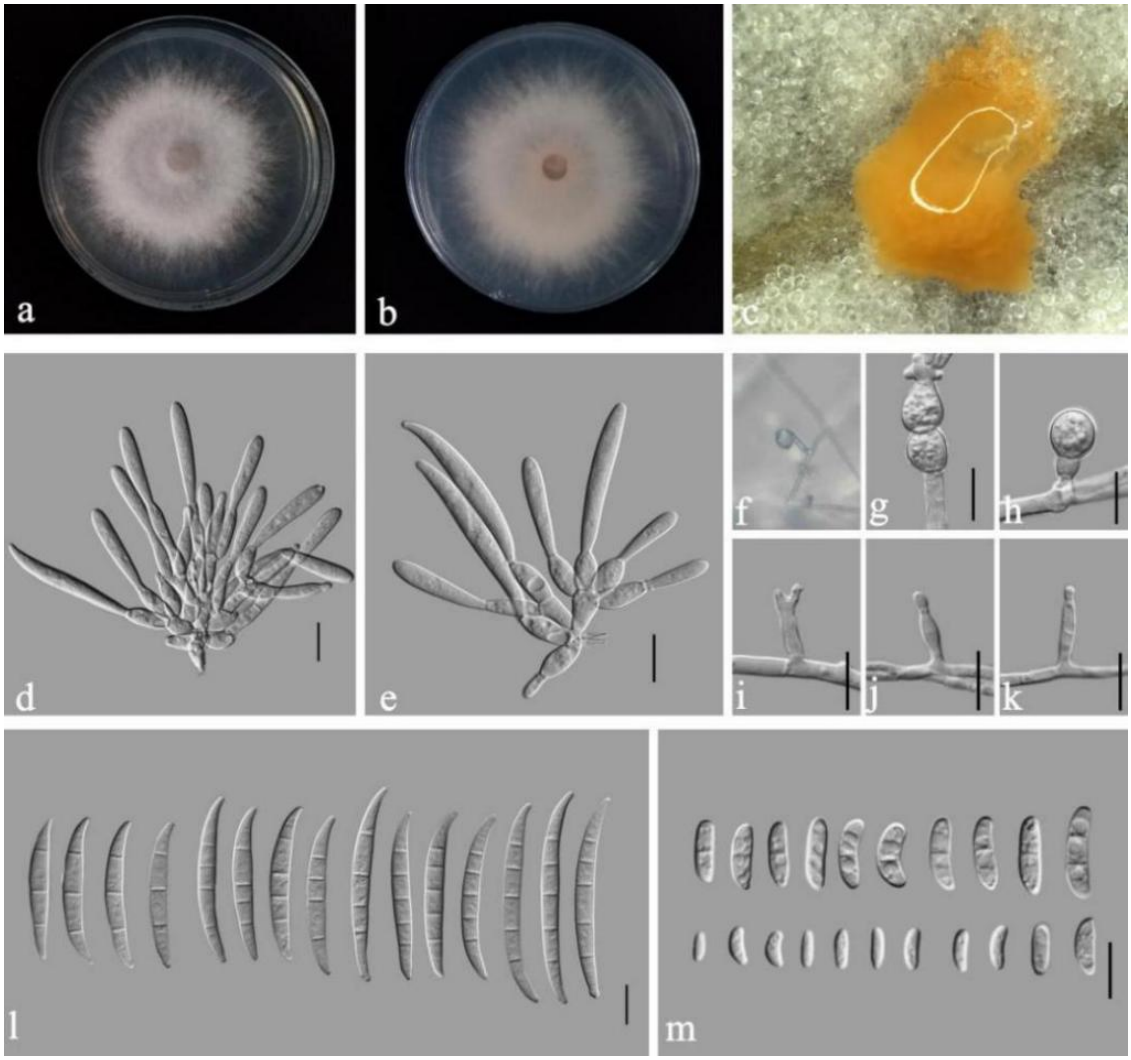

Figure 19 – *Fusarium grosmichelii* (ZHKUCC 23-0910). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false

head. g–h Chlamydospores. i–k Aerial conidiophores phialides and polyphialides. l Sporodochial conidia. m. Aerial microconidia. Scale bars: 10 μm.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, two strains belonging to this study clustered with *F. grosmichelii* (Fig. 5). Morphologically, our strains are similar to the type description of *F. grosmichelii* by Maryani et al. (2019). Thus, we identified those as *F. grosmichelii*. This species has been found only in a few plant genera, including *Musa*, *Oryza*, *Vigna* and *Tibouchina* (Maryani et al. 2019, Wang et al. 2022, Shipman 2022, Rana et al. 2022, Ujat et al. 2021, Chen et al. 2023a). Therefore, *Strelitzia reginae* and *Antirrhinum majus* are the first reported new host records of *F. grosmichelii*.

Fusarium guangdongense Y.X. Zhang, K.D. Hyde, L.T. Nie & Manawas., sp. nov. Fig. 20

Index Fungorum number: IF902567; FacesofFungi number: FoF15239

Etymology – The name refers to "Guangdong Province" where the fungus was collected.

Asexual morph: *Sporodochia* off-white, formed on CLA. *Sporodochial conidiophores* verticillately branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* subcylindrical, 10–16 × 2–4 μm ($\overline{x}$ = 13 × 3 μm, n = 50). *Sporodochial conidia* slender, apical cell curved, basal cell foot-shaped, (1–)3–7(–10)-septate, hyaline; 1-septate conidia: 70 × 4 μm (n = 1); 2-septate conidia: 70 × 4 μm (n = 1); 3-septate conidia: (32–)34–66 × 3–5 μm ($\overline{x}$ = 50 × 4 μm, n = 50); 4-septate conidia: 4–75 × 3–5 μm ($\overline{x}$ = 63 × 4 μm, n = 50); 5-septate conidia: 67–96 × 3–5 μm ($\overline{x}$ = 78 × 4 μm, n = 50); 6-septate conidia: (65–)69–101 × 3–5 μm ($\overline{x}$ = 84 × 4 μm, n = 50); 7-septate conidia: (68–)70–107 × 3–5 μm ($\overline{x}$ = 89 × 4 μm, n = 50); 8-septate conidia: 67–106(–111) × 3–5 μm ($\overline{x}$ = 88 × 4 μm, n = 23); 9-septate conidia: (80–)89–101(–120) × 4–5 μm ($\overline{x}$ = 95 × 4 μm, n = 7); 10-septate conidia: 94–100 × 4–5 μm ($\overline{x}$ = 97 × 4 μm, n = 2). *Aerial conidiophores* unbranched or rarely branched, often reduced to single phialides. *Conidiogenous cells* subcylindrical, phialides and polyphialides, (3–)4–22 × 2–4 μm ($\overline{x}$ = 13 × 3 μm, n = 50). *Aerial microconidia* in small false heads, fusiform, and obovoid, 0–1-septate; aseptate conidia: 6–16 × 4–4 μm ($\overline{x}$ = 10 × 3 μm, n = 50); 1-septate conidia: 12–20 × (3–)4–5 μm ($\overline{x}$ = 16 × 4 μm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Colonial growth on PDA was 5 mm/d at 25 ℃. Surface view: light purple to pink, floccose, regular margin. In reverse; purple in the centre, white margin. Sporodochia produced on CLA after 60 days. Colonial growth rate on OA was 4 mm/d at 25 ℃ per day. Colony surface purple in the center, white at the margin, aerial mycelia raised, dense; reverse purple in the center.

Material examined – China, Guangdong Province, Guangzhou City, on a stem of *Cymbidium* sp. (*Orchidaceae*), 17 October 2021, YX Zhang, JW Chen, C Chen (MHZU 23-0222, holotype); ZHKUCC 23-0920, ex-type; living culture ZHKUCC 23-0921; Guangdong Province, Zhongshan City, on leaf of *Dendrobium nobile* (*Orchidaceae*), 20 August 2021, YX Zhang, ZL Mai, C Chen, Jingwen Chen, living cultures, ZHKUCC 23-0917, ZHKUCC 23-0918, and ZHKUCC 23-0919; Guangdong Province, Foshan City, on leaf of *Heptapleurum heptaphyllum* (*Araliaceae*), 3 October 2021, JY Lin, living cultures, ZHKUCC 23-0922, ZHKUCC 23-0923, and ZHKUCC 23-0924.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, eight isolates formed a distinct clade which is closely related to *F. sanyaense*, *F. mangiferae* and *F. proliferatum* (Fig. 3). Our isolates differ from these closely related species by developing different numbers of septa of macroconidia and much larger macroconidia (1–10)-septate, 34–120 × 4–6 μm in our strains vs (1–4)-septate, 20–61 × 2–4 in *F. proliferatum* (Yilmaz et al. 2021) vs 3–5-septate, 25.3–67.2 × 2.7–5.1 in *F. sanyaense* (Han et al. 2023) vs 3–5-septate, 43.1–61.4 × 1.9–3.4 in *F. mangiferae* (Britz et al. 2002). Based on the phylogenetic placement and morphological variations herein, we introduce *F. guangdongense* as a novel species.

Fusarium menglaense Karun., Tibpromma & X.F. Liu, Mycosphere 14(1): 559 (2023) Fig. 21

Index Fungorum number: IF845347; Facesoffungi number: FoF13272

Asexual morph: *Sporodochia* off-white, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* sub-cylindrical, 10–16 × 2–4 µm ($\overline{x}$ = 13 × 3 µm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, (0–1)3–5(–7)-septate, hyaline; aseptate conidia: (36–)38–47 × 4–5 µm ($\overline{x}$ = 42 × 3 µm, n = 13); 1-septate conidia: 39–48 × 4–5 µm ($\overline{x}$ = 43 × 4 µm, n = 6); 2-septate conidia: 36–50 × 4–5 µm ($\overline{x}$ = 42 × 5 µm, n = 11); 3-septate conidia: 37–48(–50) × 4–5 µm ($\overline{x}$ = 42 × 4 µm, n = 50); 4-septate conidia: 37–49(–51) × 4–6 µm ($\overline{x}$ = 43 × 5 µm, n = 50); 5-septate conidia: (39–)41–55 × 4–5 µm ($\overline{x}$ = 47 × 5 µm, n = 50); 6-septate conidia: 41–50 × 4–5 µm ($\overline{x}$ = 46 × 5 µm, n = 13); 7-septate conidia: 44–4 × 5 µm ($\overline{x}$ = 46 × 5 µm, n = 2). *Conidiogenous cells* subcylindrical, molophialides, smooth and thin-walled, (3–)5–23(–27) × 2–4 µm ($\overline{x}$ = 14 × 3 µm, n = 50). *Aerial microconidia* in small false heads, reniform, fusiform and obovoid, 0–1-septate; aseptate conidia: 6–15 × 2–4 µm ($\overline{x}$ = 10 × 3 µm, n = 50); 1-septate conidia: 9–17 × 3–4 µm ($\overline{x}$ = 13 × 4 µm, n = 50). *Chlamydospores* globose to subglobose, single or in pairs, 7–16 × 7–15 µm ($\overline{x}$ = 11 × 11 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 5 mm/d at 25 ℃. Surface view: light purple in the centre, floccose, filamentous margin. In reverse; purple in the centre, white at the margin. Sporodochia produced on CLA after 30 days.

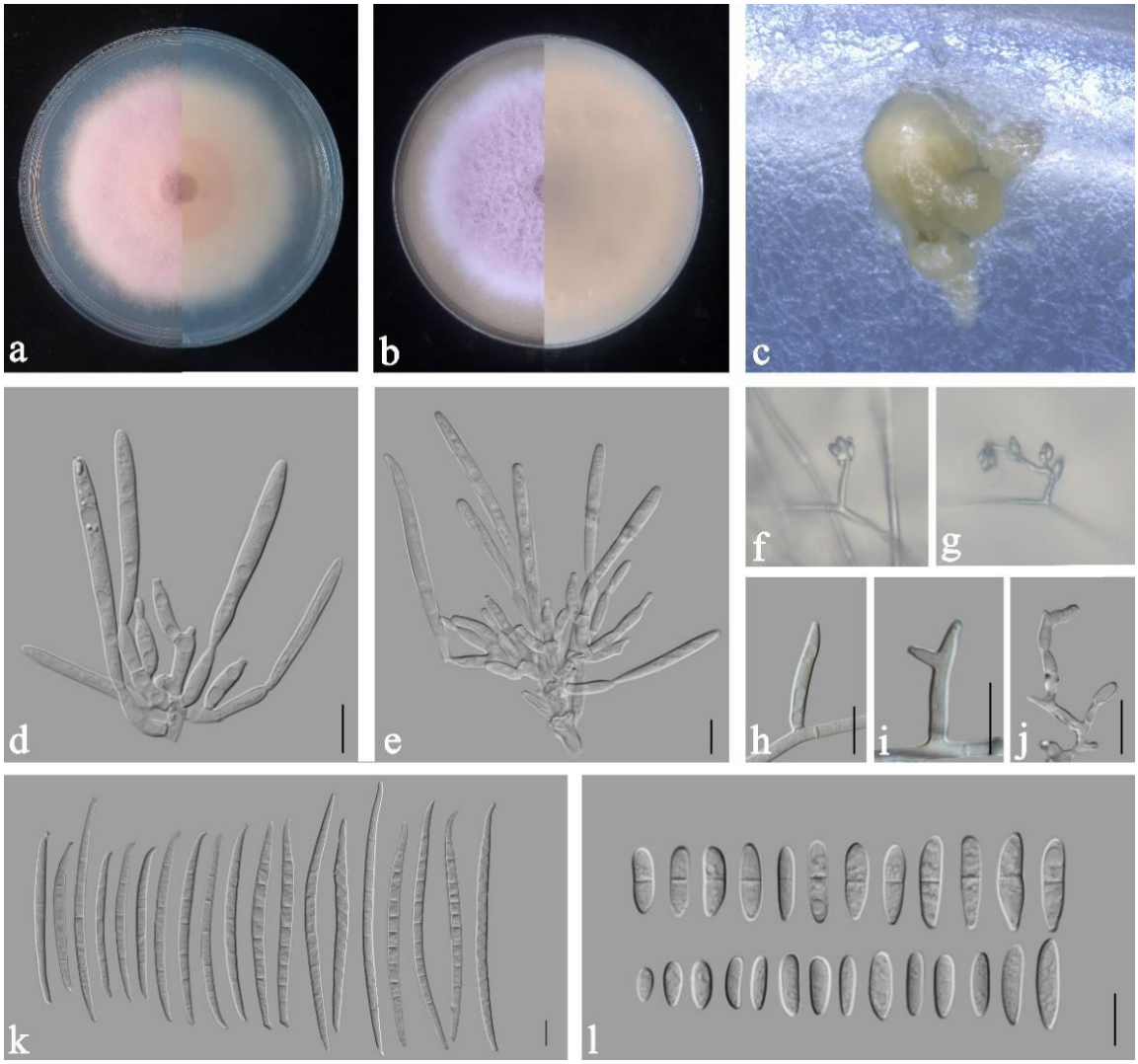

Figure 20 – *Fusarium guangdongense* (ZHKUCC 23-0920, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f–g Aerial conidial false heads. h–j Aerial conidiophores phialides and polyphialides. k Sporodochial conidia. l Aerial microconidia. Scale bars: 10 µm.

Material examined – China, Guangdong Province, Guangzhou City, on stem of *Antirrhinum majus* (*Plantaginaceae*), 26 February 2022, JC. Wang, R Li, XD Zheng, living cultures, ZHKUCC 23-0897, ZHKUCC 23-0898, ZHKUCC 23-0899.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, our strains clustered with *F. menglaense* with 77% ML bootstrap support and 0.99 BYPP value (Fig. 5). Our strains share overlapping characters with *F. menglaense*, except macroconidia which were not observed in the type strain of *F. menglaense* (Liu et al. 2023). Therefore, we identified our strains as *F. menglaense*. To date, *F. menglaense* was identified only from *Rhinolophus malayanus* (Liu et al. 2023). Herein we report the first record of *F. menglaense* from *Antirrhinum majus*.

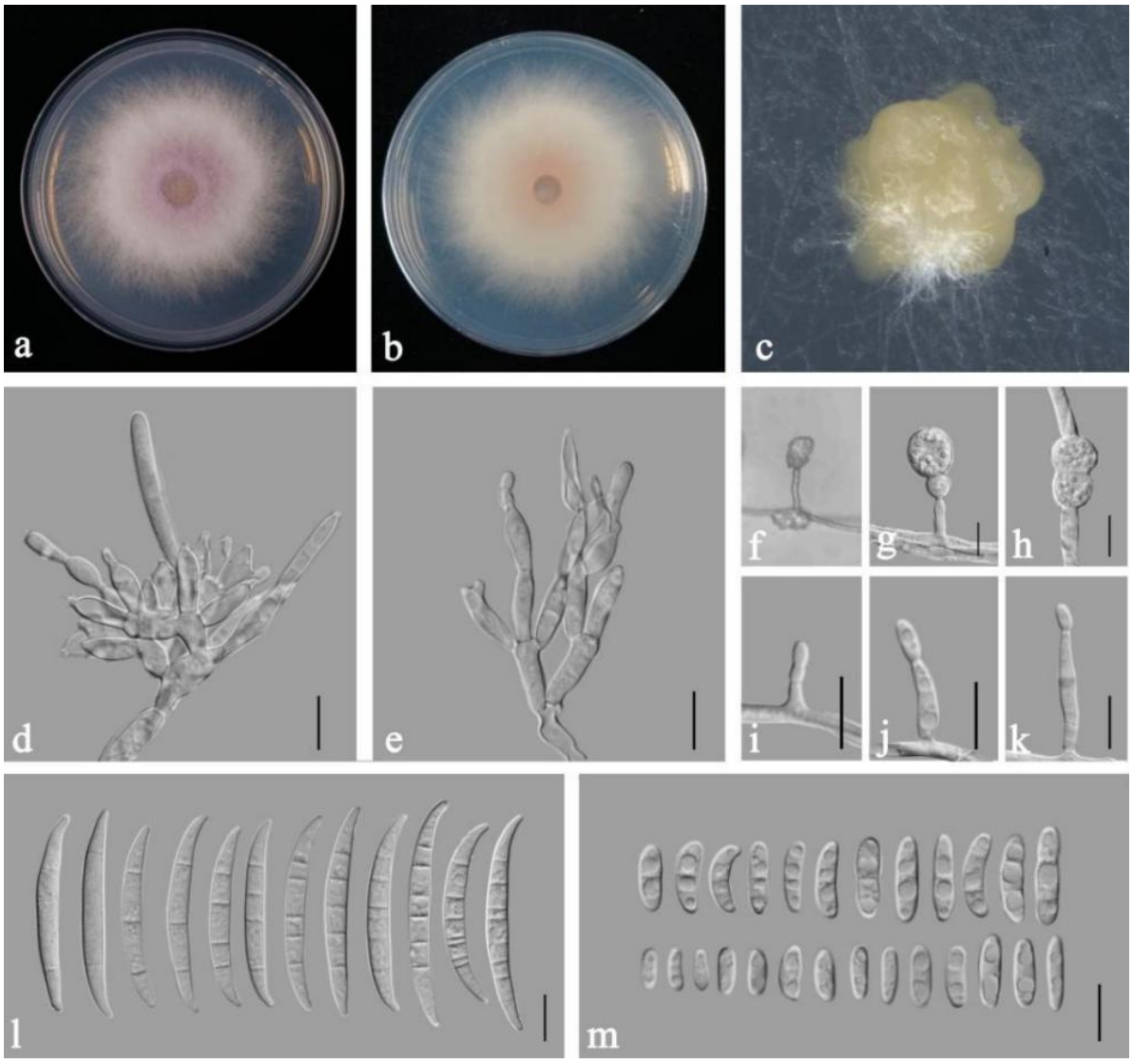

Figure 21 – *Fusarium menglaense* (ZHKUCC 23-0897). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Fusarium nirenbergiae L. Lombard & Crous, Persoonia 41: 29 (2018) Fig. 22

Index Fungorum number: IF826845; Facesoffungi number: FoF13413

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subulate to subcylindrical, 10–18 × 3–5 μm ($\overline{x}$ = 13 × 4 μm, n = 50). *Sporodochial conidia* apical cell curved, basal cell foot-shaped, 3–5-septate, 3-septate conidia: (30–)33–44 × 4–5 μm ($\overline{x}$ = 38 × 4 μm, n = 50); 4-septate conidia: 36–47 × 4–5

μm ($\bar{x}$ = 41 × 5 μm, n = 50); 5-septate conidia: 37–49 × 3–6 μm ($\bar{x}$ = 43 × 5 μm, n = 50). *Conidiogenous cells* subcylindrical, molophialides, (5–)8–19 × 2–5 μm ($\bar{x}$ = 13 × 3 μm, n = 50). *Aerial microconidia* in small false heads, oval to reniform, 0–2-septate; aseptate conidia: 6–15 × 2–4 μm ($\bar{x}$ = 9 × 3 μm, n = 50); 1-septate conidia: 11–16 × 3–4 μm ($\bar{x}$ = 14 × 4 μm, n = 50); 2-septate conidia: 16–23 × 4–5 μm ($\bar{x}$ = 18 × 4 μm, n = 6). *Chlamydospores* globose to subglobose, single or in pairs, 7–13 × 6–11 μm ($\bar{x}$ = 9 × 8 μm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 5 mm/d at 25 ℃. Surface view: white, floccose, filamentous margin. In reverse; light orange in the centre. Sporodochia produced on CLA after 30 days.

Material examined – China, Guangdong Province, Guangzhou City, on petiole of *Strelitzia reginae* (*Musaceae*), 19 April 2021, YX Zhang, C Chen, SQ Ma, living culture, ZHKUCC 23-0905; Guangdong Province, Zhaoqing City, on stem of *Bougainvillea spectabilis* (*Nyctaginacea*e), 4 November 2021, YX Zhang, living culture, ZHKUCC 23-0906; Jiangxi Province, Yichun City, on bulb of *Lilium brownii* (*Liliaceae*), May 2022, Chunping You, living culture, ZHKUCC 23-0907; Guangdong Province, Zhuhai City, on leaf of *Hymenocallis littoralis* (*Amaryllidaceae*), 16 February 2022, YH Lin, living culture, ZHKUCC 23-0908.

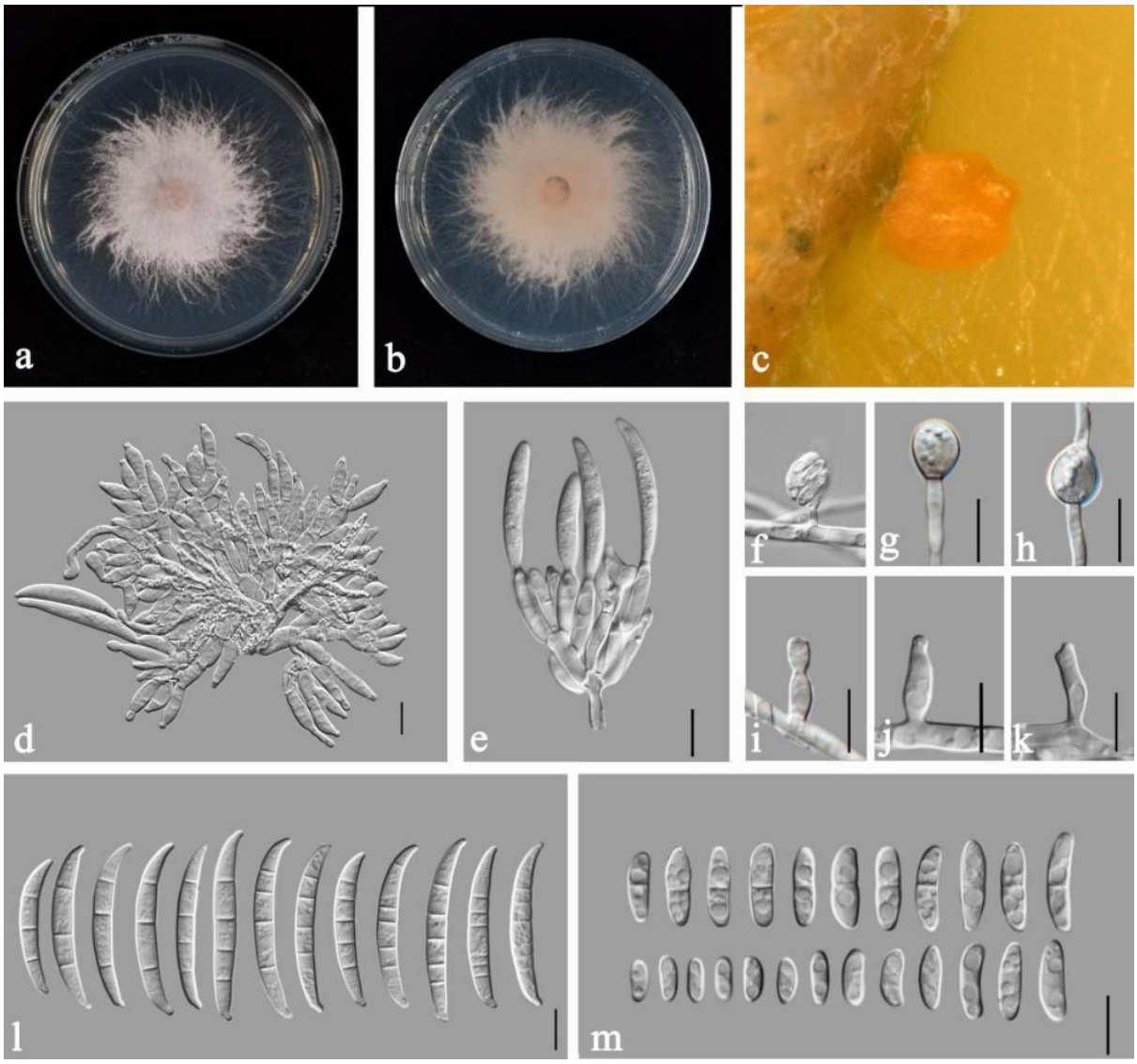

Figure 22 – *Fusarium nirenbergia*e (ZHKUCC 23-0907). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides and polyphialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, four isolates from our study, grouped with *F. nirenbergiae* strains (Fig. 5), share overlapping morphological characteristics (Lombard et al. 2019). Therefore, herein, we identified our strains as *F. nirenbergiae*. Previous studies showed that this species was associated with *Crocus sativus*, *Caryota* sp., *Dianthus caryophyllus*, *Musa* sp., *Passiflora edulis*, *Secale cereale*, and *Setaria* sp. (Lombard et al. 2019, Wang et al. 2022, Mirghasempour et al. 2022). To our knowledge, this is the first report of *F. nirenbergiae* from *Strelitzia reginae*, *Bougainvillea spectabilis* and *Hymenocallis littoralis*.

Fusarium odoratissimum Maryani, L. Lombard, Kema & Crous, Stud. Mycol. 92: 159 (2018) Fig. 23

Index Fungorum number: IF826800; Facesoffungi number: FoF16737

Asexual morph: *Sporodochia* yellow, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 10–20(–23) × 2–5 µm ($\overline{x}$ = 13 × 3 µm, n = 50). *Sporodochial conidia* falcate, curved and slender, apical cell curved, basal cell foot-shaped, (1–)3–5-septate, hyaline; 1-septate conidia: 30–40 × 3–4 µm ($\overline{x}$ = 36 × 4 µm, n = 3); 2-septate conidia: 24–37 × 4–5 µm ($\overline{x}$ = 36 × 4 µm, n = 2); 3-septate conidia: 32–45 × 4–5 µm ($\overline{x}$ = 38 × 4 µm, n = 50); 4-septate conidia: 37–50 × 4–5 µm ($\overline{x}$ = 42 × 4 µm, n = 50); 5-septate conidia: 43–50 × 3–4 µm ($\overline{x}$ = 46 × 4 µm, n = 50). *Conidiogenous cells* subcylindrical, molophialides6–27 × 2–4 µm ($\overline{x}$ = 13 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval, fusiform, obovoid and reniform, aseptate, 5–10(–13) × 3–4 µm ($\overline{x}$ = 7 × 3 µm, n = 50). *Chlamydospores* single or in pairs, globose to subglobose, 13–15 × 12–15 µm ($\overline{x}$ = 13 × 13 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 7 mm/d at 25 ℃. Surface view: white, floccose, irregular margin. In reverse; white. Sporodochia produced on CLA after 30 days.

Material examined – China, Guangdong Province, Guangzhou City, on a stem of *Callistemon rigidus* (*Myrtaceae Juss.*), 28 December 2022, LT Nie, YH Lin (MHZU 24-0012, holotype, dried culture); ZHKUCC 24-0051, ex-type; living culture, ZHKUCC 24-0052.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, two isolates from the present study formed a sister clade with *F. rosae-roxburghii* and *F. odoratissimum*, with 88% ML bootstrap support and 0.99 BYPP value (Fig. 5). Morphologically, our isolates differ from its closely related species by macroconidial size (24–45 × 4–5 µm in *F. callistemonis* vs 11.5–26 × 2–3 µm in *F. rosae-roxburghii* vs 59–75 × 6–8 µm in *F. odoratissimum*). In addition, microconidia of these three species also differ, being 5–10 × 3–4 µm in *F. callistemonis*, 8–16 × 6 µm in *F. rosae-roxburghii* and 4–21 × 2–3.5 µm in *F. odoratissimum* (Maryani et al. 2019, Zhang et al. 2023a). However, in pairwise nucleotide comparisons among the three species, they share differences of less than 1.0% in all gene regions. Based on fewer variations and overlapping morphology, we introduce our isolates as *F. odoratissimum* and reduce *F. rosae-roxburghii* to synonymy with *F. odoratissimum. Fusarium odoratissimum* has been identified only from *Musa* spp. and *Albizzia julibrissin* (Lombard et al. 2019). This is the first report of *F. odoratissimum* from *Callistemon rigidus*.

Fusarium temperatum Scaufl. & Munaut, Mycologia 103(3): 593 (2011) Fig. 24

Index Fungorum number: IF518089; Facesoffungi number: FoF16738

Asexual morph: *Sporodochia* orange, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, (5–)9–23(–25) × 3–5 µm ($\overline{x}$ = 15 × 4 µm, n = 50). *Sporodochial conidia* apical cell curved to hooked, basal cell foot-shaped, (1)3–5(–7)-septate, 1-septate conidia: 52 × 5 µm(n = 1); 3-septate conidia: (41–)46–59 × 4–6 µm ($\overline{x}$ = 51 × 4 µm, n = 50); 4-septate conidia: 44–70 × 4–6 µm ($\overline{x}$ = 56 × 5 µm, n = 50); 5-septate conidia: (44–)47–67 × 4–6 µm ($\overline{x}$ = 57 × 5 µm, n = 50); 6-septate conidia: (40–)42–59(–61)× 3–5 µm ($\overline{x}$ = 50 × 4 µm, n = 25); 7-septate conidia: 50–56 × 5–6 µm ($\overline{x}$ = 53 × 4 µm, n = 5). *Conidiogenous cells* subcylindrical, phialides and polyphialides, 4–23(–25) × 2–4 µm ($\overline{x}$ = 14 × 3

μm, n = 50). *Aerial conidia* in small false, oval to fusiform, 0–1(2)-septate; aseptate conidia: 5–14 × 2–4 μm ($\overline{x}$ = 9 × 3 μm, n = 50); 1-septate conidia: 14–21 × 3–4 μm ($\overline{x}$ = 16 × 4 μm, n = 50); 2-septate conidia: 14–23 × 4–6 μm ($\overline{x}$ = 19 × 5 μm, n = 23). *Chlamydospores* not observed. Sexual morph: not observed.

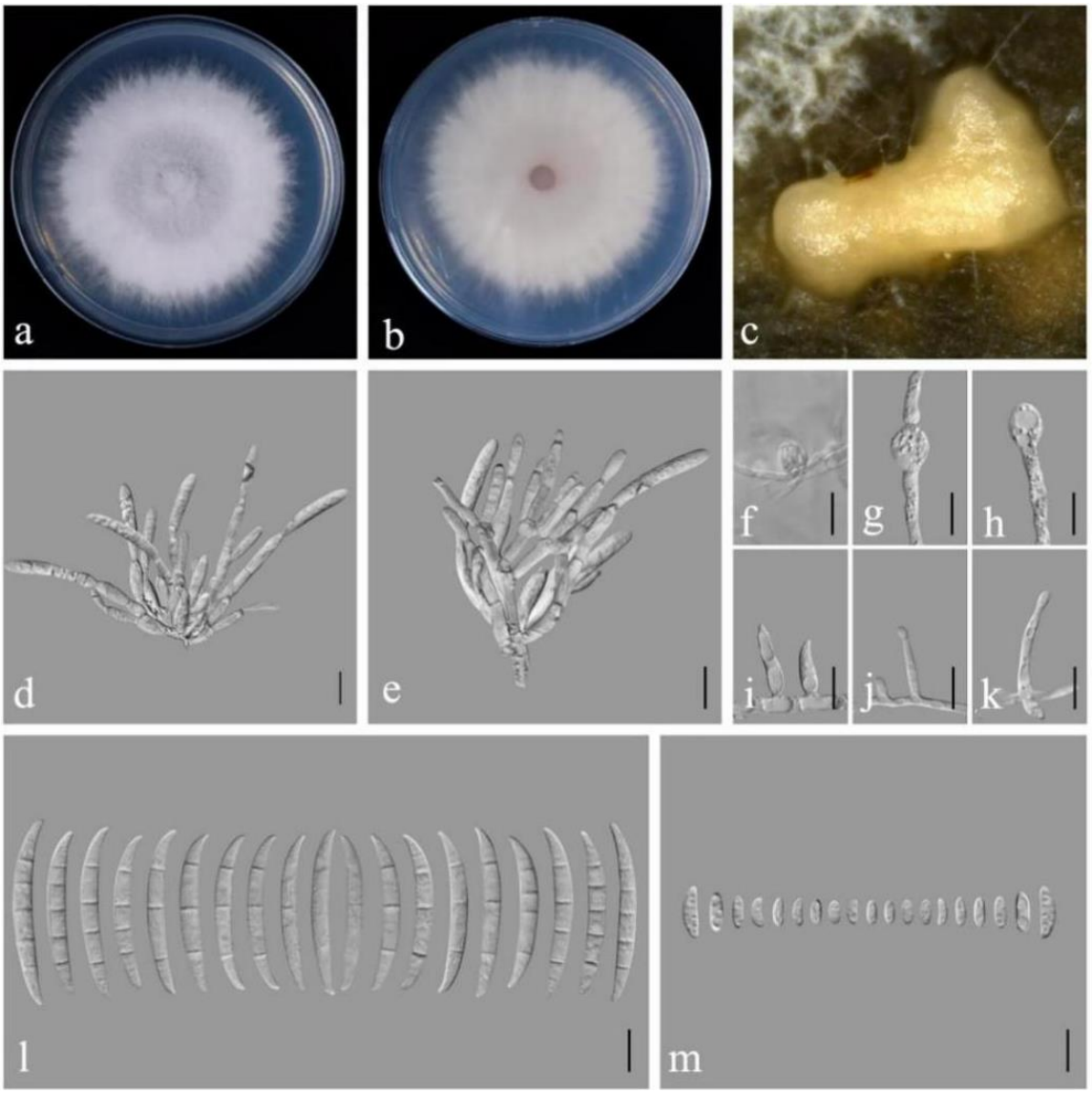

Figure 23 – *Fusarium odoratissimum* (ZHKUCC 24-00051). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Culture characteristics – Growth rate on PDA was 7 mm/d at 25 ℃. Surface view: light purple, floccose, regular margin. In reverse; light pink in the centre. Sporodochia produced on CLA after 7 days.

Material examined – China, Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, on the root of *Campanula medium* (*Campanulaceae*), 2 November 2021, L Li, N Mo, living culture, ZHKUCC 23-0934.

Notes – In the phylogenetic analysis of the *Fusarium fujikuroi* species complex, isolates from the present study clustered together with *F. temperatum* with 98% ML bootstrap support and 1.00 BYPP value (Fig. 3). Apart from the larger macroconidia than *F. temperatum* (Scauflaire et al. 2011) our isolates share overlapping morphological characteristics that are similar to

F. temperatum. Therefore, based on phylogenetic placement and morphology, we identified our isolates as *F. temperatum*. This species is a major pathogen on *Zea mays*, causing maize ear rot (Scauflaire et al. 2011). *Fusarium temperatum* also has been isolated from humans (Yilmaz et al. 2021). However, this is the first record of *F. temperatum* isolated from *Campanula medium.*

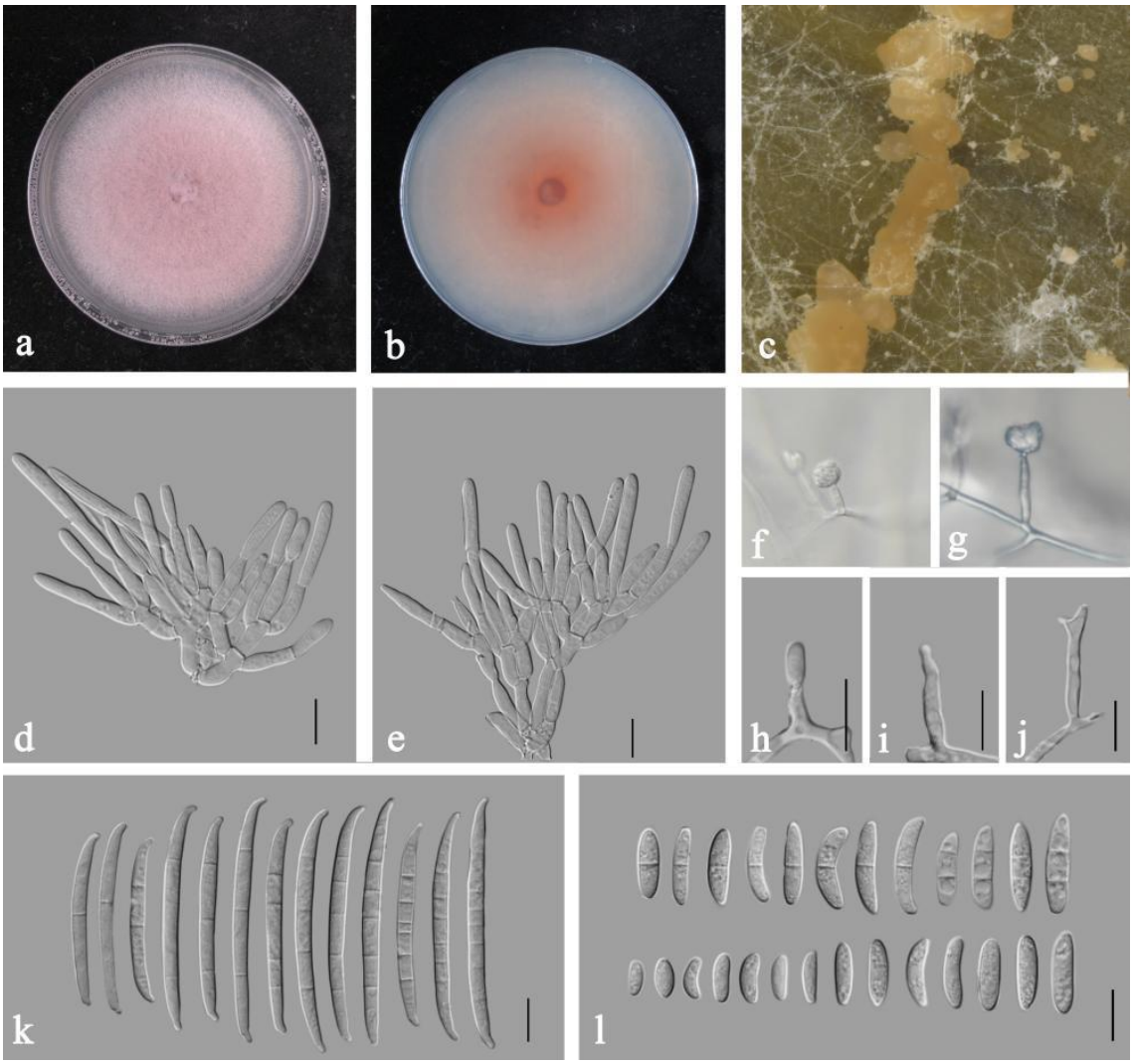

Figure 24 – *Fusarium temperatum* (ZHKUCC 23-0934). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f–g Aerial conidial false heads. h–j Aerial conidiophores phialides and polyphialides. k Sporodochial conidia. l Aerial microconidia. Scale bars: 10 μm.

Fusarium triseptatum L. Lombard & Crous, Persoonia 41: 34 (2018) Fig. 25

Index Fungorum number: IF826847; Facesoffungi number: FoF16739

Asexual morph: *Sporodochia* orange, formed on SNA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 8–20 × 3–5 μm ($\overline{x}$ = 13 × 4 μm, n = 50). *Sporodochial conidia* slender, apical cell curved, basal cell foot-shaped, (1–2–)3–5-septate, hyaline; 1-septate conidia: 49–57 × 4–5(–6) μm ($\overline{x}$ = 53 × 4 μm, n = 2); 2-septate conidia: 52 × 5 μm (n = 1); 3-septate conidia: 37–53(–55) × 4–5 μm ($\overline{x}$ = 45 × 3 μm, n = 50); 4-septate conidia: (41–)44–60(–62) × 4–5(–6) μm ($\overline{x}$ = 51 × 4 μm, n = 50); 5-septate conidia: 46–60(–62) × 3–5 μm ($\overline{x}$ = 54× 5 μm, n = 50). *Conidiogenous cells* subcylindrical, molophialides, 3–20(–22) × 2–4 μm ($\overline{x}$ = 11 × 3 μm, n = 50). *Aerial microconidia* in small false, oval to reiform, 0–1-septate; aseptate conidia: 5–13(–17) × 3–4 μm ($\overline{x}$ = 8 × 3 μm, n = 50); 1-septate conidia: 12–17 × 3–5 μm

($\bar{x}$ = 15 × 3 µm, n = 50). *Chlamydospores* globose to subglobose, single or in pairs, 7–11 × 7–11 µm ($\bar{x}$ = 9 × 9 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 6 mm/d at 25 ℃. Surface view: white, floccose, filamentous margin. In reverse; colony light pink in the centre. Sporodochia produced after 30 days on SNA.

Material examined – China, Guangdong Province, Guangzhou City, on stem of *Aglaonema commutatum* (*Araceae*), 1 November 2021, Lin Li, and Na Mo, living culture ZHKUCC 23-0900, ZHKUCC 23-0901, ZHKUCC 23-0902; Guangdong Province, Guangzhou City, on sheath of *Strelitzia reginae* (*Musaceae*), 1 November 2021, Y.X. Zhang, C. Chen, and S.Q. Ma, living culture, ZHKUCC 23-0903.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, four strains in this study (ZHKUCC 23-0900, ZHKUCC 23-0901, ZHKUCC 23-0902, ZHKUCC 23-0903) clustered with the *F. triseptatum* ex-type strain and other representative strains (Fig. 5). Except the Macroconidia of our strains are larger than *F. triseptatum*, other characteristics are similar to the type description (Lombard et al. 2019). Therefore, our strains are identified as *F. triseptatum*. This species can cause the blight of *Gossypium hirsutum* and *Ipomoea batatas* and is also found in Sago starch and humans (Lombard et al. 2019). However, this is the first report of *F. triseptatum* from *Aglaonema commutatum* and *Strelitzia reginae*.

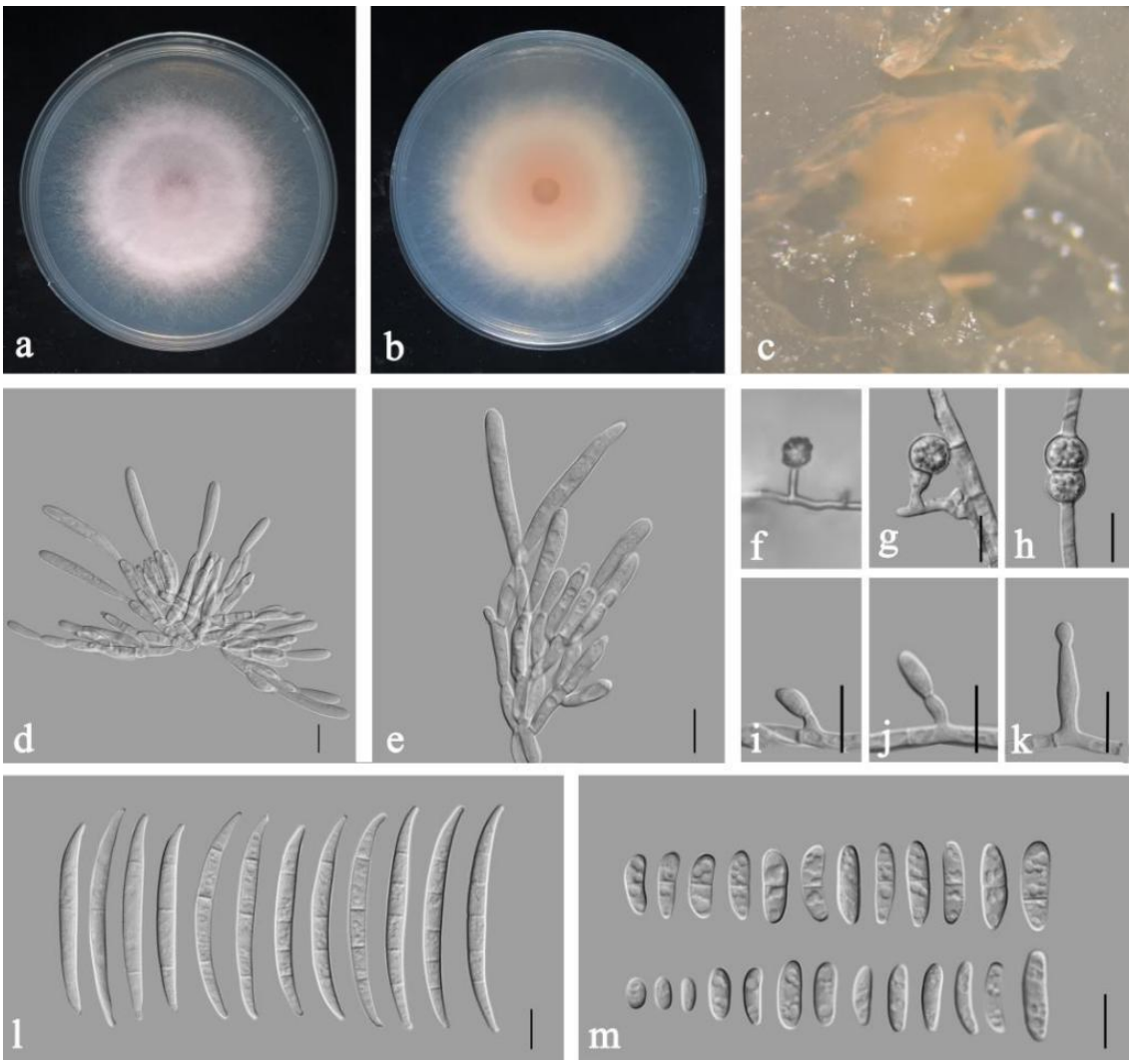

Figure 25 – *Fusarium triseptatum* (ZHKUCC 23-0900). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on SNA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 µm.

***Fusarium* sp.** Fig. 26

Asexual morph: *Sporodochia* not observed. Conidiophores borne on aerial mycelia. *Aerial macroconidia* straight to falcate, apical cells bluntly rounded to curved, papillate, basal cells no significant foot-shaped, 1–3-septate, hyaline, 1-septate conidia: 13–22 × 2–3 µm ($\overline{x}$ = 18 × 3 µm, n = 50); 2-septate conidia: 16–25 × 2–3 µm ($\overline{x}$ = 20 × 3 µm, n = 50); 3-septate conidia: 19–36 × 2–3 µm ($\overline{x}$ = 26 × 3 µm, n = 50). *Aerial microconidia* in small false heads, reniform to subclavate, 0–1-septate, aseptate conidia: 8–18(–21) × 4–5 µm ($\overline{x}$ = 12 × 4 µm, n = 50), 1-septate conidia: 11–27(–29) × 2–6 µm ($\overline{x}$ = 18 × 4 µm, n = 50). *Chlamydospores* globose to subglobose, formed intercalarily or terminally, singly or in pairs, 7–10 × 7–10 µm ($\overline{x}$ = 9 × 9 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Colonial growth on PDA was 7 mm/d at 25 ℃. Surface view: white, cottony, irregular margins. In reverse; colony light pink in the centre. Colonial growth rate on OA was 7 mm/d at 25 ℃. Colony surface white in the center, aerial mycelia raised, dense, with an undulate margin; reverse white.

Material examined – China, Guangdong Province, Guangzhou City, on a stem of *Cordyline fruticosa* (*Asparagaceae*), 28 December 2022, LT Nie, YH Lin (MHZU 24-0011, dried culture); living cultures ZHKUCC 24-0049, ZHKUCC 24-0050.

Notes – In the phylogenetic analysis of the *Fusarium oxysporum* species complex, five isolates from this study developed a distinct lineage with 99% ML bootstrap support and 1.00 BYPP value (Fig. 5). Phylogenetically, these isolates have a close relationship with *F. cili*, *F. phialophorum*, *F. rosae-roxburghii* and *F. odoratissimum*. Even though these isolates clustered separately, when we compared the nucleotide variations within the *F. cili*, *F. phialophorum*, *F. rosae-roxburghii* and *F. odoratissimum* cluster, it showed fewer variations. Moreover, it is difficult to delineate *F. cili*, *F. phialophorum*, and *F. odoratissimum* with these approaches. Therefore, treat our two isolates as *Fusarium* sp. Future studies are necessary to understand the relationship among *F. cili*, *F. phialophorum*, and *F. odoratissimum* together with our isolates.

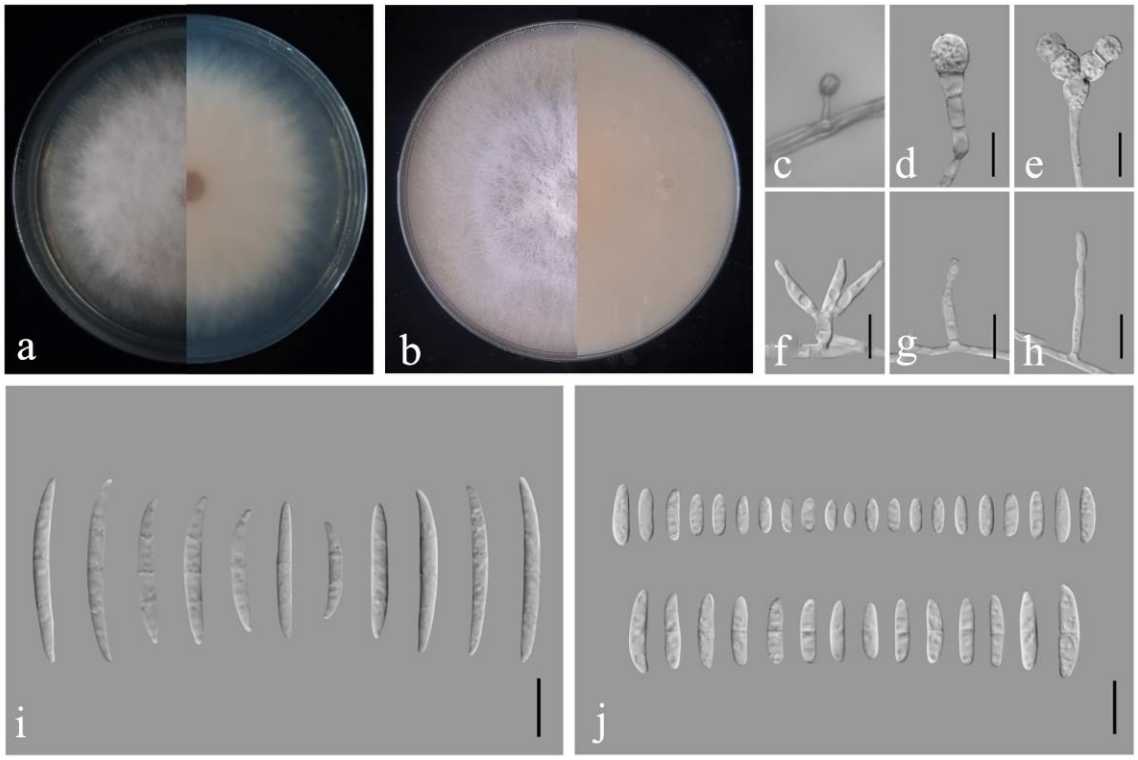

Figure 26 – *Fusarium* sp. (ZHKUCC 24-0049). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Aerial conidial false head. d–e Chlamydospores. f–h Aerial conidiophores phialides. i Aerial macroconidia. j Aerial microconidia. Scale bars: 10 µm.

Neocosmospora E.F. Sm., Bull. U.S. Department of Agriculture 17: 45 (1899)

Neocosmospora species were previously known as *Fusarium solani* species complex (FSSC; O'Donnell 2000) and assigned to a sect. *Martiella* (Wollenweber 1913). For the taxonomic treatment, Sandoval-Denis et al. (2019), Crous et al. (2021), Wijayawardene et al. (2022) and Perera et al. (2023) were followed.

Neocosmospora guangdongensis Y.X. Zhang, K.D. Hyde, C. Chen & Manawas., sp. nov. Fig. 27

Index Fungorum number: IF902568; FacesofFungi number: FoF16628

Etymology – The name refers to "Guangdong Province", where the fungus was collected.

Asexual morph: *Sporodochia* white, formed on CLA. *Sporodochial conidiophores* irregularly branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* subcylindrical, 11–21(–23) × 3–5 µm ($\overline{x}$ = 16 × 4 µm, n = 50). *Sporodochial conidia* apical cell blunt, basal cell foot-shaped, (3–)4–6(–8)-septate; 3-septate conidia: 36 × 5 µm; 4-septate conidia: (44–)50–69(–72) × 5–8 µm ($\overline{x}$ = 61 × 6 µm, n = 50); 5-septate conidia: 57–73 × 6–8 µm ($\overline{x}$ = 66 × 7 µm, n = 50); 6-septate conidia: 62–68 × 5–7 µm ($\overline{x}$ = 68 × 7 µm, n = 50); 7-septate conidia: 63–76 × 6–8 µm ($\overline{x}$ = 70 × 7 µm, n = 31); 8-septate conidia: 69 × 6 µm. *Aerial conidiophores* bearing terminal or lateral phialides. *Conidiogenous cells* subcylindrical, 15–89 × 2–6 µm ($\overline{x}$ = 53 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval, reniform, and fusiform, 0–1-septate; aseptate conidia: 5–20 × 2–5 µm ($\overline{x}$ = 9 × 4 µm, n = 50); 1-septate conidia: 13–21 × 4–6 µm ($\overline{x}$ = 16 × 5 µm, n = 50). *Chlamydospores* not observed. Sexual morph: not observed.

Culture characteristics – Colonial growth rate on PDA was 5 mm/d at 25 ℃. Surface view: white, floccose, regular margin. In reverse; white. Sporodochia produced on CLA after 30 days. Colonial growth rate on OA was 4 mm/d at 25 ℃. Colony surface white, aerial mycelia raised, dense, and margin entire; reverse light orange in the center.

Material examined – China, Guangdong Province, Zhaoqing City, on a stem of *Paphiopedilum* sp. (*Orchidaceae*), 4 November. 2021, YX Zhang (MHZU 23-0225, holotype); ZHKUCC 23-0938, ex-type; living cultures, ZHKUCC 23-0939, and ZHKUCC 23-0940.

Notes – In the phylogenetic analysis of *Neocosmospora* (Fig. 7), our strains developed a distinct clade with 100% ML bootstrap support and 1.00 BYPP values which is closely related to *N. maoershanica*, *N. paraeumartii*, *N. oblonga* and *N. longissima.* The microconidia of our isolates were larger than *N. maoershanica* (Zeng & Zhuang 2023) and *N. longissima* (Sandoval-Denis et al. 2019) (5–21 × 2–6 µm, $\overline{x}$ = 12.5 × 4.5 µm vs. 3–13 × 2–4 µm vs 5–13 × 2–5 µm, $\overline{x}$ = 7 × 3 µm). In addition, macroconidia were not observed in *N. maoershanica* and *N. oblonga* (Sandoval-Denis et al. 2019). Our strains are identified as a new species based on morphological and phylogenetic results.

Neocosmospora keratoplastica (Geiser, O'Donnell, D.P.G. Short & Ning Zhang) Sand. -Den. & Crous, Persoonia 41: 120 (2017) Fig. 28

Index Fungorum number: IF822900; Facesoffungi number: FoF16740

Asexual morph: *Sporodochia* yellow, formed on CLA. *Sporodochial conidiophores* branched, verticillate, dense. *Sporodochial conidiogenous cells* subcylindrical, 13–20 × 3–5 µm ($\overline{x}$ = 16 × 4 µm, n = 50). *Sporodochial conidia* apical cell blunt, basal cell blunt to foot-shaped, (0–)1–4(–5)-septate, 0-septate conidia: (23–)25–35× 4–6 µm ($\overline{x}$ = 30 × 6 µm, n = 11); 1-septate conidia: (17–)20–38(–40)× 4–6 µm ($\overline{x}$ = 27 × 5 µm, n = 50); 2-septate conidia: 22–35 × 4–7 µm ($\overline{x}$ = 29 × 5 µm, n = 50); 3-septate conidia: 29–39 × 5–7 µm ($\overline{x}$ = 34 × 6 µm, n = 50); 4-septate conidia: (24–)33–42(–44)× 5–7 µm ($\overline{x}$ = 36 × 6 µm, n = 50); 5-septate conidia: 28–39 × 5–7 µm ($\overline{x}$ = 35 × 6 µm, n = 6). *Conidiogenous cells* subcylindrical, 35–73 × 2–4 µm ($\overline{x}$ = 49 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval, ellipsoidal to subcylindrical, 0–1-septate; aseptate conidia: 8–16 × 3–5(–6) µm ($\overline{x}$ = 12 × 4 µm, n = 50); 1-septate conidia: 14–22 × 4–6 µm ($\overline{x}$ = 18 × 5 µm,

n = 50). *Chlamydospores* globose to subglobose, single or in pairs, 7–11 × 6–10 µm ($\overline{x}$ = 9 × 8 µm, n = 50). Sexual morph: not observed.

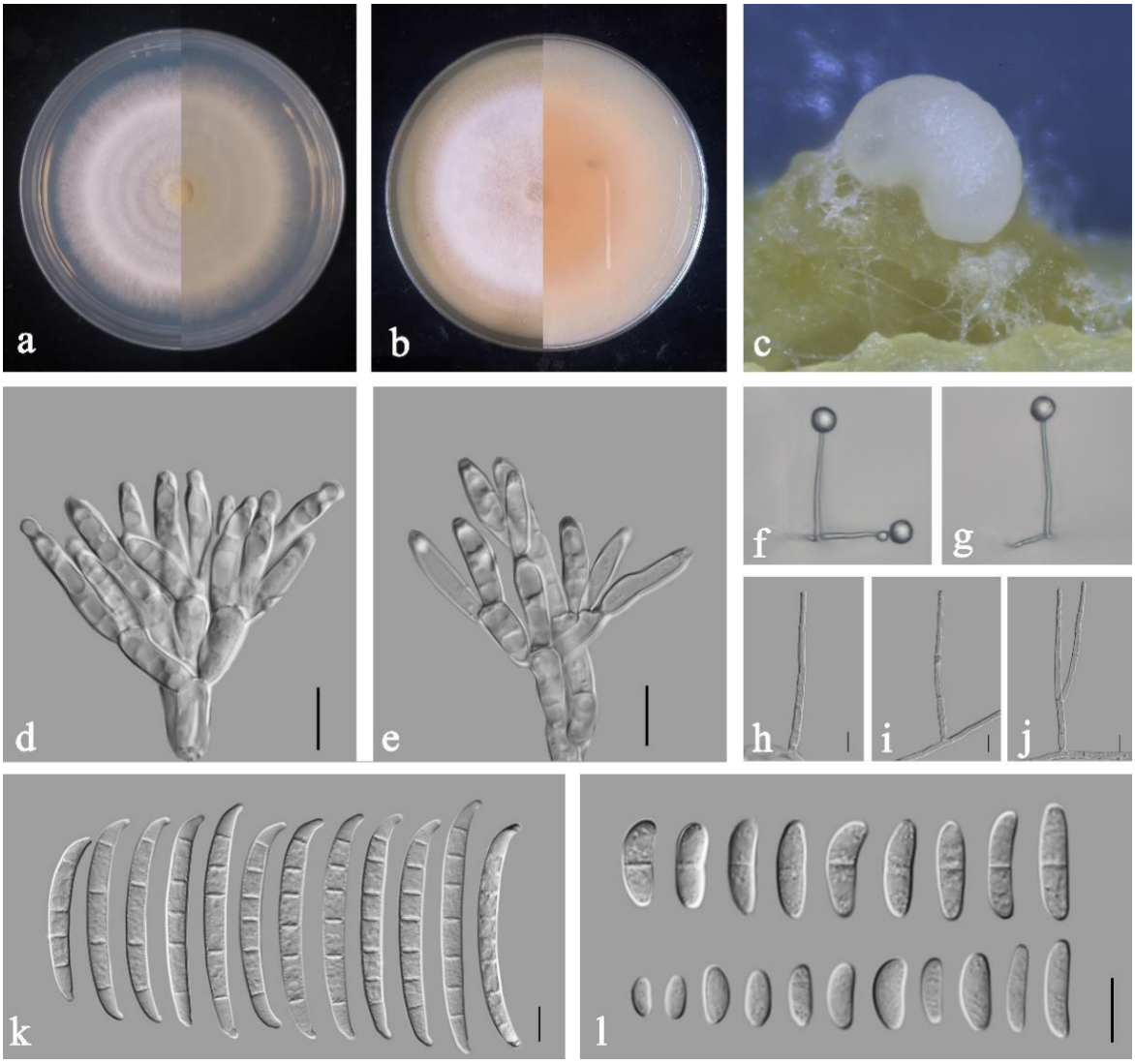

Figure 27 – *Neocosmospora guangdongensis* (ZHKUCC 23-0938, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c. Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f–g Aerial conidial false heads. h–j Aerial conidiophores phialides. k Sporodochial conidia. l. Aerial microconidia. Scale bars: 10 µm.

Culture characteristics – Colonial growth rate on PDA was 4 mm/d at 25 °C. Surface view; white, floccose, regular margin. In reverse; white. On SNA, sporodochia produced after 25 days.

Material examined – China, Guangdong Province, Guangzhou City, on stem of *Strelitzia reginae* (*Musaceae*), 19 April 2022, YX Zhang, C. Chen, SQ Ma, living cultures, ZHKUCC 23-0941, ZHKUCC 23-0942, and ZHKUCC 23-0943.

Notes – In the phylogenetic analysis, three isolates from our study clustered with *Neocosmospora keratoplastica* with 100% ML bootstrap support and 0.99 BYPP value (Fig. 7). The sporodochial conidia of our isolates are smaller with *N. keratoplastica,* and other morphological characteristics are similar to those of the original description of *N. keratoplastica* (Sandoval-Denis & Crous 2018). Based on this evidence, isolates from this study are identified as *N. keratoplastica*. This species is a well-known pathogen of animal infections and human corneal infections (Short et al. 2013, Fernando et al. 2015). It is also occasionally found in plant material and soil (Chehri et al. 2015, Shaffer et al. 2017, Gonzalez et al. 2020). This is the first report of *N. keratoplastica* from *Strelitzia reginae* worldwide.

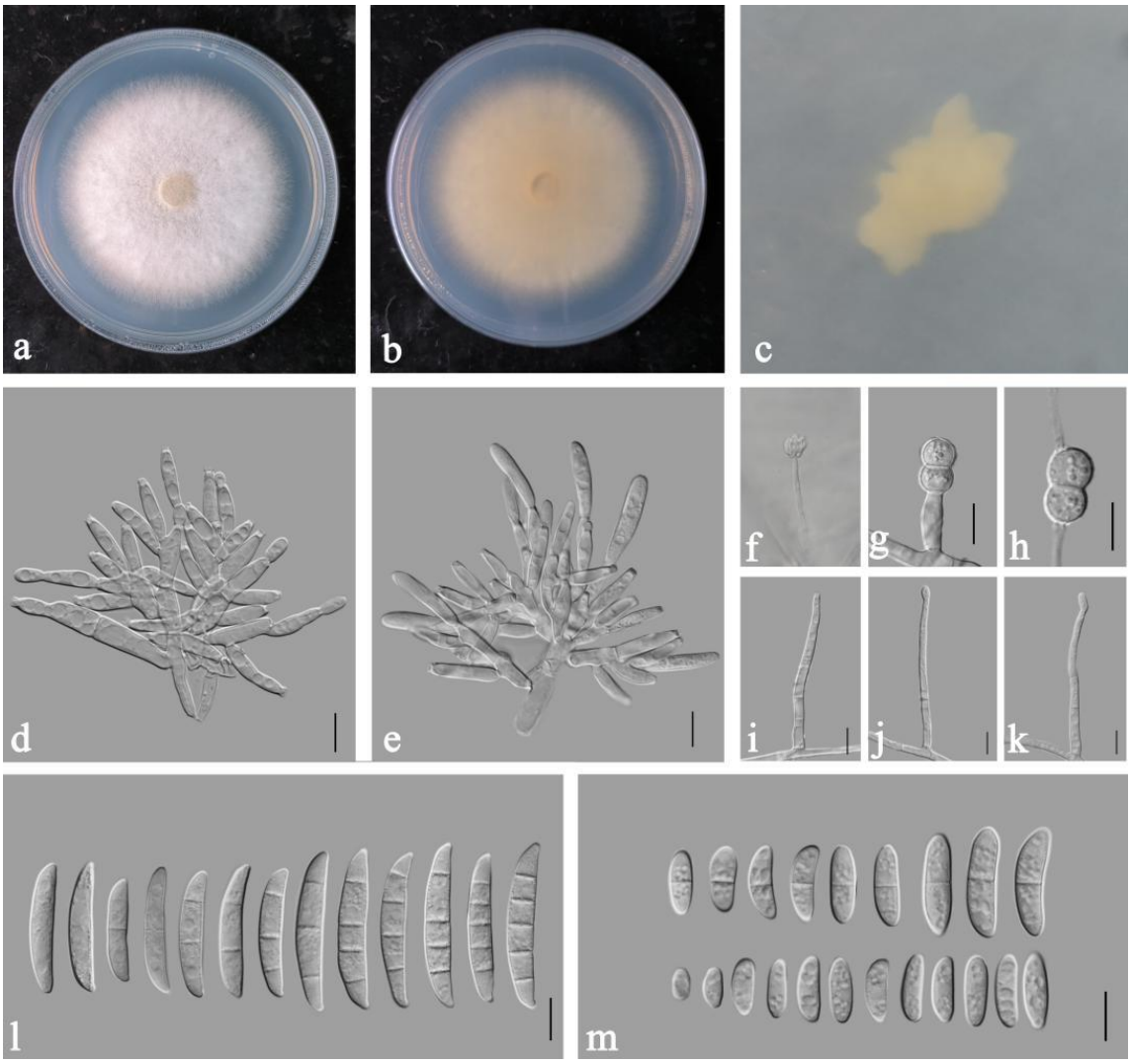

Figure 28 – *Neocosmospora keratoplastica* (ZHKUCC 23-0941). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on SNA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false heads. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Neocosmospora paphiopedili Y.X. Zhang, K.D. Hyde, C. Chen & Manawas., sp. nov. Fig. 29

Index Fungorum number: IF902571; Facesoffungi number: FoF16629

Etymology – Referring to the host of this fungus, *Paphiopedilum* sp.

Sexual morph: *Perithecia* orange to dark-red, globose, papillate, superficial, solitary, or gregarious. *Asci* subcylindrical, 68–82 × 4–7 μm ($\overline{x}$ = 75 × 6 μm, n = 19). *Ascospores* obliquely uniseriate or irregularly biseriate at apex of asci, ellipsoidal to subfusiform, 1-septate, 10–12 × 4–5 μm ($\overline{x}$ = 10 × 5 μm, n = 50), yellow brown to golden yellow, thick-walled. *Asexual morph*: *Sporodochia* not observed. *Conidiophores* arising from aerial mycelia. *Aerial macroconidia*, apical cell blunt, basal cell foot-shaped, (1–)3–4(–5)-septate; 1-septate conidia: 24–26 × 5 μm ($\overline{x}$ = 25 × 5 μm, n = 2); 2-septate conidia: 32–35 × 5–6 μm ($\overline{x}$ = 34 × 5 μm, n = 4); 3-septate conidia: 33–50 × 4–6 μm ($\overline{x}$ = 42 × 6 μm, n = 50); 4-septate conidia: 40–54 (–58) × 5–7 μm ($\overline{x}$ = 49 × 6 μm, n = 50); 5-septate conidia: (42–) 47–59 × 5–7 μm ($\overline{x}$ = 51 × 6 μm, n = 15). *Conidiophores* unbranched, simple, bearing terminal single phialides. *Conidiogenous cells* subcylindrical, smooth and slender, 21–74 × 2–5 μm ($\overline{x}$ = 51 × 4 μm, n = 50). *Aerial microconidia* in small false heads, fusoid and obovoid, 0–1-septate; aseptate conidia: 7–18 × 3–6 μm ($\overline{x}$ = 13 × 4 μm, n = 50); 1-septate conidia:

16–25(–29) × 4–6 µm ($\bar{x}$ = 20 × 5 µm, n = 50). *Chlamydospores* globose to subglobose, single, in pairs or clusters, 6–12 × 5–10 µm ($\bar{x}$ = 8 × 7 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 6 mm/d at 25 ℃. Surface view: white, regular margin. In reverse; white. On CLA, perithecia produced after 30 days. Colonial growth rate on OA was 3 mm/d at 25 ℃. Colony surface white, aerial mycelia raised, dense; reverse white.

Material examined – China, Guangdong Province, Zhongshan City, on stem of *Paphiopedilum* sp. (*Orchidaceae*), 20 Aug. 2021, YX Zhang, ZL Mai, C. Chen, JW Chen (MHZU 23-0224, holotype); ZHKUCC 23-0935, ex-type; Guangdong Province, Shaoguan City, on stem of *Spathiphyllum floribundum* (*Araceae*), 17 Jul. 2021, YX Zhang, living cultures, ZHKUCC 23-0936, and ZHKUCC 23-0937.

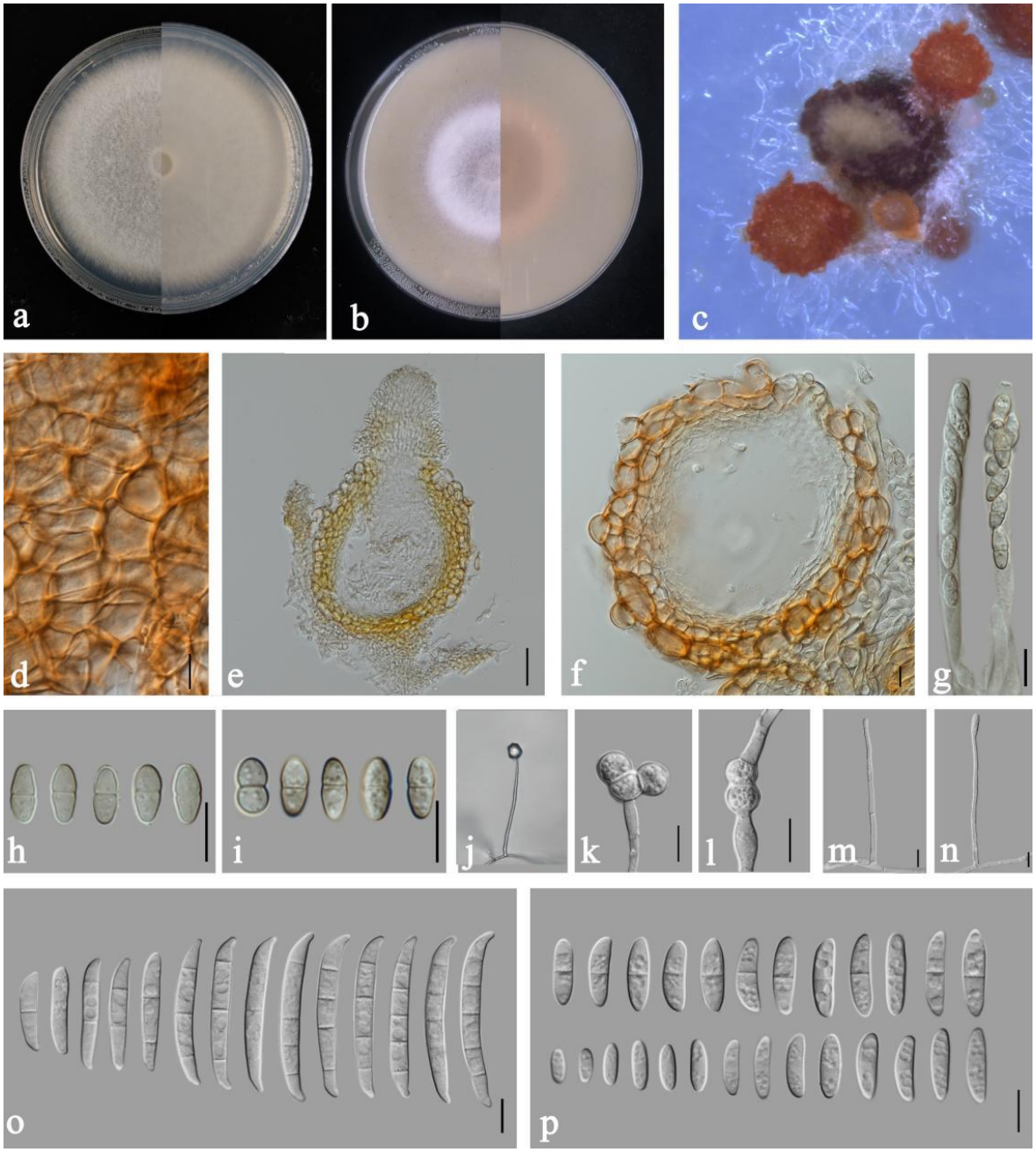

Figure 29 – *Neocosmospora paphiopedili* (ZHKUCC 23-0935, ex-type). a 7-day-old PDA culture (surface, reverse). b 7-day-old OA culture (surface, reverse). c Perithecia. d Peridium cells. e–f Section through a perithecium. g Asci. h–i Ascospores. j Aerial conidial false head. k–l Chlamydospores. m–n Aerial conidiophores phialides. o Aerial macroconidia. p Aerial microconidia. Scale bars: e = 50 µm, f–p = 10 µm.

Notes – In the phylogenetic analysis of *Neocosmospora* three isolates from the present study formed a single lineage with 100% ML bootstrap support and 1.00 BYPP values which is close to *N. solani* (Fig. 7). The macroconidia of our strains (33–54 × 4–7 µm) slightly differ from *N. solani* (36–48 × 4.5–6 µm) (Schroers et al. 2016). The nucleotide differences between *N. paphiopedili* (ZHKUCC 23-0935) and *N. solani* (CBS 101018T) are 1.83% (24/1312) in *rpb1*, 2.52% (43/1704) in *rpb2* and 1.68% (12/714) in *tef1-α*. Based on morphological and molecular data and according to the guidelines of Jayawardena et al. (2021), the strains in this study are identified as new species.

Neocosmospora pseudensiformis Samuels, Mycologia 103(6): 1323 (2011) Fig. 30

Index Fungorum number: IF519838; Facesoffungi number: FoF16741

Asexual morph: *Sporodochia* off-white, formed on CLA. *Sporodochial conidiophores* branched, irregular, dense. *Sporodochial conidiogenous cells* subcylindrical, 11–24(–26) × 3–5 µm ($\overline{x}$ = 17 × 4 µm, n = 50). *Sporodochial conidia* apical cell blunt and slightly curved, basal cell foot-shaped, (4–)5–7(–9)-septate, 4-septate conidia: 48–63 × 6–7 µm ($\overline{x}$ = 54 × 6 µm, n = 5); 5-septate conidia: (50–)54–71(–73)× 6–8 µm ($\overline{x}$ = 61 × 7 µm, n = 50); 6-septate conidia: 60–75 × 6–9 µm ($\overline{x}$ = 68 × 7 µm, n = 50); 7-septate conidia: (61–)63–82 × 6–8 µm ($\overline{x}$ = 71 × 7 µm, n = 50); 8-septate conidia: (66–)70–82 × 3–5 µm ($\overline{x}$ = 76 × 7 µm, n = 15); 9-septate conidia: 91 × 7–8 µm ($\overline{x}$ = 91 × 8 µm, n = 2). *Conidiogenous cells* subcylindrical, (14–)29–66(–69) × 3–4 µm ($\overline{x}$ = 45 × 3 µm, n = 50). *Aerial microconidia* in small false heads, oval to subcylindrical, 0–1-septate; aseptate conidia: 8–20(–22) × 3–5 µm ($\overline{x}$ = 12 × 4 µm, n = 50); 1-septate conidia: 14–22 × (3–)4–5 µm ($\overline{x}$ = 17 × 5 µm, n = 50). *Chlamydospores* globose to subglobose, single or in pairs, 4–12 × 5–10 µm ($\overline{x}$ = 7 × 7 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate; 4 mm per day on PDA at 25 °C. Upper view; white, orange in the centre, aerial mycelia sparse, and regular margin. In reverse; white, orange in the centre. On CLA, sporodochia produced after 30 days.

Material examined – China, Guangdong Province, Zhongshan City, on a stem of *Chaenomeles sinensis* (*Rosaceae*), 22 October 2021, Y.X. Zhang, living culture, ZHKUCC 23-0947.

Notes – In the phylogenetic analysis of the present study, one strain from our isolates clustered with *Neocosmospora pseudensiformis* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 7). Our collection is morphologically similar to those of *N. pseudensiformis* (Nalim et al. 2011), and thus we identified our isolate as *N. pseudensiformis.* To date, the only reported host for this species is *Cocos nucifera* (Sandoval-Denis et al. 2019). Herein we first report *N. pseudensiformis* from *Chaenomeles sinensis*.

Neocosmospora solani (Mart.) L. Lombard & Crous, Stud. Mycol. 80: 228 (2015) Fig. 31

Index Fungorum number: IF810964; Facesoffungi number: FoF14358

Asexual morph: *Sporodochia* off-white, formed on CLA. *Sporodochial conidiophores* branched, irregular, dense. *Sporodochial conidiogenous cells* subcylindrical, 21–38(–42) × 6–8 µm ($\overline{x}$ = 30 × 7 µm, n = 50). *Sporodochial conidia* apical cell blunt, basal cell foot-shaped, 1–3-septate, 1-septate conidia: 23–32(–35) × 4–7 µm ($\overline{x}$ = 28 × 5 µm, n = 16); 2-septate conidia: 26–33 × 5–6 µm ($\overline{x}$ = 29 × 6 µm, n = 11); 3-septate conidia: 29–40 × 5–7 µm ($\overline{x}$ = 35 × 6 µm, n = 50). *Conidiogenous cells* subcylindrical, (4–)6–80(–90) × 2–5 µm ($\overline{x}$ = 23 × 4 µm, n = 50). *Aerial microconidia* in small false heads, oval, reniform, ellipsoidal to subcylindrica, 0–1-septate; aseptate conidia: 8–17(–22) × 4–6 µm ($\overline{x}$ = 13 × 5 µm, n = 22); 1-septate conidia: 6–25× 3–6 µm ($\overline{x}$ = 17 × 5 µm, n = 50). *Chlamydospores* subglobose to globose, single, in pairs or clumps, 5–10 × 4–12 µm ($\overline{x}$ = 7 × 8 µm, n = 50). Sexual morph: not observed.

Culture characteristics – Growth rate on PDA was 4 mm/d at 25 °C. Surface view; white, floccose, regular margin. In reverse; white. Sporodochia produced on CLA after 20 days.

Material examined – China, Guangdong Province, Guangzhou City, on a sheath of *Strelitzia reginae* (*Musaceae*), 19 April 2022, YX Zhang, C Chen, SQ Ma, living cultures, ZHKUCC 23-

0944, and ZHKUCC 23-0945; Jiangxi Province, Yichun City, on a bulb of *Lilium brownii* (*Liliaceae*), 7 May 2022, Chunping You, living culture, ZHKUCC 23-0946.

Notes – Three isolates from this study grouped with *Neocosmospora solani* with 94% ML bootstrap support and 0.85 BYPP value (Fig. 7). Our isolates are similar to *N. solani* (Schroers et al. 2016), and thus, we identify this taxon as *N. solani*.

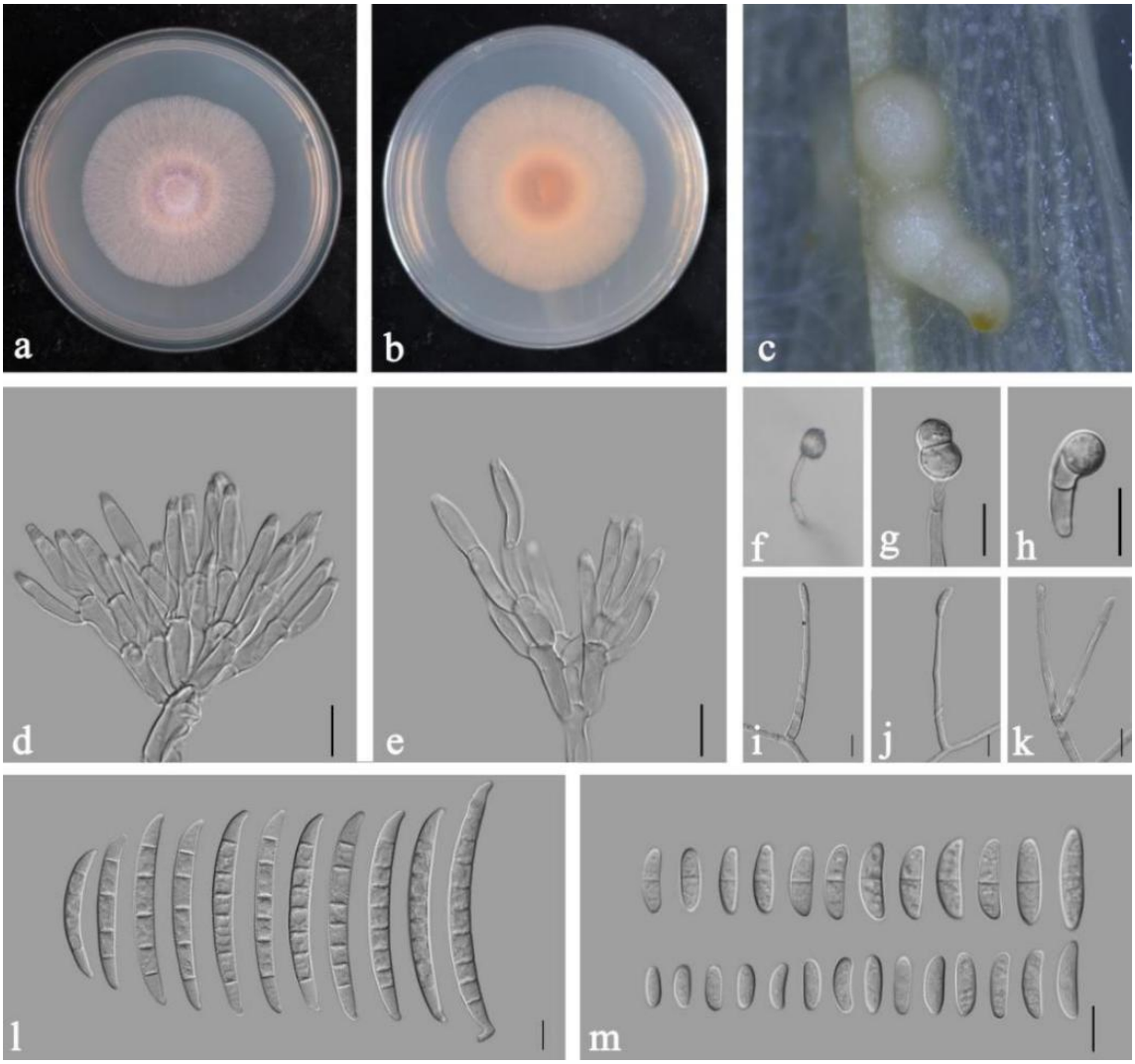

Figure 30 – *Neocosmospora pseudensiformis* (ZHKUCC 23-0947). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

DISCUSSION

Correct species identification is important in plant pathology, particularly for early detection and disease control (Jayawardena et al. 2021, Manawasinghe et al. 2021, Chen et al. 2023b). Thus, pathogen identification and classification are crucial for developing a control strategy. Currently, species identification in mycology mostly relies on molecular phylogeny, supplemented by morphology. However, defining what is a species in the most cryptic and specious genera is still challenging (Manawasinghe et al. 2021, Bhunjun et al. 2022). In the present study, based on molecular phylogeny and morphology, 24 species with one undetermined isolate belonging to *Albonectria*, *Fusarium*, and *Neocosmospora* were isolated and identified from various ornamental plants from Southern China. Our study enhances the current understanding of the species richness of these three genera in the ornamental plant industry. A total of 18 *Fusarium* species with one

unnamed species were identified from four *Fusarium* species complexes, namely, the *F. fujikuroi* species complex, *F. nisikadoi* species complex, *F. oxysporum* species complex, and the *F. tricinctum* species complex. *Fusarium oxysporum* species complex has the highest number of isolates with 33 isolates defined as nine species. Similar results were observed in previous studies in which most fusarioid pathogens associated with ornamentals are from *Fusarium oxysporum* species complex and *Fusarium fujikuroi* species complex (Gullino et al. 2015, Srivastava et al. 2018, Kamali-Sarvestani et al. 2022, Zhang et al. 2021, 2022).

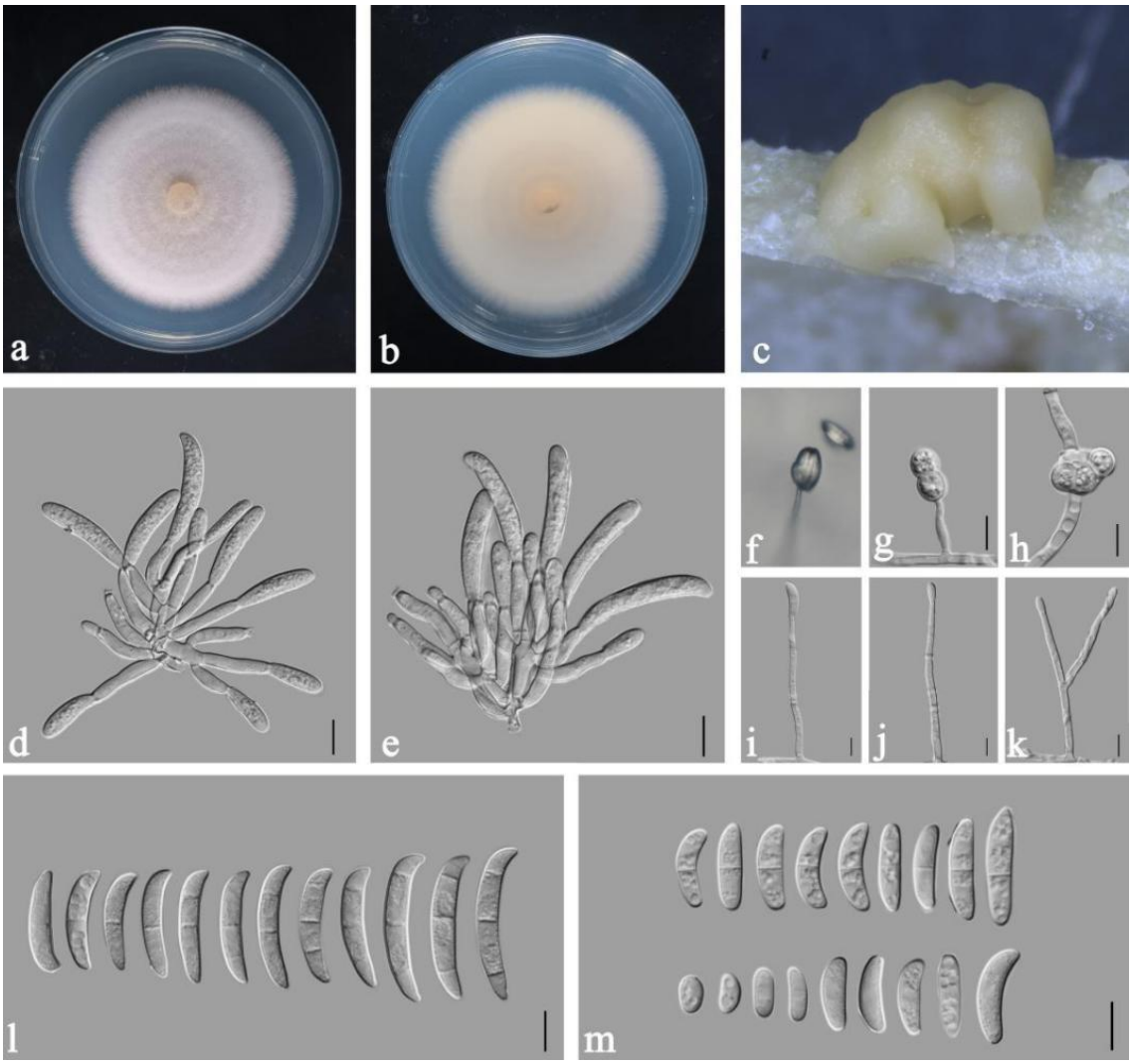

Figure 31 – *Neocosmospora solani* (ZHKUCC 23-0946). a–b 7-day-old PDA culture (surface, reverse). c Sporodochia on CLA. d–e Sporodochia conidiophores, phialides. f Aerial conidial false head. g–h Chlamydospores. i–k Aerial conidiophores phialides. l Sporodochial conidia. m Aerial microconidia. Scale bars: 10 μm.

Morphology plays a key role in species delineation, especially when it comes to addressing the taxonomy and nomenclature of most specious fungal genera such as *Fusarium*. With the acceptance of one fungus, one name (Taylor 2011), *Fusarium* was accepted over *Gibberella*, and the genus was typified with *F. sambucinum* (Geiser et al. 2013, Rossman et al. 2013). *Fusarium* s. str. species have *Gibberella* sexual morphs, whereas other fusarioid genera have more nectria-like sexual morphs, although the asexual morphs of these genera are characterized by curved, hyaline macroconidia. These macroconidia have apical and basal cells with characteristic shapes (Crous et al. 2021). *Neocosmospora* species are distinguished by red perithecia, whereas purple or blackish perithecia are formed in *Fusarium* (*Gibberella*). Despite this, asexually, *Neocosmospora* species

develop macroconidia, which resemble *Fusarium* and those of the other fusarioid genera (Crous et al. 2021). Over the years, *F. solani* species complex has undergone several taxonomic revisions (Matuo & Snyder 1973, Gerlach & Nirenberg1982, Lombard et al. 2015) and Sandoval-Denis et al. (2019) accepted *F. solani* species complex as *Neocosmospora*. Within the former broader concept of *Fusarium, Albonectria* was initially known as the *F. decemcellulare* species complex, and it is currently accepted as a separate genus (Lombard et al. 2015, Crous et al. 2021). *Albonectria* species are defined by white perithecia and 3-septate, pale yellow-brown, faintly striate ascospores (Rossman et al. 1999), while *Fusarium* produces 1–3-septate, hyaline to pale yellow-brown and smooth ascospores (Crous et al. 2021). Asexually, these taxa develop fusarioid-like conidia characterised by multi-septate macroconidia, and microconidia can be present, and chlamydospores are absent (Crous et al. 2021).

For the micro-morphological characterisation of fusarioid species, CLA (Yilmaz et al. 2021, Han et al. 2023) and SNA (Nirenberg & O'Donnell 1998, Aoki & O'Donnell 1999, Aoki et al. 2001) have been previously used as the standard media. In our study, both CLA and SNA were used to induce sporulation. We observed that some species (e.g., *F. contaminatum*, *F. nirenbergiae*, and *F. curvatum*) could produce macroconidia in both CLA and SNA. However, some species could produce macroconidia only on CLA (*F. duoseptatum*, *F. concentricum* and *N. keratoplastica*), whereas undetermined species in this study produced macroconidia only on SNA. Following these observations, it is recommended to use both CLA and SNA to observe more detail of macroconidia of fusarioid species (Leslie & Summerell 2006, Crous et al. 2021, this study). Although morphology plays a role at the generic level classification among fusarioid taxa, in the absence of sexual morphs, it is less likely distinguish closely related species conclusively. Furthermore, most of the endophytic isolations tend to be sterile on artificial media. In the present study, we introduced our novel species based on phylogenetic placement and nucleotide variations.

The molecular phylogeny of fusarioid species is subjected to long-term discussions. Following the recent taxonomic treatments by Crous et al. (2021) nine gene regions with protein-coding genes, including *act1*, *his3*, *CaM*, *rpb1*, *rpb2*, *tef1-α*, and *tub2* have been used for identification and taxonomy in fusarioid fungi. However, different taxonomists have suggested using different combinations of loci to achieve correct identification (Crous et al. 2021, Han et al. 2023, this study). Herein, we employed six loci, ITS, *CaM*, *rpb1*, *rpb2*, *tef1-α* and *tub2*, following Lombard et al. (2019), Crous et al. (2021), Yilmaz et al. (2021), Sandoval-Denis et al. (2019) and Wang et al. (2022). Among these loci, *rpb1*, *rpb2* and *tef1-α* are the most informative genes for the *Fusarium oxysporum* species complex, *Fusarium fujikuroi* species complex, and *Neocosmospora* species identification. Similar to Lombard et al. (2019), we observed that adding *rpb2* and *tub2* provides a better resolution to delineate new taxa in the *Fusarium oxysporum* species complex. For better species delineation in *Fusarium fujikuroi* species complex and *Neocosmospora*, *tef1-α* and *rpb2* are the most effective (Wang et al. 2022). However, we observed that *rpb1* also improves delineation of taxa. As an example, adding the *rpb1* gene region helps to separate *F. concentricum* from its closely related species, and simultaneously, statistical support of the main clade of the *Fusarium fujikuroi* species complex phylogenetic tree was significantly increased when adding the *rpb1* gene region (this study). O'Donnell (2000) and Al-Hatmi et al. (2019) mentioned that the *CaM* region yields conflicting clade resolutions in the *Fusarium fujikuroi* species complex observed in the present study. In our study, the *rpb1*, *rpb2*, *tef1-α*, and *tub2* datasets gave the best *Fusarium fujikuroi* species complex resolution. Furthermore, for *Neocosmospora*, we observed that *rpb2* and *tef1-α* could delineate species well, while ITS and *rpb1* could increase the statistical support. Eight isolates from this study developed a clade with *F. rosae-roxburghii*, *F. odoratissimum*, *F. cili*, and *F. phialophorum*. Based on morphology, phylogenetic placement, and sequence variations, three isolates from this study were identified as *F. odoratissimum* and we synonymised *F. rosae-roxburghii* under *F. odoratissimum*. However, in this study, the remaining five strains clustered in this species complex are not synonymised as further analysis is required. It is noteworthy to mention that once we add more representative strains to this clade, the phylogenetic placements of each strain changes, and it is difficult to define the species boundaries

within this complex. Future studies are necessary to understand how much inter-species diversity will be accepted to justify introducing a new species in the *Fusarium oxysporum* species complex.

In the present study, diseased samples were collected from 24 host species. Among these, we defined nine *Fusarium* species from 13 host species (Supplementary Table 2). Our results reflect the high species richness of fusarioid taxa associated with ornamental plants in South China. However, species discussed in the present study are generally not host-specific, with examples like *Fusarium oxysporum* capable of infecting over 500 different host species (Farr & Rossman 2024). Furthermore, these associations vary from monocot plants to woody perennials as well as soil (Crous et al. 2021, Farr & Rossman 2024, this study). Interestingly, the lifestyles of these species can vary with the host association and environmental factors. *Fusarium oxysporum* is associated with plants as an endophyte or pathogen (Rana et al. 2017). This species has the ability to produce chlamydospores, which serve as the primary survival structure in the absence of a host (Nelson 1981). Similarly, species of Fusarium and allied genera have broad relationships with their hosts, which need to be better understood in the future.

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Supplementary Table 1 Species and their hosts from this study.

Species name	Hosts	New hosts
Albonectria		
Albonectria schimae	*Schima superba*	
Fusarium		
***F. fujikuroi* species complex**		
Fusarium annulatum	*Paliurus hemsleyanus*, *Dendrobium nobile*	*Phalaenopsis aphrodite*, *Rosa chinensis*
Fusarium concentricum		*Spathiphyllum floribundum*, *Bougainvillea glabra*, *Philodendron tatei*
Fusarium cymbidii	*Cymbidium sinense*	
Fusarium dendrobii	*Dendrboium* sp.	
Fusarium fujikuroi		*Philodendron tatei*
Fusarium guangdongense	*Cymbidium* sp., *Dendrobium nobile*, *Heptapleurum heptaphyllum*	
Fusarium temperatum		*Campanula medium*
***F. nisikadoi* species complex**		
Fusarium anoectochili	*Anoectochilus roxburghii*	
***F. oxysporum* species complex**		
F. contaminatum		*Anoectochilus roxburghii*, *Zygocactus truncatus*
Fusarium curvatum	*Cymbidium sinense*	*Dendrobium* sp.
Fusarium duoseptatum		*Strelitzia reginae*
Fusarium grosmichelii		*Strelitzia reginae*, *Antirrhinum majus*
Fusarium menglaense		*Antirrhinum majus*
Fusarium nirenbergiae	*Lilium brownii*	*Strelitzia reginae*, *Bougainvillea spectabilis*, *Hymenocallis littoralis*
Fusarium odoratissimum		*Callistemon rigidus*
Fusarium triseptatum		*Aglaonema commutatum*, *Strelitzia reginae*
Fusarium sp.	*Cordyline fruticosa*, *Arrhenatherum elatius*	
***F. tricinctum* species complex**		
Fusarium avenaceum		*Hydrangea macrophylla*
Fusarium dendranthematis	*Dendranthema morifolium*	
Neocosmospora		
Neocosmospora guangdongensis	*Paphiopedilum* sp.	
Neocosmospora keratoplastica		*Strelitzia reginae*
Neocosmospora paphiopedili	*Paphiopedilum* sp., *Spathiphyllum floribundum*	
Neocosmospora pseudensiformis		*Chaenomeles sinensis*
Neocosmospora solani	*Strelitzia reginae*, *Lilium brownii*	

Supplementary Table 2 GenBank accession numbers used in this study.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
Albonectria							
A. guizhouensis	CGMCC3.25472T	OR034252	OR043728	OR043878	OR043930	OR043779	OR753368
A. guizhouensis	GUCC 198015.1	OR034253	OR043729	OR043879	OR043931	OR043780	OR043824
A. albosuccinea	NRRL 20459	JAADYS010000048.1	–	JAADYS010002360.1	–	JX171471	JX171585
A. rigidiuscula	CBS 133754	MW827602	MW834269	–	–	MW834177	MW833995
A. schimae	**ZHKUCC 24-0768T**	**–**	**–**	**PP983148**	**PP983175**	**PP983166**	**PP983202**
A. schimae	**ZHKUCC 24-0769**	**–**	**–**	**PP983149**	**PP983176**	**PP983167**	**PP983203**
A. verrucosa	NRRL 22566	–	–	–	–	JX171500	JX171613
Setofusarium setosum	CBS 635.92T	MW827634	–	MW834294	–	JX171539	JX171651
Fusarium							
***Fusarium fujikuroi* species complex**							
F. acutatum	CBS 401.97	–	MW402458	MW402124	MW402322	MW402652	MW402813
F. acutatum	CBS 402.97T	–	MW402459	MW402125	MW402323	MW402653	MW402768
F. acutatum	CBS 739.97	–	AF158329	AF160276	MW402348	MW402696	MN193883
F. agapanthi	NRRL 54463T	–	KU900611	KU900630	KU900635	KU900620	KU900625
F. agapanthi	CBS 100193	–	MW402363	MW401959	MW402160	MW402491	MW402727
F. agapanthi	NRRL 54464	–	KU900613	MN193856	KU900637	MW402718	KU900627
F. aglaonematis	ZHKUCC 22-0077	–	ON330434	ON330437	ON330440	ON330446	ON330443
F. aglaonematis	ZHKUCC 22-0078	–	ON330435	ON330438	ON330441	ON330447	ON330444
F. aglaonematis	ZHKUCC 22-0079T	–	ON330436	ON330439	ON330442	ON330448	ON330445
F. ananatum	CBS 118516T	–	MW402376	LT996091	MN534089	MW402507	LT996137
F. ananatum	CBS 118517	–	MN534157	MN533988	MN534090	MW402508	MN534229
F. ananatum	CBS 118518	–	MW402377	MW401979	MW402179	–	MW402730
F. andiyazi	CBS 119857T	–	MN534175	MN193854	LT996113	MW402524	LT996138
F. andiyazi	CBS 119856	–	MN534174	MN533989	MN534081	MW402523	MN534286
F. annulatum	CBS 137537	–	MW402414	MW402060	MW402259	MW402586	MW402749
F. annulatum	CBS 792.91	–	MW402481	MW402153	MW402354	MW402706	MW402774
F. annulatum	CBS 143605	–	MW402435	MW402094	MW402293	MW402615	MW402760
F. annulatum	CBS 258.54T	–	MT010908	MT010994	MT011041	MT010944	MT010983
F. annulatum	CBS 533.95	–	MW402470	MW402138	MW402338	–	MW402817
F. annulatum	CBS 139334	–	MW402417	MW402065	MW402264	MW402592	MW402750
F. annulatum	CBS 115.97	–	MW402373	MW401973	MW402173	MW402503	MW402785
F. annulatum	**ZHKUCC 23-0925**	–	–	**PQ031184**	**PQ031163**	**PQ212640**	**PQ139063[a],**

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
							PQ139092[b]
F. annulatum	**ZHKUCC 23-0926**	–	–	**PQ031185**	**PQ031164**	**PQ212641**	**PQ139064[a], PQ139093[b]**
F. annulatum	**ZHKUCC 23-0927**	–	–	**PQ031186**	**PQ031165**	**PQ212642**	**PQ139065[a], PQ139094[b]**
F. annulatum	**ZHKUCC 23-0928**	–	–	**PQ031187**	**PQ031166**	**PQ212643**	**PQ139066[a], PQ139095[b]**
F. anthophilum	CBS 222.76ET	–	MW402451	MW402114	MW402312	MW402641	MW402811
F. anthophilum	CBS 119858	–	MN534158	MN533990	MN534091	MW402525	MN534232
F. anthophilum	CBS 119859	–	MN534164	MN533991	MN534092	MW402526	MN534233
F. aquaticum	LC13615	–	MW566273	MW580446	MW533728	MW024437	MW474392
F. aquaticum	LC13616	–	MW566274	MW580447	MW533729	MW024438	MW474393
F. aquaticum	LC7502T	–	MW566275	MW580448	MW533730	MW024439	MW474394
F. awaxy	CBS 119831	–	MN534167	MN534056	MN534108	MW402514	MN534237
F. awaxy	CBS 119832	–	MN534170	MN534057	MN534106	MW402515	MN534240
F. awaxy	CBS 139380	–	MN534172	MN534058	MN534107	MW402597	MN534238
F. awaxy	LGMF 1930T	–	MK766940	MG839004	MG839013	–	MK766941
F. babinda	NRRL 25807T	–	–	AF160305	–	–	MN534245
F. bactridioides	CBS 100057T	–	MN534173	MN533993	MN534112	MW402490	MN534235
F. bactridioides	NRRL.20476	–	AF158343	AF160290	U34434	–	–
F. begoniae	CBS 452.97T	–	MN534163	MN533994	MN534101	MW402675	MN534243
F. begoniae	CBS 403.97	–	MW402460	MN193858	U61543	MW402654	MN193886
F. begoniae	CBS 110283	–	MW402370	MW401969	MW402170	MW402500	MW402784
F. begoniae	CBS 110282	–	–	MW401968	MW402169	–	–
F. brachiariae	CML 3032T	–	–	MT901348	MT901321	–	MT901314
F. brachiariae	CML 3163	–	–	MT901349	MT901322	–	MT901315
F. brevicatenulatum	CBS 404.97T	–	–	MN533995	MN534063	MW402655	MN534295
F. brevicatenulatum	CBS 100196	–	–	MN193859	–	MW402492	MN193887
F. bulbicola	CBS 220.76T	–	MW402450	KF466415	KF466437	KF466394	KF466404
F. caapi	CML 3657T	–	–	MT901350	MT901323	–	MT901316
F. caapi	CML 3658	–	–	MT901351	MT901324	–	MT901317
F. casha	PPRI 21883T	–	–	MF787261	MF787255	–	MN605059
F. casha	PPRI 20462	–	–	MF787262	MF787256	–	MN605060
F. casha	PPRI 20468	–	–	MF787263	MF787257	–	MN605061
F. chinhoyiense	NRRL 25221T	–	MN534196	MN534050	MN534082	MW402711	MN534262

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. chinhoyiense	NY 001B5	–	MN534197	MN534051	MN534083	MW402725	MN534263
F. chuoi	CBS 148464T	–	OK626304	OK626308	OK626310	OK626306	OK626302
F. circinatum	CBS 405.97T	–	MN534199	MN533997	MN534097	MW402656	MN534252
F. circinatum	CBS 117843	–	–	MW401978	MW402178	MW402506	MW402786
F. circinatum	CBS 119864	–	MW402389	MW401996	MW402196	MW402528	MW402736
F. coicis	NRRL 66233T	–	LT996178	KP083251	LT996115	KP083269	KP083274
F. concentricum	CBS 450.97T	–	MW402467	AF160282	MW402334	MW402674	JF741086
F. concentricum	CBS 453.97	–	MN534216	MN533998	MN534123	MW402676	MN534264
F. concentricum	LC13617	–	–	MW580453	MW533735	MW024444	MW474399
F. concentricum	CBS 102157	–	MW402367	MW401963	MW402164	MW402496	MW402728
F. concentricum	**ZHKUCC 23-0929**	–	–	**PQ031149**	**PQ031167**	**PQ212644**	**PQ139067[a], PQ139096[b]**
F. concentricum	**ZHKUCC 23-0930**	–	–	**PQ031150**	**PQ031168**	**PQ212645**	**PQ139068[a], PQ139097[b]**
F. concentricum	**ZHKUCC 23-0931**	–	–	**PQ031151**	**PQ031169**	**PQ212646**	**PQ139069[a], PQ139098[b]**
F. curculicola	PPRI 20458T	–	–	MF787266	MF787258	–	MN605062
F. curculicola	PPRI 20464	–	–	MF787267	MF787259	–	MN605063
F. curculicola	PPRI 20386	–	–	MF787268	MF787260	–	MN605064
F. cymbidii	**ZHKUCC 23-0914T**	–	–	**PQ031173**	**PQ031152**	**PQ201873**	**PQ139060[a], PQ139081[b]**
F. cymbidii	**ZHKUCC 23-0915**	–	–	**PQ031174**	**PQ031153**	**PQ201874**	**PQ139061[a], PQ139082[b]**
F. cymbidii	**ZHKUCC 23-0916**	–	–	**PQ031175**	**PQ031154**	**PQ201875**	**PQ139062[a], PQ139083[b]**
F. dendrobii	**ZHKUCC 24-0047T**	–	–	**PP983150**	**PP983177**	**PP983168**	**PQ660161[a], PQ602156[b]**
F. dendrobii	**ZHKUCC 24-0048**	–	–	**PP983151**	**PP983178**	**PP983169**	**PQ660162[a], PQ602157[b]**
F. denticulatum	CBS 406.97	–	MN534185	MN533999	MN534067	MW402657	MN534273
F. denticulatum	CBS 407.97T	–	MN534186	MN534000	MN534068	MW402658	MN534274
F. denticulatum	CBS 735.97	–	AF158322	AF160269	U61550	–	LT996143
F. dhileepanii	BRIP 71717T	–	–	OK509072	–	–	OK533536
F. dlaminii	CBS 175.88	–	MN534150	MN534002	MN534138	MW402623	MN534256
F. dlaminii	CBS 481.94	–	MN534151	MN534003	MN534139	MW402679	MN534257

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. dlaminii	CBS 119860T	–	MW402388	MW401995	MW402195	KU171681	KU171701
F. echinatum	CBS 146497T	–	MW834110	MW834273	MW834301	MW834187	MW834004
F. echinatum	CBS 146496	–	MW834109	MW834272	MW834300	MW834186	MW834003
F. elaeagni	LC13627T	–	MW566293	MW580466	MW533748	MW024457	MW474412
F. elaeagni	LC13628	–	MW566294	MW580467	MW533749	MW024458	MW474413
F. elaeagni	LC13629	–	MW566295	MW580468	MW533750	MW024459	MW474414
F. erosum	LC18579	–	OQ125640	OQ126065	OQ126319	OQ125773	OQ126517
F. erosum	CGMCC3.23518T	–	OQ125648	OQ126066	OQ126321	OQ125772	OQ126518
F. ficicrescens	CBS 125177	–	MN534176	MN534006	MN534071	MW402545	MN534281
F. ficicrescens	CBS 125178T	–	KU603958	KU604452	KP662896	MW402546	KT154002
F. ficicrescens	CBS 125181	–	MN534177	MN534007	MN534072	MW402548	MN534282
F. fracticaudum	CMW 25245T	–	–	KJ541059	KJ541051	LT996196	LT996144
F. fractiflexum	NRRL 28852T	–	AF158341	AF160288	AF160315	–	LT575064
F. fredkrugeri	CBS 408.97	–	MW402461	MW402126	MW402324	–	MW402814
F. fredkrugeri	CBS 144209T	–	LT996181	LT996097	LT996118	LT996199	LT996147
F. fredkrugeri	CBS 144495	–	LT996180	LT996096	LT996117	LT996198	LT996146
F. fredkrugeri	NRRL 26152	–	–	MW402159	–	MW402714	MW402778
F. fujikuroi	CBS 221.76T	–	–	MN534010	MN534130	MW402640	KU604255
F. fujikuroi	CBS 186.56	–	MW402447	MW402108	MW402306	MW402632	MW402765
F. fujikuroi	CBS 257.52	–	MW402454	MW402119	MW402317	MW402645	MW402812
F. fujikuroi	**ZHKUCC 23-0932**	–	–	**PQ031188**	**PQ031170**	**PQ212647**	**PQ139070[a], PQ139099[b]**
F. fujikuroi	**ZHKUCC 23-0933**	–	–	**PQ031189**	**PQ031171**	**PQ212648**	**PQ139071[a], PQ139100[b]**
F. gigantea	CMM 3557T		–	KY490537	–	–	MT188557
F. globosum	CBS 428.97T		MN534218	KF466417	MN534124	MW402668	KF466406
F. globosum	CBS 429.97		–	MW402130	MW402329	–	–
F. globosum	CBS 430.97		MN534219	MN534013	MN534125	–	MN534265
F. guangdongense	**ZHKUCC 23-0917**	–	–	**PQ031176**	**PQ031155**	**PQ212632**	**PQ139073[a], PQ139084[b]**
F. guangdongense	**ZHKUCC 23-0918**	–	–	**PQ031177**	**PQ031156**	**PQ212633**	**PQ139074[a], PQ139085[b]**
F. guangdongense	**ZHKUCC 23-0919**	–	–	**PQ031178**	**PQ031157**	**PQ212634**	**PQ139075[a], PQ139086[b]**

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	*CaM*	*tef1-α*	*tub2*	*rpb1*	*rpb2*
F. guangdongense	**ZHKUCC 23-0920T**	–	–	**PQ031179**	**PQ031158**	**PQ212635**	**PQ139076[a], PQ139087[b]**
F. guangdongense	**ZHKUCC 23-0921**	–	–	**PQ031180**	**PQ031159**	**PQ212636**	**PQ139077[a], PQ139088[b]**
F. guangdongense	**ZHKUCC 23-0922**	–	–	**PQ031181**	**PQ031160**	**PQ212637**	**PQ139078[a], PQ139089[b]**
F. guangdongense	**ZHKUCC 23-0923**	–	–	**PQ031182**	**PQ031161**	**PQ212638**	**PQ139079[a], PQ139090[b]**
F. guangdongense	**ZHKUCC 23-0924**	–	–	**PQ031183**	**PQ031162**	**PQ212639**	**PQ139080[a], PQ139091[b]**
F. guttiforme	CBS 409.97T	–	MT010901	MT010999	MT011048	MT010938	MT010967
F. guttiforme	NRRL 22945	–	AF158350	AF160297	U34420	JX171505	JX171618
F. hechiense	LC13644T	–	MW566321	MW580494	MW533773	MW024482	MW474440
F. hechiense	LC13645	–	MW566322	MW580495	MW533774	MW024483	MW474441
F. hechiense	LC13646	–	MW566323	MW580496	MW533775	MW024484	MW474442
F. hipposidericola	KUMCC 21-0725	–	OR022055	OR025994	OR025939	–	OR025910
F. hipposidericola	KUMCC 21-0726	–	OR022056	OR025995	OR025940	–	OR025911
F. hipposidericola	KUMCC 21-0727	–	OR022057	OR025996	OR025941	–	OR025912
F. konzum	CBS 119849T	–	LT996182	LT996098	MN534095	MW402519	MW402733
F. konzum	CBS 139382	–	MW402418	MW402071	MW402270	MW402598	MW402804
F. konzum	CBS 139383	–	MN534200	MN534014	MN534094	MW402599	MN534244
F. lactis	CBS 411.97T	–	MN534178	MN193862	MN534077	MW402659	MN534275
F. lactis	CBS 420.97	–	MN534181	MN534015	MN534078	MW402667	MN534296
F. longicornicola	NRRL 52706T	–	MW402487	JF740788	MW402360	–	JF741114
F. longicornicola	NRRL 52712	–	MW402488	JF740794	MW402361	MW402716	JF741120
F. longicornicola	NRRL 52713	–	MW402489	JF740795	MW402362	MW402717	JF741121
F. lumajangense	InaCCF872T	–	–	LS479441	LS479433	–	LS479850
F. lumajangense	InaCCF993	–	–	LS479442	LS479434	–	LS479851
F. madaense	CBS 146648	–	MW402436	MW402095	MW402294	MW402616	MW402761
F. madaense	CBS 146651	–	MW402437	MW402096	MW402295	MW402617	MW402762
F. madaense	CBS 146656	–	MW402438	MW402097	MW402296	MW402618	MW402763
F. madaense	CBS 146669T	–	MW402439	MW402098	MW402297	MW402619	MW402764
F. mangiferae	CBS 120994T	–	MN534224	MN534017	MN534128	MW402530	MN534271
F. mangiferae	CBS 119853	–	MN534225	MN534016	MN534140	MW402522	MN534270
F. mangiferae	NRRL 25226	–	AF158334	AF160281	U61561	MW402712	HM068353

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. marasasianum	CMW 25512	–	MN534208	MN534018	MN534113	–	MN534249
F. mexicanum	NRRL 53147T	–	–	GU737282	GU737494	MG838088	MN724973
F. mexicanum	NRRL 47473	–	GU737389	GU737416	GU737308	LR792579	LR792615
F. mindanaoense	PD20.05T	–	LC720610	LC720609	LC720611	LC720612	LC720608
F. mirum	CML 3859T	–	–	MK895725	MK907329	–	MK907308
F. mirum	CML 3858	–	–	MK895726	MK907328	–	MK907307
F. mundagurra	RGB5717T	–	MN534214	KP083256	MN534146	–	KP083276
F. musae	CBS 624.87T	–	MW402474	FN552086	FN545368	MW402689	MW402772
F. musae	CBS 115315	–	–	MW401974	MW402174	–	–
F. musae	NRRL 28893	–	FN552070	FN552092	FN545374	–	FN552114
F. napiforme	CBS 748.97T	–	MN534192	MN193863	MN534085	MW402701	MN534291
F. napiforme	CBS 135139	–	MN534183	MN534019	MN534084	MW402572	MN534290
F. napiforme	CBS 135141	–	–	MW402045	MW402244	MW402573	MW402797
F. nirenbergiae	CBS 744.97	–	AF158365	AF160312	U34424	–	LT575065
F. nygamai	CBS 572.94	–	MW402473	MW402141	MW402341	–	MW402819
F. nygamai	CBS 749.97T	–	MW402479	MW402151	MW402352	MW402703	EF470114
F. nygamai	CBS 834.85	–	MW402482	MW402154	MW402355	MW402707	MW402821
F. ophioides	CBS 118512T	–	MN534209	MN534022	MN534118	–	MN534303
F. ophioides	CBS 118510	–	MN534201	MN534020	MN534121	–	MN534301
F. ophioides	CBS 118511	–	MN534204	MN534021	MN534122	–	MN534299
F. panlongense	LC13656T	–	MW566337	MW580510	MW533789	MW024498	MW474456
F. panlongense	MUCL 55950	–	LT575151	LT574905	LT575070	–	LT574986
F. parvisorum	CMW 25267T	–	–	KJ541060	KJ541055	–	LT996150
F. phyllophilum	CBS 216.76T	–	KF466333	MN193864	KF466443	MW402637	KF466410
F. phyllophilum	CBS 246.61	–	MW402453	MW402118	MW402316	MW402644	–
F. pilosicola	NRRL 29124T	–	MN534159	MN534055	MN534099	–	MN534248
F. pilosicola	NRRL 29123	–	MN534165	MN534054	MN534098	–	MN534247
F. pininemorale	CMW 25243	–	MN534211	MN534026	MN534115	–	MN534250
F. planum	CGMCC3.23517T	–	OQ125677	OQ126125	OQ126352	OQ125871	OQ126555
F. planum	LC18578	–	OQ125678	OQ126126	OQ126351	OQ125875	OQ126556
F. planum	LC18411	–	OQ125679	OQ126124	OQ126350	OQ125872	OQ126561
F. prieskaense	CBS 146498	–	MW834112	MW834275	MW834303	MW834190	MW834007
F. prieskaense	CPC 30825	–	MW834111	MW834274	MW834302	MW834189	MW834006
F. prieskaense	CBS 146499	–	MW834113	MW834276	MW834304	MW834191	MW834008
F. proliferatum	CBS 480.96ET	–	MN534217	MN534059	MN534129	–	MN534272

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. pseudoanthophilum	CBS 414.97T	–	MW402463	MW402128	MW402326	MW402661	–
F. pseudoanthophilum	CBS 415.97	–	–	MW402129	MW402327	MW402662	–
F. pseudoanthophilum	CBS 745.97	–	MW402476	MW402148	MW402349	MW402697	MW402820
F. pseudoanthophilum	CBS 746.97	–	MW402477	MW402149	MW402350	MW402698	–
F. pseudocircinatum	CBS 449.97T	–	MN534190	AF160271	MN534069	MW402673	MN534277
F. pseudocircinatum	CBS 455.97	–	MN534184	MN534029	MN534070	–	MN534276
F. pseudocircinatum	NRRL 36939	–	–	MN193866	–	MW402715	MW402779
F. pseudonygamai	CBS 417.97T	–	AF158316	AF160263	MN534066	MW402664	MN534285
F. pseudonygamai	CBS 416.97	–	MN534194	MN534030	MN534064	MW402663	MN534283
F. pseudonygamai	CBS 484.94	–	MN534195	MN534031	MN534065	MW402681	MN534284
F. ramigenum	CBS 418.97	–	MN534187	KF466423	MN534145	MW402665	KF466412
F. ramigenum	CBS 526.97	–	MN534188	MN534032	MN534086	MW402682	MN534292
F. sacchari	CBS 223.76ET	–	AF158331	MW402115	MW402313	–	JX171580
F. sacchari	CBS 121683	–	–	MW402002	MW402202	MW402534	MW402789
F. sacchari	CBS 139376	–	–	MW402069	MW402268	MW402596	MW402803
F. sanyaense	CGMCC3.23523	–	OQ125641	OQ126093	OQ126322	OQ125859	OQ126547
F. sanyaense	LC18540	–	OQ125642	OQ126095	OQ126308	OQ125861	OQ126549
F. sanyaense	LC18537	–	OQ125643	OQ126094	OQ126323	OQ125860	OQ126548
F. secorum	NRRL 62593T	–	KJ189235	KJ189225	–	–	–
F. secorum	NRRL 62594	–	KJ189238	KJ189228	–	–	–
F. siculi	CBS 142222T	–	LT746189	LT746214	LT746346	–	LT746327
F. siculi	CPC 27189	–	LT746190	LT746215	LT746347	–	LT746328
F. sororula	CBS 137242T	–	–	KJ541067	KJ541057	LT996206	LT996153
F. sterilihyposum	NRRL 25623T	–	AF158353	MN193869	AF160316	MW402713	MN193897
F. sterilihyposum	NRRL 53991	–	GU737386	GU737413	GU737305	–	–
F. sterilihyposum	NRRL 53997	–	GU737387	GU737414	GU737306	–	–
F. sterilihyposum	NRRL 54011	–	GU737388	GU737415	GU737307	–	–
F. subglutinans	CBS 747.97ET	–	MW402478	MW402150	MW402351	MW402700	MW402773
F. subglutinans	CBS 215.76	–	MN534171	MN534061	MN534109	MW402636	MN534241
F. subglutinans	CBS 479.94	–	MN534166	MN534036	MN534105	MW402678	MN534236
F. succisae	CBS 219.76ET	–	AF158344	AF160291	U34419	MW402639	MW402766
F. succisae	CBS 187.34	–	MW402448	MW402109	MW402307	–	MW402810
F. sudanense	CBS 454.97T	–	MN534179	MN534037	MN534073	MW402677	MN534278
F. sudanense	CBS 675.94	–	MN534182	MN534038	MN534074	MW402693	MN534279
F. temperatum	MUCL 52463T	–	MW402486	–	MW402359	–	MW402776

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. temperatum	CBS 135538	–	MN534168	MN534039	MN534111	MW402575	MN534239
F. temperatum	CBS 135539	–	MN534169	KF956083	KF956079	MW402576	MN534242
F. temperatum	NRRL 25622	–	AF158354	AF160301	AF160317	–	LT970765
F. temperatum	**ZHKUCC 23-0934**	–	–	**PQ031148**	**PQ031172**	**PQ212649**	**PQ139072[a], PQ139101[b]**
F. terricola	CBS 483.94T	–	MN534189	MN534042	MN534076	MW402680	LT996156
F. terricola	CBS 119850	–	MN534180	MN534041	MN534075	MW402520	MN534280
F. thapsinum	CBS 539.79	–	MW402472	MW402140	MW402340	MW402686	MW402818
F. thapsinum	CBS 776.96	–	–	MN534044	MN534080	MW402704	MN534289
F. thapsinum	CBS 100312	–	MW402365	MW401961	MW402162	MW402494	MW402780
F. thapsinum	CBS 100313	–	MW402366	MW401962	MW402163	MW402495	MW402781
F. tjaetaba	NRRL 66243T	–	LT996187	KP083263	–	KP083267	KP083275
F. tupiense	NRRL 53984T	–	GU737377	GU737404	GU737296	LR792583	LR792619
F. tupiense	CML345	–	–	DQ452861	DQ445783	–	–
F. tupiense	NRRL 53996	–	–	DQ452860	DQ445782	–	–
F. udum	CBS 178.32	–	MW402442	AF160275	U34433	MW402624	LT996172
F. udum	CBS 419.97	–	MW402464		MW402328	MW402666	MW402769
F. udum	CBS 747.79	–	MN534154	MN193872	MN534141	MW402699	MN534258
F. udum	NRRL 25199ET	–	–	KY498862	KY498892	–	KY498875
F. verticillioides	CBS 218.76ET	–	MW402449	MW402113	MW402311	MW402638	–
F. verticillioides	CBS 447.95	–	MW402466	MW402133	MW402332	MW402671	MW402770
F. verticillioides	CBS 579.78	–	–	MW402143	MW402343	–	MW402837
F. verticillioides	CBS 734.97	–	AF158315	MW402146	MW402346	MW402694	EF470122
F. volatile	CBS 143874T	–	MK984595	LR596007	LR596008	–	LR596006
F. volatile	NRRL 25615	–	AF158357	AF160304	AF160320	–	–
F. werrikimbe	CBS 125535	–	MN534203	MW928846	MN534104	MW928821	MN534304
F. xishuangbannaense	KUMCC 21-0432T	–	OR022064	OR026004	OR025949	OR022023	OR025920
F. xishuangbannaense	KUMCC 21-0731	–	OR022065	OR026005	OR025950	OR022024	OR025921
F. xylarioides	CBS 258.52ET	–	MW402455	MN193874	AY707118	MW402646	HM068355
F. xylarioides	CBS 749.79	–	AF158326	MN534049	MN534143	MW402702	MN534259
F. xyrophilum	NRRL 62710	–	–	MN193875	–	MW402720	MN193903
F. xyrophilum	NRRL 62721T	–	–	MN193877	–	MW402721	MN193905
F. xyrophilum	NRRL 66890	–	–	MN193876	–	MW402724	MN193904
***Fusarium tricinctum* species complex**							
F. aconidiale	CBS 147772T	MZ064464	MZ078177	MZ078246	–	MZ078192	MZ078218

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. acuminatum	LC13791	MW016644	–	MW620105	MW533990	MW024672	MW474630
F. acuminatum	LC13799	MW016652	–	MW620113	MW533998	MW024680	MW474638
F. alpinum	CGMCC3.20818T	MW016689	–	MW620150	MW534035	MW024717	MW474675
F. alpinum	LC6034	MW016686	–	MW620147	MW534032	MW024714	MW474672
F. alpinum	LC6037	MW016687	–	MW620148	MW534033	MW024715	MW474673
F. alpinum	LC2854	MW016685	–	MW620146	MW534031	MW024713	MW474671
F. avenaceum	CBS 408.86NT	–	–	MW928836	–	MG282372	MG282401
F. avenaceum	GUCC 191095.1T	MZ724838	–	OR043880	OR043932	–	OR043825
F. avenaceum	LC13801	MW016655	–	MW620116	MW534001	MW024683	MW474641
F. avenaceum	LC13802	MW016656	–	MW620117	MW534002	MW024684	MW474642
F. avenaceum	LC13804	MW016658	–	MW620119	MW534004	MW024686	MW474644
F. avenaceum	**ZHKUCC 24-0774**	–	–	**PP983160**	**PP983187**	**PP983173**	**PP983197**
F. avenaceum	**ZHKUCC 24-0775**	–	–	**PP983161**	**PP983188**	**PP983174**	**PP983198**
F. californicum	145796T	MK880138	–	MK878579	MK878574	MK878584	MK878569
F. californicum	BL24	MK880134	–	MK878575	MK878570	MK878580	MK878565
F. californicum	BL28	MK880136	–	MK878577	MK878572	MK878582	MK878567
F. campestre	CBS 148994T	–	ON960621	ON960701	ON960669	ON960653[a], ON960637[b]	ON960685[a], ON960669[b]
F. campestre	KG508	–	ON960633	ON960713	ON960681	ON960665[a], ON960649[b]	ON960697[a], ON960681[b]
F. chongqingense	CGMCC3.20821T	MW016677	–	MW620138	MW534023	MW024705	MW474663
F. chongqingense	LC13813	MW016675	–	MW620136	MW534021	MW024703	MW474661
F. chongqingense	LC13814	MW016676	–	MW620137	MW534022	MW024704	MW474662
F. citricola	CPC27805T	LT746245	–	LT746197	–	LT746290	LT746310
F. citricola	CPC 27067	LT746242	–	LT746194	–	LT746287	LT746307
F. citricola	CPC 27069	LT746243	–	LT746195	–	–	LT746308
F. citriforme	CBS 253.50T	–	–	KR071775	–	MW928802	MW928823
F. concolor	NRRL 13994T	–	–	MH742650	–	MH742492	MH742569
F. dendranthematis	**ZHKUCC 24-0772T**	–	–	**PP983158**	**PP983185**	**PP983171**	**PP983195**
F. dendranthematis	**ZHKUCC 24-0773**	–	–	**PP983159**	**PP983186**	**PP983172**	**PP983196**
F. diversisporum	KNUF 21 F39	–	OP186043	OP186041	–	OP186042	–
F. diversisporum	BBA 11129	–	MZ921621	MZ921930	–	MZ921690	MZ921801
F. flocciferum	CBS 831.85	–	–	–	–	JX171514	JX171627
F. gamsii	CBS 143610T	LT970824	–	LT970788	–	–	LT970760

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. gamsii	CBS 143609	LT970823	–	LT970787	–	–	LT970759
F. iranicum	CBS 143608T	LT970821	–	LT970785	–	–	LT970757
F. iranicum	CBS 143611	LT970822	–	LT970786	–	–	LT970758
F. iranicum	LC1112	MW016678	–	MW620139	MW534024	MW024706	MW474664
F. juglandicola	CBS 147773T	MZ064461	MZ078174	MZ078243	–	MZ078190	MZ078215
F. paeoniae	CGMCC3 20817T	MW016681	–	MW620142	MW534027	MW024709	MW474667
F. paeoniae	LC13815	MW016679	–	MW620140	MW534025	MW024707	MW474665
F. paeoniae	LC7358	MW016683	–	MW620144	MW534029	MW024711	MW474669
F. petersiae	CBS 143231T	MG386078	–	MG386159	MW534026	MG386138	MG386149
F. petersiae	JW14005	MG386079	–	MG386160	–	MG386139	MG386150
F. reticulatum	CBS 473.76ET	–	–	MW928841	–	MW928816	–
F. rosendophyticum	CGMCC3.25480T	MZ724841	OR043757	–	OR043955	OR043802	OR043855
F. rosendophyticum	GUCC 190163 2	OR034269	OR043758	–	OR043956	OR043803	OR043856
F. rosiradicicola	CGMCC3.25482T	MZ724834	OR043761	OR043914	OR043959	OR043806	OR043858
F. rosiradicicola	GUCC 191073.1	MZ724836	OR043763	OR043916	OR043961	–	OR043860
F. rosiradicicola	GUCC 191098.1	MZ724840	OR043766	OR043918	OR043964	OR043809	OR043863
F. salinense	CPC 26457	LT746240	–	LT746192	–	LT746285	LT746305
F. salinense	CPC 26973T	LT746241	–	LT746193	–	LT746286	LT746306
F. sinense	CBS 122710T	EF531229	–	EF531235	EF531241	–	–
F. sinense	CBS 122711	EF531230	–	EF531238	EF531242	–	–
F. torulosum	NRRL 22748T	–	–	OL772877	–	JX171502	JX171615
F. torulosum	NRRL 52772	–	–	OL772887	–	OL773039	MH582377
F. torulosum	JW 24001	MZ890423	MZ921608	MZ921918	MZ921822	MZ921680	MZ921788
F. tricinctum	CBS 393.93T	HM068317	–	AB674263	–	JX171516	JX171629
F. tricinctum	LC13819	MW016693	–	MW620154	MW534039	MW024721	MW474679
***Fusarium nisikadoi* species complex**							
F. anoectochili	**ZHKUCC 24-0770T**	–	–	**PP983152**	**PP983179**	**PP983189**	**PQ584292[a], PQ593046[b]**
F. anoectochili	**ZHKUCC 24-0771**	–	–	**PP983153**	**PP983180**	**PP983190**	**PQ584293[a], PQ593047[b]**
F. commune	CBS 110090	–	–	AF362263	–	MW928803	MW934368
F. concolor	CBS 183.34T	–	–	MH742650	–	MH742492	MH742569
F. falsibabinda	LC13610T	–	–	MW580433	–	MW024424	MW474379
F. gaditjirri	CBS 116011	–	–	–	–	–	HQ662690
F. gaditjirri	NRRL 45417	–	–	MN193881	–	–	MN193909

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. lyarnte	CBS 125536T	–	–	EF107118	–	JX171549	JX171661
F. miscanthi	CBS 577.97T	–	–	MN193878	–	JX171521	JX171634
F. miscanthi	LC7503	MW016565	–	MW594318	–	MW024593	MW474551
F. nisikadoi	BBA 69015T	–	–	KR909358	MW533922	MG282391	MG282421
F. nisikadoi	NRRL 25179	–	–	MN193879	–	MN193935	MN193907
F. paranisikadoi	CGMCC 3.20826T	MW016561	–	MW594314	MW533918	MW024589	MW474547
F. paranisikadoi	LC2819	MW016562	–	MW594315	MW533919	MW024590	MW474548
F. paranisikadoi	LC2823	MW016563	–	MW594316	MW533920	MW024591	MW474549
F. paranisikadoi	LC2824	MW016564	–	MW594317	MW533921	MW024592	MW474550
***Fusarium oxysporum* species complex**							
F. callistephi	CBS 187.53T	–	MH484693	MH484966	MH485057	–	MH484875
F. callistephi	CBS 115423	–	MH484723	MH484996	MH485087	–	MH484905
F. carminascens	CBS 144738T	–	MH484755	MH485028	MH485119	MW928801	MH484937
F. carminascens	CBS 144739	–	MH484752	MH485025	MH485116	–	MH484934
F. carminascens	CBS 144740	–	MH484753	MH485026	MH485117	–	MH484935
F. carminascens	CBS 144741	–	MH484754	MH485027	MH485118	–	MH484936
F. cili	GUCC 190024.1 = CGMCC3.25476 T	–	OR043735	OR043885	OR043937	OR043785	OR043830
F. cili	GUCC 190024.2	–	OR043736	OR043886	OR043938	OR043786	OR043831
F. contaminatum	CBS 111552	–	MH484718	MH484991	MH485082	–	MH484900
F. contaminatum	CBS 114899T	–	MH484719	MH484992	MH485083	–	MH484901
F. contaminatum	CBS 117461	–	MH484729	MH485002	MH485093	–	MH484911
F. contaminatum	**ZHKUCC 23-0888**	–	**PQ273167**	**PQ306362**	**PQ256789**	**PQ468005**	**PQ356481**
F. contaminatum	**ZHKUCC 23-0889**	–	**PQ273168**	**PQ306363**	**PQ256790**	**PQ468006**	**PQ356482**
F. contaminatum	**ZHKUCC 23-0890**	–	**PQ273169**	**PQ306364**	**PQ256791**	**PQ468007**	**PQ356483**
F. contaminatum	**ZHKUCC 23-0891**	–	**PQ273170**	**PQ306365**	**PQ256792**	**PQ468008**	**PQ356484**
F. contaminatum	**ZHKUCC 23-0892**	–	**PQ273171**	**PQ306366**	**PQ256793**	**PQ468009**	**PQ356485**
F. contaminatum	**ZHKUCC 23-0893**	–	**PQ273172**	**PQ306367**	**PQ256794**	**PQ468010**	**PQ356486**
F. contaminatum	**ZHKUCC 23-0904**	–	**PQ273173**	**PQ316050**	**PQ256795**	**PQ468011**	**PQ356487**
F. cugenangense	CBS 130304	–	MH484739	MH485012	MH485103	–	MH484921
F. cugenangense	CBS 130308	–	MH484738	MH485011	MH485102	–	MH484920
F. cugenangense	CBS 131393	–	MH484746	MH485019	MH485110	–	MH484928
F. curvatum	CBS 247.61	–	MH484694	MH484967	MH485058	–	MH484876
F. curvatum	CBS 238.94T	–	MH484711	MH484984	MH485075	–	MH484893
F. curvatum	CBS 141.95	–	MH484712	MH484985	MH485076	–	MH484894

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. curvatum	**ZHKUCC 23-0912**	–	**PQ273174**	**PQ316051**	**PQ512068**	**PQ468012**	**PQ356488**
F. curvatum	**ZHKUCC 23-0913**	–	**PQ273175**	**PQ316052**	**PQ512069**	**PQ468013**	**PQ356489**
F. duoseptatum	InaCC F916T	–	–	LS479688	–	LS479495	LS479239
F. duoseptatum	LC13740	–	–	MW594326	MW533930	MW024601	MW474559
F. duoseptatum	LC13741	–	–	MW594327	MW533931	MW024602	MW474560
F. duoseptatum	CBS 102026	–	MH484714	MH484987	MH485078	–	MH484896
F. duoseptatum	**ZHKUCC 23-0894**	–	**PQ273176**	**PQ316053**	**PQ512070**	**PQ468014**	**PQ356490**
F. duoseptatum	**ZHKUCC 23-0895**	–	**PQ273177**	**PQ316054**	**PQ256796**	**PQ468015**	**PQ356491**
F. duoseptatum	**ZHKUCC 23-0896**	–	**PQ273178**	**PQ316055**	**PQ256797**	**PQ468016**	**PQ356492**
F. duoseptatum	**ZHKUCC 23-0911**	–	**PQ273179**	**PQ316056**	**PQ256798**	**PQ468017**	**PQ356493**
F. elaeidis	CBS 217.49T	–	MH484688	MH484961	MH485052	MW928805	MH484870
F. elaeidis	CBS 218.49	–	MH484689	MH484962	MH485053	–	MH484871
F. elaeidis	CBS 255.52	–	MH484692	MH484965	MH485056	–	MH484874
F. fabacearum	CBS 144743T	–	MH484757	MH485030	MH485121	MW928806	MH484939
F. fabacearum	CBS 144742	–	MH484756	MH485029	MH485120	MZ921691	MH484938
F. fabacearum	CBS 144744	–	MH484758	MH485031	MH485122	–	MH484940
F. foetens	CBS 120665	–	MH484736	MH485009	MH485100	–	MH484918
F. glycines	CBS 176.33	–	MH484686	MH484959	MH485050	–	MH484868
F. glycines	CBS 144746T	–	MH484760	MH485033	MH485124	MW928809	MH484942
F. glycines	CBS 200.89	–	MH484706	MH484979	MH485070	–	MH484888
F. glycines	CBS 144745	–	MH484759	MH485032	MH485123	–	MH484941
F. glycines	CBS 214.49	–	MH484687	MH484960	MH485051	–	MH484869
F. gossypinum	CBS 116613T	–	MH484727	MH485000	MH485091	–	MH484909
F. gossypinum	CBS 116611	–	MH484725	MH484998	MH485089	–	MH484907
F. gossypinum	CBS 116612	–	MH484726	MH484999	MH485090	–	MH484908
F. grosmichelii	InaCC F833 T	–	–	LS479744	–	LS479548	LS479295
F. grosmichelii	JXF4-32	–	–	OL771393	OL771401	OL771377	OL771385
F. grosmichelii	JXN4-10	–	–	OL771395	OL771403	OL771379	OL771387
F. grosmichelii	JXF4-6	–	–	OL771394	OL771402	OL771378	OL771386
F. grosmichelii	**ZHKUCC 23-0909**	–	**PQ273180**	**PQ316057**	**PQ256799**	**PQ468018**	**PQ356494**
F. grosmichelii	**ZHKUCC 23-0910**	–	**PQ273181**	**PQ316058**	**PQ256800**	**PQ468019**	**PQ476266**
F. hoodiae	CBS 132474T	–	MH484747	MH485020	MH485111	–	MH484929
F. inflexum	CBS 716.74 T	–	AF158366	AF008479	U34435	JX171469	JX171583
F. kalimantanense	InaCC F917 T	–	–	LS479690	–	LS479497	LS479241
F. kalimantanense	InaCC F918	–	–	LS479691	–	–	LS479242

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. kalimantanense	InaCC F922	–	–	LS479695	–	–	LS479246
F. languescens	CBS 646.78	–	MH484699	MH484972	MH485063	–	MH484881
F. languescens	CBS 645.78T	–	MH484698	MH484971	MH485062	MW928813	MH484880
F. languescens	CBS 413.90	–	MH484708	MH484981	MH485072	–	MH484890
F. languescens	CBS 872.95	–	MH484713	MH484986	MH485077	–	MH484895
F. libertatis	CBS 144749T	–	MH484762	MH485035	MH485126	–	MH484944
F. libertatis	CBS 144748	–	MH484750	MH485023	MH485114	–	MH484932
F. libertatis	CBS 144747	–	MH484751	MH485024	MH485115	–	MH484933
F. menglaense	KUMCC 21-0717	–	OR022059	OR025999	OR025944	OR022018	OR025915
F. menglaense	KUMCC 21-0718	–	OR022060	OR026000	OR025945	OR022019	OR025916
F. menglaense	**ZHKUCC 23-0897**	–	**PQ304865**	**PQ316059**	**PQ512071**	**PQ468020**	**PQ476267**
F. menglaense	**ZHKUCC 23-0898**	–	**PQ304866**	**PQ316060**	**PQ512072**	**PQ468021**	**PQ476268**
F. menglaense	**ZHKUCC 23-0899**	–	**PQ304867**	**PQ316061**	**PQ512073**	**PQ468022**	**PQ476269**
F. nirenbergiae	CBS 840.88T	–	MH484705	MH484978	MH485069	–	MH484887
F. nirenbergiae	CBS 115416	–	MH484720	MH484993	MH485084	–	MH484902
F. nirenbergiae	CBS 129.81	–	MH484703	MH484976	MH485067	–	MH484885
F. nirenbergiae	CBS 744.79	–	MH484700	MH484973	MH485064	–	MH484882
F. nirenbergiae	CBS 196.87 = NRRL 26219	–	MH484704	MH484977	MH485068	–	MH484886
F. nirenbergiae	**ZHKUCC 23-0905**	–	**PQ304868**	**PQ316062**	**PQ512074**	**PQ468023**	**PQ476270**
F. nirenbergiae	**ZHKUCC 23-0906**	–	**PQ304869**	**PQ316063**	**PQ512075**	**PQ468024**	**PQ476271**
F. nirenbergiae	**ZHKUCC 23-0907**	–	**PQ304870**	**PQ316064**	**PQ512076**	**PQ468025**	**PQ476272**
F. nirenbergiae	**ZHKUCC 23-0908**	–	**PQ304871**	**PQ316065**	**PQ512077**	**PQ468026**	**PQ476273**
F. odoratissimum	InaCC F822T	–	–	LS479828	–	LS479618	–
F. odoratissimum (*F. rosae-roxburghii*)	GUCC 190111.1 = CGMCC3.25479 T	–	OR043755	OR043910	–	OR043800	OR043853
F. odoratissimum (*F. rosae-roxburghii*)	GUCC 190111.2	–	OR043756	OR043911	–	OR043801	OR043854
F. odoratissimum	**ZHKUCC 24-0051**	–	**PP983164**	**PP983156**	**PP983183**	**PP983170**	**PP983191**
F. odoratissimum	**ZHKUCC 24-0052**	–	**PP983165**	**PP983157**	**PP983184**	**PP983199**	**PP983192**
F. oxysporum	CBS 221.49	–	MH484690	MH484963	MH485054	–	MH484872
F. oxysporum	CPC 25822	–	MH484761	MH485034	MH485125	–	MH484943
F. oxysporum	CBS 144134ET	–	MH484771	MH485044	MH485135	–	MH484953
F. oxysporum	CBS 144135	–	MH484772	MH485045	MH485136	–	MH484954
F. pharetrum	CBS 144751T	–	MH484770	MH485043	MH485134	MW928815	MH484952

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
F. pharetrum	CBS 144750	–	MH484769	MH485042	MH485133	–	MH484951
F. phialophorum	InaCC F971 T	–	–	LS479741	–	LS479544	LS479292
F. phialophorum	InaCC F826	–	–	LS479700	–	LS479505	LS479251
F. sangayamense	InaCC F960 T	–	–	LS479732	–	LS479537	LS479283
F. tardicrescens	NRRL 36113 T	–	–	LS479665	–	LS479474	LS479217
F. trachichlamydosporum	CBS 102028T	–	MH484715	MH484988	MH485079	–	MH484897
F. triseptatum	CBS 258.50T	–	MH484691	MH484964	MH485055	MW928820	MH484873
F. triseptatum	CBS 116619	–	MH484728	MH485001	MH485092	–	MH484910
F. triseptatum	CBS 119665	–	MH484734	MH485007	MH485098	–	MH484916
F. triseptatum	CBS 130302	–	MH484742	MH485015	MH485106	–	MH484924
F. triseptatum	**ZHKUCC 23-0900**	–	**PQ304872**	**PQ316066**	**PQ512078**	**PQ468027**	**PQ476274**
F. triseptatum	**ZHKUCC 23-0901**	–	**PQ304873**	**PQ316067**	**PQ512079**	**PQ468028**	**PQ476275**
F. triseptatum	**ZHKUCC 23-0902**	–	**PQ304874**	**PQ316068**	**PQ512080**	**PQ468029**	**PQ476276**
F. triseptatum	**ZHKUCC 23-0903**	–	**PQ304875**	**PQ316069**	**PQ512081**	**PQ468030**	**PQ476277**
F. udum	CBS 177.31	–	MH484684	MH484957	MH485048	–	MH484866
F. veterinarium	CBS 109898T	–	MH484717	MH484990	MH485081	–	MH484899
F. veterinarium	CBS 117787	–	MH484730	MH485003	MH485094	–	MH484912
F. veterinarium	CBS 117790	–	MH484731	MH485004	MH485095	–	MH484913
F. vanleeuwenii	CBS 148372 = JW 10008ET	–	MZ921585	MZ921896	–	MZ921669	MZ921765
F. vanleeuwenii	CBS 148375 = JW 10003	–	MZ921581	MZ921892	–	–	MZ921761
F. vanleeuwenii	CBS 148374 = JW 10001	–	MZ921579	MZ921890	–	–	MZ921759
***Fusarium* sp.**	**ZHKUCC 23-0885T**	–	**PQ304876**	**PQ316070**	**PQ512082**	**PQ468031**	**PQ476278**
***Fusarium* sp.**	**ZHKUCC 23-0886**	–	**PQ304877**	**PQ316071**	**PQ512083**	**PQ468032**	**PQ476279**
***Fusarium* sp.**	**ZHKUCC 23-0887**	–	**PQ304878**	**PQ316072**	**PQ512084**	**PQ468033**	**PQ476280**
***Fusarium* sp.**	**ZHKUCC 24-0049**	–	**PP983162**	**PP983154**	**PP983181**	**PP983170**	**PP983191**
***Fusarium* sp.**	**ZHKUCC 24-0050**	–	**PP983163**	**PP983155**	**PP983182**	**PP983199**	**PP983192**
Neocosmospora							
Geejayessia atrofusca	NRRL 22316	AF178423	–	AF178361	–	–	EU329502
G. cicatricum	CBS 125552	HQ728145	–	HM626644	–	–	HQ728153
N. acutispora	CBS 145461T	LR583700	–	LR583593	–	MW834210	LR583814
N. addoensis	CBS 146510T	MW173042	–	MW248741	–	MW218098	MW446575

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
N. akasia	CBS 146880T	MN954357	–	MT009971	–	–	MT009931[a], MT010011[b]
N. ambrosia	CBS 571.94ET	EU329669	–	FJ240350	–	MW834211	EU329503
N. ampla	CBS 202.32T	LR583701	–	LR583594	–	MW834212	LR583815
N. anhuiensis	CGMCC 3.24869	OQ842733	–	OQ866530	–	–	OQ866525
N. aquatica	KUNCC 22-12459	OP876713	–	OQ064518	–	–	–
N. aquatica	KUNCC 22-12460	OP876716	–	OQ064520	–	–	–
N. aurantia	CGMCC 3.24866	OQ842731	–	OQ866528	–	–	OQ866523
N. awan	CBS 146882T	MN954345	–	MT009973	–	–	MT009919[a], MT009999[b]
N. bataticola	CBS 144398T	AF178408	–	AF178344	–	MW218100	FJ240381
N. borneensis	CBS 145462ET	AF178415	–	AF178352	–	MW834213	EU329515
N. bostrycoides	CBS 144.25NT	LR583704	–	LR583597	–	MW218101	LR583818
N. brevicona	CBS 204.31ET	LR583707	–	LR583600	–	MW218103	LR583821
N. brevis	CBS 144387T	LR583708	–	LR583601	–	–	LR583822
N. caricae	ES216	OK422517	–	OK539517	–	–	OK415858
N. caricae	ES216-R	OK422519	–	OK539519	–	–	OK415860
N. caricae	ES216-MT	OK422518	–	OK539518	–	–	OK415859
N. catenata	CBS 143229T	KC808256	–	KC808214	–	MW218105	KC808355
N. citricola	CBS 146513T	MW173048	–	MW248747	–	MW218108	MW446581
N. crassa	CBS 144386T	LR583709	–	LR583604	–	MW218109	LR583823
N. crassa	VG211 = CPC 37122	–	–	MW248760	–	–	MW446594
N. crassa	NRRL 46703 = FMR 8281	–	–	HM347126	–	–	EU329661
N. cryptoseptata	CBS 145463T	AF178414	–	AF178351	–	MW834215	EU329510
N. cucurbitae	CBS 616.66T	LR583711	–	DQ247592	–	MW834217	LR583825
N. cyanescens	CBS 518.82T	AB190389	–	LR583605	–	MW218110	LR583826
N. diminuta	CBS 144390T	LR583713	–	LR583607	–	MW834218	LR583828
N. dimorpha	CGMCC 3.24867	OQ842732	–	OQ866529	–	–	OQ866524
N. drepaniformis	NRRL 62941T	KM406633	–	KM406626	–	–	KM406640[a], KM406647[b]
N. duplosperma	NRRL 62583T	KC691581	–	KC691553	–	KC691611	KC691642[a], KC691671[b]
N. elegans	CBS 144396ET	AF178401	–	AF178336	–	MW218113	FJ240380

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
N. epipeda	CBS 146523T	MW827624	–	MW834285	–	MW834219	MW834022
N. euwallaceae	CBS 135854T	JQ038014	–	JQ038007	–	JQ038021	JQ038028
N. falciformis	CBS 475.67T	MG189935	–	LT906669	–	MW218114	LT960558
N. ferruginea	CBS 109028T	DQ094446	–	DQ246979	–	MW834221	EU329581
N. floridana	NRRL 62628T	KC691563	–	KC691535	–	KC691593	KC691624[a], KC691653[b]
N. galbana	CGMCC 3.24868	OQ842730	–	OQ866532	–	–	OQ866527
N. gamsii	CBS 143207T	DQ094420	–	DQ247103	–	MW834223	EU329622
N. gamtoosensis	CBS 146502T	MW173063	–	MW248762	–	MW218116	MW446611
N. gannanensis	NJFU-JX12 T	LC702041	–	LC701609	–	LC701945	LC701981
N. gannanensis	NJFU-JX13	LC702042	–	LC701610	–	LC701946	LC701982
N. gannanensis	NJFU-JX14	LC702043	–	LC701611	–	LC701947	LC701983
N. geoasparagicola	CBS 148937T	ON763207	–	ON745622	–	ON759290	ON759301
N. geoasparagicola	CPC 39931	ON763208	–	ON745623	–	ON759291	ON759302
N. geoasparagicola	CPC 39932	ON763209	–	ON745624	–	ON759292	ON759303
N. guangdongensis	**ZHKUCC 23-0938T**	**PQ179766**	–	**PQ442946**	–	**PQ375364**	**PQ381281[a], PQ423899[b]**
N. guangdongensis	**ZHKUCC 23-0939**	**PQ179767**	–	**PQ442947**	–	**PQ375365**	**PQ381282[a], PQ423900[b]**
N. guangdongensis	**ZHKUCC 23-0940**	**PQ179768**	–	**PQ442948**	–	**PQ375366**	**PQ381283[a], PQ423901[b]**
N. haematococca	CBS 119600ET	KM231797	–	DQ247510	–	–	LT960561
N. hengyangensis	HMAS 254518	KY829446	–	KY829448	–	–	–
N. hypothenemi	CBS 145464T	LR583715	–	JF740850	–	MW218117	JF741176
N. illudens	CBS 147303	AF178393	–	AF178326	–	JX171488	JX171601
N. ipomoeae	CBS 833.97	LR583719	–	LR583611	–	MW218120	LR583833
N. keleraja	CBS 125722PT	JF433039	–	DQ247515	–	MW834226	LR583835
N. keratoplastica	CBS 490.63T	LR583721	–	LT906670	–	MW218121	LT960562
N. keratoplastica	CBS 144389	LR583722	–	LR583613	–	MW218122	LR583836
N. keratoplastica	NRRL 52704	–	–	JF740786	–	–	JF741112
N. keratoplastica	**ZHKUCC 23-0941**	**PQ179769**	–	**PQ442949**	–	**PQ375367**	**PQ381284[a], PQ423902[b]**
N. keratoplastica	**ZHKUCC 23-0942**	**PQ179770**	–	**PQ442950**	–	**PQ375368**	**PQ381285[a], PQ423903[b]**

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
N. keratoplastica	**ZHKUCC 23-0943**	**PQ179771**	–	**PQ442951**	–	**PQ375369**	**PQ381286[a], PQ423904[b]**
N. kuroshio	CBS 142642T	LR583723	–	KX262216	–	MW834227	LR583837
N. kurunegalensis	CBS 119599T	JF433036	–	DQ247511	–	MW834228	LR583838
N. lerouxii	CBS 146514T	MW173069	–	MW248768	–	MW218123	MW446617
N. lichenicola	CBS 509.63T	LR583728	–	LR583618	–	MW834229	LR583843
N. liriodendri	CBS 117481T	AF178404	–	AF178340	–	MW218124	EU329506
N. lithocarpi	LC1113 T	MW016711	–	MW620172	–	MW024739	MW474697
N. liupanshuiensis	GUCC 190115.1	MZ724849	–	OR043923	–	OR043814	OR043869
N. liupanshuiensis	GUCC 190201.1 = CGMCC3.25481 T	MZ724850	–	OR043924	–	OR043815	–
N. longissima	CBS 126407T	LR583731	–	LR583621	–	MW834230	LR583846
N. macrospora	CBS 142424T	LT746266	–	LT746218	–	MW218125	LT746331
N. magnoliae	MFLUCC 17-2615	MT215508	–	MT212207	–	–	MT212200
N. mahasenii	CBS 119594T	JF433045	–	DQ247513	–	MW834231	LT960563
N. maoershanica	CGMCC 3.24870	OQ842734	–	OQ866531	–	–	OQ866526
N. martii	CBS 142423T	LT746264	–	LT746216	–	–	LT746329
N. mekan	CBS 146885T	MN954342	–	MT009956	–	–	MT009916[a], MT009996[b]
N. merkxiana	CBS 146525T	MW827627	–	MW834288	–	MW834233	MW834025
N. metavorans	CBS 135789T	LR583738	–	LR583627	–	MW218127	LR583849
N. mori	CBS 145467T	DQ094305	–	AF178358	–	MW834235	EU329499
N. neerlandica	CBS 232.34T	MW827629	–	MW847906	–	MW834237	MW847903
N. nelsonii	CBS 309.75T	MW827630	–	MW847907	–	MW834238	MW847904
N. nirenbergiana	CBS 145469T	AF178403	–	AF178339	–	–	EU329505
N. noneumartii	CBS 115658T	LR583745	–	LR583630	–	MW218129	MW446618
N. obliquiseptata	NRRL 62611T	KC691576	–	KC691548	–	KC691606	KC691637[a], KC691666[b]
N. oblonga	CBS 130325T	LR583746	–	LR583631	–	MW834239	LR583853
N. oligoseptata	CBS 143241T	KC691566	–	KC691538	–	KC691596	LR583854
N. pallidimors	KUMCC 20-0007T	MT031915	–	MT024983	–	–	–
N. paphiopedili	**ZHKUCC 23-0935T**	**PQ179763**	–	**PQ442943**	–	**PQ367248**	**PQ381278[a], PQ423896[b]**
N. paphiopedili	**ZHKUCC 23-0936**	**PQ179764**	–	**PQ442944**	–	**PQ367249**	**PQ381279[a], PQ423897[b]**

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
N. paphiopedili	**ZHKUCC 23-0937**	**PQ179765**	–	**PQ442945**	–	**PQ367250**	**PQ381280[a], PQ423898[b]**
N. papillata	NRRL 62943T	KM406635	–	KM406628	–	–	–
N. papillata	NRRL 62944	KM406634	–	KM406627	–	–	KM406648
N. paraeumartii	CBS 487.76T	LR583747	–	DQ247549	–	MW834240	LR583855
N. parceramosa	CBS 115695T	JX435199	–	JX435149	–	–	JX435249
N. passiflorae	IBFS07	FJ200220	–	JX524768	–	–	–
N. passiflorae	IBFS09	FJ200222	–	–	–	–	–
N. passiflorae	IBFS08	FJ200221	–	–	–	–	–
N. perseae	CBS 144142T	LT991940	–	LT991902	–	MW218130	LT991909
N. petroliphila	CBS 203.32	DQ094320	–	DQ246835	–	MW218131	LR583857
N. phaseoli	NRRL 31041T	AY220239	–	AY220193	–	–	JX171643
N. piperis	CBS 145470T	AF178422	–	AF178360	–	MW834241	EU329513
N. pisi	CBS 123669ET	LR583753	–	LR583636	–	MW834242	LR583862
N. plagianthi	NRRL 22632	AF178417	–	AF178354	–	JX171501	JX171614
N. populicola	NJFU-JS02 T	LC702061	–	LC701601	–	LC701929	LC701965
N. populicola	NJFU-JS03	LC702062	–	LC701602	–	LC701930	LC701966
N. populicola	NJFU-JS04	LC702063	–	LC701603	–	LC701931	LC701967
N. protoensiformis	CBS 145471T	AF178399	–	AF178334	–	MW834244	EU329498
N. pseudensiformis	CBS 130.78	LR583759	–	DQ247635	–	MW834245	LR583868
N. pseudensiformis	CBS 125729T	KC691584	–	DQ247512	–	–	KC691645
N. pseudensiformis	CBS 241.93	JX435198	–	JX435148	–	–	JX435248
N. pseudensiformis	**ZHKUCC 23-0947**	**PQ179775**	–	**PQ442955**	–	**PQ528007**	**PQ381290[a], PQ423908[b]**
N. pseudopisi	CBS 266.50T	MW827631	–	MW834290	–	MW834246	MW834027
N. pseudoradicicola	CBS 145472T	JF740899	–	JF740757	–	MW218133	JF741084
N. pseudotonkinensis	CBS 143038T	LR583758	–	LR583640	–	–	LR583867
N. quercicola	CBS 141.90T	LR583760	–	DQ247634	–	MW834247	LR583869
N. rectiphora	CBS 125727T	JF433034	–	DQ247509	–	MW834249	LR583871
N. regularis	CBS 230.34T	LR583763	–	LR583643	–	–	MW834029
N. rekana	CMW 52862T	MN249094	–	MN249151	–	–	MN249137[a], MN249108[b]
N. riograndensis	UFMG CM F12570T	KT186366	–	KX534002	–	–	KX534003
N. robusta	CBS 145473T	AF178405	–	AF178341	–	MW834251	EU329507

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers					
		ITS	***CaM***	***tef1-α***	***tub2***	***rpb1***	***rpb2***
N. samuelsii	CBS 114067T	LR583764	–	LR583644	–	MW834252	LR583874
N. silvicola	CBS 123846T	LR583766	–	LR583646	–	MW834254	LR583876
N. solani	CBS 140079ET	KT313633	–	KT313611	–	MW218134	KT313623
N. solani	CBS 101018T ex-type of *N. rubicola*	LR583770	–	LR583651	–	–	LR583878
N. solani	CBS 144393 = MUCL 34689	–	–	LR583655	–	–	LR583882
N. solani	CBS 111722	LR583771	–	LR583652	–	–	LR583879
N. solani	**ZHKUCC 23-0944**	**PQ179772**	–	**PQ442952**	–	**PQ375370**	**PQ381287[a], PQ423905[b]**
N. solani	**ZHKUCC 23-0945**	**PQ179773**	–	**PQ442953**	–	**PQ375371**	**PQ381288[a], PQ423906[b]**
N. solani	**ZHKUCC 23-0946**	**PQ179774**	–	**PQ442954**	–	**PQ375372**	**PQ381289[a], PQ423907[b]**
N. spathulata	CBS 145474T	EU329674	–	DQ246882	–	MW218137	EU329542
N. stercicola	CBS 142480T	LR583778	–	KY556525	–	–	LR583886
N. stercicola	CBS 142481T	LR583779	–	LR583658	–	MW834255	LR583887
N. striatispora	MFLUCC 18-0582	ON775553	–	ON892545	–	–	–
N. suttoniana	CBS 143214T	DQ094617	–	DQ247163	–	MW218138	EU329630
N. thailandica	MFLUCC 17-2630	ON787624	–	ON892546	–	–	–
N. theobromae	BPI 453072NT	–	–	LR583660	–	–	–
N. tonkinensis	CBS 115.40T	MG189941	–	LT906672	–	MW218140	LT960564
N. tuaranensis	NRRL 22231T	KC691570	–	KC691542	–	KC691600	KC691631[a], KC691660[b]
N. tumidisperma	NJFU-JX26 T	LC702053	–	LC701621	–	LC701957	LC701993
N. tumidisperma	NJFU-JX27	LC702054	–	LC701622	–	LC701958	LC701994
N. tumidisperma	NJFU-JX28	LC702055	–	LC701623	–	LC701959	LC701995[a]
N. variasi	CBS 146888T	MN954356	–	MT009967	–	–	MT009913[b], MT009993
N. vasinfecta	CBS 325.54IT	KM231803	–	LR583664	–	–	KM232370
N. vasinfecta	CBS 446.93T	LR583791	–	LR583670	–	MW834257	LR583898
N. warna	CBS 146891T	MN954346	–	MT009955	–	–	MT009920[a], MT010000[b]

Abbreviations: ITS: internal transcribed spacer regions, *CaM*: calmodulin, *tef1-α*: translation elongation factor 1-alpha, *tub2*: β-tubulin, *rpb1*: RNA polymerase largest subunit I, and *rpb2*: RNA polymerase largest subunit II. BBA: Biologische Bundesanstalt fu¨r Land-und Forstwirtschaft, Institute

fu¨r Mikrobiologie, Berlin, Germany; BPI: U.S. National Fungus Collections, USDA-ARS, Beltsville, MD, USA; CBS: Westerdijk Fungal Biodiverity Institute (WIFB), Utrecht, The Netherlands; CGMCC: China General Microbiological Culture Collection Centre, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; CML: Coleção Micológica de Lavras, Universidade Federal de Lavras, Minas Gerais, Brazil; CMW: Culture Collection, Tree Protection Co-operative Programme, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa; CPC: Culture collection of Pedro Crous, housed at the Westerdijk Institute; FMR: Facultat de Medicina i Ciències de la Salut, Reus, Spain; FRC: Fusarium Research Center, Pennsylvannia State University, PA, USA; GUCC: Department of Plant Pathology Culture Collection, Agriculture College, Guizhou University, China; HMAS: Herbarium Mycologicum Academiae Sinicae, Chinese Academy of Sciences, Beijing, China; InaCC: Indonesian Culture Collection, Research Center for Biology, Indonesian Institute of Sciences (LIPI) Cibinong, Indonesia; KUMCC: Kunming Institute of Botany Culture Collection, Yunnan, China; LC: working collection of Lei Cai, State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, P.R. China; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCL: Mycothèque de l´Université Catholique de Louvain, Louvain-la-Neuve, Belgium; NRRL: Agricultural Research Service Culture Collection, National Center for Agricultural Utilization Research, USDA, Peoria, IL, USA; NY: University of Pretoria, South Africa; the working collection of the author Neriman Yilmaz; PD: Collection of the Dutch National Plant Protection Organization, Wageningen, The Netherlands; PPRI: Plant Protection Research Institute, Pretoria, South Africa; RGB: Royal Botanical Gardens Trust, Sydney, New South Wales, Australia; UFMG: Coleção de Micro-organismos, DNA e Células da Universidade Federal de Minas Gerais, Belo Horizonte, Brazil; ZHKUCC: Zhongkai University of Agriculture and Engineering culture collection, Guangdong, P.R. China.

The strains and sequences in this study are in bold. Ex-type cultures in bold with “T”. Epi-type with “ET”. Neotype with “NT”. The *rpb2* sequences obtained using 5f/7cr primer pair “[a]”. The *rpb2* sequences obtained using 7cf/11 primer pair “[b]”.