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Diversity of pathogenic ascomycetes on ancient *Platycladus orientalis* in Beijing based on multilocus phylogeny and morphology

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Abstract

Ancient *Platycladus orientalis* is a precious heritage with significant historical, cultural, ecological, and landscape value. Under urban environmental stress and tree aging, diseases of ancient *P. orientalis* in Beijing have become increasingly severe; however, little is known about the diversity of these fungal pathogens. In this study, symptomatic samples were collected from 15 parks or temples in Beijing, from which a total of 56 fungal taxa were isolated from the interfaces between diseased and healthy tissues. Based on pathogenicity assays, multilocus phylogenetic analysis and morphological observation, 45 ascomycete species, belonging to 6 orders, 8 families, and 17 genera, were confirmed as the pathogens of *P. orientalis*, exhibiting varying levels of virulence. Among these, 5 species are described as new to science, namely *Curvularia platycladi*, *C. platycladicola*, *Epicoccum platycladi*, *Fusarium beijingensis*, and *Toxicocladosporium quinquagintatreanum*, and 30 species represent new host records. This study establishes a foundational framework for future research on disease diagnosis and risk assessment in ancient trees.

Keywords: Ancient trees, fungal pathogens, phylogeny, taxonomy, new taxa, pathogenicity

Introduction

Ancient trees hold unique historical, cultural, ecological, and landscape value (Cannon et al. 2022). They play key roles in biodiversity conservation, maintaining ecosystem stability, habitat provision, and the delivery of social and cultural benefits to people (Piovesan et al. 2022; Huang et al. 2023; Pasques and Munné-Bosch 2024). *Platycladus orientalis* (Cupressaceae), native to China and the Korean Peninsula, is an evergreen conifer well known for its strong ecological adaptability and long lifespan (Jiao et al. 2026). It is widely used for afforestation and urban greening, and has now been introduced and naturalized worldwide (Li et al. 2016). Beijing, a famous historic city, harbors numerous ancient trees. A total of 40,529 ancient trees have been recorded to date, of which *P. orientalis* accounts for 55.69% (Zhao 2022;

45 Zhang 2024). Most of these were planted during the Ming and Qing dynasties, while a
46 few individuals are older, even exceeding a thousand years. Ancient *P. orientalis*,
47 regarded as symbols of auspiciousness and longevity due to their robust vitality and
48 evergreen nature, are commonly found in prominent historical and cultural sites, such
49 as palaces, parks, and temples in Beijing (Jiao et al. 2024).

50 Ancient *P. orientalis* remains in a prolonged over-mature stage, leading to declines
51 in physiological functions and stress resistance (Lindenmayer et al. 2012; Jiao et al.
52 2026). More seriously, multiple adverse factors, including urban environmental stress
53 and human activities, significantly increase the risk of disease (Webb et al. 2023). In a
54 two-year field survey, we found that diseases of ancient *P. orientalis* in Beijing are
55 severe, mainly caused by fungal pathogens, and significantly affect their health and
56 ornamental value. Leaf blight is the most common disease, initially manifesting as
57 chlorosis or brown spots on leaves that gradually enlarge and eventually leading to
58 leaf desiccation and defoliation (Jiao et al. 2024, 2025a, b). Dieback progresses
59 downward from the shoot tip, causing necrosis and defoliation, with black pycnidia
60 usually observed on infected tissues (Liu et al. 2022; Yin et al. 2025). Canker is
61 characterized by necrosis and cracking of the epidermis on branches or trunks,
62 forming raised or sunken lesions (Graniti 1998; Guo 2023). Some pathogens with
63 higher virulence can also penetrate into the xylem, thereby exacerbating the disease
64 (Guo 2023). Trunk rot occurs occasionally but is the most damaging disease. This
65 disease initially forms dark brown, water-soaked lesions on the bark, then gradually
66 invades the phloem and xylem (Shortle and Dudzik 2012), resulting in wood decay
67 and cavity formation, which seriously threaten the survival of ancient *P. orientalis*.

68 Studies on leaf blight of *P. orientalis* first began in China. As early as 1922, leaf
69 blight of *P. orientalis* caused by *Alternaria pruni* was reported in China (Zhu 1922).
70 Subsequently, *Didymascella thujina* (syn. *Keithia thujina*) was identified as the causal
71 agent of *P. orientalis* leaf blight in Beijing (Zhao and Zhan 1979). This pathogen later
72 spread to North America and Europe, where it caused epidemics of leaf blight of *P.*
73 *orientalis* (Phillips and Burdekin 1992). Dai et al. (1992) identified *Chloroscypha*
74 *platycladus* as the causal agent of *P. orientalis* leaf blight in Jiangsu, and this
75 pathogen was then discovered in Hebei and Gansu Provinces (Liu et al. 1995; Liu
76 2015). Until 2021, *Alternaria alternata* and *Pestalotiopsis paeoniicola* were identified
77 as the causal agents of leaf blight of ancient *P. orientalis* in Shaanxi based on
78 phylogenetic and morphological studies (Li et al. 2021). Recently, our team used
79 current phylogenetic and taxonomic approaches combined with Koch's postulates
80 verification to identify nine fungal species from three genera causing leaf blight of
81 ancient *P. orientalis* in Beijing (Jiao et al. 2024, 2025a, b). In contrast, studies on stem
82 diseases of *P. orientalis* are still scarce. *Neofusicoccum occulatum* was identified as
83 the causal agent of branch dieback of *P. orientalis* in Shandong (Liu et al. 2022). Four
84 fungal pathogens were reported to cause branch cankers of *P. orientalis* in Chongqing,
85 namely *Seiridium unicorne*, *Pestalotiopsis kenyaana*, *Neofusicoccum occulatum* and
86 *Diaporthe arecae* (syn. *Diaporthe pseudophoenicicola*) (Guo 2023). Stem wilt of *P.*
87 *orientalis* seedlings was reported in India and Pakistan, caused by *Fusarium*
88 *oxysporum* and *Neocosmospora solani* (syn. *Fusarium solani*), respectively

(Raghavendra et al. 2007; Dara et al. 2023). Accurate identification of pathogenic fungi is crucial for the diagnosis and management of diseases of *P. orientalis*.

From 2023 to 2025, disease samples were collected from 15 distribution areas of ancient *P. orientalis* in Beijing. Putative pathogenic fungal strains were isolated from the interfaces between diseased and healthy tissues. The objectives of this study were to (i) identify fungal species causing diseases of ancient *P. orientalis* based on multilocus phylogenetic analyses and morphological characteristics, and (ii) evaluate their pathogenicity through in situ inoculation on the stems of three-year-old *P. orientalis* seedlings.

Materials and methods

Sample collection and fungal isolation

From 2023 to 2025, disease samples with typical symptoms of leaf blight, branch or stem dieback, canker, and rot were collected from 15 sites across the main distribution areas of ancient *P. orientalis* in Beijing (Suppl. materials 1, 2). The number of samples collected depended on disease incidence in each organ and the area surveyed. Plant parts with symptoms were carefully removed from the trees, placed in sterile bags, labeled, stored at low temperature, and transported to the laboratory. Following Senanayake et al. (2020), putative pathogenic fungal strains were isolated from the interface between diseased and healthy tissues. Single spore or hyphal tip isolation were used to obtain axenic cultures (Senanayake et al. 2020). The following media were used to culture fungal strains and induce sporulation: potato dextrose agar (PDA), oatmeal agar (OA), carnation leaf agar (CLA) and synthetic nutrient-poor agar (SNA). The plates were incubated at 25 °C for 5–15 days in the dark or under ultraviolet light. The specimens were air-dried and deposited at Institute of Microbiology, Beijing Forestry University (BJFU). All living cultures obtained in this study were deposited at the China General Microbiological Culture Collection Center (CGMCC).

DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from fresh mycelium grown on PDA using a DNA extraction kit (Aidlab Biotechnologies Co., Ltd., Beijing, China). Polymerase chain reaction (PCR) was performed in a 25 µL reaction volume containing 12.5 µL 2 × PCR Master Mix (TransGen Biotech Co., Ltd., Beijing, China), 8.5 µL double-distilled water, 2 µL genomic DNA, and 1 µL of each forward and reverse primer (stock of 10 pM). The internal transcribed spacer (ITS) was amplified using the primer pair ITS5/ITS4 (White et al. 1990); the large subunit (LSU) with LR0R/LR7 (Vilgalys and Hester 1990); the translation elongation factor 1- α (*tef1- α*) with EF1-728F/EF1-986R (Carbone & Kohn 1999), EF1-983F/EF1-2218R (Schoch et al. 2009), or EF1/EF2 (O'Donnell et al. 1998); beta-tubulin (*tub2*) with T1/T2 (O'Donnell and Cigelnik 1997), Bt2a/Bt2b (Glass and Donaldson 1995), or

Bt-2Fd/Bt-4Rd (Woudenberg et al. 2009); actin (*act*) with ACT-512F/ACT-783R (Carbone & Kohn 1999); calmodulin (*cam*) with CL1/CL2A (O'Donnell et al. 2000); glyceraldehyde-3-phosphate dehydrogenase (*gapdh*) with GPD1/GPD2 (Berbee et al. 1999); the RNA polymerase II largest subunit (*rpb1*) with RPB1-Fa/RPB1-G2R (O'Donnell et al. 2010); and the RNA polymerase II second largest subunit (*rpb2*) with fRPB2-5F/fRPB2-7cR (Liu et al. 1999), respectively. PCR amplicons were purified and sequenced at Sangon Biotech Co., Ltd. (Beijing, China). Sequence quality was evaluated by examining chromatograms, and the sequences were assembled and edited in BioEdit v.7.0.9.0 (Hall 1999). All sequence data generated in this study were submitted to GenBank to obtain accession numbers (Table 1).

Phylogenetic analysis

The newly generated sequences were first subjected to preliminary species identification using NCBI BLASTn (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), and relevant reference sequences were downloaded from the GenBank database following recent taxonomic treatments (Table 2). Sequences were aligned using MAFFT v.7 (<http://mafft.cbrc.jp/alignment/server/>). The sequence alignments were trimmed using BioEdit v.7.0.9.0 to remove ambiguous regions at both ends, with manual adjustments performed when necessary. Loci for each genus were concatenated to construct multilocus datasets, and appropriate taxa were selected as outgroups for phylogenetic analyses.

Phylogenetic analyses were performed using Maximum Likelihood (ML), Bayesian Inference (BI), and Maximum Parsimony (MP) methods. ML analyses were conducted using RAxML-HPC BlackBox v.8.2.10 under the GTR + GAMMA model with 1,000 bootstrap replicates (Stamatakis 2014). BI analyses were performed using MrBayes v.3.2.7 under a partitioned model, with four Markov Chain Monte Carlo (MCMC) chains run for 1–10 million generations depending on the dataset (Ronquist et al. 2012). Trees were sampled every 1,000 generations, with the first 25% discarded as burn-in. The remaining 75% were used to calculate Bayesian posterior probabilities (PP) in the majority-rule consensus tree. MP analyses were conducted in PAUP v.4.0b10 using heuristic searches with tree-bisection-reconnection (TBR) branch swapping and 1,000 random addition replicates (Swofford 2002). Ambiguous regions in the alignment were excluded, and gaps were treated as missing data. Clade support was evaluated using 1,000 bootstrap replicates with Maxtrees set to 1,000 and other default parameters implemented in PAUP (Hillis and Bull 1993). Phylogenetic trees were edited in Adobe Illustrator and visualized using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree>).

Morphological characterization

Colony morphology was observed on PDA, and colony diameters were measured after 5 to 14 days to calculate growth rates. Appropriate media were selected for sporulation induction. Some strains produced conidia on PDA over time under normal

conditions, whereas others required induction by additional stimuli, such as ultraviolet light, sterilized pine needles, or carnation leaves. Microscopic sections were prepared and examined after sporulation. Morphological characters were observed and photographed using a stereomicroscope (Nikon SMZ800N, Tokyo, Japan) and a compound microscope (Nikon Eclipse E600, Tokyo, Japan). At least 30 measurements were taken for each structure, and means were calculated.

Pathogenicity assays

No species were isolated exclusively from leaves. Thus, stems of three-year-old *P. orientalis* seedlings were used for in situ inoculations. The seedlings were healthy, approximately 1 m in aboveground height, 12 mm in basal stem diameter, and soil-grown in pots. Pathogenicity assays were conducted following Bhunjun et al. (2021). Stems were surface-sterilized by wiping with cotton soaked in 75% ethanol for 1 min, followed by 10% sodium hypochlorite for 1 min, and then rinsed three times with sterile water. Wounds (5 mm diam.) were created on the stems using a sterile scalpel, and agar plugs containing the mycelium of each strain were applied to the wound sites. Agar plugs without mycelium were used as controls. The inoculation sites were then covered with cotton moistened with sterile water and sealed with Parafilm to maintain moisture. A single strain was randomly selected from each species as the representative strain for inoculation, with 6 potted seedlings inoculated per strain. The experiment was repeated once. All inoculated seedlings were placed in a greenhouse at 14–28 °C and 60–75% relative humidity under a 12 h light/dark cycle and watered regularly to maintain moisture until symptoms appeared. Lesion lengths were recorded 30 days after inoculation. The inoculated fungus was successfully re-isolated from the lesions and confirmed as the same species based on cultural and morphological characteristics, as well as ITS region sequencing, thereby fulfilling Koch's postulates.

The pathogenicity of each representative strain was assessed based on lesion shape (Fs), lesion color (Cs), and lesion length (Ls), and the evaluation criteria were summarized in Table 3. Data analysis was performed following Du et al. (2025) and Sekandarpour et al. (2025). Trait values were normalized to a 0–1 range using Min–Max scaling. Principal component analysis (PCA) was performed on the standardized data using the `prcomp` function in R (v.4.3.1). The loadings were used to estimate the relative contribution of each trait. Absolute loadings were normalized into trait weights, and a weighted sum was calculated to derive a comprehensive pathogenicity index (PDI). The calculation formula was as follows: $PDI = w_{Fs} \cdot Fs' + w_{Cs} \cdot Cs' + w_{Ls} \cdot Ls'$. Strains were ranked according to their PDI values, with higher values indicating greater pathogenicity.

Results

Fungal isolation

In total, 142 symptomatic samples were collected from 15 distribution areas of

ancient *P. orientalis* in Beijing, from which 236 fungal strains were isolated. Based on cultural morphology on PDA and analysis of highly informative loci (ITS, *tef1-α* and *rpb2*), these strains were preliminarily classified into 56 taxa. Pathogenicity assays filtered out 11 non-pathogenic taxa, and 105 representative strains from the remaining 45 pathogenic taxa were selected for further study based on sampling localities and sequence divergence. The details of these strains are mentioned in Table 1.

Phylogenetic analyses

Multilocus phylogenetic analyses assigned 105 isolates from ancient *P. orientalis* to 45 ascomycete species belonging to 2 classes, 6 orders, 8 families, and 17 genera, including *Aplosporella*, *Botryosphaeria*, *Curvularia*, *Cytospora*, *Diplodia*, *Dothiorella*, *Epicoccum*, and *Fusarium* (*F. fujikuroi*, *F. incarnatum–equiseti*, *F. lateritium*, *F. sambucinum*, and *F. tricinctum* species complexes), *Juxtiphoma*, *Neocosmospora*, *Neofusicoccum*, *Nothophoma*, *Pestalotiopsis*, *Phaeobotryon*, *Seiridium*, *Toxicocladosporium* and *Vacuiphoma*. Phylogenetic trees based on ML, BI, and MP analyses of the same dataset showed no topological conflicts. Therefore, only the ML trees are shown, with support values from all three analyses. Among these taxa, 5 species were identified as new to science, namely *Curvularia platycladi*, *C. platycladicola*, *Epicoccum platycladi*, *Fusarium beijingense*, and *Toxicocladosporium quinquagintatreanum* all of which formed distinct and well-supported clades in the phylogenetic tree (Figs. 1–4). In addition, 40 known species were identified, including *Aplosporella javeedii*, *A. prunicola*, *Botryosphaeria dothidea*, *Curvularia intermedia*, *C. pseudobrachyspora*, *Cytospora acericola*, *C. diopuiensis*, *C. qingshuiensis*, *C. xinglongensis*, *Diplodia neojuniperi*, *Dothiorella acericola*, *D. plurivora*, *Epicoccum dendrobii*, *E. lolii*, *E. nigrum*, *E. rosae*, *Fusarium annulatum*, *F. brachygibbosum*, *F. castaneophilum*, *F. citri-sinensis*, *F. clavus*, *F. compactum*, *F. graminearum*, *F. gummosum*, *F. ipomoeae*, *F. iranicum*, *F. lateritium*, *F. mucidum*, *F. nanum*, *Juxtiphoma yunnanensis*, *Neocosmospora solani*, *Neofusicoccum occulatum*, *Nothophoma gossypicola*, *N. pruni*, *N. quercina*, *Phaeobotryon mali*, *P. platycladi*, *Pestalotiopsis clavata*, *Seiridium unicornae*, and *Vacuiphoma oculihominis* (Suppl. material 3).

Taxonomy

Curvularia platycladi N. Jiao & Y. Zhang, sp. nov.

MycoBank No:

Fig. 5

Etymology. Name refers to the host genus *Platycladus*, from which it was collected.

Typus. China • Beijing, Dongcheng District, Temple of Heaven, on diseased branches of ancient *Platycladus orientalis*, 9 July 2024, Ning Jiao and Zhe Zhang (holotype BJFU-TT1.1, ex-holotype culture CGMCC3.29551).

Description. Associated with branch dieback of ancient *Platycladus orientalis*.
Sexual morph: not observed. **Asexual morph:** *Hyphae* subhyaline to brown, septate, branched, smooth to asperulate, 2–4 µm diam. *Conidiophores* usually occur at right angles to the hyphae, producing conidia apically or laterally, mononematous, septate, straight or flexuous, smooth or geniculate at the apex, simple or branched, pale brown to brown, basal cell not swollen, 35.5–127.5 × 4.0–6.5 µm ($\bar{x}$ = 75.1 × 4.8 µm, n = 30). *Conidiogenous cells* smooth-walled, terminal or intercalary, proliferating sympodially, pale brown, subcylindrical, slightly swollen or flared towards the apex, 5.5–11.5 × 4–6.5 µm ($\bar{x}$ = 7.5 × 5.3 µm, n = 30). *Conidia* subcylindrical or ellipsoidal, pale brown to brown, 1–3 distoseptate, nearly straight, a slight protrusion slightly off-center, nearly smooth with fine guttules, thick-walled, 16.5–23 × 7.5–10.8 µm ($\bar{x}$ = 19.8 × 9.1 µm, n = 50).

Culture characteristics. Growth rate on PDA 8.5 mm/d at 25 °C in the dark. Colonies velvety, mostly flat with the centre slightly raised, margins regular. Upper surface pale gray with whitish margins; reverse with black radiating stripes and white margins.

Additional material examined. China • Beijing, Haidian District, Fragrant Hills Park, on diseased branches of ancient *Platycladus orientalis*, 28 June 2024, Ning Jiao and Zhe Zhang (BJFU-XS14.4, culture CGMCC3.29550).

Notes. Two isolates from ancient *P. orientalis* formed a distinct clade with strong support in the phylogenetic tree (ML/PP/MP = 97/1/87). They were closely related to *C. spicifera*; however, the relationship between these two taxa showed low support. *tefl-α* and *gapdh* are the main markers used to distinguish species in this genus, although the degree of interspecific divergence is highly variable among species. Our strains differed from ex-type strain of *C. spicifera* (CBS 274.52) by 6 bp with 6 gaps in *tefl-α* (869 bp) and 1 bp in *gapdh* (450 bp). Morphologically, the conidiophores of *C. spicifera* are repeatedly geniculate, whereas those of our strains are smooth or simple geniculate at the apex (Zibani et al. 2024). Moreover, the conidia of *C. spicifera* are distinctly longer than those of our strains (18.5–26 × 7.5–9.5 µm vs. 16.5–23 × 7.5–10.8 µm) and differ in septum number (3–4 vs. 1–3) (Zibani et al. 2024; comparison of closely related taxa see Suppl. material 4). Phylogenetic and morphological evidence support the recognition of these isolates as a new species within the genus *Curvularia*.

Curvularia platycladicola N. Jiao & Y. Zhang, sp. nov.

Mycobank No:

Fig. 6

Etymology. Name refers to the host genus *Platycladus* and Latin “-cola” = inhabiting.

Typus. China • Beijing, Dongcheng District, Imperial Ancestral Temple, on diseased branches of ancient *Platycladus orientalis*, 6 November 2024, Ning Jiao and Zhe Zhang (holotype BJFU-TM10.1, ex-holotype cultures CGMCC3.29554 and CGMCC3.29555).

Description. Associated with branch dieback of ancient *Platycladus orientalis*.

Sexual morph: not observed. **Asexual morph:** *Hyphae* subhyaline to pale brown, septate, branched, smooth to asperulate, 2.5–5 µm diam. *Conidiophores* semi- to macronematous, mononematous, septate, simple, slightly geniculate, subhyaline to grayish brown, smooth to asperulate, thick-walled, 58.5–125.5 × 2.8–7.0 µm ($\bar{x}$ = 68.5 × 6.5 µm, n = 30). *Conidiogenous cells* terminal, polytretic, proliferating sympodially, pale brown, with darkened scars, subcylindrical to swollen, 6.0–22.8 × 4.5–9.0 µm ($\bar{x}$ = 12.0 × 6.3 µm, n = 30). *Conidia* straight to slightly curved, 3 distoseptate, verruculose, smooth-walled, with the central septa darkened, the third cell from base unequally enlarged, apical and basal cell subhyaline to pale brown, middle pale brown to dark brown, 21.8–30.0 × 13.0–19.3 µm ($\bar{x}$ = 26.3 × 15.6 µm, n = 50).

Culture characteristics. Growth rate on PDA 10.5 mm/d at 25 °C in the dark. Upper surface felted, gray with white margins; reverse with black radiating stripes and white margins.

Notes. Morphologically, the conidia of our isolates were larger than those of *C. americana* (21.8–30.0 × 13.0–19.3 µm vs. 13–28 × 7–15 µm) (Madrid et al. 2014). In addition, our strains generally produced 2–5 conidia per conidiogenous cell, whereas *C. americana* produced 2–10 (Madrid et al. 2014; see Suppl. material 4 for details). In the phylogenetic tree, the strains formed a distinct clade with strong support (ML/PP/MP = 100/1/100). Although *tefl-α* for *C. americana* is unavailable in GenBank, our strains differed from the ex-type strain of *C. americana* (UTHSC 08-3414) by 3 bp with 1 gap in ITS (450 bp) and 6 bp in *gapdh* (439 bp), sufficient to distinguish these two species. Therefore, this taxon is herein described as a new species.

Epicoccum platycladi N. Jiao & Y. Zhang, sp. nov.

Mycobank No:

Fig. 7

Etymology. Name refers to the host genus *Platycladus*, from which it was collected.

Typus. China • Beijing, Shijingshan District, Fahai Temple, on diseased branches of ancient *Platycladus orientalis*, 5 December 2024, Ning Jiao and Zhe Zhang (holotype BJFU-FHS1.7, ex-holotype culture CGMCC3.29659).

Description. Associated with leaf blight and branch canker of ancient *Platycladus orientalis*. **Sexual morph:** not observed. **Asexual morph:** *Conidiomata* pycnidial, immersed in the media, solitary, globose to subglobose, covered with hyphal outgrowths, blackish brown, ostiolate, 115–160 × 90–135 µm. *Ostiole* single, sometimes with an elongated, pale brown neck, slightly papillate. *Hyphae* hyaline to pale brown, smooth and thin walled, septate, 2.9–4.2 µm wide. *Pycnidial wall* pseudoparenchymatous, composed of oblong to isodiametric cells, 3–6 layers, 19–45 µm thick, outer wall of 1–3 pigmented layers. *Conidiogenous cells* phialidic, hyaline, smooth-walled, ampulliform to doliiform, 4–10.5 × 3.5–6.5 µm. *Conidia* hyaline, smooth-walled, aseptate, ellipsoidal to oblong, reniform, straight to slightly curved, mostly with 2 polar guttules, 2.9–5.8 × 1.5–3.1 µm ($\bar{x}$ = 5 × 2.1 µm, n = 50).

Culture characteristics. Growth rate on PDA 10.5 mm/d at 25 °C in the dark.

Colonies dense, flat, with filamentous margins. Upper surface grey to greyish brown with white margins; reverse grey with a black centre and a white margin. Growth rate on OA 9 mm/d at 25 °C in the dark. Hyphae slightly radiating, both surfaces grey to dark grey, with a darker centre.

Additional material examined. China • Beijing, Mentougou District, Jietai Temple, on diseased leaves of ancient *Platycladus orientalis*, 29 June 2024, Ning Jiao and Zhe Zhang (BJFU-JTS2.3, culture CGMCC3.29660).

Notes. Phylogenetically, strains CGMCC3.29659 and CGMCC3.29660 formed a distinct clade with strong support (ML/PP/MP = 100/1/100). They were closely related to *E. keratinophilum*, *E. pseudokeratinophilum*, and *Epicoccum* sp. However, these strains differed from *Epicoccum* sp. CBS 141022 by 2.75% (17/596 bp) in *rpb2*, and from *E. keratinophilum* CBS 142455 and *E. pseudokeratinophilum* MFLUCC 18-1593 by at least 2.99% (25/837 bp). Similarly, the *tub2* sequences showed at least 1.61% (5/311 bp) divergence from these strains. Morphologically, our strains were similar to *E. pseudokeratinophilum* in producing ellipsoidal to oblong conidia, mostly with two polar guttules; however, their conidia are shorter ($2.9\text{--}5.8 \times 1.5\text{--}3.1 \mu\text{m}$ vs. $4.8\text{--}6.9 \times 1.3\text{--}3 \mu\text{m}$) (Chethana et al. 2019; see Suppl. material 4 for details). In addition, their cultural characteristics on PDA are distinctly different: colonies of *E. pseudokeratinophilum* had a dark grey olivaceous surface toward the margin with a white centre (Chethana et al. 2019), whereas those of our strains were greyish brown with a darker centre and a white margin. Based on phylogenetic and morphological evidence, these strains are described here as a new species.

Fusarium beijingensis N. Jiao & Y. Zhang, sp. nov.

MycoBank No:

Fig. 8

Etymology. Named after Beijing, where the holotype specimen was collected.

Typus. China • Beijing, Huairou District, Hongluo Temple, on diseased leaves of ancient *Platycladus orientalis*, 4 July 2024, Ning Jiao and Zhe Zhang (holotype BJFU-HLS7.2, ex-holotype culture CGMCC3.29618).

Description. Associated with leaf blight and branch canker of ancient *Platycladus orientalis*. **Sexual morph:** not observed. **Asexual morph:** *Sporodochia* cream to pale orange, formed on CLA. *Sporodochial conidiophores* irregularly branched and densely packed, consisting of a short, smooth- and thin-walled stipe. *Sporodochial conidiogenous cells* cylindrical to subcylindrical, smooth, thin-walled, $9\text{--}11 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 10 \times 4 \mu\text{m}$, $n = 30$). *Macroconidia* falcate, curved dorsiventrally, apical cell curved, with a slightly papillate apex, basal cell foot-shaped, hyaline, 3–4(–5)-septate, 3-septate conidia: $(25\text{--})28\text{--}33 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 29 \times 4 \mu\text{m}$, $n = 50$); 4-septate conidia: $27\text{--}37 \times 4\text{--}5 \mu\text{m}$ ($\bar{x} = 32 \times 5 \mu\text{m}$, $n = 30$); 5-septate conidia: $29\text{--}37 \times 4\text{--}5 \mu\text{m}$ ($\bar{x} = 35 \times 5 \mu\text{m}$, $n = 8$). *Aerial conidiophores* unbranched and reduced to single conidiogenous cells. *Conidiogenous cells* ampulliform to subcylindrical, molophilialides, $10\text{--}16(21) \times 2\text{--}4 \mu\text{m}$ ($\bar{x} = 14 \times 3 \mu\text{m}$, $n = 30$). *Microconidia* oval, obovoid to reniform, 0–2-septate, aseptate conidia: $8\text{--}13 \times 2\text{--}4 \mu\text{m}$ ($\bar{x} = 11 \times 3 \mu\text{m}$, n

= 30); 1-septate conidia: $12\text{--}25 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 18 \times 4 \mu\text{m}$, $n = 50$); 2-septate conidia: $16\text{--}25 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 22 \times 4 \mu\text{m}$, $n = 50$). *Chlamydospores* terminal, subglobose to globose, chains, thick-walled, hyaline, $8\text{--}15 \times 7\text{--}13 \mu\text{m}$ ($\bar{x} = 11 \times 9 \mu\text{m}$, $n = 30$)

Culture characteristics. Growth rate on PDA 9 mm/d at 25 °C in the dark. Upper surface pink, white at the margin, flat, with an irregular filamentous margin; reverse dark pink with a white margin. Growth rate on OA 6 mm/d at 25 °C in the dark. Colonies flat with sparse aerial hyphae, white in the centre, a pink zone, and a white outer margin; reverse concolorous. Sporodochia produced on CLA after 20 d.

Additional materials examined. China • Beijing, Haidian District, Summer Palace, on diseased leaves of ancient *Platycladus orientalis*, 20 June 2024, Ning Jiao and Zhe Zhang (BJFU-YHY3.2, culture CGMCC3.29615); Beijing, Dongcheng District, Temple of Heaven, on diseased branches of ancient *Platycladus orientalis*, 9 July 2024, Ning Jiao and Zhe Zhang (BJFU-TT16.1, culture CGMCC3.29616); Beijing, Mentougou District, Jietai Temple, on diseased branches of ancient *Platycladus orientalis*, 29 June 2024, Ning Jiao and Zhe Zhang (BJFU-JTS3.2, culture CGMCC3.29617); Beijing, Dongcheng District, Zhongshan Park, on diseased branches of ancient *Platycladus orientalis*, 9 September 2023, Ying Zhang and Ning Jiao (BJFU-ZS18.2, culture CGMCC3.29619).

Notes. Phylogenetically, five strains formed a distinct clade with strong support (ML/BI/MP = 97/1/99) and were closely related to *F. reticulatum*. *Fusarium reticulatum* was introduced by Montagne (1843) with an inadequate protologue. Recently, Liu et al. (2025) re-described this species with falciform macroconidia, $20.7\text{--}36.8 \times 3.8\text{--}4.5 \mu\text{m}$, 3–5-septate, and napiform and oval microconidia, $7.1\text{--}16.6 \times 2.8\text{--}6.2 \mu\text{m}$, 0–1-septate. However, our strains differed in conidial size, especially in microconidial shape (for details, please see Suppl. material 4). Since the *rpb2* sequence of the ex-type strain of *F. reticulatum* (CBS 473.76) is unavailable, these two taxa were compared based on *tefl-a* and *rpb1*. Our strains showed 98.4% similarity (10/632 bp) in *tefl-a* and 99.1% similarity (7/833 bp) in *rpb1* to CBS 473.76. Therefore, our strains are recognized as a new member of the *F. tricinctum* species complex. Notably, this species was isolated from most distribution areas of ancient *P. orientalis* in Beijing, suggesting that it is a common pathogen on this host.

Toxicocladosporium quinquagintatreanum N. Jiao, J. Wang & Y. Zhang, sp. nov.

MycoBank No:

Fig. 9

Etymology. Named after Courtyard No. 53, Imperial Ancestral Temple, where the holotype specimen was collected.

Typus. China • Beijing, Dongcheng District, Imperial Ancestral Temple, on diseased stems of ancient *Platycladus orientalis*, 5 November 2024, Ning Jiao and Jing Wang (holotype BJFU-TM8.2, ex-holotype culture CGMCC3.29337).

Description. Associated with brown rot of stems of ancient *Platycladus orientalis*.

Sexual morph: not observed. **Asexual morph:** *Mycelium* consisting of branched,

septate, smooth to verruculose, 2–3.5 μm wide hyphae; walls and septa becoming dark brown and thickened with age. **Conidiophores** dimorphic. **Macroconidiophores** arising from hyphae, macronematous, erect, unbranched or branched, thick-walled, smooth to slightly verruculose, subcylindrical, straight to flexuous, 19–73 $\times$ 3–5.5 μm , 1–5-septate. **Microconidiophores** reduced to conidiogenous cells, subcylindrical, 9–21 $\times$ 3–4 μm , 0–2-septate. **Conidiogenous cells** integrated, terminal or lateral, smooth to slightly verruculose, brown, proliferating sympodially with 1–2 apical loci; scars truncate, thickened and darkened, 2–3 μm wide. **Conidia** catenulate in branched or unbranched chains, thick-walled; **primary ramoconidia** pale brown to brown, smooth to finely verruculose, 0–2-septate, subcylindrical, 8–19 $\times$ 2–5 μm ($\bar{x}$ = 12.6 $\times$ 4 μm , n = 50); **secondary ramoconidia** brown, finely verruculose, 0–1-septate, ellipsoidal, fusiform to subcylindrical, 8–17 $\times$ 3–4 μm ($\bar{x}$ = 11.9 $\times$ 4.1 μm , n = 50); scars darkened, thickened, 1–2 μm wide. **Intercalary conidia** subcylindrical, finely verruculose, 0–1-septate, brown, 9.5–16 $\times$ 2–4 μm ($\bar{x}$ = 12.7 $\times$ 3.2 μm , n = 50). **Terminal conidia** fusoid-ellipsoidal, brown, finely verruculose, 7–14 $\times$ 3–4 μm ; hila thickened and darkened, 0.5–1 μm wide.

Culture characteristics. Growth rate on PDA 1.5 mm/d at 25 °C in the dark. Upper surface folded, velvety, gray-olivaceous with entire margin; reverse dark brown. Growth rate on SNA 0.8 mm/d at 25 °C in the dark. Colonies flat, gray-olivaceous, with sparse aerial mycelium with even, smooth margins.

Additional material examined. China • Beijing, Dongcheng District, Imperial Ancestral Temple, on diseased stems of ancient *Platycladus orientalis*, 5 November 2024, Ning Jiao and Jing Wang (BJFU-TM2.1, culture CGMCC 3.29338).

Notes. Phylogenetic analyses revealed that the two strains formed a distinct, well-supported clade (ML/BI/MP = 99/1/98), which was recovered as sister to *T. irritans* and *T. eucalyptorum*. However, they differed from the ex-type strain of *T. irritans* (CBS 185.58) by 1 bp with 1 gap in ITS (375 bp), 2 bp in *act* (180 bp), 14 bp in *rpb2* (795 bp), and 6 bp with 4 gaps in *tub2* (387 bp), and from that of *T. eucalyptorum* (IRAN 4589C) by 4 bp in ITS (375 bp) and 1 bp in *act* (180 bp), as *rpb2* and *tub2* sequences are unavailable for the latter. Morphologically, our strains resembled *T. irritans* but differed by having distinctly longer secondary ramoconidia (8–17 $\times$ 3–4 vs. 6–10 $\times$ 3–5 μm) and slightly longer conidial scars (1–2 vs. 1–1.5 μm) (Crous et al. 2007; Bakhshi and Kheiri 2023). By contrast, they were readily distinguished from *T. eucalyptorum* by their larger macroconidiophores with fewer septa (19–73 $\times$ 3–5.5 μm , 1–5-septate vs. 45–100 $\times$ 2–3 μm , 2–10-septate) (Bakhshi et al. 2022; see Suppl. material 4 for details). Based on the combined phylogenetic and morphological evidence, we describe these two strains as a new species of *Toxicocladosporium*. Notably, this also represents the first record of this genus on *P. orientalis*.

Pathogenicity assay

Pathogenicity assays revealed that the representative strains of these 45 species caused necrotic lesions on stems of *P. orientalis* seedlings 30 days after inoculation,

whereas no symptoms were observed in the controls (Fig. 10). By comparing morphological characteristics and ITS sequences, the strains re-isolated from lesions were identical to the inoculated fungus, fulfilling Koch's postulates.

Based on PCA of lesion shape (Fs), lesion color (Cs), and lesion length (Ls) data, the normalized weights for Fs, Cs, and Ls were 0.390186, 0.267974, and 0.34184, respectively, and the PDI values for each strain were calculated. Pathogenicity declined with decreasing PDI values (5). Some species caused longer sunken lesions on stems that extended into the xylem, whereas others caused necrosis of the epidermis and phloem, resulting in raised lesions (Fig. 10).

In summary, 45 fungal species from *P. orientalis* were confirmed as pathogenic, exhibiting varying levels of virulence, including 5 novel species and 30 new host records (Table 4).

Discussion

This study revealed that pathogenic fungal species associated with ancient *P. orientalis* in Beijing are highly diverse. Based on multilocus phylogenetic analyses and morphological observations, 105 isolates from ancient *P. orientalis* were identified as 45 ascomycete species belonging to 2 classes, 6 orders, 8 families, and 17 genera. Notably, five species were identified as new to science, along with 30 new host records. These findings significantly expand the known diversity of pathogenic fungi associated with the host *P. orientalis*. The composition of fungal pathogens associated with ancient *P. orientalis* showed a complex structure, with taxa across multiple orders, families, and genera. This pattern is similar to studies on fungal pathogens causing conifer dieback around Tbilisi and fungal diversity associated with cypress diseases in Beijing (Danelia et al. 2021; Bi et al. 2025), both suggesting that *P. orientalis* in urban environments supports diverse communities of pathogenic fungi. However, the higher species richness observed in this study further highlights the unique microbial composition of ancient trees.

Taxa identified in this study are commonly associated with plant diseases, and many of their members have been reported from *P. orientalis*. Species of *Cytospora* and *Seiridium* are associated with stem cankers of *P. orientalis*, such as *Cytospora ailanthicola*, *C. albodisca*, *C. discostoma*, *C. donglingensis*, *C. platycladi*, *C. platycladicola*, *C. verrucosa*, and *Seiridium unicorne* (Fan et al. 2020; Pan et al. 2021; Guo 2023; Lin et al. 2024; Bi et al. 2025; Jiang et al. 2025). Members of *Alternaria*, *Curvularia*, and *Pestalotiopsis* are associated with leaf blight and branch dieback of *P. orientalis*, such as *Alternaria alternata*, *Curvularia inaequalis*, *C. spicifera*, *Pestalotiopsis kenyana*, and *P. paeoniicola* (Danelia et al. 2021; Li et al. 2021; Guo 2023; Jiao et al. 2025b). In addition, species of *Botryosphaeriaceae* and *Didymellaceae* have been reported in association with dieback and cankers of *P. orientalis*, such as *Botryosphaeria dothidea*, *Dothiorella alpina*, *D. sarmentorum*, *Neofusicoccum occulatum*, *Phaeobotryon platycladi*, *P. rhois*, *P. xizangense*, *Epicoccum nigrum*, and *Nothophoma quercina* (Dissanayake et al. 2016; Zhang et al. 2016; Pan et al. 2019; Danelia et al. 2021; Lin et al. 2023; Bi et al. 2025; Zhou et al.

2025). Fusarioid pathogens are known to cause a wide range of plant diseases but are rarely reported on *P. orientalis*, with only *Fusarium oxysporum*, *F. proliferatum*, and *Neocosmospora solani* causing wilt and damping-off of seedlings (Raghavendra et al. 2007; Zakeri et al. 2011; Dara et al. 2023). In contrast, the present study revealed a greater diversity of fusarioid taxa from ancient *P. orientalis* in Beijing. This discrepancy may be attributed to tree age and habitat, although limited sampling scope also restricted the detection of fungal pathogens. Additionally, several previously unreported taxa, including *Juxtiphoma*, *Toxicocladosporium* and *Vacuiphoma*, were isolated from ancient *P. orientalis*. Future nationwide surveys and fungal isolations are needed to better understand the pathogens associated with ancient trees.

In our previous studies, nine fungal species causing leaf blight of ancient *P. orientalis* in Beijing were reported, including *Alternaria alternata*, *A. cantlous*, *A. platycladi*, *A. subcucurbitae*, *Bipolaris setariae*, *B. sorokiniana*, *Nothophoma juglandis*, *N. platycladus*, and *N. spiraeae* (Jiao et al. 2024, 2025a, b). In the present study, pathogenicity assays revealed an additional 45 pathogenic fungal species. In total, 54 fungal pathogens from ancient *P. orientalis* in Beijing have now been documented, belonging to the classes *Dothideomycetes* and *Sordariomycetes*, with members of *Botryosphaeriaceae*, *Didymellaceae* and *Nectriaceae* showing higher species richness. Notably, twelve fungal species isolated from blighted leaves in this study were also recovered from branches or stems of the host, suggesting cross-tissue pathogenicity (Doehlemann et al. 2017).

Pathogenicity assessments based on lesion shape, lesion color, and lesion length revealed clear differences in virulence among species on the stems of *P. orientalis* seedlings. Some species caused sunken lesions that extended into the xylem, indicating strong infective and destructive capacity, whereas others caused raised necrotic lesions in the epidermal and phloem tissues. These differences reflect variation in the infection strategies of pathogenic fungi, including tissue penetration ability, cell wall-degrading enzyme activity, and vascular colonization capacity (Kubicek et al. 2014). In particular, in urban ecosystems, multiple abiotic stresses influence host–pathogen interactions, potentially leading to an underestimation of pathogen virulence (Aguilar-Trigueros et al. 2025). Nevertheless, these findings provide an essential taxonomic and pathological reference for disease diagnosis and risk assessment in ancient trees.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

Adherence to national and international regulations

All the fungal strains used in this study have been legally obtained, respecting the Convention on Biological Diversity (Rio Convention).

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Author contributions

Conceptualisation: YZ; Data curation: NJ, ZZ; Formal analysis: NJ, ZZ, JYW; Funding acquisition: AT, YZ; Investigation: NJ, ZZ, JW; Project administration: YZ; Resources: AT, YZ; Supervision: YZ, NJ; Visualisation: NJ, ZZ, JYW; Writing – original draft: NJ; Writing – review and editing: All authors. All authors read and approved the final manuscript.

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Data availability

All data generated or analyzed during this study are included in this published article or in the supplementary materials, and all newly generated sequences have been submitted in GenBank.

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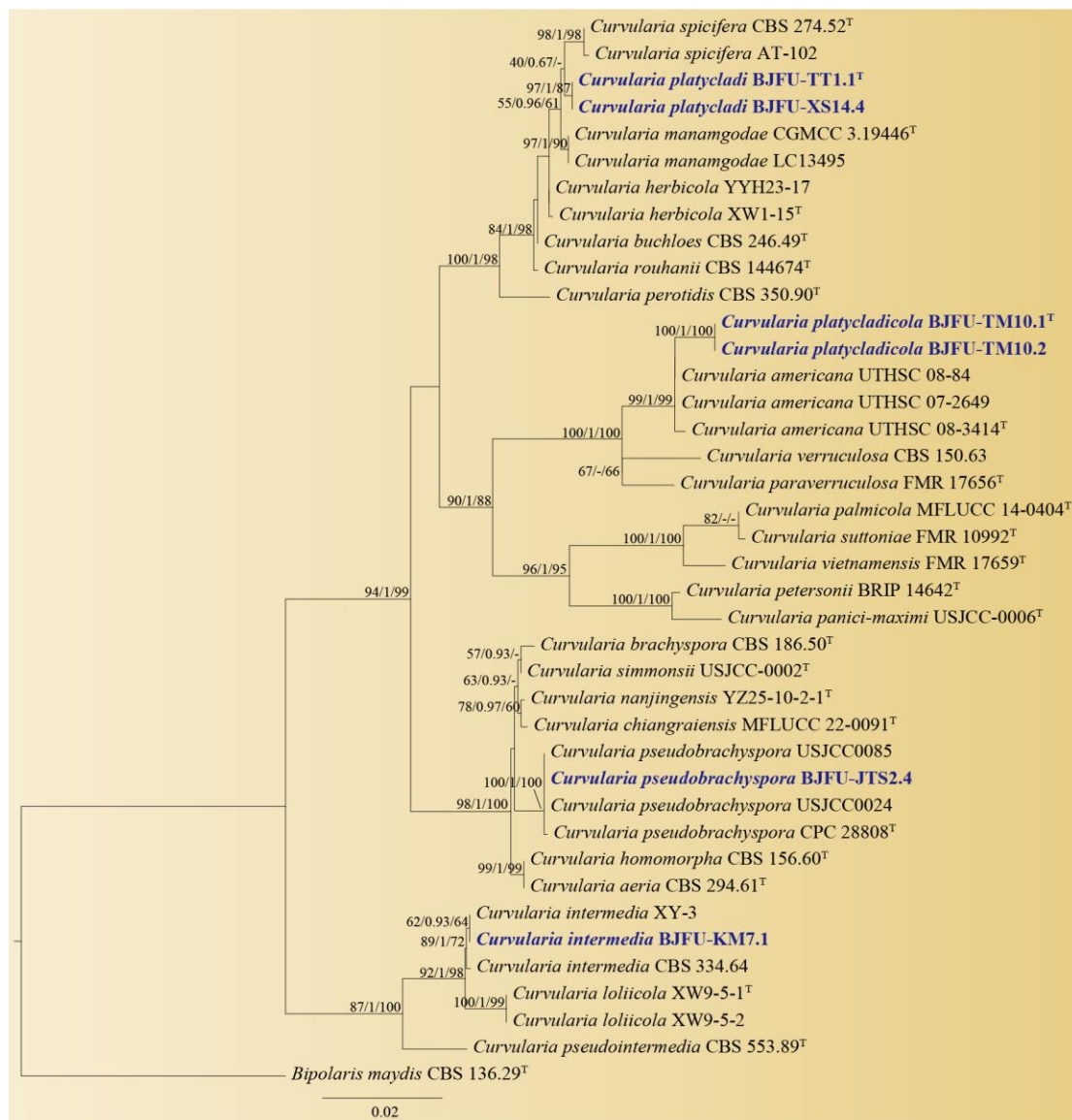


Figure 1. Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *gapdh* and *tefl-α* sequence data of species belonging to *Curvularia*. The tree was rooted with *Bipolaris maydis* CBS 136.29. RAxML bootstrap support values $\geq 50\%$, Bayesian posterior probabilities ≥ 0.90 , and Maximum parsimony bootstrap support values $\geq 50\%$ were indicated at the nodes as ML/PP/MP. The scale bar indicated 0.02 changes. The type strains were marked with superscript “T”, and isolates from the current study were shown in blue. The maximum likelihood alignment matrix contained 378 distinct alignment patterns, with 13.09% undetermined characters or gaps. The best-scoring RAxML tree with a final ML optimization likelihood value of -5457.626 was presented. Estimated base frequencies were as follows: A = 0.233, C = 0.306, G = 0.240, T = 0.221; substitution rates AC = 0.78774, AG = 2.07128, AT = 0.93858, CG = 0.70831, CT = 6.42500, GT = 1.00000.

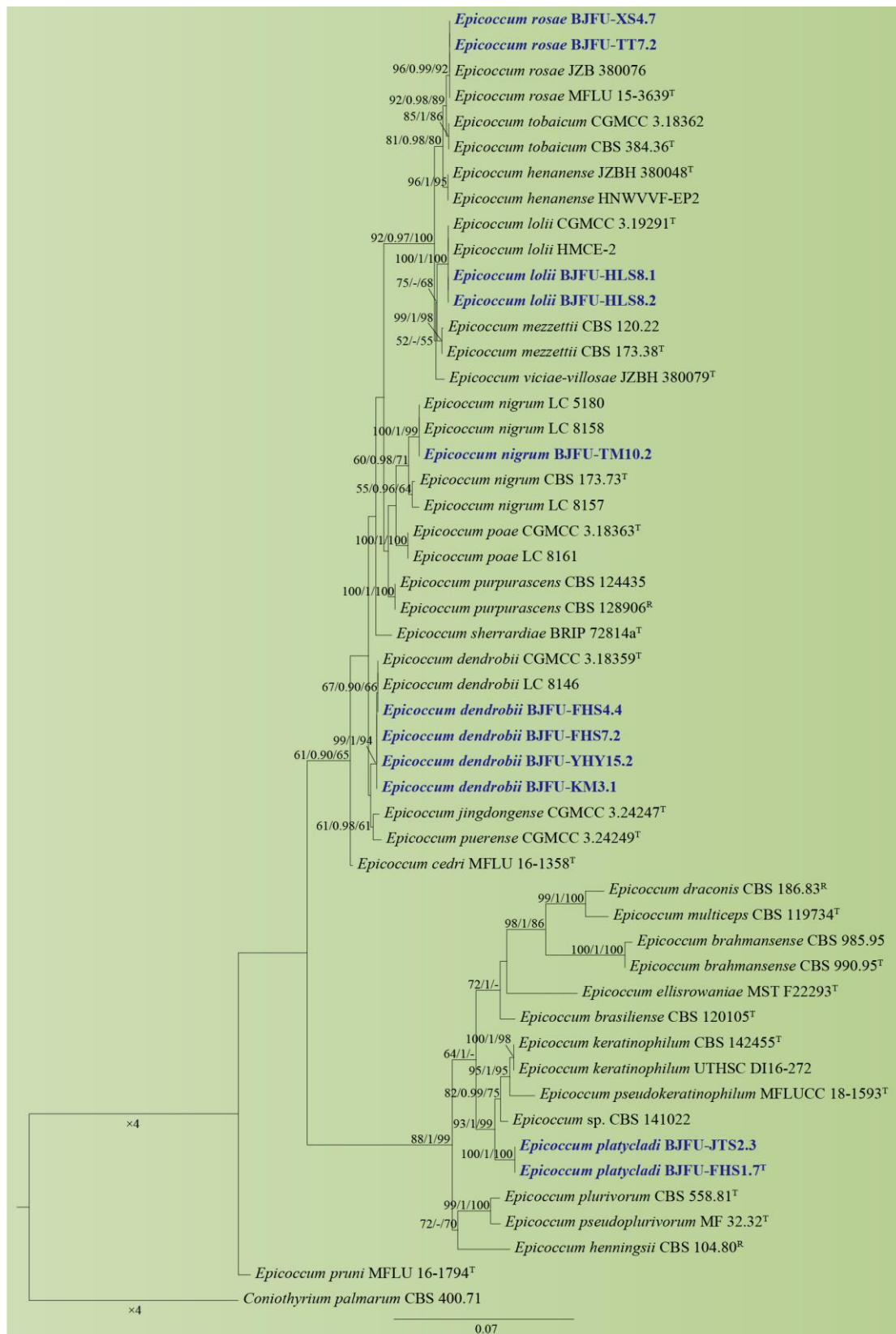


Figure 2. Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU, *rpb2* and *tub2* sequence data of species belonging to *Epicoccum*. The tree was rooted with *Coniothyrium palmarum* CBS 400.71. RAxML bootstrap support values $\geq 50\%$, Bayesian posterior probabilities ≥ 0.90 , and Maximum parsimony

bootstrap support values $\geq 50\%$ were indicated at the nodes as ML/PP/MP. The scale bar indicated 0.07 changes. The type strains were marked with superscript “T”, representative strains with superscript “R”, and isolates from the current study were shown in blue. The maximum likelihood alignment matrix contained 591 distinct alignment patterns, with 13.35% undetermined characters or gaps. The best-scoring RAxML tree with a final ML optimization likelihood value of -9338.685 was presented. Estimated base frequencies were as follows: A = 0.239, C = 0.250, G = 0.273, T = 0.237; substitution rates AC = 2.12568, AG = 6.29029, AT = 1.86450, CG = 1.47868, CT = 16.09828, GT = 1.00000.

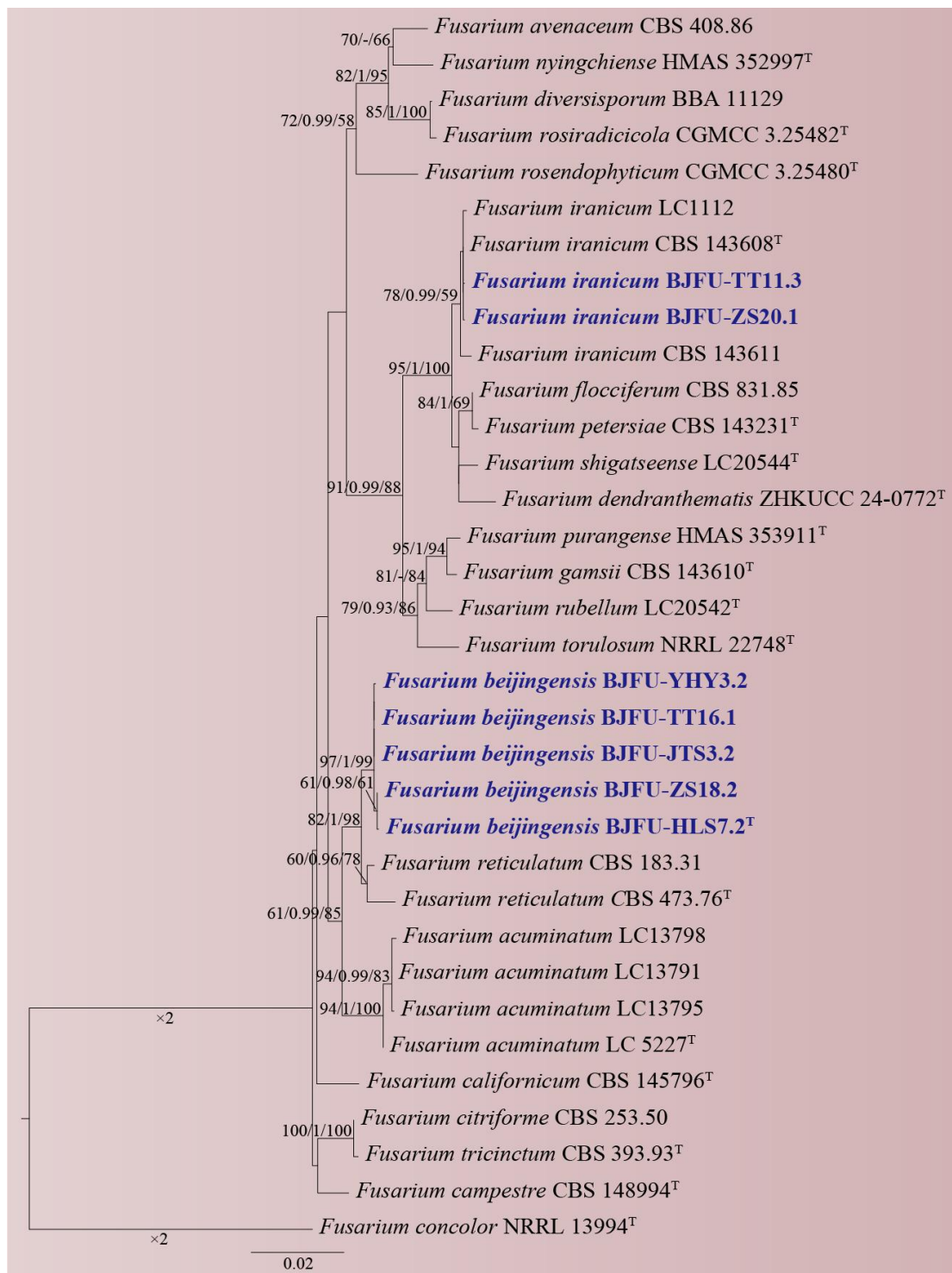


Figure 3. Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *cam*, *tef1-α*, *rpb1*, *rpb2* and *tub2* sequence data of species belonging to *Fusarium tricinctum* species complex. The tree was rooted with *Fusarium concolor* NRRL 13994. RAxML bootstrap support values $\geq 50\%$, Bayesian posterior probabilities ≥ 0.90 , and Maximum parsimony bootstrap support values $\geq 50\%$ were indicated at the nodes as ML/PP/MP. The scale bar indicated 0.02 changes. The type strains were marked with superscript “T”, and isolates from the current study were shown in blue. The maximum likelihood alignment matrix contained 617 distinct alignment patterns.

with 35.77% undetermined characters or gaps. The best-scoring RAxML tree with a final ML optimization likelihood value of -9914.516 was presented. Estimated base frequencies were as follows: A = 0.247, C = 0.259, G = 0.248, T = 0.246; substitution rates AC = 1.56654, AG = 5.16596, AT = 1.30590, CG = 0.82265, CT = 11.79053, GT = 1.00000.

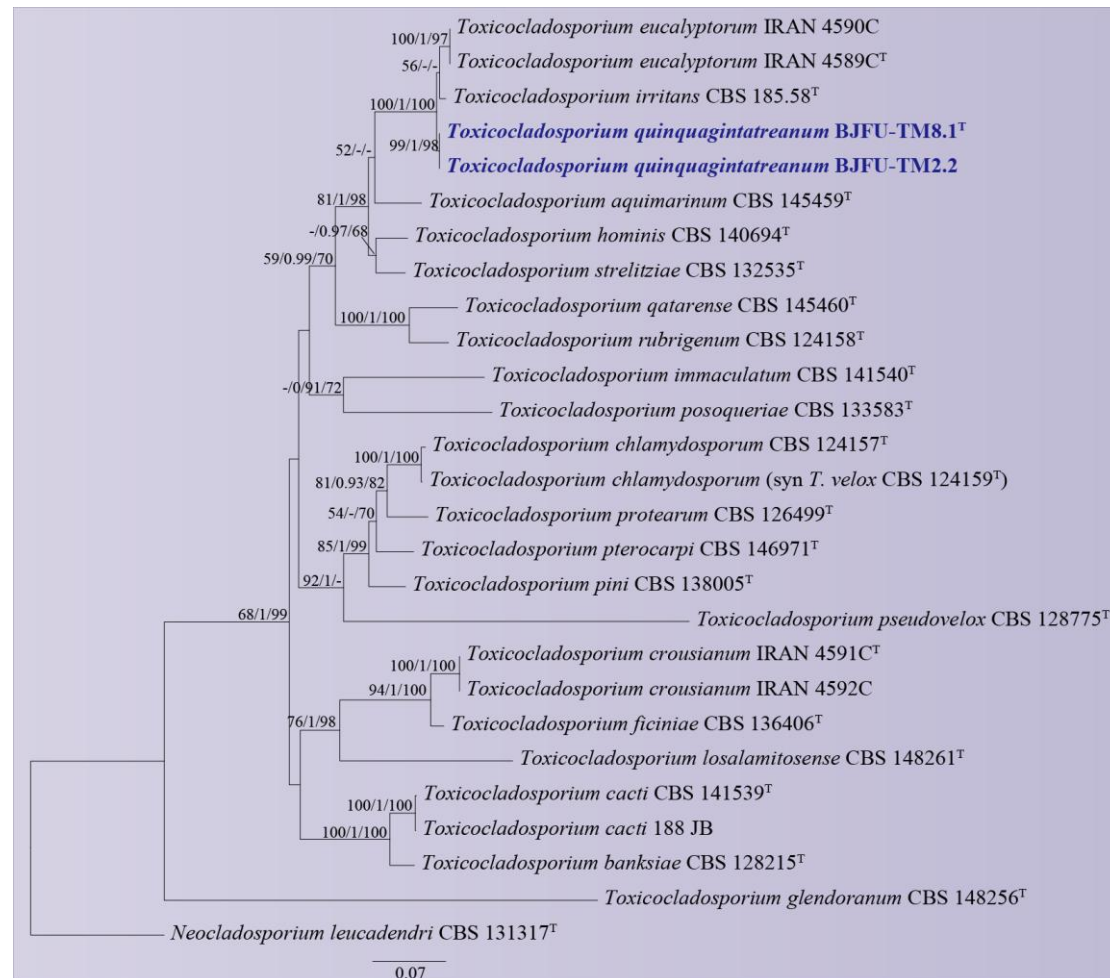


Figure 4. Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU, *act*, *rpb2* and *tub2* sequence data of species belonging to *Toxicocladosporium*. The tree was rooted with *Neocladosporium leucadendri* CBS 131317. RAxML bootstrap support values $\geq 50\%$, Bayesian posterior probabilities ≥ 0.90 , and Maximum parsimony bootstrap support values $\geq 50\%$ were indicated at the nodes as ML/PP/MP. The scale bar indicated 0.07 changes. The type strains were marked with superscript “T”, and isolates from the current study were shown in blue. The maximum likelihood alignment matrix contained 900 distinct alignment patterns, with 12.97% undetermined characters or gaps. The best-scoring RAxML tree with a final ML optimization likelihood value of -16420.217 was presented. Estimated base frequencies were as follows: A = 0.238, C = 0.258, G = 0.285, T = 0.219; substitution rates AC = 2.10807, AG = 4.03119, AT = 2.03773, CG = 1.43148, CT = 8.62601, GT = 1.00000.



Figure 5. *Curvularia platycladi* (CGMCC3.29551). **A, B** Colony obverse and reverse on PDA after 5 d at 25°C; **C–E** Conidiophores and conidiogenous cells; **F, G** Conidia. Scale bars: 10 µm (**C–G**).

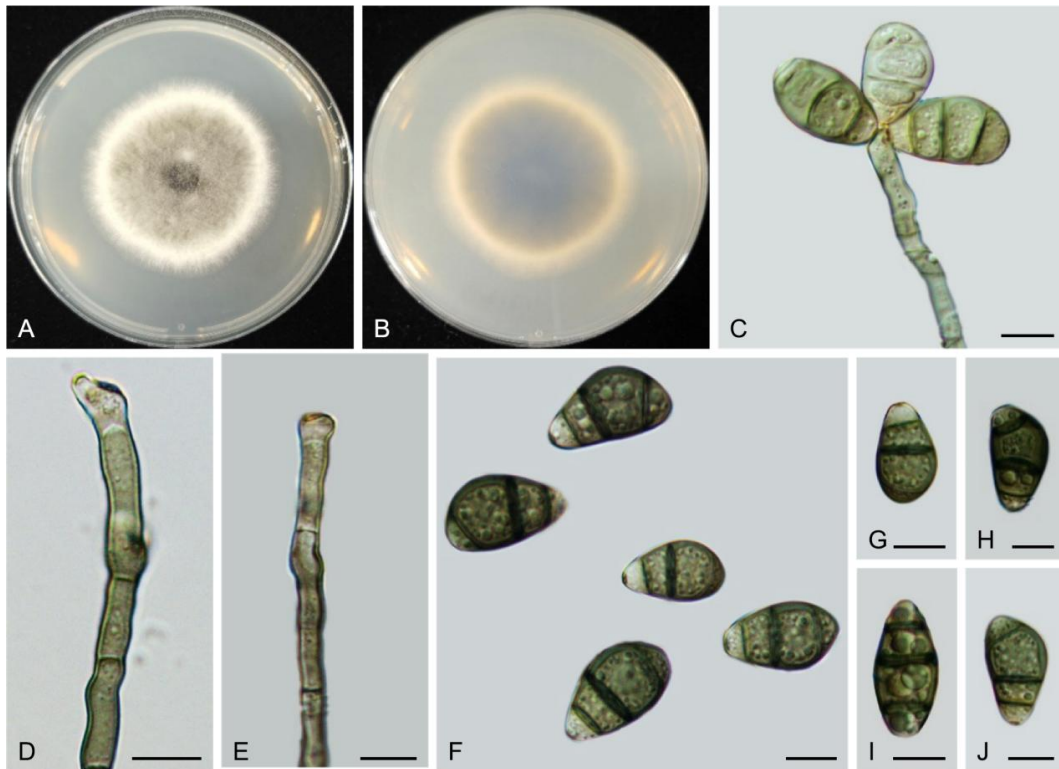


Figure 6. *Curvularia platycladicola* (CGMCC3.29554). **A, B** Colony obverse and reverse on PDA after 5 d at 25°C; **C–E** Conidiophores and conidiogenous cells; **F–J** Conidia. Scale bars: 10 µm (**C–J**).

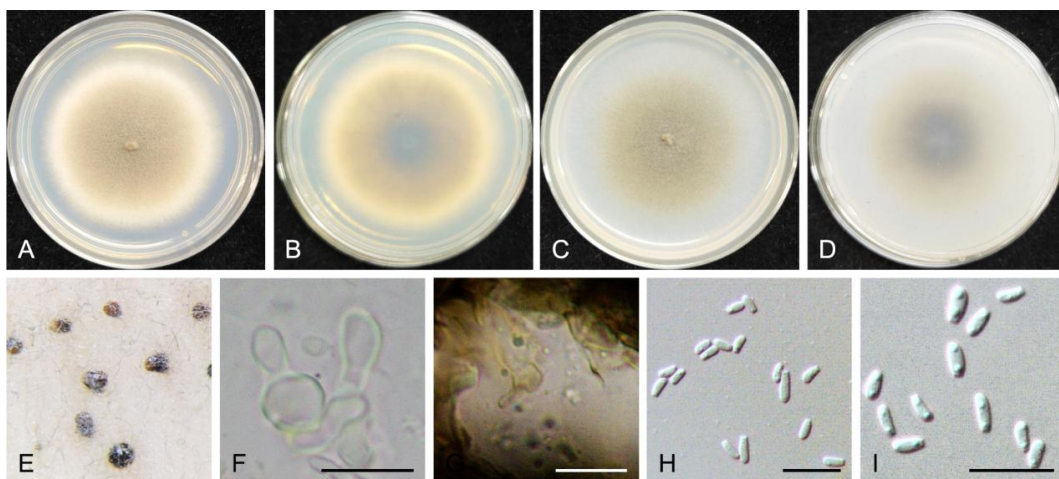


Figure 7. *Epicoccum platycladi* (CGMCC3.29659). **A, B** Colony obverse and reverse on PDA after 7 d at 25°C; **C, D** Colony obverse and reverse on OA after 7 d at 25°C; **E** Conidiomata formed on OA; **F, G** Conidiophore and conidiogenous cells; **H, I** Conidia. Scale bars: 10 µm (**F–I**).

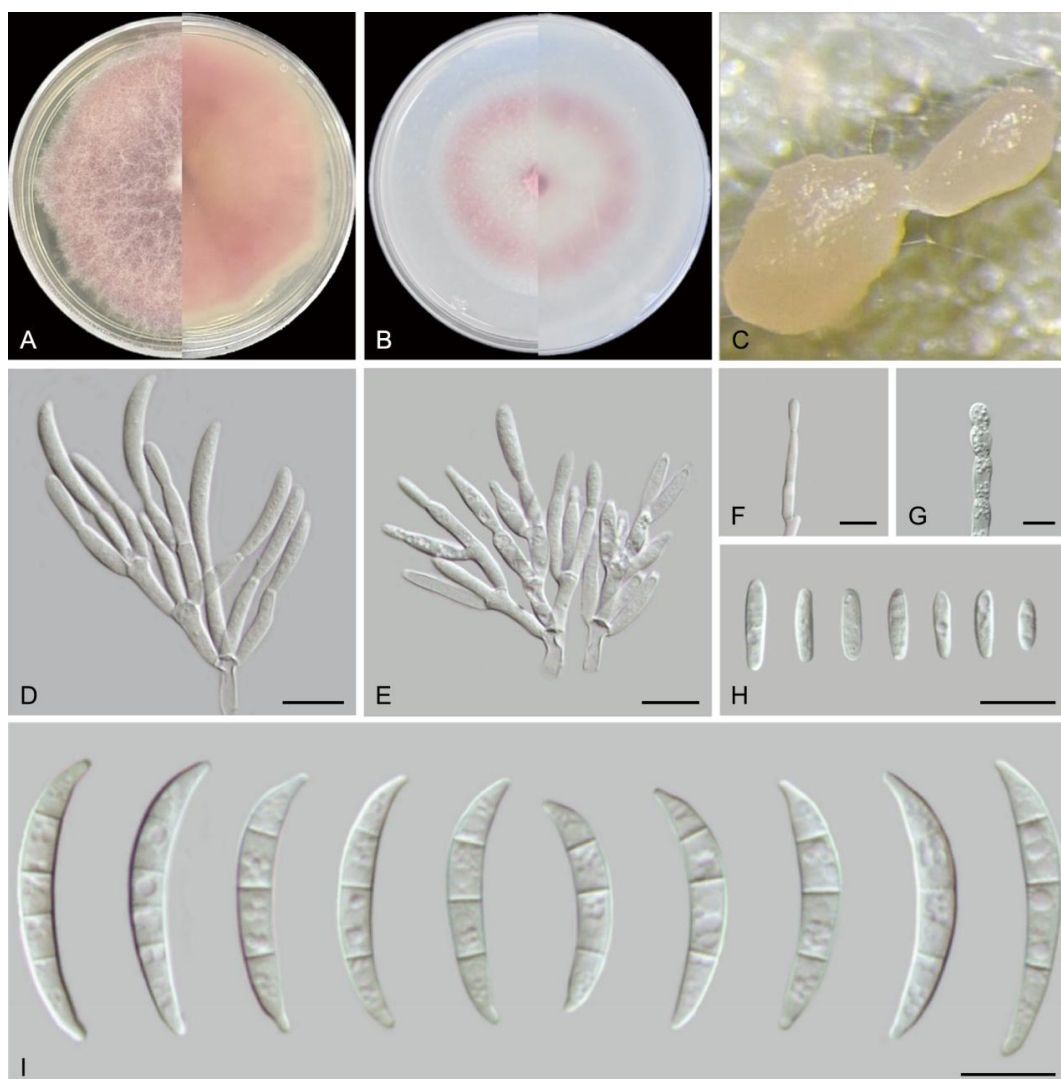


Figure 8. *Fusarium beijingsensis* (CGMCC3.29618). **A** Colony obverse and reverse on PDA after 7 d at 25°C; **B** Colony obverse and reverse on OA after 7 d at 25°C; **C** Sporodochia formed on CLA; **D, E** Sporodochial conidiophores and phialides; **F** Aerial conidiophores and monophialides; **G** Chlamydospores; **H** Microconidia; **I** Macroconidia. Scale bars: 10 µm (**D–I**).

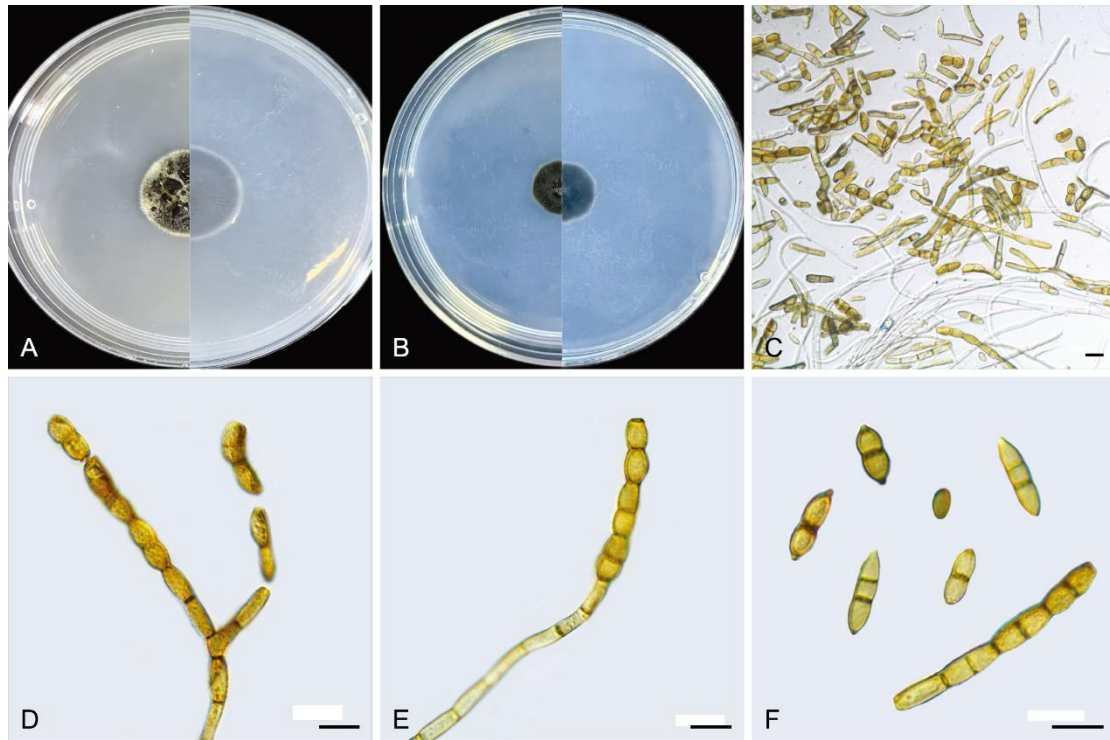


Figure 9. *Toxicocladosporium quinquagintatreanum* (CGMCC3.29337). **A** Colony obverse and reverse on PDA after 14 d at 25°C; **B** Colony obverse and reverse on SNA after 14 d at 25°C; **C–F** Mycelium, conidiophores, ramoconidia and conidia. Scale bars: 10 µm (**C–F**).

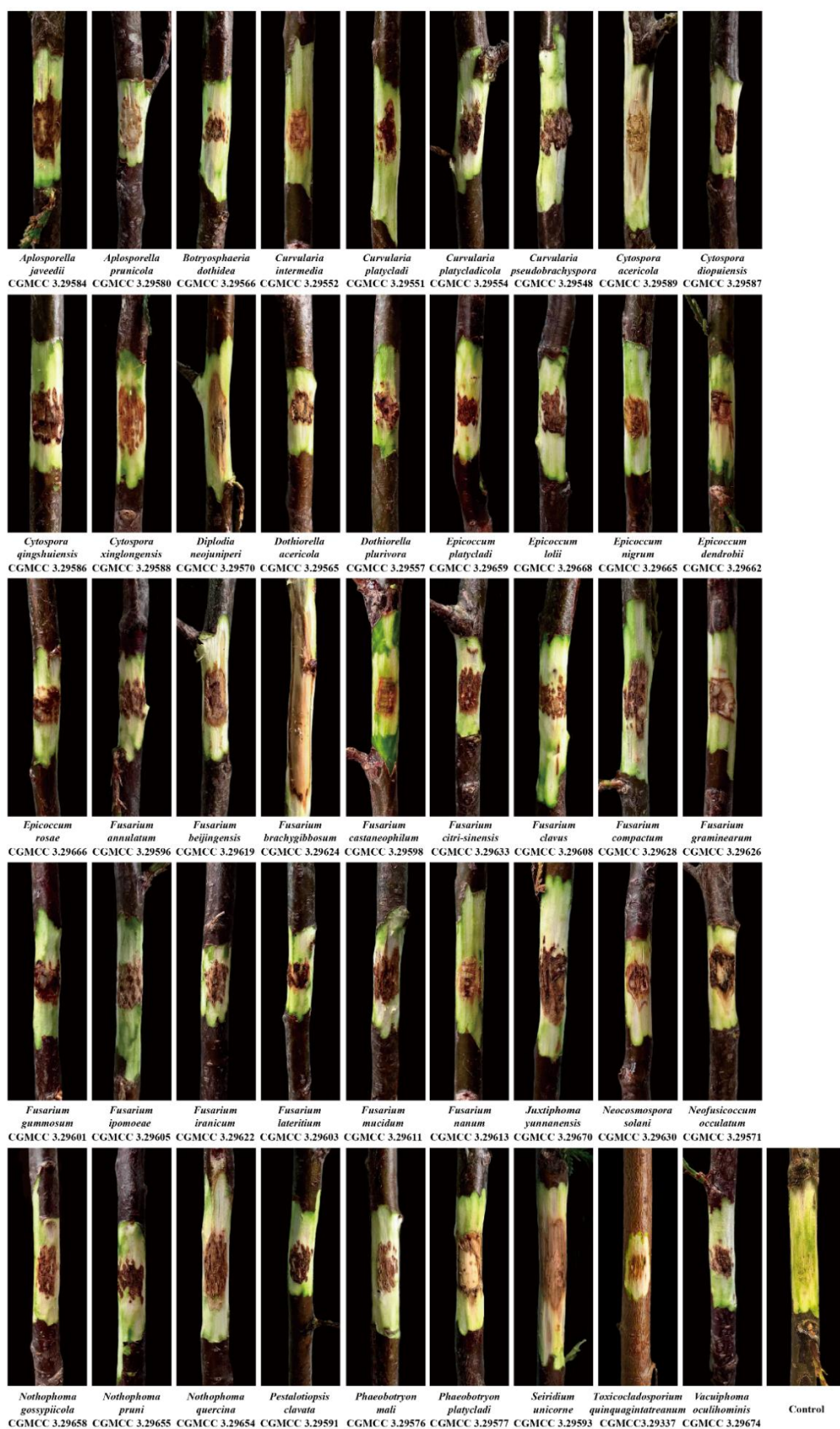


Figure 10. Lesions on stems of 3-year-old *Platycladus orientalis* seedlings after 30 d inoculation with representative strains of 45 species.

1083

1084 **Table 1.** Details of strains obtained from ancient *Platyclusus orientalis* in Beijing.

Species	Accession number	Location	Isolation source	GenBank Accession number								
				ITS	LSU	<i>tefl-a</i>	<i>tub2</i>	<i>rpb1</i>	<i>rpb2</i>	<i>act</i>	<i>cam</i>	<i>gapdh</i>
<i>Aplosporella javeedii</i>	BJFU-TT11.2 =	Dongcheng District,	Blighted	PZ2918		PZ3356						
	CGMCC3.29582	Temple of Heaven	leaves	47	—	09	—	—	—	—	—	—
	BJFU-TZY1.1 =	Dongcheng District,	Cankered	PZ2918		PZ3356						
	CGMCC3.29583	Temple of Heaven	branches	48	—	10	—	—	—	—	—	—
	BJFU-TT14.2 =	Fengtai District,	Cankered	PZ2918		PZ3356						
<i>A. prunicola</i>	CGMCC3.29584	Taiziyu Ancient Tree Cluster Park	branches	49	—	11	—	—	—	—	—	—
	BJFU- FHS3.8 =	Shijingshan District,	Cankered	PZ2918		PZ3356						
	CGMCC3.29580	Fahai Temple	branches	50	—	12	—	—	—	—	—	—
	BJFU- FHS3.9 =	Shijingshan District,	Cankered	PZ2918		PZ3356						
	CGMCC3.29581	Fahai Temple	branches	51	—	13	—	—	—	—	—	—
<i>Botryosphaeria dothidea</i>	BJFU-BH8.1 =	Xicheng District,	Branches with	PZ2918		PZ3356	PZ3356					
	CGMCC3.29566	Beihai Park	dieback	52	—	14	93	—	—	—	—	—
	BJFU-ZS19.1 =	Dongcheng District,	Branches with	PZ2918		PZ3356	PZ3356					
	CGMCC3.29567	Zhongshan Park	dieback	53	—	15	94	—	—	—	—	—
	BJFU-TT2.3 =	Dongcheng District,	Branches with	PZ2918		PZ3356	PZ3356					
<i>Curvularia intermedia</i>	CGMCC3.29568	Temple of Heaven	dieback	54	—	16	95	—	—	—	—	—
	BJFU-KM7.1 =	Dongcheng District,	Branches with	PZ2918		PZ3356						PZ3359
	CGMCC3.29552	Kongmiao and Imperial College museum	dieback	55	—	17	—	—	—	—	—	06

<i>C. platycladi</i>	BJFU-XS14.4 = CGMCC3.29550	Haidian District, Fragrant Hills Park	Branches with dieback	PZ2918 57	—	PZ3356 19	—	—	—	—	—	PZ3359 08
	BJFU-TT1.1 = CGMCC3.29551 ^T	Dongcheng District, Temple of Heaven	Branches with dieback	PZ2918 58	—	PZ3356 20	—	—	—	—	—	PZ3359 09
	BJFU-TM10.1 = CGMCC3.29554 ^T	Dongcheng District, Imperial Ancestral Temple	Branches with dieback	PZ2918 59	—	PZ3356 21	—	—	—	—	—	PZ3359 10
<i>C. platycladicola</i>	BJFU-TM10.2 = CGMCC3.29555	Dongcheng District, Imperial Ancestral Temple	Branches with dieback	PZ2918 60	—	PZ3356 22	—	—	—	—	—	PZ3359 11
	BJFU-JTS2.4 = CGMCC3.29548	Mentougou District, Jietai Temple	Branches with dieback	PZ2918 56	—	PZ3356 18	—	—	—	—	—	PZ3359 07
	BJFU-TZY3.1 = CGMCC3.29589	Fengtai District, Taiziyu Ancient Tree Cluster Park	Cankered branches	PZ2918 61	—	PZ3356 23	PZ3356 96	—	PZ3357 76	PZ3356 87	—	—
<i>C. diopuiensis</i>	BJFU-TZY5.2 = CGMCC3.29590	Fengtai District, Taiziyu Ancient Tree Cluster Park	Cankered branches	PZ2918 62	—	PZ3356 24	PZ3356 97	—	PZ3357 77	PZ3356 88	—	—
	BJFU-YHY12.3 = CGMCC3.29587	Haidian District, Summer Palace	Cankered branches	PZ2918 63	—	PZ3356 25	PZ3356 98	—	PZ3357 78	PZ3356 89	—	—
	BJFU-JTS3.1 = CGMCC3.29585	Mentougou District, Jietai Temple	Cankered branches	PZ2918 64	—	PZ3356 26	PZ3356 99	—	PZ3357 79	PZ3356 90	—	—
<i>C. qingshuiensis</i>	BJFU-HLS6.3 = CGMCC3.29586	Huairou District, Hongluo Temple	Cankered branches	PZ2918 65	—	PZ3356 27	PZ3357 00	—	PZ3357 80	PZ3356 91	—	—

<i>C. xinglongensis</i>	BJFU-XS3.1 =	Haidian District,	Cankered	PZ2918	—	PZ3356	PZ3357	—	PZ3357	PZ3356	—	—
	CGMCC3.29588	Fragrant Hills Park	branches	66	—	28	01	—	81	92	—	—
	BJFU-ZS6.1 =	Dongcheng District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
<i>Diplodia neojuniperi</i>	CGMCC3.29569	Zhongshan Park	dieback	67	—	29	02	—	—	—	—	—
	BJFU-TZY2.2 =	Fengtai District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29570	Taiziyu Ancient Tree Cluster Park	dieback	68	—	30	03	—	—	—	—	—
<i>Dothiorella acericola</i>	BJFU-YHY13.2 =	Haidian District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29559	Summer Palace	dieback	69	—	31	04	—	—	—	—	—
	BJFU-XS14.1 =	Haidian District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29560	Fragrant Hills Park	dieback	70	—	32	05	—	—	—	—	—
	BJFU-HLS4.2 =	Huairou District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29561	Hongluo Temple	dieback	71	—	33	06	—	—	—	—	—
	BJFU-TZS3.1 =	Mentougou District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29562	Tanzhe Temple	dieback	72	—	34	07	—	—	—	—	—
	BJFU-JTS3.2 =	Mentougou District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29563	Jietai Temple	dieback	73	—	35	08	—	—	—	—	—
	BJFU-TT6.1 =	Dongcheng District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29564	Temple of Heaven	dieback	74	—	36	09	—	—	—	—	—
	BJFU-YHY12.2 =	Haidian District,	Blighted	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29565	Summer Palace	leaves	75	—	37	10	—	—	—	—	—
	BJFU-TT10.2 =	Dongcheng District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
<i>D. plurivora</i>	CGMCC3.29556	Temple of Heaven	dieback	76	—	38	11	—	—	—	—	—
	BJFU-TT15.4 =	Dongcheng District,	Branches with	PZ2918	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29557	Temple of Heaven	dieback	77	—	39	12	—	—	—	—	—

<i>E. dendrobii</i>	BJFU-TT4.1 = CGMCC3.29558	Dongcheng District, Temple of Heaven	Blighted leaves	PZ2918 78	—	PZ3356 40	PZ3357 13	—	—	—	—	—
	BJFU-FHS4.4 = CGMCC3.29661	Shijingshan District, Fahai Temple	Cankered stems	PZ2918 79	PZ2919 50	—	PZ3357 14	—	PZ3357 82	—	—	—
	BJFU-FHS7.2 = CGMCC3.29662	Shijingshan District, Fahai Temple	Blighted leaves	PZ2918 80	PZ2919 51	—	PZ3357 15	—	PZ3357 83	—	—	—
	BJFU-YHY15.2 = CGMCC3.29663	Haidian District, Summer Palace	Cankered stems	PZ2918 81	PZ2919 52	—	PZ3357 16	—	PZ3357 84	—	—	—
	BJFU-KM3.1 = CGMCC3.29664	Dongcheng District, Kongmiao and Imperial College museum	Cankered branches	PZ2918 82	PZ2919 53	—	PZ3357 17	—	PZ3357 85	—	—	—
<i>E. lolii</i>	BJFU-HLS8.1 = CGMCC3.29668	Huairou District, Hongluo Temple	Cankered branches	PZ2918 83	PZ2919 54	—	PZ3357 18	—	PZ3357 86	—	—	—
	BJFU-HLS8.2 = CGMCC3.29669	Huairou District, Hongluo Temple	Cankered branches	PZ2918 84	PZ2919 55	—	PZ3357 19	—	PZ3357 87	—	—	—
<i>E. nigrum</i>	BJFU-TM10.2 = CGMCC3.29665	Dongcheng District, Imperial Ancestral Temple	Cankered stems	PZ2918 85	PZ2919 56	—	PZ3357 20	—	PZ3357 88	—	—	—
<i>E. platycladi</i>	BJFU-FHS1.7 = CGMCC3.29659 ^T	Shijingshan District, Fahai Temple	Cankered branches	PZ2918 88	PZ2919 59	—	PZ3357 23	—	PZ3357 91	—	—	—
	BJFU-JTS2.3 = CGMCC3.29660	Mentougou District, Jietai Temple	Blighted leaves	PZ2918 89	PZ2919 60	—	PZ3357 24	—	PZ3357 92	—	—	—
<i>E. rosae</i>	BJFU-XS4.7 = CGMCC3.29666	Haidian District, Fragrant Hills Park	Cankered branches	PZ2918 86	PZ2919 57	—	PZ3357 21	—	PZ3357 89	—	—	—

<i>Fusarium annulatum</i>	BJFU-TT7.2 =	Dongcheng District,	Blighted	PZ2918	PZ2919	—	PZ3357	—	PZ3357	—	—	—
	CGMCC3.29667	Temple of Heaven	leaves	87	58	—	22	—	90	—	—	—
	BJFU-TT15.3 =	Dongcheng District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29596	Temple of Heaven	branches	90	—	41	25	42	93	—	74	—
<i>F. beijingensis</i>	BJFU-TT15.4 =	Dongcheng District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29597	Temple of Heaven	branches	91	—	42	26	43	94	—	75	—
	BJFU-YHY3.2 =	Haidian District,	Blighted	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29615	Summer Palace	leaves	15	—	66	46	67	18	—	99	—
<i>F. brachygibbosum</i>	BJFU-TT16.1 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3359	—
	CGMCC3.29616	Temple of Heaven	branches	16	—	67	47	68	19	—	00	—
	BJFU-JTS3.2 =	Mentougou District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3359	—
	CGMCC3.29617	Jietai Temple	branches	17	—	68	48	69	20	—	01	—
<i>F. castaneophilum</i>	BJFU-HLS7.2 =	Huairou District,	Blighted	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3359	—
	CGMCC3.29618 ^T	Hongluo Temple	leaves	18	—	69	49	70	21	—	02	—
	BJFU-ZS18.2 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3359	—
	CGMCC3.29619	Zhongshan Park	branches	19	—	70	50	71	22	—	03	—
<i>F. brachygibbosum</i>	BJFU-TT13.2 =	Dongcheng District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29624	Temple of Heaven	branches	92	—	43	27	44	95	—	76	—
	BJFU-YHY3.6 =	Haidian District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29625	Summer Palace	branches	93	—	44	28	45	96	—	77	—
<i>F. castaneophilum</i>	BJFU-XS9.1 =	Haidian District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29598	Fragrant Hills Park	stems	94	—	45	29	46	97	—	78	—
	BJFU-FHS8.3 =	Shijingshan District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29599	Fahai Temple	branches	95	—	46	30	47	98	—	79	—

<i>F. citri-sinensis</i>	BJFU-XS9.2 =	Haidian District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3357	—	PZ3358	—
	CGMCC3.29600	Fragrant Hills Park	stems	96	—	47	31	48	99	—	80	—
	BJFU-XS15.4 =	Haidian District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29632	Fragrant Hills Park	branches	97	—	48	32	49	00	—	81	—
<i>F. clavus</i>	BJFU-TT6.3 =	Dongcheng District,	Cankered	PZ2918	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29633	Temple of Heaven	branches	98	—	49	33	50	01	—	82	—
	BJFU-TT3.2 =	Dongcheng District,	Cankered	PZ2918	—	PZ3356	—	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29608	Temple of Heaven	branches	99	—	50	—	51	02	—	83	—
<i>F. compactum</i>	BJFU-FHS4.2 =	Shijingshan District,	Cankered	PZ2919	—	PZ3356	—	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29628	Fahai Temple	branches	00	—	51	—	52	03	—	84	—
<i>F. ipomoeae</i>	BJFU-FHS4.4 =	Shijingshan District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29605	Fahai Temple	branches	01	—	52	34	53	04	—	85	—
	BJFU-FHS4.5 =	Shijingshan District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29606	Fahai Temple	branches	02	—	53	35	54	05	—	86	—
<i>F. iranicum</i>	BJFU-TT6.1 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29607	Temple of Heaven	branches	03	—	54	36	55	06	—	87	—
	BJFU-TT11.3 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29622	Temple of Heaven	branches	04	—	55	37	56	07	—	88	—
	BJFU-ZS20.1 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29623	Zhongshan Park	branches	05	—	56	38	57	08	—	89	—
<i>F. graminearum</i>	BJFU-TM11.1 =	Dongcheng District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29626	Imperial Ancestral Temple	branches	06	—	57	39	58	09	—	90	—
<i>F. gummosum</i>	BJFU-YHY5.1 =	Haidian District,	Cankered	PZ2919	—	PZ3356	PZ3357	PZ3358	PZ3358	—	PZ3358	—
	CGMCC3.29601	Summer Palace	branches	07	—	58	40	59	10	—	91	—

<i>F. lateritium</i>	BJFU-YHY5.3 =	Haidian District,	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3358	
	CGMCC3.29602	Summer Palace	branches	08	—	59	41	60	11	—	92	—
	BJFU-TT4.3 =	Dongcheng District,	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3358	
	CGMCC3.29603	Temple of Heaven	branches	09	—	60	42	61	12	—	93	—
	BJFU-TT4.1 =	Dongcheng District,	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3358	
<i>F. mucidum</i>	CGMCC3.29604	Temple of Heaven	branches	10	—	61	43	62	13	—	94	—
	BJFU-TT16.1 =	Dongcheng District,	Cankered	PZ2919		PZ3356		PZ3358	PZ3358		PZ3358	
	CGMCC3.29611	Temple of Heaven	branches	11	—	62	—	63	14	—	95	—
	BJFU-XS1.2 =	Haidian District,	Cankered	PZ2919		PZ3356		PZ3358	PZ3358		PZ3358	
	CGMCC3.29612	Fragrant Hills Park	branches	12	—	63	—	64	15	—	96	—
<i>F. nanum</i>		Dongcheng District,										
	BJFU-KM2.3 =	Kongmiao and	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3358	
	CGMCC3.29613	Imperial College	branches	13	—	64	44	65	16	—	97	—
		museum										
	BJFU-DT8.1 =	Dongcheng District,	Blighted	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3358	
<i>Juxtiphoma yunnanensis</i>	CGMCC3.29614	Ditan Park	leaves	14	—	65	45	66	17	—	98	—
	BJFU-TT5.1 =	Dongcheng District,	Cankered	PZ2919	PZ2919		PZ3357		PZ3358			
	CGMCC3.29670	Temple of Heaven	stems	20	61	—	51	—	23	—	—	—
	BJFU-YHY17.1 =	Haidian District,	Blighted	PZ2919	PZ2919		PZ3357		PZ3358			
	CGMCC3.29671	Summer Palace	leaves	21	62	—	52	—	24	—	—	—
<i>Neocosmospora solani</i>	BJFU-ZS17.4 =	Dongcheng District,	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3359	
	CGMCC3.29630	Zhongshan Park	stems	22	—	71	53	72	25	—	04	—
	BJFU-XS14.1 =	Haidian District,	Cankered	PZ2919		PZ3356	PZ3357	PZ3358	PZ3358		PZ3359	
	CGMCC3.29631	Fragrant Hills Park	stems	23	—	72	54	73	26	—	05	—
	BJFU-XS1.2 =	Haidian District,	Blighted	PZ2919		PZ3356	PZ3357					
<i>Neofusicoccum occulatum</i>	CGMCC3.29571	Fragrant Hills Park	leaves	24	—	73	55	—	—	—	—	—

	Accession	Location	Plant part	Number of samples	Number of samples	Number of samples	Number of samples	Number of samples	Number of samples	Number of samples	Number of samples	Number of samples
	BJFU-TT1.3 =	Dongcheng District,	Blighted	PZ2919	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29572	Temple of Heaven	leaves	25	—	74	56	—	—	—	—	—
	BJFU-BH4.2 =	Xicheng District,	Branches with	PZ2919	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29573	Beihai Park	dieback	26	—	75	57	—	—	—	—	—
	BJFU-RT1.1 =	Chaoyang District,	Branches with	PZ2919	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29574	Ritan Park	dieback	27	—	76	58	—	—	—	—	—
<i>Nothophoma</i>		Dongcheng District,										
<i>gossypiicola</i>	BJFU-KM7.4 =	Kongmiao and	Cankered	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29658	Imperial College museum	stems	28	63	—	59	—	27	—	—	—
<i>N. pruni</i>		Dongcheng District,										
	BJFU-TM3.2 =	Imperial Ancestral	Blighted	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29655	Temple	leaves	29	64	—	60	—	28	—	—	—
	BJFU-TM3.3 =	Dongcheng District,	Blighted	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29656	Imperial Ancestral Temple	leaves	30	65	—	61	—	29	—	—	—
	BJFU-TM1.2 =	Dongcheng District,	Cankered	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29657	Imperial Ancestral Temple	branches	31	66	—	62	—	30	—	—	—
<i>N. quercina</i>		Mentougou District,	Cankered	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29651	Jietai Temple	branches	32	67	—	63	—	31	—	—	—
	BJFU-HLS4.2 =	Huairou District,	Blighted	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29652	Hongluo Temple	leaves	33	68	—	64	—	32	—	—	—
	BJFU-YHY13.2 =	Haidian District,	Cankered	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29653	Summer Palace	branches	34	69	—	65	—	33	—	—	—

<i>Pestalotiopsis clavata</i>	BJFU-HLS10.3 =	Huairou District,	Cankered	PZ2919	PZ2919	—	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29654	Hongluo Temple	branches	35	70	—	66	—	34	—	—	—
	BJFU-FHS5.6 =	Mentougou District,	Cankered	PZ2919	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29591	Jietai Temple	branches	36	—	77	67	—	—	—	—	—
<i>Phaeobotryon mali</i>	BJFU-FHS6.3 =	Shijingshan District,	Cankered	PZ2919	—	PZ3356	PZ3357	—	—	—	—	—
	CGMCC3.29592	Fahai Temple	branches	37	—	78	68	—	—	—	—	—
	BJFU-BH5.1 =	Xicheng District,	Cankered	PZ2919	PZ2919	PZ3356	—	—	—	—	—	—
	CGMCC3.29575	Beihai Park	branches	38	71	79	—	—	—	—	—	—
<i>P. platycladi</i>	BJFU-BH5.2 =	Xicheng District,	Cankered	PZ2919	PZ2919	PZ3356	—	—	—	—	—	—
	CGMCC3.29576	Beihai Park	branches	39	72	80	—	—	—	—	—	—
	BJFU-HLS10.1 =	Huairou District,	Cankered	PZ2919	PZ2919	PZ3356	—	—	—	—	—	—
	CGMCC3.29577	Hongluo Temple	branches	40	73	81	—	—	—	—	—	—
<i>Seiridium unicorne</i>	BJFU-HLS5.1 =	Huairou District,	Cankered	PZ2919	PZ2919	PZ3356	—	—	—	—	—	—
	CGMCC3.29578	Hongluo Temple	branches	41	74	82	—	—	—	—	—	—
	BJFU-TT8.1 =	Dongcheng District,	Cankered	PZ2919	PZ2919	PZ3356	—	—	—	—	—	—
	CGMCC3.29579	Temple of Heaven	branches	42	75	83	—	—	—	—	—	—
<i>Toxicocladosporium quinquagintatre anum</i>	BJFU-HLS5.3 =	Huairou District,	Cankered	PZ2919	PZ2919	PZ3356	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29593	Hongluo Temple	branches	43	76	84	69	—	35	—	—	—
	BJFU-BH7.2 =	Xicheng District,	Cankered	PZ2919	PZ2919	PZ3356	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29594	Beihai Park	branches	44	77	85	70	—	36	—	—	—
<i>Toxicocladosporium quinquagintatre anum</i>	BJFU-CL5.2 =	Changping District,	Cankered	PZ2919	PZ2919	PZ3356	PZ3357	—	PZ3358	—	—	—
	CGMCC3.29595	Ming Tombs	branches	45	78	86	71	—	37	—	—	—
	BJFU-TM8.1 =	Dongcheng District,	Rotted stems	PX3261	PX3543	—	PX5121	—	PX5121	PX3527	—	—
	CGMCC3.29337 ^T	Imperial Ancestral Temple		37	34	—	49	—	47	16	—	—

	BJFU-TM2.2 = CGMCC3.29338	Dongcheng District, Imperial Ancestral Temple	Rotted stems	PX3261 38	PX3543 35	—	PX5121 50	—	PX5121 48	PX3527 17	—	—
<i>Vacuiphoma oculihominis</i>	BJFU-YHY6.3 = CGMCC3.29672	Haidian District, Summer Palace	Blighted leaves	PZ2919 46	PZ2919 79	—	PZ3357 72	—	PZ3358 38	—	—	—
	BJFU-JTS3.1 = CGMCC3.29673	Mentougou District, Jietai Temple	Cankered branches	PZ2919 47	PZ2919 80	—	PZ3357 73	—	PZ3358 39	—	—	—
	BJFU-TZY3.1 = CGMCC3.29674	Fengtai District, Taiziyu Ancient Tree Cluster Park	Cankered branches	PZ2919 48	PZ2919 81	—	PZ3357 74	—	PZ3358 40	—	—	—
	BJFU-YHY11.1 = CGMCC3.29675	Haidian District, Summer Palace	Blighted leaves	PZ2919 49	PZ2919 82	—	PZ3357 75	—	PZ3358 41	—	—	—

1085 **Notes.** T: ex-type strains; CGMCC: China General Microbiological Culture Collection Center, Beijing, China.

1086

1087 **Table 2.** GenBank accession numbers of relevant species used in phylogenetic analyses.

Species	Strain Numbers	GenBank Accession Numbers									References
		ITS	LSU	<i>tef1-a</i>	<i>tub2</i>	<i>rpb1</i>	<i>rpb2</i>	<i>act1</i>	<i>cam</i>	<i>gapdh</i>	
<i>Alanphillipsia aloecicola</i>	CBS 138896 ^T	KP004 444	KP004 472	MT592027							Wu et al. (2024)
<i>Aplosporella hesperidica</i>	CBS 732.79 ^T	KX464 083	—	—	—	—	—	—	—	—	Bi et al. (2025)
<i>A. javeedii</i>	CFCC 50054 ^T	KP208 840	—	KP208846	—	—	—	—	—	—	Wu et al. (2024); Bi et al. (2025)
<i>A. javeedii</i>	CFCC 50052	KP208 838	—	KP208844	—	—	—	—	—	—	Wu et al. (2024); Bi et al. (2025)
<i>A. prunicola</i>	CBS 121167 ^T	KF766	—	—	—	—	—	—	—	—	Wu et al. (2024); Bi et al.

		147									(2025)
<i>A. prunicola</i>	STE-U 6326	EF564 375	—	—	—	—	—	—	—	—	Wu et al. (2024); Bi et al. (2025)
<i>A. yalgorensis</i>	MUCC511 ^T	EF591 926	—	EF591977	—	—	—	—	—	—	Bi et al. (2025)
<i>A. yalgorensis</i>	MUCC512	EF591 927	—	EF591978	—	—	—	—	—	—	Bi et al. (2025)
<i>A. yanqingensis</i>	CFCC 58791 ^T	OQ651 164	—	OQ692924	—	—	—	—	—	—	Lin et al. (2023); Bi et al. (2025)
<i>Bipolaris maydis</i>	CBS 136.29 ^T	KJ909 769	—	KM093793	—	—	—	—	—	KM03 4845	Raza et al. (2019)
<i>Botryosphaeria dothidea</i>	CBS 115476 ^T	AY236 949	—	AY236898	AY236927	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. dothidea</i> (syn. <i>B. qinlingensis</i>)	CFCC 52984	MK43 4301	—	MK425020	MK425022	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. dothidea</i> (syn. <i>B. qinlingensis</i>)	CFCC 52985	MK43 4302	—	MK425021	MK425023	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. dothidea</i> (syn. <i>B. wangensis</i>)	CERC 2298 ^T	KX278 002	—	KX278107	KX278211	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. dothidea</i> (syn. <i>B. wangensis</i>)	CERC 2299	KX278 003	—	KX278108	KX278212	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. ramosa</i> (syn. <i>B. pseudoramosa</i>)	CERC 1999	KX277 988	—	KX278093	KX278197	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>B. ramosa</i> (syn. <i>B. pseudoramosa</i>)	CERC 2001 ^T	KX277 989	—	KX278094	KX278198	—	—	—	—	—	Zhang et al. (2021); Zhang et al. (2025b)
<i>Coniothyrium</i>	CBS 400.71	MH86	MH87	—	KT389792	—	KT389	—	—	—	Wang et al. (2024)

<i>palmarum</i>		0184	1954				592				
<i>Curvularia aeria</i>	CBS 294.61 ^T	HE861 850	—	—	—	—	—	—	—	HF565 450	Raza et al. (2019)
<i>C. americana</i>	UTHSC 07-2649	HE861 834	—	—	—	—	—	—	—	HF565 486	Madrid et al. (2014)
<i>C. americana</i>	UTHSC 08-84	HG779 015	—	—	—	—	—	—	—	HG779 115	Madrid et al. (2014)
<i>C. americana</i>	UTHSC 08-3414 ^T	HE861 833	—	—	—	—	—	—	—	HF565 488	Madrid et al. (2014); Raza et al. (2019)
<i>C. brachyspora</i>	CBS 186.50 ^T	KJ922 372	—	KM230405	—	—	—	—	—	KM06 1784	Raza et al. (2019)
<i>C. buchloes</i>	CBS 246.49 ^T	KJ909 765	—	KM196588	—	—	—	—	—	KM06 1789	Raza et al. (2019)
<i>C. chiangraiensis</i>	MFLUCC 22-0091 ^T	OP581 428	—	OP859017	—	—	—	—	—	OP859 013	Zhao et al. (2025a)
<i>C. herbicola</i>	XW1-15 ^T	PV973 433	—	PV995209	—	—	—	—	—	PV995 193	Zhao et al. (2025a)
<i>C. herbicola</i>	YYH23-17	PV973 432	—	PV995208	—	—	—	—	—	PV995 192	Zhao et al. (2025a)
<i>C. homomorpha</i>	CBS 156.60 ^T	JN192 380	—	JN601014	—	—	—	—	—	JN600 970	Raza et al. (2019)
<i>C. intermedia</i>	CBS 334.64	HG778 991	—	—	—	—	—	—	—	HG779 155	Raza et al. (2019); Zhao et al. (2025a)
<i>C. intermedia</i>	XY-3	OQ300 329	—	OQ338160	—	—	—	—	—	OQ338 159	Zhao et al. (2025a)
<i>C. loliicola</i>	XW9-5-1 ^T	PV973	—	PV995217	—	—	—	—	—	PV995	Zhao et al. (2025a)

		443								201	
<i>C. loliicola</i>	XW9-5-2	PV973	–	PV995218	–	–	–	–	–	PV995	Zhao et al. (2025a)
		441								202	
<i>C. manamgodae</i>	CGMCC3.19446 ^T	MN21	–	MN263971	–	–	–	–	–	MN26	Raza et al. (2019)
		5677								4110	
<i>C. manamgodae</i>	LC13495	MN21	–	MN263972	–	–	–	–	–	MN26	Raza et al. (2019)
		5678								4111	
<i>C. nanjingensis</i>	YZ25-10-2-1 ^T	PV973	–	PV995214	–	–	–	–	–	PV995	Zhao et al. (2025a)
		438								198	
<i>C. palmicola</i>	MFLUCC 14-0404 ^T	MF621	–	–	–	–	–	–	–	–	Zhao et al. (2025a)
		582									
<i>C. panici-maximi</i>	USJCC-0006 ^T	MN04	–	MN053009	–	–	–	–	–	MN05	Zhao et al. (2025a)
		4757								3040	
<i>C. paraverruculosa</i>	FMR 17656 ^T	LR736	–	LR736649	–	–	–	–	–	LR736	Zhao et al. (2025a)
		641								646	
<i>C. perotidis</i>	CBS 350.90 ^T	JN192	–	JN601021	–	–	–	–	–	KJ415	Raza et al. (2019)
		385								394	
<i>C. petersonii</i>	BRIP 14642 ^T	MH41	–	MH433668	–	–	–	–	–	MH43	Raza et al. (2019)
		4905								3650	
<i>C. pseudobrachyspora</i>	CPC 28808 ^T	MF490	–	MF490862	–	–	–	–	–	MF490	Marin-Felix et al. (2017); Raza et al. (2019)
		819								841	
<i>C. pseudobrachyspora</i>	USJCC–0024	MT410	–	MZ971258	–	–	–	–	–	MZ97	Ferdinandez et al. (2023)
		576								1272	
<i>C. pseudobrachyspora</i>	USJCC–0085	OQ275	–	OQ332412	–	–	–	–	–	OQ269	Ferdinandez et al. (2023)
		232								643	
<i>C. pseudointermedia</i>	CBS 553.89 ^T	MN68	–	MN688871	–	–	–	–	–	MN68	Zhao et al. (2025a)

		8819								8846	
<i>C. rouhanii</i>	CBS 144674 ^T	KX139 030	–	MG428687	–	–	–	–	–	MG42 8694	Zhao et al. (2025a)
<i>C. simmonsii</i>	USJCC-0002 ^T	MN04 4753	–	MN053005	–	–	–	–	–	MN05 3011	Ferdinandez et al. (2021)
<i>C. spicifera</i>	CBS 274.52 ^T	JN192 387	–	JN601023	–	–	–	–	–	JN600 979	Raza et al. (2019); Zhao et al. (2025a)
<i>C. spicifera</i>	AT-102	OP218 259	–	OP223188	–	–	–	–	–	OP223 176	Zhao et al. (2025a)
<i>C. suttoniae</i>	FMR 10992 ^T	HE861 828	–	LR736651	–	–	–	–	–	HF565 479	Zhao et al. (2025a)
<i>C. verruculosa</i>	CBS 150.63	KP400 652	–	KP735695	–	–	–	–	–	KP645 346	Raza et al. (2019)
<i>C. vietnamensis</i>	FMR 17659 ^T	LR736 642	–	LR736647	–	–	–	–	–	LR736 644	Zhao et al. (2025a)
<i>Cytospora acericola</i>	CFCC 55995	PP988 706	–	OQ862398	OQ862488	–	–	OR052 754	–	–	Lin et al. (2024)
<i>C. acericola</i>	CFCC 55994 ^T	PP988 705	–	OQ862397	OQ862487	–	–	OR052 753	–	–	Lin et al. (2024)
<i>C. diopuiensis</i>	CFCC 55527	OQ344 754	–	OQ398763	OQ398792	–	OQ398 736	OQ410 626	–	–	Li et al. (2024)
<i>C. diopuiensis</i>	CFCC 55479	OQ344 753	–	OQ398762	OQ398791	–	OQ398 735	OQ410 625	–	–	Li et al. (2024b)
<i>C. diopuiensis</i>	MFLUCC 18-1419 ^T	MK91 2137	–	–	–	–	–	MN68 5819	–	–	Shang et al. (2020); Lin et al. (2024)
<i>C. fugax</i>	CBS 203.42 ^T	PP988	–	KX965162	KX964971	–	KX965	KX964	–	–	Fan et al. (2020); Lin et al.

		848					540	798			(2024)
<i>C. hippophaes</i>	CBS 259.88 ^R	PP988	—	KX965167	KX964976	—	KX965	KX964	—	—	Lin et al. (2024)
		856					543	804			
<i>C. hippophaes</i>	CFCC 58942	PP988	—	OQ862362	—	—	—	OR052	—	—	Lin et al. (2024)
		857						719			
<i>C. juniperina</i>	CFCC 50501 ^T	MH93	—	MH933507	—	—	MH93	MH93	—	—	Lin et al. (2024)
		3632					3602	3539			
<i>C. lumnitzericola</i>	MFLUCC	MG97	—	—	—	—	MH25	MH25	—	—	Lin et al. (2024)
	17-0508 ^T	5778					3461	3457			
<i>C. pingbianensis</i>	MFLUCC	MK91	—	—	—	—	MN68	MN68	—	—	Lin et al. (2024); Jiang et al.
	18-1204 ^T	2135					5826	5817			(2025)
<i>C. platycladi</i>	CFCC 50504 ^T	MH93	—	MH933516	MH933581	—	MH93	MH93	—	—	Fan et al. (2020)
		3645					3610	3552			
<i>C. platycladi</i>	CFCC 50505	MH93	—	MH933517	MH933582	—	MH93	MH93	—	—	Fan et al. (2020)
		3646					3611	3553			
<i>C. populina</i>	CFCC 89644 ^T	KF765	—	KU710930	KR045681	—	KU710	KU711	—	—	Li et al. (2024); Lin et al.
		686					969	007			(2024)
<i>C. qingshuiensis</i>	CFCC 56268 ^T	PP988	—	—	—	—	—	OR052	—	—	Lin et al. (2024)
		956						735			
<i>C. qingshuiensis</i>	CFCC 56349	PP988	—	OQ862377	OQ862474	—	—	OR052	—	—	Lin et al. (2024)
		957						736			
<i>C. thailandica</i>	MFLUCC	MG97	—	—	—	—	MH25	MH25	—	—	Lin et al. (2024)
	17-0262 ^T	5776					3463	3459			
<i>C. thailandica</i>	MFLUCC 17-0263	MG97	—	—	—	—	MH25	MH25	—	—	Lin et al. (2024)
		5777					3464	3460			
<i>C. xinglongensis</i>	CFCC 52458 ^T	MK43	—	—	—	—	MK57	MK44	—	—	Jiang et al. (2020); Lin et al.

		227									
<i>D. plurivora</i>	IRAN 1538C	KC898 229	–	KC898212	–	–	–	–	–	–	Abdollahzadeh et al. (2014)
<i>D. plurivora</i>	IRAN 1537C	KC898 226	–	KC898209	–	–	–	–	–	–	Abdollahzadeh et al. (2014)
<i>D. plurivora</i>	IRAN 1552C	KC898 228	–	KC898211	–	–	–	–	–	–	Abdollahzadeh et al. (2014)
<i>Epicoccum brahmansense</i>	CBS 990.95 ^T	MN97 3514	MN94 3720	–	MT005614	–	MT018 120	–	–	–	Wang et al. (2024)
<i>E. brahmansense</i>	CBS 985.95	MN97 3513	MN94 3719	–	MT005613	–	MT018 119	–	–	–	Wang et al. (2024)
<i>E. brasiliense</i>	CBS 120105 ^T	GU237 760	GU238 049	–	GU237588	–	KT389 627	–	–	–	Wang et al. (2024)
<i>E. cedri</i>	MFLU 16-1358 ^T	KY711 170	KY711 172	–	KY711168	–	–	–	–	–	Wang et al. (2024)
<i>E. dendrobii</i>	CGMCC 3.18359 ^T	KY742 093	KY742 247	–	KY742335	–	MT018 084	–	–	–	Chen et al. (2017); Wang et al. (2024)
<i>E. dendrobii</i>	LC 8146	KY742 094	KY742 248	–	KY742336	–	MT018 085	–	–	–	Chen et al. (2017); Wang et al. (2024)
<i>E. draconis</i>	CBS 186.83 ^R	GU237 795	GU238 070	–	GU237607	–	KT389 628	–	–	–	Wang et al. (2024)
<i>E. ellisrowaniae</i>	MST F22293 ^T	OR731 309	OR731 314	–	OR737780	–	OR737 779	–	–	–	Gomzhina and Gasich (2025)
<i>E. henanense</i>	HNWVVF-EP2	MW86 1394	MW86 1424	–	MW861468	–	MW86 1498	–	–	–	Abeywickrama et al. (2023)
<i>E. henanense</i>	JZBH 380048 ^T	MW86	MW86	–	MW861467	–	MW86	–	–	–	Abeywickrama et al. (2023)

		1393	1423			1497					
<i>E. henningsii</i>	CBS 104.80 ^R	GU237	GU238	—	GU237612	—	KT389	—	—	—	Wang et al. (2024)
		731	081				629				
<i>E. jingdongense</i>	CGMCC 3.24247 ^T	OP648	OP837	—	OP854577	—	OP716	—	—	—	Wang et al. (2024)
		072	098				613				
<i>E. keratinophilum</i>	CBS 142455 ^T	LT592	LN907	—	LT592999	—	LT593	—	—	—	Valenzuela-Lopez et al. (2018)
		930	414				068				
<i>E. keratinophilum</i>	UTHSC DI16-272	LT592	LN907	—	LT593000	—	LT593	—	—	—	Valenzuela-Lopez et al. (2018)
		931	415				069				
<i>E. lolii</i>	CGMCC 3.19291 ^T	MK05	MK05	—	MK051180	—	MK05	—	—	—	Xu et al. (2024)
		1174	1177				1183				
<i>E. lolii</i>	HMCE-2	MK05	MK05	—	MK051181	—	MK05	—	—	—	Xu et al. (2024)
		1175	1178				1184				
<i>E. mezzettii</i>	CBS 120.22	MN97	MN94	—	MT005597	—	MT018	—	—	—	Hou et al. (2020a)
		3497	3702				096				
<i>E. mezzettii</i>	CBS 173.38 ^T	MN97	MN94	—	MT005596	—	MT018	—	—	—	Hou et al. (2020a)
		3496	3701				095				
<i>E. multiceps</i>	CBS 119734 ^T	MN97	MN94	—	MT005612	—	MT018	—	—	—	Wang et al. (2024)
		3512	3718				118				
<i>E. nigrum</i>	LC 8158	KY742	KY742	—	KY742353	—	KY742	—	—	—	Chen et al. (2017)
		111	265				180				
<i>E. nigrum</i>	LC 5180	KY742	KY742	—	KY742351	—	KY742	—	—	—	Chen et al. (2017)
		109	263				178				
<i>E. nigrum</i>	CBS 173.73 ^T	FJ4269	GU237	—	FJ427107	—	KT389	—	—	—	Chen et al. (2017); Wang et al.
		96	975				632				(2024)
<i>E. nigrum</i>	LC 8157	KY742	KY742	—	KY742352	—	KY742	—	—	—	Chen et al. (2017)

		110	264			179					
<i>E. plurivorum</i>	CBS 558.81 ^T	MH86	MH87	–	GU237647	–	KT389	–	–	–	Wang et al. (2024)
		1377	3128				634				
<i>E. poae</i>	CGMCC 3.18363 ^T	KY742	KY742	–	KY742355	–	KY742	–	–	–	Chen et al. (2017); Wang et al.
		113	267				182				(2024)
<i>E. poae</i>	LC 8161	KY742	KY742	–	KY742356	–	KY742	–	–	–	Chen et al. (2017)
		114	268				183				
<i>E. pruni</i>	MFLU 16-1794 ^T	KY711	KY711	–	KY711167	–	KY711	–	–	–	Wang et al. (2024)
		169	171				173				
<i>E. pseudokeratinophilum</i>	MFLUCC 18-1593 ^T	MH82	–	–	MH853666	–	MH85	–	–	–	Chethana et al. (2019); Wang et al. (2024)
		7002					3659				
<i>E. pseudoplurivorum</i>	MF 32.32 ^T	MH65	MH65	–	PP750329	–	PP750	–	–	–	Gomzhina and Gasich (2025)
		1566	1607				308				
<i>E. puerense</i>	CGMCC 3.24249 ^T	OP648	OP837	–	OP854585	–	OP716	–	–	–	Wang et al. (2024)
		080	105				621				
<i>E. purpurascens</i>	CBS 124435	MN97	MN94	–	MT005586	–	MT018	–	–	–	Hou et al. (2020a)
		3486	3691				081				
<i>E. purpurascens</i>	CBS 128906 ^R	MN97	MN94	–	MT005588	–	MT018	–	–	–	Hou et al. (2020a)
		3488	3693				083				
<i>E. rosae</i>	JZB 380076	MW86	MW86	–	MW861486	–	MW86	–	–	–	Abeywickrama et al. (2023)
		1412	1442				1516				
<i>E. rosae</i>	MFLU 15-3639 ^T	MG82	MG82	–	–	–	–	–	–	–	Wanasinghe et al. (2018); Wang et al. (2024)
		8900	9010								
<i>E. sherrardiae</i>	BRIP 72814a ^T	OR947	–	–	–	–	OR964	–	–	–	Gomzhina and Gasich (2025)
		070					966				
<i>Epicoccum</i> sp.	CBS 141022	MN97	MN94	–	MT005615	–	MT018	–	–	–	Xu et al. (2024)

		3515	3721				121				
<i>E. tobaicum</i>	CGMCC 3.18362	KY742 107	KY742 261	—	KY742349	—	—	—	—	—	Hou et al. (2020a); Wang et al. (2024)
<i>E. tobaicum</i>	CBS 384.36 ^T	MN97 3493	MN94 3698	—	MT005593	—	MT018 092	—	—	—	Hou et al. (2020a); Wang et al. (2024)
<i>E. viciae-villosae</i>	JZBH 380079 ^T	MW86 1418	MW86 1448	—	MW861492	—	MW86 1522	—	—	—	Gomzhina and Gasich (2025)
<i>Fusarium acuminatum</i>	LC13798	MW01 6651	—	MW620112	MW533997	MW02 4679	—	—	—	—	Wang et al. (2022)
<i>F. acuminatum</i>	LC13791	MW01 6644	—	MW620105	MW533990	MW02 4672	MW47 4630	—	—	—	Wang et al. (2022); Zhang et al. (2024)
<i>F. acuminatum</i>	LC13795	MW01 6648	—	MW620109	MW533994	MW02 4676	—	—	—	—	Wang et al. (2022)
<i>F. acuminatum</i>	LC5227 ^T	—	—	MW534000	—	MW02 4682	MW62 0115	—	MW474640	—	Wang et al. (2022)
<i>F. annulatum</i>	CBS 258.54 ^T	—	—	MT010994	MT011041	MT010 944	MT010 983	—	MT010908	—	Zhang et al. (2024)
<i>F. annulatum</i>	CBS 139334	—	—	MW402065	MW402264	MW40 2592	MW40 2750	—	MW402417	—	Zhang et al. (2024)
<i>F. annulatum</i>	CBS 533.95	—	—	MW402138	MW402338	—	MW40 2817	—	MW402470	—	Zhang et al. (2024)
<i>F. annulatum</i>	CBS 143605	—	—	MW402094	MW402293	MW40 2615	MW40 2760	—	MW402435	—	Zhang et al. (2024)
<i>F. annulatum</i>	CBS 115.97	—	—	MW401973	MW402173	MW40 2503	MW40 2785	—	MW402373	—	Zhang et al. (2024)
<i>F. aurantii</i>	BBA 65609 ^T	—	—	PQ000452	PQ000532	—	PQ000	—	PQ000774	—	Costa et al. (2024)

<i>F. avenaceum</i>	CBS 408.86 ^T	–	–	MW928836	–	MG28 2372	MG28 2401	–	–	–	Zhang et al. (2024)
<i>F. brachygibbosum</i>	CBS 131017	–	–	PQ260820	PQ273935	PQ280 844	PQ274 107	–	PQ240150	–	Sandoval-Denis et al. (2025)
<i>F. brachygibbosum</i>	NRRL 13829	–	–	JABFET010 000489	JABFET010 000093	JX171 460	JX171 574	–	JABFET000 000000	–	Sandoval-Denis et al. (2025)
<i>F. brachygibbosum</i>	NRRL 20954 ^T	–	–	MW233075	PQ273940	MW23 3246	MW23 3418	–	PQ240155	–	Sandoval-Denis et al. (2025)
<i>F. californicum</i>	CBS 145796 ^T	MK88 0138	–	MK878579	MK878574	MK87 8584	MK87 8569	–	–	–	Zhang et al. (2024)
<i>F. camelliae</i>	GUCC 21010 ^T	–	–	OP757314	–	–	OP800 100	–	–	–	Costa et al. (2024)
<i>F. campestre</i>	CBS 148994 ^T	–	–	ON960701	–	ON960 653	ON960 685	–	ON960621	–	Zhang et al. (2024)
<i>F. castaneophilum</i>	CFCC 70814 ^T	–	–	PP946923	PP946929	PP946 937	PP946 935	–	PP946917	–	Zhang et al. (2025a)
<i>F. castaneophilum</i>	CFCC 70815	–	–	PP946924	PP946930	PP946 938	PP946 936	–	PP946918	–	Zhang et al. (2025a)
<i>F. caulicola</i>	GUCC 191051.1 ^T	MZ724 827	–	OR043883	OR043935	OR043 783	OR043 828	–	OR043733	–	Zhang et al. (2023)
<i>F. citriforme</i>	CBS 253.50	–	–	KR071775	–	MW92 8802	MW92 8823	–	–	–	Zhang et al. (2024)
<i>F. citri-sinensis</i>	YZU 191316	–	–	MW855826	–	–	MW85 5854	–	–	–	Costa et al. (2024)
<i>F. citri-sinensis</i>	BBA 67503 ^T	–	–	PQ000509	PQ000590	–	PQ000	–	PQ000832	–	Costa et al. (2024)

							673				
<i>F. clavus</i>	CBS 126202 ^T	–	–	MN170456	–	–	MN170389	–	MN170322	–	Xia et al. (2019); Zhang et al. (2023)
<i>F. clavus</i>	NRRL 34035	–	–	GQ505637	–	–	GQ505815	–	GQ505549	–	Xia et al. (2019)
<i>F. compactum</i>	CBS 186.31 ^T	–	–	GQ505648	–	–	GQ505826	–	GQ505560	–	Xia et al. (2019); Zhang et al. (2023)
<i>F. concentricum</i>	CBS 450.97 ^T	–	–	AF160282	MW402334	MW402674	JF741086	–	MW402467	–	Zhang et al. (2024)
<i>F. concolor</i>	NRRL 13994 ^T	–	–	MH742650	–	MH742492	MH742569	–	–	–	Zhang et al. (2024)
<i>F. dendranthematis</i>	ZHKUCC 24-0772 ^T	–	–	PP983158	PP983185	PP983171	PP983195	–	–	–	Zhang et al. (2024)
<i>F. diversisporum</i>	BBA 11129	–	–	MZ921930	–	MZ921690	MZ921801	–	MZ921621	–	Zhang et al. (2024)
<i>F. elaeagni</i>	CGMCC 3.20822 ^T	MW016426	–	MW580466	MW533748	MW024457	MW474412	–	MW566293	–	Zhang et al. (2024)
<i>F. flocciferum</i>	CBS 831.85	–	–	–	–	JX171514	JX171627	–	–	–	Zhang et al. (2024)
<i>F. fujianense</i>	CFCC 57576 ^T	–	–	ON734389	ON734409	–	ON734369	–	–	–	Costa et al. (2024)
<i>F. fujikuroi</i>	CBS 221.76 ^T	MW827608	–	MN534010	MN534130	MW402640	KU604255	–	–	–	Zhang et al. (2024)
<i>F. gamsii</i>	CBS 143610 ^T	LT970821	–	LT970785	–	–	LT970757	–	–	–	Zhang et al. (2024)
<i>F. gerlachii</i>	CBS 119175 ^T	–	–	MW233118	JAGDUY01	MW23	MW23	–	PQ240192		Sandoval-Denis et al. (2025)

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<i>F. gerlachii</i>	CBS 123666	–	–	DQ459744	DQ459642	PQ280 875	PQ274 138	–	PQ240193		Sandoval-Denis et al. (2025)
<i>F. graminearum</i>	CBS 123657	–	–	PQ260861	PQ273983	JX171 531	MW23 3447	–	PQ240205		Sandoval-Denis et al. (2025)
<i>F. graminearum</i>	CBS 136009 ^T	–	–	KT855185	PQ273993	PQ280 894	KT855 211	–	PQ240215		Sandoval-Denis et al. (2025)
<i>F. gummosum</i>	ZJUE 1738 ^T	–	–	–	–	–	PX437 982	–	–	–	Xiao et al. (2025)
<i>F. gummosum</i>	ZJUE 1694	–	–	–	–	–	PX437 981	–	–	–	Xiao et al. (2025)
<i>F. hechiense</i>	CGMCC 3.20824 ^T	MW01 6454	–	MW580494	MW533773	MW02 4482	MW47 4440	–	MW566321	–	Zhang et al. (2024)
<i>F. ipomoeae</i>	LC7940	MK28 0798	–	MK289642	–	MK28 9856	MK28 9796	–	MK289695	–	Wang et al. (2019)
<i>F. ipomoeae</i>	CGMCC 3.19496 ^T	MK28 0832	–	MK289599	MW533878	MK28 9859	MK28 9752	–	MK289704	–	Wang et al. (2019); Zhang et al. (2023)
<i>F. ipomoeae</i>	LC12166	MK28 0791	–	MK289600	–	MK28 9860	MK28 9753	–	MK289706	–	Wang et al. (2019); Zhang et al. (2023)
<i>F. iranicum</i>	CBS 143608 ^T	LT970 821	–	LT970785	–	–	LT970 757	–	–	–	Zhang et al. (2024)
<i>F. iranicum</i>	LC1112	MW01 6678	–	MW620139	MW534024	MW02 4706	MW47 4664	–	–	–	Zhang et al. (2024)
<i>F. iranicum</i>	CBS 143611	LT970 822	–	LT970786	–	–	LT970 758	–	–	–	Zhang et al. (2024)
<i>F. lateritium</i>	NRRL 13622 ^T	–	–	AY707173	–	JX171	JX171	–	–	–	Costa et al. (2024)

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<i>F. lateritium</i>	GUCC 197048.1	OR034 260	–	OR043898	OR043945	–	OR043 842	–	–	–	Costa et al. (2024)
<i>F. mucidum</i>	CBS 102394	–	–	MN170484	–	–	MN17 0417	–	MN170350	–	Xia et al. (2019); Zhang et al. (2023)
<i>F. mucidum</i>	CBS 102395 ^T	–	–	MN170485	–	–	MN17 0418	–	MN170351	–	Xia et al. (2019); Zhang et al. (2023)
<i>F. nanum</i>	NRRL 32993	GQ505 709	–	GQ505620	–	–	GQ505 798	–	GQ505532	–	Wang et al. (2019)
<i>F. nanum</i>	CGMCC 3.19498 ^T	MK28 0794	–	MK289602	–	MK28 9871	MK28 9755	–	MK289651	–	Wang et al. (2019); Zhang et al. (2023)
<i>F. nanum</i>	NRRL 22244	GQ505 685	–	GQ505596	–	–	GQ505 774	–	GQ505508	–	Wang et al. (2019)
<i>F. nyingchiense</i>	HMAS 352997 ^T	–	–	*	–	*	*	–	–	–	Zhao et al. (2025b)
<i>F. persicinum</i>	CBS 479.83 ^T	–	–	MN170495	–	–	MN17 0428	–	MN170361	–	Zhang et al. (2023)
<i>F. petersiae</i>	CBS 143231 ^T	MG38 6078	–	MG386159	–	MG38 6138	MG38 6149	–	–	–	Zhang et al. (2024)
<i>F. purangense</i>	HMAS 353911 ^T	PV754 419	–	PV764498	–	PV764 436	PV764 458	–	–	–	Zhao et al. (2025b)
<i>F. radicigenum</i>	GUCC 197221.1 ^T	OR034 267	–	OR043909	OR043954	OR043 799	–	–	OR043754	–	Zhang et al. (2023)
<i>F. ramsdenii</i>	BRIP 62306a ^T	OL330 776	–	OL332732	OL332734	–	OL332 733	–	–	–	Costa et al. (2024)
<i>F. reticulatum</i>	CBS 473.76 ^T	–	–	MW928841	–	MW92 8816	–	–	–	–	Zhang et al. (2024); Zhao et al. (2025b)

<i>F. reticulatum</i>	CBS 183.31	–	–	OL772753	–	OL772 905	OL773 057	–	–	–	Zhao et al. (2025b)
<i>F. rosendophyticum</i>	CGMCC 3.25480 ^T	MZ724 841	–	–	OR043955	OR043 802	OR043 855	–	OR043757	–	Zhang et al. (2024)
<i>F. rosiradicicola</i>	CGMCC 3.25482 ^T	MZ724 834	–	OR043914	OR043959	OR043 806	OR043 858	–	OR043761	–	Zhang et al. (2024)
<i>F. rubellum</i>	LC20542 ^T	–	–	PQ453263	–	PQ456 843	PQ453 431	–	–	–	Zhao et al. (2025b)
<i>F. sagittatum</i>	NRRL 64094	–	–	MW233211	–	MW23 3383	MW23 3555	–	–	–	Sandoval-Denis et al. (2025)
<i>F. sagittatum</i>	CBS 151958 ^T	–	–	MW233212	–	MW23 3384	MW23 3556	–	PQ240282	–	Sandoval-Denis et al. (2025)
<i>F. shigatseense</i>	LC20544 ^T	–	–	PQ453267	–	PQ456 847	PQ453 435	–	–	–	Zhao et al. (2025b)
<i>F. stilboides</i>	CBS 115043	–	–	PQ000526	PQ000613	–	PQ000 689	–	PQ000857	–	Costa et al. (2024)
<i>F. stilboides</i>	CBS 746.79 ^T	–	–	MW928843	–	MW92 8817	MW92 8832	–	–	–	Costa et al. (2024)
<i>F. tangerinum</i>	LLC3501 ^T	–	–	OP487189	–	OP486 357	OP486 758	–	OP486067	–	Ai et al. (2025)
<i>F. torulosum</i>	NRRL 22748 ^T	–	–	OL772877	–	JX171 502	JX171 615	–	–	–	Zhang et al. (2024)
<i>F. tricinctum</i>	CBS 393.93 ^T	HM06 8317	–	AB674263	–	JX171 516	JX171 629	–	–	–	Zhang et al. (2024)
<i>F. wenshanense</i>	KUNCC 3512 ^T	PV469 235	–	PV413189	PV476708	PV435 815	PV521 352	–	PV442465	–	Fan et al. (2025)

<i>F. xishuangbannaense</i>	KUMCC 21-0432 ^T	–	–	OR026004	OR025949	OR022 023	OR025 920	–	OR022064	–	Zhang et al. (2024)
<i>Geejayessia atrofusca</i>	NRRL 22316	AF178 423	–	AF178361	–	JX171 496	EU329 502	–	–	–	Zhang et al. (2024)
<i>G. cicatricum</i>	CBS 125552	HQ728 145	–	HM626644	–	–	HQ728 153	–	–	–	Zhang et al. (2024)
<i>Juxtiphoma eupyrena</i>	CBS 374.91 ^T	FJ4269 99	GU238 072	–	FJ427110	–	LT623 268	–	–	–	Hou et al. (2020b); Yasanthika et al. (2021)
<i>J. kolkmaniorum</i>	CBS 146005 ^T	MN82 3568	MN82 3419	–	MN824742	–	MN82 4593	–	–	–	Hou et al. (2020b); Yasanthika et al. (2021)
<i>J. yunnanensis</i>	KUMCC 20-0227 ^T	MW60 0334	MW58 7029	–	MW602383	–	MW60 3001	–	–	–	Yasanthika et al. (2021)
<i>Neocladosporium leucadendri</i>	CBS 131317 ^T	JQ044 436	JQ044 455	–	KY706602	–	LT799 755	LT821 376	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>Neocosmospora breviconia</i>	CBS 204.31 ^T	LR583 707	–	LR583600	–	MW21 8103	LR583 821	–	MW218057	–	Zhang et al. (2024)
<i>N. paphiopedili</i>	ZHKUCC 23-0935 ^T	PQ179 763	–	PQ442943	–	PQ367 248	PQ381 278	–	–	–	Zhang et al. (2024)
<i>N. solani</i>	GUCC 190159.1	MZ724 846	–	OR043928	OR043974	OR043 817	OR043 873	–	OR043777	–	Zhang et al. (2023)
<i>N. solani</i>	CBS 140079 ^T	KT313 633	–	KT313611	–	MW21 8134	KT313 623	–	MW218088	–	Sandoval-Denis et al. (2019); Zhang et al. (2024)
<i>N. suttoniana</i>	CBS 143214 ^T	DQ094 617	–	DQ247163	–	MW21 8138	EU329 630	–	MW218092	–	Sandoval-Denis et al. (2019); Zhang et al. (2024)
<i>N. suttoniana</i>	CBS 143224	MG18 9940	–	KC808197	–	MW21 8139	KC808 336	–	MW218093	–	Sandoval-Denis et al. (2019)

<i>Neofusicoccum hongkongense</i>	CERC 2973 ^T	KX278052	–	KX278157	KX278261	–	–	–	–	–	Bi et al. (2025)
<i>N. illicii</i>	CGMCC 3.18310 ^T	KY350149	–	–	KY350155	–	–	–	–	–	Bi et al. (2025)
<i>N. illicii</i>	CGMCC 3.18311	KY350150	–	KY817756	KY350156	–	–	–	–	–	Bi et al. (2025)
<i>N. moracearum</i>	MELU 19-2758 ^T	NR174834	–	MW183808	–	–	–	–	–	–	Bi et al. (2025)
<i>N. occulatum</i>	CBS 128008 ^T	EU301030	–	EU339509	EU339472	–	–	–	–	–	Bi et al. (2025)
<i>N. occulatum</i>	MUCC 286	EU736947	–	EU339511	EU339474	–	–	–	–	–	Bi et al. (2025)
<i>N. podocarpi</i>	CBS 115065	MT587507	–	MT592222	MT592714	–	–	–	–	–	Bi et al. (2025)
<i>N. podocarpi</i>	CBS 131677 ^T	MT587508	–	MT592223	MT592715	–	–	–	–	–	Bi et al. (2025)
<i>Neomicrosphaeropsis elaeagni</i>	MFLUCC 16-2389 ^T	MH069666	MH069672	–	MH069691	–	MH069684	–	–	–	Yasanthika et al. (2021)
<i>Neopestalotiopsis protearum</i>	CBS 114178 ^T	LT853103	–	LT853201	LT853251	–	LT853151	–	–	–	Bi et al. (2025)
<i>Nothophoma anigozanthi</i>	CBS 381.91 ^T	GU237852	GU238039	–	GU237580	–	KT389655	–	–	–	Zhang et al. (2025b)
<i>N. brennandiae</i>	CBS 145912 ^T	MN823579	MN823430	–	MN824753	–	MN824604	–	–	–	Zhang et al. (2025b)
<i>N. brennandiae</i>	JW 1066	MN823578	MN823429	–	MN824752	–	MN824603	–	–	–	Zhang et al. (2025b)

<i>N. gossypiicola</i>	UTHSC: DI16-294	LT592 943	LN907 437	–	LT593012	–	LT593 082	–	–	–	Gomzhina and Gasich (2025)
<i>N. gossypiicola</i>	CBS 377.67 ^T	GU237 845	GU238 079	–	GU237611	–	KT389 658	–	–	–	Zhang et al. (2025b)
<i>N. macrospora</i>	CBS 140674 ^T	LN880 536	LN880 537	–	LN880539	–	LT593 073	–	–	–	Zhang et al. (2025b)
<i>N. multilocularis</i>	AUMC 12003 ^T	–	KY996 744	–	–	–	–	–	–	–	Zhang et al. (2025b)
<i>N. pruni</i>	MFLUCC 18-1601	MH82 7005	MH82 7026	–	MH853669	–	MH85 3662	–	–	–	Zhang et al. (2025b); Chethana et al. (2019)
<i>N. pruni</i>	MFLUCC 18-1600 ^T	MH82 7007	MH82 7028	–	MH853671	–	MH85 3664	–	–	–	Chethana et al. (2019)
<i>N. quercina</i>	MFLUCC 18-1588	MH82 7008	MH82 7029	–	MH853672	–	MH85 3665	–	–	–	Zhang et al. (2025b)
<i>N. quercina</i>	CBS 633.92 ^R	GU237 900	EU754 127	–	GU237609	–	KT389 657	–	–	–	Zhang et al. (2025b)
<i>N. raii</i>	MCC 1082 ^T	MF664 467	–	–	MF664468	–	–	–	–	–	Zhang et al. (2025b)
<i>N. variabilis</i>	CBS 142457 ^T	LT592 939	LN907 428	–	LT593008	–	LT593 078	–	–	–	Zhang et al. (2025b)
<i>Pestalotiopsis clavata</i>	MFLUCC 12-0268 ^T	JX398 990	–	JX399056	JX399025	–	–	–	–	–	Razaghi et al. (2024)
<i>P. clavata</i>	KNUF 21-006	ON409 988	–	ON456329	LC710316	–	–	–	–	–	Lim et al. (2022)
<i>P. doitungensis</i>	MFLUCC 14-0115	MK99 3574	–	MK975832	MK975837	–	–	–	–	–	Luo et al. (2024)

<i>P. rhois</i>	CFCC 89662 ^T	KM03 0584	KM03 0591	KM030598	–	–	–	–	–	–	Zhou et al. (2025)
<i>P. spiraeae</i>	CFCC 53925 ^T	OM04 9420	OM04 9432	–	–	–	–	–	–	–	Zhou et al. (2025)
<i>P. xizangense</i>	CFCC 71501 ^T	PV264 863	PV264 865	PV268116	–	–	–	–	–	–	Zhou et al. (2025)
<i>P. xizangense</i>	LZ204	PV264 864	PV264 866	PV268117	–	–	–	–	–	–	Zhou et al. (2025)
<i>Seiridium cancrinum</i>	CBS 226.55 ^T	LT853 089	MH55 4241	LT853186	LT853236	–	LT853 137	–	–	–	Razaghi et al. (2024); Bi et al. (2025)
<i>S. cancrinum</i>	CBS 907.85	LT853 090	–	LT853187	LT853237	–	LT853 138	–	–	–	Bi et al. (2025)
<i>S. cupressi</i>	IMI 052254 ^T	LT853 083	MH55 4240	LT853180	LT853230	–	LT853 131	–	–	–	Bi et al. (2025)
<i>S. cupressi</i>	CBS 122616	LT853 082	–	LT853179	LT853229	–	LT853 130	–	–	–	Bi et al. (2025)
<i>S. neocupressi</i>	CBS 142626	LT853 080	–	LT853177	LT853227	–	LT853 128	–	–	–	Bi et al. (2025)
<i>S. neocupressi</i>	CBS 142625 ^T	LT853 079	MH55 4329	LT853176	LT853226	–	LT853 127	–	–	–	Bi et al. (2025)
<i>S. unicorne</i>	CBS 143871	MK07 9339	–	MK058482	MK058487	–	MK05 8477	–	–	–	Razaghi et al. (2024)
<i>S. unicorne</i>	CBS 538.82 ^T	LT853 088	MH55 4269	LT853185	LT853235	–	LT853 136	–	–	–	Bi et al. (2025)
<i>Toxicocladosporium aquimarinum</i>	CBS 145459 ^T	MK39 4101	MK39 2187	–	LR536054	–	LR536 052	LR536 050	–	–	Fotedar et al. (2019)

<i>T. banksiae</i>	CBS 128215 ^T	HQ599 598	HQ599 599	–	KY706597	–	LT799 767	LT821 371	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. cacti</i>	CBS 141539 ^T	KY752 806	KY752 819	–	KY706587	–	LT799 768	LT821 361	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. cacti</i>	188 JB	KY752 803	KY752 816	–	KY706584	–	LT799 770	LT821 358	–	–	Bezerra et al. (2017)
<i>T. chlamydosporum</i>	CBS 124157 ^T	FJ7902 83	FJ7903 01	–	KY706598	–	LT799 778	LT821 372	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. chlamydosporum</i> (<i>T. velox</i>)	CBS 124159 ^T	FJ7902 88	FJ7903 06	–	KY706609	–	LT799 779	LT821 383	–	–	Bezerra et al. (2017)
<i>T. crousianum</i>	IRAN 4591C ^T	ON817 215	ON817 198	–	–	–	–	ON814 477	–	–	Bakhshi et al. (2022)
<i>T. crousianum</i>	IRAN 4592C	ON817 216	ON817 199	–	–	–	–	ON814 478	–	–	Bakhshi et al. (2022)
<i>T. eucalyptorum</i>	IRAN 4589C ^T	ON817 217	ON817 200	–	–	–	–	ON814 479	–	–	Bakhshi et al. (2022)
<i>T. eucalyptorum</i>	IRAN 4590C	ON817 218	ON817 201	–	–	–	–	ON814 480	–	–	Bakhshi et al. (2022)
<i>T. ficiniae</i>	CBS 136406 ^T	KF777 190	KF777 241	–	KY706599	–	LT799 780	LT821 373	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. glendoranum</i>	CBS 148256 ^T	OK664 717	OK663 756	–	–	–	–	OK651 126	–	–	Crous et al. (2021b)
<i>T. hominis</i>	CBS 140694 ^T	LN834 444	KY752 829	–	KY706600	–	LT799 781	LT821 374	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. immaculatum</i>	CBS 141540 ^T	KY752 815	KY752 828	–	KY706596	–	LT799 782	LT821 370	–	–	Bezerra et al. (2017); Fotedar et al. (2019)

<i>T. irritans</i>	CBS 185.58 ^T	EU040 243	EU040 243	–	KY706601	–	LT799 783	LT821 375	–	–	Crous et al. (2007); Bezerra et al. (2017)
<i>T. losalamitosense</i>	CBS 148261 ^T	OK664 743	OK663 782	–	OK651215	–	OK651 175	OK651 135	–	–	Crous et al. (2021b)
<i>T. pini</i>	CBS 138005 ^T	KJ869 160	KJ869 217	–	KY706603	–	LT799 784	LT821 377	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. posoqueriae</i>	CBS 133583 ^T	NR121 555	KC005 803	–	KY706604	–	LT799 785	LT821 378	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. protearum</i>	CBS 126499 ^T	HQ599 586	HQ599 587	–	KY706605	–	LT799 786	LT821 379	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. pseudovelox</i>	CBS 128775 ^T	JF4998 47	JF4998 67	–	KY706606	–	LT799 970	LT821 380	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. pterocarp</i>	CBS 146971 ^T	MZ064 422	MZ064 479	–	MZ078263	–	MZ078 198	MZ07 8148	–	–	Crous et al. (2021a)
<i>T. qatarense</i>	CBS 145460 ^T	MK39 2186	MK39 2188	–	LR536055	–	LR536 053	LR536 051	–	–	Fotedar et al. (2019)
<i>T. rubrigenum</i>	CBS 124158 ^T	FJ7902 87	FJ7903 05	–	KY706607	–	LT799 787	LT821 381	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>T. strelitziae</i>	CBS 132535 ^T	NR111 765	JX069 858	–	KY706608	–	LT799 788	LT821 382	–	–	Bezerra et al. (2017); Fotedar et al. (2019)
<i>Vacuiphoma laurina</i>	CBS 1196367 ^T	MN97 3551	MN94 3758	–	MT005654	–	MT018 195	–	–	–	Hou et al. (2020a)
<i>V. oculihominis</i>	UTHSC DI16-308 ^T	LT592 954	LN907 451	–	LT593023	–	LT593 093	–	–	–	Hou et al. (2020a)

1088 **Notes.** T: ex-type; R: representative strains; – : Sequence unavailable; *: Sequences are from the cited original references, without GenBank
1089 accession numbers.

1090 **Table 3.** Pathogenicity evaluation criteria.

Trait	Score/Unit	Description
Lesion Shape (Fs)	0–4	0: flat/healthy, no visible damage;
		1: slightly raised, low tissue damage;
		2: clearly raised, moderate damage;
		3: slightly sunken, tissue beginning to necrotize;
		4: severely sunken, tissue necrosis obvious, high tissue damage.
Lesion Color (Cs)	0–2	0: green/healthy, no visible lesion;
		1: pale brown to brown, moderate necrosis;
		2: dark brown to black, severe necrosis;
Lesion Length (Ls)	mm	Measured lesion length for 45 strains, indicates extent of tissue damage.

1091

Table 4. Pathogenicity assessment of representative strains from 45 fungal species.

Species	Record status	Strain number	Lesion shape score (Fs) ^a	Lesion color score (Cs) ^b	Length of the lesions (Ls, mm) ^c	Pathogenicity index (PDI)
<i>Aplosporella javeedii</i>	Non-new host record	CGMCC3.29584	2	2	14.67 ± 1.63 c-g	0.583
<i>Aplosporella prunicola</i>	Non-new host record	CGMCC3.29580	2	1	13.83 ± 1.72 d-i	0.442
<i>Botryosphaeria dothidea</i>	Non-new host record	CGMCC3.29566	3	2	7.67 ± 1.21 q	0.623
<i>Curvularia intermedia</i>	New host record	CGMCC3.29552	3	1	12.00 ± 2.61 h-k	0.525
<i>Curvularia platycladi</i>	New species	CGMCC3.29551	3	2	16.67 ± 1.37 c	0.697
<i>Curvularia platycladicola</i>	New species	CGMCC3.29554	2	2	10.83 ± 1.47 j-p	0.552
<i>Curvularia pseudobrachyspora</i>	New host record	CGMCC3.29548	2	2	8.50 ± 1.38 pq	0.533
<i>Cytospora acericola</i>	New host record	CGMCC3.29589	3	1	21.17 ± 1.47 b	0.6
<i>Cytospora diopuiensis</i>	New host record	CGMCC3.29587	3	2	11.50 ± 1.38 i-n	0.655
<i>Cytospora qingshuiensis</i>	Non-new host record	CGMCC3.29586	2	2	10.33 ± 1.03 j-p	0.547
<i>Cytospora xinglongensis</i>	New host record	CGMCC3.29588	3	1	15.53 ± 2.79 cd	0.554
<i>Diplodia neojuniperi</i>	New host record	CGMCC3.29570	4	2	13.83 ± 3.97 d-i	0.771
<i>Dothiorella acericola</i>	New host record	CGMCC3.29565	4	2	9.00 ± 1.41 m-q	0.732
<i>Dothiorella plurivora</i>	New host record	CGMCC3.29557	2	2	9.33 ± 1.03 k-q	0.539
<i>Epicoccum dendrobii</i>	New host record	CGMCC3.29662	1	1	16.17 ± 0.98 cd	0.364
<i>Epicoccum lolii</i>	New host record	CGMCC3.29668	2	2	11.50 ± 1.87 i-n	0.557
<i>Epicoccum nigrum</i>	Non-new host record	CGMCC3.29665	3	1	11.67 ± 3.50 h-m	0.522
<i>Epicoccum platycladi</i>	New species	CGMCC3.29659	2	1	9.17 ± 1.47 l-q	0.404
<i>Epicoccum rosae</i>	New host record	CGMCC3.29666	2	2	14.83 ± 3.60 c-f	0.584
<i>Fusarium annulatum</i>	New host record	CGMCC3.29596	2	2	11.17 ± 1.47 j-p	0.554
<i>Fusarium beijingsensis</i>	New species	CGMCC3.29619	4	2	15.33 ± 1.37 c-e	0.783
<i>Fusarium brachygibbosum</i>	New host record	CGMCC3.29624	4	2	41.83 ± 3.54 a	1
<i>Fusarium castaneophilum</i>	New host record	CGMCC3.29598	3	1	12.50 ± 1.52 f-j	0.529
<i>Fusarium citri-sinensis</i>	New host record	CGMCC3.29633	1	2	10.33 ± 1.63 j-p	0.45
<i>Fusarium clavus</i>	New host record	CGMCC3.29608	1	1	8.67 ± 1.21 o-q	0.302
<i>Fusarium compactum</i>	New host record	CGMCC3.29628	2	1	16.00 ± 1.55 cd	0.46
<i>Fusarium graminearum</i>	New host record	CGMCC3.29626	3	2	12.50 ± 1.64 f-j	0.663

<i>Fusarium gummosum</i>	New host record	CGMCC3.29601	2	2	10.50 ± 1.05 j-p	0.549
<i>Fusarium ipomoeae</i>	New host record	CGMCC3.29605	2	2	8.50 ± 1.05 pq	0.533
<i>Fusarium iranicum</i>	New host record	CGMCC3.29622	2	1	12.17 ± 1.17 g-j	0.429
<i>Fusarium lateritium</i>	New host record	CGMCC3.29603	2	2	11.83 ± 2.14 h-l	0.56
<i>Fusarium mucidum</i>	New host record	CGMCC3.29611	1	2	11.17 ± 1.94 j-p	0.457
<i>Fusarium nanum</i>	New host record	CGMCC3.29613	1	1	13.00 ± 1.90 e-j	0.338
<i>Juxtiphoma yunnanensis</i>	New host record	CGMCC3.29670	3	2	14.67 ± 1.21 c-g	0.68
<i>Neocosmospora solani</i>	Non-new host record	CGMCC3.29630	4	2	10.33 ± 2.07 j-p	0.743
<i>Neofusicoccum occulatum</i>	Non-new host record	CGMCC3.29571	4	2	14.17 ± 1.47 c-h	0.774
<i>Nothophoma gossypicola</i>	New host record	CGMCC3.29658	3	1	15.00 ± 1.10 c-f	0.549
<i>Nothophoma pruni</i>	New host record	CGMCC3.29655	2	2	10.67 ± 1.63 j-p	0.55
<i>Nothophoma quercina</i>	Non-new host record	CGMCC3.29654	3	2	20.67 ± 1.97 b	0.73
<i>Pestalotiopsis clavata</i>	New host record	CGMCC3.29591	2	2	14.83 ± 2.14 c-f	0.584
<i>Phaeobotryon mali</i>	New host record	CGMCC3.29576	3	2	10.67 ± 1.21 j-p	0.648
<i>Phaeobotryon platycladi</i>	Non-new host record	CGMCC3.29577	4	2	20.33 ± 3.50 b	0.824
<i>Seiridium unicorne</i>	Non-new host record	CGMCC3.29593	3	1	21.83 ± 2.23 b	0.605
<i>Toxicocladosporium quinquagintatreanum</i>	New species	CGMCC3.29337	3	1	8.83 ± 1.72 n-q	0.499
<i>Vacuiphoma oculihominis</i>	New host record	CGMCC3.29674	2	2	11.33 ± 1.37 i-o	0.556
Control	—	—	0	0	0 r	0

1093 **Notes.** a: The lesion shape score for each strain, based on the extent of raised and sunken lesions on all its inoculated seedlings (Normalized
1094 weight: $w_{Fs} = 0.390186$). b: The lesion color score for each strain, based on the extent of lesion discoloration on all its inoculated seedlings
1095 (Normalized weight: $w_{Cs} = 0.267974$). c: Mean lesion length ± standard deviation (SD) (Normalized weight: $w_{Ls} = 0.34184$). Different letters
1096 indicate significant differences, with $P < 0.05$ according to Duncan's post hoc test.

Supplementary material 1

Disease symptoms of ancient *Platycladus orientalis* in the field

Authors: Ning Jiao, Zhe Zhang, Ying Zhang

Data type: png

Explanation note: **A–C.** Symptoms of leaf blight on ancient *P. orientalis* with necrotic lesions and chlorosis. **D, E.** Dieback symptoms on ancient *P. orientalis*, with necrotic branches and foliage. **F.** Canker symptoms on branches of ancient *P. orientalis*. **G, H.** Rot symptoms on trunks of ancient *P. orientalis*, with discoloration, bark cracking, and wood decay. **I.** Canker symptoms on trunks of ancient *P. orientalis*, with blister-like lesions.

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Link:

Supplementary material 2

Collection sites of diseased samples from ancient *Platycladus orientalis* in Beijing

Authors: Ning Jiao, Zhe Zhang, Ying Zhang

Data type: png

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Link:

Supplementary material 3

Phylogenetic trees

Authors: Ning Jiao, Zhe Zhang, Jingyan Wang

Data type: zip

Explanation note: Phylogenetic tree of the strains of known species isolated from ancient *Platycladus orientalis*, together with closely related taxa, based on maximum likelihood analyses using concatenated multilocus sequence data. RAxML bootstrap support values $\geq 50\%$, Bayesian posterior probabilities ≥ 0.90 , and Maximum parsimony bootstrap support values $\geq 50\%$ were indicated at the nodes as ML/PP/MP. The type strains were marked with superscript “T”, representative strains with superscript “R”, and the strains newly obtained in this study were shown in blue.

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Link:

Supplementary material 4

Comparison of morphology and base-pair differences among ex-type strains of the new species and related taxa.

Authors: Ning Jiao, Zhe Zhang, Jingyan Wang

Data type: xlsx

Explanation note: “NA” indicates the sequence unavailability.

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Link:

Supplementary material 5

Alignments for phylogenetic analyses

Authors: Ning Jiao, Zhe Zhang, Jingyan Wang

Data type: zip

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