ENDOPHYTIC FUNGI FROM *TETRADIUM RUTICARPUM* AND THEIR ABILITY TO PRODUCE ANTIMICROBIAL ACTIVITIES

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IN
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ABSTRACT

This study presents a comprehensive investigation of the endophytic fungal community associated with the traditional medicinal plant *Tetradium ruticarpum*, revealing its taxonomic diversity, ecological drivers, and bioactive potential. Through extensive sampling across multiple tissues, geographic locations, and culture media, we identified 935 fungal isolates spanning three phyla, six classes, 21 orders, 54 families, and 84 genera. The community was dominated by Ascomycota (99.5%), primarily Sordariomycetes (61.9%) and Dothideomycetes (35.4%). *Diaporthe* was the most abundant genus (26.8%), followed by *Colletotrichum* (9.9%), *Fusarium* (9.2%), and *Alternaria* (6.1%). Among the remaining 82 rare genera, all except *Hypoxylon*, *Nigrospora* were reported for the first time from this host. Recovery of endophytes was influenced by medium, tissue, and region, with PDA (429 isolates, 71 genera), leaves (408 isolates), and the Daodi production area (Jiangxi Province, 744 isolates, 63 genera), yielding the highest numbers and diversity.

A total of 12 novel fungal species were discovered exclusively from this host, including *Amphisphaeria chenzhouensis*, *A. tetradiana*, *Cyphellophora guangxiensis*, *Diaporthe hunanensis*, *D. jiangxiensis*, *D. tetradii*, *Funiliomyces jiangxiensis*, *Fusarium jiangxiensis*, *Nemania jiangxiensis*, *Pseudokeissleriella tetradii*, *Tetradiomyces jiangxiensis*, and *Zasmidium guangxiensis*. These findings further enriched the taxonomy of endophytic fungi by leading to the establishment of a new family, Funiliomycetaceae, and a new genus, *Tetradiomyces*. Additionally, three species, *Coryneum castaneicola, Exophiala pisciphila*, and *Nigrograna jinghongensis* were documented as new host records for *T. ruticarpum*. This significant taxonomic expansion underscores *T. ruticarpum* as a valuable reservoir for fungal biodiversity and a promising source of novel fungal lineages.

Antimicrobial screening using the agar plug method identified 35 strains from 12 genera with inhibitory activity against three pathogenic bacteria (*Escherichia* coli, *Xanthomonas campestris*, and *Staphylococcus* aureus) and two pathogenic fungi (*Aspergillus niger* and *Candida albicans*). Antimicrobial screening using the agar plug method identified 35 strains from 12 genera with inhibitory activity against three pathogenic bacteria (*E. coli*, *X. campestris*, and *S. aureus*) and two pathogenic fungi (*A. niger* and *C. albicans*). Among them, *Epicoccum* sp. 2 (JAUCC 6839), *Epicoccum* sp. 2 (JAUCC 3794), and *Penicillifer* sp. 1 (JAUCC 4286) showed inhibitory activity against two pathogens. In particular, *Epicoccum* sp. 2 (JAUCC 6839) exhibited strong inhibition against *X. campestris* (32.7 mm), and two *Fusarium* strains (JAUCC 5568 and JAUCC 3841) demonstrated notable inhibition of *A. niger* (26.7 mm).

This study provides a comprehensive overview of *T. ruticarpum* endophytic fungi, revealing high taxonomic richness with several new taxa, distinct tissue- and region-specific patterns, and notable antimicrobial potential. These findings lay a foundation for exploring their roles in host physiology and their biotechnological applications in agriculture and drug discovery.

Keywords: Antimicrobial Properties, Fungal Community, Endophytes, Medicinal Plant, Multi-locus Phylogeny, Novel Taxa

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ABBREVIATIONS AND SYMBOLS

e.g.	for example
et al.	and others
i.e.	that is
ibid.	ibidem
min	minute
mm	millimetre
nov.	novum (Latin for new thing)
s	second
sp.	species
spp.	species (plural)
°C	degree centigrade
$\bar{x}$	average
µm	micrometer
µl	microliter
%	percent

CHAPTER 1

INTRODUCTION

1.1 Background and Importance

Abundant worldwide, most fungi are inconspicuous because of the small size of their structures and their cryptic lifestyles in soil or on dead matter. However, fungi can grow in almost all habitats on earth to withstand extremes in temperature, water activity, and carbon source (Raspor & Zupan, 2006). The world of fungi is an abundant and diverse kingdom, which plays a crucial role in various ecosystems as mycorrhiza, endophytes, saprophytes and pathogens and has immense potential to provide valuable resources for human health and industry, but the role of an individual species in nature is unclear (Schmit & Mueller, 2007). Mycologists estimate that there may be between 2.2 million and 3.8 million total species (Hawksworth & Lucking, 2017), but there are only about 148,000 species of fungi, which have been identified and described (Cheek et al., 2020).

Symbiosis between a fungus and a plant is a widespread phenomenon in nature. The relationship between fungi and plants is diverse and essential for ecosystem functioning (Alam et al., 2021), which can range from mutualism through commensalism to parasitism in a continuous manner. In the process of mutual influence, fungi form three corresponding types of interactions with hosts: mutualistic (beneficial endophytes), commensalistic (non-beneficial/virulent endophytes) and pathogenic (virulent pathogens), depending on the physiological status or specific circumstances that host plants experience. According to these three modes of action, fungal strains can increase, have no palpable effects on, or decrease host fitness and cause host disease (Kogel et al., 2006).

Therefore, understanding the diversity within the fungal-plant microbiome is crucial for sustainable agriculture, ecosystem management, and conservation efforts. It can help us harness beneficial interactions while mitigating negative impacts caused by plant pathogens.

China boasts a rich biodiversity and a long history with diverse ethnic cultures (Mi et al., 2021). It is home to approximately 11,000 species of medicinal plants (Zhang & Yang, 2012). However, due to the long growth cycle, low yield, and protection efforts for some species, the demand for medicinal plant resources is challenging to meet. *Tetradium ruticarpum*, commonly known as “Wu zhu yu”, is widely used in Chinese herbal medicine for treating headache, vomiting, and gastrointestinal disorders, as documented in traditional Chinese medicine history (Yang et al., 2017). Presently, most studies on *T. ruticarpum* focus on extracting active components and evaluating their pharmacological effects. The chemical compounds isolated from *T. ruticarpum* mainly include alkaloids such as evodiamine (EVO), rutaecarpine (RUT), dehydroevodiamine (DHE), as well as quinolone alkaloids, terpenoids, flavonoids, phenolic acids, and volatile oils (Li & Wang, 2020). Pharmacological studies have revealed the remarkable therapeutic potential of *T. ruticarpum* fruit extracts and their bioactive components in the treatment of tumors, cardiovascular disorders, microbial infections, Alzheimer's disease, and obesity in clinical practice (Li & Wang, 2020; Tian et al., 2019).

In recent years, with the advancements in various emerging biological technologies, research on fungi has garnered increased attention and resulted in the accumulation of a substantial number of fungal resources. *Tetradium ruticarpum*, a plant known for its diverse range of bioactive compounds, has gained attention due to its potential therapeutic applications. However, research on fungi from *T. ruticarpum* remains relatively limited. This study delves into the unexplored realm of fungal biodiversity associated with *T. ruticarpum* and investigates their capacity to produce antimicrobial agents. Fungi are known to synthesize various secondary metabolites, some of which exhibit potent antimicrobial properties. Through isolation, identification, and screening processes, we aim to shed light on the diversity of fungi inhabiting *T. ruticarpum* and their antimicrobial activities. The findings could potentially lead to the discovery of novel bioactive compounds for pharmaceutical and agricultural applications.

1.2 Overview of Endophytic Fungi

1.2.1 General Concepts of Endophytic Fungi

The term “endophyte” originates from 1809, when the German botanist Heinrich Friedrich Link introduced “entophytae” to describe fungi living inside plants with a partially parasitic habit (Link, 1809). In 1866, Bary formally introduced the term “endophyte” (from Greek endo, “inside” and phytón, “plant”) to designate all organisms that colonize internal plant tissues, thereby distinguishing them from those that inhabit plant surfaces (de Bary, 1866). Since then, as research on endophytes has advanced, the concept has continued to evolve. In 1991, Petrini proposed a widely accepted definition of endophytes: organisms that inhabit plant organs at some stage of their life cycle and colonize internal tissues without causing apparent harm to the host (Petrini, 1991). Stone et al. (2000) further refined the concept by defining endophytes as microorganisms that reside within the tissues or organs of healthy plants throughout their entire life cycle or during specific stages, without eliciting obvious disease symptoms in the host, or only causing transient, symptomless infections.

With the increasing discovery and recognition of endophytic fungi, the definition of endophytic fungi has developed nearly 26 versions so far (Liao et al., 2025). Many scholars have interpreted endophyte from different perspectives, giving it more meanings, but this has also caused some confusion to a certain extent. For example, Bills (1996) and Bayman et al. (1997) suggest that mycorrhizal fungi also belong to endophytes. But Liao et al. (2025) suggested setting a clear boundary between mycorrhizal fungi and endophyte, as they have different lifestyles. Therefore, taking into account colonization dynamics, disease-causing potential, benefits to hosts, and lifestyle plasticity of endophytes, Liao et al. (2025) propose the following updated definition: asymptomatic microbial partners that intimately co-inhabit healthy plant tissues, confer benefits to their hosts, co-evolve with them, and shift their lifestyles in response to plant developmental stages and environmental stresses.

1.2.2 The Biodiversity of Endophytic Fungi

Endophytic fungi represent a highly diverse group of microorganisms. Approximately 1.5 million fungal species are estimated to exist on Earth, of which about one million are endophytic in nature (Strobel & Daisy, 2003). Their biodiversity spans multiple taxonomic groups, including Ascomycota, Basidiomycota, Chytridiomycota, Mucoromycota, Zygomycota, and others, with Ascomycetes being the most prevalent. Rashmi et al. (2019) provided a comprehensive global list of endophytic fungi, documenting 2,771 species from 877 genera, with the majority (87.38%) belonging to the phylum Ascomycota. In addition, the most speciose genera reported among endophytic fungi are *Penicillium,* followed by *Colletotrichum*, *Alternaria*, *Fusarium*, *Pestalotiosi*s, and *Aspergillus*. In a review spanning over 30 years of research in Korea, Eo et al. (2022) documented 855 endophytic fungal taxa across 50 families, 108 genera, and 132 species, with Ascomycetes representing approximately 93% of the total.

Endophytic fungal diversity is also influenced by tissue type (e.g., leaves, stems, roots, barks, fruits and flowers). Harrison and Griffin (2020) reported that stems harbored the greatest endophyte diversity in woody species, while roots supported the highest richness in grasses. Huang et al. (2008) reported 1160 endophytic strains from the 29 traditional Chinese medicinal plants and found a similar richness between different tissues: leaves (549), stems (568), flowers (28), roots (four) and fruits (11). Chauhan et al. (2019) examined endophytic fungi in *Ensete ventricosum* collected from three geographic regions and found substantial variation in isolation frequency. They recovered 53 strains from Dega, 46 strains from Weina-dega and nine strains from Kefil-kola. They also observed that old leaves yielded far more isolates than young leaves, with 85 isolates obtained from old leaves and 23 from young leaves, indicating that leaf age strongly influences endophyte colonization.

Climate conditions can affect the diversity of endophytic fungi. The abundance and diversity of endophytic fungi may be relatively low in cold environments compared to warmer regions (U'Ren et al., 2012). However, in cold or even extreme environments, endophytic fungi still survive and form symbiotic relationships with the surrounding plants (Zhang et al., 2019b). According to Li et al.

(2012), endophytic fungi isolated from five dominant plant species in Baima Snow Mountain, Southwest China, exhibited notable adaptation to cold environments.

1.2.3 Identification of Endophytic Fungi

Accurate identification of endophytic fungi is foundational to understanding their ecological roles and potential applications. This process typically involves three interconnected approaches: morphological characteristics, molecular analyses, and complementary advanced techniques. These methods are often used in combination to establish a comprehensive framework for taxonomic classification and characterization (dos Reis et al., 2022).

1.2.3.1 Morphological identification

Morphological identification remains a widely used method for preliminary classification, particularly in ecological studies or resource-limited settings where molecular tools are unavailable. After purification, fungal isolates are grouped based on macro- and micromorphological traits (Dhayanithy et al., 2019; Jayatilake & Munasinghe, 2020). Macroscopic characteristics include colony features such as surface and reverse colour, texture (e.g., cottony, powdery), topography, and growth rate on culture media (e.g., PDA, MEA), which enable initial grouping into distinct morphotypes. Microscopic observations focus on reproductive structures (conidiophores, spores) and hyphal traits (septation, branching), often aided by staining (e.g., lactophenol cotton blue) and microculture techniques (dos Banhos et al., 2014). However, morphological classification has limitations: it does not always reflect phylogenetic relationships, and non-sporulating species often require molecular methods for accurate resolution (Li et al., 2016b, 2016c; Yao et al., 2017; Du et al., 2020). For example, Tibpromma et al. (2018) identified endophytic fungi from healthy leaves of *Pandanaceae* in southern Thailand by first grouping 22 isolates into eight morphotypes based on cultural characteristics, followed by species-level identification through morphological examination and phylogenetic analyses of DNA sequence data, which led to the discovery of a new genus, seven new species, and nine known species. Moreover, many other studies have applied similar morphotype-based preliminary screening before molecular confirmation, highlighting its practicality in endophyte diversity research.

1.2.3.2 Molecular identification

Molecular identification enables accurate species-level classification and is essential for studying fungal biodiversity. The standard procedure begins with DNA extraction from pure cultures, followed by PCR amplification of target regions. The Internal Transcribed Spacer (ITS) region is widely recognized as the primary fungal barcode due to its high interspecific variability and flanking conserved regions, making it ideal for distinguishing most species (Nilsson et al., 2019; Schoch et al., 2012). Resulting sequences are compared to reference databases (e.g., GenBank) using BLAST tools to determine taxonomic affinity. For closely related species where ITS lacks sufficient resolution, additional protein-coding genes such as actin (ACT), beta-tubulin (TUB), translation elongation factor 1-alpha (TEF-1α), and calmodulin (CAL) are employed to improve discrimination, along with other loci such as RNA polymerase II largest subunit (RPB1) and second largest subunit (RPB2), chitin synthase (CHS), glyceraldehyde-3-phosphate dehydrogenase (GPD), and mating-type genes. For example, sequence data of the protein-coding gene *tef*-1 was used to describe new species in the *Cantharellus cibarius* complex, clarifying taxonomic boundaries and demonstrating its critical role in resolving closely related fungal taxa (Buyck & Hofstetter, 2011). Reeb et al. (2004) demonstrated that RPB2 is highly informative for multilocus phylogenetic studies of euascomycetes. Additionally, RPB1 and RPB2 have proven valuable in resolving phylogeny in *Fusarium* (O'Donnell et al., 2010; Schoch et al., 2009), while CAL and TUB are frequently used for species delimitation in *Aspergillus* (Samson et al., 2014). This multi-locus approach provides a more robust genetic foundation for classification and helps to overcome the limitations associated with relying solely on morphological characteristics.

1.2.3.3 Complementary and advanced techniques

Beyond the traditional morphological and core molecular methods, a range of advanced techniques further support the accurate identification, comprehensive characterization, and in-depth functional understanding of endophytic fungi. Molecular identification is augmented by high-throughput sequencing (HTS) technologies, which enable the simultaneous analysis of hundreds of samples and are particularly effective for identifying non-culturable taxa, expanding the scope of biodiversity assessments (Breitenwieser et al., 2020; Nilsson et al., 2019). Advanced imaging techniques, such as confocal laser scanning microscopy (CLSM), visualize fungal colonization patterns within plant tissues, linking taxonomic identity to ecological niches (Fracchia et al., 2023). Functional characterization complements identification through in vitro assays for traits like plant growth promotion (Verma et al., 2001) and metabolomic profiling using tools such as liquid chromatography-mass spectrometry (LC-MS) and nuclear magnetic resonance (NMR), which connect fungal identity to biosynthetic potential (Kusari et al., 2014). Emerging technologies, including single-cell genomics, facilitate the study of unculturable endophytes (Grün & van Oudenaarden, 2015), while integrated multi-omics approaches (genomics, transcriptomics, metabolomics) provide a systems-level understanding of endophyte-host interactions (Shishodia et al., 2025). Together, these techniques enhance the depth and accuracy of endophytic fungal identification and characterization.

1.2.4 The Relationship between Endophytic Fungi and Host Plants

The interaction between endophytes and their hosts is highly complex. Most endophytic fungi in plants have formed a mutualistic symbiotic relationship with their host plants due to their long-term coexistence within them. The construction of endophytic fungal communities in plants is not random. The response of plants to the colonization of endophytic fungi is also conducive to enhancing the immune system of plants. During the symbiotic combination of endophytic fungi and plants, endophytic fungi can promote plant growth and enhance the resistance of plants to biological stresses (pathogenic bacteria, insects, pests, and herbivores) and abiotic stresses (drought, salt, heat, and cold) (Lata et al., 2018; Moghaddam et al., 2021; Singh et al., 2011; Yan et al., 2019).

1.2.4.1 The genetic influence of endophytic fungi on host plants

The distribution and community structure of endophytic fungi are influenced by factors such as genetic background (Higgins et al., 2014). Some endophytic fungal populations are confined to particular host species or families, and even to specific genetic background (genotypes) of a species (D’Amico et al., 2008; Dai et al., 2003). Some endophytic fungal isolates can switch between parasitic and mutualistic lifestyles depending on the genotype of the host they colonize (Redman et al., 2001; Unterseher & Schnittler, 2010).

1.2.4.2 Endophytic fungi promote the growth of host plants

Some endophytic fungi enhance the growth and fitness of their host plants by producing growth-promoting hormones like indole-3-acetic acid, indole-3-acetonitrile, and cytokinins. They can also aid plant development by improving the uptake of essential nutrients such as nitrogen and phosphorus (Zhang et al., 2006; Hartley & Gange, 2009). Guo and Wang (2001) reported that *Mycena dendrobii* facilitates *Gastrodia elata* seed germination and growth by secreting indoleacetic acid.

1.2.4.3 Endophytic fungi promote disease resistance of host plants

Many studies have shown that endophytic fungi can enhance the disease resistance of host plants. Cui et al. (2021) reported that endophytic fungi boost host plant resistance to herbivorous animals, pests, and pathogenic microbes. The endophytic fungus *Piriformospora indica* has been demonstrated as an effective biocontrol agent against *Cymbidium mosaic* virus (Safeer & Thara, 2022). The endophytic fungus *Neotyphodium* colonizes tall fescue ryegrass, enhancing host plant protection and stability under stressful conditions; in this mutualistic relationship, the ryegrass facilitates fungal propagation through seeds containing fungal hyphae (Tan & Zou, 2001).

1.2.4.4 Endophytic fungi enhance the stress resistance of the host plants

Numerous studies have investigated endophyte-plant interactions, particularly their role in enhancing plant tolerance to abiotic stress (Jia et al., 2016; Khare et al., 2018; Munir et al., 2022). Enhanced biotic stress tolerance in host plants has been linked to bioactive compounds synthesized by endophytic fungi (Tan & Zou, 2001; Zhang et al., 2006). Endophytic fungi could produce a vast variety of antioxidant compounds that could protect their hosts by enhancing tolerance to abiotic stresses (Rodriguez & Redman, 2008). Brotman et al. (2013) demonstrated that the endophytic fungus *Trichoderma asperelloides* enhances salt stress tolerance in cucumber (*Cucumis sativus*) seedlings under 100 mM NaCl conditions.

1.2.4.5 Endophytic fungi promote the accumulation of bioactive components

Several endophytic fungi have the ability to stimulate secondary metabolite accumulation in their plant hosts (Chen et al., 2016). Endophytic fungi can induce host plants to produce their characteristic bioactive compounds. For instance, *Colletotrichum gloeosporioides* has been shown to stimulate artemisinin production in hairy root cultures of *Artemisia annua* (Wang et al., 2006). Potshangbam et al. (2017) reported that inoculation with *Penicillium citrinum* and *Aspergillus terreus* leads to improved biomass yield in sunflower plants. In addition, many endophytic fungi can not only promote the massive accumulation of secondary metabolites produced by the host, but also generate various types of chemical components themselves. A landmark discovery was reported when Stierle et al. (1995) first isolated the anticancer drug paclitaxel from *Taxomyces andreanae*, an endophytic fungus associated with the Pacific yew (*Taxus brevifol*ia).

1.2.5 Enzymatic Activities of Endophytic Fungi

1.2.5.1 Enzymatic diversity in endophytic fungi

Endophytic fungi produce a broad spectrum of enzymes, including hydrolytic enzymes such as cellulases, xylanases, pectinases, proteases, and lipases, as well as oxidative and detoxifying enzymes like laccases, peroxidases, cytochrome P450 monooxygenases, and antioxidant enzymes (Borges et al., 2009; Usman et al., 2023). For example, cellulases from *Aspergillus* spp. degrade cellulose into fermentable sugars, while laccases from *Trametes* spp. can oxidize lignin-like compounds. This enzymatic diversity underlies endophytes' ability to colonize plant tissues, survive environmental stress, and mediate a variety of ecological functions (Sahoo et al., 2025).

1.2.5.2 Functional roles in plant–fungus interactions

Enzymes are critical for establishing and maintaining symbiosis with host plants. Hydrolytic enzymes facilitate tissue penetration and stable colonization; for instance, pectinases from *Fusarium* and *Aspergillus* spp. soften plant tissues, allowing fungal entry while indirectly enhancing plant defense (de Vries & Visser, 2001). These enzymes also support nutrient acquisition: certain diazotrophic endophytes (e.g., *Gloeocercospora* spp.) produce nitrogenase for atmospheric nitrogen fixation (Rosenblueth et al., 2018), while phosphatases (from *Penicillium* spp.) enhance phosphorus solubilization, promoting plant growth (Wakelin et al., 2007). Additionally, stress-responsive enzymes like superoxide dismutase (SOD) and catalase (CAT) protect both fungi and plants against oxidative damage (Hamilton et al., 2012). Together, these enzymatic functions support plant growth, resilience, and ecological stability, which in turn highlights their potential for biotechnological applications.

1.2.5.3 Applications in biotechnology and industry

Endophytic fungal enzymes have demonstrated promising utility in environmental, medical, and industrial contexts. In bioremediation, laccases and peroxidases from Phanerochaete chrysosporium degrade synthetic dyes, polycyclic aromatic hydrocarbons, and other pollutants (Kumar & Chandra, 2020). In medicine, Xylarinase from the endophytic fungus *Xylaria curta* is a novel fibrinolytic metalloprotease with thrombolytic potential, hydrolyzing fibrinogen and prolonging clotting times in vitro (Meshram et al., 2016). Agriculturally, a chitinase from the endophytic fungus *Neotyphodium* sp. in *Poa ampla* is secreted into the host apoplast and may enhance plant defense and growth (Li et al., 2004). Industrially, oleaginous endophytic fungi such as *Lasiodiplodia exigua*, *Phomopsis* spp., and *Pestalotiopsis microspora* from biodiesel plants (e.g., *Jatropha curcas* and *Ricinus communis*) produce high lipid content and carbohydrate-active enzymes, highlighting their potential for biodiesel production (Paul et al., 2020). In addition, endophytic fungi such as Penicillium daleae and Aspergillus sp. produce phytase, an enzyme that degrades anti-nutritional phytate in cereals and legumes (Adhikari & Pandey, 2019); moreover, in the pulp and paper industry, xylanases, cellulases, lipases, and laccases are employed as eco-friendly alternatives to traditional chlorine-based bleaching agents (Singh et al., 2016). The breadth of these examples illustrates the translational potential of endophytic fungal enzymes from ecological roles to practical applications.

1.2.5.4 Summary and future outlook

In summary, endophytic fungi represent a vast reservoir of enzymatic diversity that underpins both their ecological success and biotechnological potential. Their enzymes mediate symbiosis, enhance nutrient uptake, mitigate stress, and enable applications in bioremediation, medicine, and industry. Despite significant progress, many enzymes remain insufficiently characterized at molecular, structural, and functional levels. Future research integrating multi-omics approaches, structural biology, and protein engineering will be crucial to fully exploit these enzymatic resources and translate them into sustainable biotechnological solutions (Sahoo et al., 2025).

1.2.6 Secondary Metabolites: Biosynthesis, Biological Activities, and Practical Applications in Endophytic Fungi

1.2.6.1 Secondary metabolites in endophytic fungi

Endophytic fungi represent a significant and prolific reservoir of structurally diverse secondary metabolites (Kaul et al., 2012; Ratnaweera & de Silva, 2017; Rustamova et al., 2020; Singh & Kumar, 2023). These secondary metabolites from endophytic fungi refer to low-molecular-weight natural organic compounds synthesized by endophytic fungi (mainly in specific growth stages) with ecological functions (D'Souza et al., 2023). Such metabolites encompass a wide array of chemical classes, including phenols, alkaloids, polyketides, quinones, steroids, enzymes, peptides (Kaul et al., 2012; Shi et al., 2024; Zhang et al., 2006). This chemical diversity also protects host plants from pathogens by inhibiting plant pathogen growth and boosting host immune system to amplify plant defense mechanisms (Meena et al., 2019).

The discovery of taxol from the endophytic fungus *Taxomyces andreanae* (Stierle et al., 1993) marked the beginning of extensive research into endophytic fungal secondary metabolites. Following this breakthrough, researchers have increasingly focused on exploring the chemical diversity and biological potential of fungal secondary metabolites. For instance, 200 secondary metabolites have been identified and characterized from endophytic fungi associated with *Huperzia serrata* to date (Cao et al., 2021). Between 1995 and 2022, as many as 716 antibacterial compounds were reported from endophytic fungi (Deshmukh et al., 2015, 2022). Additionally, Rustamova et al. (2020) documented 221 structurally unique secondary metabolites produced by 67 endophytic fungal species. In a more recent review, Shi et al. (2024) reported 553 natural products from endophytic fungi, including 219 polyketides, 145 terpenoids, 35 steroids, 106 alkaloids, and 48 peptides within 2023. These endophyte-derived compounds collectively highlight that endophytic fungi represent a rich source of secondary metabolites.

1.2.6.2 Biosynthesis of secondary metabolites in endophytic fungi

Endophytic fungi produce a wide array of secondary metabolites with diverse chemical structures and bioactivities (Shi et al., 2024). These metabolites are typically synthesized through specific enzymatic pathways, such as polyketide synthases (PKSs), nonribosomal peptide synthetases (NRPSs), and terpene synthases, often encoded by clustered genes whose coordinated expression determines the chemical diversity of the products(Brakhage, 2013; Keller, 2019; Prakash et al., 2025). For instance, the endophytic fungus *Nigrograna mackinnonii* (isolate E5202H) produces (3E, 5E, 7E)-nona-1, 3, 5, 7-tetraene (NTE) via a PKS-based mechanism, as revealed by isotope-labeling and genomic analysis (Shaw et al., 2015). Additionally, in silico genomic mining of endophytic fungi from *Hypericum* species has uncovered multiple type I PKS biosynthetic gene clusters potentially responsible for the production of anthraquinone derivatives, such as emodin-like and bis-anthraquinones (Petijová et al., 2024). In contrast, *Gliocladium roseum* (NRRL 50072) produces volatile alkanes and esters, often referred to as "myco-diesel," which are derived from fatty acid-based biosynthetic pathways rather than PKS or NRPS routes (Strobel et al., 2008).

These biosynthetic processes are typically controlled by biosynthetic gene clusters (BGCs), which consist of co-located sets of genes encoding enzymes, transporters, and pathway-specific regulators. The diversity of BGCs generally correlates with the structural variety of metabolites a fungus can produce (Wadhwa et al., 2024). Advances in genome sequencing and bioinformatics, including tools such as antiSMASH, have enabled the identification and annotation of BGCs, revealing the hidden biosynthetic capacity of many endophytes. For instance, an endophytic strain *Fusarium* sp. R1, isolated from *Rumex madaio*, contains 37 BGCs, including PKS, NRPS, and hybrid clusters (Liu et al., 2022a). Similarly, the endophytic fungus *Calcarisporium arbuscula* NRRL 3705 harbors seven hybrid NRPS/PKS clusters and multiple terpene and indole gene clusters (Cheng et al., 2020).

1.2.6.3 Rich biological activities of endophytic fungal secondary metabolites

Endophytic fungi are recognized as prolific producers of structurally diverse secondary metabolites (Ancheeva et al.,2020; Jha et al., 2023; Gao et al., 2018; Tan & Zou, 2001). Many of these metabolites exhibit significant biological activities, including antimicrobial, anticancer, immunomodulatory, antidiabetic, insecticidal, antiviral, and antitubercular properties (Agrawal et al., 2022; Ajadi et al., 2024; Ancheeva et al., 2020; Kaul et al., 2012).

Antimicrobial activity is one of the most extensively studied properties of endophytic fungi. Deshmukh et al. (2022) reviewed 451 bioactive metabolites isolated from different groups of endophytic fungi during 2015–2021, which exhibited notable antibacterial activity. There have also been reports that the endophytic fungus *Botryosphaeria mamane* CF2-13, isolated from *Arrabidaea chica*, exhibits a broad spectrum of antimicrobial activity, particularly against *Staphylococcus aureus* and *Candida parapsilosis*. Another endophytic fungus, *Colletotrichum* sp. CG1-7, was found to possess notable antioxidant potential (Gurgel et al., 2023).

Endophytic fungi are also a valuable source of novel anticancer compounds. Prajapati et al. (2021) reviewed that 205 structurally unique anticancer compounds were obtained from 95 endophytic fungal strains collected from 16 different countries, highlighting the remarkable biosynthetic potential of endophytic fungi for cancer therapeutics between 2016 to 2020. The anticancer potential of these metabolites is particularly promising, with compounds such as paclitaxel and vinblastine analogs demonstrating potent cytotoxicity through mechanisms including microtubule stabilization, apoptosis induction, and topoisomerase inhibition (Islam et al., 2025).

Beyond antimicrobial and anticancer effects, endophytic fungi exhibit a wide range of additional biological activities. Antidiabetic properties have been reported in metabolites from *Aspergillus awamori* that inhibit α-glucosidase (Singh & Kaur, 2016), while anti-inflammatory compounds isolated from endophytic *Edenia gomezpompae* suppress key inflammatory mediators (Tan et al., 2020). Endophytic fungi also produce metabolites with notable insecticidal activity, such as the angularly prenylated indole alkaloids identified from *Fusarium sambucinum* TE-6L(Zhang et al., 2019a). Other reported activities include antiprotozoal (Pina et al., 2021), antituberculosis (Wijeratne et al., 2013), immunomodulatory (Rauf et al., 2022), and antiviral (Hawas & Abou El-Kassem, 2019, Lacerda et al., 2022), further underscoring the functional diversity of endophytic fungal secondary metabolites.

1.2.6.4 Applications of endophtyic fungal secondary metabolites

The broad-spectrum biological activities of endophytic fungal secondary metabolites have facilitated their applications across medicine, agriculture, and industrial biotechnology (Baron & Rigobelo, et al., 2023; Singh & Kumar, et al., 2023).

In medicinal, the landmark discovery of paclitaxel from *Taxomyces andreanae* established the pharmaceutical potential of these fungi, providing an alternative microbial source for this invaluable anticancer drug (Stierle et al., 1993). Since then, many studies have explored the medicinal potential of endophytic fungi. For example, Griseofulvin, mainly extracted from *Penicillium griseofulvumis,* is used for dermatophyte infections (Yu et al., 2024). Taxol produced by the endophytic fungus *Nodulisporium sylviforme* HDFS4-26 exhibits valuable application prospects in treating human breast, cervical, and ovarian cancers, attributed to its ability to induce cancer cell apoptosis (Wang et al., 2015). while taxol and camptothecin derivatives are pivotal in chemotherapy for ovarian, breast, and lung cancers (Ran et al., 2017). Beyond this, immunomodulatory compounds such as cyclosporine analogs offer promising scaffolds for developing novel immunosuppressive therapies, while antimicrobial metabolites like phonocoumarins present new avenues for combating multidrug-resistant bacterial infections (Aly et al., 2011).

In agriculture, endophytic fungal secondary metabolites play important roles as eco-friendly biopesticides and biofertilizers by inhibiting phytopathogens and promoting plant growth (Bamisile et al., 2018; Baron & Rigobelo, 2021; Lacey & Neven, 2006). Polyketides and peptides from *Talaromyces trachyspermus* R-17 suppress crown rot disease in wheat by inhibiting pathogen mycelial growth (Zhao et al., 2022), while VOCs, cell wall–degrading enzymes, siderophores, and phosphate- and zinc-solubilizing compounds produced by *Wickerhamomyces anomalus* from rice, corn, and sugarcane inhibit *Curvularia lunata*, *Fusarium moniliforme*, and *Rhizoctonia solani* (Khunnamwong et al., 2020). In addition to disease suppression, secondary metabolites with plant growth-promoting properties, such as gibberellins and auxin analogs, enhance crop yields by regulating host development (Baron & Rigobelo, 2021).

In industrial applications, endophytic fungal secondary metabolites are equally promising. In biofuel production, hydrocarbon derivatives from *Curvularia lunata*, an endophyte of *Solanum trilobatum*, resemble myco-diesel and illustrate the potential of fungal metabolites as fuel precursors (Kannan et al., 2016). In the food industry, phenolic secondary metabolites from *Cophinforma mamane* (CF2-13) show strong antioxidant activity, and the optimized extract containing caffeic acid can delay lipid oxidation in olive oil, demonstrating their value as natural antioxidants (Gurgel et al., 2024). These examples highlight the versatile industrial applications of endophytic fungal metabolites.

1.3 Current Research Status of Endophytic Fungi in Medicinal Plants

Plant endophytic fungi exist widely in medicinal plants with rich biodiversity, and have positive effects on host plants. People have been studying endophytic fungi for more than 100 years, since Vogl isolated the first endophytic fungus in ryegrass seeds in 1898 (Vogl, 1898). Especially after the discovery of paclitaxel-producing endophytic fungi *Taxomyces andreanae* from *T. brevifolia* (Stierle et al., 1993), it has stimulated the upsurge of the study of endophytic fungi. From 2005 to 2015, more than 376 endophytic fungi belonging to 83 families were isolated from 212 medicinal plants, which greatly increased the diversity of endophytic fungi (Tan et al., 2015).

Endophytic fungi of medicinal plants have rich biodiversity and play a positive role in the growth and development of plants. Some endophytic fungi can synthesize host secondary metabolites and have become a hot resource for humans to search for new drug sources. Many studies have shown that endophytic fungi can produce secondary metabolites mainly including alkaloids, polysaccharides, polyketones, terpenes, sterols, anthraquinones, flavonoids, xanthines, phenols, anthrene derivatives, furandione and cyclic peptides, etc (Aly et al., 2011; Kusari et al., 2012; Schulz et al., 2002). In the meantime, the biodiversity of these bioactive secondary metabolites showed antioxidant, bacteriostatic, insecticidal, plant growth regulation, anticancer and antitumor biological activities in various studies, which can be used in medicine, agriculture, foods and other fields with great application prospects (Adeleke & Babalola, 2021; Zhao et al., 2010).

At present, many researchers have focused on endophytic fungi and secondary metabolites of medicinal plants, including *Taxus cuspidata, Ginkgo biloba, Taxus chinensis* var. *Mairei, Wollemia nobilis, Nothapodytes foetidaz, Apodytes dimidiata* and so on (Fadiji & Babalola, 2020). There are an estimated 391,000 plant species worldwide (Díaz, 2022). Among them, thousands have known human uses, with more than 28,000 species used for medicinal purposes (Willis, 2017). The potential uses of the vast majority remain unexplored, and research on endophytic fungi in medicinal plants is far from sufficient.

1.4 The Antimicrobial Ability of Endophytic Fungi

Nowadays, the discovery of novel and active metabolites against pathogenic microbes to overcome antimicrobial resistance has become a paramount concern in the global healthcare system (Ferri et al., 2017). Endophytic fungi, which inhabit plant tissues without causing apparent harm, have emerged as prolific producers of antimicrobial metabolites (Jha et al., 2023). Secondary metabolites produced by endophytic fungi from medicinal plants often exhibit a certain inhibitory activity against a range of pathogenic microorganisms, primarily due to their antibiotic properties (Radić & Strukelj, 2012; Wen et al., 2022). The antimicrobial compounds generated by these fungi include various classes such as terpenoids, alkaloids, phenylpropanoids, aliphatic compounds, polyketides, and peptides (Adeleke & Babalola, 2021; Ezeobiora et al., 2021; Grabka et al., 2022; Narayanan & Glick, 2022).

Representative examples include palitantin, a polyketide from *Aspergillus fumigatiaffinis* isolated from healthy *Tribulus terrestris* leaves, showed strong antimicrobial activity against multidrug-resistant *Enterococcus faecalis* UW 2689 and *Streptococcus pneumoniae* 25697 (Ola et al., 2018). Four polyketide derivatives isolated from the endophytic fungus *Alternaria alternata* ZHJG5, which was obtained from the leaves of *Cercis chinensis*, exhibited potent antimicrobial activity against *Xanthomonas oryzae* pv. *oryzicola* (Xoc) and *Ralstonia solanacearum*, with MIC values ranging from 0.5 to 64 μg/mL (Zhao et al., 2021). Cytochrysins 63 and 65, derived from the endophytic fungus *Cytospora chrysosperma* HYQZ-931 associated with the desert plant *Hippophae rhamnoides*, exhibited antimicrobial activity. Compound 63 was active against *Enterococcus faecium* (MIC 25 μg/mL), while compound 65 inhibited *Staphylococcus aureus* (MIC 25 μg/mL) (Mou et al., 2021).

Likewise, the ergosterol derivative fusaristerol A (200), isolated from the endophytic *Fusarium* sp. of *Mentha longifolia*, exhibited strong activity against *Candida albicans* (MIC 8.3 μg/disc) (Ibrahim et al., 2018).

Although studies on *Tetradium ruticarpum* are limited, other members of the Rutaceae family have increasingly been recognized as reservoirs of diverse endophytic fungi with notable antimicrobial activities. For example, *Aegle marmelos* harbors *Muscodor kashayum*, which completely inhibited the growth of 75% of tested fungi/yeasts and 72% of tested bacteria (Meshram et al., 2012), and a novel species, *Alternaria marmelos*, showed strong anti-staphylococcal activity against *Staphylococcus aureus* (Meshram et al., 2013). Similarly, *Limonia acidissima* contains endophytic strains of *Aspergillus flavus* and *Aspergillus fumigatus*, which produce secondary metabolites with antibacterial and antifungal activities, as well as plant growth-promoting compounds such as indole acetic acid (IAA) and ammonia, highlighting their biotechnological and medicinal potential (Shuddhalwar et al., 2018). Endophytic fungi from *Zanthoxylum* species further illustrate the diversity and antimicrobial potential within Rutaceae. In *Z. bungeanum*, eight endophytic fungi exhibited strong and sustained antifungal activity against the host pathogens *Fusarium sambucinum* and *Pseudocercospora zanthoxyli* (Li et al., 2016b), while in *Z. simulans*, 113 isolates were obtained, of which 23 strains (20.35%) across six genera (*Penicillium*, *Colletotrichum*, *Diaporthe*, among others) displayed antimicrobial activity, suggesting their role in host defense and as sources of natural antibiotics. Moreover, *Citrus* species also host endophytic fungi with broad-spectrum antimicrobial activity. An isolate from *Citrus jambhiri* in Nigeria produced metabolites active against *S. aureus* (inhibition zone 3 mm at 1 mg/mL), containing bioactive compounds such as protocathechuic acid, IAA, and acropyrone (Eze et al., 2018). The citrus endophyte *Nemania* sp. LJZ-Y-11 exhibited >50% inhibition against nine plant pathogenic fungi and strong antibacterial effects with MIC values as low as 0.078 g/L against *Bacillus subtilis* (Li et al., 2023). In *Citrus sinensis* (Gannan navel orange), 54 endophytic strains (17 species, 12 genera) demonstrated significant antimicrobial activity, with extracts of *Geotrichum* sp. and *Diaporthe biconispora* inhibiting *Xanthomonas citri*, and *Colletotrichum gloeosporioides* extract showing potent activity against methicillin-resistant *S. aureus* (MIC = 62.5 μg/mL)

(Wang et al., 2023). Furthermore, *Muscodor* sp. LGMF1254, isolated from healthy citrus plants in Brazil, inhibited the growth of *Phyllosticta citricarpa*, the causal agent of Citrus Black Spot, via volatile organic compounds (VOCs), indicating potential as a biological control agent (Pena et al., 2016). Taken together, these studies indicate that Rutaceae plants host a diverse array of endophytic fungi with considerable antimicrobial potential.

Overall, between 1995 and 2022, 286 species of endophytic fungi have been reported with antimicrobial activity, yielding a total of 716 bioactive compounds (Deshmukh et al., 2015, 2022). Thus, endophytic fungi constitute a valuable reservoir of antimicrobial agents, representing another promising source beyond plants (Tiwari & Bae, 2022).

1.5 Screening Methods for Antimicrobial Activity of Endophytic Fungi

The exploration of endophytic fungi as rich reservoirs of antimicrobial compounds relies on a combination of classical bioassays and advanced analytical tools to comprehensively evaluate their bioactive potential. Initial screening typically employs traditional in vitro assays, including agar-based methods such as the agar plug assay (Jiménez-Esquilín et al., 2005), disk diffusion (Elleuch et al., 2010), and well diffusion (El-Desoukey, 2018), which are valued for their simplicity and suitability for detecting diffusible secondary metabolites directly from fungal cultures. Quantitative assessment is commonly achieved through broth or agar dilution methods, which determine minimum inhibitory concentrations (MICs) and offer more standardized evaluation. In the context of ecological relevance, dual-culture (co-culture) assays are frequently applied to observe antagonistic interactions between endophytes and pathogens, providing insight into direct inhibition capacity under competitive conditions (Ali et al., 2020; Jia et al., 2020).

For broader and more precise screening, bioassay-guided fractionation is often combined with chromatographic techniques such as TLC or HPLC together with overlay or bioautography assays, enabling the identification and tracking of active compounds within complex fungal extracts. More recently, high-resolution tools such as resazurin-based viability assays, flow cytometry, and bioluminescence-based reporter assays have emerged, enabling real-time, high-throughput evaluation of cell viability and antimicrobial impact. Furthermore, Omics-based approaches are increasingly applied to link observed bioactivities with specific metabolites or biosynthetic pathways, and these include genome mining for biosynthetic gene clusters (BGCs) such as NRPS or PKS as well as LC-MS/MS metabolomics (Balouiri et al., 2016; Hossain, 2024).

Despite these advances, significant challenges remain, particularly in the standardization of screening protocols across diverse fungal taxa and the attribution of antimicrobial effects to individual metabolites. Therefore, a multidisciplinary workflow that integrates phenotypic assays, chemical profiling, and molecular analysis is essential to fully harness the antimicrobial potential of endophytic fungi.

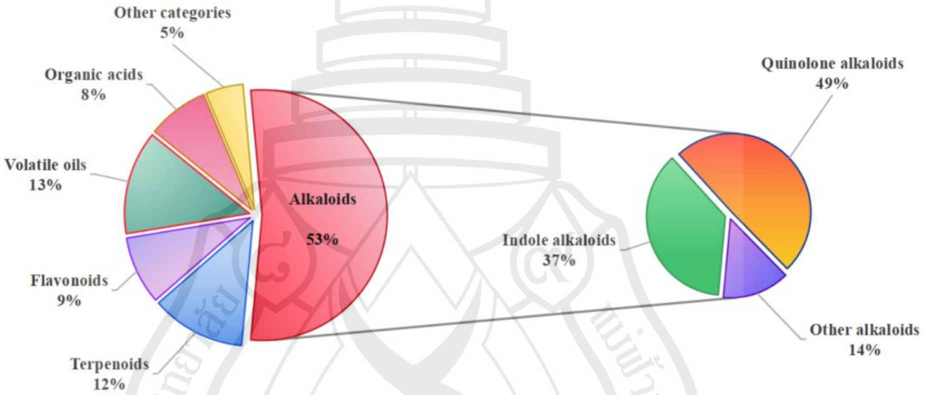
1.6 Research Progress of *Tetradium ruticarpum*

1.6.1 Botany of *Tetradium ruticarpum*

Tetradium ruticarpum (A. Juss.) T. G. Hartley is a deciduous shrub or small tree in the family Rutaceae and represents a classic medicinal plant with a history of use spanning more than 2,000 years (Na et al., 2022). It is native to East and South Asia, including China, Vietnam, Myanmar, Nepal, Bhutan, and India, and has also been introduced to Japan and Korea (World Flora Online, 2025). The species was previously placed in the genus *Euodia* as *Euodia ruticarpa*, and additional synonyms include *Ampacus ruticarpa* (A. Juss.) Kuntze and *Evodia ruticarpa* (A. Juss.) Hook. f. & Thomson. The misspelt form "*Evodia rutaecarpa*" is also widely cited in traditional Chinese medicine and herbal literature. Two intraspecific varieties are recognized under *E. rutaecarpa* (Juss.) Benth., namely *E. rutaecarpa* var. *officinalis* (Dode) Huang and *E. rutaecarpa* var. *bodinieri* (Dode) Huang (Yan et al., 2020). Hartley (1981) clarified the distinction between *Tetradium* and *Euodia*. Now, there are ten species in *Tetradium* genus (Ang et al., 2025). Botanically, *T. ruticarpum* typically grows 3–5 m tall and is characterized by opposite odd-pinnate leaves, terminal inflorescences, and dioecious flowers with 4–5 sepals, petals, stamens, and carpels. The fruit is oblate, follicle-like, and purplish red, with conspicuous oil glands, and splits into five segments at maturity, each containing a shiny black seed. The flowering period generally extends from June to August, followed by fruiting from August to November (Flora of China Editorial Committee, 2006). Given its long-standing medicinal application and broad distribution, increasing emphasis has been placed on the standardized cultivation of *T. ruticarpum* to ensure stable quality, safety, and sustainable utilization of this important medicinal resource (Li et al., 2022b; She et al., 2023; Tian et al., 2024). The dried, nearly ripe fruits of *Tetradium ruticarpum*, internationally referred to as Euodie Fructus or Evodiae Fructus and known locally as “Wuzhuyu” in China, “Goshuyu” in Japan, “Osuyu” in South Korea, and (Ngô thù, Xà lạp in Vietnamese, serve as its primary medicinal part (To et al., 2021). These fruits are derived from the official species *Euodia rutaecarpa* (Juss.) Benth. (abbreviated as ER) and its two variants, *E. rutaecarpa* (Juss.) Benth. var. *officinalis* (Dode) Huang and *E. rutaecarpa* (Juss.) Benth. var. *bodinieri* (Dode) Huang, which are now collectively recognized as *Tetradium ruticarpum* (A. Juss.) T. G. Hartley (National Pharmacopoeia Committee, 2020). Despite the taxonomic revision (i.e., being reassigned from the genus *Evodia*), *Evodia rutaecarpa* (corresponding to Euodiae Fructus in medicinal contexts) remains widely used in contemporary academic literature. Traditionally, this herb has held significant value in East Asian medicine for its ability to dispel cold, relieve pain, regulate liver qi, and alleviate vomiting (Li &Wang, 2020). The main producing areas of *T. ruticarpum* in China are located south of the Qinling Mountains, including Jiangxi, Guizhou, Guangxi, Hunan, Zhejiang, Anhui, and Yunnan provinces. Among these, Jiangxi Province is the Daodi production area, mainly distributed in Zhangshu, Fengcheng, Gaoan, and Xingan (Hao et al., 2025).

1.6.2 Phytochemistry of *Tetradium ruticarpum*

In line with its long history of medicinal use, phytochemical studies have revealed that the genus *Tetradium*, particularly *Tetradium rutaecarpa*, contains a wide array of bioactive compounds (Xu et al., 2025). *Tetradium ruticarpum* is a representative medicinal species that has been extensively investigated for its phytochemical composition and pharmacological potential (Li & Wang, 2020; Shan et al., 2020; Xiao et al., 2023a; Hao et al., 2025; Xu et al., 2025). Phytochemical analyses have revealed nearly 330 metabolites isolated and characterized from *T. ruticarpum*, including alkaloids (174), terpenoids (40), flavonoids (29), volatile oils (44), Organic acids (26), and other constituents (16) (Appendix Table A1) (Zuo et al., 2000, 2003; Yang et al., 2008; Wang et al., 2010; Lacroix et al., 2011; Wang et al., 2013b; Li et al., 2014; Qian et al., 2014; Qin, 2015; Zhao et al., 2015a; Li et al., 2016d; Ling et al., 2016; Xia et al., 2016; Su et al., 2017; Li et al., 2020a, b; Li & Wang 2020; Zhang et al., 2020b; Ma et al., 2021; Qin et al., 2021a, b; Zhao et al., 2021b; Xiao et al., 2023a; He et al., 2024; Li et al., 2024b; Hao et al., 2025; Matsuo et al., 2025; Tan et al., 2025).



Note The left pie chart displays the proportions of major compound categories, and the right sub-pie chart details subgroups of alkaloids.

Figure 1.1 Distribution of chemical constituents isolated from *Tetradium ruticarpum*

The distribution of these compounds reveals that alkaloids account for the largest proportion, representing 53% of all metabolites, followed by volatile oils (13%), terpenoids (12%), flavonoids (9%), organic acids (8%), and other categories (5%) (Figure 1.1). A more detailed breakdown of alkaloids shows that quinolone alkaloids constitute nearly half of this group (49%), with indole alkaloids comprising 37% and other alkaloid subtypes, such as quinolines, indolequinazolines, and organic amines, making up the remaining 14% (sub-pie chart in Figure 1.1). Evodiamine and rutaecarpine, two indole alkaloids, are regarded as index metabolites of the plant (Li et al., 2020a). In addition, terpenoids, particularly limonoids (33 of the 40 identified terpenoids), represent another key chemical class, with limonin highlighted as a crucial compound contributing to the pharmacological profile of *T. ruticarpum*. Flavonoids (mainly flavonols), volatile oils (notably sesquiterpenes), and organic acids further enrich the chemical diversity of this species. Collectively, these findings emphasize the chemical complexity of *T. ruticarpum*. Together, they provide a foundation for understanding its wide spectrum of biological activities and medicinal applications. Alkaloids, mainly indole and quinolone derivatives, constitute the most representative class (Li et al., 2020a), with evodiamine and rutaecarpine regarded as index compounds. In addition, the terpenoid limonin has been highlighted as another key metabolite contributing to the pharmacological activity of this plant.

1.6.3 Pharmacological Value of *Tetradium ruticarpum*

The chemical diversity of *Tetradium ruticarpum* underpins its wide-ranging biological activities (Shan et al., 2020). Modern pharmacological investigations confirm that the plant's extracts and bioactive constituents, including evodiamine, rutaecarpine, limonin, and essential oil components, possess significant therapeutic potential (Zhao et al., 2019; Li & Wang, 2020; Xiao et al., 2023a). At the level of organ and system protection, *T. ruticarpum* demonstrates direct defensive effects on cardiovascular, gastrointestinal, neural, hepatic, renal, reproductive, and skeletal systems (Lee et al., 2011; Ren et al., 2020; Tian et al., 2019; Yu et al., 2016). Rutaecarpine enhances endothelial nitric oxide synthase phosphorylation to preserve vascular integrity (Lee et al., 2021), evodiamine alleviates myocardial fibrosis via PI3K/AKT inhibition (Huang et al., 2017), its alkaloids mitigate gastric mucosal injury and oxidative stress (Ren et al., 2020; Zhao et al., 2015b), rutaecarpine and limonin attenuate neuronal damage and autophagy in cerebral ischemia and neurotoxicity (Han et al., 2019; Gao et al., 2023), and protective effects extend to the liver, kidney, prostate, and bone through antioxidative, apoptotic, and osteogenic pathways (Fukuma et al., 2018; Lee et al., 2016; Lei et al., 2023; Park et al., 2018; Zhou et al., 2023). In terms of pathological process intervention, its constituents directly modulate disease mechanisms by suppressing inflammatory signaling and cytokine release (Jayakumar et al., 2021; Yang et al., 2022c), reducing pain sensitivity through TRPV1 desensitization (Iwaoka et al., 2016) inducing apoptosis and inhibiting metastasis in diverse cancers (Luo et al., 2021; Panda et al., 2023), restoring glucose and lipid metabolism via AMPK activation and hypothalamic neuropeptide regulation (Nie et al., 2016; Shi et al., 2009), and exerting antidepressant effects through hippocampal monoamine and BDNF-TrkB modulation (Jiang et al., 2015). In addition to its organ-protective and disease-modulating effects, *T. ruticarpum* exhibits defensive activity against exogenous organisms. Its volatile oils and alkaloids inhibit pathogens, including *Staphylococcus aureus*, *Bacillus subtilis*, and *Helicobacter pylori,* consistent with its traditional use for gastrointestinal disorders (Liu et al., 2019; Na et al., 2022). Extracts and bioactive components such as evodiamine and rutaecarpine also show insecticidal activity against *Aedes albopictus* larvae and stored grain pests (*Sitophilus zeamais*) (Liu & Du, 2011; Liu et al., 2012). Beyond these effects, the plant contributes to physiological balance by enhancing antioxidant enzyme activity, reducing lipid peroxidation (Li et al., 2016a), and regulating immune homeostasis, including suppression of IgE-mediated allergic responses (Shin et al., 2007). *Tetradium ruticarpum* unifies organ protection, disease intervention, anti-exogenous defense, and homeostatic regulation, validating its traditional use and highlighting potential for modern therapeutics and functional innovations.

1.6.4 Economic Value of *Tetradium ruticarpum*

Tetradium ruticarpum is an indispensable medicinal plant with additional potential in apiculture and edible mushroom cultivation, highlighting its broad economic value. Zhang et al. (2021) documented that the plant can serve as a supplementary nectar source during summer, and its derived “Tetradium honey” shows promise for development. Li et al. (2024a) identified 297 volatile compounds in *Evodia rutaecarpa* Benth honey (ERBH), with 22 key odor-active compounds (e.g., (E)-β-damascenone, linalool, eugenol) contributing to its distinct floral, fruity, herbaceous, and woody aromas, underscoring its economic value. In addition, the branches of *T. ruticarpum* are rich in nutrients such as crude protein, cellulose, hemicellulose, lignin, and selenium, making them a valuable substrate for cultivating edible fungi. For example, Yang et al. (2016) reported that its branches supported the fruiting of *Auricularia auricula*, *Pleurotus ostreatus*, and *Tremella fuciformis*. Subsequent studies have confirmed its broader application: *Pleurotus citrinipileatus*, *Auricularia polytricha* and *Auricularia cornea* were all successfully cultivated on *T. ruticarpum* branch sawdust (Lan et al., 2022; Ye et al., 2022, 2024). Notably, Lan et al. (2022) demonstrated that a substrate containing 46.8% *T. ruticarpum* sawdust not only ensured stable yields of *P. citrinipileatus* but also produced selenium-enriched mushrooms with high-quality proteins, crude polysaccharides, and flavor-enhancing amino acids. Similarly, Ye et al. (2024) reported that a formulation containing 62.4% *T. ruticarpum* branch sawdust was optimal for *Auricularia polytricha* cultivation, yielding fruiting bodies with enhanced nutritional profiles. Based on studies demonstrating the efficacy of *T. ruticarpum*'s main active components (evodiamine, rutaecarpine), these components align with the modern cosmetics industry's growing demand for anti-ageing, antioxidant, anti-inflammatory, antibacterial, and anti-photoaging effects. Accordingly, *T. ruticarpum* extract is predicted to hold significant potential and broad application prospects in the cosmetics field (Yao et al., 2024).

1.6.5 The Antimicrobial Ability of *Tetradium ruticarpum*

Medicinal plants, particularly those within the Rutaceae family, have long been recognized as reservoirs of bioactive compounds (Sultana et al., 2024). Notably, *Tetradium ruticarpum* itself exhibits broad-spectrum antimicrobial activity which has been attributed to its diverse bioactive compounds such as quinolone alkaloids, indole alkaloids, polysaccharides, limonoids, and essential oils (Table 1.1). Specifically, quinolone alkaloids (e.g., rutaecarpine, evodiamine, and N-methyl-4(1H)-quinolone derivatives) can inhibit various bacteria such as *Staphylococcus aureus*, *Escherichia coli*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Helicobacter pylori*, and *Mycobacterium* species. They also show antifungal effects against *Candida albicans* and *Rhizoctonia solani* (Hamasaki et al., 2000; Tominaga et al., 2002, 2005; Adams et al,. 2005; Wang et al., 2013a; Mbaebie Oyedemi, 2015; Liang et al., 2017; Na et al., 2022). Ethanol extracts of *T. ruticarpum* suppress gram-positive cocci, *Pseudomonas aeruginosa*, and the fungus *Candida albicans* (Thuille, 2003). Polysaccharides from this plant inhibit multiple bacterial strains including *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Bacillus subtilis,* as well as *Candida albicans* (Fu et al., 2010). Indole alkaloids target *Xanthomonas* pathogens like *Xanthomonas oryzae* pv. *oryzae* and *Xanthomonas campestris* pv. *campestris*, and they also act against the fungus *Rhizoctonia solani* (Su et al., 2018). Limonoids (e.g., limonin) exert inhibitory effects on *Escherichia coli* and *Staphylococcus aureus*

(Liang et al., 2017), while essential oils inhibit bacteria such as *Bacillus subtilis*, *Sarcina lutea*, *Staphylococcus aureus*, and fungi including *Candida albicans* and *Aspergillus niger* (Liu et al., 2019). While medicinal plants have long been explored as sources of antimicrobial compounds, their application is often constrained by long growth cycles, complex cultivation requirements, and low yields of active constituents (Atanasov et al., 2015; Anand et al., 2019). This limitation has stimulated the search for alternative microbial resources.

Table 1.1 The antimicrobial ability of *Tetradium ruticarpum*

Category of compounds	Extracts or compounds	Antibacterial ability	Antifungal ability	References
Quinolone alkaloids	1-methy1-2-[(Z)-8-trideceny1]-4-(1H)-quinolone 1-methy1-2-[(Z)-7-trideceny1]-4-(1H)-quinolone	*Helicobacter pylori*	-	(Hamasaki et al., 2000; Tominaga et al., 2002, 2005)
	Compounds (1-5)	*Mycobacterium fortuitum, Mycobacterium smegmatis, Mycobacterium phlei*	-	(Adams et al., 2005)
	N-methyl-4(1H)-quinolone	*Staphyloccocus aureus, Staphylococcus epidermidis, Bacillus subtilis*	-	(Wang et al., 2013a)
	Rutaecarpine, Evodiamine, Sucrose	*Staphylococcus aureus*	-	(Mbaebie Oyedemi, 2015)
	1-O-β-D-glucopyranosylrutae carpine, 14-hydroxyevodiamine Evodiamine, Rutaecarpine, formyldihydro-rutaecarpin	*Escherichia coli, Staphylococcus aureus*	-	(Liang et al., 2017)
	Evocarpine 4-methoxy-3-(3-methylbut-2-enyl)-1H–quinolin-2-one	*Escherichia coli, Staphylococcus aureus*	-	
	1-methyl-2-(8E)-8-tridecenyl-4(1H)-quinolinone	*Helicobacter pylori*	-	(Na et al., 2022)
Indole alkaloid	Rhetsinine, dehydroevodiamine	*Xanthomonas oryzae pv. oryzae,* *Xanthomonas oryzae pv. Oryzicola* *Xanthomonas campestris pv. campestris*	-	(Su et al., 2018)
	Evodiamine	-	*Rhizoctonia solani*	
Ethanol extract	Ethanol extract	*Staphylococcus aureus, Staphylococcus pyogenes, Escherichia coli, Pseudomonas mirabilis, Pseudomonas aeruginosa*	*Candida albicans*	(Thuille et al., 2003)
Polysaccharides	Crude extracts	*Staphylococcus aureus, Escherichia coli* *Pseudomonas aeruginosa, Bacillus subtilis*	*Candida albicans*	(Fu et al., 2010)
Limonoids	Limonin, 6β-acetoxy-5-epilimonin	*Escherichia coli*		(Liang et al., 2017)
Essential oils	β-cis-ocimene, caryophyllene oxide	*Bacillus subtilis, Sarcina lutea, Staphylococcus aureus*	*Candida albicans* *Aspergillus niger*	(Liu et al., 2019)

1.6.6 Endophytic Fungi Associated with *Tetradium ruticarpum*

The earliest investigation of endophytic fungi from *Tetradium ruticarpum* was conducted by Zhu in 2007, who isolated a fungus identified as *Sclerotium* sp., yielding 44 bioactive compounds. However, this study did not comprehensively characterize the endophytic fungal diversity within the host (Zhu, 2007). In 2011, two independent studies aimed to isolate endophytic fungi from *T. ruticarpum* capable of producing alkaloids similar to those of the host plant, yet neither provided taxonomic identification of the obtained strains (Cao et al., 2011; Li et al., 2011). The first genus-level taxonomic study was carried out by Ho et al. (2012), who reported four endophytic genera from *T. ruticarpum*: *Cyanodermella*, *Guignardia*, *Hypoxylon*, and *Nigrospora*. Research on endophytic fungi from *T. ruticarpum* had long been lacking, until our recent work led to the description of two novel species, *Cyphellophora guangxiensis* (Mi et al., 2025b) and *Pseudokeissleriella tetradii* (Mi et al., 2025a). Though *T. ruticarpum* is recognized for its medicinal value, reports on its associated fungi remain limited. As the number of medicinal plant-related fungal studies increases (Cheek et al., 2020; Katoch et al., 2017; Kusari et al., 2013; Safaie et al., 2024), exploring the fungal diversity associated with *T. ruticarpum* could provide new insights into potential bioactive compounds.

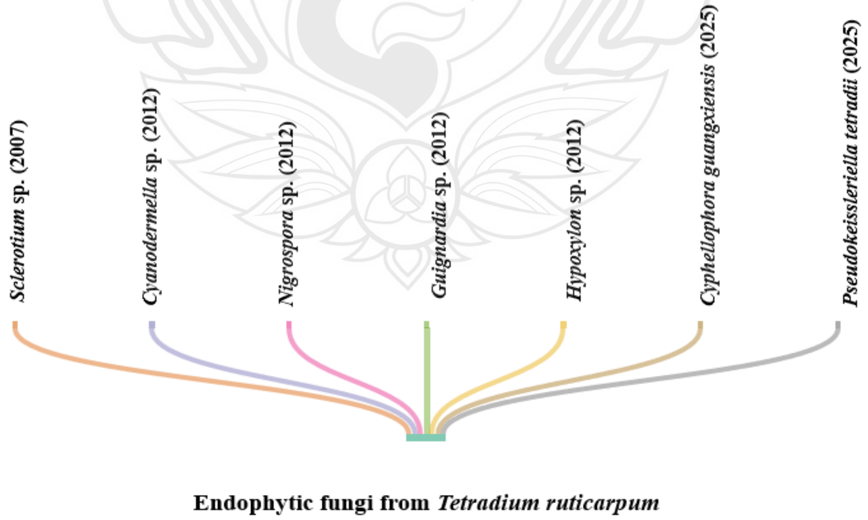


Figure 1.2 Endophytic fungi from *Tetradium ruticarpum*

1.6.7 The Antimicrobial Ability of Endophytic Fungi from *Tetradium ruticarpum*

Tetradium ruticarpum, a medicinal Rutaceae species, has been little studied in terms of its associated fungi, and only one report has documented the antibacterial potential of its endophytic fungi (Ho et al., 2012). According to reports in the literature, *Cyanodermella* sp., an endophytic isolate from *T. ruticarpum*, exhibited strong antagonistic activity against 12 phytopathogens, including the fungal pathogens *Cynlidocladiella lageniformis* CL01, *Fusarium oxysporum* f. sp. *lilii* Fol-04, and *Monilinia fructicola* TW01, as well as the bacterial pathogen *Ralstonia solanacearum* PW2, with an inhibition index of 3 (inhibition zone >10 mm). Although studies on *T. ruticarpum* are limited, other members of the Rutaceae family have increasingly been recognized as reservoirs of diverse endophytic fungi with notable antimicrobial activities. For example, *Aegle marmelos* harbors *Muscodor kashayum*, which completely inhibited the growth of 75% of tested fungi/yeasts and 72% of tested bacteria (Meshram et al., 2012), and a novel species, *Alternaria marmelos*, showed strong anti-staphylococcal activity against *Staphylococcus aureus* (Meshram et al., 2013). Similarly, *Limonia acidissima* contains endophytic strains of *Aspergillus flavus* and *Aspergillus fumigatus*, which produce secondary metabolites with antibacterial and antifungal activities, as well as plant growth-promoting compounds such as indole acetic acid (IAA) and ammonia, highlighting their biotechnological and mcgent (Pena et al., 2016). Taken together, these studies indicate that Rutaceae plants host a diverse array of endophytic fungi with considerable antimicrobial potential. By analogy, as a medicinal member of the Rutaceae, *T. ruticarpum* is likely to harbor endophytic fungi with significant antibacterial and antifungal activities; however, this remains largely unexplored. Taken together, these studies indicate that Rutaceae plants host a diverse array of endophytic fungi with considerable antimicrobial potential. By analogy, *T. ruticarpum*, as a medicinal member of the Rutaceae, is likely to harbor endophytic fungi with significant antibacterial and antifungal activities; however, this remains largely unexplored.

1.7 Research Objectives

1.7.1 Isolation and Identification of Endophytic Fungi

To isolate and identify fungi associated with *Tetradium ruticarpum* at the genus level based on the ITS gene region and at the species level based on morphology and multigene phylogenetic evidence.

1.7.2 Screening of Antimicrobial Properties

To screen and test endophytic fungi associated with *Tetradium ruticarpum* with antimicrobial properties against fungal and bacterial pathogens.

1.8 Research Significance

1.8.1 Fill the Gap in the Research of Endophytic Fungi in *Tetradium ruticarpum*

In recent years, the study of endophytic fungi has become a hot topic and has accumulated a large number of bacterial resources. Endophytic fungi have become an important source for obtaining novel compounds. However, there is limited research on the endophytic fungi in *T. ruticarpum* (Cao et al., 2011; Ho et al., 2012; Li et al., 2011; Zhu, 2007). At present, research on *T. ruticarpum* mainly focuses on phytochemical constituents, pharmacological effects, and cultivation practices. In addition, with the expansion of the planting area and the extension of years, various diseases occurred one after another. It has been reported in the literature (Gao et al., 2012; Lian et al., 2012), there are five fungi-diseases, namely rust (pathogenetic fungi: *Coleosporium* sp.), leaf spot (pathogenetic fungi: *Phyllostica* sp.), powdery mildew (pathogenetic fungi: *Oidium* sp.), spot (pathogenetic fungi: *Leptosphaeria* sp.) and pedicels rot (pathogenetic fungi: *Alternaria* sp.). In recent years, several pathogenic fungi associated with *T. ruticarpum* have aslo been reported, including *Alternaria alternata* (Xiang et al., 2021), *Coleosporium euodiicola* (Sun et al., 2024a), and *Colletotrichum siamense* (Sun et al., 2025). In this study, we mainly focused on the endophytic fungi of *T. ruticarpum*. Samples were collected from four regions in southern China (Jiangxi, Hunan, Anhui, and Guangxi provinces). Endophytic fungi were subsequently isolated, purified, and preliminarily identified based on ITS sequence analysis. This study provides the first basic data on the community richness of endophytic fungi associated with *T. ruticarpum*.

1.8.2 Supplement Fungal Species Resources

During this investigation, some isolates were identified through polygenic phylogeny and morphological characteristics, and some novel taxonomic units were discovered in the endophytic fungi of *Tetradium ruticarpum*. The discovery of potential new fungal taxa expands the known biodiversity of endophytic fungi and enhances the available strain resources for taxonomy, ecology, and pharmaceutical exploration.

1.8.3 Lay the Foundation for the Exploration of New Antibacterial Active Substances

Tetradium ruticarpum is a commonly used medicinal plant in traditional Chinese medicine, known for its functions in warming the middle, relieving pain, and exhibiting anti-inflammatory and antibacterial activities. Modern studies have shown that its active components, such as alkaloids and volatile oils, possess promising antibacterial potential. In recent years, endophytic fungi from medicinal plants have emerged as important sources of novel natural products due to their ability to produce structurally unique and biologically active metabolites. The unique chemical composition and ecological environment of *T. ruticarpum* may endow its endophytes with high developmental potential. In this study, endophytic fungi isolated from *T. ruticarpum* were subjected to preliminary antimicrobial screening, providing a theoretical foundation and resource support for the discovery of new antimicrobial compounds, which may contribute to addressing the growing challenge of antibiotic resistance.

CHAPTER 2

RESEARCH METHODOLOGY

2.1 Sample Collection

Tetradium ruticarpum (Rutaceae) (Figure 2.1) plants were collected from 23 distinct sites in Southeast China (Jiangxi, Hunan, Anhui and Guangxi provinces) during 2020–2024 (Figure 2.2 and Table 2.1). The healthy plant tissues (root, stem, leaf, and fruit) of *T. ruticarpum* were collected randomly in Ziploc plastic bags, preserved with ice, transported to the lab and stored at 4 ℃ until processing. The distribution map of sampling locations (Figure 2.2) was created using ArcGIS, with the base map of China sourced from the map open platform (https://datav.aliyun.com/tools/atlas/index.html).

Figure 2.1 Habitats of *Tetradium ruticarpum*

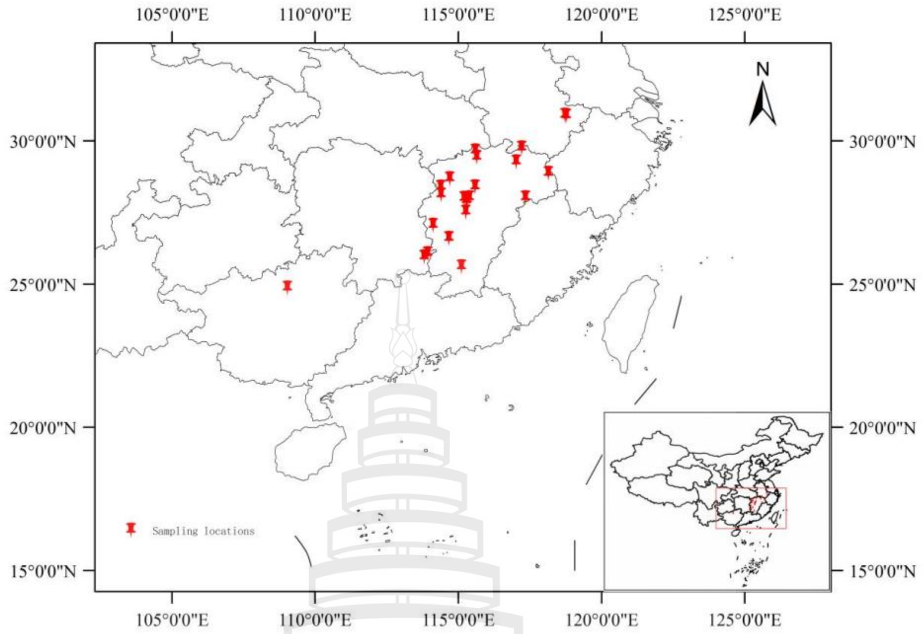


Figure 2.2 Distribution map of sampling locations of *Tetradium ruticarpum* in southern China

Table 2.1 Information on sample collection sites

Collection sites	Abbreviation	Location (Latitude, Longitude, Altitude)	Collection Date
Xiaochang Town, Luocheng Mulao Autonomous County, Hechi, Guangxi	GXHCLC	24.8667°N, 109.0333°E, unavailable	19 May 2022, 9 September 2023
Dui Zaixia, Guidong County, Chenzhou, Hunan	HNCZDZ	25.9500°N, 113.8100°E, unavailable	9 September 2023
Wei Xia, Guidong County, Chenzhou, Hunan	HNCZWX	26.0667°N, 113.9333°E, 868m	10 November 2021
Tongjiawan, Xuanzhou District, Xuancheng, Anhui	AHXCTJ	30.9000°N, 118.7300° E, 17.76m	8 September 2023
Jinbei Street, Xuanzhou District, Xuancheng, Anhui	AHXCJB	30.8833°N, 118.7833°E, 46m	22 May 2022
Tongxin Village, Wanzai County, Yichun, Jiangxi	JXYCTX	28.3836°N, 114.3890°E, 655m	4 April 2021
Shanghong, Tonggu County, Yichun, Jiangxi	JXYCTG	28.6852°N, 114.7067°E, 483.6m	12 July 2021
Liansheng Village, Wanzai County, Yichun, Jiangxi	JXYCLS	28.1173°N, 114.3997°E, unavailable	27 July 2021
Xiexi Town, Fengcheng, Yichun, Jiangxi	JXYCFC	28.3944°N 115.5965°E, 35.8m	27 September 2024

Table 2.1 (continued)

Collection sites	Abbreviation	Location (Latitude, Longitude, Altitude)	Collection Date
Fujia Village, Linjiangzhen, Zhangshu, Yichun, Jiangxi	JXZSLJ	28.0130°N, 115.3919°E, unavailable	15 November 2020
Luotang, Yicheng, Zhangshu, Yichun, Jiangxi	JXZSYC	27.9931°N, 115.2123°E, 45m	21 September 2021
Shuangjin Farm, Zhangshu, Yichun, Jiangxi	JXZSSJ	27.9333°N, 115.3166°E, unavailable	10 October 2022
Changfuzhen, Zhangshu, Yichun, Jiangxi	JXZSCF	27.9200°N, 115.2900°E, unavailable	16 October 2023
Tianxi Village, Wan'an County, Ji'an, Jiangxi	JXJAWA	26.6000°N, 114.6833°E, unavailable	11 April 2021
Xinshi Village, Xingan County, Ji'an, Jiangxi	JXJAXG	27.5244°N, 115.2650°E, unavailable	30 September 2022
Heshan, Yongxin County, Ji'an, Jiangxi	JXJAYX	27.0575°N, 114.1271°E, unavailable	6 November 2020
Dabu Town , Ganxian District, Ganzhou, Jiangxi	JXGZGX	25.6121°N, 115.1211°E, 412.9m	26 July 2022
Liyang Town, Changjiang District, Jingdezhen, Jiangxi	JXJDZC	29.2707°N, 117.0332°E, 40.6m	29 June 2022
Jinggongqiao Town, Changjiang District, Jingdezhen, Jiangxi	JXJDZF	29.7595°N, 117.2206°E, 76.1m	7 November 2022
Hongyuan Hejialong, Ruichang, Jiujiang, Jiangxi	JXJJRC	29.6500°N, 115.6000°E, unavailable	23 March 2021, 24 March 2023
Hepu Village, Dean, Jiujiang, Jiangxi	JXJJDA	29.4333°N, 115.6500°E, unavailable	11 November 2023
Hongqiao, Guixi, Yingtan, Jiangxi	JXYTWF	28.0132°N, 117.3490°E, unavailable	4 August 2021, 24 June 2022
Yuzhi, Zihu Town, Yushan County, Shangrao, Jiangxi	JXSRYS	28.8667°N, 118.1500°E, unavailable	28 April 2023

2.2 Surface Sterilization and Isolation of Endophytic Fungi

Endophytic fungi were isolated using the surface sterilization method described by Senanayake et al. (2020) and slightly modified according to the characteristics of *Tetradium ruticarpum*. The healthy roots, stems, leaves, and fruits of *T. ruticarpum* were first washed with running tap water to remove residual soil, then blotted dry with sterile filter paper and transferred to an ultra-clean workbench for surface disinfection.

During disinfection, 75% (v/v) ethanol soaking durations were adapted to the structural traits of different tissues: roots and stems for 1 min, and leaves and fruits for 45 s. Thereafter, all tissues were uniformly soaked in a sodium hypochlorite solution (3.3% available chlorine) for 1 min, followed by three rinses with sterile distilled water to eliminate residual disinfectant, and finally blotted dry on sterile filter paper. To maximize the diversity of endophytic fungi isolated, surface-sterilized plant organs were cut into small fragments (ca. 5 mm^2) and cultured on six different media: potato dextrose agar (PDA), malt extract agar (MEA), yeast-starch agar (YpSs), rose-bengal agar (RBA), potato carrot agar (PCA), and oatmeal agar (OA) (Table 2.2). These Petri dishes were sealed, incubated at 25 °C, and examined every day. When fungi grew out from the tissue segment, a few hyphal fragments were picked up and transferred to new plates (the same as isolation media) to obtain pure cultures. The pure endophytic strains were deposited in the Jiangxi Agricultural University Culture Collection (JAUCC), Nanchang, China, while the dry cultures were stored in the Herbarium of Fungi, Jiangxi Agricultural University (HFJAU), Nanchang, China. For newly published species, the Faces of Fungi (FoF) numbers were obtained following Jayasiri et al. (2015), and the Index Fungorum numbers were registered according to the guidelines of Index Fungorum (2025).

Table 2.2 Culture medium used for isolation of fungal endophytes

Medium name	Composition (g/L)	References
Malt extract agar (MEA)	Malt extract 30, Peptone 5, agar 15, Chloramphenicol 0.1	(Luo, 2022)
Potato dextrose agar (PDA)	Potato 200, Dextrose 20, agar 15	(Rodriguez & Redman, 2008)
Potato carrot agar (PCA)	Potato 200 g, Carrots 200 g, Agar 15 g	(Luo, 2022)
Oatmeal agar (OA)	Oatmeal 50, agar 20	(Luo, 2022)
Rose Bengal agar (RBA)	Mycological peptone 5, glucose 10, potassium dihydrogen phosphate 1, magnesium sulfate 0.5, Rose Bengal 0.0333, agar 15	(Luo, 2022)
Yeast-starch agar (YpSs)	Starch 15, yeast extract 4, K_2PO4 1, $MgSO_47H_2O$ 1, agar 20	(Wilkins & Schöller, 2009)

To ensure that the isolated strains were truly endophytic fungi, three types of blank control experiments were performed. (1) During the separation process, 3 medium plates were opened and placed on the ultra-clean table to see if any fungi could appear after the plate was cultured at 28 °C for 7 days. (2) The sterile water of the last rinsed tissue was coated on the PDA medium plate and cultured at 28 °C for 7 days. (3) The surface-sterilized plant tissue was pasted on the medium plate for 20 min, and then the sterilized plant material was removed and cultured at 28 °C for 7 days. After the cultivation of the above medium plate, if no colony grew out of the control plate, it indicates that the effectiveness of surface sterilization and the fungi isolated were not fungal epiphytes but fungal endophytes (Kong, 2019).

2.3 Morphological and Cultural Characterisation

The fungal isolates were identified based on a comprehensive morphological analysis, which included both macroscopic and microscopic features. The colony morphology and pigmentation of fungal cultures grown on medium were carefully documented. Fungal fruiting bodies from pure cultures were examined under a Nikon SMZ-1270 stereomicroscope (Nikon Corporation, Japan). Hyphal structures, conidia, and conidiophores were observed under a Nikon ECLIPSE Ni-U compound microscope equipped with a Nikon DS-Fi3 camera (Nikon Corporation, Tokyo, Japan). Measurements were taken using PhotoRuler Ver. 1.1 software (The Genus Inocybe, Hyogo, Japan), and the images were processed with Adobe Photoshop CS6 Extended version 10.0 (Adobe Systems, USA).

2.4 Molecular Identification and DNA Sequencing

Fresh mycelium scraped from the margin of colonies on medium plates was used for DNA extraction by using a cetyltrimethylammonium bromide (CTAB) method (Doyle & Doyle, 1987). For molecular identification of the fungi, the internal transcribed spacer (ITS) region was sequenced first for all isolates to determine potential genera and species. The BLAST tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi) was used to compare the resulting sequences with those in GenBank. To reveal the phylogenetic relationships and taxonomic distinction of species, different primers were selected for amplification according to the genetic markers recommended in the recent bibliography of each genus. The primer pairs and amplification conditions for each of the chosen gene regions in this study are provided in Table 2.3. The amplification reactions will be carried out according to the manufacturer's instructions: The PCR amplification reactions were carried out in a 25 μL reaction volume, including 12.5 μL 2×Taq PCR MasterMix (Qingke, Changsha, China), 1 μL each forward and reverse primer (0.2 μM), 1 μL template DNA (circa 50–100 ng) and 9.5 μL ddH$_2$O. Successful products were purified and sequenced by QingKe Biotechnology Co. (Changsha, China). All sequences were assembled with edited with SeqMan v. 7.1.0 (DNASTAR, Inc., Madison, WI) and deposited in GenBank (https://www.ncbi.nlm.nih.gov/).

Table 2.3 Loci used in this study with PCR primers and process

Locus	Primers	Sequence (5'-3')	PCR amplification on procedures	References
ITS	ITS1 ITS4	TCCGTAGGTGAACCTGCGG TCCTCCGCTTATTGATATGC	95 °C, 5 min; 35 cycles of 95 °C 30 s, 50 °C 30 s, 72 °C, 30 s; 72 °C 10min; 4°C on hold	(White et al., 1990)
LSU	LROR LR5	ACCCGCTGAACTTAAGC ATCCTGAGGGAAACTTC	95 °C, 5 min; 35 cycles of 95 °C 30 s, 50 °C 30 s; 72 °C 30 s; 72 °C 10min; 4°C on hold	(Vilgalys & Hester, 1990; Rehner & Samuels, 1994)
SSU	NS1 NS4	GTAGTCATATGCTTGTCTC CTTCCGTCAATTCCTTTAAG	95 °C, 5 min; 35 cycles of 95 °C 30 s, 50 °C 30 s, 72 °C 30 s, 72 °C 10min; 4°C on hold	(White et al., 1990)
CAL	CAL228F CAL737R	GAGTTCAAGGAGGCCTTCTCCC CATCTTTCTGGCCATCATGG	95 °C, 5 min; 35 cycles of 95 °C 15 s, 54 °C 20 s, 72 °C 1min; 72 °C 10min; 4°C on hold	(Carbone & Kohn, 1999)
HIS	CYLH3F H3-1b	AGGTCCACTGGTGGCAAG GCGGGCGAGCTGGATGTCCTT	95 °C, 5 min; 35 cycles of 95 °C 30 s, 57 °C 30 s, 72 °C 1min; 72 °C 10min; 4°C on hold	(Crous et al., 2004; Glass & Donaldson, 1995)
ACT	ACT-512F ACT-783R	ATGTGCAAGGCCGGTTTCGC TACGAGTCCTTCTGGCCCAT	95 °C, 5 min; 35 cycles of 95 °C 30 s, 55 °C 30 s, 72 °C 30s, 72 °C 10min; 4°C on hold	(Carbone & Kohn, 1999)

Table 2.3 (continued)

Locus	Primers	Sequence (5'-3')	PCR amplification on procedures	References
TEF1	EF1-728F	CATCGAGAAGTTCGAGAAGG	95 °C, 5 min; 35 cycles of 95 °C 30 s, 54 °C 20 s, 72 °C 1min; 72 °C 10min; 4℃ on hold	(Carbone & Kohn, 1999)
	EF1-986R	TACTTGAAGGAACCCTTACC		
	EF-1	ATGGGTAAGGARGACAAGAC	95◦C,3 min; 35 cycles of 95◦C 30 s, 52◦C 30 s, 72°C 1 min; 72°C 10 min; 4°C on hold	(O'Donnell et al., 1998)
	EF-2	GGARGTACCAGTSATCATG		
TUB2	T1	AACATGCGTGAGATTGTAAGT	95 °C, 5 min; 35 cycles of 95 °C 30 s, 55 °C 30 s; 72 °C 1min; 72 °C 10min; 4℃ on hold	(Glass & Donaldson, 1995；O'Donnell & Cigelnik, 1997)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC		
	T1	AACATGCGTGAGATTGTAAGT	95 °C, 5 min; 35 cycles of 95 °C 30 s, 55 °C, 30 s; 72 °C, 30s; 72 °C, 10min; 4℃ on hold	(O'Donnell & Cigelnik, 1997)
	T2	TAGTGACCCTTGGCCCAGTTG		
	T1	AACATGCGTGAGATTGTAAGT	95 °C, 5 min; 35 cycles of 95 °C 30 s, 55 °C, 30 s; 72 °C, 30s; 72 °C, 10min; 4℃ on hold	(O'Donnell & Cigelnik, 1997)
	T22	TCTGGATGTTGTTGGGAATCC		
	Bt2a	GGTAACCAAATCGGTGCTGCTTTC	95 °C, 5 min; 35 cycles of 95 °C 30 s, 60 ℃, 30 s, 72 °C, 30s; 72 °C, 10min; 4℃ on hold	(Glass & Donaldson, 1995)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC		
RPB1	Fa	CAYAARGARTCYATGATGGGWC	94°C, 90 s; 5 cycles of 94°C 45 s, 54°C 45 s, 72°C 2 min; 5 cycles of 94°C 45 s, 53°C 45 s, 72°C 2 min; 35 cycles of 94°C 45 s, 52℃ 45 s, 72 °C 2 min; 72°C 10 min; 4℃ on hold	(O'Donnell et al., 2010)
	R8	CAATGAGACCTTCTCGACCAGC		
	F8	TTCTTCCACGCCATGGCTGGTCG	94°C 90 s; 5 cycles of 94 °C 45 s, 56°C 45 s, 72°C 2 min; 5 cycles of 94°C 45 s, 55°C 45 s, 72°C 2 min; 35 cycles of 94°C 45 s, 54°C 45 s, 72°C 2 min; 72°C 10 min; 4℃ on hold	
	G2R	GTCATYTGDGTDGCDGGYTCDCC		
RPB2	fRPB2-5F	GATGATCGAGATCACTTCGG	94°C 2 min; 35 cycles of 94°C ,30s; 55–61°C, 30 s; 68 °C for 90-180s; 72◦C 10 min; 4℃ on hold	(Liu et al., 1999)
	fRPB2-7cR	CCCATAGCTTGTTTGCCCAT		
	ACT-783R	TACGAGTCCTTCTGGCCCAT		

2.5 Phylogenetic Analyses

All the sequence data generated in this study were subjected to BLAST searches in the nucleotide database of GenBank (https://blast.ncbi.nlm.nih.gov/) to determine their most probable closely related taxa. Sequence data were retrieved from GenBank based on highly similar taxa and recent publications. Newly sequences will be checked and assembled by using BioEdit v 7.2.5 (Hall, 1999). The FASTA files of the single genetic locus dataset were generated using OFPT (Zeng et al., 2023) and aligned with the online MAFFT version 7 service (https://mafft.cbrc.jp/alignment/software) under default settings (Katoh et al., 2019), and then manually adjusted using BioEdit version 7.2.5 to maximize alignment accuracy and minimize gaps. Gaps were treated as missing data. The combined sequence alignments were obtained from PhyloSuite v.1.2.2 (Zhang et al., 2020a).

Phylogenetic analysis of both individual and combined aligned data were based on Maximum Likelihood (ML) and Bayesian Inference analysis (BI). Maximum Likelihood (ML) analyses were performed on the concatenated datasets using IQ-TREE v1.6 (http://iqtree.cibiv.univie.ac.at/) with a partition strategy, and the best-fit substitution models for each partition were determined by IQ-TREE (Trifinopoulos et al., 2016). Clade support for the ML analyses was assessed using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1,000 replicates (Guindon et al., 2010) and 1,000 replicates of the ultrafast bootstrap (UFB) (Hoang et al., 2018). Nodes with support values of both SH-aLRT ≥ 80 and UFB ≥ 95 were considered supported, nodes with one of SH-aLRT ≥ 80 or UFB ≥ 95 were weakly supported, and nodes with both SH-aLRT < 80 and UFB < 95 were unsupported, and other parameters were used for the default settings (Brunke & Smetana, 2019; Yu et al., 2023).

The Bayesian Inference analysis (BI) was conducted in MrBayes 3.2.6 (Ronquist et al., 2012). The best evolution model for single genes was estimated by using Akaike information criterion (AIC) implemented in MrModeltest v. 2.3 (Nylander et al., 2004) via PAUP v. 4.0b10 (Swofford, 2002). Posterior probabilities (PP) were estimated via a Markov Chain Monte Carlo (MCMC) sampling approach (Zhaxybayeva & Gogarten, 2002). Two parallel runs, each consisting of four chains, were executed for 100 million generations with a stop value of 0.01, a temperature setting of 0.2, and sampling every 1,000 generations. A relative burn-in of 25.0% was applied for diagnostics. The trees resulting from ML and BI analyses were visualized using FigTree v.1.4.4 (Rambaut, 2018), and subsequently the layout was edited with the online service tvBOT (https://www.chiplot.online/tvbot.html) (Xie et al., 2023). Genetic distances of different genetic loci from species belonging to different genera were calculated using the Kimura 2-parameter (K2P) model in MEGA-X software (Kumar et al., 2018).

The genealogical concordance phylogenetic species recognition (GCPSR) approach was applied using the pairwise homoplasy index (PHI) test to evaluate species boundaries and detect potential recombination events (Quaedvlieg et al., 2014). The PHI test was performed in SplitsTree4 v4.17.1 to assess the degree of recombination among closely related taxa (Bruen et al., 2006; Huson & Bryant, 2006; Quaedvlieg et al., 2014). Multi-locus concatenated alignments of closely related species were analyzed. A PHI test result with $\Phi w < 0.05$ was considered indicative of significant recombination within the dataset. Relationships among related taxa were further visualized by constructing split graphs based on concatenated datasets using the LogDet transformation and splits decomposition methods, and the resulting graphs were edited in Microsoft PowerPoint 2021.

2.6 Preliminary Analysis of Endophytic Fungal Communities

To comprehensively assess the composition and diversity of cultivable endophytic fungi associated with *Tetradium ruticarpum*, a total of 935 fungal strains were analyzed. These isolates were obtained from four types of plant tissues, namely roots, stems, leaves, and fruits, collected across 23 sampling sites distributed in four provinces. Fungal isolation was conducted using six different culture media, including potato dextrose agar (PDA), malt extract agar (MEA), yeast-starch agar (YpSs), rose-bengal chloramphenicol agar (RBA), potato carrot agar (PCA), and oatmeal agar (OA), in order to capture a wide range of fungal diversity.

The relative isolation frequency (RF) was used to quantify the abundance of cultivable endophytic fungi from *Tetradium ruticarpum* (Du et al., 2020; Sun et al., 2008). After surface sterilization and isolation, each distinct colony morphotype was purified as a single isolate and identified by ITS sequencing. For each taxon i, RF was calculated as:

$$(\text{RF}, \%) = \frac{N_i}{N} \times 100\%$$

where N is the total number of isolates and Ni is the number of isolates belonging to taxon i. RF was the ratio of the number of isolates of a certain genus or taxon to the total number of isolates and was expressed as a percentage.

Genera with a relative frequency of isolation greater than 10% in the samples were considered dominant. Common genera had relative frequencies ranging from 5% to 10%, while those with frequencies below 5% were classified as rare (Luo, 2022).

Venn diagrams (https://www.interactivenn.net/index2.html) were used to visualize overlapping genera between tissues, media, and locations. The preliminary analysis was performed using Microsoft Excel (version 2021), focusing on descriptive comparisons rather than statistical inference due to unbalanced sampling.

Data reflecting the diversity of cultivable endophytic fungi from *Tetradium ruticarpum* were visualized as a Sankey diagram using the free online tool SankeyMATIC (Steve Bogart; available at www.sankeymatic.com) to intuitively illustrate the taxonomic composition and genus-level abundance distribution.

2.7 Pre-screening of Antimicrobial Activity of the Endophytic Fungi Associated with *Tetradium ruticarpum*

2.7.1 Test Microorganisms

Previous studies have reported that the secondary metabolites (e.g., berberine and evodiamine) from *Tetradium ruticarpum* demonstrate significant antimicrobial activity against various pathogens (Table 1.1). As microbial symbionts often evolve to produce complementary defensive metabolites within medicinal plants (D'Souza et al., 2023), we hypothesized that its endophytic fungi might share this antimicrobial capacity. To evaluate the antimicrobial potential of the endophytic fungi of *T.*

ruticarpum, we selected five pathogens historically susceptible to *T. ruticarpum* extracts (Table 2.4): two fungal pathogens (*Aspergillus niger* ATCC 16404 and *Candida albicans* ATCC 10231) and three bacterial pathogens (*Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, *Xanthomonas campestris* NCPPB 571). These pathogens were maintained at Nutrient Agar slants and stored at 4°C.

Table 2.4 Pathogenic microorganisms used in this study

Pathogen	**New Code**	**Strain Name**	**Strain Number**	**Effects of Pathogens**	**Source**	**References**
Pathogenic bacteria	PE	*Escherichia coli*	ATCC 25922	Gram-negative bacillus; causes UTIs, traveller's diarrhea, dysentery, HUS, pneumonia, meningitis, and wound infections.	College of Food Science and Engineering, Jiangxi Agricultural University	(Kaper et al., 2004; Levine et al., 1977)
	PX	*Xanthomonas campestris*	NCPPB 57	Gram-negative pathogen, causes black rot	Shanghai Microbiological Culture Collection Co., Ltd.	(Vicente & Holub, 2013)
	PS	*Staphylococcus aureus*	ATCC 259213	Major gram-positive pathogen; responsible for a wide range of human infections.	College of Food Science and Engineering, Jiangxi Agricultural University	(Tong et al., 2015)
Pathogenic fungi	PA	*Aspergillus niger*	ATCC 16404	Opportunistic filamentous fungus; commonly associated with food spoilage and human infections.	College of Food Science and Engineering, Jiangxi Agricultural University	(Gautam et al., 2011; Sharma, 2012)
	PC	*Candida albicans*	ATCC 10231	The most common human fungal pathogen; causes mucosal and systemic infections.	Shanghai Microbiological Culture Collection Co., Ltd.	(Tsui et al., 2016)

2.7.2 Screening Antagonistic Endophytes by Agar Plug Diffusion Assay (Pretest)

A total of 935 endophytic fungal isolates from *Tetradium ruticarpum* were activated on PDA medium, with 635 strains successfully revived for preliminary screening. These strains were cultivated at 25°C for 7 days, and mycelial colonies were cut into 6mm agar plugs using a sterile plastic straw under laminar airflow. To enhance screening efficiency, each Petri dish contained agar plugs from five different fungal strains, evenly spaced on the agar surface to avoid overlapping inhibition zones. Two independent replicate plates were prepared for each set of five strains (i.e., each strain was tested in two separate plates).

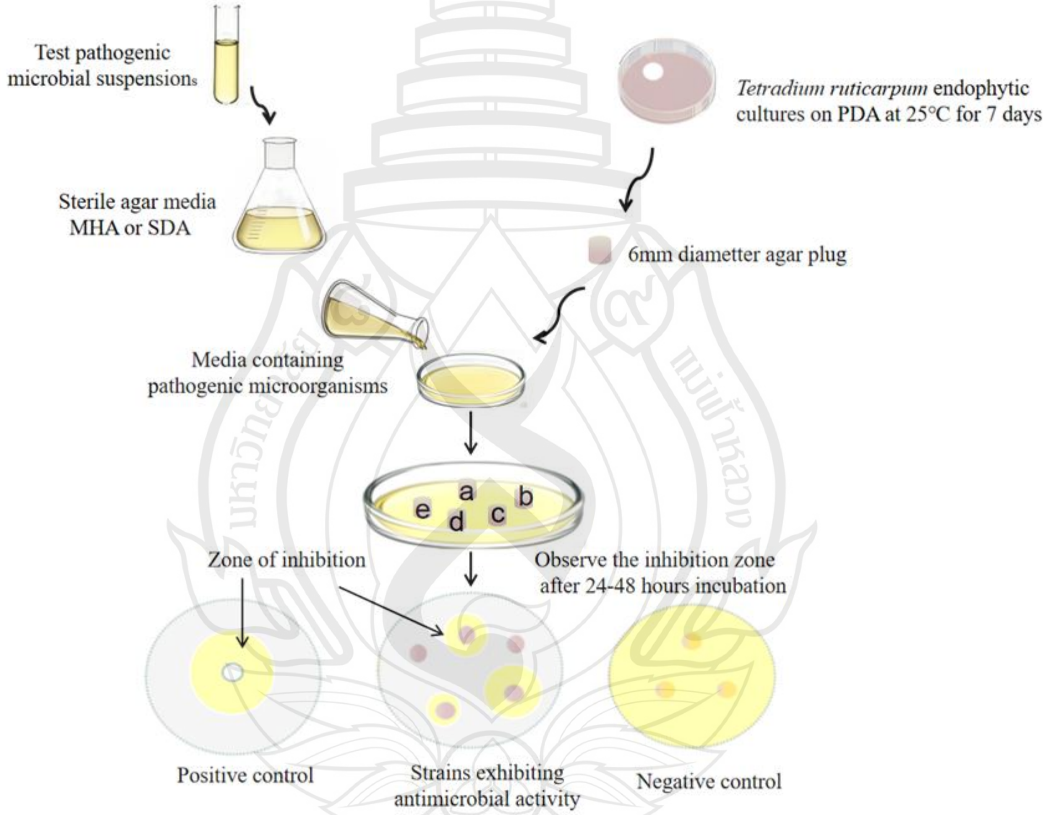


Figure 2.3 Pre agar plug diffusion assay steps

Test pathogens (*Staphylococcus aureus*, *Escherichia coli*, *Xanthomonas campestris*, *Candida albicans*, and *Aspergillus niger*) were suspended at standardized densities (6.7×10^5 cells/mL for bacteria; 5×10^4 spores/mL for fungi) and mixed with Mueller–Hinton Agar (MHA) or Sabouraud Dextrose Agar (SDA) at 45°C before solidification (Mapook et al., 2009; Zhang et al., 2009). Agar plugs from fungal isolates were transferred to pathogen-containing plates. Penicillin (10 μg) served as the positive control for *S. aureus*, while ciprofloxacin (5 μg) was used for validating antibacterial activity against *E. coli* and *X. campestris*. Nystatin (10 μg) was applied as the antifungal control for *C. albicans* and *A. niger*. Sterile PDA plugs without fungal hyphae were included as the negative control. The agar plugs approximately 6 mm in diameter from the isolates were transferred to solid medium plates containing target pathogenic microorganisms. The plates were then refrigerated at 4°C overnight to allow complete diffusion of the antibiotics, followed by incubation at 30°C for 24-48 hours (Zhang et al., 2009). After incubation, the presence of an inhibition zone around the agar plug indicates that the strain exhibits antagonistic activity and has a certain inhibitory effect on the pathogen. Such strains will be selected for further formal test. The steps used are given in Figure 2.3.

2.7.3 Screening Antagonistic Endophytes by Agar Plug Diffusion Assay (Formal Test)

According to the results of the pretest, endophytic fungal strains demonstrating inhibitory activity against at least one of the five pathogens (*Staphylococcus aureus*, *Escherichia coli*, *Xanthomonas campestris*, *Candida albicans*, and *Aspergillus niger*) were selected for formal validation. The method of formal agar plug diffusion assay is similar to the pretest, just with some modifications (Figure 2.4). The endophytic fungi with certain antimicrobial properties were reactivated on PDA medium at 25°C for 7 days. Then the fungal colonies were cut into 6-mm diameter agar plugs under sterile laminar airflow, ensuring the mycelium side of each plug was fully in contact with the pathogen-containing agar surface. Three plugs from the same strain were arranged in a triangular pattern on each plate. Bacterial pathogens (*S. aureus*, *E. coli*, and *X. campestris*) were incorporated into MHA, while fungal pathogens (*C. albicans* and *A. niger*) were embedded in SDA. Following overnight refrigeration at 4°C to facilitate metabolite diffusion, plates were incubated at 30°C for 24–48 hours. After incubation, inhibition (ZOI) was measured using a ruler and compared against positive controls (ciprofloxacin, penicillin, or nystatin).

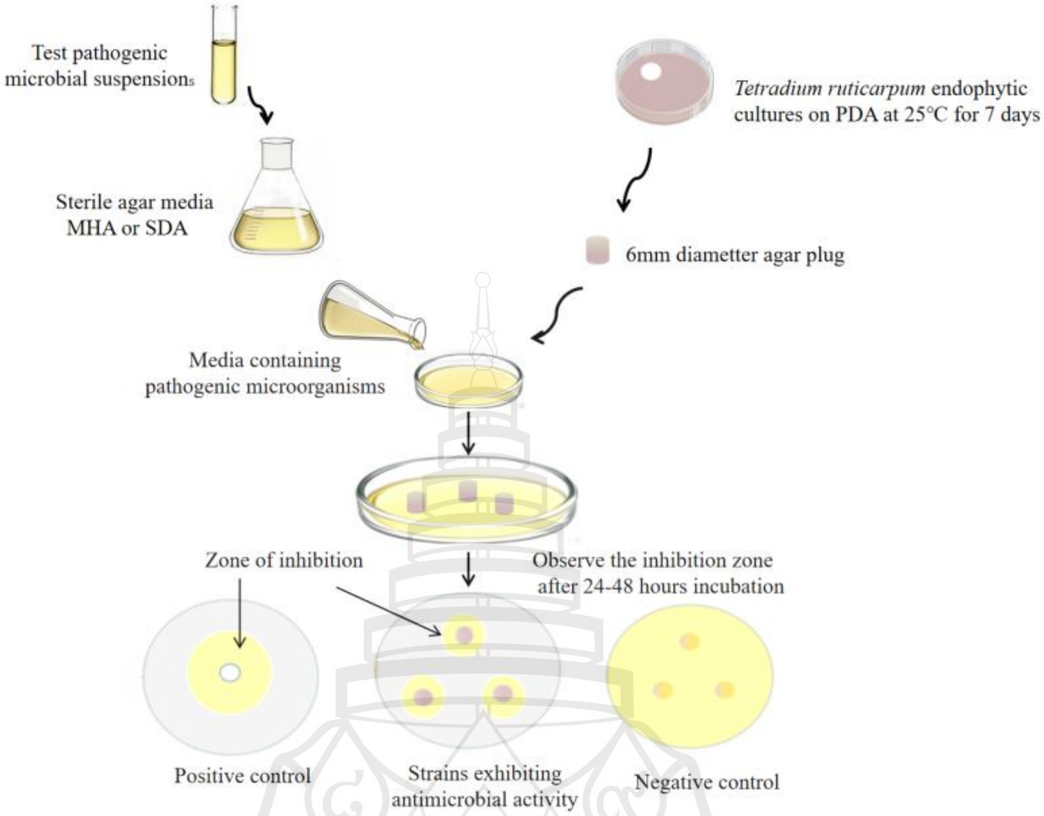


Figure 2.4 Formal agar plug diffusion assay steps

2.7.4 Calculation and Statistical Analyses

Agar plug assays were used to evaluate the antimicrobial activity of the endophytic fungal isolates, and the diameter of each zone of inhibition (ZOI) around each agar plug was measured in millimeters (mm) using a ruler. All assays were performed in triplicate (n = 3), and ZOI values were recorded in Microsoft Excel 2021. Descriptive statistics (mean and standard deviation) were calculated in Excel, and results are reported as mean ± SD (n = 3). The inhibitory performance of each fungal isolate was compared to that of a standard antibiotic disc used as a positive control, and all statistical summaries and bar-graph visualizations of the ZOI data were generated using Microsoft Excel 2021.

CHAPTER 3

RESULTS

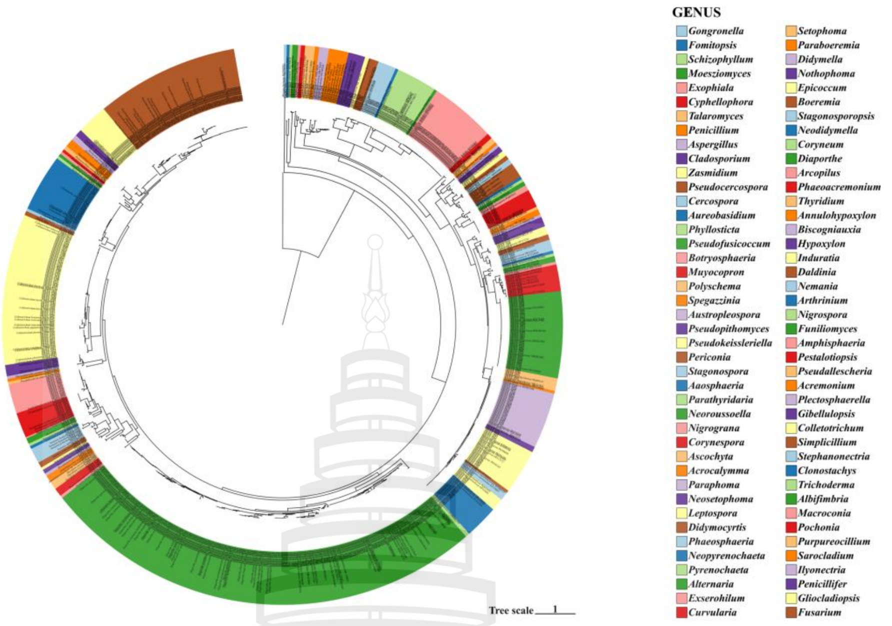
3.1 Diversity of Culturable Endophytic Fungi in *Tetradium ruticarpum*

In this study, a total of 935 cultivable endophytic fungal strains were successfully isolated from different tissues of *Tetradium ruticarpum* (roots, stems, leaves, and fruits) collected at 23 representative sampling sites across four major production provinces in China: Anhui, Guangxi, Hunan, and Jiangxi. All isolates were subjected to molecular identification by sequencing the internal transcribed spacer (ITS) region, followed by BLAST searches against the NCBI GenBank database to obtain their closest taxonomic affiliations. To further confirm the reliability of identification, representative ITS sequences were selected for phylogenetic analysis. The resulting phylogenetic tree clearly revealed clustering of isolates into distinct clades corresponding to established fungal taxonomic groups (Figure 3.1). Interestingly, several isolates formed well-supported, divergent clades separated from known reference taxa, suggesting the presence of potentially novel lineages of endophytic fungi in *T. ruticarpum*.

A total of 935 endophytic fungal isolates obtained from *Tetradium ruticarpum* were taxonomically assigned to three phyla, six classes, 21 orders, 54 families, and 84 genera. The hierarchical connections among these taxa are depicted in a Sankey diagram (Figure 3.2), revealing the broad taxonomic diversity and compositional structure of the endophytic fungal assemblage. At the phylum level (Figure 3.3A), Ascomycota was the dominant phylum, accounting for 99.5% (930 isolates), while Basidiomycota and Mucoromycota accounted for 0.4% (four isolates) and 0.1% (one isolate), respectively. At the class level (Figure 3.3B), three classes within Ascomycota (Sordariomycetes, 61.9%; Dothideomycetes, 35.4%; and Eurotiomycetes, 2.1%) dominated the assemblage. Minor representation was observed for Agaricomycetes and Ustilaginomycetes (Basidiomycota) and Mucoromycetes (Mucoromycota), each comprising less than 0.2% of the total isolates. At the order level (Figure 3.3C), the 935 *T. ruticarpum* endophytic fungal isolates displayed a skewed distribution, with the top 10 most abundant orders as follows: Diaporthales (253 isolates, 27.1%), Pleosporales (236 isolates, 25.2%), Hypocreales (159 isolates, 17.0%), Glomerellales (94 isolates, 10.1%), Botryosphaeriales (67 isolates, 7.2%), Amphisphaeriales (39 isolates, 4.2%), Eurotiales (17 isolates, 1.8%), Mycosphaerellales (17 isolates, 1.8%), Xylariales (17 isolates, 1.8%), and Thyridiales (10 isolates, 1.1%). The remaining orders were rare, each containing fewer than 10 isolates, including Cladosporiales, Togniniales, Chaetothyriales, Muyocopronales, Ustilaginales, Agaricales, Dothideales, Microascales, Mucorales, Polyporales and Sordariales. At the family level (Figure 3.3D), the top five dominant families are Diaporthaceae (251 isolates, 26.8%), Nectriaceae (111 isolates, 11.9%), Didymellaceae (99 isolates, 10.6%), Glomerellaceae (93 isolates, 9.9%), and Pleosporaceae (70 isolates, 7.5%), which account for over 65% (66.7% total) of isolates. Additionally, 15 families (e.g., Chaetomiaceae, Clavicipitaceae) have only one isolate each (0.1% each). The remaining families each contain 2–8 isolates, with their individual proportions ranging from 0.2% to 0.9%. The specific information of the isolated strains is shown in Table 3.1.

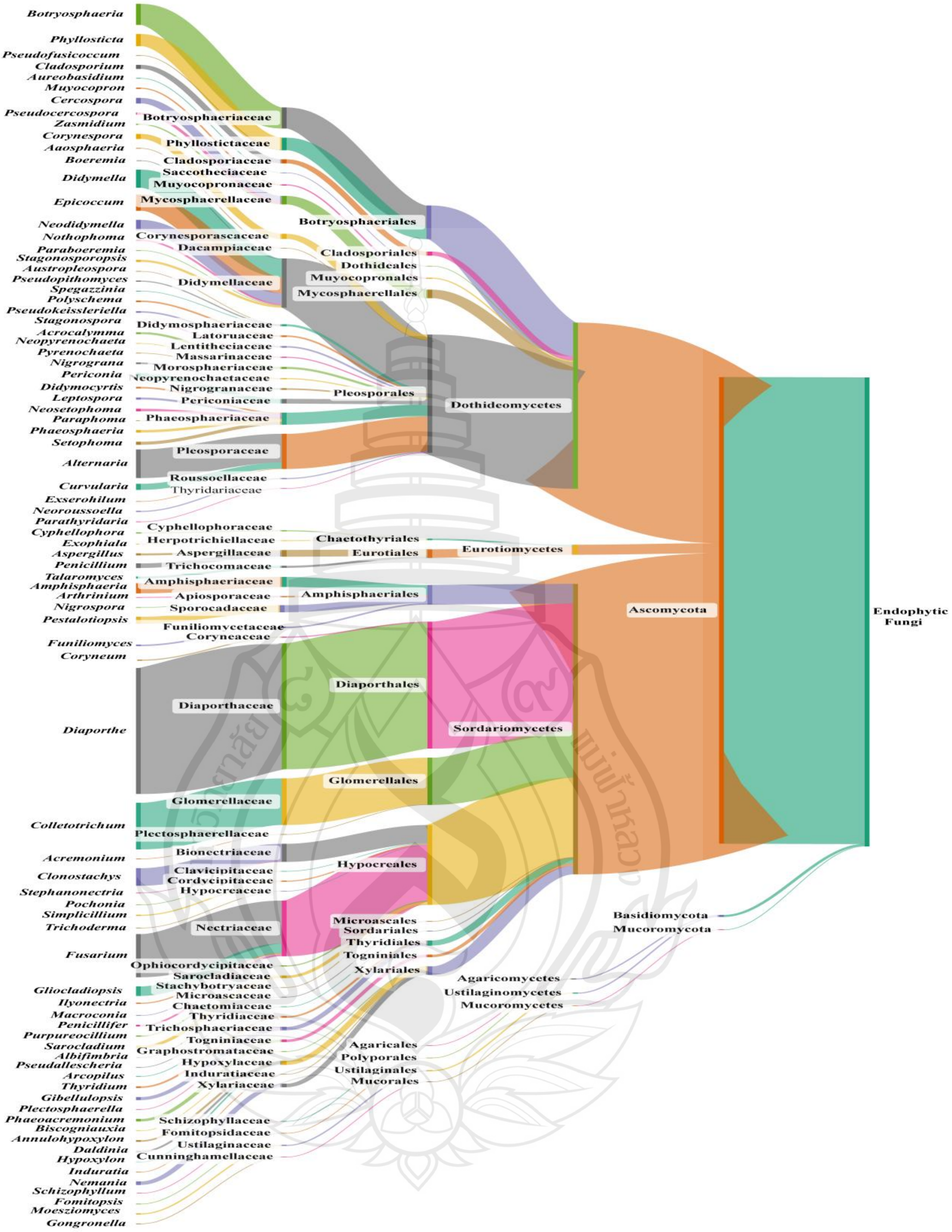
At the genus level, the distribution of endophytic fungi isolated from *Tetradium ruticarpum* (a total of 935 isolates, representing 84 genera) exhibited a highly uneven pattern (Figure 3.4, Table 3.2). Genera with a relative frequency of isolation greater than 10% in the samples were considered dominant. Common genera had relative frequencies ranging from 5% to 10%, while those with frequencies below 5% were classified as rare. Genera were categorized based on their relative frequency (RF). According to the relative frequency (RF%) values, the genus *Diaporthe* (251 isolates) was the only dominant genus, accounting for the largest proportion of 26.8%. Three genera, namely *Colletotrichum* (93 isolates, 9.9%), *Fusarium* (86 isolates, 9.2%) and *Alternaria* (57 isolates, 6.1%), were categorized as Common. These three genera accounted for 236 isolates (25.2%) and, together with *Diaporthe*, comprised over 52% of the total isolates, representing the core of the community. The majority of genera have relatively low isolate numbers, falling under the “Rare” category. These included *Botryosphaeria* (42 isolates, 4.5%), *Didymella* (36 isolates, 3.9%), *Clonostachys* (35 isolates, 3.7%), *Epicoccum* (32 isolates, 3.4%), *Phyllosticta* (24 isolates, 2.6%), *Neodidymella* (21 isolates, 2.2%), *Amphisphaeria* (20 isolates, 2.1%), *Gliocladiopsis*

(19 isolates, 2.0%), *Pestalotiopsis* (14 isolates, 1.5%), *Curvularia* (12 isolates, 1.3%), *Cercospora* (11 isolates, 1.2%), *Corynespora* (10 isolates, 1.1%), *Penicillium* (nine isolates, 1.0%), *Periconia* (nine isolates, 1.0%). Genera represented by eight or fewer isolates (RF < 1%) included *Cladosporium* (eight isolates, 0.9%), *Nemania* (seven isolates, 0.7%), *Gibellulopsis* and *Setophoma* (six isolates each, 0.6%), *Neosetophoma*, *Phaeoacremonium*, *Phaeosphaeria*, and *Sarocladium* (five isolates each, 0.5%), *Aspergillus*, *Leptospora*, *Pseudocercospora*, *Stagonosporopsis*, and *Talaromyces* (four isolates each, 0.4%), as well as *Acrocalymma*, *Annulohypoxylon*, *Funiliomyces*, *Daldinia*, *Didymocyrtis*, *Nigrograna*, *Nothophoma*, *Penicillifer*, *Polyschema*, *Pseudokeissleriella*, and *Thyridium* (three isolates each, 0.3%). In addition, 12 genera, including *Coryneum*, *Cyphellophora*, *Hypoxylon*, *Ilyonectria*, *Moesziomyces*, *Muyocopron*, *Neoroussoella*, *Pseudopithomyces*, *Purpureocillium*, *Simplicillium*, *Stagonospora*, and *Zasmidium,* were represented by two isolates each (0.2%). Furthermore, 30 genera such as *Aaosphaeria*, *Acremonium*, *Albifimbria*, *Arcopilus*, *Arthrinium*, *Ascochyta*, *Aureobasidium*, *Austropleospora*, *Biscogniauxia*, *Boeremia*, *Exophiala*, *Exserohilum*, *Fomitopsis*, *Gongronella*, *Induratia*, *Macroconia*, *Neopyrenochaeta*, *Nigrospora*, *Paraboeremia*, *Paraphoma*, *Parathyridaria*, *Plectosphaerella*, *Pochonia*, *Pseudallescheria*, *Pseudofusicoccum*, *Pyrenochaeta*, *Schizophyllum*, *Spegazzinia*, *Stephanonectria*, and *Trichoderma* were represented by a single isolate each (0.1%).



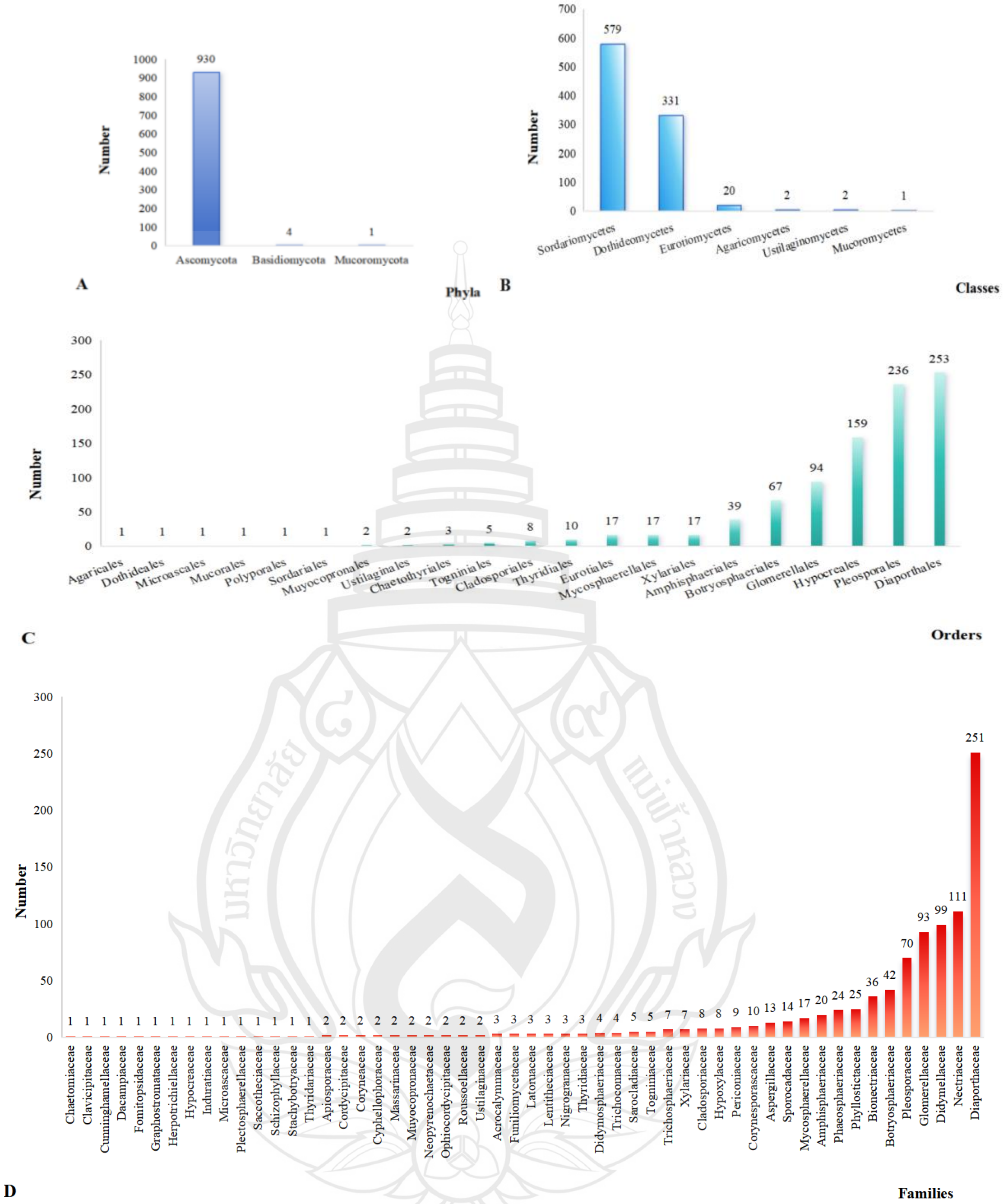
Note Circular phylogenetic tree constructed using the maximum likelihood method based on concatenated ITS datasets, including 935 sequences of endophytic fungi from *Tetradium ruticarpum* and their 269 closest sequences from GenBank. *Rhizopus koreanus* EML-HO95-1 (KU058202) (Mucoromycota) was used as the outgroup for the phylogenetic analysis. Maximum-likelihood phylogenies were inferred using IQ-TREE under the Edge-linked partition model (GTR+F+I+G4 for the ITS locus) with 10,000 ultrafast bootstraps. The maximumlikelihood matrix had 911 distinct alignment patterns with 56.4 % undetermined characters or gaps. The alignment of 1205 sequences resulted in 1135 columns, 764 parsimony-informative characters, 63 singleton sites, and 308 constant characters. The current best maximum likelihood tree had a final likelihood value of -35518.834. Different colours indicate independent genera, with a total of 84 genera.

Figure 3.1 Phylogenetic relationships derived from maximum likelihood analyses of concatenated ITS datasets



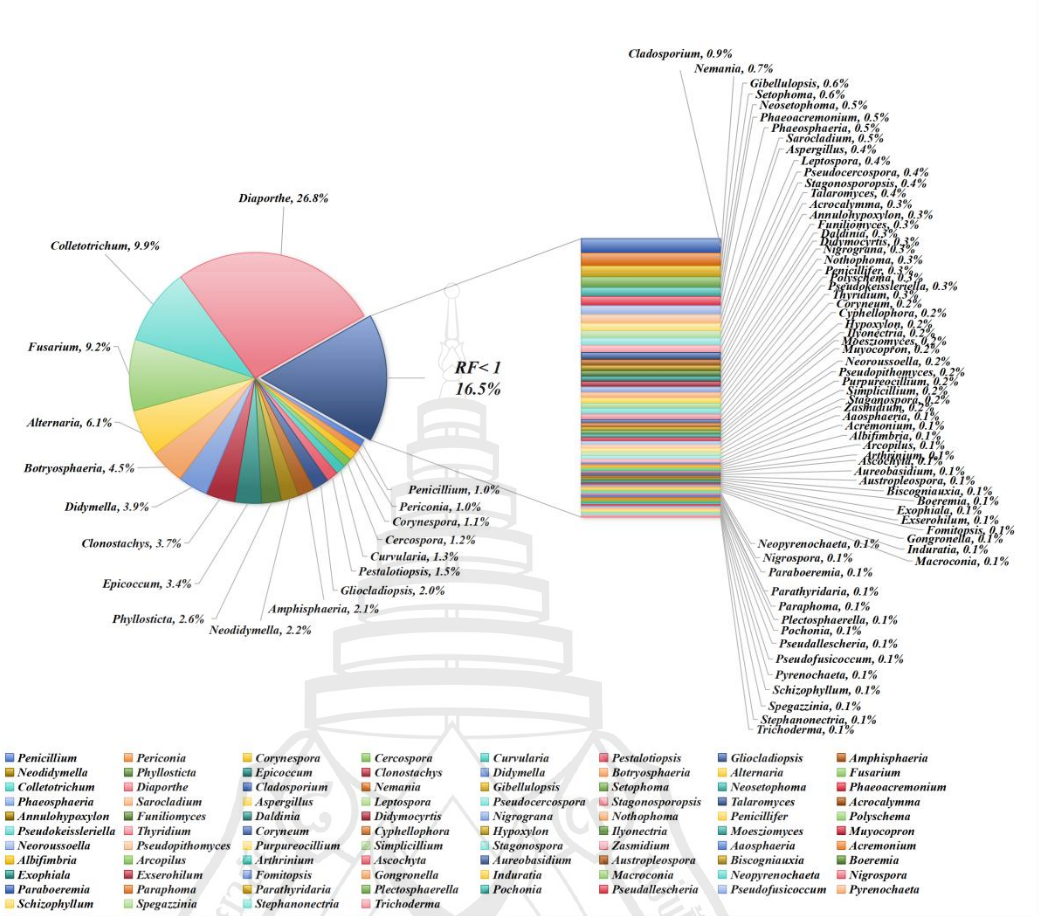
Note Sankey diagram illustrating the taxonomic composition of endophytic fungi associated with *Tetradium ruticarpum*, encompassing three phyla, six classes, 21 orders, 54 families and 84 genera. The width of each flow represents the number of taxa at the lower taxonomic level.

Figure 3.2 Diversity of culturable endophytic fungi isolated from *Tetradium ruticarpum*



Note Distribution of 935 *Tetradium ruticarpum* endophytic fungal isolates at the phylum (A), class (B), order (C), and family (D) levels. The bar charts represent the number of isolates.

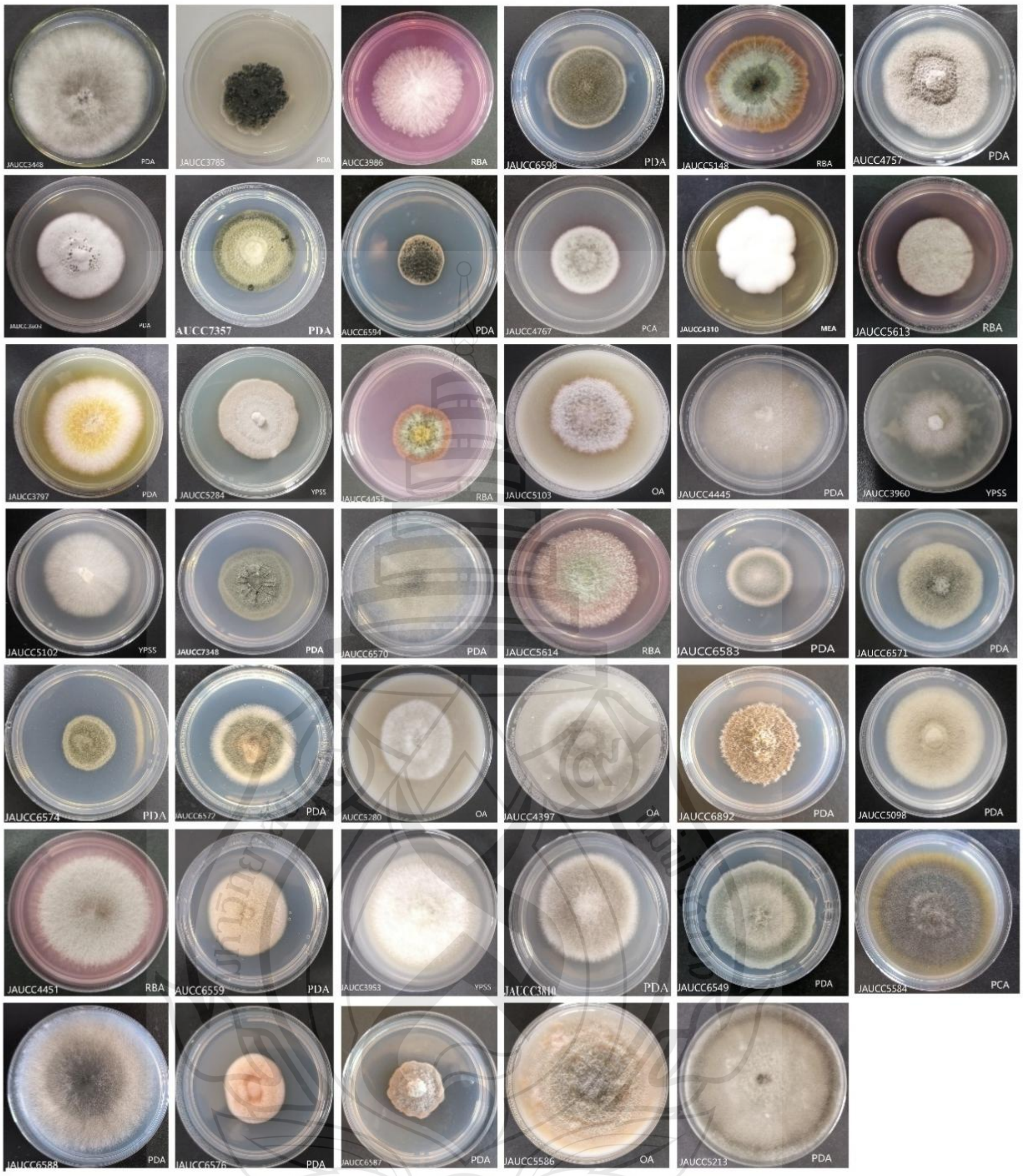
Figure 3.3 Number of isolates at different taxonomic levels



Note Pie–bar combination chart illustrating the genus-level distribution of the 935 endophytic fungal isolates obtained from *Tetradium ruticarpum*.

Figure 3.4 Genus-level percentage contribution of the 84 genera

We conducted morphological observations of the 935 isolates from *Tetradium ruticarpum* and captured colony photographs for all strains. Figures 3.5–3.7 present representative front-view colony images of genera across six fungal classes, including 41 genera in Dothideomycetes, 34 genera in Sordariomycetes, five genera in Eurotiomycetes, one genus in Ustilaginomycetes, two genera in Agaricomycetes, and one genus in Mucoromycetes.

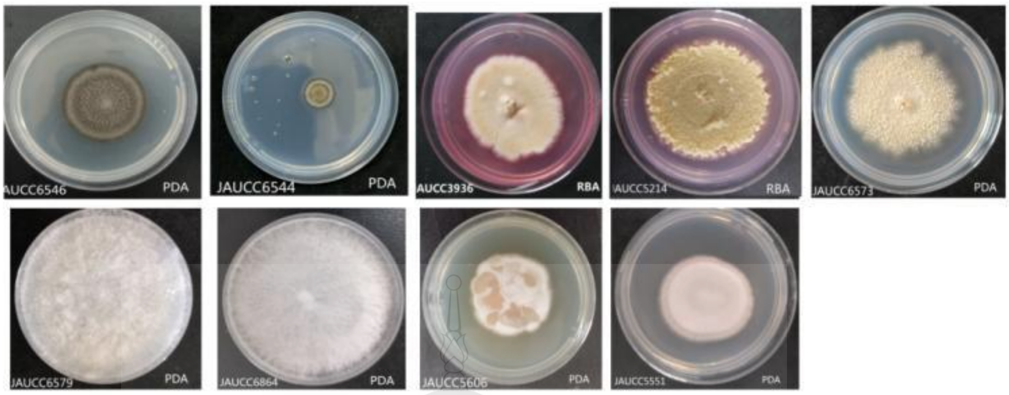


Note Colony morphology of 41 genera in Dothideomycetes in different media. Strain numbers are indicated at the lower left of each colony image, while the culture medium type is at the lower right.

Figure 3.5 Colony morphology of representative genera in Dothideomycetes

Note Colony morphology of 34 genera in Sordariomycetes in different media. Strain numbers are indicated at the lower left of each colony image, while the culture medium type is at the lower right.

Figure 3.6 Colony morphology of representative genera in Sordariomycetes



Note Colony morphology of nine genera in Eurotiomycetes, Ustilaginomycetes, Agaricomycetes, and Mucoromycetes in different media. Strain numbers are indicated at the lower left of each colony image, while the culture medium type is at the lower right.

Figure 3.7 Colony morphology of representative genera in Eurotiomycetes, Ustilaginomycetes, Agaricomycetes, and Mucoromycetes

Table 3.1 Culturable endophytic fungi in *Tetradium ruticarpum* based on ITS sequence

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3443	PV578841	*Epicoccum thailandicum*		*Epicoccum* sp. 2	leaf	PDA	JXJAYX
JAUCC 3445	PV578842	*Diaporthe sojae*	PQ499369	*Diaporthe* sp. 5	leaf	PDA	JXJAYX
JAUCC 3446	PV578843	*Alternaria alternata*	MW580740	*Alternaria* sp. 1	leaf	PDA	JXJAYX
JAUCC 3447	PV578844	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXJAYX
JAUCC 3448	PV578845	*Botryosphaeria dothidea*	KF293865	*Botryosphaeria* sp. 1	leaf	PDA	JXJAYX
JAUCC 3449	PV578846	*Diaporthe phaseolorum*	OQ555455	*Diaporthe* sp. 40	leaf	PDA	JXJAYX
JAUCC 3450	PV578847	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXJAYX
JAUCC 3451	PV578848	*Clonostachys rosea*	MT945217	*Clonostachys* sp. 3	root	PCA	JXZSYC
JAUCC 3452	PV578849	*Alternaria alternata*	MH881064	*Alternaria* sp. 1	leaf	PCA	JXZSYC
JAUCC 3453	PV578850	*Diaporthe penetriteum*	OQ703348	*Diaporthe* sp. 10	stem	PCA	JXYCTG
JAUCC 3454	PV578851	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PDA	JXZSYC
JAUCC 3455	PV578852	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	HNCZWX
JAUCC 3456	PV578853	*Didymella glomerata*	PQ219349	*Didymella* sp. 1	leaf	PCA	JXZSYC
JAUCC 3457	PV578854	*Arcopilus flavigenus*	MN562032	*Arcopilus* sp. 1	root	PDA	JXJAYX
JAUCC 3458	PV578855	*Trichoderma spirale*	PV400361	*Trichoderma* sp. 1	root	PDA	JXJAYX
JAUCC 3459	PV578856	*Clonostachys rosea*		*Clonostachys* sp. 3	root	OA	JXYCTX
JAUCC 3460	PV578857	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PCA	JXYCLS
JAUCC 3461	PV578858	*Didymella glomerata*	MG832523	*Didymella* sp. 1	leaf	PCA	JXZSYC
JAUCC 3462	PV578859	*Alternaria alternata*	KP172289	*Alternaria* sp. 1	leaf	MEA	JXZSYC
JAUCC 3783	PV578860	*Colletotrichum kahawae*	PP594911	*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3784	PV578861	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	MEA	JXZSLJ
JAUCC 3785	PV578862	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3786	PV578863	*Clonostachys rosea*		*Clonostachys* sp. 3	leaf	RBA	JXJJRC
JAUCC 3787	PV578864	*Amphisphaeria mangrovei*	MG844283	*Amphisphaeria* sp. 1	root	RBA	JXJJRC
JAUCC 3788	PV578865	*Diaporthe amygdali*	KF453978	*Diaporthe* sp. 40	leaf	PCA	JXJJRC
JAUCC 3789	PV578866	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	leaf	PDA	JXZSLJ
JAUCC 3790	PV578867	*Colletotrichum kahawae*	JN222974	*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ
JAUCC 3791	PV578868	*Colletotrichum kahawae*	MK569272	*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ
JAUCC 3792	PV578869	*Diaporthe sojae*	ON035597	*Diaporthe* sp. 5	leaf	PDA	JXZSLJ
JAUCC 3793	PV578870	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	MEA	JXJJRC
JAUCC 3794	PV578871	*Epicoccum thailandicum*		*Epicoccum* sp. 2	leaf	PDA	JXZSLJ
JAUCC 3795	PV578872	*Phyllosticta machili*	OQ996254	*Phyllosticta* sp. 2	leaf	PDA	JXZSLJ
JAUCC 3796	PV578873	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	MEA	JXJJRC
JAUCC 3797	PV578874	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PCA	JXJJRC
JAUCC 3798	PV578875	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXZSYC
JAUCC 3799	PV578876	*Fusarium proliferatum*		*Fusarium* sp. 12	root	PDA	JXYCTG
JAUCC 3800	PV578877	*Neodidymella thailandicum*	NR_156400	*Neodidymella* sp. 1	root	RBA	JXZSYC
JAUCC 3801	PV578878	*Colletotrichum boninense*		*Colletotrichum* sp. 5	leaf	RBA	HNCZWX
JAUCC 3802	PV578879	*Diaporthe amygdali*		*Diaporthe* sp. 40	leaf	PCA	JXJJRC
JAUCC 3803	PV578880	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3804	PV578881	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	leaf	PDA	JXZSLJ
JAUCC 3805	PV578882	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3806	PV578883	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3807	PV578884	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3808	PV578885	*Alternaria alternata*	PQ415966	*Alternaria* sp. 1	leaf	RBA	JXZSYC
JAUCC 3809	PV578886	*Alternaria alternata*	ON350803	*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3810	PV578887	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3811	PV578888	*Cladosporium cladosporioides*		*Cladosporium* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3812	PV578889	*Diaporthe nobilis*	KJ609010	*Diaporthe* sp. 17	leaf	PDA	JXJJRC
JAUCC 3813	PV578890	*Epicoccum nigrum*	KP900241	*Epicoccum* sp. 1	leaf	MEA	HNCZWX
JAUCC 3814	PV578891	*Diaporthe eres*	OM536179	*Diaporthe* sp. 18	leaf	PCA	JXJJRC
JAUCC 3815	PV578892	*Diaporthe amygdali*		*Diaporthe* sp. 40	leaf	PCA	JXJJRC
JAUCC 3816	PV578893	*Diaporthe caryae*	MW784828	*Diaporthe* sp. 48	stem	PCA	JXJJRC
JAUCC 3817	PV578894	*Diaporthe hongkongensis*	MW202974	*Diaporthe* sp. 37	stem	PCA	JXJJRC
JAUCC 3818	PV578895	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ
JAUCC 3819	PV578896	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	RBA	JXJJRC
JAUCC 3820	PV578897	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PCA	JXJJRC
JAUCC 3821	PV578898	*Diaporthe pseudooculi*		*Diaporthe* sp. 13	leaf	PDA	JXZSLJ
JAUCC 3822	PV578899	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ
JAUCC 3823	PV578900	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3824	PV578901	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	RBA	JXYCTG
JAUCC 3825	PV578902	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSLJ
JAUCC 3827	PV578903	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PCA	JXJJRC
JAUCC 3828	PV578904	*Diaporthe pseudooculi*		*Diaporthe* sp. 13	stem	PDA	JXZSLJ
JAUCC 3829	PV578905	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	OA	JXYCLS
JAUCC 3830	PV578906	*Diaporthe hubeiensis*		*Diaporthe* sp. 7	stem	PCA	JXJJRC
JAUCC 3831	PV578907	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	stem	PDA	JXZSLJ
JAUCC 3832	PV578908	*Botryosphaeria dothidea*	KF293862	*Botryosphaeria sp.*1	stem	PDA	JXZSLJ
JAUCC 3833	PV578909	*Diaporthe sojae*		*Diaporthe* sp. 5	stem	PCA	JXJJRC
JAUCC 3834	PV578910	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	stem	PDA	JXZSLJ
JAUCC 3835	PV578911	*Diaporthe caryae*	MK626954	*Diaporthe* sp. 48	stem	PCA	JXJJRC
JAUCC 3836	PV578912	*Diaporthe discoidispora*	MN816410	*Diaporthe* sp. 14	stem	PCA	JXJJRC
JAUCC 3837	PV578913	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	stem	PDA	JXZSLJ
JAUCC 3838	PV578914	*Diaporthe sojae*		*Diaporthe* sp. 5	stem	PCA	JXJJRC
JAUCC 3839	PV578915	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	stem	RBA	JXJJRC
JAUCC 3840	PV578916	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	OA	JXYTWF
JAUCC 3841	PV578917	*Fusarium falciforme*	MN252111	*Fusarium* sp. 3	stem	PCA	JXZSLJ
JAUCC 3842	PV578918	*Diaporthe longicolla*	MG686131	*Diaporthe* sp. 21	stem	PCA	JXZSLJ
JAUCC 3843	PV578919	*Fusarium falciforme*		*Fusarium* sp. 3	stem	PCA	JXZSLJ
JAUCC 3844	PV578920	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3845	PV578921	*Diaporthe pseudophoenicicola*	OP591389	*Diaporthe* sp. 30	stem	PDA	JXZSLJ
JAUCC 3846	PV578922	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PDA	JXZSLJ
JAUCC 3847	PV578923	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	MEA	JXYTWF
JAUCC 3848	PV578924	*Diaporthe hubeiensis*	MW578679	*Diaporthe* sp. 7	stem	PCA	JXJJRC
JAUCC 3849	PV578925	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	stem	OA	JXZSLJ
JAUCC 3850	PV578926	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	YpSs	JXZSLJ
JAUCC 3851	PV578927	*Diaporthe caryae*		*Diaporthe* sp. 45	stem	PCA	JXJJRC
JAUCC 3852	PV578928	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	stem	PCA	JXJJRC
JAUCC 3853	PV578929	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	YpSs	JXZSLJ
JAUCC 3854	PV578930	*Botryosphaeria dothidea*	OP926952	*Botryosphaeria* sp.1	stem	YpSs	JXZSLJ
JAUCC 3855	PV578931	*Diaporthe perseae*	OQ271286	*Diaporthe* sp. 31	stem	YpSs	JXZSLJ
JAUCC 3856	PV578932	*Didymella glomerata*		*Didymella* sp. 1	stem	YpSs	JXZSLJ
JAUCC 3857	PV578933	*Clonostachys rosea*	PP216444	*Clonostachys* sp. 3	stem	PCA	JXYTWF
JAUCC 3858	PV578934	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	YpSs	JXYCLS
JAUCC 3859	PV578935	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	RBA	JXYCLS
JAUCC 3860	PV578936	*Diaporthe perseae*		*Diaporthe* sp. 31	stem	PCA	JXZSLJ
JAUCC 3861	PV578937	*Botryosphaeria dothidea*	OP926951	*Botryosphaeria* sp.1	stem	MEA	JXZSLJ
JAUCC 3862	PV578938	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	stem	MEA	JXZSLJ
JAUCC 3863	PV578939	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	YpSs	JXJJRC
JAUCC 3864	PV578940	*Pestalotiopsis microspora*	KM438014	*Pestalotiopsis* sp. 4	stem	MEA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3865	PV586274	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	MEA	JXZSLJ
JAUCC 3866	PV586275	*Botryosphaeria dothidea*	KF516940	*Botryosphaeria* sp.1	stem	MEA	JXZSLJ
JAUCC 3867	PV586276	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PCA	JXJJRC
JAUCC 3868	PV586277	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	MEA	JXJJRC
JAUCC 3869	PV586278	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	MEA	JXZSLJ
JAUCC 3870	PV586279	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	MEA	JXZSLJ
JAUCC 3871	PV586280	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	MEA	JXZSLJ
JAUCC 3872	PV586281	*Diaporthe caryae*		*Diaporthe* sp. 42	leaf	OA	JXJJRC
JAUCC 3873	PV586282	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	MEA	JXZSLJ
JAUCC 3874	PV586283	*Diaporthe perseae*		*Diaporthe* sp. 31	stem	MEA	JXZSLJ
JAUCC 3875	PV586284	*Diaporthe discoidispora*	KY011887	*Diaporthe* sp. 14	stem	MEA	JXZSLJ
JAUCC 3876	PV586285	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	YpSs	HNCZWX
JAUCC 3877	PV586286	*Diaporthe cotoneastri*	KX866907	*Diaporthe* sp. 36	leaf	OA	JXJJRC
JAUCC 3878	PV586287	*Epicoccum nigrum*	PQ381249	*Epicoccum* sp. 1	leaf	OA	JXJJRC
JAUCC 3879	PV586288	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PCA	JXZSLJ
JAUCC 3880	PV586289	*Fusarium ngaiotongaense*		*Fusarium* sp. 5	stem	YpSs	JXYTWF
JAUCC 3881	PV586290	*Fusarium falciforme*		*Fusarium* sp. 3	stem	PCA	JXZSLJ
JAUCC 3882	PV586291	*Diaporthe caryae*		*Diaporthe* sp. 42	leaf	OA	JXJJRC
JAUCC 3883	PV586292	*Fusarium ngaiotongaense*		*Fusarium* sp. 5	stem	YpSs	JXYTWF
JAUCC 3884	PV586293	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PCA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon 's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3885	PV586294	*Clonostachys rosea*		*Clonostachys* sp. 3	stem	PCA	JXYCLS
JAUCC 3886	PV586295	*Diaporthe perseae*		*Diaporthe* sp. 31	stem	PDA	JXZSLJ
JAUCC 3887	PV586296	*Didymella glomerata*		*Didymella* sp. 1	stem	PDA	JXZSLJ
JAUCC 3888	PV586297	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	OA	JXYCLS
JAUCC 3889	PV586298	*Diaporthe ongicolla*		*Diaporthe* sp. 21	stem	PDA	JXZSLJ
JAUCC 3890	PV586299	*Diaporthe hubeiensis*	MW578680	*Diaporthe* sp. 7	stem	PDA	JXZSLJ
JAUCC 3891	PV586300	*Alternaria alternata*		*Alternaria* sp. 1	leaf	OA	JXJJRC
JAUCC 3892	PV586301	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PDA	JXZSLJ
JAUCC 3893	PV586302	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	stem	PDA	JXZSLJ
JAUCC 3894	PV586303	*Diaporthe perseae*		*Diaporthe* sp. 31	stem	PDA	JXZSLJ
JAUCC 3895	PV586304	*Diaporthe pseudophoenicicola*	OR416454	*Diaporthe* sp. 16	stem	PDA	JXZSLJ
JAUCC 3896	PV586305	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	MEA	HNCZWX
JAUCC 3897	PV586306	*Diaporthe huangshanensis*		*Diaporthe* sp. 32	leaf	OA	JXJJRC
JAUCC 3898	PV586307	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	OA	JXZSLJ
JAUCC 3899	PV586308	*Diaporthe clematidina*	NR_170819	*Diaporthe* sp. 15	stem	OA	JXJJRC
JAUCC 3900	PV586309	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	OA	JXZSLJ
JAUCC 3901	PV586310	*Penicillium rolfsii*	MT729953	*Penicillium* sp. 3	root	OA	JXZSYC
JAUCC 3902	PV586311	*Diaporthe perseae*		*Diaporthe* sp. 31	stem	OA	JXZSLJ
JAUCC 3903	PV586312	*Fusarium fujikuro*	MW016449	*Fusarium* sp. 17	stem	YpSs	JXYTWF
JAUCC 3904	PV586313	*Neosetophoma poaceicola*	PP592443	*Neosetophoma* sp. 1	stem	OA	JXJJRC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3905	PV586314	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	OA	JXJJRC
JAUCC 3906	PV586315	*Diaporthe hubeiensis*		*Diaporthe* sp. 7	stem	MEA	JXJJRC
JAUCC 3907	PV586316	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	MEA	JXJJRC
JAUCC 3908	PV586317	*Daldinia eschscholtzii*	MW261783	*Daldinia* sp. 1	stem	RBA	JXZSLJ
JAUCC 3910	PV586318	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	RBA	JXZSLJ
JAUCC 3911	PV586319	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ
JAUCC 3912	PV586320	*Diaporthe cotoneastri*		*Diaporthe* sp. 36	stem	RBA	JXZSLJ
JAUCC 3913	PV586321	*Corynespora cassiicola*	MK530519	Corynespora sp. 1	stem	RBA	JXZSLJ
JAUCC 3914	PV586322	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	MEA	JXJJRC
JAUCC 3915	PV586323	*Fusarium sp.*		*Fusarium* sp. 13	stem	RBA	JXJJRC
JAUCC 3916	PV586324	*Daldinia eschscholtzii*		*Daldinia* sp. 1	stem	RBA	JXZSLJ
JAUCC 3917	PV586325	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ
JAUCC 3919	PV586326	*Diaporthe nobilis*	OM950739	*Diaporthe* sp. 17	leaf	MEA	JXJJRC
JAUCC 3920	PV586327	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ
JAUCC 3921	PV586328	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ
JAUCC 3922	PV586329	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PDA	JXZSLJ
JAUCC 3923	PV586330	*Alternaria alternata*		*Alternaria* sp. 1	leaf	MEA	JXJJRC
JAUCC 3924	PV586331	*Arthrinium arundinis*	GU566268	*Arthrinium* sp. 1	root	MEA	JXJJRC
JAUCC 3925	PV586332	*Neodidymella thailandicum*	MT470668	*Neodidymella* sp. 1	leaf	YpSs	HNCZWX
JAUCC 3926	PV586333	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3927	PV586334	*Diaporthe caryae*	MN788609	*Diaporthe* sp. 1	stem	PCA	JXZSYC
JAUCC 3928	PV586335	*Diaporthe pseudooculi*	PV361429	*Diaporthe* sp. 13	stem	PDA	JXZSLJ
JAUCC 3929	PV586336	*Diaporthe huangshanensis*	MN219730	*Diaporthe* sp. 32	stem	PDA	JXZSLJ
JAUCC 3930	PV586337	*Epicoccum nigrum*	OP117272	*Epicoccum* sp. 1	leaf	PDA	HNCZWX
JAUCC 3931	PV586338	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	YpSs	HNCZWX
JAUCC 3932	PV586339	*Stagonosporopsis cucurbitacearum*	MT466519	*Stagonosporopsis* sp.2	stem	PDA	JXZSLJ
JAUCC 3933	PV586340	*Alternaria alternata*		*Alternaria* sp. 1	stem	MEA	JXZSLJ
JAUCC 3934	PV586341	*Daldinia eschscholtzii*		*Daldinia* sp. 1	stem	MEA	JXZSLJ
JAUCC 3935	PV586342	*Muyocopron lithocarpi*	MT137780	*Muyocopron* sp. 1	leaf	PDA	HNCZWX
JAUCC 3936	PV586343	*Aspergillus sydowii*	OM670095	Aspergillus sp. 1	leaf	RBA	JXZSLJ
JAUCC 3937	PV586344	*Diaporthe pseudooculi*		*Diaporthe* sp. 13	stem	MEA	JXZSLJ
JAUCC 3938	PV586345	*Diaporthe pseudooculi*	PQ462623	*Diaporthe* sp. 13	stem	MEA	JXZSLJ
JAUCC 3940	PV586346	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	PDA	JXYCTX
JAUCC 3941	PV586347	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	PDA	JXZSLJ
JAUCC 3942	PV586348	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	RBA	JXZSLJ
JAUCC 3944	PV586349	*Corynespora cassiicola*	PP346164	*Corynespora* sp. 1	stem	RBA	JXYCTX
JAUCC 3945	PV586350	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	PDA	JXZSLJ
JAUCC 3947	PV586351	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	stem	YpSs	JXZSLJ
JAUCC 3948	PV586352	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ
JAUCC 3949	PV586353	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3950	PV586354	*Diaporthe celastrina*		*Diaporthe* sp. 27	stem	OA	JXZSLJ
JAUCC 3952	PV586355	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	OA	JXZSLJ
JAUCC 3953	PV586356	*Setophoma yingyisheniae*	PQ499147	*Setophoma* sp. 1	leaf	YpSs	JXZSLJ
JAUCC 3954	PV586357	*Diaporthe unshiuensis*	MN816428	*Diaporthe* sp. 4	stem	OA	JXZSLJ
JAUCC 3955	PV586358	*Fusarium oxysporum*		*Fusarium* sp. 11	stem	PCA	JXYTWF
JAUCC 3956	PV586359	*Clonostachys rosea*		*Clonostachys* sp. 3	stem	YpSs	JXYCLS
JAUCC 3957	PV586360	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PCA	JXZSLJ
JAUCC 3958	PV586361	*Clonostachys rosea*		*Clonostachys* sp. 3	stem	PCA	JXYTWF
JAUCC 3960	PV586362	*Pseudopithomyces palmicola*	MT557070	*Pseudopithomyces* sp. 1	stem	YpSs	JXZSYC
JAUCC 3961	PV586363	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	MEA	JXZSYC
JAUCC 3962	PV586364	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	RBA	JXJJRC
JAUCC 3963	PV586365	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3964	PV586366	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3965	PV586367	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3966	PV586368	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3967	PV586369	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3968	PV586370	*Penicillium javanicum*	PP385147	*Penicillium* sp. 4	root	YpSs	JXZSLJ
JAUCC 3969	PV586371	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	YpSs	JXZSLJ
JAUCC 3970	PV586372	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	PCA	JXZSYC
JAUCC 3971	PV586373	*Aspergillus parasiticus*	MK178553	*Aspergillus* sp. 2	root	MEA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3972	PV586374	*Diaporthe nobilis*	MZ127379	*Diaporthe* sp. 17	stem	RBA	JXZSLJ
JAUCC 3974	PV586375	*Penicillium janthinellum*	GU934553	*Penicillium* sp. 5	root	MEA	JXZSLJ
JAUCC 3975	PV586376	*Fusarium falciforme*		*Fusarium* sp. 3	root	RBA	JXZSLJ
JAUCC 3976	PV586377	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	root	RBA	JXJJRC
JAUCC 3977	PV586378	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PDA	JXZSYC
JAUCC 3978	PV586379	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	root	MEA	JXZSLJ
JAUCC 3979	PV586380	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem		JXZSLJ
JAUCC 3980	PV586381	*Diaporthe fukushi*	JN198407	*Diaporthe* sp. 25	stem	RBA	JXZSLJ
JAUCC 3981	PV586382	*Corynespora cassiicola*	MG825670	Corynespora sp. 1	root	MEA	JXZSLJ
JAUCC 3982	PV586383	*Diaporthe huangshanensis*	PV252443	*Diaporthe* sp. 32	stem	PDA	JXZSYC
JAUCC 3983	PV586384	*Epicoccum thailandicum*		*Epicoccum* sp. 2	root	RBA	JXZSLJ
JAUCC 3984	PV586385	*Colletotrichum gigasporum*	PP663777	*Colletotrichum* sp. 7	root	RBA	JXZSLJ
JAUCC 3985	PV586386	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	PDA	JXZSYC
JAUCC 3986	PV586387	*Pseudofusicoccum violaceum*	OQ659875	*Pseudofusicoccum* sp. 1	root	RBA	JXZSLJ
JAUCC 3987	PV586388	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 16	stem	MEA	JXZSLJ
JAUCC 3989	PV586389	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSLJ
JAUCC 3990	PV586390	*Diaporthe pseudophoenicicola*		*Diaporthe* sp. 30	stem	PDA	JXZSLJ
JAUCC 3992	PV586391	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXZSLJ
JAUCC 3994	PV586392	*Diaporthe cotoneastri*	MK311290	*Diaporthe* sp. 26	leaf	RBA	JXJJRC
JAUCC 3995	OK087600	*Dactylaria acerosa*	OR543730	*Funiliomyces* sp. 1	root	PDA	JXZSLJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 3996	PV586393	*Fusarium solani*	MZ275213	*Fusarium* sp. 16	root	PDA	JXZSLJ
JAUCC 3998	PV586394	*Diaporthe caryae*		*Diaporthe* sp. 42	stem	RBA	JXJJRC
JAUCC 3999	PV586395	*Diaporthe amygdali*		*Diaporthe* sp. 40	stem	RBA	JXJJRC
JAUCC 4000	PV586396	*Diaporthe sojae*		*Diaporthe* sp. 5	stem	RBA	JXJJRC
JAUCC 4211	PV586397	*Didymella glomerata*		*Didymella* sp. 1	leaf	MEA	JXYCTX
JAUCC 4212	PV586398	*Diaporthe citrichinensis*	PP383956	*Diaporthe* sp. 46	leaf	MEA	JXYCTX
JAUCC 4213	PV586399	*Diaporthe huangshanensis*		*Diaporthe* sp. 32	leaf	MEA	JXYCTX
JAUCC 4214	PV586400	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	MEA	JXYCTX
JAUCC 4215	PV586401	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	MEA	JXYCTX
JAUCC 4216	PV586402	*Didymella glomerata*		*Didymella* sp. 1	leaf	MEA	JXYCTX
JAUCC 4217	PV586403	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	MEA	JXYCTX
JAUCC 4218	PV586404	*Diaporthe apiculata*	PQ319521	*Diaporthe* sp. 8	leaf	YpSs	JXYCTX
JAUCC 4219	PV586405	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	OA	JXYCTX
JAUCC 4220	PV586406	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	OA	JXYCTX
JAUCC 4221	PV586407	*Diaporthe eres*	OM867499	*Diaporthe* sp. 18	leaf	OA	JXYCTX
JAUCC 4222	PV586408	*Diaporthe eres*		*Diaporthe* sp. 18	leaf	OA	JXYCTX
JAUCC 4223	PV586409	*Diaporthe fukushi*		*Diaporthe* sp. 25	leaf	OA	JXYCTX
JAUCC 4224	PV586410	*Diaporthe oraccinii*		*Diaporthe* sp. 2	leaf	OA	JXYCTX
JAUCC 4225	PV586411	*Diaporthe citrichinensis*	MK626893	*Diaporthe* sp. 46	leaf	OA	JXYCTX
JAUCC 4226	PV586412	*Diaporthe cotoneastri*		*Diaporthe* sp. 26	leaf	OA	JXYCTX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4227	PV586413	*Diaporthe eres*	MK335738	*Diaporthe* sp. 18	leaf	OA	JXYCTX
JAUCC 4228	PV586414	*Diaporthe biguttulata*	OM538401	*Diaporthe* sp. 33	leaf	OA	JXYCTX
JAUCC 4229	PV586415	*Epicoccum nigrum*	OM106448	*Epicoccum* sp. 1	leaf	OA	JXYCTX
JAUCC 4230	PV586416	*Diaporthe castaneae*	KC763096	*Diaporthe* sp. 29	leaf	PDA	JXYCTX
JAUCC 4231	PV586417	*Diaporthe celastrina*		*Diaporthe* sp. 27	leaf	PDA	JXYCTX
JAUCC 4232	PV586418	*Diaporthe heterophyllae*	MW959685	*Diaporthe* sp. 24	leaf	PDA	JXYCTX
JAUCC 4233	PV586419	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	PDA	JXYCTX
JAUCC 4234	PV586420	*Fusarium solani*		*Fusarium* sp. 16	leaf	RBA	JXZSYC
JAUCC 4235	PV586421	*Diaporthe citrichinensis*	MZ648260	*Diaporthe* sp. 46	leaf	PDA	JXYCTX
JAUCC 4236	PV586422	*Didymella glomerata*		*Didymella* sp. 1	leaf	PDA	JXYCTX
JAUCC 4237	PV586423	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	HNCZWX
JAUCC 4238	PV586424	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	PCA	JXYCTX
JAUCC 4239	PV586425	*Diaporthe australiana*	OM574685	*Diaporthe* sp. 22	leaf	OA	JXYCTX
JAUCC 4240	PV586426	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	OA	JXYCTX
JAUCC 4241	PV586427	*Diaporthe oraccinii*		*Diaporthe* sp. 2	leaf	PDA	JXYCTX
JAUCC 4242	PV586428	*Diaporthe amygdali*		*Diaporthe* sp. 40	leaf	PCA	JXYCTX
JAUCC 4243	PV586429	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	PCA	JXYCTX
JAUCC 4244	PV586430	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	OA	JXYCTX
JAUCC 4245	PV586431	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	YpSs	JXYCTX
JAUCC 4246	PV586432	*Didymella glomerata*		*Didymella* sp. 1	leaf	PDA	JXYCTX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4247	PV586433	*Epicoccum nigrum*	KP689180	*Epicoccum* sp. 1	leaf	PCA	HNCZWX
JAUCC 4248	PV586434	*Diaporthe celastrina*		*Diaporthe* sp. 27	leaf	PCA	JXYCTX
JAUCC 4249	PV586435	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	OA	JXYCTX
JAUCC 4250	PV586436	*Diaporthe oraccinii*		*Diaporthe* sp. 2	leaf	PCA	JXYCTX
JAUCC 4251	PV586437	*Diaporthe nobilis*	MT877032	*Diaporthe* sp. 17	leaf	OA	JXYCTX
JAUCC 4252	PV586438	*Diaporthe oraccinii*		*Diaporthe* sp. 2	leaf	MEA	JXYCTX
JAUCC 4253	PV586439	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	YpSs	JXYCTX
JAUCC 4254	PV586440	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	PCA	JXYCTX
JAUCC 4255	00869215	*Dactylaria acerosa*		*Funiliomyces* sp. 1	root	PDA	JXZSYC
JAUCC 4256	PV586441	*Diaporthe huangshanensis*		*Diaporthe* sp. 32	leaf	OA	JXYCTX
JAUCC 4257	PV586442	*Alternaria alternata*	MT102830	*Alternaria* sp. 1	leaf	OA	JXYCTX
JAUCC 4258	PV586443	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	YpSs	JXYCTX
JAUCC 4259	PV586444	*Diaporthe eres*		*Diaporthe* sp. 41	leaf	PDA	JXYCTX
JAUCC 4260	PV586445	*Diaporthe fukushi*		*Diaporthe* sp. 25	leaf	YpSs	JXYCTX
JAUCC 4261	PV586446	*Diaporthe amygdali*		*Diaporthe* sp. 40	leaf	OA	JXYCTX
JAUCC 4262	PV586447	*Colletotrichum boninense*	MZ312519	*Colletotrichum* sp. 5	leaf	PDA	HNCZWX
JAUCC 4263	PV586448	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	PDA	JXYCTX
JAUCC 4264	PV586449	*Gliocladiopsis tenuis*	OP876701_	*Gliocladiopsis* sp. 1	root	PDA	JXYCTX
JAUCC 4265	PV586450	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXYCTX
JAUCC 4266	PV586451	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	YpSs	JXYCTX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4267	PV586452	*Clonostachys rosea*		*Clonostachys* sp. 3	root	YpSs	JXJJRC
JAUCC 4268	PV586453	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	PDA	JXYCTX
JAUCC 4269	PV586454	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	OA	JXJJRC
JAUCC 4270	PV586455	*Talaromyces pinophilus*	MH059546	*Trichoderma* sp. 2	root	PDA	JXJJRC
JAUCC 4271	PV586456	*Clonostachys rosea*		*Clonostachys* sp. 3	root	YpSs	JXYCTX
JAUCC 4272	PV586457	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXYCTX
JAUCC 4273	PV586458	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	RBA	JXJJRC
JAUCC 4274	PV586459	*Diaporthe sojae*		*Diaporthe* sp. 5	stem	RBA	JXJJRC
JAUCC 4275	PV586460	*Stagonospora tainanensis*	MH855607	*Stagonospora* sp. 2	leaf	RBA	JXYCTX
JAUCC 4276	PV586461	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	RBA	JXYCTX
JAUCC 4277	PV586462	*Setophoma yingyisheniae*	PQ499147	*Setophoma* sp. 1	leaf	RBA	JXYCTX
JAUCC 4278	PV586463	*Diaporthe eres*		*Diaporthe* sp. 18	leaf	RBA	JXYCTX
JAUCC 4279	PV586464	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	RBA	JXYCTX
JAUCC 4280	PV586465	*Diaporthe padi var. padi*	KC343170	*Diaporthe* sp. 43	leaf	RBA	JXYCTX
JAUCC 4281	PV586466	*Setophoma yingyisheniae*		*Setophoma* sp. 1	leaf	MEA	JXYCTX
JAUCC 4282	PV586467	*Setophoma yingyisheniae*	MK511937	*Setophoma* sp. 1	leaf	YpSs	JXYCTX
JAUCC 4283	PV586468	*Diaporthe sojae*		*Diaporthe* sp. 5	leaf	OA	JXZSYC
JAUCC 4284	PV586469	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	RBA	JXYCTX
JAUCC 4285	PV586470	*Diaporthe unshiuensis*	MW722993	*Diaporthe* sp. 4	leaf	RBA	JXYCTX
JAUCC 4286	PV586471	*Penicillifer diparietisporus*	MK387971	*Penicillifer* sp. 1	root	PDA	JXYCTX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4287	PV586472	*Clonostachys rosea*	OM436895	*Clonostachys* sp. 3	root	OA	JXJJRC
JAUCC 4288	PV586473	*Didymella glomerata*		*Didymella* sp. 1	leaf	MEA	JXYCTX
JAUCC 4289	PV586474	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	PDA	JXJJRC
JAUCC 4290	PV586475	*Didymella glomerata*		*Didymella* sp. 1	leaf	YpSs	JXYCTX
JAUCC 4291	PV586476	*Clonostachys rosea*	LT220554	*Clonostachys* sp. 3	root	PDA	JXYCTX
JAUCC 4292	PV586477	*Clonostachys rosea*		*Clonostachys* sp. 3	root	OA	JXYCTX
JAUCC 4293	PV586478	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	PDA	JXYCTX
JAUCC 4294	PV586479	*Diaporthe biguttulata*		*Diaporthe* sp. 33	leaf	RBA	JXYCTX
JAUCC 4295	PV586480	*Setophoma yingyisheniae*		*Setophoma* sp. 1	leaf	YpSs	JXYCTX
JAUCC 4296	PV586481	*Penicillifer diparietisporus*	MN400088	*Penicillifer* sp. 1	root	MEA	JXJJRC
JAUCC 4297	PV586482	*Gliocladiopsis tenuis*	EF495240	*Gliocladiopsis* sp. 1	root	RBA	JXJJRC
JAUCC 4298	PV586483	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4299	PV586484	*Amphisphaeriaqujingensis*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4300	PV586485	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXYCTX
JAUCC 4301	PV586486	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	YpSs	JXJJRC
JAUCC 4302	PV586487	*Diaporthe hongkongensis*	MT470613	*Diaporthe* sp. 37	leaf	YpSs	HNCZWX
JAUCC 4303	PV586488	*Fusarium sp.*		*Fusarium* sp. 13	root	RBA	JXJJRC
JAUCC 4304	PV586489	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	RBA	JXJJRC
JAUCC 4305	PV586490	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	YpSs	JXJJRC
JAUCC 4306	PV586491	*Gliocladiopsis tenuis*	MK371764	*Gliocladiopsis* sp. 1	root	YpSs	JXJJRC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4307	PV586492	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	PDA	JXJJRC
JAUCC 4308	PV586493	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4309	PV586494	*Induratia fengyangensis*	HM034853	*Induratia* sp. 1	leaf	OA	HNCZWX
JAUCC 4310	PV586495	*Aaosphaeria arxii*	MT786363	*Aaosphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4311	PV586496	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	PDA	JXJJRC
JAUCC 4312	PV586497	*Diaporthe australiana*		*Diaporthe* sp. 22	leaf	RBA	HNCZWX
JAUCC 4313	PV586498	*Fusarium proliferatum*		*Fusarium* sp. 12	root	RBA	JXYCTG
JAUCC 4359	PV586499	*Diaporthe hongkongensis*	MW578708	*Diaporthe* sp. 37	leaf	RBA	HNCZWX
JAUCC 4360	PV586500	*Diaporthe caryae*	OP315346	*Diaporthe* sp. 1	stem	RBA	JXJAWA
JAUCC 4361	PV586501	*Didymella glomerata*	PQ219326	*Didymella* sp. 1	stem	RBA	JXJAWA
JAUCC 4362	PV586502	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	RBA	JXJAWA
JAUCC 4363	PV586503	*Diaporthe caryae*	MW722991	*Diaporthe* sp. 1	stem	RBA	JXJAWA
JAUCC 4364	PV586504	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	RBA	JXJAWA
JAUCC 4365	PV586505	*Diaporthe unshiuensis*	PQ559809	*Diaporthe* sp. 4	stem	RBA	JXJAWA
JAUCC 4366	PV586506	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	RBA	JXJAWA
JAUCC 4367	PV586507	*Diaporthe oraccinii*		*Diaporthe* sp. 2	stem	RBA	JXJAWA
JAUCC 4368	PV586508	*Diaporthe psoraleae-pinnatae*	PQ325601	*Diaporthe* sp. 4	stem	OA	HNCZWX
JAUCC 4369	PV586509	*Epicoccum nigrum*	PP542542	*Epicoccum* sp. 1	leaf	RBA	HNCZWX
JAUCC 4370	PV586510	*Diaporthe apiculata*		*Diaporthe* sp. 8	stem	PCA	JXJAWA
JAUCC 4371	PV586511	*Diaporthe caryae*	PP594911	*Diaporthe* sp. 1	stem	RBA	JXJAWA

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4372	PV586512	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	stem	RBA	JXJAWA
JAUCC 4373	PV586513	*Diaporthe silvicola*	ON179817	*Diaporthe* sp. 34	stem	RBA	JXJAWA
JAUCC 4374	PV586514	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	stem	PDA	JXJAWA
JAUCC 4375	PV586515	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	RBA	JXJAWA
JAUCC 4376	PV586516	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	RBA	HNCZWX
JAUCC 4377	PV586517	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	RBA	JXJAWA
JAUCC 4378	PV586518	*Amphisphaeria qujingensis*		*Amphisphaeria* sp. 1	root	PCA	JXZSYC
JAUCC 4379	PV586519	*Diaporthe penetriteum*		*Diaporthe* sp. 10	stem	RBA	JXJAWA
JAUCC 4380	PV586520	*Diaporthe penetriteum*		*Diaporthe* sp. 10	stem	RBA	JXJAWA
JAUCC 4381	PV586521	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	stem	RBA	JXJAWA
JAUCC 4382	PV586522	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	RBA	JXJAWA
JAUCC 4383	PV586523	*Diaporthe hubeiensis*		*Diaporthe* sp. 7	stem	RBA	JXJAWA
JAUCC 4384	PV586524	*Colletotrichum karsti*	MH298862	*Colletotrichum* sp. 1	fruit	PCA	JXYCTG
JAUCC 4385	PV586525	*Diaporthe caryae*	OQ727287	*Diaporthe* sp. 48	fruit	PDA	JXYCTG
JAUCC 4386	PV586526	*Diaporthe caryae*	OQ727288	*Diaporthe* sp. 48	fruit	PCA	JXYCTG
JAUCC 4387	PV586527	*Colletotrichum karsti*		*Colletotrichum* sp. 1	fruit	PCA	JXYCTG
JAUCC 4388	PV586528	*Diaporthe penetriteum*		*Diaporthe* sp. 10	fruit	PCA	JXYCTG
JAUCC 4389	PV586529	*Colletotrichum karsti*		*Colletotrichum* sp. 1	fruit	MEA	JXYCTG
JAUCC 4390	PV586530	*Diaporthe amygdali*		*Diaporthe* sp. 40	fruit	RBA	JXYCTG
JAUCC 4391	PV586531	*Diaporthe eucalyptorum*		*Diaporthe* sp. 39	fruit	PCA	JXYCTG

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4392	PV586532	*Diaporthe apiculata*		*Diaporthe* sp. 8	fruit	PDA	JXYCTG
JAUCC 4393	PV586533	*Diaporthe apiculata*	OP218109	*Diaporthe* sp. 8	fruit	RBA	JXYCTG
JAUCC 4394	PV586534	*Colletotrichum karsti*		*Colletotrichum* sp. 1	fruit	YpSs	JXYCTG
JAUCC 4395	PV586535	*Diaporthe apiculata*		*Diaporthe* sp. 8	fruit	OA	JXYCTG
JAUCC 4396	PV586536	*Diaporthe biguttulata*		*Diaporthe* sp. 33	fruit	MEA	JXYCTG
JAUCC 4397	PV586537	*Didymocyrtis cladoniicola*	OR879285	*Didymocyrtis* sp. 1	fruit	OA	JXYCTG
JAUCC 4398	PV586538	*Diaporthe apiculata*		*Diaporthe* sp. 8	fruit	OA	JXYCTG
JAUCC 4399	PV586539	*Aspergillus aculeatus_*		*Aspergillus* sp. 3	fruit	PDA	JXYCLS
JAUCC 4402	PV586540	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PCA	JXYCLS
JAUCC 4403	PV586541	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	RBA	JXYCLS
JAUCC 4404	PV586542	*Nemania primolutea*	MN84444	*Nemania* sp. 4	leaf	RBA	JXJDZC
JAUCC 4405	PV586543	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	JXYCLS
JAUCC 4406	PV586544	*Diaporthe apiculata*		*Diaporthe* sp. 8	fruit	YpSs	JXYCTG
JAUCC 4407	PV586545	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	fruit	YpSs	JXYCTG
JAUCC 4408	PV586546	*Coryneum castaneicola*	MH683559	*Coryneum* sp. 1	stem	OA	JXYTWF
JAUCC 4409	PV586547	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4410	PV586548	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4411	PV586549	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXJAWA
JAUCC 4412	PV586550	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4413	PV586551	*Colletotrichum fioriniae*	OP687070	*Colletotrichum* sp. 2	fruit	MEA	JXYCLS

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4414	PV586552	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	fruit	PDA	JXYCLS
JAUCC 4415	PV586553	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	fruit	MEA	JXYCLS
JAUCC 4416	PV586554	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	OA	JXZSYC
JAUCC 4417	PV586555	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	fruit	OA	JXZSYC
JAUCC 4418	PV586556	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	PCA	JXZSYC
JAUCC 4419	PV586557	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	YpSs	JXZSYC
JAUCC 4420	PV586558	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	PDA	JXZSYC
JAUCC 4421	PV586559	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	YpSs	JXZSYC
JAUCC 4422	PV586560	*Botryosphaeria dothidea*		*Botryosphaeria sp.*1	fruit	RBA	JXZSYC
JAUCC 4423	PV586561	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	YpSs	JXZSYC
JAUCC 4424	PV586562	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	fruit	YpSs	JXZSYC
JAUCC 4425	PV586563	*Diaporthe sojae*		*Diaporthe* sp. 5	fruit	YpSs	JXZSYC
JAUCC 4426	PV586564	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	YpSs	JXYTWF
JAUCC 4427	PV586565	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	stem	RBA	JXYCTG
JAUCC 4428	PV586566	*Diaporthe apiculata*		*Diaporthe* sp. 8	stem	MEA	JXYCTG
JAUCC 4429	PV586567	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	stem	PDA	JXYCTG
JAUCC 4430	PV586568	*Didymella glomerata*		*Didymella* sp. 1	stem	RBA	JXYCTX
JAUCC 4431	PV586569	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	stem	PDA	JXYCTX
JAUCC 4432	PV586570	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	stem	PDA	JXYCTX
JAUCC 4433	PV586571	*Diaporthe fusicola*	MK626914	*Diaporthe* sp. 9	stem	RBA	JXYCTG

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4434	PV586572	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4435	PV586573	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4436	PV586574	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4437	PV586575	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	RBA	JXJAWA
JAUCC 4438	PV586576	*Diaporthe celastrina*		*Diaporthe* sp. 27	leaf	RBA	JXJAWA
JAUCC 4439	PV586577	*Didymella glomerata*		*Didymella* sp. 1	leaf	YpSs	JXJAWA
JAUCC 4440	PV586578	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	RBA	JXJAWA
JAUCC 4441	PV586579	*Didymella glomerata*		*Didymella* sp. 1	leaf	YpSs	JXJAWA
JAUCC 4443	PV586580	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXJAWA
JAUCC 4444	PV586581	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXJAWA
JAUCC 4445	PV586582	*Austropleospora ochracea*	MT799859	*Austropleospora* sp. 1	leaf	PDA	JXJAWA
JAUCC 4446	PV586583	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4447	PV586584	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4448	PV586585	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJAWA
JAUCC 4449	PV586586	*Didymella glomerata*		*Didymella* sp. 1	leaf	MEA	JXJAWA
JAUCC 4450	PV586587	*Clonostachys rogersoniana*	MH421856	*Clonostachys* sp. 2	root	PCA	JXYCTG
JAUCC 4451	PV586588	*Paraphoma chrysanthemicola*	MH063750	*Paraphoma* sp. 1	leaf	RBA	JXJAWA
JAUCC 4452	PV586589	*Nothophoma quercina*	MH635156	*Nothophoma* sp. 1	leaf	RBA	JXJAWA
JAUCC 4453	PV586590	*Nothophoma quercina*		*Nothophoma* sp. 1	leaf	RBA	JXJAWA
JAUCC 4454	PV586591	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	RBA	HNCZWX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4455	PV586592	*Nothophoma quercina*		*Nothophoma* sp. 1	leaf	RBA	JXJAWA
JAUCC 4456	PV586593	*Diaporthe celastrina*	OP163782	*Diaporthe* sp. 27	leaf	PCA	JXJAWA
JAUCC 4457	PV586594	*Clonostachys rogersoniana*		*Clonostachys* sp. 2	root	PDA	JXYCTG
JAUCC 4458	PV586595	*Diaporthe hongkongensis*	OP020699	*Diaporthe* sp. 37	stem	PDA	HNCZWX
JAUCC 4729	PV586596	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	PDA	JXZSYC
JAUCC 4730	PV586597	*Pestalotiopsis nanjingensis*	OR342044	*Pestalotiopsis* sp. 2	stem	PDA	JXZSYC
JAUCC 4731	PV586598	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	PDA	JXZSYC
JAUCC 4732	PV586599	*Diaporthe ceratozamiae*	KU360597	*Diaporthe* sp. 44	stem	PDA	JXZSYC
JAUCC 4733	PV586600	*Diaporthe unshiuensis*	MT043829	*Diaporthe* sp. 4	stem	PDA	JXZSYC
JAUCC 4734	PV586601	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	stem	YpSs	JXZSYC
JAUCC 4735	PV586602	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	YpSs	JXZSYC
JAUCC 4736	PV586603	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	stem	RBA	JXYCTX
JAUCC 4737	PV586604	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	stem	RBA	JXYCTX
JAUCC 4738	PV586605	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	RBA	JXYCTX
JAUCC 4739	PV586606	*Setophoma yingyisheniae*		*Setophoma* sp. 1	stem	RBA	JXYCTX
JAUCC 4740	PV586607	*Diaporthe huangshanensis*		*Diaporthe* sp. 32	stem	RBA	JXYCTX
JAUCC 4741	PV586608	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	PDA	JXYCTG
JAUCC 4742	PV586609	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	MEA	JXYCTG
JAUCC 4743	PV586610	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	RBA	JXYCTG
JAUCC 4744	PV586611	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	MEA	JXYCTG

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4745	PV586612	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXJAWA
JAUCC 4746	PV586613	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	RBA	JXJAWA
JAUCC 4747	PV586614	*Diaporthe discoidispora*		*Diaporthe* sp. 14	leaf	RBA	JXJAWA
JAUCC 4748	PV586615	*Diaporthe amygdali*		*Diaporthe* sp. 40	leaf	RBA	JXJAWA
JAUCC 4749	PV586616	*Diaporthe citrichinensis*		*Diaporthe* sp. 46	leaf	RBA	JXYCTG
JAUCC 4750	PV586617	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	PCA	JXYCTG
JAUCC 4751	PV586618	*Didymella glomerata*		*Didymella* sp. 1	leaf	PCA	JXYCTG
JAUCC 4752	PV586619	*Diaporthe clematidina*		*Diaporthe* sp. 15	leaf	MEA	JXYCTG
JAUCC 4753	PV586620	*Diaporthe caryae*	PV252444	*Diaporthe* sp. 48	leaf	MEA	JXYCTG
JAUCC 4754	PV586621	*Diaporthe penetriteum*		*Diaporthe* sp. 10	leaf	PDA	JXYCTG
JAUCC 4755	PV586622	*Diaporthe caryae*		*Diaporthe* sp. 1	leaf	RBA	JXYCTG
JAUCC 4756	PV586623	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	RBA	JXYCTG
JAUCC 4757	PV586624	*Muyocopron lithocarpi*	OM287122	*Muyocopron* sp. 1	leaf	PDA	JXYCTG
JAUCC 4758	PV586625	*Diaporthe apiculata*		*Diaporthe* sp. 8	leaf	RBA	JXYCTG
JAUCC 4759	PV586626	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	OA	JXYCLS
JAUCC 4760	PV586627	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	YpSs	JXYCLS
JAUCC 4761	PV586628	*Phyllosticta capitalensis*	OP897171	*Phyllosticta* sp. 1	leaf	OA	JXYCLS
JAUCC 4762	PV586629	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	leaf	RBA	JXYCLS
JAUCC 4763	PV586630	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	RBA	JXYCLS
JAUCC 4764	PV586631	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	MEA	JXYTWF

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4765	PV586632	*Corynespora cassiicola*		*Corynespora* sp. 1	leaf	YpSs	JXYTWF
JAUCC 4766	PV586633	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXYTWF
JAUCC 4767	PV586634	*Corynespora cassiicola*		*Corynespora* sp. 1	leaf	PCA	JXYTWF
JAUCC 4768	PV586635	*Corynespora cassiicola*		*Corynespora* sp. 1	leaf	PCA	JXYTWF
JAUCC 4769	PV586636	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXYTWF
JAUCC 4770	PV586637	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXYCLS
JAUCC 4771	PV586638	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXYTWF
JAUCC 4772	PV586639	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	OA	JXYCLS
JAUCC 4773	PV586640	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	leaf	OA	JXYCLS
JAUCC 4774	PV586641	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	MEA	JXYTWF
JAUCC 4775	PV586642	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	MEA	JXYCLS
JAUCC 4776	PV586643	*Phyllosticta capitalensis*	PP494776	*Phyllosticta* sp. 1	leaf	PDA	JXYCLS
JAUCC 4777	PV586644	*Diaporthe biguttulata*		*Diaporthe* sp. 33	leaf	RBA	JXYCTG
JAUCC 4778	PV586645	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXYTWF
JAUCC 4779	PV586646	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	leaf	PCA	JXYTWF
JAUCC 4780	PV586647	*Alternaria alternata*		*Alternaria* sp. 1	leaf	OA	JXYCLS
JAUCC 4782	PV586648	*Colletotrichum plurivorum*	OL439887	*Colletotrichum* sp. 8	leaf	PDA	JXZSYC
JAUCC 4783	PV586649	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	MEA	JXZSYC
JAUCC 4784	PV586650	*Diaporthe sojae*		*Diaporthe* sp. 5	leaf	PDA	JXZSYC
JAUCC 4786	PV586651	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	RBA	JXZSYC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4787	PV586652	*Colletotrichum fructicola*	MN075714	*Colletotrichum* sp. 10	leaf	MEA	JXZSYC
JAUCC 4788	PV586653	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PCA	JXZSYC
JAUCC 4789	PV586654	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXZSYC
JAUCC 4790	PV586655	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXZSYC
JAUCC 4791	PV586656	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSYC
JAUCC 4792	PV586657	*Phyllosticta capitalensis*	JN791605	*Phyllosticta* sp. 1	leaf	PCA	JXZSYC
JAUCC 4793	PV586658	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXZSYC
JAUCC 4794	PV586659	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	MEA	JXZSYC
JAUCC 4796	PV586660	*Diaporthe sojae*		*Diaporthe* sp. 5	leaf	YpSs	JXZSYC
JAUCC 4797	PV586661	*Colletotrichum liaoningense*	PP504320	*Colletotrichum* sp. 4	leaf	PCA	JXZSYC
JAUCC 4798	PV586662	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	YpSs	JXZSYC
JAUCC 4799	PV586663	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSYC
JAUCC 4800	PV586664	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	PDA	JXZSYC
JAUCC 4801	PV586665	*Colletotrichum plurivorum*		*Colletotrichum* sp. 8	leaf	RBA	JXZSYC
JAUCC 4802	PV586666	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	leaf	PDA	JXZSYC
JAUCC 4803	PV586667	*Diaporthe sojae*		*Diaporthe* sp. 5	leaf	MEA	JXZSYC
JAUCC 4804	PV586668	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PCA	JXZSYC
JAUCC 4805	PV586669	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	YpSs	JXZSYC
JAUCC 4806	PV586670	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXZSYC
JAUCC 4807	PV586671	*Diaporthe unshiuensis*		*Diaporthe* sp. 4	leaf	PDA	JXZSYC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4808	PV586672	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	YpSs	JXZSYC
JAUCC 4809	PV586673	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXZSYC
JAUCC 4810	PV586674	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PDA	JXZSYC
JAUCC 4811	PV586675	*Colletotrichum gigasporum*		*Colletotrichum* sp. 7	leaf	YpSs	JXZSYC
JAUCC 4812	PV586676	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	RBA	JXZSYC
JAUCC 4813	PV586677	*Colletotrichum plurivorum*		*Colletotrichum* sp. 8	leaf	RBA	JXZSYC
JAUCC 4814	PV586678	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	RBA	JXZSYC
JAUCC 4815	PV586679	*Neodidymella thailandicum*	PV383420	*Neodidymella* sp. 1	leaf	RBA	JXZSYC
JAUCC 4816	PV586680	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	YpSs	JXZSYC
JAUCC 4817	PV586681	*Phyllosticta capitalensis*	MF170677	*Phyllosticta* sp. 1	leaf	YpSs	JXZSYC
JAUCC 4818	PV586682	*Alternaria alternata*		*Alternaria* sp. 1	leaf	MEA	JXZSYC
JAUCC 4819	PV586683	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	PCA	JXZSYC
JAUCC 4820	PV586684	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	MEA	JXZSYC
JAUCC 4821	PV586685	*Neodidymella thailandicum*		*Neodidymellaa* sp. 1	leaf	PCA	JXZSYC
JAUCC 4822	PV586686	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	OA	JXZSYC
JAUCC 4823	PV586687	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	OA	JXZSYC
JAUCC 4824	PV586688	*Pseudocercospora tabernaemontanae*	KC677911	*Pseudocercospora* sp. 1	leaf	PDA	JXZSYC
JAUCC 4825	PV586689	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PCA	JXZSYC
JAUCC 4826	PV586690	*Cercospora capsici*	KT193658	*Cercospora* sp. 1	leaf	PCA	JXZSYC
JAUCC 4827	PV586691	*Cercospora capsici*		*Cercospora* sp. 1	leaf	MEA	JXZSYC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4828	PV586692	*Fusarium proliferatum*		*Fusarium* sp. 12	leaf	MEA	JXZSYC
JAUCC 4829	PV586693	*Curvularia geniculata*	KY310634	*Curvularia* sp. 1	root	MEA	JXZSYC
JAUCC 4830	PV586694	*Clonostachys rosea*		*Clonostachys* sp. 3	root	OA	JXZSYC
JAUCC 4831	PV586695	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXZSYC
JAUCC 4832	PV586696	*Alternaria alternata*		*Alternaria* sp. 1	root	MEA	JXZSYC
JAUCC 4833	PV586697	*Diaporthe caryae*	MK626952	*Diaporthe* sp. 48	fruit	MEA	JXZSYC
JAUCC 4834	PV586698	*Curvularia geniculata*		*Curvularia* sp. 1	fruit	RBA	JXZSYC
JAUCC 4835	PV586699	*Cercospora capsici*		*Cercospora* sp. 1	fruit	RBA	JXZSYC
JAUCC 4836	PV586700	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	RBA	JXYCTX
JAUCC 4837	PV586701	*Cercospora capsici*	HQ700356	*Cercospora* sp. 1	leaf	RBA	JXZSYC
JAUCC 4838	PV586702	*Clonostachys rosea*		*Clonostachys* sp. 3	root	RBA	JXYCTG
JAUCC 4839	PV586703	*Fusarium oxysporum*		*Fusarium* sp. 11	root	RBA	JXYCTG
JAUCC 4840	PV586704	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	RBA	JXJJRC
JAUCC 4841	PV586705	*Fusarium sp.*		*Fusarium* sp. 13	root	RBA	JXJJRC
JAUCC 4842	PV586706	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4843	PV586707	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXYCTG
JAUCC 4844	PV586708	*Moesziomyces antarcticus*	MK409383	*Moesziomyces* sp. 1	leaf	RBA	JXYTWF
JAUCC 4845	PV586709	*Fusarium proliferatum*		*Fusarium* sp. 12	root	YpSs	JXYTWF
JAUCC 4846	PV586710	*Fusarium equiseti*		*Fusarium* sp. 1	root	YpSs	JXYTWF
JAUCC 4847	PV586711	*Fusarium proliferatum*		*Fusarium* sp. 12	root	PCA	JXYTWF

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 4849	PV586712	*Fusarium proliferatum*		*Fusarium* sp. 12	root	YpSs	JXYTWF
JAUCC 4850	PV586713	*Annulohypoxylon stygium*	FJ008986	*Annulohypoxylon* sp. 1	stem	RBA	JXGZGX
JAUCC 4851	PV586714	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	MEA	JXYTWF
JAUCC 4852	PV586715	*Fusarium oxysporum*	MW412760	*Fusarium* sp. 11	root	PDA	JXYTWF
JAUCC 4853	PV586716	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PCA	JXYTWF
JAUCC 4854	PV586717	*Fusarium proliferatum*		*Fusarium* sp. 12	root	PCA	JXYTWF
JAUCC 4855	PV586718	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PCA	JXYTWF
JAUCC 4856	PV586719	*Talaromyces pinophilus*		*Trichoderma* sp. 2	root	MEA	JXYTWF
JAUCC 4857	PV586720	*Biscogniauxia petrensis*	MN341573	*Biscogniauxia* sp. 1	root	PDA	JXYCLS
JAUCC 4858	PV586721	*Fusarium falciforme*		*Fusarium* sp. 3	root	RBA	JXYCTG
JAUCC 4859	PV586722	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4860	PV586723	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PDA	JXJJRC
JAUCC 4861	PV586724	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	leaf	MEA	JXZSYC
JAUCC 4862	PV586725	*Purpureocillium roseum*	MT560196	*Purpureocillium* sp. 1	stem	YpSs	JXYCLS
JAUCC 5048	PV586726	*Cladosporium halotolerans*	MT796131	*Cladosporium* sp. 2	root	YpSs	JXJDZC
JAUCC 5049	PV586727	*Diaporthe hongkongensis*	MW202983	*Diaporthe* sp. 37	stem	RBA	JXJDZC
JAUCC 5050	PV586728	*Diaporthe huangshanensis*		*Diaporthe* sp. 32	stem	RBA	JXJDZC
JAUCC 5051	PV586729	*Didymocyrtis cladoniicola*		*Didymocyrtis* sp. 1	stem	YpSs	JXJDZC
JAUCC 5052	PV586730	*Diaporthe caryae*	MK429860	*Diaporthe* sp. 1	stem	PCA	JXJDZC
JAUCC 5053	PV586731	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	PDA	AHXCJB

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5054	PV586732	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXYTWF
JAUCC 5055	PV586733	*Nemania diffusa*	LC685777	*Nemania* sp.3	leaf	OA	JXYTWF
JAUCC 5057	PV586734	*Coryneum castaneicola*		*Coryneum* sp. 1	stem	OA	JXYTWF
JAUCC 5087	PV586735	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	root	PCA	JXJDZC
JAUCC 5088	PV586736	*Clonostachys rosea*		*Clonostachys* sp. 3	root	RBA	AHXCJB
JAUCC 5089	PV586737	*Fusarium proliferatum*		*Fusarium* sp. 12	root	RBA	JXJDZC
JAUCC 5091	PV586738	*Cladosporium cladosporioides*	OP315346	*Cladosporium* sp. 1	root	MEA	JXJDZC
JAUCC 5092	PV586739	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	AHXCJB
JAUCC 5093	PV586740	*Diaporthe caryae*		*Diaporthe* sp. 1	root	PCA	AHXCJB
JAUCC 5094	PV586741	*Phaeoacremonium alvesii*		*Phaeoacremonium* sp. 1	root	PDA	AHXCJB
JAUCC 5096	PV586742	*Alternaria alternata*	MN822506	*Alternaria* sp. 1	stem	RBA	AHXCJB
JAUCC 5097	PV586743	*Didymocyrtis cladoniicola*		*Didymocyrtis* sp. 1	stem	YpSs	JXJDZC
JAUCC 5098	PV586744	*Neosetophoma poaceicola*		*Neosetophoma* sp. 1	stem	PDA	AHXCJB
JAUCC 5099	PV586745	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	YpSs	JXJDZC
JAUCC 5100	PV586746	*Nemania primolutea*		*Nemania* sp. 4	leaf	RBA	JXJDZC
JAUCC 5101	PV586747	*Neosetophoma qimenensis*	PQ807173	*Neosetophoma* sp. 2	leaf	RBA	JXJDZC
JAUCC 5102	PV586748	*Spegazzinia tessarthra*	JQ673429	*Spegazzinia* sp. 1	leaf	YpSs	AHXCJB
JAUCC 5103	PV586749	*Stagonosporopsis valerianellae*		Stagonosporopsis sp. 1	leaf	OA	AHXCJB
JAUCC 5139	PV586750	*Amphisphaeria curvaticonidia*		*Amphisphaeria* sp. 1	root	MEA	JXJDZC
JAUCC 5140	PV586751	*Phaeoacremonium alvesii*	NR_136054	*Phaeoacremonium* sp. 1	root	YpSs	AHXCJB

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5141	PV586752	*Phaeoacremonium alvesii*		*Phaeoacremonium* sp. 1	root	YpSs	AHXCJB
JAUCC 5142	PV586753	*Fusarium sp.*		*Fusarium* sp. 2	root	MEA	GXHCLC
JAUCC 5143	PV586754	*Fusarium perseae*	OP020705	*Fusarium* sp. 7	root	RBA	GXHCLC
JAUCC 5144	PV586755	*Fusarium oxysporum*		*Fusarium* sp. 11	root	RBA	GXHCLC
JAUCC 5145	PV586756	*Clonostachys rose*		*Clonostachys* sp. 3	root	RBA	GXHCLC
JAUCC 5146	PV586757	*Fusarium sporotrichioides*	ON860846	*Fusarium* sp. 8	root	PCA	GXHCLC
JAUCC 5147	PV586758	*Penicillium janthinellum*	KM268666	*Penicillium* sp. *5*	root	YpSs	GXHCLC
JAUCC 5148	PV586759	*Aureobasidium pullulans*	PV363903	*Aureobasidium* sp.	stem	RBA	JXJDZC
JAUCC 5149	PV586760	*Ascochyta medicaginicola*	KX381183	*Ascochyta* sp. 1	leaf	OA	AHXCJB
JAUCC 5150	PV586761	*Alternaria alternata*		*Alternaria* sp. 1	leaf	YpSs	JXGZGX
JAUCC 5151	PV586762	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXGZGX
JAUCC 5152	PV586763	*Aspergillus aculeatus_*	ON790320	*Aspergillus* sp. 3	leaf	MEA	JXGZGX
JAUCC 5153	PV586764	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PCA	JXGZGX
JAUCC 5154	PV586765	*Curvularia trifolii*	PP837870	*Curvularia* sp. 4	leaf	YpSs	JXGZGX
JAUCC 5155	PV586766	*Alternaria alternata*		*Alternaria* sp. 1	leaf	YpSs	JXGZGX
JAUCC 5156	PV586767	*Periconia macrospinosa*		*Periconia* sp. 3	leaf	OA	JXGZGX
JAUCC 5157	PV586768	*Periconia macrospinosa*	KT385782	*Periconia* sp. 3	leaf	PCA	JXGZGX
JAUCC 5194	PV586769	*Phaeoacremonium alvesii*		*Phaeoacremonium* sp. 1	root	RBA	AHXCJB
JAUCC 5195	PV586770	*Fusarium sp.*		*Fusarium* sp. 2	root	RBA	GXHCLC
JAUCC 5197	PV586771	*Acrocalymma arengae*	NR_185734	*Acrocalymma* sp. 1	stem	RBA	JXJDZC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5201	PV586772	*Didymella glomerata*		*Didymella* sp. 1	leaf	MEA	JXGZGX
JAUCC 5202	PV586773	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXGZGX
JAUCC 5203	PV586774	*Periconia echinochloae*	MW081310	*Periconia* sp. 2	leaf	RBA	JXGZGX
JAUCC 5204	PV586775	*Fusarium falciforme*		*Fusarium* sp. 3	root	RBA	JXYCTG
JAUCC 5205	PV586776	*Clonostachys rogersoniana*		*Clonostachys* sp. 2	root	RBA	JXYCTG
JAUCC 5206	PV586777	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXZSYC
JAUCC 5207	PV586778	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	RBA	HNCZWX
JAUCC 5208	PV586779	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	root	YpSs	HNCZWX
JAUCC 5209	PV586780	*Penicillium janthinellum*	KM013447	*Penicillium* sp. 5	root	RBA	HNCZWX
JAUCC 5210	PV586781	*Fusarium oxysporum*		*Fusarium* sp. 11	root	PDA	HNCZWX
JAUCC 5211	PV586782	*Fusarium oxysporum*		*Fusarium* sp. 11	root	YpSs	HNCZWX
JAUCC 5212	PV586783	*Didymella glomerata*		*Didymella* sp. 1	root	RBA	HNCZWX
JAUCC 5213	PV586784	*Paraboeremia selaginellae*	KT224856	*Paraboeremia* sp. 1	root	PCA	HNCZWX
JAUCC 5214	PV586785	*Penicillium crustosum*	MT298910	*Penicillium* sp. 1	root	RBA	HNCZWX
JAUCC 5215	PV586786	*Pochonia chlamydosporia*	MH483889	*Pochonia* sp. 1	root	RBA	HNCZWX
JAUCC 5216	PV586787	*Clonostachys rosea*		*Clonostachys* sp. 3	root	RBA	HNCZWX
JAUCC 5217	PV586788	*Penicillium pulvillorum*	MK450709	*Penicillium* sp. 2	root	PDA	HNCZWX
JAUCC 5218	PV586789	*Didymella glomerata*		*Didymella* sp. 1	root	YpSs	HNCZWX
JAUCC 5219	PV586790	*Fusarium oxysporum*		*Fusarium* sp. 11	root	OA	HNCZWX
JAUCC 5220	PV586791	*Alternaria alternata*		*Alternaria* sp. 1	root	MEA	HNCZWX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5221	PV586792	*Ilyonectria robusta*	OK31701	*Ilyonectria* sp. 1	root	RBA	HNCZWX
JAUCC 5222	PV586793	*Alternaria alternata*		*Alternaria* sp. 1	root	PDA	JXZSYC
JAUCC 5223	PV586794	*Fusarium falciforme*		*Fusarium* sp. 3	root	OA	GXHCLC
JAUCC 5224	PV586795	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	root	MEA	JXJDZC
JAUCC 5225	PV586796	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	root	PDA	JXJDZC
JAUCC 5226	PV586797	*Didymella sancta*	MH861588	*Didymella* sp. 2	root	PDA	JXJDZC
JAUCC 5227	PV586798	*Fusarium proliferatum*		*Fusarium* sp. 12	root	PDA	JXJDZC
JAUCC 5228	PV586799	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	root	PCA	JXJDZC
JAUCC 5229	PV586800	*Diaporthe caryae*		*Diaporthe* sp. 1	stem	PCA	JXZSYC
JAUCC 5230	PV586801	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	stem	MEA	HNCZWX
JAUCC 5231	PV586802	*Diaporthe hongkongensis*		*Diaporthe* sp. 38	stem	YpSs	HNCZWX
JAUCC 5232	PV586803	*Pseudopithomyces maydicus*	MN783091	*Pseudopithomyces* sp. 2	stem	RBA	HNCZWX
JAUCC 5233	PV586804	*Amphisphaeria micheliae*		*Amphisphaeria* sp. 2	stem	RBA	HNCZWX
JAUCC 5234	PV586805	*Pestalotiopsis trachycarpicola*		*Pestalotiopsis* sp. 3	stem	YpSs	HNCZWX
JAUCC 5235	PV586806	*Alternaria alternata*		*Alternaria* sp. 1	stem	YpSs	HNCZWX
JAUCC 5236	PV586807	*Diaporthe palmicola*	KF496905	*Diaporthe* sp. 19	stem	YpSs	HNCZWX
JAUCC 5237	PV586808	*Diaporthe sojae*		*Diaporthe* sp. 5	stem	YpSs	HNCZWX
JAUCC 5238	PV586809	*Pestalotiopsis hainanensis*	MG820096	*Pestalotiopsis* sp. 1	stem	OA	HNCZWX
JAUCC 5239	PV586810	*Diaporthe penetriteum*		*Diaporthe* sp. 10	stem	PCA	HNCZWX
JAUCC 5240	PV586811	*Gliocladiopsis tenuis*		*Gliocladiopsis* sp. 1	stem	RBA	HNCZWX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5241	PV586812	*Annulohypoxylon bovei var. microspora*	EF026141	*Annulohypoxylon* sp. 2	stem	PCA	JXYTWF
JAUCC 5242	PV586813	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	PCA	JXJDZC
JAUCC 5243	PV586814	*Cladosporium cladosporioides*	KF876823	*Cladosporium* sp. 1	stem	MEA	JXJDZC
JAUCC 5244	PV586815	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	RBA	JXYTWF
JAUCC 5245	PV586816	*Alternaria alternata*		*Alternaria* sp. 1	stem	PDA	HNCZWX
JAUCC 5246	PV586817	*Alternaria alternata*		*Alternaria* sp. 1	stem	MEA	AHXCJB
JAUCC 5247	PV586818	*Didymella sancta*		*Didymella* sp. 2	stem	PDA	AHXCJB
JAUCC 5248	PV586819	*Thyridium endophyticum*	MT271971	*Thyridium* sp. 1	stem	RBA	AHXCJB
JAUCC 5249	PV586820	*Neodidymella thailandicum*		*Neodidymella* sp. 1	stem	RBA	GXHCLC
JAUCC 5250	PV586821	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	leaf	YpSs	HNCZWX
JAUCC 5251	PV586822	*Cercospora capsici*		*Cercospora* sp. 1	leaf	RBA	HNCZWX
JAUCC 5253	PV586823	*Alternaria longissima*	KY982678	*Alternaria* sp. 3	leaf	RBA	HNCZWX
JAUCC 5254	PV586824	*Colletotrichum boninense*		*Colletotrichum* sp. 5	leaf	PDA	HNCZWX
JAUCC 5255	PV586825	*Colletotrichum boninense*		*Colletotrichum* sp. 5	leaf	PDA	HNCZWX
JAUCC 5256	PV586826	*Phaeosphaeria musae*	OR438358	*Phaeosphaeria* sp. 1	leaf	RBA	HNCZWX
JAUCC 5257	PV586827	*Colletotrichum boninense*		*Colletotrichum* sp. 5	leaf	RBA	HNCZWX
JAUCC 5258	PV586828	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	HNCZWX
JAUCC 5259	PV586829	*Colletotrichum boninense*		*Colletotrichum* sp. 5	leaf	RBA	HNCZWX
JAUCC 5260	PV586830	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	RBA	HNCZWX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5261	PV586831	*Phaeosphaeria musae*		*Phaeosphaeria* sp. 1	leaf	RBA	HNCZWX
JAUCC 5262	PV586832	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	RBA	HNCZWX
JAUCC 5263	PV586833	*Nemania diffusa*		*Nemania* sp. 3	leaf	RBA	JXYTWF
JAUCC 5264	PV586834	*Diaporthe hongkongensis*		*Diaporthe* sp. 37	leaf	RBA	JXYTWF
JAUCC 5265	PV586835	*Diaporthe caryae*		*Diaporthe* sp. 42	leaf	PCA	JXYTWF
JAUCC 5266	PV586836	*Colletotrichum plurivorum*		*Colletotrichum* sp. 8	leaf	PCA	JXYTWF
JAUCC 5267	PV586837	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	YpSs	JXJDZC
JAUCC 5268	PV586838	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	leaf	PCA	JXJDZC
JAUCC 5269	PV586839	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	AHXCJB
JAUCC 5270	PV586840	*Didymella glomerata*		*Didymella* sp. 1	leaf	PDA	AHXCJB
JAUCC 5271	PV586841	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PCA	AHXCJB
JAUCC 5272	PV586842	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJDZC
JAUCC 5273	PV586843	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXJDZC
JAUCC 5274	PV586844	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	MEA	JXJDZC
JAUCC 5275	PV586845	*Alternaria alternata*		*Alternaria* sp. 1	leaf	MEA	JXJDZC
JAUCC 5276	PV586846	*Periconia byssoides*	LC014582	*Periconia* sp. 1	leaf	YpSs	JXJDZC
JAUCC 5277	PV586847	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PCA	JXJDZC
JAUCC 5278	PV586848	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXJDZC
JAUCC 5279	PV586849	*Diaporthe goulteri*	ON197578	*Diaporthe* sp. 6	leaf	RBA	JXJDZC
JAUCC 5280	PV586850	*Periconia byssoides*		*Periconia* sp. 1	leaf	OA	JXJDZC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5281	PV586851	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	PCA	GXHCLC
JAUCC 5282	PV586852	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	PCA	GXHCLC
JAUCC 5283	PV586853	*Pestalotiopsis trachycarpicola*		*Pestalotiopsis* sp. 3	leaf	PCA	GXHCLC
JAUCC 5284	PV586854	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	YpSs	GXHCLC
JAUCC 5285	PV586855	*Alternaria alternata*		*Alternaria* sp. 1	leaf	YpSs	GXHCLC
JAUCC 5286	PV586856	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	PDA	GXHCLC
JAUCC 5287	PV586857	*Stagonosporopsis valerianellae*	KP128007	*Stagonosporopsis* sp. 1	leaf	YpSs	AHXCJB
JAUCC 5288	PV586858	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	YpSs	AHXCJB
JAUCC 5289	PV586859	*Curvularia falsilunata*	MN215660	*Curvularia* sp. 3	leaf	PCA	AHXCJB
JAUCC 5290	PV586860	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PCA	AHXCJB
JAUCC 5291	PV586861	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PCA	AHXCJB
JAUCC 5292	PV586862	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	AHXCJB
JAUCC 5293	PV586863	*Fusarium graminearum*	MW722991	*Fusarium* sp. 10	leaf	RBA	AHXCJB
JAUCC 5294	PV586864	*Neodidymella thailandicum*		*Neodidymella* sp. 1	stem	RBA	JXJDZF
JAUCC 5295	PV586865	*Colletotrichum fioriniae*		*Colletotrichum* sp. 2	stem	PDA	JXYTWF
JAUCC 5296	PV586866	*Fusarium proliferatum*		*Fusarium* sp. 12	root	PDA	GXHCLC
JAUCC 5297	PV586867	*Phaeoacremonium alvesii*		*Phaeoacremonium* sp. 1	root	PDA	AHXCJB
JAUCC 5298	00869213	*Dactylaria acerosa*		*Funiliomyces* sp. 1	root	PDA	JXGZGX
JAUCC 5299	PV586868	*Purpureocillium roseum*		*Purpureocillium* sp. 1	root	PDA	JXGZGX
JAUCC 5300	PV586869	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	RBA	JXGZGX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5301	PV586870	*Clonostachys rosea*		*Clonostachys* sp. 3	root	MEA	JXGZGX
JAUCC 5302	PV586871	*Fusarium falciforme*		*Fusarium* sp. 3	root	MEA	AHXCJB
JAUCC 5303	PV586872	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXGZGX
JAUCC 5540	PV586873	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PDA	JXGZGX
JAUCC 5541	PV586874	*Gibellulopsis nigrescens*	MH856082	*Gibellulopsis* sp. 1	root	PCA	JXJAXG
JAUCC 5542	PV586875	*Fusarium decemcellulare*	LC055813	*Fusarium* sp. 15	root	MEA	AHXCJB
JAUCC 5543	PV586876	*Clonostachys rosea*		*Clonostachys* sp. 3	root	RBA	JXJAXG
JAUCC 5544	PV586877	*Diaporthe caryae*		*Diaporthe* sp. 42	stem	RBA	JXGZGX
JAUCC 5545	PV586878	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	RBA	JXJAXG
JAUCC 5546	PV586879	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	RBA	JXJDZF
JAUCC 5547	PV586880	*Alternaria padwickii*	GU373650	*Alternaria* sp. 2	stem	RBA	JXJDZF
JAUCC 5548	PV586881	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	RBA	JXJDZF
JAUCC 5549	PV586882	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	PCA	JXGZGX
JAUCC 5550	PV586883	*Annulohypoxylon stygium*		*Annulohypoxylon* sp. 1	stem	RBA	JXGZGX
JAUCC 5551	PV586884	*Gongronella butleri*	MK336439	Gongronella sp. 1	stem	PDA	JXGZGX
JAUCC 5552	PV586885	*Fusarium equiseti*	MH707080	*Fusarium* sp. 1	stem	PCA	JXJDZF
JAUCC 5553	PV586886	*Fusarium equiseti*		*Fusarium* sp. 1	stem	PCA	JXJDZF
JAUCC 5554	PV586887	*Fusarium proliferatum*		*Fusarium* sp. 12	leaf	OA	JXJAXG
JAUCC 5555	PV586888	*Fusarium biseptatum*	MG543699	*Fusarium* sp. 4	leaf	PDA	JXJDZF
JAUCC 5556	PV586889	*Nemania dendrobii*		*Nemania* sp. 2	leaf	OA	JXSRYS

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5557	PV586890	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PCA	JXSRYS
JAUCC 5558	PV586891	*Fusarium oxysporum*		*Fusarium* sp. 11	leaf	OA	JXJAXG
JAUCC 5559	PV586892	*Fusarium equiseti*		*Fusarium* sp. 1	leaf	RBA	JXJAXG
JAUCC 5560	PV586893	*Periconia byssoides*		*Periconia* sp. 1	leaf	MEA	JXJDZF
JAUCC 5561	PV586894	*Fusarium equiseti*		*Fusarium* sp. 1	leaf	PCA	JXJDZF
JAUCC 5562	PV586895	*Fusarium oxysporum*		*Fusarium* sp. 11	leaf	OA	JXJDZF
JAUCC 5563	PV586896	*Curvularia eragrostidis*	PP887992	*Curvularia* sp. 6	leaf	RBA	JXJAXG
JAUCC 5564	PV586897	*Curvularia aeria*	OR101252	*Curvularia* sp. 5	leaf	RBA	JXJAXG
JAUCC 5565	PV586898	*Periconia byssoides*	OR237684	*Periconia* sp. 1	leaf	YpSs	JXJDZF
JAUCC 5566	PV586899	*Phaeosphaeria papayae*	KT224848	*Phaeosphaeria* sp. 3	leaf	YpSs	JXJDZF
JAUCC 5567	PV586900	*Colletotrichum truncatum*	OR975570	*Colletotrichum* sp. 6	root	PDA	JXZSSJ
JAUCC 5568	PV586901	*Fusarium falciforme*		*Fusarium* sp. 3	root	PDA	JXZSSJ
JAUCC 5569	PV586902	*Fusarium decemcellulare*		*Fusarium* sp. 15	root	MEA	AHXCJB
JAUCC 5570	PV586903	*Epicoccum thailandicum*		*Epicoccum* sp. 2	root	PDA	JXJAXG
JAUCC 5571	PV586904	*Sarocladium implicatum*	JQ69216	*Sarocladium* sp. 1	stem	PCA	JXGZGX
JAUCC 5572	PV586905	*Sarocladium implicatum*		*Sarocladium* sp. 1	stem	PDA	JXGZGX
JAUCC 5573	PV586906	*Diaporthe incompleta*	NR_152471	*Diaporthe* sp. 35	stem	RBA	JXGZGX
JAUCC 5574	PV586907	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	stem	MEA	JXJAXG
JAUCC 5575	PV586908	*Diaporthe jiangxiensis*		*Diaporthe* sp. 47	stem	PDA	JXZSSJ
JAUCC 5576	PV586909	*Curvularia geniculata*		*Curvularia* sp. 1	stem	MEA	JXJAXG

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5577	PV586910	*Neodidymella thailandicum*		*Neodidymella* sp. 1	stem	RBA	JXJDZF
JAUCC 5578	PV586911	*Fusarium ngaiotongaense*	MW016714	*Fusarium* sp. 6	stem	MEA	JXJAXG
JAUCC 5579	PV586912	*Epicoccum thailandicum*	OP163601	*Epicoccum* sp. 2	stem	MEA	JXGZGX
JAUCC 5580	PV586913	*Sarocladium implicatum*		Sarocladium sp. 1	stem	MEA	JXGZGX
JAUCC 5581	PV586914	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	PDA	JXJDZF
JAUCC 5582	PV586915	*Sarocladium implicatum*		*Sarocladium* sp. 1	stem	PDA	JXGZGX
JAUCC 5583	PV586916	*Plectosphaerella cucumerina*	MZ350158	*Plectosphaerella* sp. 1	leaf	PDA	AHXCJB
JAUCC 5584	PV586917	*Curvularia geniculata*		*Curvularia* sp. 1	leaf	PCA	JXJAXG
JAUCC 5585	PV586918	*Alternaria alternata*		*Alternaria* sp. 1	leaf	MEA	JXZSSJ
JAUCC 5586	PV586919	*Boeremia linicola*	OP596032	*Boeremia* sp. 1	leaf	OA	JXJDZF
JAUCC 5587	PV586920	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	OA	JXSRYS
JAUCC 5588	PV586921	*Colletotrichum karsti*	PQ624705	*Colletotrichum* sp. 1	leaf	PCA	JXSRYS
JAUCC 5589	PV586922	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PCA	JXJAXG
JAUCC 5590	PV586923	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	MEA	JXJDZF
JAUCC 5591	PV586924	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PCA	JXJDZF
JAUCC 5592	PV586925	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	PCA	JXJDZF
JAUCC 5593	PV586926	*Didymella glomerata*		*Didymella* sp. 1	leaf	PCA	JXJDZF
JAUCC 5594	PV586927	*Alternaria alternata*		*Alternaria* sp. 1	leaf	YpSs	JXJDZF
JAUCC 5595	PV586928	*Curvularia lunata*	MG642982	*Curvularia* sp. 2	leaf	RBA	JXJAXG
JAUCC 5596	PV586929	*Corynespora cassiicola*		*Corynespora* sp. 1	leaf	OA	JXJDZF

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5597	PV586930	*Periconia byssoides*		*Periconia* sp. 1	leaf	OA	JXJDZF
JAUCC 5598	PV586931	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PCA	JXJDZF
JAUCC 5599	PV586932	*Clonostachys rosea*		*Clonostachys* sp. 3	root	RBA	JXJDZF
JAUCC 5600	PV586933	*Epicoccum thailandicum*	PQ643459	*Epicoccum* sp. 2	root	RBA	JXJAXG
JAUCC 5601	PV586934	*Fusarium proliferatum*		*Fusarium* sp. 12	root	RBA	JXJAXG
JAUCC 5602	PV586935	*Ilyonectria radicicola*	KF894993	*Ilyonectria* sp. 2	root	RBA	JXJAXG
JAUCC 5603	PV586936	*Colletotrichum truncatum*	MF990608	*Colletotrichum* sp. 6	root	PDA	JXZSSJ
JAUCC 5604	PV586937	*Gibellulopsis nigrescens*		*Gibellulopsis* sp. 1	stem	PDA	JXGZGX
JAUCC 5605	PV586938	*Sarocladium implicatum*		*Sarocladium* sp. 1	stem	PDA	JXGZGX
JAUCC 5606	PV586939	*Moesziomyces bullatus*	OQ415397	*Moesziomyces* sp. 2	leaf	PDA	JXGZGX
JAUCC 5607	PV586940	*Corynespora cassiicola*		*Corynespora* sp. 1	leaf	MEA	JXJDZF
JAUCC 5608	PV586941	*Periconia byssoides*	OR805513	*Periconia* sp. 1	leaf	PCA	JXJDZF
JAUCC 5609	PV586942	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXSRYS
JAUCC 5610	PV586943	*Fusarium proliferatum*		*Fusarium* sp. 12	leaf	RBA	JXJDZF
JAUCC 5611	PV586944	*Alternaria alternata*		*Alternaria* sp. 1	leaf	RBA	JXSRYS
JAUCC 5612	PV586945	*Diaporthe cotoneastri*		*Diaporthe* sp. 36	leaf	RBA	JXSRYS
JAUCC 5613	PV586946	*Didymella glomerata*		*Didymella* sp. 1	leaf	RBA	JXSRYS
JAUCC 5614	PV586947	*Stagonospora bicolor*	PP217004	*Stagonospora* sp. 1	leaf	RBA	JXSRYS
JAUCC 5615	PV586948	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	JXZSSJ
JAUCC 5616	PV586949	*Amphisphaeria mangrovei*		*Amphisphaeria* sp. 1	root	PCA	JXJDZF

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 5617	PV586950	*Fusarium oxysporum*		*Fusarium* sp. 11	root	RBA	JXJDZF
JAUCC 5618	PV586951	*Albifimbria verrucaria*	KX138396	*Albifimbria* sp. 1	root	PDA	JXJDZF
JAUCC 5619	PV586952	*Talaromyces pinophilus*	KU729085	*Trichoderma* sp. 2	root	RBA	JXJDZF
JAUCC 5620	PV586953	*Fusarium biseptatum*		*Fusarium* sp. 4	root	RBA	JXJDZF
JAUCC 5621	PV586954	*Clonostachys epichloe*	PQ382814	*Clonostachys* sp. 1	stem	PCA	JXJDZF
JAUCC 5622	PV586955	*Colletotrichum truncatum*		*Colletotrichum* sp. 6	stem	PDA	JXZSSJ
JAUCC 5623	PV586956	*Diaporthe eres*		*Diaporthe* sp. 18	stem	MEA	JXJDZF
JAUCC 5624	PV586957	*Diaporthe discoidispora*		*Diaporthe* sp. 14	stem	OA	JXJDZF
JAUCC 5625	PV586958	*Colletotrichum truncatum*		*Colletotrichum* sp. 6	leaf	PDA	JXJDZF
JAUCC 6543	PV586959	*Penicillifer diparietisporus*		*Penicillifer* sp. 1	root	PDA	GXHCLC
JAUCC 6544	PV586960	*Exophiala pisciphila*	OW983546	*Exophiala* sp. 1	root	PDA	HNCZDZ
JAUCC 6545	PV586961	*Thyridium curvatum*	PQ803355	*Thyridium* sp. 2	root	PDA	GXHCLC
JAUCC 6546	PV082617	*Cyphellophora deltoidea*	NR_153555	*Cyphellophora* sp. 1	root	PDA	GXHCLC
JAUCC 6547	PV082616	*Cyphellophora deltoidea*		*Cyphellophora* sp. 1	root	PDA	GXHCLC
JAUCC 6548	PV586962	*Thyridium cornearis*	MH865903	*Thyridium* sp. 3	root	PDA	GXHCLC
JAUCC 6549	PV586963	*Alternaria alternata*		*Alternaria* sp. 1	fruit	PDA	JXZSCF
JAUCC 6550	PV586964	*Pestalotiopsis trachycarpicola*	OR002107	*Pestalotiopsis* sp. 3	fruit	PDA	JXJJDA
JAUCC 6551	PV586965	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	PDA	JXJJDA
JAUCC 6552	PV586966	*Alternaria alternata*		*Alternaria* sp. 1	fruit	PDA	JXJJDA
JAUCC 6553	PV586967	*Colletotrichum fructicola*	MK041479	*Colletotrichum* sp. 10	fruit	PDA	GXHCLC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6554	PV586968	*Colletotrichum plurivorum*		*Colletotrichum* sp. 8	fruit	PDA	AHXCTJ
JAUCC 6555	PV586969	*Colletotrichum nymphaeae*		*Colletotrichum* sp. 3	fruit	PDA	GXHCLC
JAUCC 6556	PV586970	*Nigrospora hainanensis*	OQ473493	*Nigrospora* sp. 1	fruit	PDA	GXHCLC
JAUCC 6558	PV586971	*Neosetophoma poaceicola*		*Neosetophoma* sp. 1	fruit	PDA	JXJJDA
JAUCC 6559	PV586972	*Phaeosphaeria musae*		*Phaeosphaeria* sp. 1	fruit	PDA	JXJJDA
JAUCC 6560	PV586973	*Fusarium lateritium*		*Fusarium* sp. 14	fruit	PDA	GXHCLC
JAUCC 6561	PV586974	*Phaeosphaeria oryzae*	OK510235	*Phaeosphaeria* sp. 2	fruit	PDA	GXHCLC
JAUCC 6562	PV586975	*Cladosporium cladosporioides*	MF044039	*Cladosporium* sp. 1	fruit	PDA	JXJJDA
JAUCC 6563	PV586976	*Macroconia gigas*	OR654960	*Macroconia* sp. 1	fruit	PDA	JXJJDA
JAUCC 6564	PV586977	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	GXHCLC
JAUCC 6565	PV586978	*Corynespora cassiicola*		*Corynespora* sp. 1	fruit	PDA	GXHCLC
JAUCC 6566	PV586979	*Fusarium proliferatum*	MZ400581	*Fusarium* sp. 12	fruit	PDA	GXHCLC
JAUCC 6567	PV586980	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	GXHCLC
JAUCC 6568	PV586981	*Alternaria alternata*		*Alternaria* sp. 1	fruit	PDA	JXZSCF
JAUCC 6569	PV586982	*Simplicillium subtropicum*	AB604001	*Simplicillium* sp. 1	stem	PDA	AHXCTJ
JAUCC 6570	PV330325	*Pseudokeissleriella bambusicola*	PP545294	*Pseudokeissleriella* sp. 1	stem	PDA	AHXCTJ
JAUCC 6571	PV586983	*Neopyrenochaeta telephoni*	MZ422998	*Neopyrenochaeta* sp. 1	stem	PDA	HNCZDZ
JAUCC 6572	PV586984	*Nigrograna jinghongensis*	PQ895912	*Nigrograna* sp. 1	stem	PDA	AHXCTJ
JAUCC 6573	PV586985	*Talaromyces trachyspermus*	MT279505	*Talaromyces* sp. 1	stem	PDA	HNCZDZ
JAUCC 6574	PV586986	*Pyrenochaeta inflorescentiae*	GU361962	*Pyrenochaeta* sp. 1	stem	PDA	JXJJDA

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6575	PV586987	*Gibellulopsis nigrescens*		*Gibellulopsis* sp. 1	stem	PDA	HNCZDZ
JAUCC 6576	PV586988	*Neoroussoella_solani*	OQ789363	*Neoroussoella* sp. 1	stem	PDA	AHXCTJ
JAUCC 6577	PV586989	*Neoroussoella solani*		*Neoroussoella* sp. 1	stem	PDA	AHXCTJ
JAUCC 6578	PV330326	*Pseudokeissleriella bambusicola*		*Pseudokeissleriella* sp. 1	stem	PDA	AHXCTJ
JAUCC 6579	PV586990	*Fomitopsis tianshanensis*	MN148256	*Fomitopsis* sp. 1	stem	PDA	AHXCTJ
JAUCC 6581	PV586991	*Gibellulopsis nigrescens*	KC156644	*Gibellulopsis* sp. 1	stem	PDA	AHXCTJ
JAUCC 6582	PQ895913	*Nigrograna jinghongensis*		*Nigrograna* sp. 1	stem	PDA	AHXCTJ
JAUCC 6583	PV586992	*Acrocalymma arengae*		*Acrocalymma* sp.1	stem	PDA	AHXCTJ
JAUCC 6584	PV586993	*Acrocalymma arengae*		*Acrocalymma* sp. 1	stem	PDA	AHXCTJ
JAUCC 6585	PV586994	*Simplicillium subtropicum*		*Simplicillium* sp. 1	stem	PDA	AHXCTJ
JAUCC 6586	PV330327	*Pseudokeissleriella bambusicola*		*Pseudokeissleriella* sp. 1	stem	PDA	AHXCTJ
JAUCC 6587	PV586995	*Parathyridaria ramulicola*	MN788609	*Parathyridaria* sp. 1	stem	PDA	AHXCTJ
JAUCC 6588	PV586996	*Exserohilum rostratum*	MW362495	*Exserohilum* sp. 1	leaf	PDA	JXZSCF
JAUCC 6589	PV586997	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXJJDA
JAUCC 6590	PV586998	*Diaporthe nobilis*		*Diaporthe* sp. 17	leaf	PDA	JXZSCF
JAUCC 6591	PV586999	*Cladosporium cladosporioides*		*Cladosporium* sp. 1	leaf	PDA	GXHCLC
JAUCC 6592	PV587000	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXZSCF
JAUCC 6593	PV587001	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXZSCF
JAUCC 6594	PV587002	*Zasmidium pearceae*	NR_185743	*Zasmidium* sp. 1	leaf	PDA	GXHCLC
JAUCC 6595	PV587003	*Diaporthe caryae*		*Diaporthe* sp. 1	leaf	PDA	JXZSCF

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6596	PV587004	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXZSCF
JAUCC 6597	PV587005	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXZSCF
JAUCC 6598	PV587006	*Cladosporium cladosporioides*		*Cladosporium* sp. 1	leaf	PDA	JXJJDA
JAUCC 6599	PV587007	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXZSCF
JAUCC 6600	PV587008	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXZSCF
JAUCC 6601	PV587009	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXJJDA
JAUCC 6602	PV587010	*Cladosporium cladosporioides*		*Cladosporium* sp. 1	leaf	PDA	JXJJDA
JAUCC 6603	PV587011	*Cercospora capsici*		*Cercospora* sp. 1	leaf	PDA	JXJJDA
JAUCC 6604	PV587012	*Phyllosticta capitalensis*		*Phyllosticta* sp. 1	leaf	PDA	JXJJDA
JAUCC 6605	PV587013	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXJJDA
JAUCC 6606	PV587014	*Pestalotiopsis microspora*		*Pestalotiopsis* sp. 4	leaf	PDA	JXJJDA
JAUCC 6607	PV587015	*Penicillium jiangxiense*		*Penicillium* sp. 6	stem	PDA	HNCZDZ
JAUCC 6838	PV587016	*Pseudallescheria angusta*	MT803042	*Pseudallescheria* sp. 1	root	RBA	JXJJRC
JAUCC 6839	PV587017	*Epicoccum thailandicum*		*Epicoccum* sp. 2	root	RBA	JXZSSJ
JAUCC 6840	PV587018	*Clonostachys rosea*		*Clonostachys* sp. 3	root	PCA	JXSRYS
JAUCC 6841	PV587019	*Fusarium biseptatum*		*Fusarium* sp. 4	root	PDA	JXZSSJ
JAUCC 6842	PV587020	*Colletotrichum nymphaeae*		*Colletotrichum* sp. 3	fruit	PDA	GXHCLC
JAUCC 6843	PV587021	*Botryosphaeria dothidea*		*Botryosphaeria* sp. 1	fruit	PDA	GXHCLC
JAUCC 6844	PV587022	*Fusarium lateritium*	MT940457	*Fusarium* sp. 14	fruit	PDA	GXHCLC
JAUCC 6845	PV587023	*Fusarium lateritium*		*Fusarium* sp. 14	fruit	PDA	GXHCLC

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6846	PV587024	*Colletotrichum plurivorum*		*Colletotrichum* sp. 8	fruit	PDA	AHXCTJ
JAUCC 6847	PV587025	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	PDA	AHXCTJ
JAUCC 6848	PV587026	*Fusarium equiseti*		*Fusarium* sp. 1	fruit	PDA	AHXCTJ
JAUCC 6849	PV587027	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	PDA	AHXCTJ
JAUCC 6850	PV587028	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	PDA	AHXCTJ
JAUCC 6851	PV587029	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	fruit	PDA	AHXCTJ
JAUCC 6852	PV587030	*Fusarium equiseti*		*Fusarium* sp. 1	fruit	PDA	GXHCLC
JAUCC 6853	PV587031	*Colletotrichum nymphaeae*		*Colletotrichum* sp. 3	fruit	PDA	GXHCLC
JAUCC 6854	PV587032	*Colletotrichum kahawae*		*Colletotrichum* sp. 9	fruit	PDA	GXHCLC
JAUCC 6855	PV587033	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	AHXCTJ
JAUCC 6856	PV587034	*Colletotrichum nymphaeae*		*Colletotrichum* sp. 3	fruit	PDA	GXHCLC
JAUCC 6857	PV587035	*Colletotrichum nymphaeae*		*Colletotrichum* sp. 3	fruit	PDA	AHXCTJ
JAUCC 6858	PV587036	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	AHXCTJ
JAUCC 6859	PV587037	*Fusarium proliferatum*		*Fusarium* sp. 12	fruit	PDA	GXHCLC
JAUCC 6860	PV587038	*Fusarium graminearum*		*Fusarium* sp. 10	fruit	PDA	GXHCLC
JAUCC 6861	PV587039	*Fusarium equiseti*	MK611672	*Fusarium* sp. 1	fruit	PDA	GXHCLC
JAUCC 6862	PV587040	*Amphisphaeria micheliae*	MT756625	*Amphisphaeria* sp. 2	stem	RBA	HNCZWX
JAUCC 6863	PV587041	*Botryosphaeria dothidea*		*Botryosphaeria* sp.1	stem	PDA	HNCZDZ
JAUCC 6864	PV587042	*Schizophyllum commune*	OQ78461	*Schizophyllum* sp.	stem	PDA	AHXCTJ
JAUCC 6865	PV587043	*Stephanonectria keithii*	MG748630	*Stephanonectria* sp. 1	stem	PDA	AHXCTJ

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6866	PV587044	*Gibellulopsis nigrescens*		*Gibellulopsis* sp. 1	stem	PDA	AHXCTJ
JAUCC 6867	PV587045	*Acremonium antarcticum*	KU183664	*Acremonium* sp. 1	stem	PDA	AHXCTJ
JAUCC 6868	PQ895912	*Nigrograna jinghongensis*		*Nigrograna* sp. 1	stem	PDA	AHXCTJ
JAUCC 6869	PV587046	*Colletotrichum gigasporum*		*Colletotrichum* sp. 7	stem	PDA	AHXCTJ
JAUCC 6870	PV587047	*Fusarium proliferatum*		*Fusarium* sp. 12	stem	PDA	JXSRYS
JAUCC 6871	PV587048	*Didymella glomerata*		*Didymella* sp. 1	stem	PDA	JXSRYS
JAUCC 6872	PV587049	*Gibellulopsis nigrescens*		*Gibellulopsis* sp. 1	stem	PDA	JXZSSJ
JAUCC 6873	PV587050	*Didymella glomerata*		*Didymella* sp. 1	stem	PDA	JXSRYS
JAUCC 6874	PV587051	*Diaporthe pseudomangiferae*		*Diaporthe* sp. 11	stem	PDA	JXZSSJ
JAUCC 6875	PV587052	*Diaporthe pseudomangiferae*		*Diaporthe* sp. 11	stem	PDA	JXZSSJ
JAUCC 6876	PV587053	*Pestalotiopsis trachycarpicola*		*Pestalotiopsis* sp. 3	stem	PDA	JXSRYS
JAUCC 6877	PV587054	*Didymella glomerata*		*Didymella* sp. 1	stem	PDA	JXSRYS
JAUCC 6878	PV587055	*Pestalotiopsis mangiferae*		*Pestalotiopsis* sp. 4	stem	PDA	JXSRYS
JAUCC 6879	PV587056	*Fusarium acuminatum*	PP336551	*Fusarium* sp. 9	leaf	PDA	JXSRYS
JAUCC 6880	PV587057	*Epicoccum nigrum*		*Epicoccum* sp. 1	leaf	PDA	JXJJRC
JAUCC 6881	PV587058	*Diaporthe celastrina*		*Diaporthe* sp. 28	leaf	PDA	JXJJRC
JAUCC 6882	PV587059	*Curvularia trifolii*		*Curvularia* sp. 4	leaf	PDA	JXJDZF
JAUCC 6883	PV587060	*Diaporthe celastrina*		*Diaporthe* sp. 27	leaf	PDA	JXSRYS
JAUCC 6884	PV587061	*Didymella glomerata*		*Didymella* sp. 1	leaf	PDA	JXSRYS
JAUCC 6885	PV587062	*Epicoccum nigrum*	PQ788684	*Epicoccum* sp. 1	leaf	PDA	JXSRYS

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6886	PV587063	*Stagonosporopsis valerianellae*		*Stagonosporopsis* sp. 1	leaf	PDA	JXSRYS
JAUCC 6887	PV587064	*Neosetophoma poaceicola*		*Neosetophoma* sp. 1	leaf	PDA	JXSRYS
JAUCC 6888	PV587065	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	PDA	GXHCLC
JAUCC 6889	PV587066	*Diaporthe phaseolorum*		*Diaporthe* sp. 20	leaf	PDA	GXHCLC
JAUCC 6890	PV587067	*Neodidymella thailandicum*		*Neodidymella* sp. 1	leaf	PDA	GXHCLC
JAUCC 6891	PV587068	*Corynespora cassiicola*		Corynespora sp. 1	leaf	PDA	GXHCLC
JAUCC 6892	PV587069	*Leptospora rubella*	OP237234	*Leptospora* sp. 1	leaf	PDA	GXHCLC
JAUCC 6893	PV587070	*Leptospora rubella*		*Leptospora* sp. 1	leaf	PDA	GXHCLC
JAUCC 6894	PV587071	*Curvularia falsilunata*		*Curvularia* sp. 3	leaf	PDA	GXHCLC
JAUCC 6895	PV587072	*Diaporthe pseudooculi*		*Diaporthe* sp. 13	leaf	PDA	GXHCLC
JAUCC 6896	PV587073	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	GXHCLC
JAUCC 6897	PV587074	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	GXHCLC
JAUCC 6898	PV587075	*Diaporthe pseudooculi*		*Diaporthe* sp. 12	leaf	PDA	GXHCLC
JAUCC 6899	PV587076	*Colletotrichum karsti*		*Colletotrichum* sp. 1	leaf	PDA	GXHCLC
JAUCC 6900	PV587077	*Pseudocercospora elaeodendri*	KC172073	*Pseudocercospora* sp. 2	leaf	PDA	JXJJDA
JAUCC 6901	PV587078	*Alternaria alternata*		*Alternaria* sp. 1	leaf	PDA	JXJJDA
JAUCC 6902	PV587079	*Fusarium equiseti*		*Fusarium* sp. 1	leaf	PDA	JXJJDA
JAUCC 6903	PV587080	*Diaporthe hunanensis*		*Diaporthe* sp. 3	fruit	PDA	HNCZWX
JAUCC 6904	PV587081	*Diaporthe tetradii*		*Diaporthe* sp. 23	fruit	PDA	HNCZWX
JAUCC 6907	PV587082	*Pseudocercospora elaeodendri*		*Pseudocercospora* sp. 2	fruit	PDA	HNCZWX

Table 3.1 (continued)

Strain number	Accession number	The closest match taxon	The closest taxon's accession number	Taxon proposed	Tissue	Medium	Sampling Sites (Abbreviation)
JAUCC 6908	PV587083	*Penicillium jiangxiense*	MT611183	*Penicillium* sp. 6	fruit	PDA	HNCZWX
JAUCC 7345	PV587084	*Hypoxylon pilgerianum*	KY610412	*Hypoxylon* sp. 1	leaf	PDA	AHXCTJ
JAUCC 7346	PV587085	*Hypoxylon pilgerianum*		*Hypoxylon* sp. 1	root	PDA	AHXCTJ
JAUCC 7347	PV587086	*Polyschema sclerotigenum*		*Polyschema* sp. 1	root	PDA	JXYCFC
JAUCC 7348	PV587087	*Polyschema sclerotigenum*		*Polyschema* sp. 1	root	PDA	JXYCFC
JAUCC 7349	PV587088	*Polyschema sclerotigenum*		*Polyschema* sp. 1	root	PDA	JXYCFC
JAUCC 7350	PV587089	*Nemania dendrobii*	MZ463138	*Nemania* sp. 2	leaf	PDA	JXYCFC
JAUCC 7351	PV587090	*Zasmidium pearceae*		*Zasmidium* sp. 1	leaf	PDA	JXYCFC
JAUCC 7352	PV587091	*Didymella glomerata*		*Didymella* sp. 1	leaf	PDA	JXYCFC
JAUCC 7353	PV587092	*Curvularia intermedia*	KU856621	*Curvularia* sp. 7	leaf	PDA	JXYCFC
JAUCC 7354	PV587093	*Nemania bipapillata*	MW079960	*Nemania* sp. 1	leaf	PDA	JXYCFC
JAUCC 7355	PV587094	*Leptospora macarangae*		*Leptospora* sp. 2	leaf	PDA	JXYCFC
JAUCC 7356	PV587095	*Leptospora macarangae*	OR229714	*Leptospora* sp. 2	leaf	PDA	JXYCFC
JAUCC 7357	PV587096	*Pseudocercospora elaeodendri*	HQ328000	*Pseudocercospora* sp. 2	leaf	PDA	JXYCFC
JAUCC 7358	PV587097	*Diaporthe tetradii*		*Diaporthe* sp. 23	leaf	PDA	HNCZDZ
JAUCC 7359	PV587098	*Diaporthe hunanensis*		*Diaporthe* sp. 3	leaf	PDA	HNCZDZ

Note The closest taxon's accession number is used for ITS phylogenetic analysis. *Rhizopus koreanus* EML-HO95-1 (KU058202) was used as an outgroup for phylogenetic analysis.

Table 3.2 Number of isolates, isolation frequency, and dominance status of endophytic fungal genera isolated from *Tetradium ruticarpum*

Genus	Number of Isolates	RF (%)	Dominance Status
Aaosphaeria	1	0.1%	Rare
Acremonium	1	0.1%	Rare
Acrocalymma	3	0.3%	Rare
Albifimbria	1	0.1%	Rare
Alternaria	57	6.1%	Common
Amphisphaeria	20	2.1%	Rare
Annulohypoxylon	3	0.3%	Rare
Arcopilus	1	0.1%	Rare
Arthrinium	1	0.1%	Rare
Ascochyta	1	0.1%	Rare
Aspergillus	4	0.4%	Rare
Aureobasidium	1	0.1%	Rare
Austropleospora	1	0.1%	Rare
Biscogniauxia	1	0.1%	Rare
Boeremia	1	0.1%	Rare
Botryosphaeria	42	4.5%	Rare
Cercospora	11	1.2%	Rare
Cladosporium	8	0.9%	Rare
Clonostachys	35	3.7%	Rare
Colletotrichum	93	9.9%	Common
Corynespora	10	1.1%	Rare
Coryneum	2	0.2%	Rare
Curvularia	12	1.3%	Rare
Cyphellophora	2	0.2%	Rare
Daldinia	3	0.3%	Rare
Diaporthe	251	26.8%	Dominant
Didymella	36	3.9%	Rare
Didymocyrtis	3	0.3%	Rare
Epicoccum	32	3.4%	Rare
Exophiala	1	0.1%	Rare
Exserohilum	1	0.1%	Rare
Fomitopsis	1	0.1%	Rare
Funiliomyces	3	0.3%	Rare
Fusarium	86	9.2%	Common

Table 3.2 (continued)

Genus	Number of Isolates	RF (%)	Dominance Status
Gibellulopsis	6	0.6%	Rare
Gliocladiopsis	19	2.0%	Rare
Gongronella	1	0.1%	Rare
Hypoxylon	2	0.2%	Rare
Ilyonectria	2	0.2%	Rare
Induratia	1	0.1%	Rare
Leptospora	4	0.4%	Rare
Macroconia	1	0.1%	Rare
Moesziomyces	2	0.2%	Rare
Muyocopron	2	0.2%	Rare
Nemania	7	0.7%	Rare
Neodidymella	21	2.2%	Rare
Neopyrenochaeta	1	0.1%	Rare
Neoroussoella	2	0.2%	Rare
Neosetophoma	5	0.5%	Rare
Nigrograna	3	0.3%	Rare
Nigrospora	1	0.1%	Rare
Nothophoma	3	0.3%	Rare
Paraboeremia	1	0.1%	Rare
Paraphoma	1	0.1%	Rare
Parathyridaria	1	0.1%	Rare
Penicillifer	3	0.3%	Rare
Penicillium	9	1.0%	Rare
Periconia	9	1.0%	Rare
Pestalotiopsis	14	1.5%	Rare
Phaeoacremonium	5	0.5%	Rare
Phaeosphaeria	5	0.5%	Rare
Phyllosticta	24	2.6%	Rare
Plectosphaerella	1	0.1%	Rare
Pochonia	1	0.1%	Rare
Polyschema	3	0.3%	Rare
Pseudallescheria	1	0.1%	Rare
Pseudocercospora	4	0.4%	Rare
Pseudofusicoccum	1	0.1%	Rare
Pseudokeissleriella	3	0.3%	Rare
Pseudopithomyces	2	0.2%	Rare

Table 3.2 (continued)

Genus	Number of Isolates	RF (%)	Dominance Status
Purpureocillium	2	0.2%	Rare
Pyrenochaeta	1	0.1%	Rare
Sarocladium	5	0.5%	Rare
Schizophyllum	1	0.1%	Rare
Setophoma	6	0.6%	Rare
Simplicillium	2	0.2%	Rare
Spegazzinia	1	0.1%	Rare
Stagonospora	2	0.2%	Rare
Stagonosporopsis	4	0.4%	Rare
Stephanonectria	1	0.1%	Rare
Talaromyces	4	0.4%	Rare
Thyridium	3	0.3%	Rare
Trichoderma	1	0.1%	Rare
Zasmidium	2	0.2%	Rare

3.2 Comparative Analysis of Endophytic Fungi across Media, Plant Tissues, and Provinces

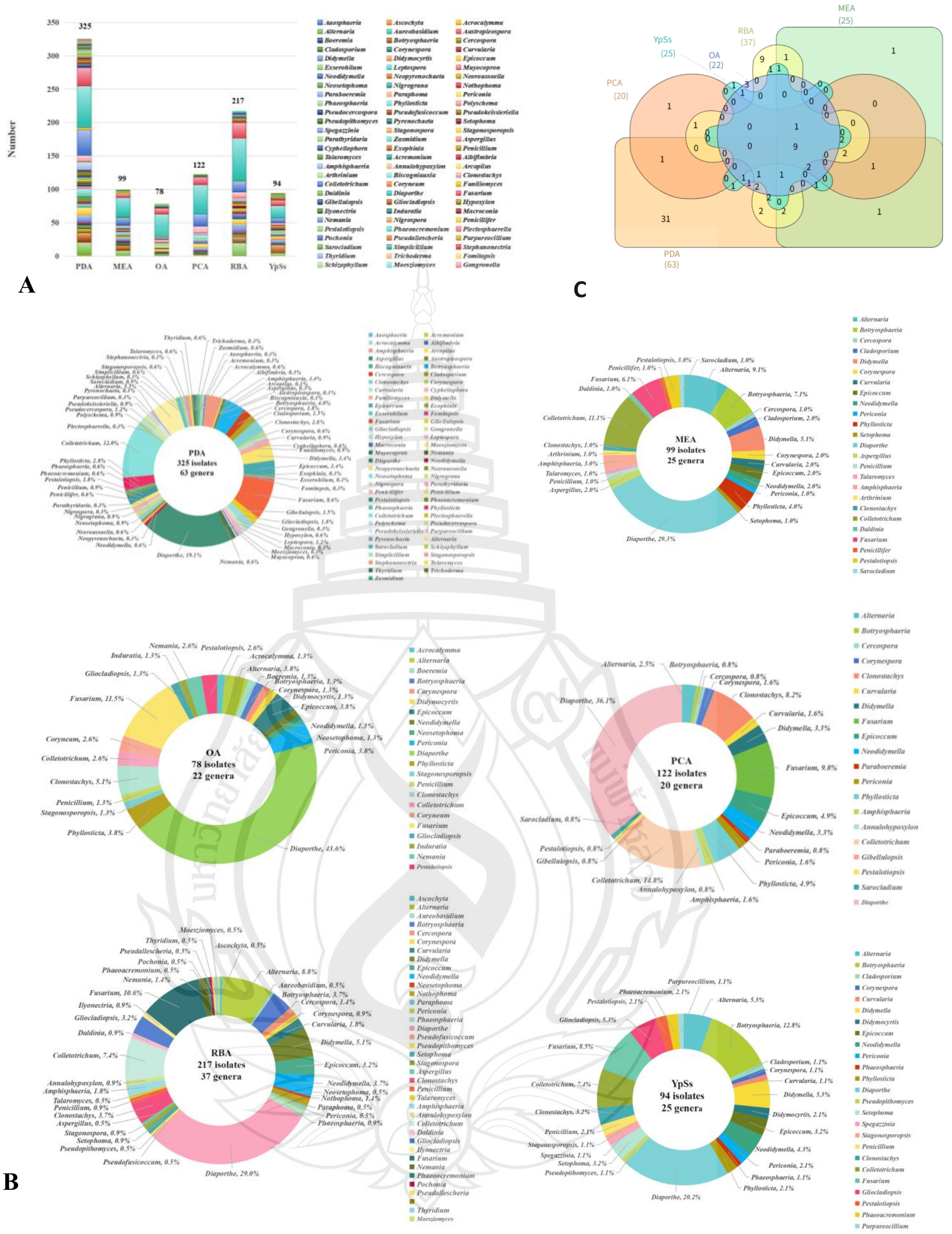
The diversity and abundance of cultivable endophytes are influenced by multiple factors, including culture media composition, host tissue type, and geographic location. In this study, we focused on comparing the distribution of isolates across various culture media, plant tissues, and four provinces. A comparative analysis was performed to identify isolation preferences and evaluate factors shaping the endophytic fungi of *Tetradium ruticarpum*. The distribution of culturable endophytic fungal isolates across different categories is summarized in Table 3.3.

3.2.1 Influence of Culture Media on Isolation Yield and Fungal Diversity Composition

In our study, six culture media (PDA, RBA, PCA, MEA, YpSs, and OA) were employed for isolating fungi from *Tetradium ruticarpum* tissues. Among the six media used, potato dextrose agar (PDA) yielded the highest number of isolates (325 isolates, 34.8%), which represented 63 genera. This was followed by RBA (217 isolates, 23.2%, 38 genera) and PCA (122 isolates, 13.0%, 20 genera). Fewer isolates and lower generic richness were recovered from MEA (99 isolates, 10.6%, 25 genera), YpSs (94 isolates, 10.1%, 25 genera), and OA (78 isolates, 8.3%, 22 genera) (Figure 3.8A, B). At the genus level, *Diaporthe* consistently dominated across all six media, ranking first in relative abundance in each (Figure 3.8B). Its prevalence was highest on OA and PCA, constituting 43.6% and 36.1% of isolates on these media, respectively. On other media, its relative abundance was 29.0% on RBA, 29.3% on MEA, 19.1% on PDA, and 20.2% on YpSs. The composition of the subsequent dominant genera varied with the medium: on PDA, *Diaporthe* was followed by *Colletotrichum* (12.0%) and *Fusarium* (8.6%); on RBA, by *Fusarium* (10.6%) and *Alternaria* (8.8%); and on PCA, by *Colletotrichum* (14.8%) and *Fusarium* (9.8%). On OA, *Fusarium* (11.5%) and *Clonostachys* (5.1%) were the next most abundant after *Diaporthe*; on MEA, they were *Colletotrichum* (11.1%) and *Alternaria* (9.1%). A notable compositional shift was observed on YpSs, where *Botryosphaeria* (12.8%) emerged as the second most abundant genus, followed by *Fusarium* (8.5%).

Table 3.3 Total number of endophytic fungal isolates from *Tetradium ruticarpum* across all conditions

Category	Subcategory	Number of Isolates	Percentage (%)
Culture Media	OA	78	8.3%
	YpSs	94	10.1%
	MEA	99	10.6%
	PCA	122	13.0%
	RBA	217	23.2%
	PDA	325	34.8%
Plant Tissues	Fruits	80	8.6%
	Leaves	408	43.6%
	Roots	171	18.3%
	Stems	276	29.5%
Different Provinces	Anhui	63	6.7%
	Guangxi	55	5.9%
	Hunan	73	7.8%
	Jiangxi	744	79.6%
Total	-	935	100%



Note Three types of charts illustrating the diversity of *Tetradium ruticarpum* endophytic fungi in different culture media: (A) Bar chart showing the number and genus-level composition; (B) Donut charts illustrating the proportional composition of fungal genera across each culture medium; (C) Venn diagram displaying the shared and unique genera among the six media.

Figure 3.8 Number of endophytic fungal isolates in different culture media

Table 3.4 Generic richness of endophytic fungi from *Tetradium ruticarpum* in different culture media

Phylum	Class	Genus	PDA	MEA	OA	PCA	RBA	YpSs	Total
Ascomycota	Dothideomycetes	*Aaosphaeria*	1	-	-	-	-	-	1
		Acrocalymma	2	-	-	-	1	-	3
		Alternaria	18	9	3	3	19	5	57
		Ascochyta	-	-	1	-		-	1
		Aureobasidium	-	-	-	-	1	-	1
		Austropleospora	1	-	-	-	-	-	1
		Boeremia	-	-	1	-	-	-	1
		Botryosphaeria	13	7	1	1	8	12	42
		Cercospora	6	1	-	1	3	-	11
		Cladosporium	5	2	-	-	-	1	8
		Corynespora	2	2	1	2	2	1	10
		Curvularia	3	2	-	2	4	1	12
		Didymella	11	5	-	4	11	5	36
		Didymocyrtis	-	-	1	-	-	2	3
		Epicoccum	11	2	3	6	7	3	32
		Exserohilum	1	-	-	-	-	-	1
		Leptospora	4	-	-	-	-	-	4
		Muyocopron	2	-	-	-	-	-	2
		Neodidymella	2	2	1	4	8	4	21
		Neopyrenochaeta	1	-	-	-	-	-	1
		Neoroussoella	2	-	-	-	-	-	2
		Neosetophoma	3	-	1	-	1	-	5
		Nigrograna	3	-	-	-	-	-	3
		Nothophoma	-	-	-	-	3	-	3
		Paraboeremia	-	-	-	1	-	-	1
		Paraphoma	-	-	-	-	1	-	1
		Periconia	-	1	3	2	1	2	9
		Phaeosphaeria	2	-	-	-	2	1	5
		Phyllosticta	9	4	3	6	-	2	24
		Polyschema	3	-	-	-	-	-	3
		Pseudocercospora	4	-	-	-	-	-	4
		Pseudofusicoccum	-	-	-	-	1	-	1
		Pseudokeissleriella	3	-	-	-	-	-	3
		Pseudopithomyces	-	-	-	-	1	1	2
		Pyrenochaeta	1	-	-	-	-	-	1
		Setophoma	-	1	-	-	2	3	6
		Spegazzinia	-	-	-	-	-	1	1
		Stagonospora	-	-	-	-	2	-	2

Table 3.4 (continued)

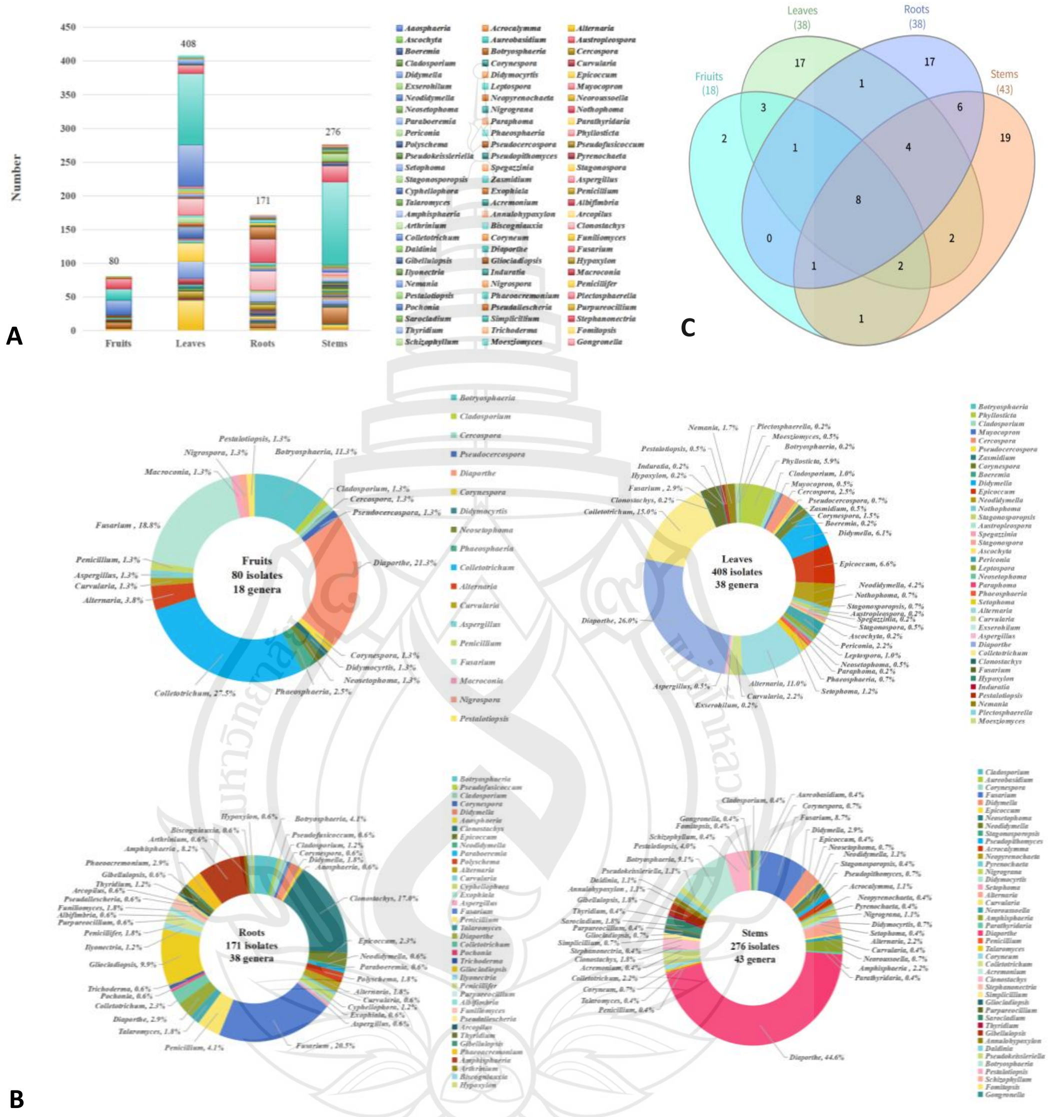
Phylum	Class	Genus	PDA	MEA	OA	PCA	RBA	YpSs	Total
		Stagonosporopsis	2	-	1	-	-	1	4
		Parathyridaria	1	-	-	-	-	-	1
		Zasmidium	2	-	-	-	-	-	2
	Eurotiomycetes	*Aspergillus*	1	2	-	-	1	-	4
		Cyphellophora	2	-	-	-	-	-	2
		Exophiala	1	-	-	-	-	-	1
		Penicillium	3	1	1	-	2	2	9
		Talaromyces	2	1	-	-	1	-	4
	Sordariomycetes	*Acremonium*	1	-	-	-	-	-	1
		Albifimbria	1	-	-	-	-	-	1
		Amphisphaeria	11	3	-	2	4	-	20
		Annulohypoxylon	-	-	-	1	2	-	3
		Arcopilus	1	-	-	-	-	-	1
		Arthrinium	-	1	-	-	-	-	1
		Biscogniauxia	1	-	-	-	-	-	1
		Clonostachys	9	1	4	10	8	3	35
		Colletotrichum	39	11	2	18	16	7	93
		Coryneum	-	-	2	-	-	-	2
		Daldinia	-	1	-	-	2	-	3
		Diaporthe	62	29	34	44	63	19	251
		Funiliomyces	3	-	-	-	-	-	3
		Fusarium	28	6	9	12	23	8	86
		Gibellulopsis	5	-	-	1	-	-	6
		Gliocladiopsis	6	-	1	-	7	5	19
		Hypoxylon	2	-	-	-	-	-	2
		Ilyonectria	-	-	-	-	2	-	2
		Induratia	-	-	1	-	-	-	1
		Macroconia	1	-	-	-	-	-	1
		Nemania	2	-	2	-	3	-	7
		Nigrospora	1	-	-	-	-	-	1
		Penicillifer	2	1	-	-	-	-	3
		Pestalotiopsis	6	3	2	1	-	2	14
		Phaeoacremonium	2	-	-	-	1	2	5
		Plectosphaerella	1	-	-	-	-	-	1
		Pochonia	-	-	-	-	1	-	1
		Pseudallescheria	-	-	-	-	1	-	1
		Purpureocillium	1	-	-	-	-	1	2
		Sarocladium	3	1	-	1	-	-	5
		Simplicillium	2	-	-	-	-	-	2
		Stephanonectria	1	-	-	-	-	-	1

Table 3.4 (continued)

Phylum	Class	Genus	PDA	MEA	OA	PCA	RBA	YpSs	Total
		Thyridium	2	-	-	-	1	-	3
		Trichoderma	1	-	-	-	-	-	1
Basidiomycota	Agaricomycetes	*Fomitopsis*	1	-	-	-	-	-	1
		Schizophyllum	1	-	-	-	-	-	1
	Ustilaginomycetes	*Moesziomyces*	1	-	-	-	1	-	2
Mucoromycota	Mucoromycetes	*Gongronella*	1	-	-	-	-	-	1
		Total	325	99	78	122	217	94	935

Regarding genus richness across culture media, several genera were recovered from multiple media types (Table 3.4, Figure 3.8C). PDA supported the broadest phylogenetic range, comprising 63 genera, followed by RBA with 37 genera, MEA and YpSs with 25 genera each, OA with 22 genera, and PCA with 20 genera. Nine genera were recovered from all media, including *Alternaria*, *Botryosphaeria*, *Corynespora*, *Epicoccum*, *Neodidymella*, *Clonostachys*, *Colletotrichum*, *Diaporthe*, and *Fusarium.* Other genera isolated from five media included *Phyllosticta* and *Pestalotiopsis* (MEA, OA, PCA, PDA, and YpSs), *Didymella* and *Curvularia* (MEA, OA, PCA, PDA, RBA), and *Penicillium* was present in five media: MEA, PDA, RBA, YpSs, and PCA. Genera recovered from four media included *Cercospora* and *Amphisphaeria* (MEA, PCA, PDA, and RBA). Genera recovered from three media included *Stagonosporopsis* (OA, PDA, and YpSs), *Cladosporium* (MEA, PDA, and YpSs), *Sarocladium* (MEA, PCA, and PDA), *Aspergillus* and *Talaromyces* (MEA, PDA, and RBA), and *Acrocalymma*, *Neosetophoma*, and *Nemania* (OA, PDA, and RBA). Certain genera were shared exclusively between two specific media combinations, such as *Gibellulopsis* (PCA and PDA), *Penicillifer* (PDA and MEA), *Annulohypoxylon* (PCA and RBA), *Didymocyrtis* (OA and YpSs), *Pseudopithomyces* (RBA and YpSs), and *Purpureocillium* (PDA and YpSs). However, some genera were recovered exclusively from a single culture medium. PDA contained 31 unique genera, such as *Muyocopron*, *Pseudocercospora*, *Zasmidium*, and *Exophiala*. RBA contained eight unique genera, including *Pseudofusicoccum* and *Aureobasidium*. OA contained three unique genera: *Boeremia*, *Coryneum*, and *Induratia*. MEA contained one unique genus, *Arthrinium*, and YpSs contained one unique genus, *Spegazzinia*. PCA contained one unique genus, *Paraboeremia*.

3.2.2 Influence of Plant Tissues on Isolation Yield and Fungal Diversity Composition



Note Three types of charts illustrating the diversity of *Tetradium ruticarpum* endophytic fungi in different plant tissues: (A) Bar chart showing the number and genus-level composition in different plant tissues; (B) Donut charts illustrating the proportional composition of fungal genera across different plant tissues; (C) Venn diagram displaying the shared and unique genera among different plant tissues.

Figure 3.9 Number of endophytic fungal isolates in different plant tissues

Table 3.5 Generic richness of endophytic fungi from *Tetradium ruticarpum* in different plant tissues

Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
Ascomycota	Dothideomycetes	*Aaosphaeria*	-	-	1	-	1
		Acrocalymma	-	-	-	3	3
		Alternaria	3	45	3	6	57
		Ascochyta	-	1	-	-	1
		Aureobasidium	-	-	-	1	1
		Austropleospora	-	1	-	-	1
		Boeremia	-	1	-	-	1
		Botryosphaeria	9	1	7	25	42
		Cercospora	1	10	-	-	11
		Cladosporium	1	4	2	1	8
		Corynespora	1	6	1	2	10
		Curvularia	1	9	1	1	12
		Didymella	-	25	3	8	36
		Didymocyrtis	1	-	-	2	3
		Epicoccum	-	27	4	1	32
		Exserohilum	-	1	-	-	1
		Leptospora	-	4	-	-	4
		Muyocopron	-	2	-	-	2
		Neodidymella	-	17	1	3	21
		Neopyrenochaeta	-	-	-	1	1
		Neoroussoella	-	-	-	2	2
		Neosetophoma	1	2	-	2	5
		Nigrograna	-	-	-	3	3
		Nothophoma	-	3	-	-	3
		Paraboeremia	-	-	1	-	1
		Paraphoma	-	1	-	-	1
		Parathyridaria	-	-	-	1	1
		Periconia	-	9	-	-	9
		Phaeosphaeria	2	3	-	-	5
		Phyllosticta	0	24	-	-	24
		Polyschema	-	-	3	-	3
		Pseudocercospora	1	3	-	-	4
		Pseudofusicoccum	-	-	1	-	1
		Pseudokeissleriella	-	-	-	3	3
		Pseudopithomyces	-	-	-	2	2
		Pyrenochaeta	-	-	-	1	1
		Setophoma	-	5	-	1	6
		Spegazzinia	-	1	-	-	1

Table 3.5 (continued)

Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
		Stagonospora	-	2	-	-	2
		Stagonosporopsis	-	3	-	1	4
		Zasmidium	-	2	-	-	2
	Eurotiomycetes	*Aspergillus*	1	2	1	-	4
		Cyphellophora	-	-	2	-	2
		Exophiala	-	-	1	-	1
		Penicillium	1	-	7	1	9
		Talaromyces	-	-	3	1	4
	Sordariomycetes	*Acremonium*	-	-	-	1	1
		Albifimbria	-	-	1	-	1
		Amphisphaeria	-	-	14	6	20
		Annulohypoxylon	-	-	-	3	3
		Arcopilus	-	-	1	-	1
		Arthrinium	-	-	1	-	1
		Biscogniauxia	-	-	1	-	1
		Clonostachys	-	1	29	5	35
		Colletotrichum	22	61	4	6	93
		Coryneum	-	-	-	2	2
		Daldinia	-	-	-	3	3
		Diaporthe	17	106	5	123	251
		Funiliomyces	-	-	3	-	3
		Fusarium	15	12	35	24	86
		Gibellulopsis	-	-	1	5	6
		Gliocladiopsis	-	-	17	2	19
		Hypoxylon	-	1	1	-	2
		Ilyonectria	-	-	2	-	2
		Induratia	-	1	-	-	1
		Macroconia	1	-	-	-	1
		Nemania	-	7	-	-	7
		Nigrospora	1	-	-	-	1
		Penicillifer	-	-	3	-	3
		Pestalotiopsis	1	2	-	11	14
		Phaeoacremonium	-	-	5	-	5
		Plectosphaerella	-	1	-	-	1
		Pochonia	-	-	1	-	1
		Pseudallescheria	-	-	1	-	1
		Purpureocillium	-	-	1	1	2
		Sarocladium	-	-	-	5	5
		Simplicillium	-	-	-	2	2
		Stephanonectria	-	-	-	1	1

Table 3.5 (continued)

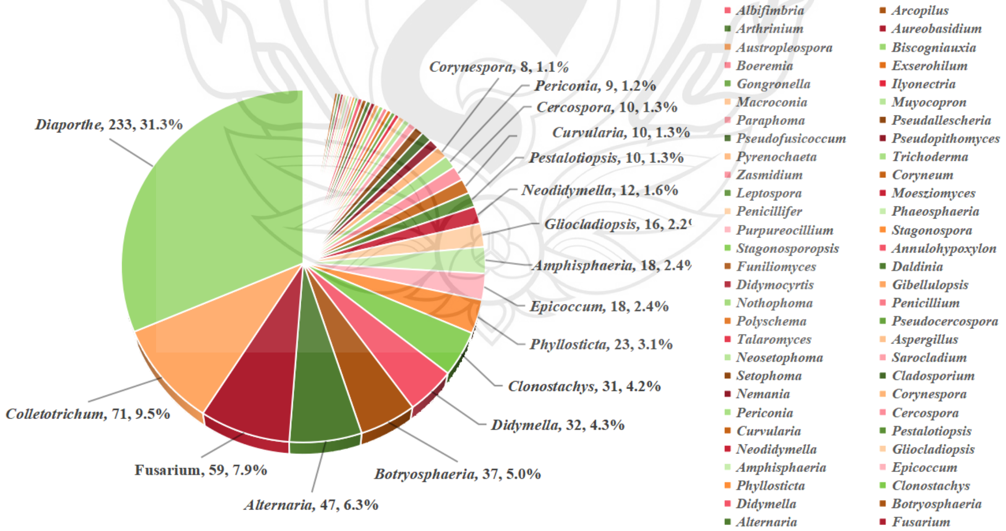
Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
		Thyridium	-	-	2	1	3
		Trichoderma	-	-	1	-	1
Basidiomycota	Agaricomycetes	*Fomitopsis*	-	-	-	1	1
		Schizophyllum	-	-	-	1	1
	Ustilaginomycetes	*Moesziomyces*	-	2	-	-	2
Mucoromycota	Mucoromycetes	*Gongronella*	-	-	-	1	1
		Total	80	408	171	276	935

In this study, endophytic fungal isolates were obtained from four different tissues of *Tetradium ruticarpum*, namely the roots, stems, leaves, and fruits. The number of isolates and corresponding generic richness were greatest in leaves (408 isolates, 43.6%; 38 genera), followed by stems (276 isolates, 29.5%; 43 genera), roots (171 isolates, 18.3%; 38 genera), and fruits (80 isolates, 8.6%; 18 genera), from a total of 935 isolates (Figure 3.9A, B). The fungal community composition and dominance structure varied markedly across tissues (Figure 3.9). Stem tissues were strongly dominated by *Diaporthe*, which accounted for the largest proportion of stem isolates (44.6%), followed by *Botryosphaeria* (9.1%) and *Fusarium* (8.7%). Leaf tissues exhibited the highest taxonomic richness, with *Diaporthe* (26.0%), *Colletotrichum* (15.0%), and *Alternaria* (11.0%) as the predominant genera. Root tissues were dominated by *Fusarium* (20.5%) and *Clonostachys* (17.0%), followed by *Gliocladiopsis* (9.9%) and *Amphisphaeria* (8.2%). Fruit tissues were co-dominated by *Colletotrichum* (27.5%) and *Diaporthe* (21.3%), while *Fusarium* (18.8%) and *Botryosphaeria* (11.3%) were also relatively abundant. Across all four plant tissues, numerous other genera were represented by only one or two isolates each.

Endophytic fungi from *Tetradium ruticarpum* were isolated from stems, roots, leaves, and fruits, comprising 43, 38, 38, and 18 genera, respectively (Table 3.5, Figure 3.9C). Among them, eight genera, including *Botryosphaeria*, *Cladosporium*, *Corynespora*, *Alternaria*, *Curvularia*, *Diaporthe*, *Colletotrichum*, and *Fusarium,* were detected in all four tissues (roots, stems, leaves, and fruits). Genera recovered from three tissues included *Aspergillus* (fruits, leaves, and roots), *Didymella, Epicoccum, Neodidymella, and Clonostachys* (leaves, roots, and stems), *Neosetophoma* and *Pestalotiopsis* (fruits, leaves, and stems), and *Penicillium* (fruits, roots, and stems). Genera shared between two tissues included *Cercospora*, *Pseudocercospora*, and *Phaeosphaeria* (fruits and leaves), *Hypoxylon* (leaves and roots), *Stagonosporopsis* and *Setophoma* (leaves and stems), *Didymocyrtis* (fruits and stems), and *Talaromyces*, *Gliocladiopsis*, *Purpureocillium*, *Thyridium*, *Gibellulopsis*, and *Amphisphaeria* (roots and stems). Additionally, several genera were recovered exclusively from a single tissue, such as *Ascochyta,* *Phyllosticta*, *Muyocopron*, *Zasmidium*, *Boeremia*, *Nothophoma*, *Austropleospora*, *Spegazzinia*, *Stagonospora*, *Periconia*, *Leptospora*, *Paraphoma*, *Exserohilum*, *Induratia*, *Nemania*, *Plectosphaerella*, and *Moesziomyces* from leaves, *Pseudofusicoccum*, *Aaosphaeria*, *Paraboeremia*, *Polyschema*, *Cyphellophora*, *Exophiala*, *Pochonia*, *Trichoderma*, *Ilyonectria*, *Penicillifer*, *Albifimbria*, *Pseudallescheria*, *Arcopilus*, *Phaeoacremonium*, *Arthrinium*, *Biscogniauxia*, *Funiliomyces* from roots, *Acrocalymma*, *Aureobasidium*, *Pseudopithomyces*, *Pseudokeissleriella*, *Neopyrenochaeta*, *Pyrenochaeta*, *Nigrograna*, *Neoroussoella*, *Thyridariaceae*, *Coryneum*, *Acremonium*, *Stephanonectria*, *Simplicillium*, *Sarocladium*, *Annulohypoxylon*, *Daldinia*, *Schizophyllum*, and *Fomitopsis*, *Gongronella* from stems, and *Macroconia* and *Nigrospora* from fruits.

3.2.3 Influence of Different Provinces on Isolation Yield and Fungal Diversity Composition

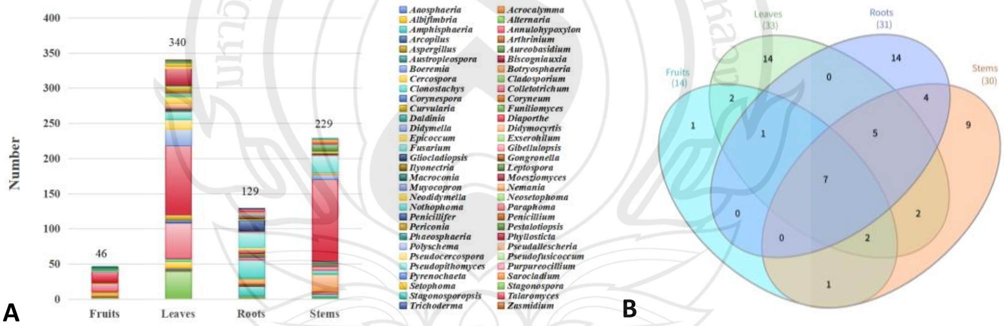
3.2.3.1 Community composition of endophytic fungi from *Tetradium ruticarpum* in Jiangxi Province



Note Pie chart illustrating the taxonomic distribution of the 744 endophytic fungal isolates from *Tetradium ruticarpum* at the genus level in Jiangxi Province.

Figure 3.10 Number of genera recovered from *Tetradium ruticarpum* in Jiangxi Province

In this study, a total of 744 endophytic fungal isolates were recovered from the roots, stems, leaves, and fruits of *Tetradium ruticarpum* collected from 18 sampling sites in Jiangxi Province during 2020–2024. These 744 isolates were further classified into 62 different genera (Figure 3.10). Among these 62 genera, 17 genera had a relative frequency greater than 1%, and their specific isolate numbers and relative proportions are as follows: *Diaporthe* (233 isolates, 31.3%), *Colletotrichum* (71 isolates, 9.5%), *Fusarium* (59 isolates, 7.9%), *Alternaria* (47 isolates, 6.3%), *Botryosphaeria* (37 isolates, 5.0%), *Didymella* (32 isolates, 4.3%), *Clonostachys* (31 isolates, 4.2%), *Phyllosticta* (23 isolates, 3.1%), *Amphisphaeria* (18 isolates, 2.4%), *Epicoccum* (18 isolates, 2.4%), *Gliocladiopsis* (16 isolates, 2.2%), *Neodidymella* (12 isolates, 1.6%), *Cercospora* (10 isolates, 1.3%), *Curvularia* (10 isolates, 1.3%), *Pestalotiopsis* (10 isolates, 1.3%), *Periconia* (nine isolates, 1.2%), and *Corynespora* (eight isolates, 1.1%). Notably, *Diaporthe* stood out as the absolute dominant genus, accounting for over 30% of the total isolates, while *Colletotrichum*, *Fusarium*, and *Alternaria* also exhibited relatively high proportions. These key genera collectively constitute the core components of the endophytic fungal community associated with *T. ruticarpum* in Jiangxi Province.



Note Stacked bar chart (A) and Venn diagram (B) showing the composition and overlap of endophytic fungal genera isolated from four tissues (fruits, leaves, roots, and stems) of *Tetradium ruticarpum* collected in Jiangxi Province.

Figure 3.11 Number and overlap of genera recovered from *Tetradium ruticarpum* in Jiangxi Province

Among the 744 endophytic fungal isolates obtained from *Tetradium ruticarpum* in Jiangxi Province, 129 originated from roots, 229 from stems, 340 from leaves, and 46 from fruits (Figure 3.11A). The community was dominated by *Diaporthe* (31.3%) and *Colletotrichum* (26.1%), followed by *Botryosphaeria* (10.9%) and *Alternaria* (6.5%). Other genera, including *Fusarium*, *Aspergillus*, *Cercospora*, *Cladosporium*, *Curvularia*, *Didymocyrtis*, *Macroconia*, *Neosetophoma*, *Pestalotiopsis*, and *Phaeosphaeria*, were detected at low relative abundances (<5%). From the leaf tissues, 340 endophytic fungal isolates were obtained, belonging to 33 genera. The leaf-associated community was dominated by *Diaporthe* (28.8%) and *Colletotrichum* (14.7%), followed by *Alternaria* (11.8%) and *Didymella* (7.1%). Other relatively abundant genera included *Phyllosticta* (6.8%), *Epicoccum* (3.8%), and *Fusarium* (3.2%), while the remaining genera, such as *Cercospora*, *Periconia*, *Neodidymella*, and *Curvularia*, occurred at lower proportions (<3%). In the roots, 129 isolates representing 31 genera were obtained. The dominant genera were *Clonostachys* (19.4%) and *Fusarium* (17.1%), followed by *Gliocladiopsis* (11.6%) and *Amphisphaeria* (10.9%). Moderate abundances were observed for *Botryosphaeria* (5.4%) and *Colletotrichum*, *Diaporthe*, and *Epicoccum* (each around 3%). The remaining genera, including *Funiliomyces*, *Penicillium*, *Talaromyce*s, and *Polyschema*, accounted for less than 3% of the total isolates. Similarly, 229 isolates were obtained from the stem tissues, representing 30 genera. The dominant genus was *Diaporthe* (50.66%), followed by *Botryosphaeria* and *Fusarium* (each 10.48%). Moderate abundances were recorded for *Pestalotiopsis* (3.49%) and Didymella (3.06%), while other genera, including *Clonostachys*, *Colletotrichum*, and *Sarocladium* (each 2.18%), *Amphisphaeria* (1.75%), *Annulohypoxylon*, and *Daldinia* (each 1.31%), as well as *Alternaria*, *Corynespora*, and *Didymocyrtis* (each 0.87%), were present at lower proportions (<3%).

The composition of endophytic fungal communities varied among the four tissues of *Tetradium ruticarpum* in Jiangxi province (Table 3.6, Figure 3.11B). A total of 62 genera were detected across all tissues, with seven genera (*Alternaria*, *Botryosphaeria*, *Cladosporium*, *Colletotrichum*, *Curvularia*, *Diaporthe*, and *Fusarium*) shared by fruits, roots, stems, and leaves. The roots contained the highest number of unique genera (14), including *Aaosphaeria*, *Albifimbria*, *Arcopilus*, *Arthrinium*, *Biscogniauxia*, *Funiliomyces*, *Ilyonectria*, *Penicillifer*, *Penicillium*, *Polyschema*, *Pseudallescheria*, *Pseudofusicoccum*, *Talaromyces*, and *Trichoderma*. The stems had nine exclusive genera, such as *Acrocalymma*, *Annulohypoxylon*, *Aureobasidium*, *Coryneum*, *Daldinia*, *Gongronella*, *Pseudopithomyces*, *Pyrenochaeta*, and *Sarocladium*.

The leaves contained 14 tissue-specific taxa, including *Austropleospora*, *Boeremia*, *Exserohilum*, *Leptospora*, *Moesziomyces*, *Muyocopron*, *Nemania*, *Nothophoma*, *Paraphoma*, *Periconia*, *Phyllosticta*, *Pseudocercospora*, *Stagonospora*, and *Zasmidium*. The fruit tissues showed the lowest diversity, with *Macroconia* as the only exclusive genus. Intermediate overlaps were observed among certain tissues. *Aspergillus* was shared by fruits, roots, and leaves; *Neosetophoma* and *Pestalotiopsis* occurred in fruits, stems, and leaves; and *Clonostachys*, *Corynespora*, *Didymella*, *Epicoccum*, and *Neodidymella* were detected in roots, stems, and leaves. *Amphisphaeria*, *Gibellulopsis*, *Gliocladiopsis*, and *Purpureocillium* were shared by roots and stems, while *Setophoma* and *Stagonosporopsis* were common to stems and leaves.

Table 3.6 Generic richness of endophytic fungi associated with *Tetradium ruticarpum* in different plant tissues from Jiangxi Province

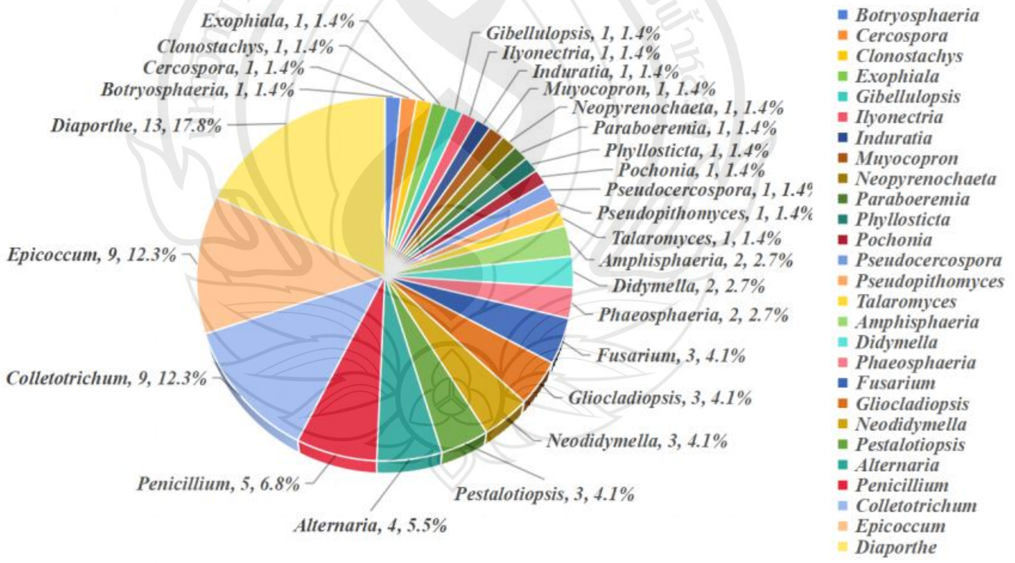
Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
Ascomycota	Dothideomycetes	*Aaosphaeria*	0	0	1	0	1
		Acrocalymma	0	0	0	1	1
		Alternaria	3	40	2	2	47
		Aureobasidium	0	0	0	1	1
		Austropleospora	0	1	0	0	1
		Boeremia	0	1	0	0	1
		Botryosphaeria	5	1	7	24	37
		Cercospora	1	9	0	0	10
		Cladosporium	1	3	2	1	7
		Corynespora	0	5	1	2	8
		Curvularia	1	7	1	1	10
		Didymella	0	24	1	7	32
		Didymocyrtis	1	0	0	2	3
		Epicoccum	0	13	4	1	18
		Exserohilum	0	1	0	0	1
		Leptospora	0	2	0	0	2
		Muyocopron	0	1	0	0	1
		Neodidymella	0	9	1	2	12
		Neosetophoma	1	2	0	1	4
		Nothophoma	0	3	0	0	3
		Paraphoma	0	1	0	0	1
		Periconia	0	9	0	0	9
		Phaeosphaeria	1	1	0	0	2
		Phyllosticta	0	23	0	0	23
		Polyschema	0	0	3	0	3

Table 3.6 (continued)

Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
		Pseudocercospora	0	3	0	0	3
		Pseudofusicoccum	0	0	1	0	1
		Pseudopithomyces	0	0	0	1	1
		Pyrenochaeta	0	0	0	1	1
		Setophoma	0	5	0	1	6
		Stagonospora	0	2	0	0	2
		Stagonosporopsis	0	1	0	1	2
		Zasmidium	0	1	0	0	1
	Eurotiomycetes	*Aspergillus*	1	2	1	0	4
		Penicillium	0	0	3	0	3
		Talaromyces	0	0	3	0	3
	Sordariomycetes	*Albifimbria*	0	0	1	0	1
		Amphisphaeria	0	0	14	4	18
		Annulohypoxylon	0	0	0	3	3
		Arcopilus	0	0	1	0	1
		Arthrinium	0	0	1	0	1
		Biscogniauxia	0	0	1	0	1
		Clonostachys	0	1	25	5	31
		Colletotrichum	12	50	4	5	71
		Coryneum	0	0	0	2	2
		Daldinia	0	0	0	3	3
		Diaporthe	15	98	4	116	233
		Funiliomyces	0	0	3	0	3
		Fusarium	2	11	22	24	59
		Gibellulopsis	0	0	1	2	3
		Gliocladiopsis	0	0	15	1	16
		Ilyonectria	0	0	1	0	1
		Macroconia	1	0	0	0	1
		Nemania	0	7	0	0	7
		Penicillifer	0	0	2	0	2
		Pestalotiopsis	1	1	0	8	10
		Pseudallescheria	0	0	1	0	1
		Purpureocillium	0	0	1	1	2
		Sarocladium	0	0	0	5	5
		Trichoderma	0	0	1	0	1
Basidiomycota	Ustilaginomycetes	*Moesziomyces*	0	2	0	0	2
Mucoromycota	Mucoromycetes	*Gongronella*	0	0	0	1	1
		Total	46	340	129	229	744

3.2.3.2 Community composition of endophytic fungi from *Tetradium ruticarpum* in Hunan Province

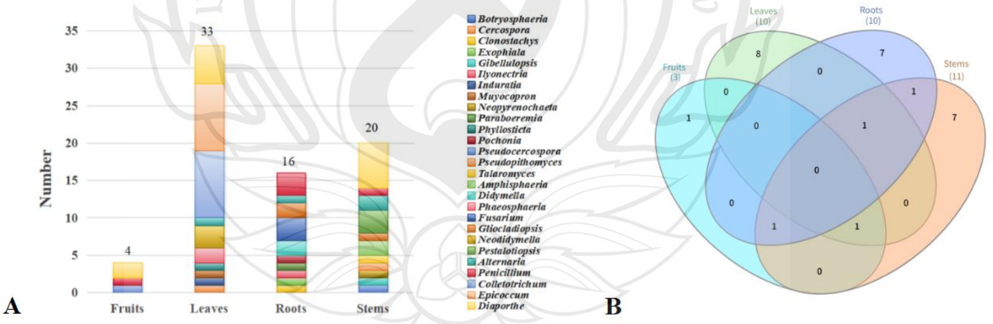
In this study, a total of 73 endophytic fungal isolates were recovered from the roots, stems, leaves, and fruits of *Tetradium ruticarpum* collected from two sampling sites in Hunan Province during 2021 and 2023. These isolates were identified as belonging to 27 genera (Figure 3.12). Among them, *Diaporthe* stood out as the core dominant genus, representing 17.8% of the total isolates (13 isolates). *Epicoccum* and *Colletotrichum* were also identified as dominant genera, each accounting for 12.3% (nine isolates). *Penicillium* and *Alternaria* were classified as common genera, contributing 6.8% (five isolates) and 5.5% (four isolates), respectively. The rare genera (relative frequency < 5%) included *Fusarium*, *Gliocladiopsis*, *Neodidymella*, and *Pestalotiopsis*, each representing 4.1% (three isolates), as well as *Amphisphaeria*, *Didymella*, and *Phaeosphaeria*, each accounting for 2.7% (two isolates). Fifteen genera were represented by a single isolate each (1.4%), including *Botryosphaeria*, *Cercospora*, *Clonostachys*, *Exophiala*, *Gibellulopsis*, *Ilyonectria*, *Induratia*, *Muyocopron*, *Neopyrenochaeta*, *Paraboeremia*, *Phyllosticta*, *Pseudocercospora*, *Pseudopithomyces*, *Pochonia*, and *Talaromyces*.



Note Pie chart illustrating the taxonomic distribution of the 73 endophytic fungal isolates from *Tetradium ruticarpum* at the genus level in Hunan Province.

Figure 3.12 Number of genera recovered from *Tetradium ruticarpum* in Hunan Province

Among the 73 endophytic fungal isolates obtained from *Tetradium ruticarpum* in Hunan Province, four isolates recovered from fruits, 33 from leaves, 16 from roots, and 20 from stems (Figure 3.13A). The number of isolates from fruits was relatively small, with these four isolates identified into three genera: *Diaporthe* (two isolates, 50.0%), *Penicillium* (one isolate, 25.0%), and *Pseudocercospora* (one isolate, 25.0%). Leaf tissues yielded the largest number of isolates, comprising 10 genera. *Colletotrichum* and *Epicoccum* were the most abundant (nine isolates each, 27.3%), followed by *Diaporthe* (five isolates, 15.2%) and *Neodidymella* (three isolates, 9.1%). The remaining genera, *Phaeosphaeria* (two isolates, 6.1%) and *Alternaria*, *Cercospora*, *Induratia*, *Muyocopron*, and *Phyllosticta* (one isolate each, 3.0%), were less frequent. Root tissues harbored 16 isolates, representing nine genera. *Fusarium* and *Penicillium* were co-dominant (three isolates each, 18.8%), followed by *Didymella* and *Gliocladiopsis* (two isolates each, 12.5%), and *Alternaria*, *Exophiala*, *Ilyonectria*, *Paraboeremia*, and *Pochonia* (one isolate each, 6.3%). Stem tissues contained 20 isolates (27.4% of total), belonging to 10 genera. *Diaporthe* was the most abundant (six isolates, 30.0%), followed by *Pestalotiopsis* (three isolates, 15.0%), *Alternaria* and *Amphisphaeria* (two isolates each, 10.0%), and *Botryosphaeria*, *Gibellulopsis*, *Gliocladiopsis*, *Neopyrenochaeta*, *Penicillium*, and *Pseudopithomyces* (one isolate each, 5.0%).



Note Stacked bar chart (A) and Venn diagram (B) showing the composition and overlap of endophytic fungal genera isolated from four tissues (fruits, leaves, roots, and stems) of *Tetradium ruticarpum* collected in Hunan Province.

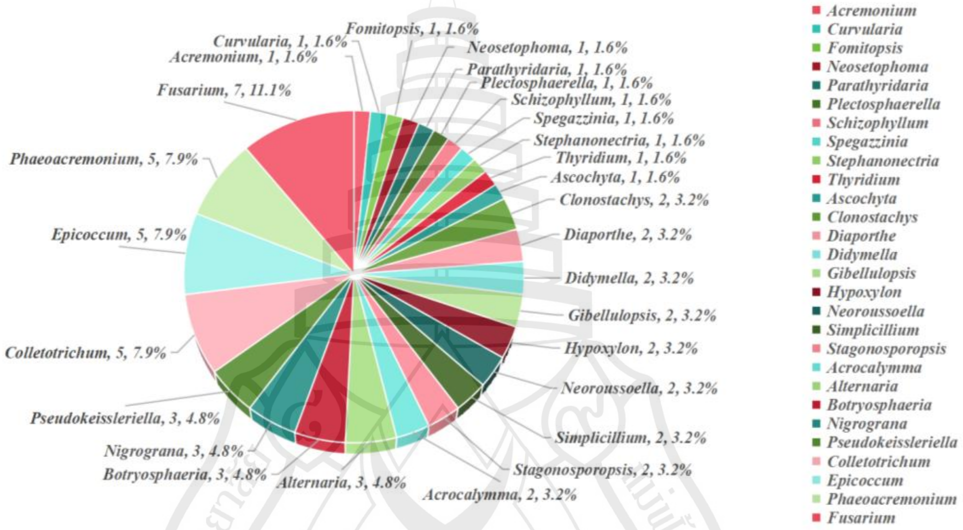
Figure 3.13 Number and overlap of genera recovered from *Tetradium ruticarpum* in Hunan Province

Table 3.7 Generic richness of endophytic fungi associated with *Tetradium ruticarpum* in different plant tissues from Hunan Province

Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
Ascomycota	Dothideomycetes	*Alternaria*	0	1	1	2	4
		Botryosphaeria	0	0	0	1	1
		Cercospora	0	1	0	0	1
		Didymella	0	0	2	0	2
		Epicoccum	0	9	0	0	9
		Muyocopron	0	1	0	0	1
		Neodidymella	0	3	0	0	3
		Neopyrenochaeta	0	0	0	1	1
		Paraboeremia	0	0	1	0	1
		Phaeosphaeria	0	2	0	0	2
		Phyllosticta	0	1	0	0	1
		Pseudocercospora	1	0	0	0	1
		Pseudopithomyces	0	0	0	1	1
	Eurotiomycetes	*Exophiala*	0	0	1	0	1
		Penicillium	1	0	3	1	5
	Eurotiomycetes	*Talaromyces*	0	0	0	1	1
	Sordariomycetes	*Amphisphaeria*	0	0	0	2	2
		Clonostachys	0	0	1	0	1
		Colletotrichum	0	9	0	0	9
		Diaporthe	2	5	0	6	13
		Fusarium	0	0	3	0	3
		Gibellulopsis	0	0	0	1	1
		Gliocladiopsis	0	0	2	1	3
		Ilyonectria	0	0	1	0	1
		Induratia	0	1	0	0	1
		Pestalotiopsis	0	0	0	3	3
		Pochonia	0	0	1	0	1
			4	33	16	20	73

Endophytic fungal communities exhibited distinct composition patterns across the four tissues of *Tetradium ruticarpum*, with a total of 27 genera detected across all tissues (Table 3.7, Figure 3.13B). No genus was found to be shared across all four tissues. Among the isolates, *Diaporthe* was shared by fruit, stem, and leaf tissues, and *Penicillium* was shared by fruit, root, and stem tissues. *Alternaria* was common to root, stem, and leaf tissues. Root and stem tissues shared *Gliocladiopsis*. Fruit tissues alone harbored *Pseudocercospora*, while root tissues contained *Clonostachys*, *Didymella*, *Exophiala*, *Fusarium*, *Ilyonectria*, *Paraboeremia*, and *Pochonia*. Stem tissues contained Amphisphaeria, *Botryosphaeria*, *Gibellulopsis*, Neopyrenochaeta, *Pestalotiopsis*, *Pseudopithomyces*, and *Talaromyces*. Leaf tissues contained *Cercospora*, *Colletotrichum*, *Epicoccum*, *Induratia*, *Muyocopron*, *Neodidymella, Phaeosphaeria,* and *Phyllosticta.*

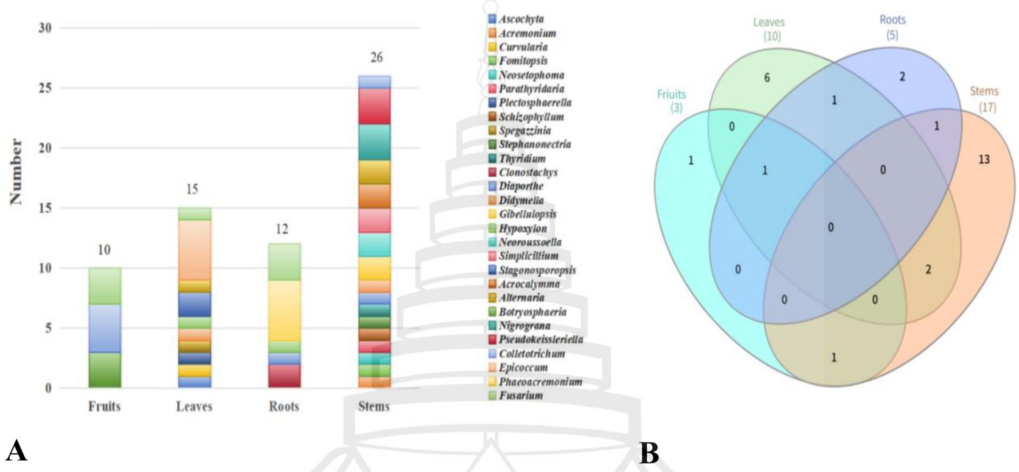
3.2.3.3 Community composition of endophytic fungi from *Tetradium ruticarpum* in Anhui Province



Note Pie chart illustrating the taxonomic distribution of the 63 endophytic fungal isolates from *Tetradium ruticarpum* at the genus level in Anhui Province.

Figure 3.14 Number of genera recovered from *Tetradium ruticarpum* in Anhui Province

In this study, a total of 63 endophytic fungal isolates were recovered from the roots, stems, leaves, and fruits of *Tetradium ruticarpum* collected from two sampling sites in Anhui Province during 2022 and 2023. These isolates were assigned to 28 genera (Figure 3.14). *Fusarium* was identified as the dominant genus, comprising seven isolates (11.1%). The common genera included *Colletotrichum*, *Epicoccum*, and *Phaeoacremonium*, each represented by five isolates (7.9%). The rare genera consisted of *Alternaria*, *Botryosphaeria*, *Nigrograna*, and *Pseudokeissleriella* (three isolates each, 4.8%), as well as *Acrocalymma*, *Clonostachys*, *Diaporthe*, *Didymella*, *Gibellulopsis*, *Hypoxylon*, *Neoroussoella*, *Simplicillium*, and *Stagonosporopsis* (two isolates each, 3.2%). Ten genera were represented by a single isolate (1.6%), namely *Acremonium*, *Ascochyta*, *Curvularia*, *Fomitopsis*, *Neosetophoma*, *Parathyridaria*, *Plectosphaerella*, *Schizophyllum*, *Spegazzinia*, *Stephanonectria*, and *Thyridium*. Overall, *Fusarium*, *Colletotrichum*, *Epicoccum*, and *Phaeoacremonium* constituted the principal components of the endophytic fungal community associated with *T. ruticarpum* in Anhui Province.



Note Stacked bar chart (A) and Venn diagram (B) showing the composition and overlap of endophytic fungal genera isolated from four tissues (fruits, leaves, roots, and stems) of *Tetradium ruticarpum* collected in Anhui Province.

Figure 3.15 Number and overlap of genera recovered from *Tetradium ruticarpum* in Anhui Province

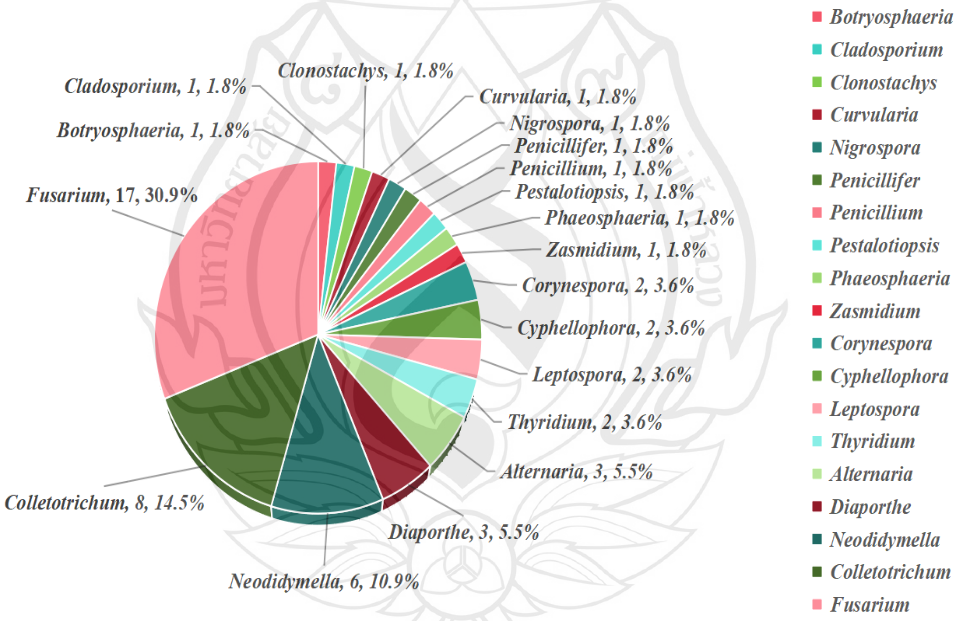
Among the 63 endophytic fungal isolates obtained from *Tetradium ruticarpum* in Anhui Province, 10 originated from fruits, 15 from leaves, 12 from roots, and 26 from stems (Figure 3.15A). Fruit tissues yielded 10 isolates, representing three genera. *Colletotrichum* was the most abundant (four isolates, 40.0%), followed by *Botryosphaeria* and *Fusarium* (three isolates each, 30.0%). Leaf tissues contained 15 isolates across 10 genera. *Epicoccum* was the most frequent (five isolates, 33.3%), followed by *Stagonosporopsis* (two isolates, 13.3%), and *Ascochyta*, *Alternaria*, *Curvularia*, *Didymella*, *Fusarium*, *Hypoxylon*, *Plectosphaerella*, and *Spegazzinia* (one isolate each, 6.7%). Root tissues harbored 12 isolates classified into five genera. *Phaeoacremonium* and *Fusarium* were the most abundant (five and three isolates, 41.7% and 25.0%, respectively), followed by *Clonostachys*, *Diaporthe*, and *Hypoxylon* (1–2 isolates, 8.3–16.7%). Stem tissues contained 26 isolates across 17 genera. *Nigrograna* and *Pseudokeissleriella* were the most frequent (three isolates each, 11.5%), followed by *Acrocalymma*, *Alternaria*, *Gibellulopsis*, *Neoroussoella*, and *Simplicillium* (two isolates each, 7.7%), and the remaining genera, including *Acremonium*, *Colletotrichum*, *Diaporthe*, *Didymella*, *Fomitopsis*, *Neosetophoma*, *Parathyridaria*, *Schizophyllum*, *Stephanonectria*, and *Thyridium* (one isolate each, 3.8%).

Table 3.8 Generic richness of endophytic fungi associated with *Tetradium ruticarpum* in different plant tissues from Anhui Province

Phylum	Class	Genus	Fruits	Leaves	Roots	Stems	Total
Ascomycota	Dothideomycetes	*Acrocalymma*	0	0	0	2	2
		Alternaria	0	1	0	2	3
		Ascochyta	0	1	0	0	1
		Botryosphaeria	3	0	0	0	3
		Curvularia	0	1	0	0	1
		Didymella	0	1	0	1	2
		Epicoccum	0	5	0	0	5
		Neoroussoella	0	0	0	2	2
		Neosetophoma	0	0	0	1	1
		Nigrograna	0	0	0	3	3
		Parathyridaria	0	0	0	1	1
		Pseudokeissleriella	0	0	0	3	3
		Spegazzinia	0	1	0	0	1
		Stagonosporopsis	0	2	0	0	2
	Sordariomycetes	*Acremonium*	0	0	0	1	1
		Clonostachys	0	0	2	0	2
		Colletotrichum	4	0	0	1	5
		Diaporthe	0	0	1	1	2
		Fusarium	3	1	3	0	7
		Gibellulopsis	0	0	0	2	2
		Hypoxylon	0	1	1	0	2
		Phaeoacremonium	0	0	5	0	5
		Plectosphaerella	0	1	0	0	1
		Simplicillium	0	0	0	2	2
		Stephanonectria	0	0	0	1	1
		Thyridium	0	0	0	1	1
Basidiomycota	Agaricomycetes	*Fomitopsis*	0	0	0	1	1
		Schizophyllum	0	0	0	1	1
			10	15	12	26	63

The composition of endophytic fungal communities in *Tetradium ruticarpum* varied among tissues in Hunan Province (Table 3.8, Figure 3.15B). Most genera were either tissue-specific or shared by two to three tissues, with no genera present in all four tissues. *Fusarium* occurred in fruit, root, and leaf, while *Diaporthe* was shared by root and stem, and *Hypoxylon* by root and leaf. Stem and leaf shared *Alternaria*, and *Didymella*, and fruit and stem shared *Colletotrichum*. Several genera were tissue-specific: *Botryosphaeria* was detected only in fruit; *Clonostachys* and *Phaeoacremonium* only in root; *Acremonium*, *Acrocalymma*, *Fomitopsis*, *Gibellulopsis*, *Neoroussoella*, *Neosetophoma*, *Nigrograna*, *Parathyridaria*, *Pseudokeissleriella*, *Schizophyllum*, *Simplicillium*, *Stephanonectria*, and *Thyridium* only in stem; and *Ascochyta*, *Curvularia*, *Epicoccum*, *Plectosphaerella*, *Spegazzinia*, and *Stagonosporopsis* only in leaf.

3.2.3.4 Community composition of endophytic fungi from *Tetradium ruticarpum* in Guangxi Province

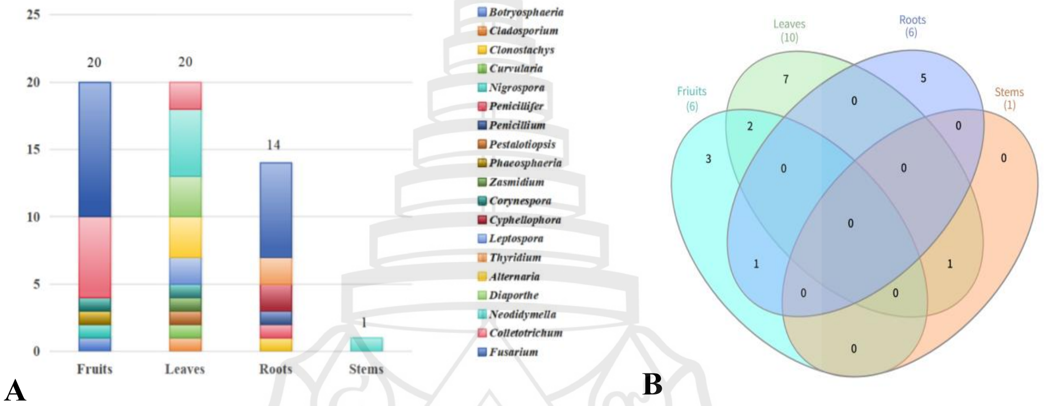


Note Pie chart illustrating the taxonomic distribution of the 63 endophytic fungal isolates from *Tetradium ruticarpum* at the genus level in Guangxi Province.

Figure 3.16 Number of genera recovered from *Tetradium ruticarpum* in Guangxi Province

A total of 55 endophytic fungal isolates were obtained from *Tetradium ruticarpum* collected in Guangxi during 2022 and 2023, representing 19 genera (Figure 3.16). *Fusarium* (17 isolates, 30.9%), *Colletotrichum* (eight isolates, 14.5%), and

Neodidymella (six isolates, 10.9%) were identified as the dominant genera. *Alternaria* and *Diaporthe* (three isolates each, 5.5%) were classified as common genera. The remaining rare genera (<5%) included *Corynespora* (two isolates, 3.6%), *Cyphellophora* (two isolates, 3.6%), *Leptospora* (two isolates, 3.6%), *Thyridium* (two isolates, 3.6%), and single-isolate genera: *Botryosphaeria*, *Cladosporium*, *Clonostachys,* *Curvularia*, *Nigrospora*, *Penicillifer*, *Penicillium*, *Pestalotiopsis*, *Phaeosphaeria*, and *Zasmidium* (one isolate each, 1.8%).



Note Stacked bar chart (A) and Venn diagram (B) showing the composition and overlap of endophytic fungal genera isolated from four tissues (fruits, leaves, roots, and stems) of *Tetradium ruticarpum* collected in Guangxi Province.

Figure 3.17 The number and overlap of genera recovered from *Tetradium ruticarpum* in Guangxi Province

Among the 55 endophytic fungal isolates obtained from *Tetradium ruticarpum* in Guangxi Province, 20 originated from fruits, 20 from leaves, 14 from roots and one from stems (Table 3.9, Figure 3.17A). Fruit tissues yielded 20 isolates representing six genera, with *Fusarium* the most abundant (10 isolates, 50.0%), followed by *Colletotrichum* (six isolates, 30.0%), and *Botryosphaeria*, *Corynespora*, *Nigrospora*, and *Phaeosphaeria* (one isolate each, 5.0%). Leaf tissues contained 20 isolates across eight genera, with *Neodidymella* the most frequent (five isolates, 25.0%), followed by *Alternaria* and *Diaporthe* (three isolates each, 15.0%), *Colletotrichum* and *Leptospora* (two isolates each, 10.0%), and *Cladosporium*, *Corynespora*, *Curvularia*, *Pestalotiopsis*, and *Zasmidium* (one isolate each, 5.0%). Root tissues harbored 14 isolates representing six genera, with *Fusarium* dominant (seven isolates, 50.0%), followed by *Cyphellophora* and *Thyridium* (two isolates each, 14.3%), and *Clonostachys*, *Penicillifer*, and *Penicillium* (one isolate each, 7.1%). Only one genus *Neodidymella* was isolated from the stem. The composition of endophytic fungal communities varied among the three tissues, with several genera shared across tissues, such as *Fusarium* in fruits and roots and *Colletotrichum* in fruits and leaves, while tissue-specific genera were also observed, reflecting a tissue-dependent distribution pattern of endophytic fungi in *T. ruticarpum*.

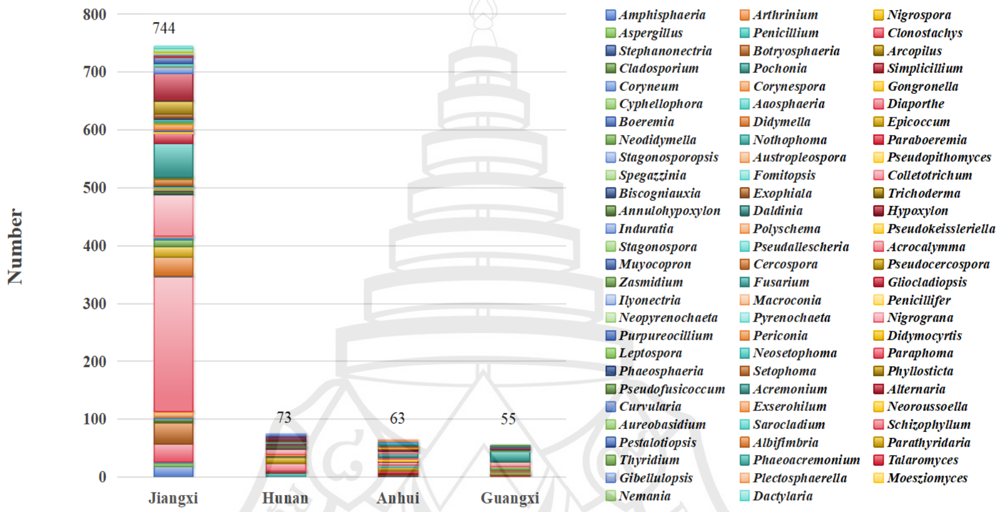
Table 3.9 Generic richness of endophytic fungi associated with *Tetradium ruticarpum* in different plant tissues from Guangxi Province

Phylum	Class	Genus	Fruit	Leaf	Root	Stem	Total
Ascomycota	Dothideomycetes	*Alternaria*	0	3	0	0	3
		Botryosphaeria	1	0	0	0	1
		Cladosporium	0	1	0	0	1
		Corynespora	1	1	0	0	2
		Curvularia	0	1	0	0	1
		Leptospora	0	2	0	0	2
		Neodidymella	0	5	0	1	6
		Phaeosphaeria	1	0	0	0	1
		Zasmidium	0	1	0	0	1
	Eurotiomycetes	*Cyphellophora*	0	0	2	0	2
		Penicillium	0	0	1	0	1
	Sordariomycetes	*Clonostachys*	0	0	1	0	1
		Colletotrichum	6	2	0	0	8
		Diaporthe	0	3	0	0	3
		Fusarium	10	0	7	0	17
		Nigrospora	1	0	0	0	1
		Penicillifer	0	0	1	0	1
		Pestalotiopsis	0	1	0	0	1
		Thyridium	0	0	2	0	2
		Total	20	20	14	1	55

In Guangxi Province, the endophytic fungal communities of *Tetradium ruticarpum* exhibited distinct tissue-specific distributions, with no single genus found across all four tissues (Figure 3.17B). *Fusarium* was shared between fruit and root, while *Colletotrichum* and *Corynespora* were shared between fruit and leaf, and *Neodidymella* occurred in both stem and leaf. Several genera were tissue-specific:

Botryosphaeria, *Nigrospora*, and *Phaeosphaeria* were detected only in fruit; *Clonostachys*, *Cyphellophora*, *Penicillifer*, *Penicillium*, and *Thyridium* were exclusive to root; and *Alternaria*, *Cladosporium*, *Curvularia*, *Diaporthe*, *Leptospora*, *Pestalotiopsis*, and *Zasmidium* were found only in leaf.

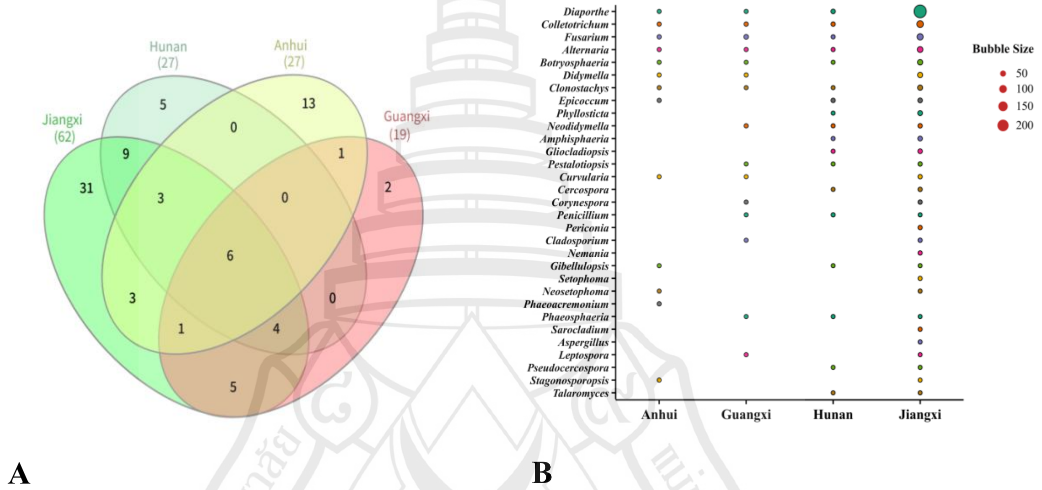
3.2.3.5 Analysis of endophytic fungal community composition of *Tetradium ruticarpum* across four provinces



Note Stacked bar chart showing the number and composition of endophytic fungal genera isolated from *Tetradium ruticarpum* in four different provinces, namely Jiangxi, Hunan, Anhui, and Guangxi.

Figure 3.18 The Number of genera recovered from *Tetradium ruticarpum* in different provinces

Overall, a total of 935 endophytic fungal isolates were obtained from *Tetradium ruticarpum* across four provinces in China. Jiangxi Province yielded the highest number of isolates (744 isolates, 63 genera), followed by Hunan (73 isolates, 27 genera), Anhui (63 isolates, 27 genera), and Guangxi (55 isolates, 19 genera) (Table 3.10, Figure 3.18). The much higher number of isolates from Jiangxi Province is partly due to uneven sampling across provinces, indicating that more balanced sampling and experimental design would be required to obtain statistically robust data. Nevertheless, the current study still provides valuable insights into the endophytic fungal communities of *T. ruticarpum*. Although the total number of isolates varied among provinces, certain genera were consistently detected. All communities in the four provinces exhibit a typical long-tail distribution, with a few dominant taxa followed by numerous rare genera, and a single genus predominated in each province, including *Diaporthe* in Jiangxi (31.3%) and Hunan (17.8%) and *Fusarium* in Anhui (11.1%) and Guangxi (30.9%). Across all provinces, *Diaporthe*, *Colletotrichum*, *Fusarium*, and *Alternaria* represented the core components of the endophytic fungal community, with relative abundances ranging from 5.5% to 31.3%, while other genera occurred at lower frequencies (see Figs. 16, 18, 20, and 22 for details).



Note Venn diagram (A) illustrating the overlap of endophytic fungal genera among four provinces for Tetradium ruticarpum, and Bubble Plot (B) showing the distribution of 31 of these genera (with isolate numbers ≥ 4) across the four provinces.

Figure 3.19 Overlap of the genera between different provinces

Table 3.10 Generic richness of endophytic fungi from *Tetradium ruticarpum* in different provinces

Phylum	Class	Genus	Jiangxi	Hunan	Anhui	Guangxi	Total
Ascomycota	Dothideomycetes	*Aaosphaeria*	1	-	-	-	1
		Acrocalymma	1	-	2	-	3
		Alternaria	47	4	3	3	57
		Aureobasidium	1	-	-	-	1
		Austropleospora	1	-	-	-	1
		Ascochyta	0	0	1	0	1
		Boeremia	1	-	-	-	1
		Botryosphaeria	37	1	3	1	42
		Cercospora	1-	1	-	-	11
		Cladosporium	7	-	-	1	8
		Corynespora	8	-	-	2	1-
		Curvularia	1-	-	1	1	12
		Didymella	32	2	2	-	36
		Didymocyrtis	3	-	-	-	3
		Epicoccum	18	9	5	-	32
		Exserohilum	1	-	-	-	1
		Leptospora	2	-	-	2	4
		Muyocopron	1	1	-	-	2
		Neodidymella	12	3	-	6	21
		Neopyrenochaeta	-	1	-	-	1
		Neoroussoella	-	-	2	-	2
		Neosetophoma	4	-	1	-	5
		Nigrograna	-	-	3	-	3
		Nothophoma	3	-	-	-	3
		Paraboeremia	-	1	-	-	1
		Paraphoma	1	-	-	-	1
		Parathyridaria	-	-	1	-	1
		Periconia	9	-	-	-	9
		Phaeosphaeria	2	2	-	1	5
		Phyllosticta	23	1	-	-	24
		Polyschema	3	-	-	-	3
		Pseudocercospora	3	1	-	-	4
		Pseudofusicoccum	1	-	-	-	1
		Pseudokeissleriella	-	-	3	-	3
		Pseudopithomyces	1	1	-	-	2
		Pyrenochaeta	1	-	-	-	1
		Setophoma	6	-	-	-	6
		Spegazzinia	-	-	1	-	1

Table 3.10 (continued)

Phylum	Class	Genus	Jiangxi	Hunan	Anhui	Guangxi	Total
		Stagonospora	2	-	-	-	2
		Stagonosporopsis	2	-	2	-	4
		Zasmidium	1	-	-	1	2
	Eurotiomycetes	*Aspergillus*	4	-	-	-	4
		Cyphellophora	-	-	-	2	2
		Exophiala	-	1	-	-	1
		Penicillium	3	5	-	1	9
		Talaromyces	3	1	-	-	4
	Sordariomycetes	*Acremonium*	-	-	1	-	1
		Albifimbria	1	-	-	-	1
		Amphisphaeria	18	2	-	-	2-
		Annulohypoxylon	3	-	-	-	3
		Arcopilus	1	-	-	-	1
		Arthrinium	1	-	-	-	1
		Biscogniauxia	1	-	-	-	1
		Clonostachys	31	1	2	1	35
		Colletotrichum	71	9	5	8	93
		Coryneum	2	-	-	-	2
		Daldinia	3	-	-	-	3
		Diaporthe	233	13	2	3	251
		Funiliomyces	3	-	-	-	3
		Fusarium	59	3	7	17	86
		Gibellulopsis	3	1	2	-	6
		Gliocladiopsis	16	3	-	-	19
		Hypoxylon	-	-	2	-	2
		Ilyonectria	1	1	-	-	2
		Induratia	-	1	-	-	1
		Macroconia	1	-	-	-	1
		Nemania	7	-	-	-	7
		Nigrospora	-	-	-	1	1
		Penicillifer	2	-	-	1	3
		Pestalotiopsis	1-	3	-	1	14
		Phaeoacremonium	-	-	5	-	5
		Plectosphaerella	-	-	1	-	1
		Pochonia	-	1	-	-	1
		Pseudallescheria	1	-	-	-	1
		Purpureocillium	2	-	-	-	2
		Sarocladium	5	-	-	-	5
		Simplicillium	-	-	2	-	2
		Stephanonectria	-	-	1	-	1

Table 3.10 (continued)

Phylum	Class	Genus	Jiangxi	Hunan	Anhui	Guangxi	Total
		Thyridium	-	-	1	2	3
		Trichoderma	1	-	-	-	1
Basidiomycota	Agaricomycetes	*Fomitopsis*	-	-	1	-	1
	Agaricomycetes	*Schizophyllum*	-	-	1	-	1
	Ustilaginomycetes	*Moesziomyces*	2	-	-	-	2
Mucoromycota	Mucoromycetes	*Gongronella*	1	-	-	-	1
			744	73	63	55	935

The endophytic fungal genera of *Tetradium ruticarpum* across Jiangxi, Hunan, Anhui, and Guangxi provinces include both cross-regional shared components and genera detected only in individual provinces (Figure 3.19A). Bubble plot of 31 genera (≥ four isolates) illustrates their distribution patterns, excluding less informative rare genera (Figure 3.19B). Among them, six genera are common to all four provinces, specifically *Clonostachys*, *Botryosphaeria*, *Alternaria*, *Fusarium*, *Colletotrichum*, and *Diaporthe*; eight genera are shared by three provinces, which are divided into three combinations: Jiangxi, Hunan, and Anhui share three genera (*Gibellulopsis*, *Epicoccum*, *Didymella*), Jiangxi, Hunan, and Guangxi share four genera (*Phaeosphaeria*, *Penicillium*, *Pestalotiopsis*, *Neodidymella*), and Jiangxi, Anhui, and Guangxi share one genus (*Curvularia*); 18 genera are shared by two provinces, covering four combinations: Jiangxi and Anhui share three genera (*Acrocalymma*, *Stagonosporopsis*, *Neosetophoma*), Jiangxi and Hunan share nine genera (*Ilyonectria*, *Muyocopron*, *Pseudopithomyces*, *Pseudocercospora*, *Talaromyces*, *Cercospora*, *Gliocladiopsis*, *Amphisphaeria*, *Phyllosticta*), Jiangxi and Guangxi share five genera (*Zasmidium*, *Leptospora*, *Penicillifer*, *Cladosporium*, *Corynespora*), and Anhui and Guangxi share one genus (*Thyridium*). In addition, there are genera detected only in individual provinces: Jiangxi has the largest number at 31 genera (e.g., *Aaosphaeria*, *Albifimbria*), Hunan has five genera (*Exophiala*, *Induratia*, *Neopyrenochaeta*, *Paraboeremia*, *Pochonia*), Anhui has 13 genera (*Acremonium*, *Fomitopsis*, *Parathyridaria*, *Plectosphaerella*, *Schizophyllum*, *Spegazzinia*, *Stephanonectria*, *Hypoxylon*, *Neoroussoella*, *Simplicillium*, *Nigrograna*, *Pseudokeissleriella*, *Phaeoacremonium*), and Guangxi has the fewest at two genera (*Nigrospora*, *Cyphellophora*). Bubble Plot (Figure 25B) showing the distribution of 31 of these genera (with isolate numbers ≥ 4) across the four provinces.

3.3 New Taxa of Endophytic Fungi in *Tetradium ruticarpum*

3.3.1 Phylogenetic Analysis

Phylogenetic analyses were performed to resolve the placement of the taxonomic novelties and other taxa of uncertain position. The resulting trees are presented and discussed in the species note.The taxa used in this study and their GenBank accession numbers are presented in Appendix Tables B1–B12.

3.3.2 Taxonomy

New species were established in accordance with the taxonomic frameworks of Chethana et al. (2021), Jayawardena et al. (2021), and Maharachchikumbura et al. (2021). The arrangement of the following taxa is based on the latest fungal classification system proposed by Hyde et al. (2024) and recent relevant publications. The taxa illustrated below are presented in alphabetical order.

Ascomycota Caval. -Sm.

Dothideomycetes sensu O.E. Erikss. & Winka

Dothideomycetidae P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker

Mycosphaerellales (Nannf.) P.F. Cannon

Mycosphaerellaceae Lindau (based on molecular data)

Zasmidium Fr. 1849

The genus *Zasmidium* was originally established by Fries in 1849, with *Z. cellare* (Pers.) Fr. designated as the type species. Arzanlou et al. (2007) demonstrated that *Zasmidium* represents the earliest valid name for Stenella-like hyphomycetes within the family Mycosphaerellaceae, which are distinguished by their conidiogenous loci and conidia bearing truncate hila (Bensch et al., 2012). As a result, numerous species formerly assigned to *Stenella* were subsequently reclassified under *Zasmidium* (Braun et al., 2010; Kamal, 2010). It is currently classified within the order

Mycosphaerellales of class Dothideomycetes. To date, approximately 150 species are currently accepted in the genus (Hyde et al., 2024).

Zasmidium guangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov.*, Figure 3.20 and Figure 3.21

Etymology: The name reflects the location "Guangxi" from where the holotype was collected.

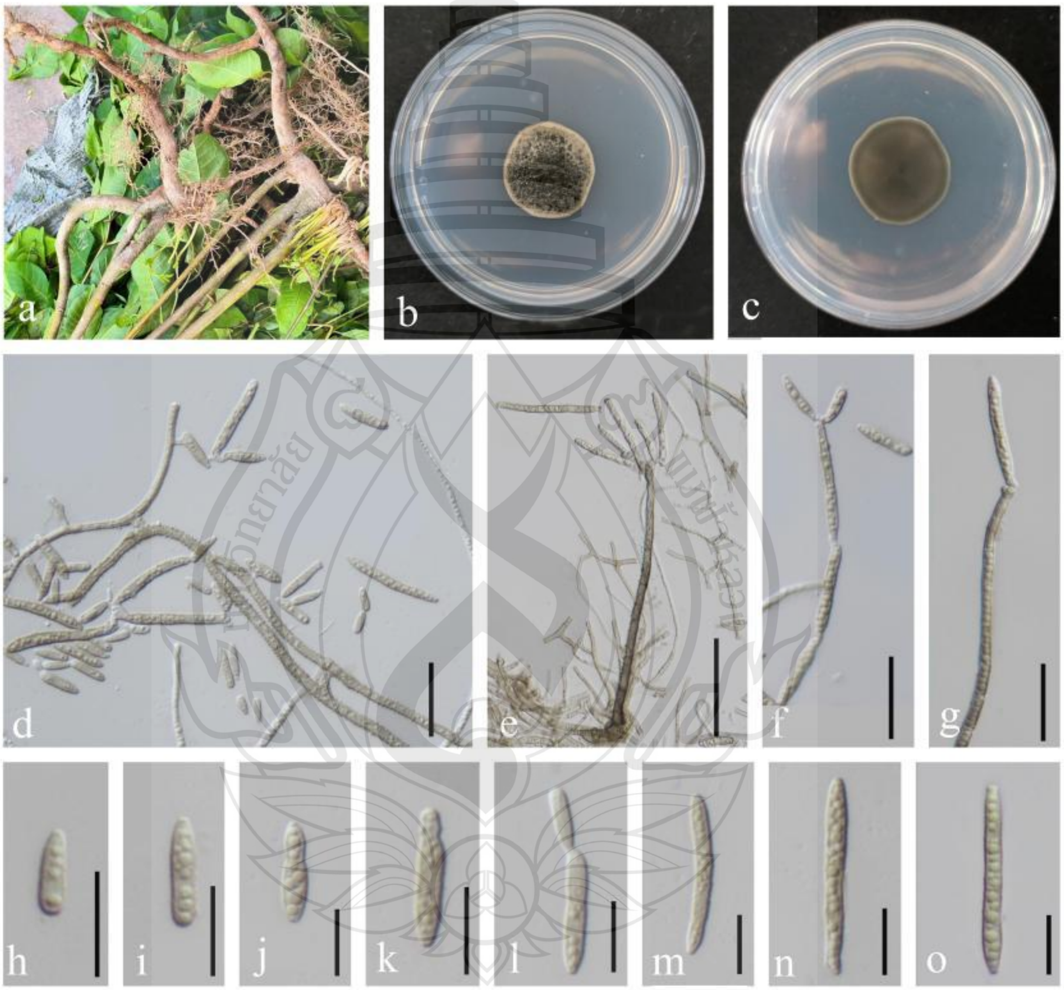
Holotype: HFJAU10886

Endophytic in the roots of *T. ruticarpum*. **Sexual morph:** Undetermined. **Asexual morph:** hyphomycetous. *Mycelium* composed of hyaline and pale brown to dark blackish-brown hyphae, verruculose, septate, branching, 1.0–2.5 µm. *Conidiophores* 33–310 × 1.2–5.2 µm ($\bar{x}$ = 145 × 4 µm, n = 25), arising singly as lateral branches of superficial hyphae, pale olivaceous brown, straight or slightly curved, almost smooth to verruculose, dendritic rugged or rugose on the surface. *Conidiogenous cells* 6–26.5 × 2.5–5 µm ($\bar{x}$ = 13 × 3 µm, n = 25), terminal, integrated, sympodial, polyblastic, cylindrical, geniculate. *Conidia* 7–50 × 2–4.5 µm ($\bar{x}$ = 20 × 2.8 µm, n = 35), solitary, occasionally branched chains, cylindrical to obclavate, 0-1-septate, light brown, thin-walled, verruculose.

Culture characteristics: Colony on PDA 22 mm diam after 2 weeks at 25 °C, the mycelium showed spreading growth with circular colony formation. The central region exhibited dark pigmentation with numerous black, bullate (blister-like) structures, while the periphery displayed lighter-colored, floccose aerial hyphae. The middle part of the reverse side of the colony is relatively dark in color, gradually lightening towards the edge, and the edge is regular.

Material examined: China, Guangxi Province, Hechi city, Luocheng, 9 September 2023, 24.8667°N, 109.0333°E, 0m asl, endophytic fungi from the healthy leaf of *T. ruticarpum*, Lixue Mi, HFJAU10886 (dry culture, holotype); ex-type living culture JAUCC 6594; Jiangxi Province, Yichun city, Fengcheng, 27 September 2024, 28.3944°N 115.5965°E, 35.9m asl, endophytic fungi from the healthy leaf of *T. ruticarpum*, Lixue Mi, dry culture HFJAU10594, living culture JAUCC 7351.

Notes: The multi-locus phylogenetic analysis showed that *Zasmidium guangxiensis* clustered as a sister taxon to *Z. aporosae* (P210X) and *Z. pearceae* (BRIP 72388b) with 99.9% ML bootstrap support in the SH-aLRT test, 100% in the UFB method, and a Bayesian probability of 0.1 (Figure 3.21). Morphologically, *Zasmidium guangxiensis* differs from *Z. aporosae* by having longer and often rugose conidiophores (up to 310 µm vs. 83 µm), geniculate polyblastic conidiogenous cells, and longer, mostly 0–1-septate conidia (up to 50 µm vs. 38 µm). Conidia in *Z. guangxiensis* are cylindrical to obclavate and verruculose, while those of *Z. aporosae* are more variable in shape. (Phengsintham et al., 2009). Therefore, we identified our new isolate (JAUCC 6544) as *Z. guangxiensis* with the first host report on *Tetradium ruticarpum* in China.



Note a Host. b, c Colonies on PDA from surface and reverse. d–g Conidiophores and developing conidia. h–o Conidia. Scale bars: d = 20, e=50, f ,g = 20µm, h–o =10 µm.

Figure 3.20 Photographs of *Zasmidium guangxiensis* (HFJAU10463, holotype)

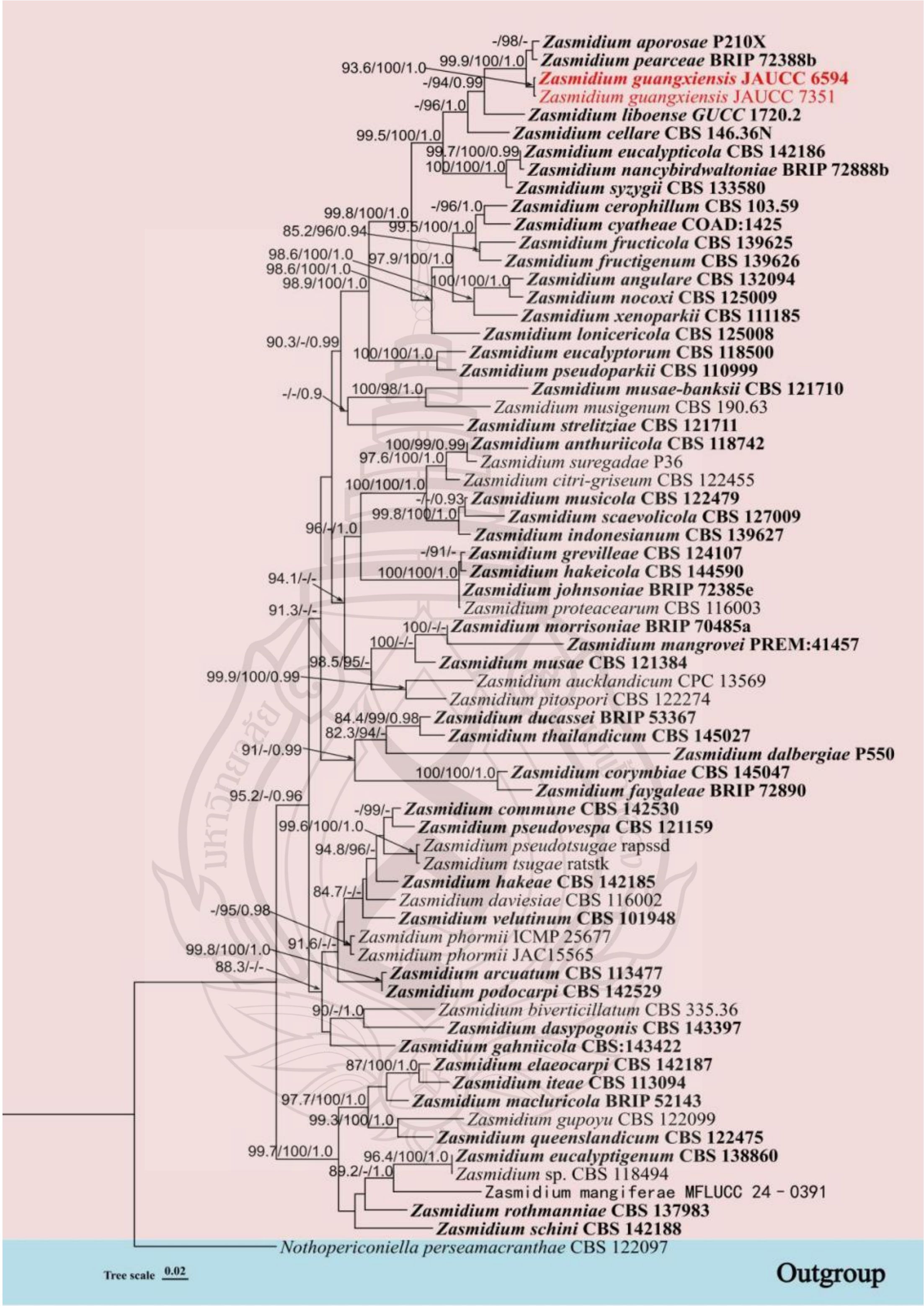


Figure 3.21 Phylogenetic tree of *Zasmidium*

Maximum likelihood (ML) phylogenetic tree of the *Zasmidium* genus based on combined ITS, LSU, and RPB2 sequence data (Figure 3.21). Sixty-seven strains are included in the combined gene analyses, comprising 2416 characters after alignment (554 characters for ITS, 809 for LSU, and 1053 for RPB2). *Nothopericoniella perseamacrantha*e (CBS 122097) was used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TNe+I+G4 for ITS, TN+F+I+G4 for LSU, TN+F+I+G4 for RPB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -21223.850 is presented. The matrix had 1012 distinct alignment patterns, with 25.48%undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for ITS, LSU, and RPB2 in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker

Pleosporales Luttrell ex M.E. Barr

Latoruaceae Crous, IMA Fungus 6(1), 176 (2015).

Latoruaceae was established by Crous et al. (2015a) to accommodate *Latorua* and *Polyschema* within Pleosporales. Following its establishment, the family was broadened to incorporate Matsushimamyces and Pseudoasteromassaria (Ariyawansa et al., 2015; Sharma et al., 2015), with subsequent additions of *Triseptata* (Boonmee et al., 2020), *Multiverruca* (Wang et al., 2023), and *Verrucohypha* (Crous et al., 2024). To date, six genera are recognized within the family. Members of Latoruaceae are mainly saprobic or weakly parasitic, occurring on twigs, leaves, soil, or decaying wood, and occasionally from human clinical specimens. They are characterized by immersed, papillate ascomata, bitunicate asci, brown fusiform ascospores, and hyphomycetous or coelomycetous asexual morphs, often with brown, septate conidia in chains (Boonmee et al., 2020b; Crous et al., 2015; Wang et al., 2023).

Tetradiomyces L.X. Mi, K.D. Hyde & D.M. Hu**,** gen. nov.

Etymology: Named after the host plant *T. ruticarpum*, from which the fungus was isolated.

Type species: *Tetradiomyces jiangxiensis* L.X. Mi, K.D. Hyde & D.M. Hu

Mycelium ranges from immersed to superficial and consists of branched, septate hyphae that vary in color from hyaline to predominantly dark brown. The hyphae include both thin-walled and verruculose types. Thin hyphae occasionally bear swollen, spherical to subspherical cells, which can occur singly or in chains, and may contain faintly visible inclusions such as oil droplets or granules. Verruculose hyphae become more prominent as cultures age.

Culture characteristics: The colonies on PDA superficial, initially dark olivaceous with dark-green and woolly, later becoming dry, wrinkled, raised, cracked, with undulate margin, reverse pale-olivaceous to yellow-white, cracked star-like from the center, with a neat edge.

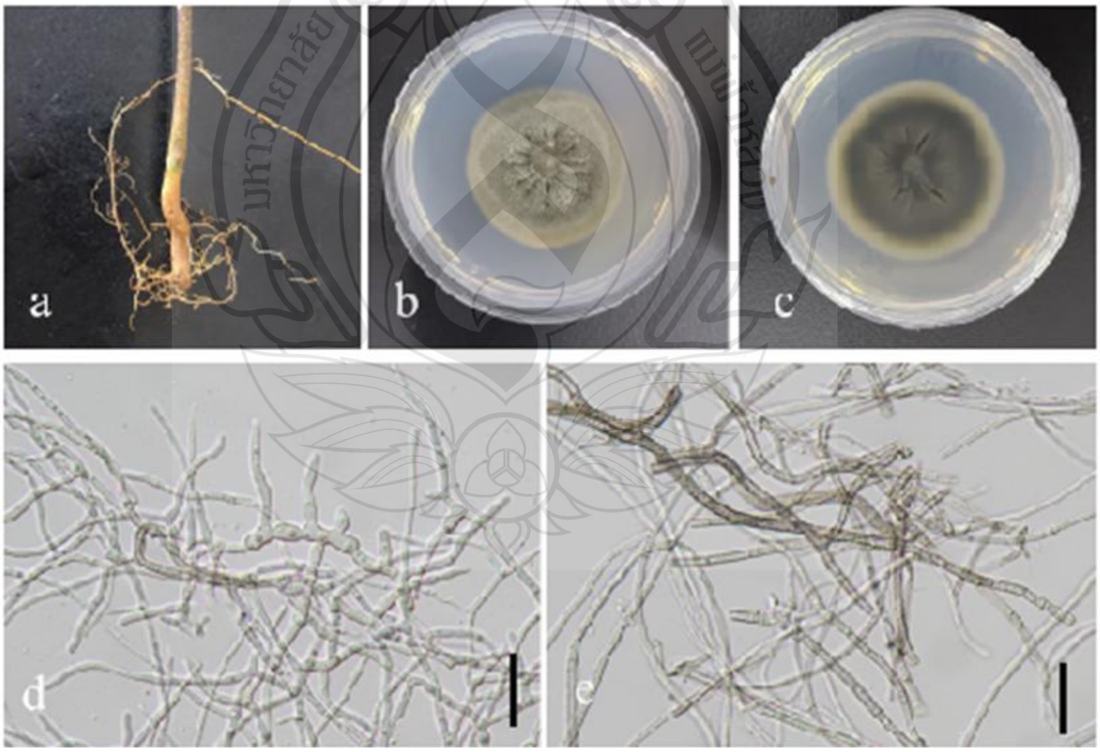
Notes: *Tetradiomyces* forms a distinct and well-supported clade (SH-aLRT/UFB/BPP = 99.4/97/1.0) as the sister clade to *Verrucohypha* within Latoruaceae, and is phylogenetically distant from other genera in the family. It is currently known only from its asexual morph, isolated as an endophyte from the roots of *T. ruticarpum*. Colonies are characterized by dark olivaceous, woolly to wrinkled surfaces with star-like cracking. Only vegetative hyphae were observed; no conidiogenous structures or conidia were produced in culture. Since sporulating structures of *Tetradiomyces* were not observed, precluding direct morphological comparison with related genera, both ITS and LSU sequence divergences were used to assess its taxonomic status (Appendix Table C1–C2). In the ITS-rDNA dataset, *Tetradiomyces* shows intergeneric genetic distances ranging from 10.80% (vs. *Multiverruca*) to 23.92% (vs. *Pseudoasteromassaria*). This minimum distance of 10.80% exceeds closer known intergeneric distances, like the 8.19% between *Multiverruca* and *Latorua*, indicating genus-level differentiation. For LSU-rDNA, *Tetradiomyces* exhibits intergeneric distances from 2.92% (vs. *Multiverruca*) to 3.99% (vs. *Triseptata*). The minimum distance of 2.92% surpasses the smallest reported intergeneric distance of 1.32% (between *Multiverruca* and *Matsushimamyces*) and aligns with typical genus-level divergence. Combined, these genetic divergences in both ITS and LSU support recognizing *Tetradiomyces* as a new genus in Latoruaceae, rather than a new species of an existing genus. Expanded sampling to obtain more species of this genus is needed to better understand the genus *Tetradiomyces*, including its taxonomic boundaries, morphological diversity, and phylogenetic placement within Latoruaceae.

Tetradiomyces jiangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov* Figure 3.22 and Figure 3.23

Etymology: The name reflects the location “Jiangxi” from where the holotype was collected.

Holotype: HFJAU10590

Dark septate endophyte (DSE) isolated on culture media from surface-sterilised roots of *Tetradium ruticarpum*. Mycelium is immersed to superficial, composed of branched, septate hyphae. Hyphae range from hyaline to dark brown (predominantly dark brown), with thin-walled and verruculose types. Thin hyphae are 1–3 µm wide, sometimes bearing swollen cells, which are spherical or subspherical, occurring singly or in chains, approximately 3.5–6 µm diameter, faintly visible inclusions (such as oil droplets, granules); verruculose hyphae are 2–4 µm wide, more prominent in older cultures.



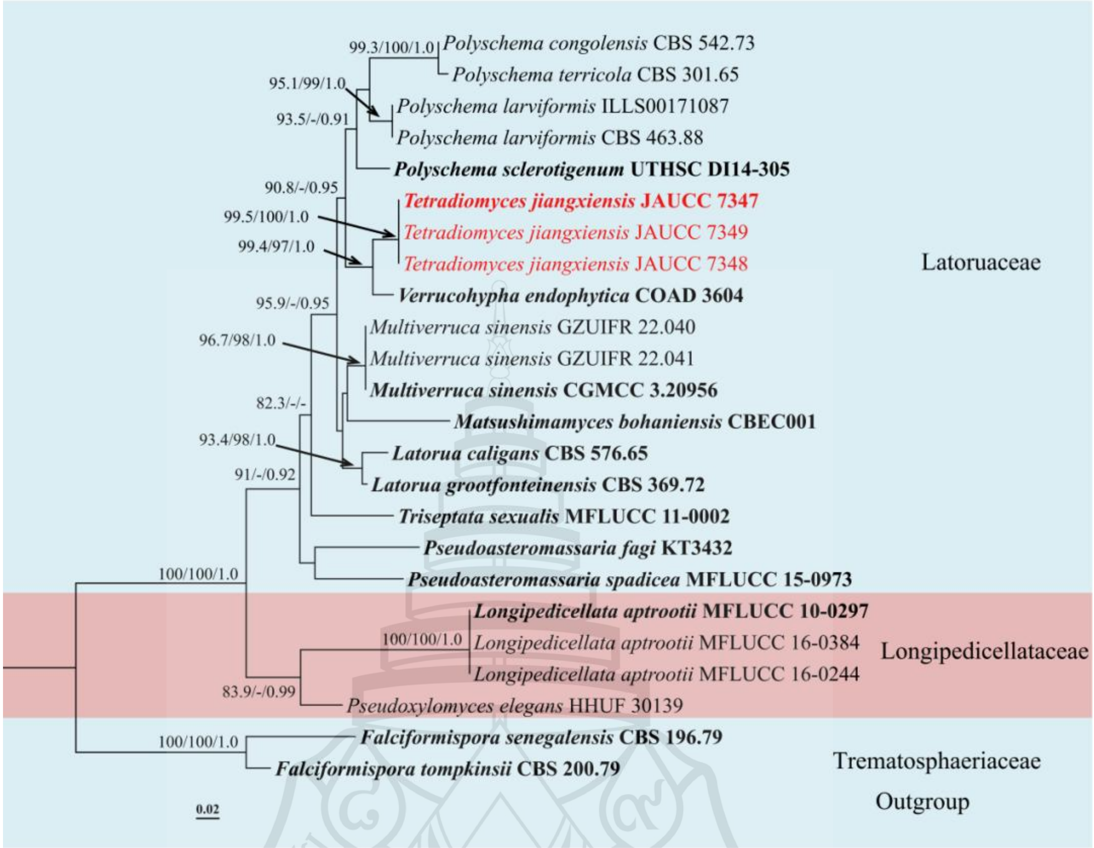
Note a Host. b, c Colonies on PDA from surface and reverse. d–e Branched or unbranched mycelia. Scale bars: d, e = 20 µm**.**

Figure 3.22 Photographs of *Tetradiomyces jiangxiensis* (HFJAU10590, holotype)

Culture characteristics: The colonies on PDA reached 36mm in diameter after 4 weeks. Superficial, initially dark olivaceous with dark-green and woolly, later becoming dry, wrinkled, raised, cracked, with undulate margin, reverse pale-olivaceous to yellow-white, cracked star-like from the center, with a neat edge.

Material examined: China, Jiangxi Province, Yichuncity, Fengcheng, 27 September 2024, 28.3944°N 115.5965°E, 35.8m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, HFJAU10590 (dry cultrue, holotype), ex-type living cultrue JAUCC 7347; ibid, from the healthy roots of *T. ruticarpum*, 27 September 2024, Lixue Mi, dry cultrue HFJAU10591, the living cultrue JAUCC 7348; ibid, from the healthy roots of *T. ruticarpum*, 27 September 2024, Lixue Mi, dry cultrue HFJAU10592, the living cultrue JAUCC 7349.

Notes: *Tetradiomyces jiangxiensis* is introduced as a novel species typifying the genus *Tetradiomyces*, represented by three isolates and described based on its asexual morph. This species was isolated as an endophyte from *Tetradium ruticarpum* (Rutaceae). Phylogenetic analysis based on combined LSU and ITS sequence data reveals that *T. jiangxiensis* forms a distinct lineage within the family Latoruaceae with strong statistical support (SH-aLRT/UFB/BPP = 92.9/96/1.0) (Figure 3.23). It forms a clade closely related to *Verrucohypha endophytica*, the type species of *Verrucohypha*. Compared to *V. endophytica*, *T. jiangxiensis* shows 94.32% identity with 31 polymorphisms, including gaps for the ITS region, and 98.6% identity with 12 polymorphisms, including gaps for the LSU region. Morphologically, *T. jiangxiensis* resembles other genera within Latoruaceae, characterized by verruculose hyphae and predominantly dark brown coloration. The main morphological differences between A and B are in hyphal size and features. *T. jiangxiensis* has thinner hyphae (1–3 µm) with swollen, spherical cells (3.5–6 µm) and faint inclusions, while *V. endophytica* shows slightly wider thin hyphae (2–3 µm) and verruculose hyphae (2.5–5 µm), with mucilaginous bubbles up to 8 µm appearing in older cultures. Notably, *T. jiangxiensis* represents the second root-associated endophytic fungus discovered in Latoruaceae after *Verrucohypha endophytica*.



Note Maximum likelihood (ML) phylogenetic tree of the *Tetradiomyces* genus and related taxa based on combined LSU and ITS sequence data. Twenty-four strains are included in the combined gene analyses, comprising 1415 characters after alignment (890 for LSU, 585 for ITS). *Falciformispora senegalensis* (CBS 196.79) and *F. tompkinsii* (CBS 200.79) are used as the outgroup taxon. Maximum likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TNe+I+G4 for LSU and ITS) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -6176.068 is presented. The matrix had 420 distinct alignment patterns, with 13.77% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for LSU and ITS in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Figure 3.23 Phylogenetic tree of *Tetradiomyces*

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

Pseudokeissleriella Jian K. Liu

Pseudokeissleriella was introduced by Yang et al. (2022b) within Lentitheciaceae (Pleosporales, Dothideomycetes) to accommodate *P. bambusicola*. This fungus was collected from the dead culms of bamboos in Sichuan Province, China (Yang et al., 2022b). The sexual morph of the genus *Pseudokeissleriella* is characterized by subglobose to globose, glabrous ascomata, and hyaline, septate, fusiform ascospores with subobtuse ends and a swollen upper cell, surrounded by a mucilaginous sheath with a central depression (Yang et al., 2022b).

Pseudokeissleriella tetradii L.X. Mi & D.M. Hu sp. *nov*., Figure 3.24 and Figure 3.25

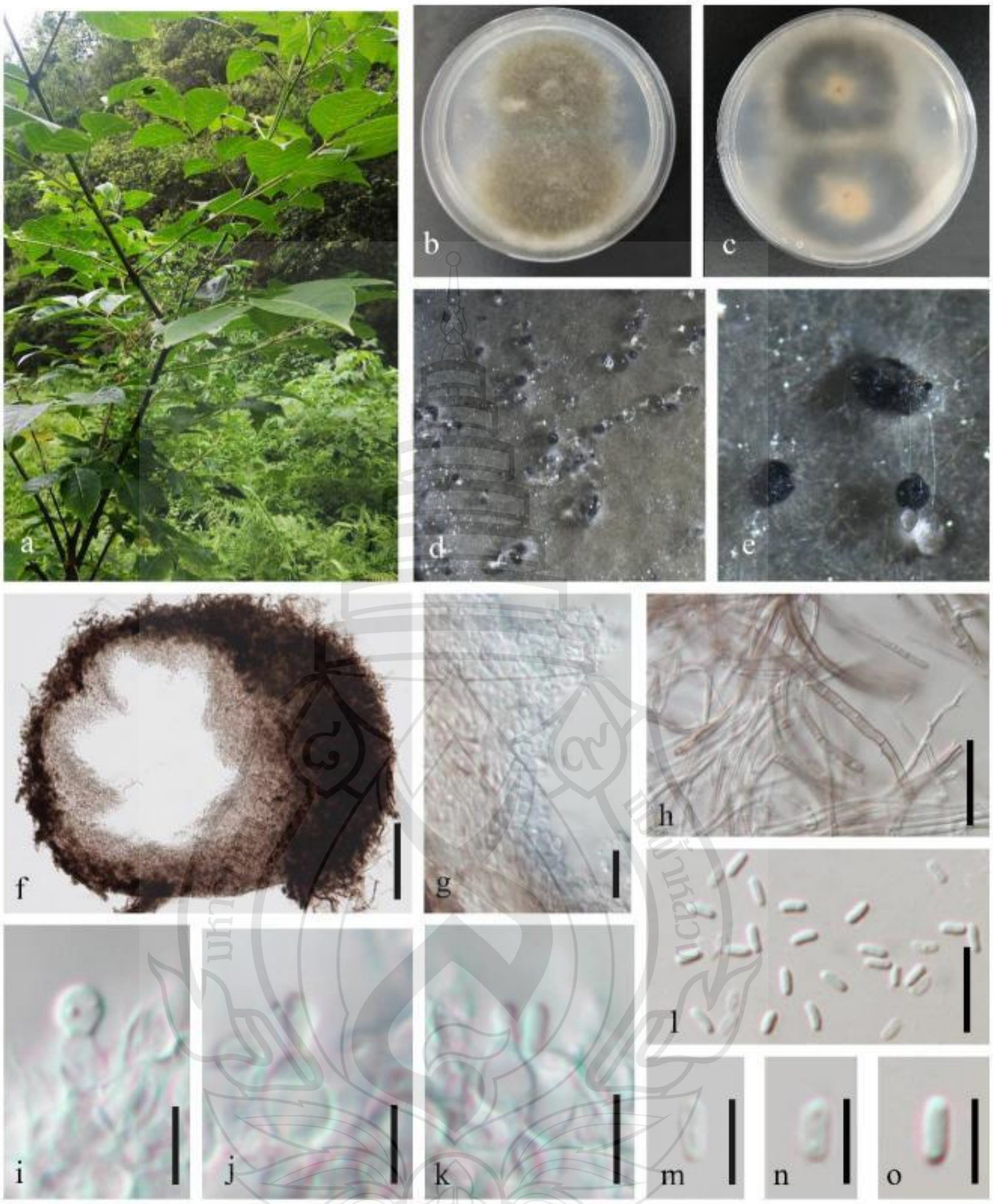
Index Fungorum Number: IF903759; Facesoffungi Number: FOF17679.

Etymology: The name reflects the host genus, *Tetradium*, from which the fungus was isolated.

Holotype: HFJAU10463

Endophytic fungi from the healthy stem of *Tetradium ruticarpum* (Rutaceae). **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Mycelium* densely branched, 1–4 µm wide, hyaline, subhyaline to pale brown, septate, smooth-walled; *Conidiomata* 150–700 µm diam, pycnidial, solitary to aggregated, globose to subglobose, black, glabrous or with few hyphal outgrowths, superficial on the agar or semi-immersed; *Ostiole* inconspicuous; *Conidiomatal wall* pseudoparenchymatous, several layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.8–4 × 1–1.5 µm ($\overline{x}$ = 3.5 × 1.3 µm; n = 50), holoblastic, hyaline, smooth-walled, ampulliform to doliiform, proliferating percurrently at apex; *Conidia* 2.8–4 × 1–1.5 µm ($\overline{x}$ = 3.5 × 1.3 µm; n = 50), hyaline, cylindrical to subcylindrical, biguttulate, rounded at both ends, straight, aseptate, thick- and smooth-walled.

Culture characteristics: Colonies growing on PDA, reaching a diameter of 40 mm after 16 d at 25 °C, nearly circular, surface slightly rough, woolly or cottony, dark grey or olive to pale white from centre to margin, reverse as the same as front. No visible pigmentation.



Note a Host. b, c Colonies on PDA from surface and reverse. d, e Conidioma on PDA. f Section through conidioma. g Section of peridium. h Mycelium. i–k Conidiogenous cells and developing conidia. l–o Conidia. Scale bars: f, g = 300 µm, all others = 10µm.

Figure 3.24 Photographs of *Pseudokeissleriella tetradii* (HFJAU10463, holotype)

Material examined: China, Anhui Province, Xuancheng City, Xuanzhou District, on the healthy stems of *Tetradium ruticarpum*, 30.88° N 118.78° E, altitude

46m, 22 May 2022, Lixue Mi, dry culture (HFJAU10463, holotype), ex-type living culture JAUCC 6570; ibid, 30.90° N, 118.73° E, altitude 17.76m, in the healthy stems of *Tetradium ruticarpum*, 8 September 2023, Lixue Mi, dry culture HFJAU10464, living culture JAUCC 6578; bid, dry culture HFJAU10465, living culture JAUCC 6586.

Notes: Our newly isolated strain *Pseudokeissleriella tetradii* (JAUCC 6570) was morphologically identified as the asexual morph (anamorph). Direct morphological comparison is unfeasible since *P. tetradii* is an asexual morph, while *P. bambusicola* (CGMCC 3.20950) was described based on its sexual morph. However, this species aligns with the anamorphic characteristics defined for Lentitheciaceae, demonstrating pycnidial conidiomata with globose morphology, enteroblastic conidiogenous cells, and unicellular cylindrical conidia that are hyaline with smooth walls (Hyde et al., 2013). Moreover, the multi-locus phylogenetic analysis (Figure 3.27) strongly supports the close relationship between *P. tetradii* and *P. bambusicola*, with high statistical support (ML bootstrap = 98.8% in SH-aLRT, UFBoot = 100%, Bayesian posterior probability = 1.0). The pairwise genetic distances between *P. tetradii* and *P. bambusicola* for different loci are as follows: ITS (2.75%), LSU (0.44%), SSU (0.00%), and TEF1 (1.28%). These values fall below the intergeneric divergence thresholds typically observed within Lentitheciaceae (Appendix Table C3–C6). Furthermore, the ITS divergence (2.75%) exceeds the intraspecific variation commonly observed in closely related fungal species (Jeewon & Hyde, 2016), supporting *P. tetradii* as a distinct species rather than an asexual morph of *P. bambusicola*. Thus, given the above morphological and molecular evidence, we introduce *P. tetradii* as a new species, representing its first documented asexual morph.

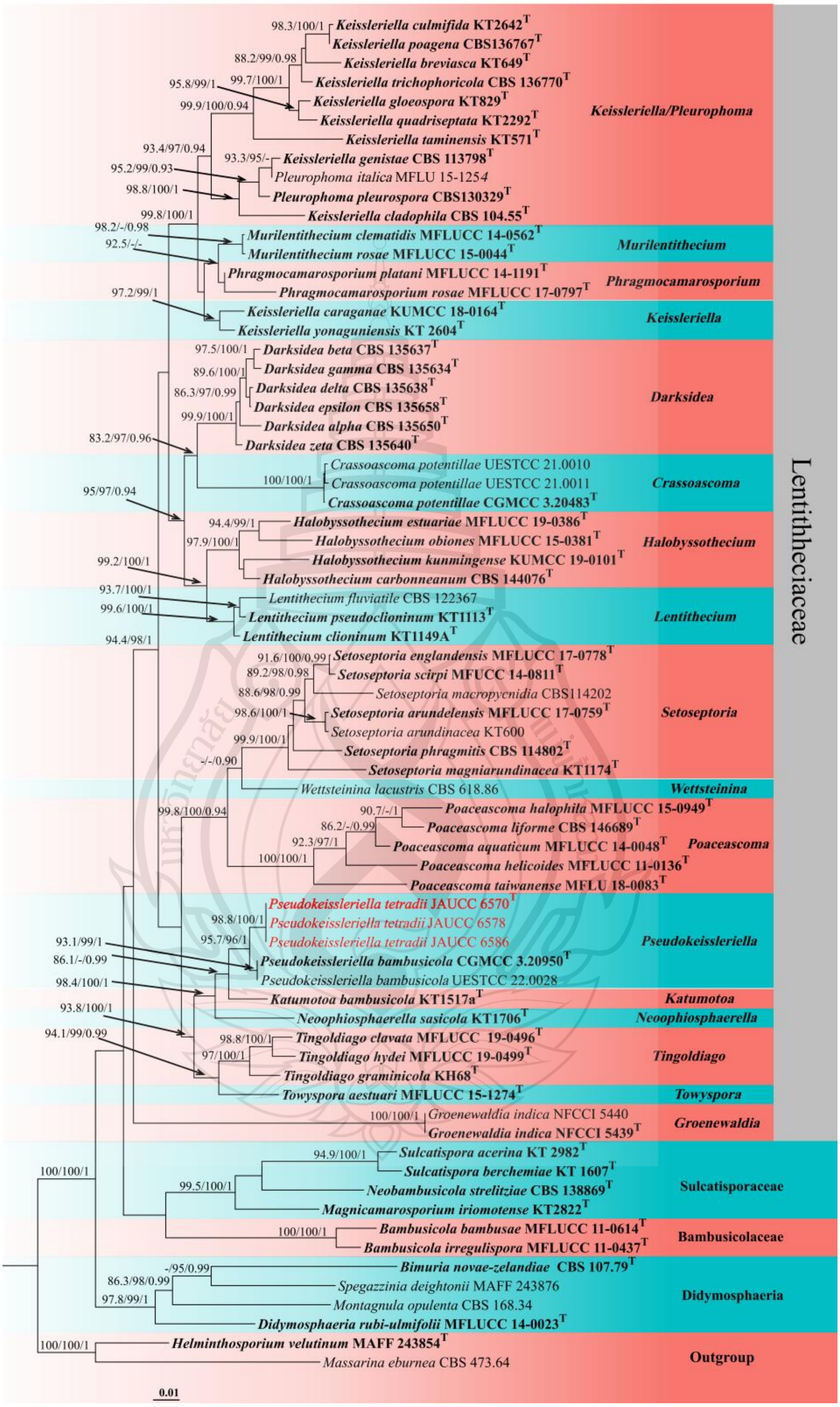


Figure 3.25 Phylogenetic tree of *Pseudokeissleriella*

Maximum likelihood (ML) phylogenetic tree of *Pseudokeissleriella* genus and related taxa based on combined ITS, LSU, SSU and TEF1 sequence data (Figure 3.25). Seventy-one strains are included in the combined gene analyses comprising 3259 characters after alignment (552 characters for ITS, 833 for LSU, 970 for SSU, 904 for TEF1). *Helminthosporium velutinum* (MAFF 243854) and *Massarina churnea* (CBS 473.64) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (K2P+I for SSU, TIM2+F+I+G4 for ITS, TIM2e+I+G4 for LSU, and GTR+F+I+G4 for TEF1) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -20049.123 is presented. The matrix had 1052 distinct alignment patterns, with 17.91% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for ITS, LSU, and TEF1, while HKY+I+G was selected for SSU in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Nigrogranaceae Jaklitsch & Voglmayr

Nigrograna Gruyter, Verkley & Crous

Nigrograna was established to accommodate the asexual species *Ni. mackinnonii* (basionym: *Pyrenochaeta mackinnonii*) (de Gruyter et al., 2013). Ahmed et al. (2014) transferred the type species *Nigrograna mackinnonii* to the genus *Biatriospora*, based on its phylogenetic proximity to the type species *Biatriospora marina*. However, Jaklitsch and Voglmayr (2016) reclassified *Nigrograna mackinnonii* back to its original genus *Nigrograna* based on phylogenetic and morphological analyses, included three additional species (*Ni. fuscidula*, *Ni. mycophila,* and *Ni. obliqua*) within *Nigrograna*, and established the family Nigrogranaceae.

Nigrograna, the sole genus in Nigrogranaceae (Pleosporales), has been morphologically characterized by its sexual and asexual forms (coelomyces or hyphomyces). The sexual morph of *Nigrograna* is characterized by globose to subglobose and black ascomata, with ostiolate, two-layered peridium, bitunicate, clavate, and fissitunicate 8-spored asci, with short pedicellate, fusoid to narrowly ellipsoid, straight or curved, 1–3-septate, and smooth or verruculose ascospores

(Jaklitsch & Voglmayr, 2016). Asexual morph (*coelomyces*) is characterized by globose to subglobose or pyriform pycnidia, filiform, solitary or branched conidiophores, hyaline, phialidic, discrete conidiogenous cells, sub-hyaline, aseptate, and ellipsoidal conidia (de Gruyter et al., 2013; Jaklitsch & Voglmayr, 2016). The hyphomycetous state is characterized by having black gregarious synnemata, septate brown conidiophores, sympodial and polyblastic conidiogenous cells and acrogenous, ellipsoidal, aseptate, hyaline conidia (Dong et al., 2020). Currently, there are 37 epithets of *Nigrograna* recorded in Index Fungorum (accession date: August 2024), all of which have molecular sequences stored in GenBank.

Nigrograna jinghongensis Wanas. & K.D. Hyde 2021, in Boonmee et al., Fungal Diversity 111: 83 (2021), Figure 3.26 and Figure 3.27

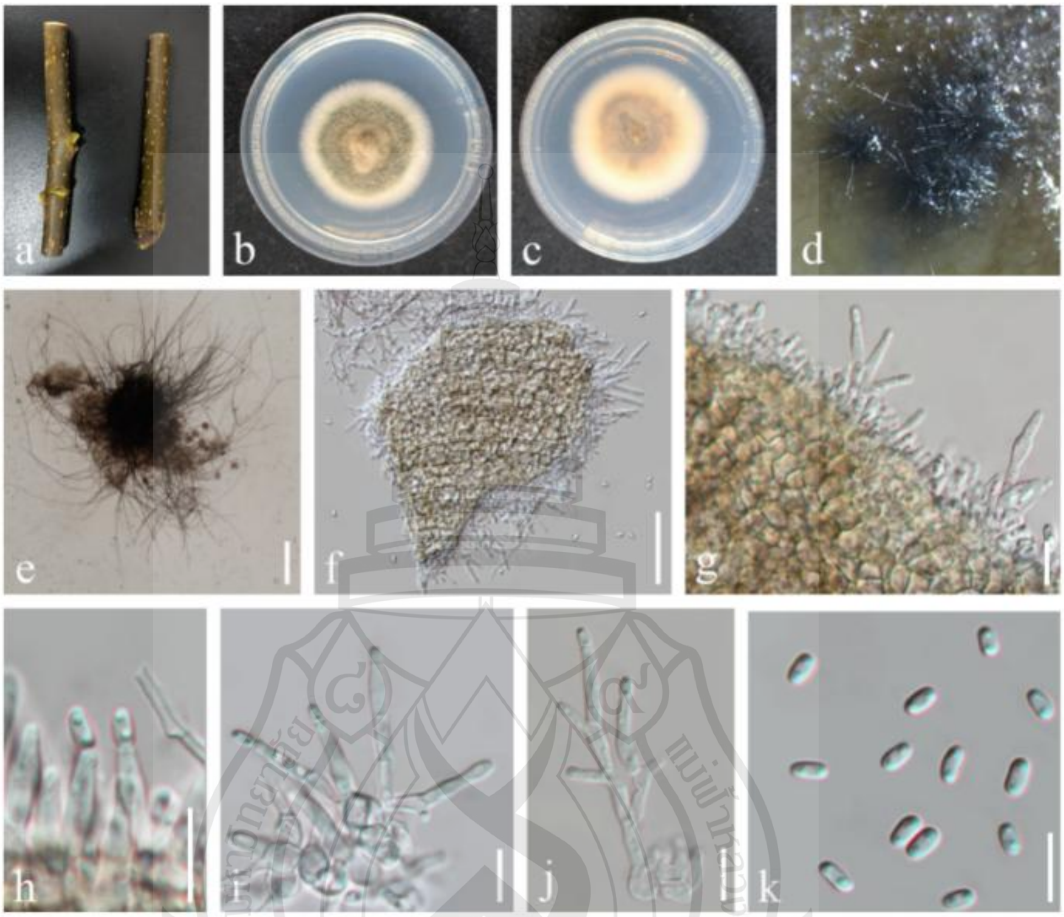
MycoBank number: MB 558601; Facesoffungi number: FoF 09951

Hyphae branched, septate, hyaline or brown, smooth, 1–2.5 µm diam. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Pycnidia* globose to subglobose, or pyriform, solitary, dark brown. *Pycnidial wall* pseudoparenchymatous, brown, hyaline near the conidiophores. *Conidiophores* arising from the pycnidial wall, up to 47 µm long and 2–3.5 µm wide (av. 2.7 µm, n = 15), filiform, septate, hyaline, simple to sparsely branched, with solitary phialides terminal. *Phialides* 4–17 × 1.5–4 µm (av. 12.1 × 2.7 µm, n = 20), variable in shape, phialidic, discrete, subcylindrical to cylindrical, ampulliform, lageniform, straight or slightly curved. *Conidia* hyaline, smooth, aseptate, subcylindrical to cylindrical, ellipsoidal, unicellular, containing 2 guttules, 4.5–6 × 2–3.5 µm (av. 5.2 × 2.5 µm, n = 40).

Culture characteristics: Colony on PDA 34 mm diam after 2 weeks at 25 °C, dense and cottony, slightly raised centre, light brown to tan, then dark green to olive with a white outer edge, nearly round, margin well-defined and even regular; the reverse side transitions from a darker brownish centre to lighter brown, then to a pale, almost white edge.

Known hosts and distribution: saprobic fungi from woody litter in Guizhou Province, China (Boonmee et al., 2021); endophytic fungi from the healthy stem of *Tetradium ruticarpum in* Anhui Province, China (this study).

Material examined: China, Anhui Province, Xuancheng city, Xiangyang district, N 30.90°, E 118.73°, elevation 17.76 m, isolated as an endophyte from the healthy stems of *Tetradium ruticarpum*, 8 Sep 2023, Lixue Mi, living culture: JAUCC 6582, dried culture: HFJAU10460; ibid., living culture: JAUCC 6868, dried culture: HFJAU10459.



Note a, the healthy stem of Tetradium ruticarpum. b, c the morphology of colonies on the front and back of PDA medium (2 weeks). d, e pycnidia. f–j conidiophores with pegs and phialides. k. conidia. Scale bars: e = 200 μm, f = 50 μm, g–k = 10 μm.

Figure 3.26 Photographs of *Nigrograna jinghongensis* (HFJAU10459)

Notes: *Nigrograna jinghongensis* (KUMUCC 21-0035 = DWX01-3 = KUN-HKAS 115776) with its sexual morph was first introduced by Boonmee et al. (2021), isolated from a dead woody litter of an undetermined host in Yunnan Province, China. In the multi-gene phylogeny, our two new endophytic isolates (JAUCC 6582 and JAUCC 6868) clustered together with the ex-type of *Ni. jinghongensis* (KUMUCC 21-0035 and KUMUCC 21-0036) with high support (SH-aLRT/UFB/BPP = 99.8/100/1) (Figure 3.27). The BLASTn searches of the LSU sequence of our strain resulted in 100%

similarity with the ex-type *Ni. jinghongensis* HKAS 115776, the TEF1 showed 99.79% similarity with *Ni. jinghongensis* DWX01-3, RPB2 showed 99.51% similarity with *Ni. jinghongensis* DWX01-3, and the ITS BLASTn results appeared to show 99.01% similarity with *Ni. jinghongensis* HKAS 115776. Accordingly, this new collection was identified as *Ni. jinghongensis*, providing its asexual morphological characteristics as a new host record.

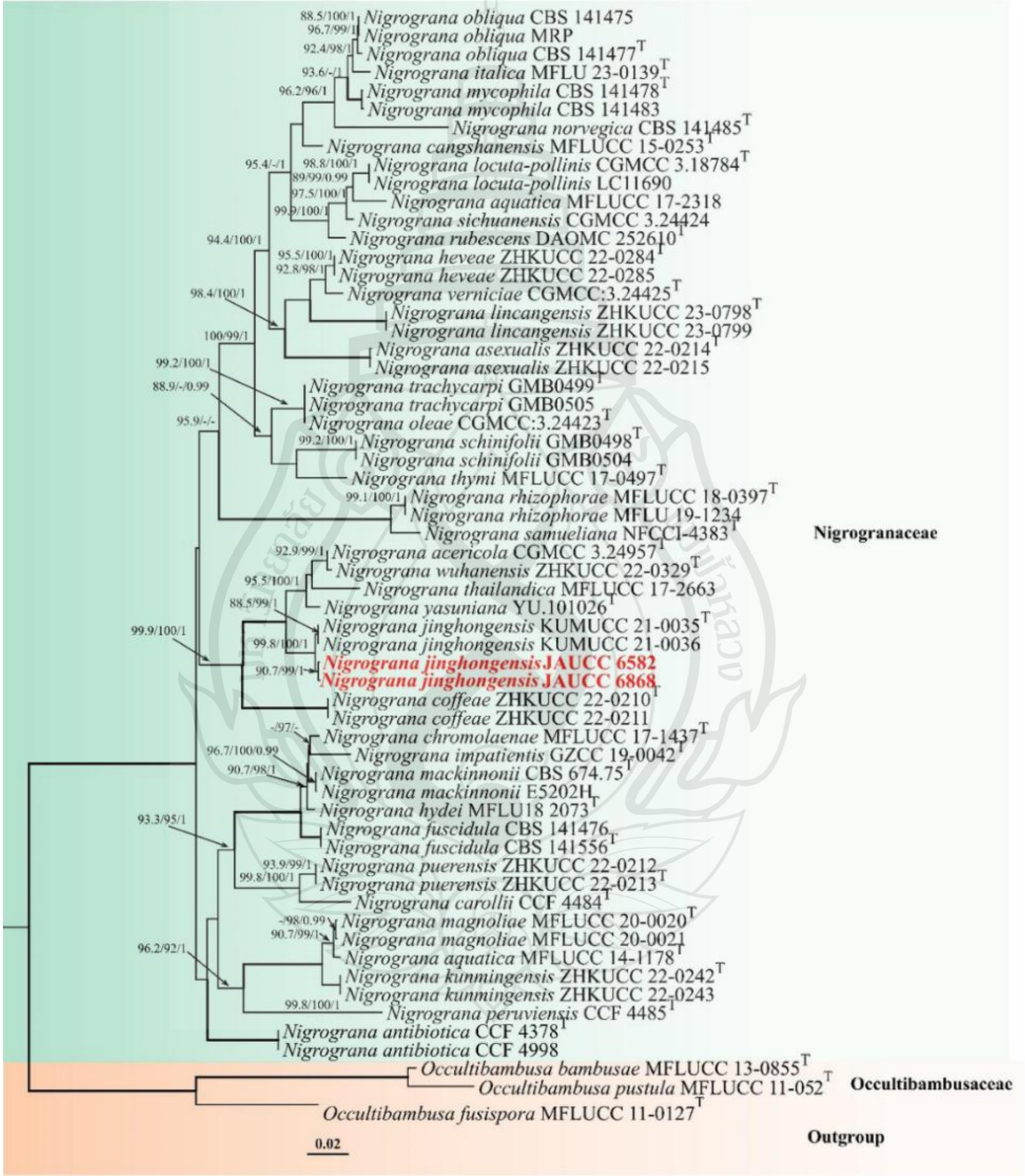


Figure 3.27 Phylogenetic tree of *Nigrograna*

Maximum likelihood (ML) phylogenetic tree of the *Nigrograna* genus based on a combined dataset of SSU, LSU, ITS, RPB2 and TEF1 sequences with *Occultibambusa bambusae* (MFLUCC 13-0855), *Occultibambusa fusispora* (MFLUCC 11-0127), and *Occultibambusa pustula* (MFLUCC 11-0502) as the outgroup taxa (Figure 3.27). Multi-locus data, including ITS: 1-1785, LSU: 1786-2589, SSU: 2590-3573, TEF1: 3574-5044 and RPB2: 5045-6098, composed of 60 strains containing our new strains *Nigrograna jinghongensis* (JAUCC6862 and JAUCC 6582) and the outgroup taxa *Occultibambusa bambusae* (MFLUCC 13-0855), *O. fusispora* (MFLUCC 11-0127), and *O. pustula* (MFLUCC 11-0502) (Table 2). The maximum likelihood matrix comprised 6098 columns, 1722 distinct patterns, 1203 parsimony-informative, 314 singleton sites, and 4581 constant sites, with 46.76% undetermined characters or gaps. The highest final likelihood value of the maximum likelihood tree is -25331.664. Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) (left), ultrafast bootstrap (UFB) (middle) and Bayesian posterior probabilities (BPP) values (right) are shown above the nodes. Only one of SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated along the branches (SH-aLRT/UFB/BPP). Thickened branches indicate branch support with SH-aLRT/UFB/BPP = 100/100/1. Strains derived from the current study are highlighted in red bold.

Class **Eurotiomycetes** Tehler ex O.E. Eriksson & K. Winka
Subclass **Chaetothyriomycetidae** Doweld
Chaetothyriales M.E. Barr
Cyphellophoraceae Hansf. ex M.E. Barr
Cyphellophora G.A. de Vries (37)

Cyphellophora de Vries (1962) was introduced to accommodate *C. laciniata*, an asexual species isolated from human skin scales. With the incorporation of phylogenetic analysis into its taxonomy, the placement of *Cyphellophora* within Chaetothyriales has become increasingly well-defined (Feng et al., 2012, 2013; Quan et al., 2020; Réblová et al., 2013). Morphologically, *Cyphellophora* has been reported in both sexual and asexual forms. The sexual morph is characterized by its scattered, subglobose to globose, dark brown, with inconspicuous ostioles ascomata that fuse with the host tissue at the base; ellipsoidal to cylindrical, short pedicel, bitunicate asci; and hyaline, septate ascospores. (Phookamsak et al., 2019; Yang et al., 2018b, 2022a). The asexual morph of *Cyphellophora* is characterized by having branched, septate hyphae; discrete or integrated phialides, intercalary, terminal, or lateral, with funnel-shaped or indistinct collarettes; and hyaline to pale brown conidia, oblong to fusiform or vermiform, either septate or aseptate (de Vries, 1962; Réblová et al., 2013). To date, 43 species have been formally accepted within *Cyphellophora* (Crous et al., 2023; Crous et al., 2024; Dos Santos Santana et al., 2025; Torres-Garcia et al., 2023).

Cyphellophora guangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov*., Figure 3.28 and Figure 3.29

Index Fungorum number: IF903758 Faces of fungi number: FoF 17680

Etymology: The name reflects the location "Guangxi" from where the holotype was collected.

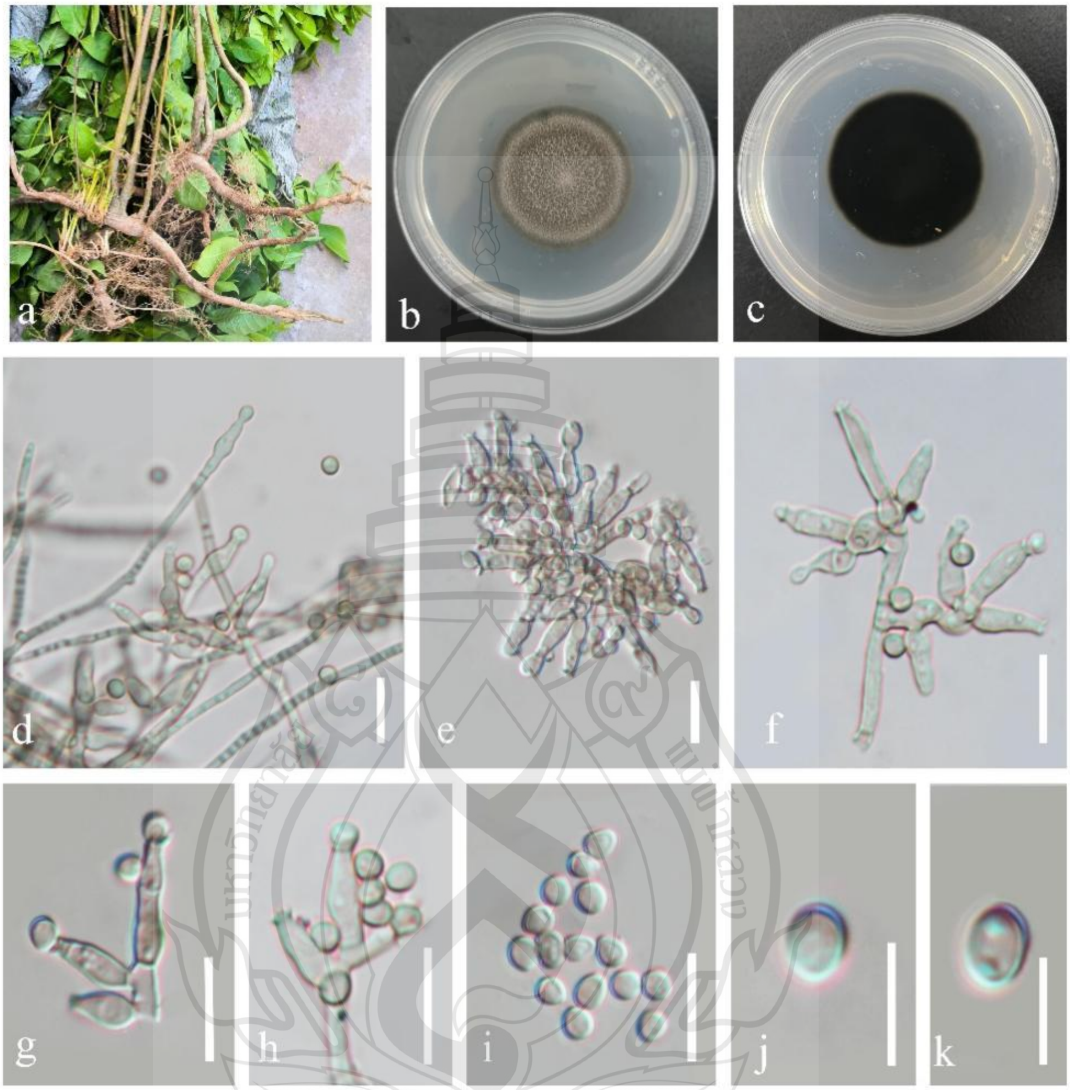
Holotype: HFJAU10461

Endophytic from the healthy root of *Tetradium ruticarpum.* **Sexual morph**: Undetermined. **Asexual morph:** Hyphomycetous. *Mycelium* densely branched, 1–2.5 µm wide, hyaline, subhyaline to pale brown, septate, constrictions at the septa, smooth-walled, with inflated cells, sometimes with excrescences in older hyphae, guttulate in young hyphae, many oil droplets in older ones. *Conidiophores* mononematous, indistinct, absent or rarely reduced to a short cell basal to the conidiogenous cells. *Conidiogenous cells* 3.4–13.5 × 2–3.5 µm ($\bar{x}$ = 8 × 2.8 µm, n = 35) monophialidic, short cylindrical to flask-shaped, intercalary, lateral or terminal, sometimes arising at short side branches of hyphae, with an inconspicuous short flaring collarette, sub-hyaline to pale olivaceous brown, thin-walled. *Conidia* one-celled, guttulate or non-guttulate, hyaline to pale brown, smooth-walled, broadly ovate or ellipsoidal, 2.5–4 × 2-3 µm ($\bar{x}$ = 3 × 2.5 µm, n = 50), aggregating in a slimy mass at the apex of the phialide.

Culture characteristics: Colonies slowly grow on PDA at 25°C and reach 30 mm in diameter after 39 days, spreading with moderate to sparse aerial mycelium, consisting of woolly-velvety texture, pale olivaceous grey in the center, margin entire; reverse olivaceous black. No diffusible pigment was produced.

Material examined: China, Guangxi Province, Hechi City, on healthy roots of *Tetradium ruticarpum* (Rutaceae), 24.8667° N 109.0333° E 0 m asl, 9 September 2023, Lixue Mi, HFJAU10461 (dry culture, holotype), ex-type living culture: JAUCC 6546;

ibid, 24.8831° N 109.0432° E 100 m asl, 12 Oct. 2024, Lixue Mi, dry culture HFJAU10462, living culture: JAUCC 6547.



Note a Host. b,c Colony on PDA (39 days). d Hyphal. e–h Conidiogenous cells and conidia. i–k Conidia. Scale bars: d–i = 10 µm; j–k = 5 µm.

Figure 3.28 Photographs of *Cyphellophora guangxiensis* (HFJAU10461, holotype)

Notes: The multi-locus phylogenetic analysis showed that *Cyphellophora guangxiensis* clustered as a sister taxon to *C. deltoidea* with 83.8% ML bootstrap support in the SH-aLRT test, 95% in the UFB method, and a Bayesian probability of 0.97 (Figure 3.29). Morphologically, *C. guangxiensis* differs from its closely related species in conidia shape and size. *Cyphellophora guangxiensis* produces broadly ovate to ellipsoidal, aseptate conidia measuring 2.5–4 × 2–3 µm, whereas *C. deltoidea* has distinctly triangular spores that are slightly smaller, measuring as 2.6–3.2 µm (Marchisio et al., 2011). *Cyphellophora clematidis* differs from *C. guangxiensis* in having larger, aseptate, ellipsoid conidia measuring (3–)4–5(–6.5) × (1.5–)2(–2.5) µm (Crous et al., 2019). In addition, *C. neerlandica* differs from *C. guangxiensis* by its subcylindrical conidia, which are significantly larger [(27–)30–33(–36) × 2 µm] with 3-septate (Crous et al., 2023). Therefore, the observed genetic divergence, in combination with its distinct morphological characteristics, prompted us to describe our isolate as a new species, *C. guangxiensis* on *Tetradium ruticarpum* from China.

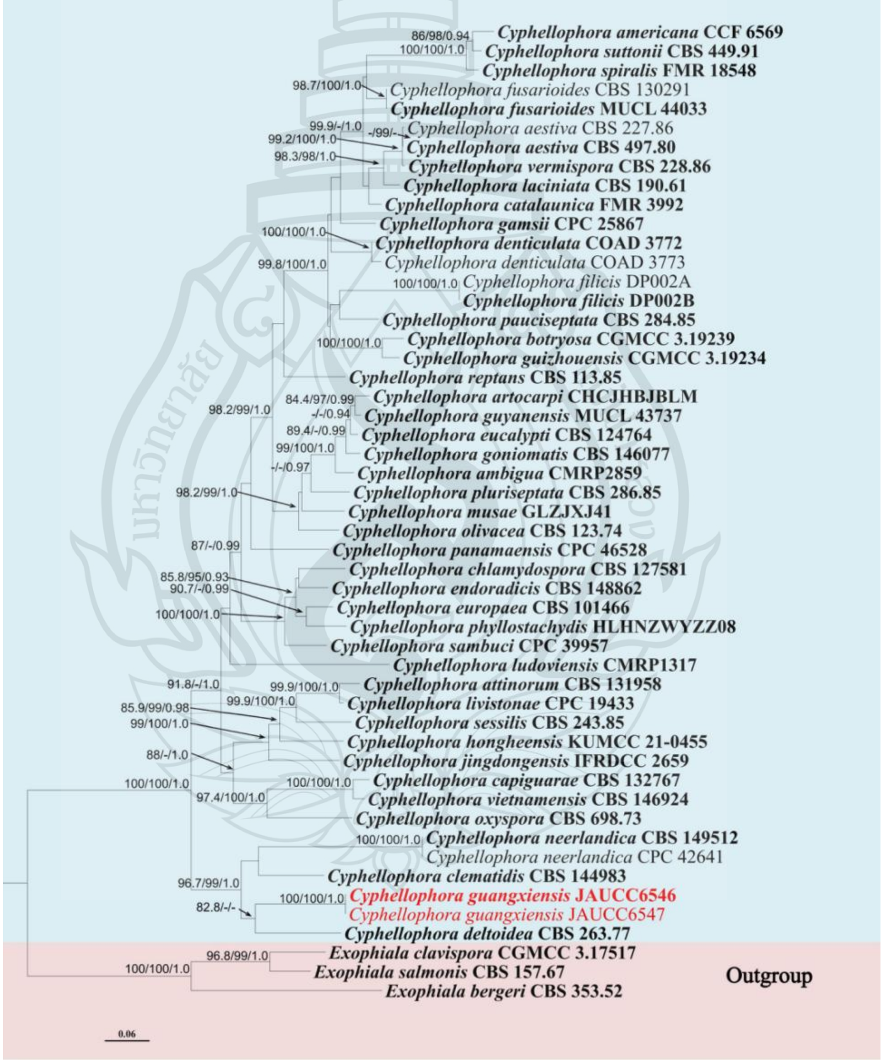


Figure 3.29 Phylogenetic tree of *Cyphellophora*

Maximum likelihood (ML) phylogenetic tree of *Cyphellophora* genus based on combined ITS, LSU, and TUB2 sequences. *Exophiala clavispora* (CGMCC 3.17517), *E. salmonis* (CBS 157.67) and *E. bergeri* (CBS 353.52) are used as the outgroup taxa (Figure 3.29). Fifty-one strains are included in the combined gene analyses comprising 2026 characters, including gaps (695characters for ITS, 861 for LSU, 470 for TEF1). The combined alignment contained 639 parsimony-informative characters, 151 singleton sites, and 1236 constant characters. The ML and BI analyses yielded similar topologies. The maximum likelihood matrix had 996 distinct alignment patterns with 21.23% undetermined characters or gaps. The best maximum likelihood tree, with a final likelihood value of -17711.474. For the BI analysis, the best nucleotide substitution model for all three loci (ITS, LSU, and TUB2) is selected by AIC in MrModeltest. The GTR+I+G model was selected for ITS and LSU, while the HKY+I+G model was selected for TUB2. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Herpotrichiellaceae Munk, Dansk bot. Ark.

Exophiala J.W. Carmich., Sabouraudia

Exophiala pisciphila McGinnis & Ajello, Figure 3.30 and Figure 3.31

Index Fungorum number: IF 314043

Endophytic fungi from the healthy root of *Tetradium ruticarpum.* **Sexual morph:** Undetermined. **Asexual morph:** hyphomycetous. *Mycelium* consisting of hyaline or pale brown, strongly torulose, branched, septate, smooth, thick-walled, 1.5–3.5 µm diam hyphae. *Conidiophores* micronematous, often reduced to single conidiogenous cells borne terminally or laterally from cylindrical or moniliform hyphae. *Conidiogenous cells* 5-12.5× 2-4.5µm ($\bar{x}$ = 8 × 3.5 µm, n = 30) either terminal or lateral on undifferentiated hyphae, more or less swollen, flask-shaped phialides, with inconspicuous, often subterminal annellated zones. *Conidia* 3–7.5× 2.5–4 µm ($\bar{x}$ = 4.3 × 3.2 µm, n = 50) usually masses of one-celled, guttulate, hyaline, smooth, broadly ovate or ellipsoidal, sometimes slightly curved, with an inconspicuous basal scar; detached conidia sometimes forming secondary conidia. Budding cells are sparse. Chlamydospores absent.

Note a, the healthy stem of *Tetradium ruticarpum*. b–d the morphology of colonies on PDA medium (1 week). e, hyphal coil. f–i unbranched or sparsely branched conidiophores with conidiogenous cells in ateral and terminal position. j–l conidia. m budding cells. Scale bars: e–i = 10 µm; j–m = 5 µm.

Figure 3.30 Photographs of *Exophiala pisciphila* (HFJAU10866)

Culture characteristics: Colonies developing slowly and reaching 11 mm diam after 1 week on PDA at 25 °C, restricted, spreading with moderate to sparse aerial mycelium, consisting of woolly-velvety texture, pale olivaceous grey in the centre, margin entire; reverse olivaceous black with white margins. No diffusible pigment was produced.

Known distribution: USA, from cranial lesions of Atlantic salmon (Langdon & McDonald, 1987); USA, Atlanta, from Ictalurus punctatus (McGinnis & Ajello, 1974); USA, New York, from smooth dogfish (Gaskins & Cheung, 1986), an opportunistic infection of skin and subcutaneous (Maher et al., 1991); USA, Georgia, from siol

(Ondeyka et al., 2003); China, Yunnan province, from *Arundinella bengalensis* (Zhang et al., 2008); Germany, Human nail (de Hoog et al., 2011); China, Yunnan Province, from an abandoned lead–zinc mining area in Huize County (Zhan, et al., 2015a); Czech Republic from Cardinal tetra (Rehulka et al., 2017); Japan, healthy roots of orchid plants (Harsonowati et al., 2020); Spain, Girona, from freshwater sediments (Torres-Garcia et al., 2023); China, Anhui Province, endophytic fungi from the healthy steam of *Tetradium ruticarpum* (this study).

Material examined: China, Hunan Province, Chenzhou city, endophytic fungi from the root of *Tetradium ruticarpum* (Rutaceae), 9 September 2023, 25.95° N 113.81° E, dry culture HFJAU10866, the living culture: JAUCC6544.

Notes: Based on phylogenetic analyses of the combined multi-gene phylogenetic analysis of ITS, LSU, SSU, and TUB2 shows that the new isolate (JAUCC 6544) grouped within the *Exophiala pisciphila* clade, with high support values with100% ML bootstrap support in the SH-aLRT test, 100% in the UFB method, and a Bayesian probability of 1.0 in Figure 3.31. The new isolate (JAUCC 6544) shares similar characteristics with the type species *E. pisciphila* (CBS 537.73), which was reported by McGinnis and Ajello (1974) from Channel Catfish. Their conidia are both aseptate and subglobose to obovoid with a narrowly truncate hilum, but they differ in size. Our isolate (3–7.5 × 2.5–4 µm) is larger than the type specimen (2–3 × 3–5 µm). We therefore identified our new isolate (JAUCC 6544) as *E. pisciphila* with the first host report on *Tetradium ruticarpum* in China.

Figure 3.31 Phylogenetic tree of *Exophiala*

Maximum likelihood (ML) phylogenetic tree of the *Exophiala* genus based on combined ITS, LSU, SSU and TUB2 sequence data (Figure 3.31). Ninety-six strains are included in the combined gene analyses comprising 3585 characters after alignment (676 characters for ITS, 851 for LSU, 1601 for SSU, 457 for TUB2). *Cyphellophora eucalypti* (CBS 124764) and *Cyphellophora fusarioides* (MUCL-44033) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TIM2e+I+G4 for ITS, TNe+I+G4 for LSU, K2P+G4 for SSU, TN+F+I+G4 for TUB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -30968.631 is presented. The matrix had 1393 distinct alignment patterns, with 49.79% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for all sequences in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Class **Sordariomycetes** O.E. Eriks. & Winka

Subclass **Hypocreomycetidae** O.E. Erikss. & Winka

Hypocreales Lindau

Nectriaceae Tul. & C. Tul.

Fusarium Link

Fusarium, established by Link (1809) with *Fus. roseum* as the type species, is a globally distributed genus comprising numerous plant and human pathogens, as well as species producing bioactive secondary metabolites (Kvas et al., 2009; Proctor et al., 2013; Hyde et al., 2020, 2023). Currently, over 120 species are accepted within 18 species complexes (Sandoval-Denis et al., 2018; Lombard et al., 2019; Yilmaz et al., 2021), while more than 400 epithets and 1858 records are listed in Index Fungorum (2025).

Fusarium jiangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov.* Figure 3.32 and Figure 3.33

Etymology: The name reflects the location “Jiangxi” from where the holotype was collected.

Holotype: HFJAU10867

Note a The healthy root of *Tetradium ruticarpum*. b,c Colonies on PDA from surface and reverse (1 week). d–g Branched or unbranched sporodochial conidiophores forming conidia. l–o Conidia. Scale bars: d–g =20 µm, h–l = 10µm.

Figure 3.32 Photographs of *Fusarium jiangxiensis* (HFJAU10867, holotype)

Endophytic in the roots of *T. ruticarpum*. **Sexual morph:** Undetermined. **Asexual morph:** *Vegetative hyphae* septate, branched, hyaline, smooth-walled, forming strands and coils, 4–11 µm wide. *Conidiophores* arise directly from the surface of the medium, with no distinct sporodochial structures observed. They are unbranched or occasionally branched, variable in length, and grow upright. *Conidiogenous cells* 10–40 × 3–5.5 µm ($\bar{x}$ = 25 × 4 µm, n = 20) monophialidic, integrated, formed terminally or intercalarily on sporodochial conidiophores, flask-shaped to slightly cylindrical. *Macroconidia* 23–60 × 2.5–6.5 µm (x̄ = 44 × 4.5 µm, n = 50), falcate to slightly curved, moderately slender, 3–5-septate, smooth-walled, hyaline, dorsiventral, tapering towards both ends, with an acutely pointed apical cell and a foot-like basal cell.

Culture characteristics: Colonies on PDA reaching 33 mm in diameter after 1 week at 25 °C, white, flat, cottony, margins irregular, with abundant aerial mycelium; reverse pale yellow.

Material examined: China, Jiangxi Province, Jiujiang City, Ruichang, 23 March 2021, 29.6595° N 115.6050° E, endophytic fungi from the healthy root of *T. ruticarpum*, Lixue Mi, HFJAU10867 (dry culture, holotype), ex-type living culture JAUCC 4303; ibid, endophytic fungi from the healthy root of *T. ruticarpum*, 23 March 2021, Lixue Mi, dry culture HFJAU10868, living culture JAUCC 4841.

Notes: The multi-locus phylogenetic analysis showed that *Fusarium jiangxiensis* clustered as a sister taxon to *Fus. zanthoxyli* within the *Fus. torreyae* species complex, with 100% ML bootstrap support in the SH-aLRT test, 100% in the UFB method, and a Bayesian posterior probability of 1.0 (Figure 3.33). Morphologically, *Fusarium jiangxiensis* produces moderately slender, falcate to slightly curved macroconidia (23–60 × 2.5–6.5 µm, 3–5-septate) with an acutely pointed apical cell and a distinct foot-shaped basal cell. In contrast, *Fus. zanthoxyli* displays a wider range of conidial morphology and septation, with macroconidia being (1–)3–5(–7)-septate, typically falcate to fusiform, often larger (up to 76.0 µm long). Additionally, *Fus. zanthoxyli* occasionally forms shorter, naviculate to clavate conidia (0–3-septate, 7.5–28.0 × 2.0–4.0 µm), which are absent in *Fus. jiangxiensis* (Zhou et al., 2016).

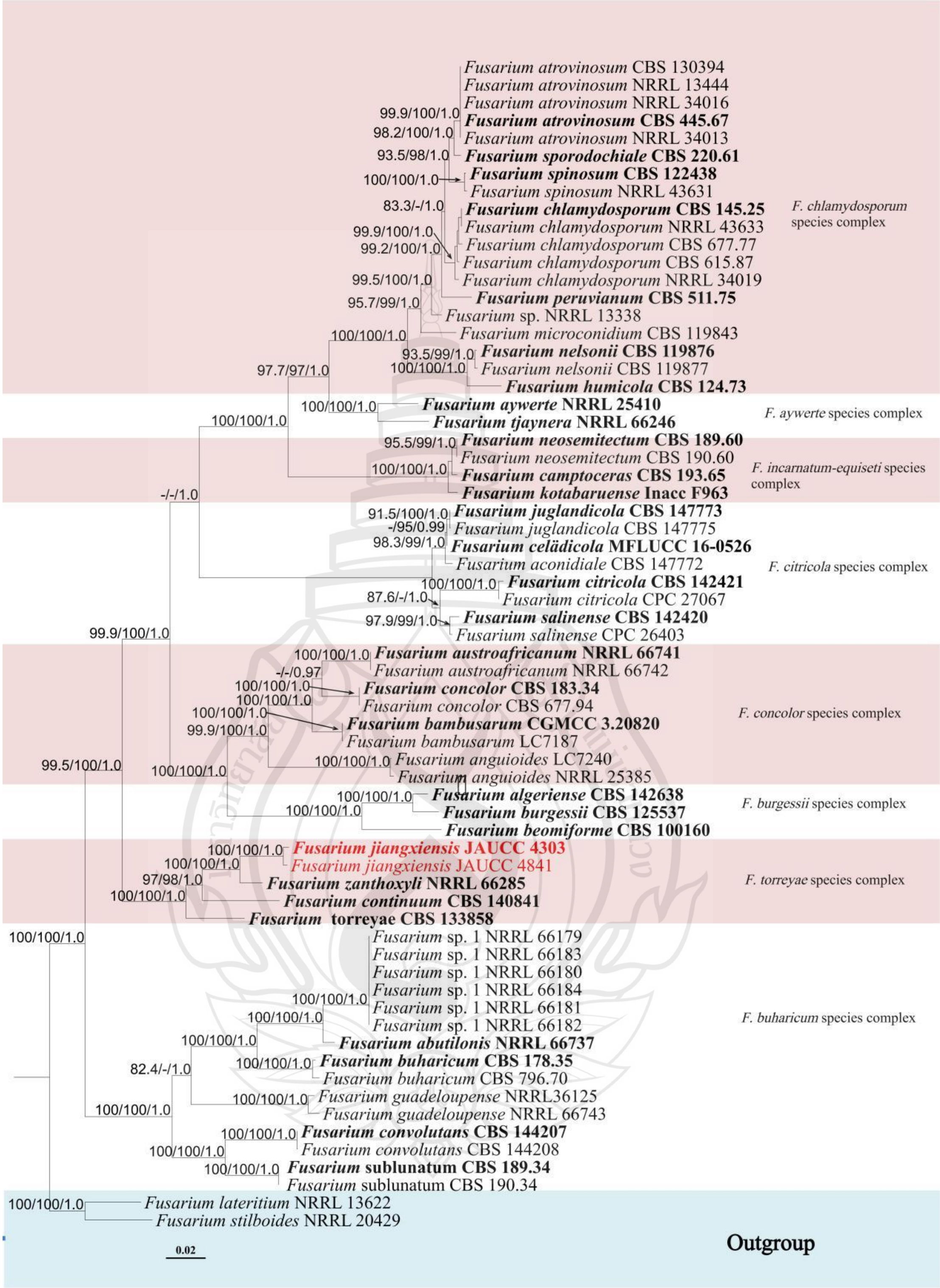


Figure 3.33 Phylogenetic tree of *Fusarium*

Maximum likelihood (ML) phylogenetic tree of *Fusarium* genus based on combined RPB1, RPB2 and TEF1 sequence data (Figure 3.33). Sixty-six strains are included in the combined gene analyses comprising 3953 characters after alignment (1575 for ITS, 1692 for LSU, 686 for TEF1). *Fusarium lateritium* (NRRL13622) and *Fusarium stilboides* (NRRL 20429) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TNe+G4 for RPB1, TIM2e+I+G4 for RPB2, SYM+I+G4 for TEF1) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -29891.729 is presented. The matrix had 1758 distinct alignment patterns, with 13.68% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. SYM+I+G was selected as the best-fit evolutionary model for RPB1 and RPB2, while GTR+I+G was selected for *tef*1 in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Subclass **Sordariomycetidae** O.E. Erikss & Winka (= Meliolomycetidae P.M. Kirk & K.D. Hyde)

Diaporthales Nannf.

Coryneaceae Corda (=Pseudovalsaceae M.E. Barr)

Coryneum Nees, Das System der Pilze and Schwamme

The genus *Coryneum* was first described by Nees von Esenbeck (1816) based on the asexual morph of *C. umbonatum*, while its sexual morph, Pseudovalsa, was later introduced by Cesati and De Notaris (1863). Rossman et al. (2015) redefined the genus, treating *Pseudovalsa* as a synonym due to nomenclatural priority. The sexual morph of *Coryneum* is characterized by immersed, aggregated, ostiolate ascomata, with pedicellate asci bearing a J-apical ring. The ascospores are hyaline to brown, one- to several-septate, often distoseptate, and usually have pale brown or hyaline terminal cells (Corda, 1839; Senanayake et al., 2017). The asexual morph is defined by acervular conidiomata that erupt through the outer periderm of the host. Its conidia are brown and transversely distoseptate, with apical and basal cells darker than the median cells, while some apical cells end in a hyaline tip (Sutton, 1975, 1980; Senanayake et al., 2017). As the sole genus in Coryneaceae (Diaporthales), it forms a distinct phylogenetic lineage.

Over 70 species have been reported, primarily from temperate regions, with five recorded in China, though molecular data remain limited for most. These fungi are commonly associated with woody hosts (e.g., *Castanea*, *Quercus*, *Prunus, Vitis*), causing mild cankers and dieback, though their pathogenicity is poorly studied (Muthumary & Sutton, 1986; Jiang et al., 2018; Wijayawardene et al., 2016). Recent taxonomic revisions highlight the need for further phylogenetic and pathological research to clarify species boundaries and ecological impacts (Hongsanan et al., 2025; Jiang et al., 2018; Long et al., 2023; Senanayake et al., 2017).

Coryneum castaneicola Berk. & M.A. Curtis, Grevillea 2:154. 1874, Figure 3.34 and Figure 3.35

Index Fungorum number: IF118810

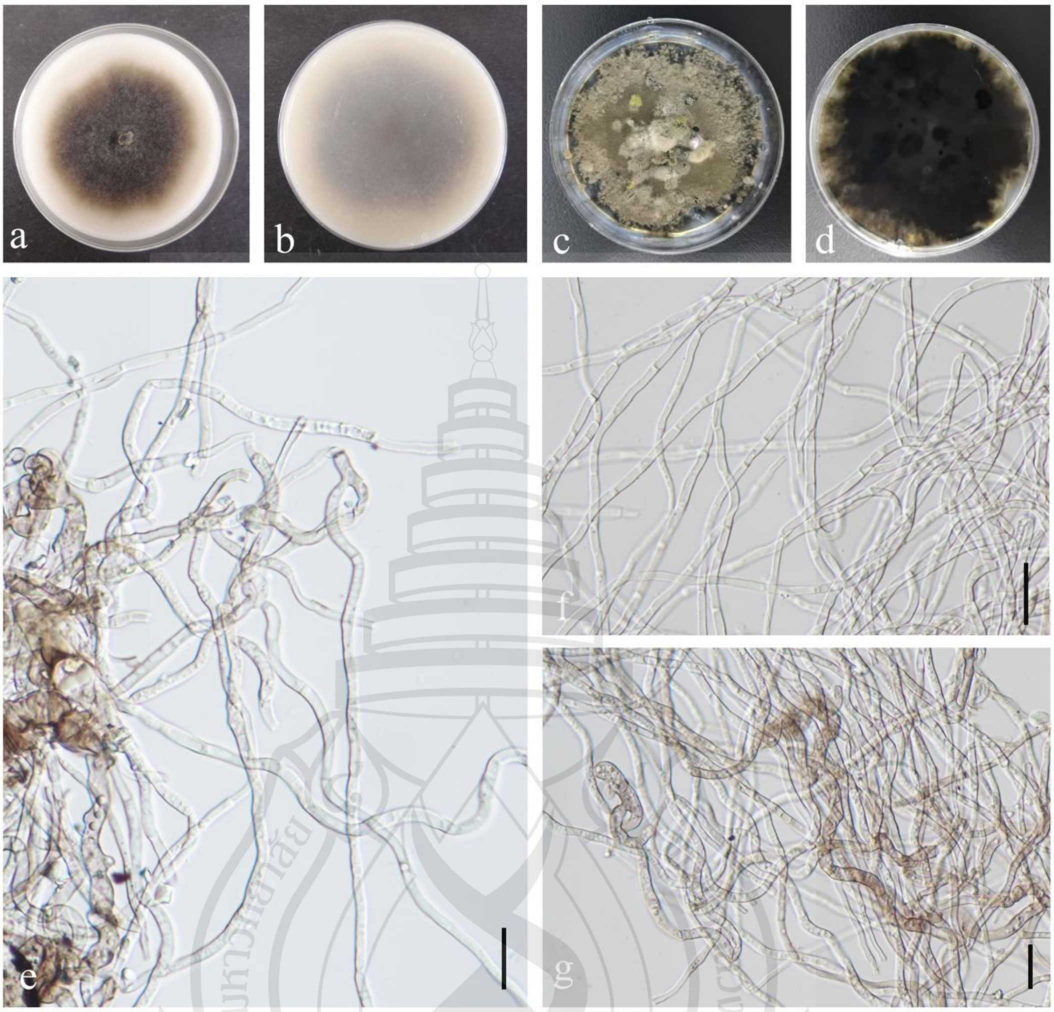
Etymology: The name reflects the location "Jiangxi" from where the holotype was collected.

Endophytic fungi isolated on culture media from surface-sterilised stems of *Tetradium ruticarpum*. Mycelium is immersed superficially, composed of branched, septate hyphae. Generative hyphae simple-septate, branched, with clamp connections, sub-hyaline to brown, thin-walled, 2–5.5 µm wide.

Culture characteristics: Colonies on OA circular, flat, with entire margin, dark brown, sparse aerial hyphae, reverse pale brown. Colonies on PDA circular, flat, with entire margin, olivaceous brown; reverse dark brown to black. Not sporulating in culture.

Known distribution: USA, Pennsylvania, Dead corticated branches of *Castane*a spp (Sutton, 1975); CHINA, Shaanxi Province, on branches of *Castanea mollissima* (Jiang et al., 2018); CHINA, Jiangxi Province, endophytic fungi from the healthy stems of *Tetradium ruticarpum* (this study).

Material examined: China, Jiangxi Province, Yingtan city, Guixi,4 August 2021, 28.0132°N, 117.3490°E, endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, HFJAU10869 (dry culture), ex-type living culture JAUCC 4408; ibid, endophytic fungi from the healthy stem of *T. ruticarpum*, 24 June 2022, Lixue Mi, dry culture HFJAU10870, living culture JAUCC 5057.



Note a,b Colonies on OA from surface and reverse (1 week). c,d Colonies on PDA from surface and reverse (1 month). e–g Branched or unbranched mycelia. Scale bars: e–g = 20 μm.

Figure 3.34 Photographs of *Coryneum castaneicola* (HFJAU10869)

Notes: Based on a nucleotide BLAST searches in GenBank database using the ITS sequence, the closest matches are *Coryneum castaneicola* (43-1 = CFCC 52315) [GenBank MH683559; identities = 512/524(98%), gaps = 10/524 (1%)], *C. modonium* D203 [GenBank MH674331; identities = 530/546 (97%), gaps = 5/546 (0%)]. The consistent 10-base gap in the ITS region, confirmed by repeated sequencing, is likely an adaptive genetic variation within *C. castaneicola*, possibly driven by environmental factors. While the ITS region in fungi is generally conserved, it can exhibit moderate sequence variation, including insertions or deletions, shaped by evolutionary pressures such as niche adaptation or host interactions. Such variations may serve as genetic markers for ecological adaptation, yet their divergence often remains below the threshold for species delimitation (Schoch et al., 2012; Nilsson et al., 2008; Ko Ko et al., 2011). The closest match for the LSU sequence is *Coryneum castaneicola* (43-1 = CFCC 52315) [GenBank MH683551; identities = 801/801 (100%), gaps = 0/801 (1%)]. For the TEF1 sequence, the closest match is *Coryneum castaneicola* CFCC 52315 [GenBank MH685731; identities = 279/281(99%), gaps = 0/281(0%)]. For the RPB2 sequence, and *Coryneum castaneicola* CFCC 52315 [GenBank MZ707110; identities = 1077/1079(99%), 0/1079(0%)]. This finding represents a new record of *C. castaneicola* with a distinct ITS sequence variant. It provides valuable insights into the genetic adaptability of *C. castaneicola* and highlights the role of environmental factors in driving genetic variation within species. Further studies on the ecological context, functional implications of this ITS variation, and efforts to obtain its asexual morph (given that this endophytic fungus currently lacks sporulating structures) are warranted to better understand the adaptive mechanisms and complete the taxonomic characterization of *C. castaneicola.*

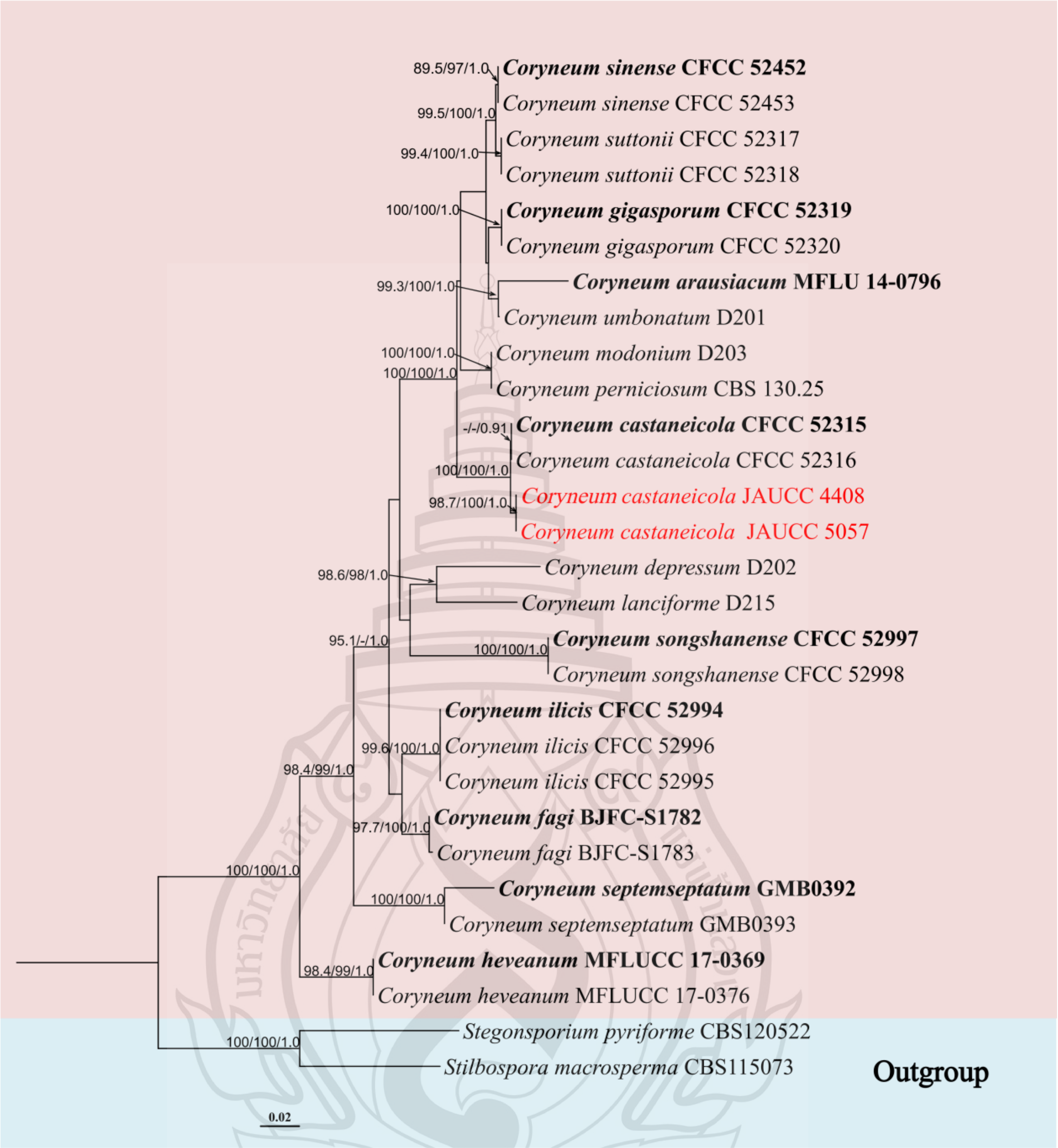


Figure 3.35 Phylogenetic tree of *Coryneum*

Maximum likelihood (ML) phylogenetic tree of the *Coryneum* genus based on combined ITS, LSU, TEF1, and RPB2 sequence data (Figure 3.35). Twenty-nine strains are included in the combined gene analyses comprising 3407 characters after alignment (576 for ITS, 838 for LSU, 912 for TEF1, 1081 for RPB2). *Stegonsporium pyriforme* (CBS120522) and *Stilbospora macrosperma* (CBS115073) are used as the outgroup taxon. Maximum likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TIMe+G4 for ITS, TNe+I for LSU, TIM2+F+G4 for TEF1, TN+F+G4 for RPB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -12898.468 is presented. The matrix had 869 distinct alignment patterns, with 23.66% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I was selected as the best-fit evolutionary model for ITS and TEF1, while GTR+I+G was selected for LSU and RPB2 in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Diaporthaceae Höhn. ex Wehm

Diaporthe Nitschke

Diaporthe is a diverse fungal genus in the family Diaporthaceae (Diaporthales, Sordariomycetes), originally established by Nitschke. Species of *Diaporthe* are globally distributed and exhibit a wide range of ecological lifestyles, including plant pathogens, endophytes, and saprobes (Thomidis & Michailides, 2009; Gomes et al., 2013; Dissanayake et al., 2017; Xiao et al., 2023b; Saravanakumar et al., 2021; da Silva Santos et al., 2022). *Diaporthe* is characterized by a coelomycetous asexual morph with pycnidial, brown to black, globose to subglobose conidiomata; cylindrical, hyaline, septate conidiophores; phialidic conidiogenous cells; and ellipsoidal or filiform, hyaline, aseptate conidia. The sexual morph, though less frequently observed, consists of immersed, black, ostiolate, globose to subglobose ascomata; unitunicate, clavate to subclavate asci with eight spores; and 1-septate, ellipsoidal, hyaline ascospores (Udayanga et al., 2014; Gao et al., 2017; Huang et al., 2021; Dissanayake et al., 2024).

Diaporthe jiangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov.* Figure 3.36 and Figure 3.37

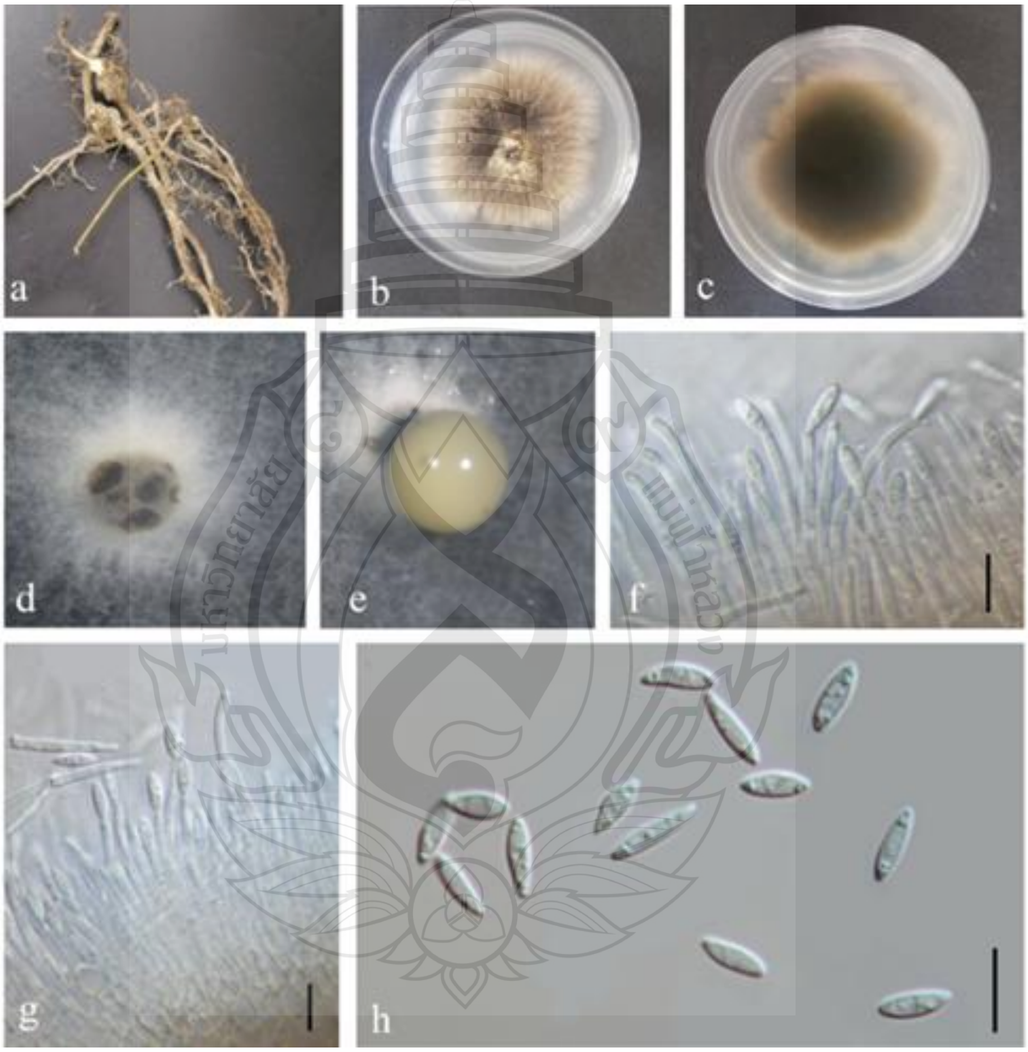
Etymology: The name reflects the location “Jiangxi” from where the holotype was collected.

Holotypes: HFJAU10871

Endophytic in healthy stems or roots of *T. ruticarpum*. **Sexual morph**: Undetermined. **Asexual morph**: *Pycnidia* on PDA, superficial, solitary or scattered, dark brown to black, globose, producing as yellow droplets extruding through the ostioles. *Conidiophores* hyaline, septate, cylindrical, straight or sinuous, densely aggregated, terminal. *Conidiogenous cells* 6.4–31.74 × 1.5–3 µm ($\bar{x}$ = 18.5 × 2 µm, n =

25) phialidic, simple, hyaline, cylindrical to subcylindrical. *Alpha conidia* 6.5–12.5 × 1.5–3.2 µm (x̄ = 9 × 2.5 µm, n = 50), L/W ratio = 3.5, ellipsoidal to clavate, biguttulate or multiguttulate, hyaline, aseptate, tapering toward both ends. *Beta conidia* not observed.

Culture characteristics: Colony on PDA 40 mm diam after 1 week at 25 °C, initially white, then turns brown to dark brown, abundant, sparse aerial hyphae, margin irregular; reverse: black pigmented at the centre, white and irregular at the margin.



Note a The healthy root of *Tetradium ruticarpum.* b,c Colonies on PDA from surface and reverse (1 week). d,e Conidiomata on PDA. f,g Conidiophores and conidiogenous cells. h Alpha conidia. Scale bars: f–h = 10 µm.

Figure 3.36 Photographs of *Diaporthe jiangxiensis* (HFJAU10871, holotype)

Material examined: China, Jiangxi Province, Yichun city, Wanzai, 4 August 2021, 28.3836°N, 114.3890°E, 655m asl, endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, HFJAU10871 (holotpye, dry cultrue), ex-type living cultrue JAUCC 3940; ibid, HFJAU10872, living cultrue JAUCC 4738; dry cultrue Yichuncity, Zhangshu , 10 October 2022, 27.9333°N, 115.3166°E, 0m asl, endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10873, living cultrue JAUCC 5575; Yingtan city, Guixi, 24 June 2022, 28.0132°N, 117.3490°E, endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10874, living cultrue JAUCC 5244; Jiangxi Province, Jingdezhen city, Changjiang, 29 June 2022, 29.2707°N, 117.0332°E, 40.6m asl, endophytic fungi from the healthy root of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10875, living cultrue JAUCC 5224; ibid, dry cultrue HFJAU10876, living cultrue JAUCC 5225; dry cultrue HFJAU10877, living cultrue JAUCC 5228; endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10878, living cultrue JAUCC 5242; Ji'An city, Xingan, 30 September 2022, 27.5244°N, 115.2650°E, endophytic fungi from the healthy stem of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10879, living cultrue JAUCC 5545.

Notes: BLASTn on the searches of the ITS sequence of *Diaporthe jiangxiensis* resulted in 98.19% similarity with *Diaporthe biconispora* MFLUCC 24-0440 (Identities = 485/498 (97%), Gaps = 4/498 (0 %)). Phylogenetically, nine strains obtained from healthy stems and roots of *T. ruticarpum* grouped in a distinct species introduced here as *D. jiangxiensis* (Figure 3.37). In the phylogenetic tree, this species is placed closer to *D. biconispora.* Morphologically, *Diaporthe jiangxiensis* differs from *D. biconispora* by its fusiform, guttulate, smaller and thinner alpha conidia (6.5× 1.5 µm *vs*. 7.7× 2.8 µm, L/W: 3.5 *vs*. 2.8) while the latter has ovate to ellipsoidal, 1–2 guttules alpha conidia (Huang et al., 2015). Therefore, we introduce *D. jiangxiensis* as a novel species and not belonging to any species complex following the recent literature (Dissanayake et al., 2024).

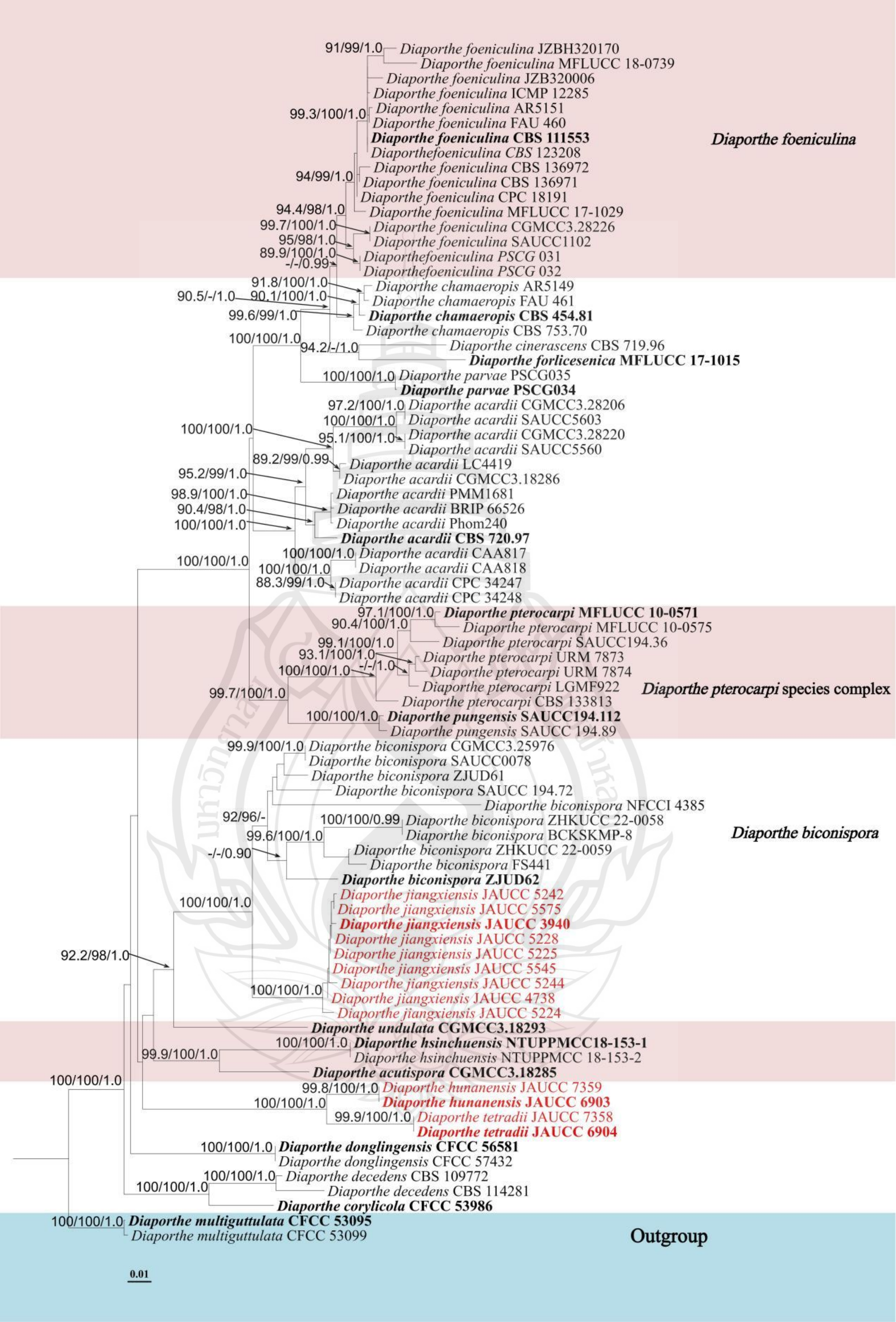


Figure 3.37 Phylogenetic tree of *Diaporthe*

Maximum likelihood (ML) phylogenetic tree of *Diaporthe* genus based on combined CAL, *HIS*, ITS, TEF1 and TUB2 sequence data (Figure 3.37). Eighty-one strains are included in the combined gene analyses comprising 2401 characters after alignment (475 for CAL, 506 for HIS 567 for ITS, 395 for TEF1, 458 for TUB2). *Diaporthe multiguttulata* (CFCC 53095) and *Diaporthe multiguttulata* (CFCC 53099) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TN+F+G4 for CAL, TN+F+G4 for HIS, TIM2e+I+G4 for ITS, HKY+F+I+G4 for TEF1*,* TIM3+F+G4 for TUB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -16219.092 is presented. The matrix had 1235 distinct alignment patterns, with 26.36% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. For the Bayesian inference analyses, the best-fit evolutionary models were determined as follows: HKY+I+G for CAL and TEF1, GTR+I+G for HIS, SYM+I+G for ITS, and GTR+G for TUB2. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

Diaporthe hunanensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov.* Figure 3.37 and Figure 3.38

Etymology: The name reflects the location “Hunan” from where the holotype was collected.

Holotypes: HFJAU10880

Endophytic in healthy fruits or leaves of *T. ruticarpum*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* superficial, solitary, scattered on PDA, dark brown to black, globose, solitary or clustered in groups. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9.5–16.5 × 1.2–2.5 µm (x̄ = 13.5 × 1.8 µm, n = 25), phialidic, cylindrical, aseptate, cylindrical, straight or sinuous, densely aggregated, terminal. *Alpha conidia* 5–10.5 × 2–4.5 µm (x̄ = 7 × 2.5 µm, n = 40), L/W ratio = 2.4, fusiform, hyaline, aseptate, muliti-guttulate, both ends obtuse. *Beta conidia* not observed.

Culture characteristics: Colonies incubated on PDA at 25 °C, originally white fluffy aerial mycelium, circular, with raised center, becoming pale yellow with age, with visible solitary conidiomata after two weeks, coated with white hypha, reverse dark brown to pale brown from center to margin.

Note a The healthy fruit of *Tetradium ruticarpum*. b, c Colonies on PDA from surface and reverse (1 week). d, e Conidiomata on PDA. f, g Conidiophores and conidiogenous cells. h Alpha conidia. Scale bars: f–h = 10μm.

Figure 3.38 Photographs of *Diaporthe hunanensis* (HFJAU10880, holotype)

Material examined: China, Hunan Province, Chenzhou city, Guidong, 9 September 2023, 25.95°N, 113.81°E, endophytic fungi from the healthy fruit of *T. ruticarpum*, Qiuyan Guo, HFJAU10880 (dry culture, holotype), ex-type living culture JAUCC 6903; 9 September 2023, 25.95°N, 113.81°E, endophytic fungi from the healthy leaf of *T. ruticarpum*, Qiuyan Guo, dry culture HFJAU10883, living culture JAUCC 7359.

Notes: Two strains (JAUCC 6903 and JAUCC 7359) obtained from healthy fruit and leaf of *T. ruticarpum* grouped in a distinct clade and not belonging to any species complex, following the recent literature. Based on the NCBI's BLAST search, the closest similar species was *D. searlei* SB-PH-S-24(Identities = 488/509 (96 %), Gaps = 6/509 (1%)). Morphologically, our strain shows typical *Diaporthe* alpha conidia: hyaline, aseptate, ellipsoidal to fusiform, and guttulate. They are herein described *Diaporthe hunnanensis* as a new species.

Diaporthe tetradii L. X. Mi, K. D. Hyde & D. M. Hu sp. *nov.*, Figure 3.37 and Figure 3.39

Etymology: The name *tetradii* refers to the host plant *Tetradium ruticarpum*, from which the fungus was isolated.

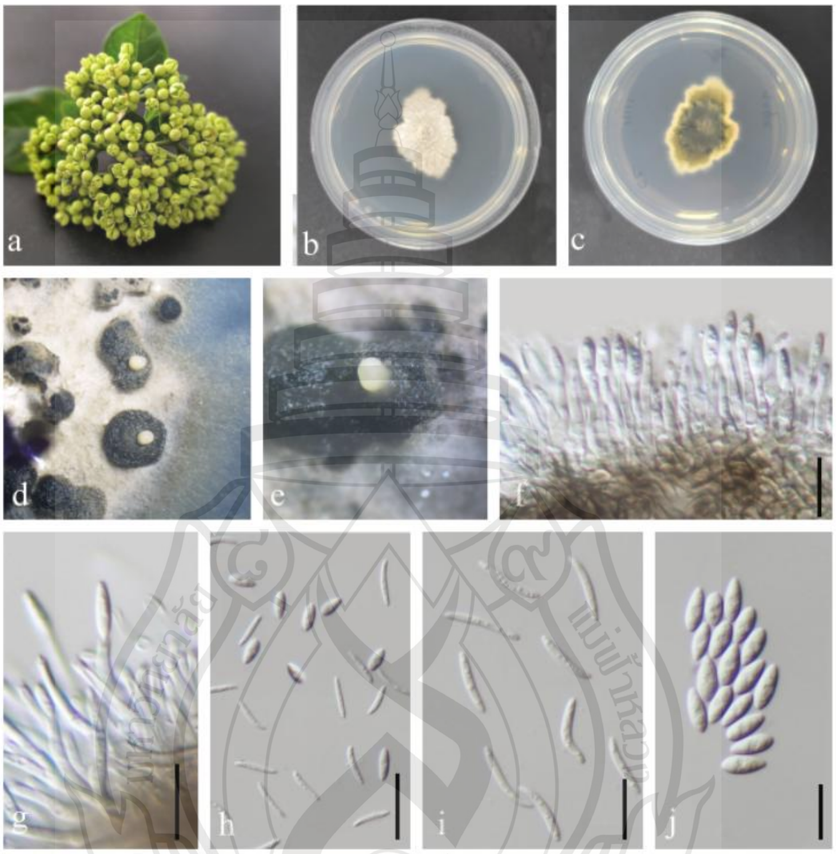
Holotype: HFJAU10881

Endophytic in healthy fruits of *T. ruticarpum*. **Sexual morph**: Undetermined. **Asexual morph**: *Pycnidia* on PDA, superficial, globose or irregular, solitary or scattered, dark brown to black, whitish translucent to yellow conidial drops and/or cirrus exuded from ostioles. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 13.5–19 × 1.5–3.5 µm ($\bar{x}$ = 18 × 2.5 µm, n = 25) phialidic, simple, hyaline, cylindrical to subcylindrical, straight or sinuous, densely aggregated, terminal, slightly tapered towards the apex. *Alpha conidia* 7–14.5 × 2.5–5.5 µm ($\bar{x}$ = 9.7× 4.2 µm, n = 50), L/W ratio = 2.3, ellipsoidal to clavate, biguttulate or multiguttulate, hyaline, aseptate, both ends obtuse or tapering toward one end. *Beta conidia* 11–18.5 × 2–3.2 µm ($\bar{x}$ = 14.3× 2.3 µm, n = 50) hyaline, aseptate, multiguttulate, filiform, straight to curved, tapering towards the apex, base truncate.

Culture characteristics: Culture incubated on PDA at 25 °C, originally white cottony, irregularly dense, felted, conidiomata erumpent at maturity, with yellowish-cream conidial drops exuding from the ostioles after 2 weeks. reverse olive green to yellowish from center to the margin.

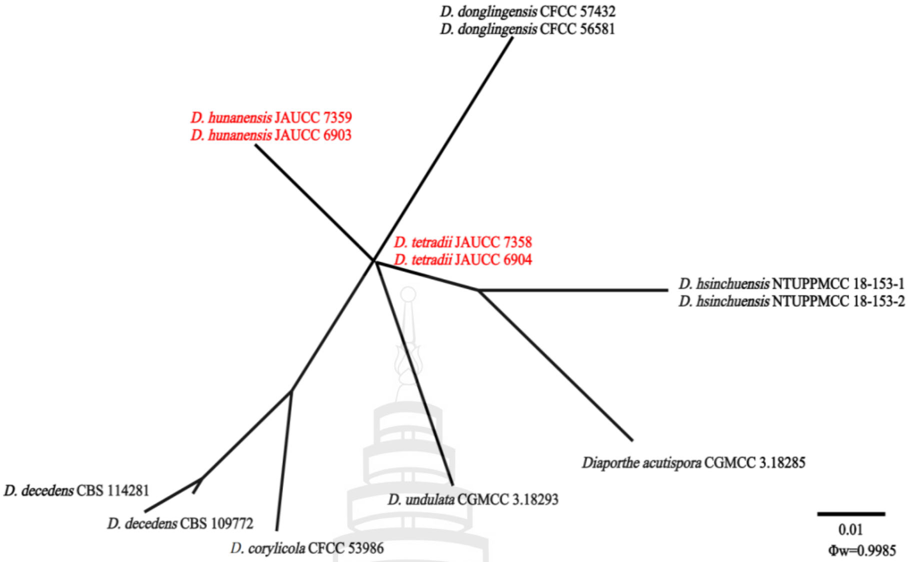
Material examined: China, Hunan Province, Chenzhou city, Guidong, 9 September 2023, 25.9500°N, 113.8100°E, endophytic fungi from the healthy fruit of *T. ruticarpum*, Lixue Mi, HFJAU10881 (dry culture, holotype), ex-type living culture

JAUCC6904; ibid, endophytic fungi from the healthy leaf of *T. ruticarpum*, 9 September 2023, Lixue Mi, dry culture HFJAU10882, ex-type living culture JAUCC7358.



Note a The healthy fruit of *Tetradium ruticarpum.* b,c Colonies on PDA from surface and reverse (1 week). d, e Conidiomata on PDA. f, g Conidiophores and conidiogenous cells. h Alpha conidia and *Beta conidia*. i *Beta conidia*. j *Alpha* conidia. Scale bars: f– g =5 µm, h= 10µm, i–g = 5 µm.

Figure 3.39 Photographs of *Diaporthe tetradii* (HFJAU10881, holotype)



Note Split graphs showing the results of *Diaporthe hunanensis, D. tetradii,* and closely related species. The PHI test used LogDet transformation and splits decomposition. It yielded Φw = 0.9985 (Φw ≥ 0.05), indicating no significant recombination within the dataset. The new taxon is highlighted in bold red.

Figure 3.40 PHI test results of *Diaporthe hunanensis* and *D. tetradii*

Notes: Phylogenetically, *Diaporthe tetradii* (JAUCC 6904 and JAUCC 7358) isolated from healthy fruit and leaf of *T. ruticarpum* formed a sister clade to *D. hunanensis*, representing a distinct lineage that does not belong to any known *Diaporthe* species complex (Figure 3.37). Morphologically, *D. tetradii* can be distinguished from *D. hunnanensis* by several distinct features: it has larger conidiogenous cells (13.5–19 × 1.5–3.5 µm vs. 9.5–16.5 × 1.2–2.5 µm) and alpha conidia (7–14.5 × 2.5–5.5 µm vs. 5–10.5 × 2–4.5 µm). In addition, the alpha conidia of *D. tetradii* are ellipsoidal to clavate, while those of *D. hunnanensis* are fusiform. Notably, beta conidia are present in *D. tetradii* (11–18.5 × 2–3.2 µm) but absent in *D. hunnanensis*. Therefore, *Diaporthe tetradii* is introduced here as a new species of endophytic fungi.

Additionally, application of the PHI test to concatenated cal, his, ITS, TEF1, and TUB2 sequences revealed no evidence of recombination among phylogenetically related species ((Figure 3.40).). Specifically, no significant recombination events were detected between *D. hunanensis*, *D. tetradii*, and closely related taxa, including *D. donglingensis*, *D. hsinchuensis*, *D. acutispora*, *D. undulata*, *D. corylicola*, and *D.*

decedens. The Φw value of 0.9985 for the combined dataset indicates that *D. hunanensis* and *D. tetradii* have not recombined with other species and represent two distinct taxa.

Subclass **Xylariomycetidae** O.E. Erikss. & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.,

Amphisphaeriaceae G. Winter

Amphisphaeria Ces. & De Not.

Amphisphaeria is the type genus of Amphisphaeriaceae with *A. umbrina* as the type species by its asexual morph characteristics (Cesati & De Notaris, 1863; Hyde et al., 1996). The sexual morph of *Amphisphaeria* is characterized by having globose ascomata with periphysate ostiolate, peridial layers composed of inner hyaline and outer brown cells, 8-spored cylindrical asci with J+ or J− apical rings, 1-septate ellipsoidal and brown ascospores (Cesati & De Notaris, 1863; Wang et al., 2004). The coelomycetous asexual morphology is characterized by globose, dark brown conidiomata, a thick-walled peridium, septate, branched hyaline conidiophores, septate hyaline annellidic conidiogenous cells, and 1-celled hyaline elongate-fusiform conidia. (Senanayake et al., 2015; Samarakoon et al., 2020). Wang et al. (2023b) were the first to introduce the hyphomycetous asexual morph of *Amphisphaeria*, which exhibits two primary types of conidium development: thallic conidogenesis and blastic conidogenesis, characterized by having polymorphic conidia.

Samarkoon et al. (2022) recognized 27 species within the *Amphisphaeria* genus, and subsequent studies have accepted an additional eight species (Samarakoon, 2023; Wang et al., 2023b; Zhang et al., 2023; Li et al., 2024c; Liu et al., 2024; Sun et al., 2025b). These organisms are predominantly saprophytic, thriving in terrestrial and marine (Phookamsak et al., 2019; Samarakoon, 2023). They are distributed across various regions in Asia, particularly China and Thailand, as well as in Europe, including England, France, Germany, and Italy (Dissanayake et al., 2020; Jaklitsch et al., 2016; Samarakoon, 2023; Samarakoon et al., 2019; Senanayake et al., 2019). Notably, *A. orixae* is the only identified endophytic species within this genus and is recognized for its production of secondary metabolites (Wang et al., 2023b). Here, we introduce two new *Amphisphaeria* species isolated from the medicinal plant in China.

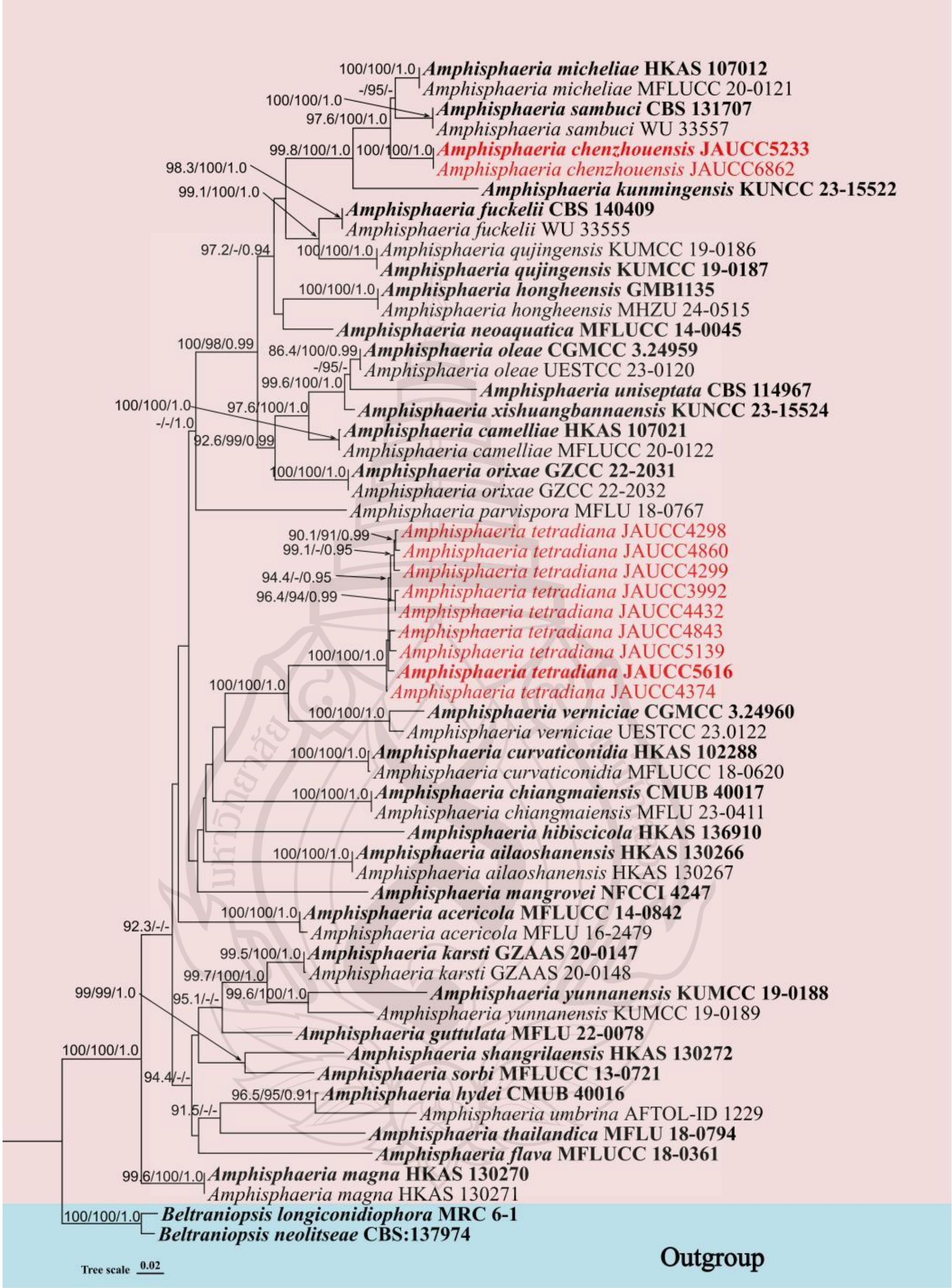


Figure 3.41 Phylogenetic tree of *Amphisphaeria*

Maximum likelihood (ML) phylogenetic tree of the *Amphisphaeria* genus based on combined ITS, LSU, RPB2, and TUB2 sequence data (Figure 3.41). Fifty-nine strains are included in the combined gene analyses comprising 4562 characters after alignment (671 for ITS, 1363 for LSU, 1059for RPB2, 1469 for TUB2). *Beltraniopsis longiconidiophora* (MRC 6-1) and *Beltraniopsis neolitseae* (CBS 137974) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TVMe+I+G4 for ITS, TNe+I+G4 for LSU, TIM2+F+I+G4 for RPB2, TPM2u+F+I+G4 for TUB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -26530.443 is presented. The matrix had 2065 distinct alignment patterns, with 45.63% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for ITS, LSU, and RPB2, while HKY+I+G was selected for TUB2 in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

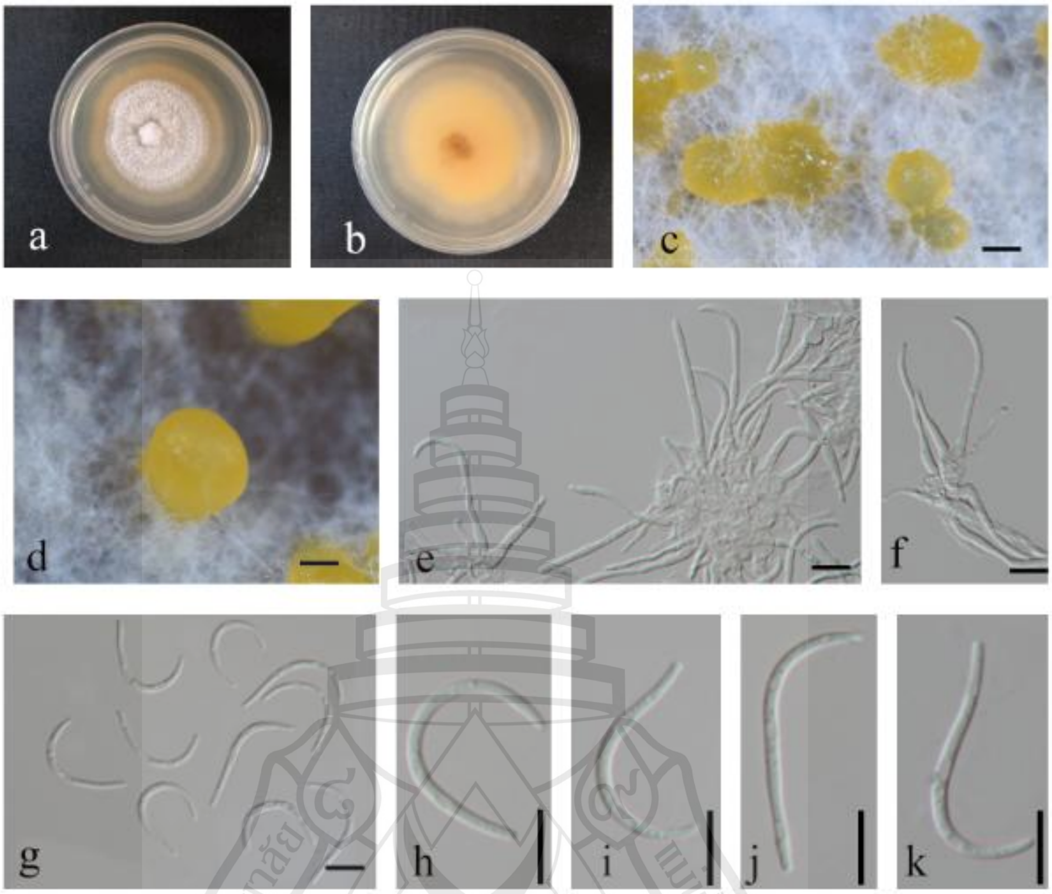
Amphisphaeria tetradiana L. X. Mi, K. D. Hyde & D. M. Hu sp. *nov.* Figure 3.41 and Figure 3.42

Etymology: Named after the genus of the host "*Tetradium ruticarpum*" on which the fungus occurs.

Holotypus: HFJAU10473

Endophytic fungi in the roots of *T. ruticarpum*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* superficial on PCA, solitary or aggregated, globose, luminous yellow. *Conidiophores* arising from the peridium, equivalent to *conidiogenous cells*. *Conidiogenous cells* 11–23 × 1.5–4 µm (x̄ = 17.7 × 2.5 µm, n = 25), elongated conical, thin-walled, hyaline, annellidic, guttulate. *Conidia* 24–42 × 1.3–3.8 µm (x̄ = 35 × 1.3 µm, n = 50), predominantly crescent-shaped or slightly curved, resembling a boomerang or sickle, curved, smooth-walled, hyaline, septate with distinct compartments.

Culture characteristics: colonies, growing slowly on PCA and reaching 47 mm diameter after 40 days at 25 °C, flat, dense, fluffy and cotton-like in centre, somewhat diffuse, blending into the agar surface at the edge, white to pale yellow. Reverse yellowish brown to pale saffron yellow, then nearly transparent from center to edges. No diffusible pigments.



Note a, b Front and reverse view of the 40-day-old colony on PCA. c–d Conidiomata in the culture. e–f Conidiophores, conidiogenous cells and conidiogenesis. g–k Conidia. Scale bars: c–d = 200 µm; e–k = 10 µm.

Figure 3.42 Photographs of *Amphisphaeria tetradiana* (HFJAU10473, holotype)

Material examined: China, Jiangxi Province, Jingdezhen city, Fuliang, 7 November 2022, 29.7595°N, 117.2206°E 71.6m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry culture (HFJAU10473, holotype), ex-type living culture JAUCC 5616; ibid., Jiujiang city, Ruichang, 23 March 2021, 29.65°N 115.60°E 73.2m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10466, the living cultrue JAUCC 4860; Yichun city, Zhangshu, 4 April 2020, 28.0130°N,115.3919°E 0 m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, living cultrue JAUCC 3992, dry cultrue HFJAU10467; Yichun city, Wanzai, 4 April 2021, 28.38°N 114.39°E 655m asl, endophytic fungi from the healthy steams of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10468, living cultrue

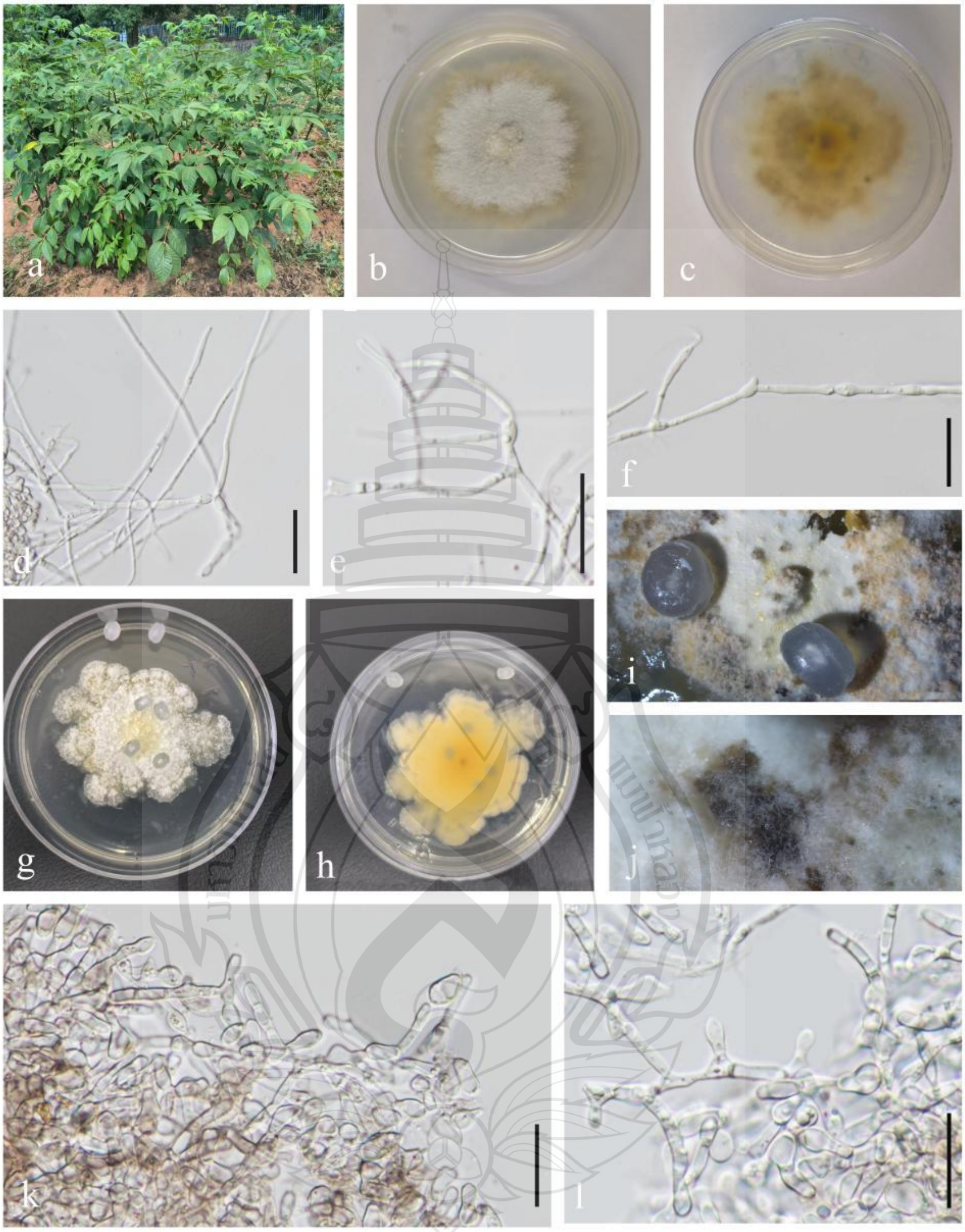
JAUCC 4432; Jiujiang city, Ruichang, 23 March 2021, 29.65°N 115.60°E 73.2m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10471, living cultrue JAUCC 4298; Jiujiang city, Ruichang, 23 March 2021, 29.65°N 115.60°E 73.2m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10472, the living cultrue JAUCC 4299; Jiangxi Province, Ji'an city, Wan'an, 11 April 2021, 26.36°N 114.41°E 0 m asl, endophytic fungi from the healthy steams of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10469, living cultrue JAUCC 4374; Jiangxi Province, Jingdezhen city, Changjiang, 29 June 2022, 29.27°N 117.03°E 40.6 m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10474, living cultrue JAUCC 5139; Jiangxi Province, Yichun city, Tonggu, 12 July 2021, 28.69°N 114.71°E, 483.6 m asl, endophytic fungi from the healthy roots of *T. ruticarpum*, Lixue Mi, dry cultrue HFJAU10470, living cultrue JAUCC 4843.

Notes: To date, most species of *Amphisphaeria* have been reported in their sexual morph, with only a few described in the asexual morph, namely *A. umbrina* and *A. sorbi* (Liu et al., 2015), *A. curvaticonidia*, and *A. camelliae* (Samarakoon et al., 2020). Our collection, obtained from healthy *Tetradium ruticarpum*, produced only the asexual morph. The sister species *A. verniciae*, which is phylogenetically close, is known exclusively from the sexual morph. Multi-gene phylogenetic analyses of ITS, LSU, TUB2, TEF1, and RPB2 sequences revealed that our nine isolates (JAUCC 4860, JAUCC 4298, JAUCC 4299, JAUCC 3992, JAUCC 4432, JAUCC 4374, JAUCC 5616, JAUCC 5139, and JAUCC 4843) clustered with *A. verniciae*, supported by strong statistical values (SH-aLRT/UFB/BPP = 100/100/1) (Figure 3.44). Given their consistent molecular differences and distinct morphological characteristics, we introduce *A. tetradiana* as a novel species.

Amphisphaeria chenzhouensis L. X. Mi, K. D. Hyde & D. M. Hu sp. *nov*., Figure 3.41 and Figure 3.43

Etymology: referring to the place where the fungus was collected

Holotype: HFJAU10475



Note a, Host. b,c Colonies on PDA (surface and reverse, 1 month). d–f Mycelium masses on PDA. g–j Colonies on PDA mixed with polypropylene (surface and reverse). k–l Mycelium masses on PDA mixed with polypropylene. Scale bars: d–f = 20 μm, k–l = 20 μm.

Figure 3.43 Photographs of *Amphisphaeria chenzhouensis* (HFJAU10475, holotype)

Culture characteristics: Colonies grew slowly on PDA medium, the colony reached 43.0 mm after one month, creamy white, flat, fluffy and velvety, sparse at the edge, reverse pale yellowish to brownish at the centre. Generative hyphae septate, branched, sub-hyaline, cylindrical, guttulate, thick-walled, 1–3 µm wide. Not sporulating in culture. Colonies on PDA mixed with polypropylene, white to yellowish, sparse, fluffy, with irregular margin, reverse yellow-brown in centre and yellow-white at the margin. Generative hyphae septate, branched, hyaline to pale brown, surface protuberances, with cells sub-globose to ovoid in shape, guttules, thick-walled, 1–3 µm wide. Not sporulating in culture.

Material examined: China, Hunan Province, Chenzhou City, Guidong, 7 November 2022, 26.0667°N, 113.9333°E, 868m asl, endophytic fungi from the healthy stems of *T. ruticarpum*, Qiuyan Guo, HFJAU10475 (dry culture, holotype), ex-type living culture JAUCC 5233; ibid., endophytic fungi from the healthy stems of *T. ruticarpum*, Qiuyan Guo, dry culture HFJAU10476, living culture JAUCC 6862.

Notes: In this study, *Amphisphaeria chenzhouensis* is described as a new species supported by phylogenetic analyses. *Amphisphaeria chenzhouensis* forms a strongly supported monophyletic clade (SH-aLRT/UFB/BPP = 100/100/1) within *Amphisphaeria*, sister to the clade of *A. micheliae* and *A. sambuci* (Figure3.43). Following the sporulation method of Wang et al. (2023), polypropylene (PP) was added to PDA medium and inoculated with the fungal mycelium to induce spore production. However, no sporulation was observed.

Funiliomycetaceae L. X. Mi, K. D. Hyde, H. Y. Song & D. M. Hu, fam. nov.

Index Fungorum number: IF904529

Etymology: from the type genus *Funiliomyces*

Type genus: *Funiliomyces* Aptroot, Studies in Mycology, 50(2): 309 (2004)

Description:Saprobic, endophytic, or epiphytic on diverse plant hosts in tropical to temperate regions. **Sexual morph:** *Ascomata* black, subglobose, immersed to erumpent. *Wall* composed of irregular layers of regularly melanized, flattened cells, with no color change in KOH. *Physes* absent. *Asci* cylindrical, 8-spored, with a thickened apex bearing a central refractive, IKI-negative apical apparatus, and enclosed by parenchymatous tissue. *Ascospores* pale brown, torpedo-shaped, 2-septate, upper cell pointed, lower cell rounded, hyaline granules or oil droplets, bearing two hyaline mucilaginous appendages. **Asexual morph:** *Mycelium* consisting of branched, septate, smooth, hyaline to pale brown hyphae, sometimes forming hyphal ropes. *Conidiophores* macronematous, mononematous, solitary or in small groups, erect, straight to flexuous, subcylindrical to cylindrical (apex sometimes inflated), simple or occasionally branched, hyaline to brown, septate, sometimes reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal or lateral, sympodial, mono- to polyblastic, hyaline to brown, cylindrical to clavate, with flat-tipped or denticulate apices; denticles (when present) large, cylindrical to geniculate, cylindrical, truncate, or pimple-like, or lacking entirely. *Conidia* solitary, hyaline to pale smoky, smooth, septate, narrowly fusiform to cylindrical, with obtuse, subobtuse, or tapering apices and truncate or rounded bases; dimensions variable among species.

Notes: A new family, Funiliomycetaceae, is proposed to accommodate a distinct, strongly supported clade comprising the genus *Funiliomyces* and several related lineages historically identified as "*Dactylaria*". In our multi-locus phylogeny, this clade was resolved as a sister to Nothodactylariaceae with maximum statistical support (SH-aLRT/UFB/BPP = 99.9/-/0.99). Furthermore, the minimum genetic distances between Funiliomycetaceae and other families in Amphisphaeriales (ITS: 0.156; LSU: 0.036; RPB2: 0.252) all exceeded the smallest inter-familial divergences observed within the order (ITS: 0.110; LSU: 0.032; RPB2: 0.208) (Appendix Table C7–C9), providing quantitative evidence that it represents an independent family-level lineage.

In addition to the strong phylogenetic and genetic distances outlined above, the establishment of Funiliomycetaceae is further supported by distinct morphological and ecological characteristics. Morphologically, although the conidial sizes of some Funiliomycetaceae species overlap with the largest conidia in Nothodactylariaceae (e.g., *Nothodactylaria fusiformis*, 16.5–23 × 2–3 μm), the entire conidial size range of the new family is substantially broader and encompasses numerous species with distinctly larger dimensions.(Table 3.11). A more definitive diagnostic feature is the diversity of its conidiogenous cells, which bear large cylindrical to geniculate denticles or lack denticles entirely. This diversity sharply contrasts with the uniform, pimple-like denticles of Nothodactylariaceae. Ecologically, Funiliomycetaceae exhibits no host specialization, unlike all known Nothodactylariaceae species, which are restricted to ferns, particularly those in the family Blechnaceae. Thus, the establishment of

Funiliomycetaceae is robustly supported by an integrative assessment of phylogenetic, morphological, and ecological evidence.

Funiliomyces Aptroot, Stud. Mycol. 50 (2): 309 (2004)

Index Fungorum number: IF500077

Type species: *Funiliomyces biseptatus* Aptroot, Stud. Mycol. 50 (2): 309 (2004)

Index Fungorum number: IF500164

Holotype: CBS H-10505

Type information: Brazil, Minas Gerais, Catas Altas, Serro do Caraça, Parque Natural do Caraça, near Funil, 1 km NW of monastery Santuário do Caraça, 20°06' S, 43°29' W, on dead leaf of Bromeliaceae in rock field, 18 Sept. 1997, A. Aptroot, holotype herb. CBS H-10505, isotypes herb. SP, living culture ex-type CBS 100373, also dried culture CBS H-10506.

Description: See Aptroot (2004) on page 309.

Emended Diagnosis: Saprobic, endophytic, or epiphytic on diverse plant hosts in tropical to temperate regions. **Sexual morph**: *Ascomata* black, subglobose, immersed to erumpent. *Wall* composed of irregular layers of regularly melanized, flattened cells, with no color change in KOH. *Physes* absent. *Asci* cylindrical, 8-spored, with a thickened apex bearing a central refractive, IKI-negative apical apparatus, and enclosed by parenchymatous tissue.. *Ascospores* pale brown, torpedo-shaped, 2-septate, upper cell pointed, lower cell rounded, hyaline granules or oil droplets, bearing two hyaline mucilaginous appendages. **Asexual morph:** *Mycelium* consisting of branched, septate, smooth, hyaline to pale brown hyphae*, s*ometimes forming hyphal ropes. *Conidiophores* macronematous, mononematous, solitary or in small groups, erect, straight to flexuous, subcylindrical to cylindrical (apex sometimes inflated), simple or occasionally branched, hyaline to brown, septate, sometimes reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal or lateral, sympodial, mono- to polyblastic, hyaline to brown, cylindrical to clavate, with flat-tipped or denticulate apices; denticles (when present) large, cylindrical to geniculate, cylindrical, truncate, or pimple-like, or lacking entirely. *Conidia* solitary, hyaline to pale smoky, smooth, septate, narrowly fusiform to cylindrical, with obtuse, subobtuse, or tapering apices and truncate or rounded bases; dimensions variable among species.

Notes: *Funiliomyces* was first described by Aptroot (2004) as a monospecific genus, containing only its type species *Fus. biseptatu*s. Our phylogenetic analyses confirm that *Dactylaria* sensu lato is polyphyletic (Figure 3.45). Its type species, *Dactylaria purpurella*, forms an independent lineage within Pezizomycotina, distantly related to the ten "*Dactylaria*" species examined in this study. This indicates that these ten species are not congeneric with the type of *Dactylaria*. Therefore, we transfer these ten species and one newly described species (*Fus. jiangxiensis*) to Funiliomyces, in accordance with the "One Fungus, One Name" principle.

This emendation expands the genus to encompass both sexual and asexual morphs. The type species, *Fus. biseptatus*, represents the sexual morph, characterized by torpedo-shaped ascospores with two nearly central septa and appendages. In contrast, the eleven other species represent the asexual morphs, producing hyaline, septate conidiophores with sympodial, denticulate conidiogenous cells and solitary, hyaline, clavate or fusoid-ellipsoid conidia. Despite these stark morphological differences, our phylogenetic analyses demonstrate that all these taxa form a coherent clade within Amphisphaeriales (Figure 3.45), justifying their inclusion in a single genus under a modern, phylogeny-based taxonomic framework.

Funiliomyces jiangxiensis L. X. Mi, K. D. Hyde, H. Y. Song & D. M. Hu, sp. nov., Figure 3.44 and Figure 3.45

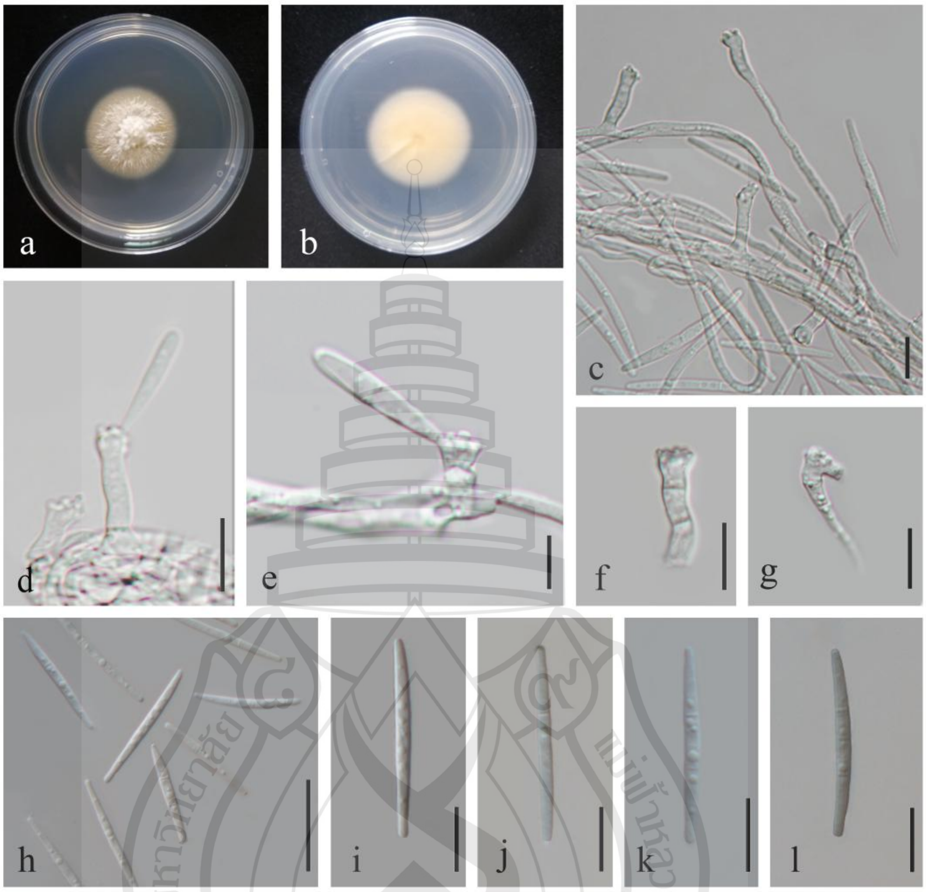
Index Fungorum number: IF904530

Etymology: The name refers to the place where the fungal was collected.

Holotype: HFJAU10125

Endophytic fungus isolated from the roots of *Tetradium ruticarpum*. **Sexual morph:** Undetermined. **Asexual morph:** *Mycelium* consisted of hyaline, smooth, branched, septate, 1.7–2.6 µm diam hyphae. *Conidiophores* (6–)8.5–17.5(–23.5) × 1.8–3.5(–4) µm ($\bar{x}$ = 12.5 × 3 µm, n = 35), macronematous, mononematous, hyaline, subcylindrical, arising from terminal or intercalary parts of aerial hyphae, moslty reduced to conidiogenous cells (rarely with a supporting cell), tapering towards the base, apex polyblastic, sympodial, inflated or geniculous-sinuous, with conspicuous, cylindrical denticles, up to 0.9 µm wide. *Conidia* 20–40 × 1.5–3.5 µm ($\bar{x}$ = 27.8 × 2.6 µm, n = 40), hyaline, narrowly fusoid-ellipsoid, 0–3-septate, guttulate, apex sub-obtuse, base truncate.

Culture characteristics: Colonies on PDA at 25 °C for 5 days, convex, white with cream margin, reverse pale brown with cream margin, no pigment in agar.



Note a,b Colonies on the front and back of PDA medium (for 5 days). c Hyphae and sporulation structures. d,e Conidiophores bearing a conidium initial on one of its denticles. f,g Conidiophores. h–l Conidia. Scale bars: c,d = 10 μm, e = 5 μm, f,g = 10 μm, h = 20 μm, i–l = 10 μm.

Figure 3.44 Photographs of *Funiliomyces jiangxiensis* (HFJAU10125, holotype)

Material examined: CHINA, Jiangxi Province, Ganzhou City, Ganxian District, 25.6121°N, 115.1211°E 412.9m asl, isolated from healthy roots of *Tetradium ruticarpum*, 26 June 2022, Lixue Mi, dry culture HFJAU10125 (holotype); ex-type JAUCC 5298; *ibid*., Yichun City, Zhangshu county-level city, 27.9931° N 115.2123° E, 46m asl, 21 September 2021, Lixue Mi, dry culture HFJAU10124; living culture: JAUCC 4255.

Notes: Based on a nucleotide BLAST search in GenBank database using the LSU sequence, the closest matches are *Dactylaria* species, including *Funiliomyces hwasunensis* (≡ *D. calliandrae*) CMML 20-35 [GenBank PQ741487; identities = 820/824 (99%), gaps = 0/824 (0%)], *Fus. calliandrae* (≡*D. calliandrae*) CPC 48004 [GenBank PV664963; identities = 805/811 (99%), gaps = 0/811 (0%)], *Fus. fragilis* (≡ *D. fragilis*) P057 [GenBank EU107290; identities = 798/807 (99%), gaps = 0/811 (0%)]. The closest match for the ITS sequence is *Fusidium griseum* Trtsf08 [GenBank GU479905; identities = 468/495 (95%), gaps = 7/495 (1%)], D. acerose ICMP 13178 [GenBank OR543730; identities = 465/494 (94%), gaps = 4/494 (4%)], and *Fus. calliandrae* (≡ *D. calliandrae*) CPC 48004 [GenBank PV664937; identities = 454/479 (95%), gaps = 6/479 (4%)]. For the RPB2 sequence, the closest matches included *Dicyma funiculosa* CBS 323.86 [GenBank KU684306; identities = 579/735 (79%), gaps = 6/735 (0%)], and *Xylaria liquidambaris* FCATAS879 [GenBank MZ707110; identities = 553/700 (79%), gaps = 8/700 (1%)]. This situation may be due to the limited availability of RPB2 gene sequences for this genus.

In the multi-gene analysis, *Funiliomyces jiangxiensis* (strains JAUCC 5298 and JAUCC 4255) forms a distinct lineage that groups with *Fus. hwasunensis* (≡ *Dactylaria hwasunensis*) and *Fus. calliandrae* (≡ *D. calliandrae*) as a sister branch, supported by high statistical values in the phylogenetic tree (SH-aLRT/UFB/BPP = 98.8/100/0.98). Morphologically, *Funiliomyces jiangxiensis* can be distinguished from *Fus. hwasunensis* by their conidiogenous cells and conidia. Specifically, *Funiliomyces jiangxiensis* develops distinct denticles on its conidiogenous cells, a feature that is absent in *Fus. hwasunensis*. Additionally, there is a notable difference in the number of septa in their conidia: *Funiliomyces jiangxiensis* has conidia with 0–3 septa, whereas *Fus. hwasunensis* produces conidia with more septa, ranging from 1 to 5. In terms of morphology, *Fus. jiangxiensis* resembles *Fus. calliandrae* but can be distinguished from it. Both have denticles on conidiogenous cells, yet those of *Fus. jiangxiensis* (0.9 μm) are shorter than *Fus. calliandrae*'s (1–3 μm). Additionally, the conidia of *Fus. jiangxiensis* (20–40 μm) are shorter than those of *Fus. calliandrae* [(37–)40–45(–47) μm]. Therefore, these distinct morphological features, combined with phylogenetic evidence, support the establishment of *Fus. jiangxiensis* as a new specie.

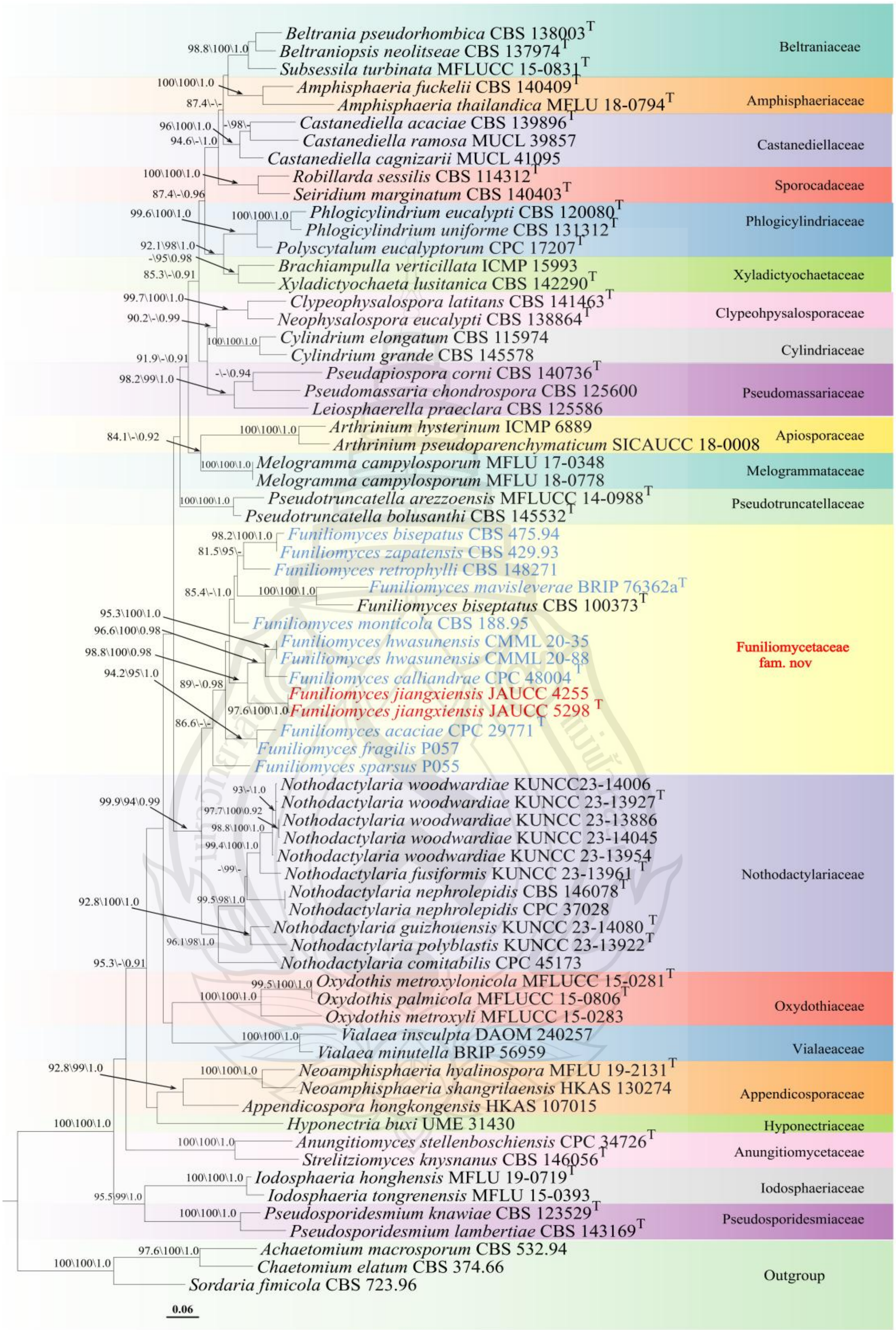


Figure 3.45 Phylogenetic tree of *Funiliomyces*

Maximum likelihood (ML) phylogenetic tree of the *Funiliomyces* genus within Amphisphaeriales based on combined LSU, ITS, and RPB2 sequence data (Figure 3.45). Seventy-one strains are included in the combined gene analyses, comprising 2642 characters after alignment (857 for LSU, 728 for ITS, and 1057 for RPB2). *Achaetomium macrosporum* (CBS 532.94), *Chaetomium elatum* (CBS 374.66), and *Sordaria fimicola* (CBS 723.96) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (GTR+I+G for LSU, ITS, and RPB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -29373.458 is presented. The matrix had 1501 distinct alignment patterns, with 37.19% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. For the Bayesian inference analyses, the best-fit evolutionary models were GTR+I+G for LSU, ITS, and RPB2. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Ex-type strains are marked with T after the strain number. The newly generated sequences are indicated in red, and species for reclassification are in blue.

Ten new combinations within the genus *Funiliomyces* are proposed based on morphological and phylogenetic evidence.

Funiliomyces acaciae (Crous) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF819073

Basionym: *Dactylaria acaciae* Crous, Persoonia 37: 321 (2016)

Holotype: CBS H-22876

Type information: USA, Hawaii, Oahu, on leaves of *Acacia koa* (Fabaceae), 30 September 2015, J.J. Le Roux (holotype CBS H-22876, culture ex-type CPC 29771 = CBS 142087).

Description: See the original description in D'Souza et al. (2002) on page 141.

Funiliomyces bisepatus (Matsushima) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: 312614

Basionym: *Dactylaria biseptata* Matsushima, Icones Microfungorum a Matsushima lectorum: 48 (1975).

Holotype: CBS H-25715.

Type information: Japan, Ohdaigahara, Nara Pref, on a rotten leaf of *Rhododendron metternichii* (Ericaceae), July 1970, MFC-4029 (holotype).

Description: See the original description in Matsushima (1975) on page 48–49.

Funiliomyces calliandrae (Crous) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: 859210

Basionym: *Dactylaria calliandrae* Crous et al. Persoonia 54: 376–377 (2025). Holotype. MFC-4029.

Type information: Brazil, Minas Gerais, Viçosa, Clonar nursery, on living leaf of *Calliandra tweediei* (Fabaceae), 25 February, 2024, P.W. Crous, HPC 4399 (holotype CBS H-25715; culture ex-type COAD 3994 = CPC 48004).

Description: See the original description in Crous et al. (2025) on page 376–377.

Funiliomyces fragilis (de Hoog) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF104169

Basionym: *Dactylaria fragilis* de Hoog, Studies in Mycology 26: 30 (1985)

Holotype: No.6074(CBS)

Type information: The Netherlands, Opsterland, Oldeterp, on cupules of *Fagus sylvatica* (Fagaceae), H.A. van der Aa, October, 1977.

Description: See the original description in de Hoog & van Oorscho (1985) on page 30.

Funiliomyces hwasunensis (H. F. Liu & H. K. Sang) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF857258

Basionym: *Dactylaria fragilis* H. F. Liu & H. K, IMA Fungus 16(e138479): 10 (2025).

Holotype: CMML 20-35H

Type information: Korea, South Jeolla Province, Hwasun, isolated from roots of *Zoysia japonica* (Poaceae), October 2020, H. Liu & H. Sang, holotype CMML 20-35H, ex-holotype CMML 20-35, ex-isotype CMML 20-88.

Description: See the original description in Liu et al. (2025) on page 12–14.

***Funiliomyces* mavisleverae** (Y.P. Tan, Bishop-Hurley & Marney) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF902836

Basionym: *Dactylaria mavisleverae* Y. P. Tan, Bishop-Hurley & Marney, Index of Australian Fungi 46: 3 (2024).

Holotype: BRIP 76362a

Type information: Australia, Queensland, Brisbane, phylloplane of unidentified ornamental plant, January, 2024, T.S. Marney, BRIP 76362a (holotype).

Description: See the original description in Tan et al. (2024) on page 3–4.

Funiliomyces monticola (R. F. Castañeda & W. B. Kendr.) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF361523

Basionym: *Dactylaria monticola* R. F. Castañeda & W. B. Kendr, University of Waterloo Biology Series, 35:30 (1991).

Holotype: INIFAT C 91/82

Type information – Cuba, Granma, Buey Arriba, La Estrella, on dead leaves of *Andira inermis*(Leguminosae), R.F. Castañeda, 14 March 1991.

Description: See the original description in Castañeda & Kendr (1991) on page 30.

***Funiliomyces retrophylli* (Crous)** L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF844283

Basionym: *Dactylaria retrophylli* Crous, Fungal Systematics and Evolution 10: 41 (2022).

Holotype: HPC 3260

Type information – Colombia, Finca El Cedral, on leaves of *Retrophyllum rospigliosii* (Podocarpaceae), M.J. Wingfield, February, 2020, HPC 3260 (holotype CBS H-24817, culture ex-type CPC 39510 = CBS 148271).

Description: See the original description in Crous et al. (2022) on page 41–42.

Funiliomyces sparsus (R. F. Castañeda & W. B. Kendr.) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF361528

Basionym: *Dactylaria sparsa* R. F. Castañeda & W. B. Kendr, University of Waterloo Biology Series. 35:33 (1991)

Holotype: INIFAT C 91/68-2,

Type information: Cuba, C. Habana, Santiago de las Vegas, on decaying leaves, R.F. Castañeda, 18 February 1990.

Description – See the original description in Castañeda & Kendr (1991), 33.

Funiliomyces zapatensis (R.F. Castañeda) L. X. Mi, H. Y. Song, D. M. Hu & K. D. Hyde, comb. nov.

Index Fungorum: IF125340

Basionym: *Dactylaria zapatensis* R.F. Castañeda, Fungi Cubenses III (La Habana): 5 (1988)

Holotype: INIFAT C85/98

Type information: Cuba, Matanzas, Ciénaga de Zapata,on fallen leaves of *Nectandra coriacea* (Lauraceae), R.F. Castañeda Ruiz, 26 May 1985.

Description – See the original description in Castañeda Ruiz (1988), 5.

Funiliomyces currently includes only a single sexual morph species, *F. biseptatus*; therefore, we summarized the asexual morphological features, lifestyle, host associations, and distribution for all species (Table 3.11) to facilitate comparison within the genus

Table 3.11 Asexual morphological features, lifestyle, host associations, and distribution of *Funiliomyces* species

Species	**Mycelium**	**Conidiophores**	**Conidiogenous cells**	**Conidia**		**Life style**	**Host**	**Country**	**References**
				Shape/colour	**Size**				
Funiliomyces acaciae	2–2.5 µm, hyaline,	7–60 × 2–3.5 µm, brown, 0–7-septate	7–25 × 2–3.5 µm, brown, with flat-tipped denticles (0.5–1.5 × 0.5 µm)	narrowly fusoid ellipsoid, 2-septate, hyaline	(16–)25–34(–37) × 2(–2.5) µm	epiphytic	*Acacia koa* (Fabaceae)	USA	(Crous et al., 2016)
F. bisepatus	1–3 µm, hyaline to moderately brown	5–20 µm × 3–3.5 µm, moderately brown, cylindrical, 0–2-septata	cylindrical, moderately brown, with successive denticles and geniculate structure	cylindrical, 2-septata, individually, hyaline to pale smoky	(22–) 27–33 (–35) × 1.5–2 µm	saprobic	*Rhododendron metternichii* (Ericaceae)	Japan	(Matsushima, 1975)
F. biseptatus	–	–	–	–	–	saprobic	*Undefined (Bromeliaceae)*	Brazil	(Aptroot, 2004)
F. calliandrae	2–3 µm, hyphae	hyaline (appearing subhyaline with age), mostly reduced to conidiogenous cells	10–25 × 3–4 µm hyaline, prominent cylindrical denticles, 1–3 × 1.5 µm	spindle-shaped, apex subobtuse, base truncate, (3–)5–6(–8)-septate, hyaline	(37–)40–45(–47) × (2.5–)3 µm	epiphytic	*Calliandra tweediei* (Fabaceae)	Brazil	(Crous et al., 2025)
F. fragilis	pale brown	15–30 × 4 µm at the base, 0–3 thin septa, subhyaline to pale brown	thin-walled, hyaline, slightly lobed; denticles absent; rhexolytic secession with inconspicuous scars	clavate, 2-septate, hyaline	18–26 × 1.5, base 0.6 µm wide	saprobic	*Fagus sylvatica* (Fagaceae)	Netherlands	(de Hoog & van Oorscho, 1985)

Table 3.11 (continued)

Species	Mycelium	Conidiophores	Conidiogenous cells	Conidia		Life style	Host	Country	References
				Shape/colour	**Size**				
F. hwasunensis	–	6–35 × 2.2–2.8 µm, hyaline, aseptate or septate	2–2.8 µm wide, terminal, integrated, hyaline	clavate, blunt end, hyaline, 1–5 septate	10–60 × 2.2–2.8 µm	endophytic	*Zoysia japonica* (Poaceae)	Korea	(Liu et al., 2025a)
F. jiangxiensis	1.7–2.6 µm, hyaline	5–37 × 2–4 µm, hyaline, septate, sometimes reduced to conidiogenous cells	4–18 × 1–4 µm, with conspicuous, cylindrical denticles, up to 0.9 µm wide	narrowly fusoid-ellipsoid, guttulate, 0–3-septate, hyaline	20–40 × 1.5–4 µm	endophytic	*Tetradium ruticarpum* (Rutaceae)	China	This study
F. mavisleverae	–	–	–	–	–	*epiphytic*	an unidentified ornamental plant	Australia	(Tan & Shivas, 2024)
F. monticola	1–1.5µm, colourless	15–40 × 2–2.5 µm, colourless, septate	12–17× 2–3 µm, with conspicuous, truncate denticles in the apical region	fusiform, 1-septate, colourless	30–37 × 1–1.5 µm	saprobic	*Andira inermis* (Leguminosae)	Cuba	(Castañeda & Kendr, 1991)
F.retrophylli	1.5–2.5 µm, hyaline	conidiophores reduced to conidiogenous cells or with supporting cell	with 1–2 × 1 µm apex denticulate	medianly 1-septate, straight to narrowly fusoid, 6–20 × 2.5–3.5	(26–)30–33(–37) × (1.5–)2 µm	epiphytic	*Retrophyllum rospigliosii* (Podocarpaceae)	Colombia	(Crous et al., 2022)

Table 3.11 (continued)

Species	Mycelium	Conidiophores	Conidiogenous cells	Conidia		Life style	Host	Country	References
				Shape/colour	Size				
F. sparsus	1–1.5 µm, pale brown	0–1-septate, pale brown uasually reduced to a conidiogenous cell.	7–12 × 3–4 µm, pale brown or almost colourless, with large, conspicuous, truncate denticles, 1.5–2 µm	subcylindrical, (2–)3-septated with a false septum near each end, colouress or almost colourless	26–36 x 1.5–2 µm	saprobic	decaying leaves (unidentified*)*	Cuba	(Castañeda & Kendr*,* 1991)
F. zapatensis	1–1.5 µm, light brown	12–60 × 1–2 µm, septate, light brown, up to 24 µm wide at apex	polyblastic, denticulate, sympodial, inflated at apex	cylindrical, 2-septata, hyaline, septa visible near extremities	18–26×1–1.5 µm	saprobic	*Nectandra coriacea* (Lauraceae)	Cuba	(Castañeda Ruiz, 1988)

Note the symbol "–" denotes no information available.

Xylariales Nannf.

Xylariaceae Tul. & C. Tul. (= Clypeosphaeriaceae G. Winter)

Nemania Gray

Nemania was established by Gray (1821) with *N. serpens* designated as the type species and is currently placed in the family Xylariaceae. Species of *Nemania* are widely distributed in both terrestrial and marine environments, occurring as endophytes, saprobes, or occasionally as pathogens (Daranagama et al., 2018; Liu et al., 2025b; Pi et al., 2021; Tibpromma et al., 2021; U'Ren et al., 2016; Zhang et al., 2024). Morphologically, members of the genus are characterized by dark brown to black, carbonaceous or brittle stromata that do not release pigments in 10% KOH, and by the presence of white, soft tissue between or beneath the perithecia. Ascospores are typically pale brown, usually without distinct germ slits and remaining intact in 10% KOH. Diagnostic features of the genus include the morphology of the germ slit, ascospore size, and stromatal characteristics (Fournier et al., 2018; Ju & Rogers, 2002). *Nemania* species are also recognized as important producers of secondary metabolites (Demir et al., 2025; Tibpromma et al., 2021). According to Index Fungorum (2025), 99 epithets are currently listed under this genus.

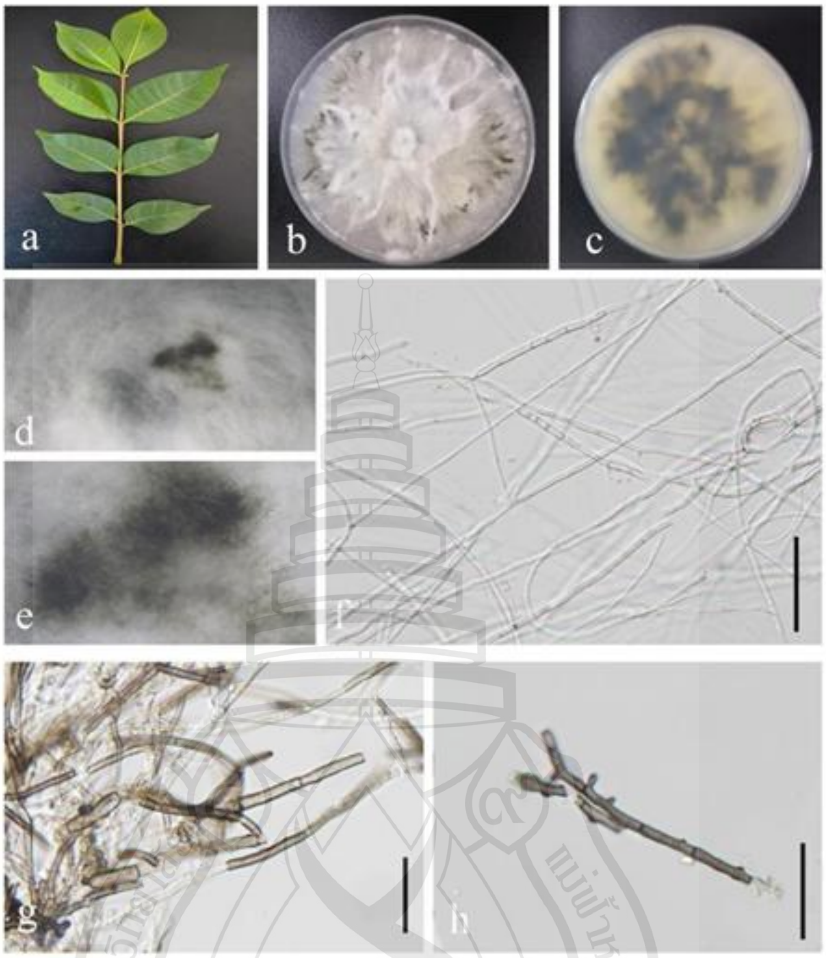
Nemania jiangxiensis L.X. Mi, K.D. Hyde & D.M. Hu sp. *nov*., Figure 3.46 and Figure 3.47

Etymology: The name reflects the location "Jiangxi" from where the holotype was collected.

Holotypus: HFJAU10884

Culture characteristics: The colony on PDA fully covered the Petri dish after 1 week at 25 °C. superficial, white in the beginning and later some mycelium becomes black, circular, entire edge, smooth, flossy, velvety and raised on the surface media; reverse white to black. Generative hyphae simple-septate, branched, sub-hyaline to brown, guttulate, thin-walled, 1.5–4 µm wide. Not sporulating in culture.

Material examined: China, Jiangxi Province, Jingdezhen City, Changjiang, 29 June 2022, 29.2707°N, 117.0332°E, 40.6m asl, endophytic fungi from the healthy leaves of *T. ruticarpum*, Lixue Mi, HFJAU10884 (dry culture, holotype), ex-type living culture JAUCC 4404; ibid, endophytic fungi from the healthy leaves of *T. ruticarpum*, 29 June 2022, Lixue Mi, dry culture HFJAU10885, the living culture JAUCC 5100.



Note a, Host; b,c Colonies on PDA (surface and reverse, 1 month); f–h Mycelium masses. Scale bars: f–h =20 μm.

Figure 3.46 Photographs of *Nemania jiangxiensis* (HFJAU10885, holotype)

Notes: Based on a nucleotide BLAST search in the GenBank database using the ITS sequence, the closest match is *Ne. primolutea* KoLRI_EL006273 [GenBank MN84442; identities = 508/514 (98.83%), gaps = 3/514 (0%)]. The closest match for the RPB2 sequence is *Ne. feicuiensis* GMBC0059 [GenBank: MW836063; identities = 876/920 (95%), gaps = 5/920 (0%)]. For the TUB2 sequence, the closest matches are *Ne. primolutea* YMJ 91102001 [GenBank EF025607; identities = 1219/1346 (91%), gaps = 13/1346 (0%)]. In our phylogenetic analyses, *Ne. jiangxiensis* grouped with *Ne. feicuiensis* (SH-aLRT/UFB/BPP = 100/100/1, Figure 3.47). *Ne. jiangxiensis* was found as an endophytic fungus in leaves of *T. ruticarpum*, while *Ne. feicuiensis* was found as a saprobic fungus on decaying wood. However, morphological comparisons between the new taxon *Nemania jiangxiensis* and *Nemania feicuiensis* could not be conducted, as only cultural characteristics are available for the former. Therefore, we introduce *Nemania jiangxiensis* as a new species based on molecular evidence.

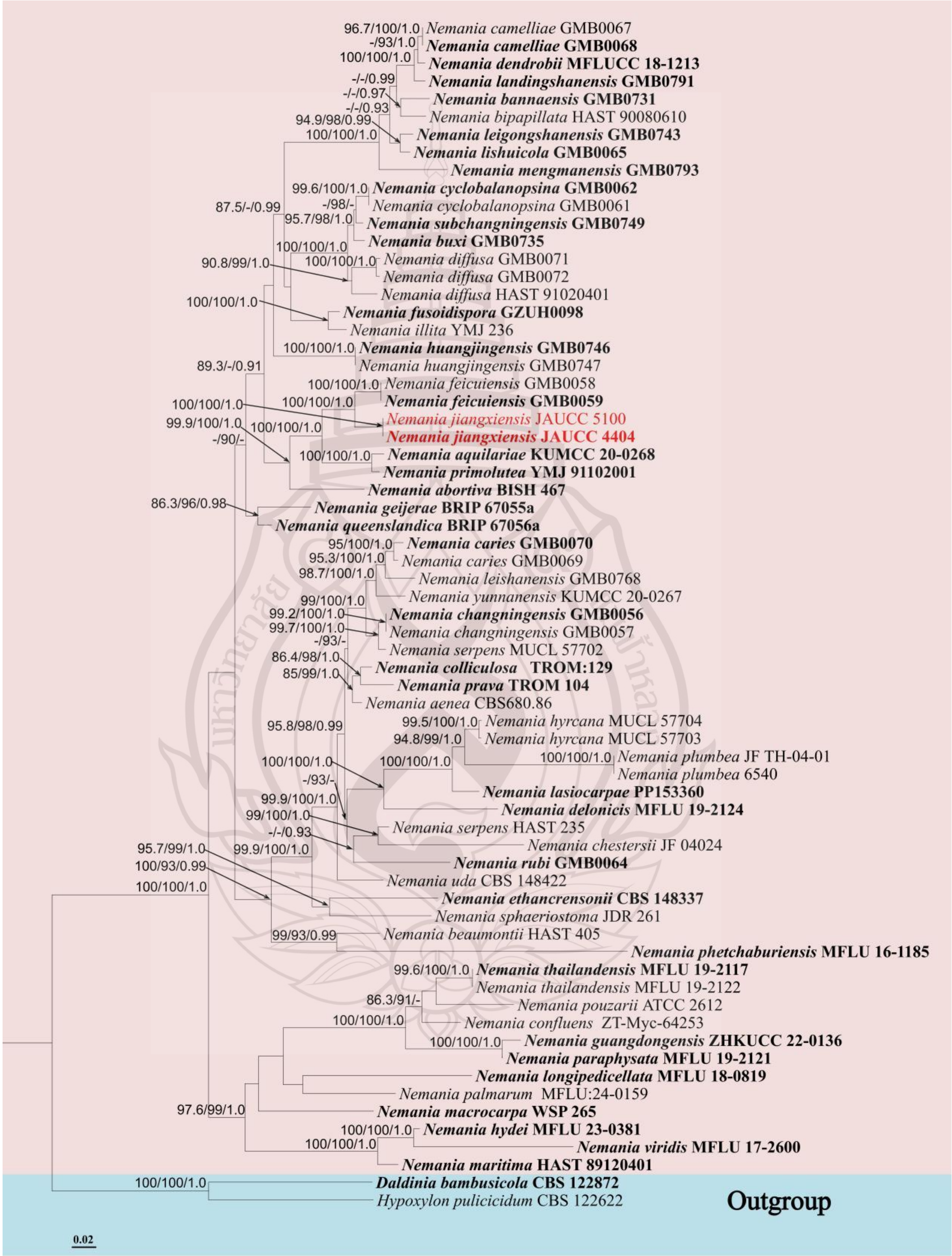


Figure 3.47 Phylogenetic tree of *Nemania*

Maximum likelihood (ML) phylogenetic tree of the *Nemania* genus based on combined ITS, LSU, RPB2*,* and TUB2 sequence data (Figure 3.47). Sixty-seven strains are included in the combined gene analyses, comprising 4022 characters after alignment (723 for ITS, 788 for LSU, 1038 for RPB2, 1473 for TUB2). *Daldinia bambusicola* (CBS 122872) and *Hypoxylon pulicicidum* (CBS 122622) are used as the outgroup taxon. Maximum-likelihood phylogenies were inferred using IQ-TREE under an Edge-linked partition model (TNe+I+G4 for ITS, TNe+I+G4 for LSU, TIM3e+I+G4 for RPB2, TN+F+I+G4 for TUB2) for 10,000 ultrafast bootstraps. The best ML tree with a final likelihood value of -37931.759 is presented. The matrix had 2084 distinct alignment patterns, with 38.56% undetermined characters or gaps. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. GTR+I+G was selected as the best-fit evolutionary model for ITS, LSU, and RPB2, while HKY+I+G was selected for TUB2 in the Bayesian inference phylogenies. SH-aLRT > 80 or UFB > 95 for ML and BYPP > 0.90 for BI is indicated above or below the branches (SH-aLRT/UFB/BPP). Type strains are in bold. The newly generated sequences are indicated in red.

3.4 Preliminary Antimicrobial Screening of the Fungal Isolates

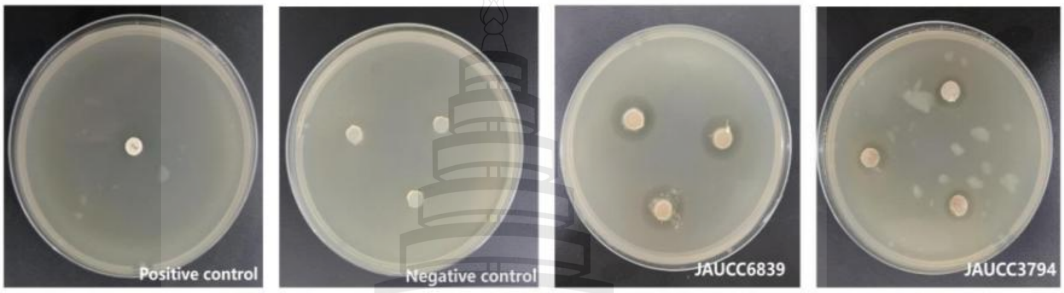
3.4.1 Agar Plug Diffusion Assay for Antibiosis Test (Pretest)

In the pretest of the agar plug diffusion assay, 35 fungal strains with antimicrobial activity were selected from 635 isolates. Among these active isolates, two strains showed inhibitory activity against *Escherichia coli*, five strains inhibited *Xanthomonas campestris*, and five strains exhibited inhibitory effects against *Staphylococcus aureus*. In addition, 25 strains demonstrated inhibitory activity against *Aspergillus niger*, whereas only a single strain inhibited Candida albicans. Notably, three of these endophytic strains exhibited inhibitory effects against two different pathogenic microorganisms. Therefore, these 35 strains were subsequently cultured for formal testing to confirm their antimicrobial activity.

3.4.2 Agar Plug Diffusion Assay for Antibiosis Test (Formal Test)

The 35 endophytic strains selected from the pretest were cultured for 7 days and then subjected to formal antimicrobial testing. The results are presented in Table 3.12. All 35 endophytic fungal strains exhibited certain antimicrobial activity in the formal assay, which was consistent with the results observed in the pre-test.

3.4.2.1 Inhibition of selected endophytes on the *Escherichia coli* growth



Note Positive control: ciprofloxacin 5 µg, 63.2 ± 0.43 mm.

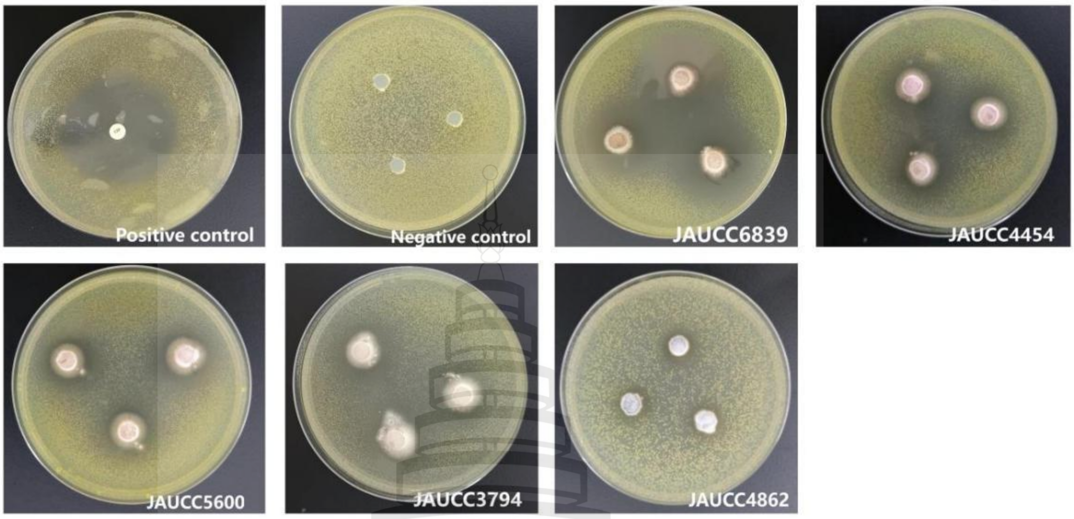
Figure 3.48 Antimicrobial prescreening of selected fungi against *Escherichia coli*

Two endophytic fungal isolates demonstrated inhibitory activity against *Escherichia coli* (ATCC 25922) in the agar plug assay (Table 3.12, Figure 3.48). *Epicoccum* sp. 3 (JAUCC 6839), isolated from root tissue, exhibited the strongest activity with an inhibition zone of 19.0 ± 0.0 mm, while *Epicoccum* sp. 2 (JAUCC 3794) from leaf tissue showed moderate inhibition with a zone of 14.0 ± 0.0 mm. However, both values were notably smaller than that of the positive control (ciprofloxacin 5 µg), which produced a zone of 63.2 ± 0.43 mm.

3.4.2.2 Inhibition of selected endophytes on the *Xanthomonas campestris* growth

Five endophytic fungal isolates exhibited varying degrees of inhibitory activity against *Xanthomonas campestris* (Table 3.12, Figure 3.49). Among them, *Epicoccum* sp. 3 (JAUCC 6839), isolated from root tissue, demonstrated the strongest inhibition with a mean inhibition zone of 32.7 ± 3.6 mm. This was followed by *Epicoccum* sp. 2 (JAUCC 5600, root) and *Epicoccum* sp. 1 (JAUCC 4454, leaf), which produced inhibition zones of 27.0 ± 0.0 mm and 23.0 ± 0.0 mm, respectively. *Epicoccum* sp. 2 (JAUCC 3794, leaf) also showed moderate activity with a zone of 18.0

± 0.0 mm. In contrast, *Penicillifer* sp. 1 (JAUCC 4286) exhibited only weak inhibition (10.0 ± 0.0 mm).



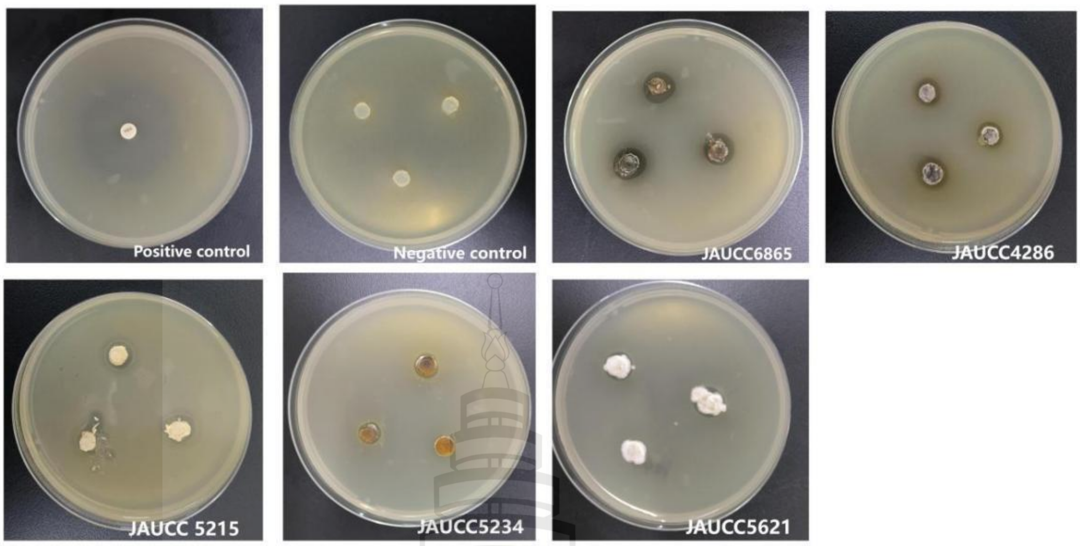
Note Positive control: Ampicillin 10µg, 42.0 ± 0.0 mm.

Figure 3.49 Antimicrobial prescreening of selected fungi against *Xanthomonas campestris*

3.4.2.3 Inhibition of selected endophytes on the *Staphylococcus aureus* growth

Among the 635 endophytic fungal isolates subjected to preliminary antibacterial screening, only five strains exhibited measurable inhibitory activity against *Staphylococcus aureus* (Table 3.12, Figure 3.50). The inhibition zone diameters ranged from 10.0 mm to 14.0 mm, indicating varying but relatively modest antibacterial potency compared to the positive control (Penicillin, 42.0 ± 0.0 mm).

The five active isolates included *Clonostachys* sp. 1 (JAUCC 5621) and *Pestalotiopsis* sp. 3 (JAUCC 5234) from stem tissues, with inhibition zones of 11.0 ± 0.0 mm and 10.0 ± 0.0 mm, respectively. Two strains, *Penicillifer* sp. 1 (JAUCC 4286) and *Pochonia* sp. 1 (JAUCC 5215), were isolated from roots, both showing inhibition zones of 12.0 ± 0.7 mm. Notably, *Stephanonectria* sp. 1 (JAUCC 6865) from stem tissues displayed the strongest activity among them, with an inhibition zone of 14.0 ± 0.0 mm. The results are summarized in Figure 3.48, which visually compares the inhibition zone diameters for each isolate. Despite the relatively small inhibition zones compared to the positive control, these isolates demonstrate potential for further investigation into bioactive secondary metabolites with activity against *S. aureus*.



Note Positive control: Penicillin 10 µg, 42.0 ± 0.0 mm.

Figure 3.50 Antimicrobial prescreening of selected fungi against *Staphylococcus aureus*

3.4.2.4 Inhibition of selected endophytes on the *Aspergillus niger* growth

Of the 35 endophytic fungal isolates evaluated for antifungal activity, 25 exhibited inhibition against *Aspergillus niger*, with inhibition zone diameters ranging from 8.7 to 26.7 mm. (Table 3.12, Figure 3.51). Notably, several strains of *Fusarium* sp. 12 demonstrated the strongest antibacterial activity, including JAUCC 5568 (26.7 ± 0.9 mm), JAUCC 5223 (25.0 ± 0.0 mm), and JAUCC 5549 (24.7 ± 0.2 mm). Additionally, *Fusarium* sp. 3 (JAUCC 3841) exhibited a comparable inhibition zone of 26.7 ± 0.9 mm. Moderate inhibition was also observed in isolates such as *Albifimbria* sp. 1 (JAUCC 5618, 22.0 ± 2.0 mm) and *Diaporthe* spp. (up to 15.7 ± 1.6 mm), while others including *Clonostachys*, *Curvularia*, and *Neosetophoma* species showed relatively weaker activity (≤14.7 mm). None of the isolates surpassed the positive control (Nystatin 10 µg, 30 mm).

Note Positive control: Nystatin 10µg, 30.0 ± 0.22 mm.

Figure 3.51 Antimicrobial prescreening of selected fungi against *Aspergillus niger*

Table 3.12 Preliminary screening results of antimicrobial activities

No.	Strain number	Possible species	Taxon Proposed	The tissue source of the strain	Zone of Inhibition (mm)				
					Pathogenic bacteria			Pathogenic fungi	
					Gram-negative bacteria		Gram-positive bacteria		
					E. coli	***X. campestris***	***S. aureus***	***A. niger***	***C. albicans***
1	JAUCC 5618	*Albifimbria verrucaria*	*Albifimbria* sp. 1	root	×	×	×	22.0 ± 2.0	×
2	JAUCC 3978	*Botryosphaeria dothidea*	*Botryosphaeria* sp. 1	root	×	×	×	×	8.0 ± 0.0
3	JAUCC 5621	*Clonostachys epichloe*	*Clonostachys* sp. 1	stem	×	×	11.0 ± 0.0	×	×
4	JAUCC 4271	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	10.7 ± 0.9	×
5	JAUCC 4272	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	14.7 ± 0.2	×
6	JAUCC 4830	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	8.7 ± 1.6	×
7	JAUCC 5088	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	10.0 ± 0.0	×
8	JAUCC 5145	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	11.7 ± 0.2	×
9	JAUCC 5540	*Clonostachys rosea*	*Clonostachys* sp. 3	root	×	×	×	12.0 ± 0.7	×
10	JAUCC 5564	*Curvularia aeria*	*Curvularia* sp. 5	leaf	×	×	×	12.7 ± 2.9	×
11	JAUCC 4312	*Diaporthe australiana*	*Diaporthe* sp. 22	leaf	×	×	×	12.3 ± 3.6	×
12	JAUCC 3804	*Diaporthe hongkongensis*	*Diaporthe* sp. 37	leaf	×	×	×	15.7 ± 1.6	×
13	JAUCC 3855	*Diaporthe perseae*	*Diaporthe* sp. 31	stem	×	×	×	14.7 ± 0.2	×
14	JAUCC 3922	*Diaporthe pseudophoenicicola*	*Diaporthe* sp. 30	leaf	×	×	×	12.0 ± 2.0	×
15	JAUCC 4383	*Diaporthe hubeiensis*	*Diaporthe* sp. 7	stem	×	×	×	10.3 ± 0.2	×
16	JAUCC 4454	*Epicoccum nigrum*	*Epicoccum* sp. 1	leaf	×	23.0 ± 0.0	×	×	×
17	JAUCC 5600	*Epicoccum thailandicum*	*Epicoccum* sp. 2	root	×	27.0 ± 0.0	×	×	×
18	JAUCC 6839	*Epicoccum thailandicum*	*Epicoccum* sp. 2	root	19.0 ± 0.0	32.7 ± 3.6		×	×

Table 3.12 (continued)

No.	Strain number	Possible species	Taxon Proposed	The tissue source of the strain	Zone of Inhibition (mm)				
					Pathogenic bacteria			Pathogenic fungi	
					Gram-negative bacteria		Gram-positive bacteria		
					E. coli	*X. campestris*	*S. aureus*	*A. niger*	*C. albicans*
19	JAUCC 3794	*Epicoccum thailandicum*	*Epicoccum* sp. 2	leaf	14.0 ± 0.0	18.0 ± 0.0		×	×
20	JAUCC 5548	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	12.0 ± 0.0	×
21	JAUCC 5549	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	24.7 ± 0.2	×
22	JAUCC 5601	*Fusarium proliferatum*	*Fusarium* sp. 12	root	×	×	×	10.7 ± 0.2	×
23	JAUCC 3910	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	20.0 ± 4.7	×
24	JAUCC 5568	*Fusarium proliferatum*	*Fusarium* sp. 12	root	×	×	×	26.7 ± 0.9	×
25	JAUCC 6567	*Fusarium proliferatum*	*Fusarium* sp. 12	fruit	×	×		17.3 ± 4.2	×
26	JAUCC 6870	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	14.0 ± 0.7	×
27	JAUCC 3900	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	10.0 ± 0.2	×
28	JAUCC 4382	*Fusarium proliferatum*	*Fusarium* sp. 12	stem	×	×	×	15.0 ± 2.0	×
29	JAUCC 3841	*Fusarium falciforme*	*Fusarium* sp. 3	stem	×	×	×	26.7 ± 0.9	×
30	JAUCC 5223	*Fusarium falciforme*	*Fusarium* sp. 3	root	×	×	×	25.0 ± 0.0	×
31	JAUCC 6558	*Neosetophoma poaceicola*	*Neosetophoma* sp. 1	fruit	×	×	×	11.7 ± 0.2	×
32	JAUCC 4286	*Penicillifer diparietisporus*	*Penicillifer* sp. 1	root	×	10.0 ± 0.0	12.0 ± 0.7		×
33	JAUCC 5234	*Pestalotiopsis trachycarpicola*	*Pestalotiopsis* sp. 3	stem	×	×	10.0 ± 0.0	×	×
34	JAUCC 5215	*Pochonia chlamydosporia*	*Pochonia* sp. 1	root	×	×	12.0 ± 0.7	×	×
35	JAUCC 6865	*Stephanonectria keithii*	*Stephanonectria* sp. 1	stem	×	×	14.0 ± 0.0	×	×

Note "×" indicates no antimicrobial activity.

3.4.2.5 Inhibition of selected endophytes on *Candida albicans* growth

Among the 635 endophytic fungal isolates screened, only one strain, *Botryosphaeria* sp. 1 (JAUCC 3978), exhibited inhibitory activity against *Candida albicans* (Table 3.12, Figure 3.52). However, the antifungal effect was relatively weak, with an inhibition zone of only 10 mm, which was significantly smaller than that of the positive control (Nystatin 10 µg, 21 mm).

Note Positive control: Nystatin 10µg, 21.0 ± 0.0mm.

Figure 3.52 Antimicrobial prescreening of selected fungi against *Candida albicans*

CHAPTER 4

DISCUSSION

4.1 Community Analysis of Endophytic Fungi From *Tetradium ruticarpum*

The high biodiversity, host specificity, tissue specificity, and spatial heterogeneity of endophytic fungi in medicinal plants have been widely confirmed (Huang et al., 2008), while the relevant characteristics of endophytic fungi in *Tetradium ruticarpum*, as an important medicinal plant, have not been fully revealed. In this study, a total of 935 cultivable endophytic fungi were isolated from the roots, stems, leaves, and fruits of *T. ruticarpum* collected from four provinces in southern China (Jiangxi, Hunan, Anhui, and Guangxi) using six different culture media.

4.1.1 The High Richness of the Endophytic Fungal Community of *Tetradium ruticarpum*

Based on internal transcribed spacer (ITS) sequences, the taxonomic analysis of 935 endophytic fungal isolates from *Tetradium ruticarpum* revealed a highly richness yet structurally skewed community, encompassing three phyla, six classes, 21 orders, 54 families, spanning 84 genera. The vast majority of isolates (99.5%) belonged to the phylum Ascomycota, underscoring its dominance in the culturable fungal assemblage of this medicinal plant. Within Ascomycota, the classes Sordariomycetes (61.9%) and Dothideomycetes (35.4%) were particularly prevalent, together forming the core of the endophytic mycobiota in *T. ruticarpum*. This finding is consistent with the global survey of endophytic fungi by Rashmi et al. (2019), who summarized data from multiple plant species and found that endophytic fungi were predominantly classified within the phylum Ascomycota (87.38%), with Sordariomycetes (35.1%) and Dothideomycetes (25.7%) being the most represented classes. In contrast, Li et al. (2016c) reported that among endophytic fungi associated with *Zanthoxylum bungeanum* (Rutaceae), 96% of isolates belonged to Ascomycota, but Dothideomycetes (63.3%) rather than Sordariomycetes (32.7%) were predominant, indicating a different community structure compared with that of *T. ruticarpum*. The dominant fungal orders in *T. ruticarpum* were Diaporthales (27.1%), Pleosporales (25.2%), Hypocreales (17.0%), and Glomerellales (10.1%), exhibiting a distinct composition compared with *Oxalis latifolia* (Oxalidaceae), where endophytic fungi were mainly distributed in Xylariales (56%), followed by Diaporthales (19%) and Glomerellales (13%) (Hussein et al., 2024). As for the families in *T. ruticarpum*, the dominant ones were Diaporthaceae (26.8%), Nectriaceae (11.9%), and Didymellaceae (10.5%).

At the genus level, the endophytic fungal community of *Tetradium ruticarpum* exhibits a distinct hierarchical structure, characterized by the dominance of one genus, three common genera, and a high richness of rare genera. Specifically, among the 84 identified genera, only one genus (*Diaporthe*) is classified as dominant. It accounts for 251 isolates, corresponding to a relative frequency (RF) of 26.8% and representing over a quarter of the total 935 isolates. This is followed by 3 common genera (*Colletotrichum*, *Fusarium*, and *Alternaria*) with moderate abundances. *Colletotrichum* comprises 93 isolates (9.9%), *Fusarium* includes 86 isolates (9.2%), and *Alternaria* contains 57 isolates (6.1%). Together, these three genera contribute 236 isolates, making up 25.2% of the total community. In contrast, the remaining 79 genera are categorized as rare, with 76 of them having an RF of ≤4.5%. Among these rare genera, four genera (*Botryosphaeria*, *Clonostachys*, *Didymella*, *Epicoccum*) fall into the moderately rare range (3.4–4.5%) with 32–42 isolates each. The vast majority, however, are highly rare. This group includes 72 genera, each with 1–9 isolates and an RF of ≤1.5%. Examples include *Aaosphaeria*, *Acremonium*, and *Arcopilus*, each represented by 1 isolate and an RF of 0.1%. This distribution highlights the strong unevenness in genus-level abundance within the endophytic community of *T. ruticarpum.* Different medicinal plants harbor varying compositions and proportions of endophytic fungal genera. For example, a study of endophytic fungi from *Zanthoxylum simulans* yielded 113 isolates from leaves and stems, with 23 exhibiting antimicrobial activity. These bioactive strains were distributed across six genera: *Penicillium* (26.09%), *Colletotrichum* (21.74%), *Diaporthe* (21.74%), *Daldinia* (17.39%), *Alternaria* (8.70%), and *Didymella* (4.34%) (Kuo et al., 2021). In addition, Among the 84 genera identified, only *Hypoxylon* and *Nigrospora* had been previously reported by Ho et al. (2012); the remaining 82 genera represent new records from *Tetradium ruticarpum*. Collectively, these results significantly enhance our understanding of the endophytic fungal diversity associated with *T. ruticarpum*.

4.1.2 Distribution of Dominant, Common, and Rare Fungal Genera in *Tetradium ruticarpum*

The endophytic fungal community of *Tetradium ruticarpum* exhibits a hierarchical structure at the genus level, characterized by a single dominant genus, a few common genera, and numerous rare genera.In this community structure, a few taxa make up the majority of isolates, whereas most taxa are present at low frequencies. This pattern is commonly observed in endophytic fungal assemblages across diverse plant species (Magurran & Henderson, 2003). It reflects ecological specialization, competitive dynamics, and adaptation to microenvironmental conditions within host tissues, such as secondary metabolite composition and tissue-specific niches.

4.1.2.1 One dominant genus in *Tetradium ruticarpum*

Diaporthe is a widely distributed endophytic fungal genus frequently reported from medicinal plants such as *Artemisia argyi* (Gu et al., 2022), *Astragalus membranaceus* (Kim et al., 2017), *Camptotheca acuminata* (Liu et al., 2021), *Litsea kobuskiana* (Sun et al., 2024b), *Vochysia divergens* and *Stryphnodendron adstringens* (Noriler et al., 2018). In this study, 251 *Diaporthe* isolates were obtained from *T. ruticarpum*, representing 26.8% of all endophytic fungi. Similarly, *Diaporthe* was identified as the predominant genus in both *Copaifera langsdorffii* and *C. pubiflora* (de Carvalho et al., 2021). In addition, our study revealed that the genus was recovered from all culture media, plant tissues, and four provinces, indicating its broad ecological amplitude and strong adaptability within *T. ruticarpum*. This widespread occurrence aligns with previous findings that *Diaporthe* is a dominant endophyte in diverse plant hosts fromtropical rainforests (Monkai et al., 2023), temperate woodlands (Chepkirui & Stadler, 2017), and arid medicinal plant communities (de Pádua et al., 2018), highlighting its remarkable environmental versatility. Furthermore, *Diaporthe* is recognized for producing structurally diverse and biologically active secondary metabolites.The ability of *Diaporthe* species to colonize multiple organs of *T. ruticarpum* may stem from their capacity to produce diverse secondary metabolites that facilitate evasion of host defense systems (Hilário & Gonçalves, 2022; Dissanayake et al., 2024). A recent review summarized 275 compounds from this genus, including terpenoids, polyketides, and alkaloids with cytotoxic, antimicrobial, antioxidant, and anti-inflammatory activities, while genomic analyses (antiSMASH) suggest substantial unexplored biosynthetic potential (Wei et al., 2023). The 251 *Diaporthe* isolates obtained from *T. ruticarpum* in this study thus represent a valuable resource for discovering pharmacologically active compounds potentially linked to the host's medicinal properties.

4.1.2.2 Three common genera in *Tetradium ruticarpum*

Colletotrichum (9.9%), *Fusarium* (9.2%), and *Alternaria* (6.1%) are common genera in *T. ruticarpum*, widely distributed across four provinces in southern China. *Colletotrichum* is a globally distributed fungal genus comprising hundreds of species associated with thousands of plant hosts. While many species are well-known pathogens, a substantial number also occur as symptomless endophytes, particularly in tropical and subtropical regions. These endophytic forms are frequently among the most common fungal residents within plant tissues and have been reported to contribute to host benefits such as enhanced stress tolerance and disease resistance (da Silva et al., 2025; Talhinhas & Baroncelli, 2021).

In our study, *Colletotrichum* was recovered from all examined tissues of *T. ruticarpum*, including fruits (22 isolates), leaves (61 isolates), roots (four isolates), and stems (six isolates). Its presence across multiple tissue types highlights its broad colonization ability and suggests potential ecological roles within this medicinal plant. Gonzaga et al. (2015) found that *Colletotrichum* was the most frequently isolated genus from the endophytic fungal communities of common bean leaves, accounting for 32.69% and 24.29% of isolates from two different varieties. Similarly, *Colletotrichum* has been reported as a dominate genus in the endophytic fungal community of *Cephalotaxus hainanensis* (Yang et al., 2015). Revathy et al. (2025) investigated the endophytic fungal community in the leaves of the black mangrove *Lumnitzera racemosa* and found that *Colletotrichum* was the most prevalent genus, accounting for 47% of the isolates, followed by *Phyllosticta* at 20% and *Escovopsis* at 14%.

As the second conmon genus, *Fusarium* is a common genus of endophytic fungi frequently associated with medicinal plants, with its proportion in the endophytic community varying among different host species. In *Glycyrrhiza glabra*, *Fusarium* was the second most dominant genus overall, following *Phoma*, representing 15.42% of the total isolates (Arora et al., 2019). Similarly, in the present study on *Tetradium* *ruticarpum*, *Fusarium* accounted for 9.2% of the total isolates and was distributed across different tissues, with 35 isolates from roots, 24 from stems, 12 from leaves, and 15 from fruits, indicating a clear preference for roots. This root predominance may be related to the ecological role of *Fusarium*, as roots, being in direct contact with the soil, are more exposed to soil-borne microorganisms, and the abundance of *Fusarium* in this niche could be associated with its involvement in host defense or soil microbe interactions. Gharibi et al. (2025) found that *Fusarium* was the most common genus, accounting for 34.37% of endophytic fungi isolated from the roots of seven medicinal Papaveraceae plants in Iran. This agrees with our study, where most *Fusarium* isolates also came from roots.

For another genus conmon, *Alternaria* is a prevalent genus of endophytic fungi widely reported from various medicinal plants, with its relative abundance differing among host species. In this study, *Alternaria* accounted for 8.6% of the total isolates and was distributed across plant tissues, with 8 from roots, 15 from stems, 22 from leaves, and five from fruits. Within the endophytic fungal community of *T. ruticarpum*, *Alternaria* belongs to the common genera. Similarly, Silva-Hughes et al. (2015) concluded that *Alternaria* is the dominant fungal genus in the native medicinal cactus *Opuntia humifusa*. Additionally, in a study on the endophytic fungal diversity of *Cornus officinalis*, *Alternaria* accounted for 31.25% of isolates and was a dominant genus primarily found in stem and leaf tissues (Zhao et al., 2020).

4.1.2.3 Seventy-nine rare genera in *Tetradium ruticarpum*

The majority of endophytic genera in *T. ruticarpum* (79 out of 84) are classified as rare, with relative frequencies ranging from 0.1% to 4.5%. These include moderately rare taxa (1–4.5%) and highly rare taxa (<1%). Rare genera, despite their low abundance, enhance the community’s functional diversity and may contribute unique ecological functions. Among the moderately rare group, *Botryosphaeria* (4.5%), *Didymella* (3.9%), and *Clonostachys* (3.7%) exhibited distinct tissue-specific colonization patterns in *T. ruticarpum*. *Botryosphaeria* was predominantly recovered from stems (25 isolates, 60%), followed by fruits (nine isolates, 21%) and roots (seven isolates, 17%), with only a single isolate from leaves (one isolate, 2%). In contrast to our findings, *Botryosphaeria* was reported as the dominant genus in the endophytic fungal community of *Cornus officinalis*, accounting for 31.25% of isolates and primarily distributed in stem and leaf tissues (Zhao et al., 2020). *Didymella* showed an opposing trend, being leaf-dominant (42 isolates, 74%), with fewer isolates from stems (11 isolates, 19%) and roots (four isolates, 7%), indicating specialization in foliar niches, possibly contributing to oxidative stress mitigation and defense against leaf-infecting pathogens. Notably, in *Glycyrrhiza glabra*, both *Botryosphaeria* and *Didymella* were represented by only a single isolate each (Arora et al., 2019), underscoring the marked variability in their abundance and tissue distribution across different host plants. Moreover, *Clonostachys* displayed strong root dominance (29 isolates, 83%), with minor occurrence in stems (five isolates, 14%) and leaves (one isolate, 3%), reflecting its adaptation to the rhizosphere microenvironment and potential involvement in nutrient cycling and antagonism against soil-borne pathogens. These contrasting distribution profiles underscore niche differentiation among moderately rare genera, highlighting their potential ecological roles in host tissue colonization and functional complementarity within the endophytic community. The genus *Clonostachys* has been frequently detected as endophytic fungi in various plants, such as *Coptis chinensis* (Ming et al., 2022) and *Camellia sinensis* (Onlamun et al., 2023). However, in the study of endophytic fungal communities in *Taxus chinensis* var. *mairei*, Wu et al. (2013) reported no isolation of *Clonostachys* species. In addition to the moderately rare genera, highly rare taxa such as *Pseudokeissleriella* from stems (0.3%) *Cyphellophora* from roots (0.2%), *Biscogniauxia* from roots (0.1%), and *Austropleospora* from leaves (0.1%). A single *Biscogniauxia* isolate, a genus primarily known as plant pathogens (Diminić et al., 2019), was recovered from the roots of *T. ruticarpum*. Previous work on *B. mediterranea* in *Quercus cerris* showed that it can switch between endophytic and pathogenic lifestyles, with its endophytic phase favored by reduced host water potential (Vannini et al., 2009). It is possible that *Biscogniauxia* in *T. ruticarpum* may also transition to a pathogenic state under certain environmental or physiological conditions, suggesting a potential risk for host health. Meanwhile, *Austropleospora*'s presence in leaves, though limited, may imply specialized interactions within the foliar microenvironment. *Austropleospora* has so far been reported only as a pathogen or saprobe (Dissanayake et al., 2021), and this is the first record of the genus as an endophyte. Collectively, a considerable number of low-frequency taxa, many of which are singletons, likely arising from random events rather than ecological factors, exhibited spatial variability alongside the majority of dominant taxa (Magurran & Henderson, 2003). These rare taxa contribute to the functional redundancy and resilience of the endophytic fungal community. However, their ecological significance is likely underestimated due to inherent limitations of culture-based isolation methods, which tend to overlook slow-growing or less competitive fungi. Integrating culture-independent techniques, such as high-throughput sequencing, would provide a more comprehensive assessment of their diversity and ecological roles.

The endophytic fungal community in *Tetradium ruticarpum* displays a characteristic "dominance–rarity" pattern, with a few genera occurring in high abundance while most are represented by rare taxa. This distribution reflects the complex ecological interactions within different host tissues and the selective bias of culture-based isolation methods that favor fast-growing fungi. Such a community structure underscores the rich diversity and functional potential of endophytes in medicinal plants. Notably, comparative studies reveal that while common genera like *Pestalotiopsis* and *Clonostachys* frequently appear in endophyte research, the detection of less common genera such as *Stephanonectria* and *Penicillifer* among the active isolates from *T. ruticarpum* suggests host-specific relationships or unique biosynthetic capabilities. Together, these findings highlight *T. ruticarpum* as a valuable reservoir for novel antimicrobial compounds, particularly those with activity against important phytopathogens.

4.2 Analysis of Endophytic Fungi across Media, Plant Tissues, and Provinces

4.2.1 The Influence of Culture Media on the Isolation Efficiency of Endophytic Fungi

The type of culture medium plays a critical role in determining both the recovery efficiency and the taxonomic richness of culturable endophytic fungi (Muggia et al., 2017). In this study, six different media, including PDA, RBA, PCA, MEA, YpSs, and OA, were employed to maximize the isolation efficiency from *Tetradium ruticarpum* (Table 2). The number of isolates obtained from the six culture media followed the order PDA(325) > RBA(217) > PCA(122)> MEA(99) > YpSs(94) > OA(78). Among them, PDA yielded the highest number of isolates and the richest genus-level diversity, contributing 31 unique genera not recovered from any other medium, which highlights its broad-spectrum suitability for culturing diverse fungal taxa. PDA was the most widely used medium in previous studies (Du et al., 2020; Ibrahim et al., 2021; Li et al., 2016c). Its nutrient-rich composition likely supports both fast-growing and slow-growing endophytes (Syamsia et al., 2021), making it the most effective single medium in this study. Cheng et al. (2023) aslo found that PDA yielded more genera from cucumber and rhizosphere samples than other tested media. Rose bengal agar (RBA) is also frequently applied for the isolation of endophytic fungi (Das et al., 2013; Kim et al., 2022; Luo, 2022; Yu & Yao, 2022; Zheng et al., 2020). In our study, RBA ranked second in both the number of isolates (217 isolates, 23.2%) and diversity (37 genera), and contributed 8 unique genera. Its selective components, such as rose-bengal, may suppress bacterial growth and fast-growing molds, thus enabling the recovery of more competitively sensitive fungi (King et al., 1979). PCA is often suitable for the growth of many fungi, such as *Alternaria* sp., *Epicoccum* sp., *Phoma* sp., and *Chaetomium* sp. (Nalawade et al., 2019; Sørensen et al., 2009). Meanwhile, PCA is also frequently used for the growth of fungal spores. For example, PCA is one of the suitable culture media for sporulation of the fungus *Myrothecium roridum* (Ranjini & Naika, 2018). In our study, PCA yielding a moderate number of isolates (122 isolates), showed the lowest genus diversity (20 genera) and yield only one unique genera, suggesting it favors more commonly occurring fungi with broad medium tolerance. The other media used in this study, namely MEA, YpSs, and OA, are also commonly employed for fungal cultivation (Luo, 2022; Nitoda et al., 2003; Ibrahim et al., 2017; Sevgili & Erkmen, 2019; Shrestha et al., 2006).

The type of culture medium influences not only fungal recovery rates but also the overall taxonomic richness and diversity.. Nine genera were consistently isolated from all six culture media, including *Alternaria*, *Botryosphaeria*, *Corynespora*, *Epicoccum, Neodidymella*, *Clonostachys*, *Colletotrichum*, *Diaporthe*, and *Fusarium*. These genera are commonly reported as endophytes from a wide range of host plants (Huang et al., 2008), reflecting their ecological versatility and strong colonization ability within plant tissues. Their consistent occurrence across multiple media in this study highlights their dominance and adaptability within *T. ruticarpum.* In addition to the genera shared by all six media, several genera were found to overlap among two to four media, indicating partial selectivity and overlapping nutrient preferences. In addition, *Diaporthe* was consistently identified as the dominant fungal genus across all six media used in this study, indicating its strong adaptability and stable distribution under varying nutrient conditions. A similar observation was reported by Orwa et al. (2020), who found that although the number of fungal isolates varied among Malt Extract Agar (MEA), Oatmeal Agar (OA), Sabouraud Dextrose Agar (SDA), and Potato Dextrose Agar (PDA) prepared at different nutrient levels, with 14 isolates obtained from MEA-L and only five from MEA-H, the dominant fungal genera including *Penicillium*, *Acremonium*, *Phoma*, and *Cladosporium* remained consistent across all media. Notably, the combination of PDA and RBA proved highly effective for the isolation of endophytic fungi from *T. ruticarpum*, accounting for 91.7% of the total genera (77 genera). Overall, these findings suggest that using multiple culture media enhances the recovery and richness of culturable endophytic fungi from *T. ruticarpum*, providing practical guidance for the selection of isolation media in future studies.

4.2.2 Analysis of Endophytic Fungal Community Composition in Different Plant Tissues

The distribution and abundance of endophytic fungi within plant tissues are influenced by tissue type, physiological conditions, and ecological interactions (Kumar & Hyde, 2004; Li et al., 2018; Sun et al., 2008). Although uneven sampling among tissues limits direct quantitative comparisons, the results provide meaningful insights into potential patterns of tissue-specific colonization and fungal richness. Among the four tissues of *Tetradium ruticarpum*, the leaf yielded the highest number of isolates (408), followed by the stem (276), root (171), and fruit (80). This tissue-dependent distribution of endophytes is consistent with observations in other medicinal plants. For instance, in *Tinospora cordifolia*, Mishra et al. (2012) reported clear tissue-specific variation in endophytic fungi, with leaves showing the highest colonization (29.4%), followed by stems (18.2%), petioles (10.1%), and roots (6.3%). A similar pattern, with the highest number of isolates recovered from leaf tissues, has also been observed in Solanum rubrum and Morinda pubescens (Jena & Tayung, 2013). These findings are consistent with previous reports, where leaves often harbor a high abundance of endophytic fungi due to their exposure to spore-rich air and relatively high nutrient content (González-Teuber et al., 2021). However, different plants exhibit distinct distribution patterns. Zheng et al. (2017) found that in *Panax notoginseng*, endophytic fungal richness was lowest in leaves (12 isolates), while higher numbers were recovered from stems (16), seeds (19), and especially roots (42). In *Dendrobium loddigesii,* a greater number of endophytes were isolated from the roots compared to the stems and leaves (Chen et al., 2010). Root-associated fungi are often shaped by complex interactions with soil microbiota and plant exudates, which may influence both fungal entry and persistence. While stem tissues are less exposed than leaves, they serve as important conduits and can support systemic colonizers (Ranathunge et al., 2012). The low fungal recovery from fruit tissues (80 strains) may be influenced by the smaller sample size in addition to several biologically inherent factors. The fruit environment appears inherently less conducive to fungal colonization, potentially due to antimicrobial metabolites, a brief developmental period, and a more resistant surface structure (Berhin et al., 2022).

Notably, species richness did not align with isolation numbers. The genera richness from high to low in different tissues were stem (43) > leaf / root (38) >fruit (18). Among these, eight genera, namely *Alternaria*, *Botryosphaeria*, *Cladosporium*, *Corynespora*, *Curvularia*, *Diaporthe*, *Colletotrichum*, and *Fusarium*, were recovered from all examined tissues of *Tetradium ruticarpum*. These genera are also commonly reported across multiple organs in diverse host plants (Arora et al., 2019; Bezerra et al., 2015; Juybari et al., 2019; Onlamun et al., 2023; Wang et al., 2017). Their widespread occurrence may result from broad tissue colonization potential and ecological versatility, and may also be facilitated by tissue-to-tissue migration, as observed in *Ageratina adenophora*, where stems act as conduits for airborne fungi to colonize roots (Fang et al., 2019). Endophytic fungal diversity and colonization density differ among plant tissues and are influenced by both the host species and its habitat (Schulz & Boyle, 2006). In our study, in addition to the shared genera and those overlapping among two or three tissues, certain genera were uniquely recovered from individual tissues, with 18 from stems, 17 from roots, 16 from leaves, and 2 from fruits. The preferential colonization of fungal endophytes in specific plant tissues or organs can be attributed to their capacity to exploit tissue-specific substrates for nutrition and the selective pressures imposed by the host environment (Liao et al., 2025; Sun et al., 2018; Wu et al., 2013). Therefore, further studies with more balanced and extensive sampling are needed to confirm these tissue-specific associations and better understand the ecological roles of endophytic fungi in *T. ruticarpum*.

4.2.3 Analysis of Endophytic Fungal Communities of *Tetradium ruticarpum* Across Four Provinces

In this study, A total of 935 endophytic fungal isolates were obtained from *Tetradium ruticarpum* samples collected from four provinces in China: Jiangxi, Hunan, Anhui, and Guangxi. Sampling was primarily concentrated in Jiangxi, the Daodi (authentic) production area of *T. ruticarpum*, with additional collections from the cultivating production areas of Hunan, Anhui, and Guangxi (Hao et al., 2025). Consequently, Jiangxi yielded the highest number of isolates (744 isolates) as well as the greatest genus-level diversity, encompassing 63 genera. The other cultivating production areas showed lower isolation numbers and genus diversity. Hunan yielded 73 isolates representing 27 genera, while Anhui produced 63 isolates representing 27 genera, and Guangxi yielded 55 isolates representing 19 genera. Among them, several genera were shared by multiple provinces, with six genera (*Clonostachys, Botryosphaeria*, *Alternaria*, *Fusarium*, *Colletotrichum,* and *Diaporthe*) common to all four provinces (Figure 3.19).

“Daodi medicinal material” refers to medicinal products cultivated and processed in specific geographic regions with designated natural conditions and ecological environments, and is recognized for its high quality (Zhao et al., 2012). As the Daodi production area of *Tetradium ruticarpum*, Jiangxi yielded more isolates and higher fungal richness. This may be attributed not only to more sampling sites but also to the natural and geographical advantages of Jiangxi as a Daodi region. This link between Daodi regions and enriched endophytic fungi is not unique, and similar patterns exist in other Daodi medicinal plants. For example, in *Paeonia ostii* ‘Feng Dan’ (a Daodi peony cultivar), the endophytic fungal community exhibited the highest richness and diversity among examined cultivars, with higher detection rates of PKS and NRPS genes (key for bioactive metabolite synthesis), suggesting that endophytic fungal diversity contributes to the quality and characteristic properties of Daodi products

(Yang et al., 2018a). Similarly, in Daodi *Dendrobium officinale*, mycorrhizal fungi like Ceratobasidiaceae were significantly enriched and positively correlated with polysaccharide content, while Serendipitaceae fungi correlated with flavonoid levels; experimental inoculation with Serendipita WX-7 further confirmed that such fungi stimulate bioactive compound accumulation, highlighting the role of endophytic and mycorrhizal communities in enhancing Daodi medicinal material quality (Zhou et al., 2025).

However, the three non-Daodi cultivation provinces also exhibited distinct assemblages of unique endophytic fungal genera, with genus-level exclusivity varying among regions, where five genera were unique to Hunan, thirteen to Anhui, and two to Guangxi. This phenomenon underscores that climatic, ecological, and geographical factors in different cultivation areas play pivotal roles in shaping region-specific assemblages of endophytic fungi, which are closely associated with *Tetradium ruticarpum*'s adaptation and growth under local environmental conditions.

4.3 Discovery of Novel Taxa and Their Taxonomic Significance

In this study, fungal endophytes isolated from *Tetradium ruticarpum* (Rutaceae) were found to belong to Ascomycota, Basidiomycota, and Mucoromycota. Consistent with most previous studies on endophytic fungi, the majority of the isolates were affiliated with Ascomycota (Arora et al., 2019; Noriler et al., 2018; Onlamun et al., 2023; Zhao et al., 2020). Several isolates showed low ITS sequence similarity (<97%) to known species and formed distinct clades in phylogenetic analyses, indicating they may represent novel species or even previously unrecognized genera. Their unique morphological features, together with molecular data, provided additional support for their classification as new taxa.

Endophytic fungi are an important source of novel fungal species (Liu et al., 2025a; Rajamanikyam et al., 2017; Tibpromma et al., 2018). During the comprehensive investigation of endophytic fungi associated with *T. ruticarpum*, several putative novel taxa were identified based on a combination of morphological characteristics and robust multi-locus phylogenetic analyses. This includes 12 novel species (*Zasmidium* *guangxiensis, Tetradiomyces jiangxiensis, Pseudokeissleriella tetradii, Cyphellophora guangxiensis, Fusarium jiangxiensis, Diaporthe jiangxiensis, Diaporthe hunanensis, Diaporthe tetradii, Amphisphaeria tetradiana, Amphisphaeria chenzhouensis, Funiliomyces jiangxiensis, Nemania jiangxiensis*), 1 novel family (Funiliomycetaceae), 1 novel genus (*Tetradiomyces*), and 3 newly host recorded species (*Coryneum castaneicola*, *Nigrograna jinghongensis* and *Exophiala pisciphila*), contributing significantly to the fungal taxonomy of endophytic communities from medicinal plants *Tetradium ruticarpum*.

In traditional mycological research, endophytic fungi were primarily identified based on morphological traits (Gopi & Jayaprakashvel, 2019). However, ascomycetes often possess only a limited set of diagnostic characters and frequently exhibit homoplasy, making accurate species-level identification challenging, and thus the introduction of molecular identification is necessary (Guo et al., 2003). Previous studies have shown that many endophytic fungi do not produce spores, making it difficult to identify their characteristics morphologically (Lin er al., 2007; Liu et al., 2025a; Tejesvi et al., 2011; Tibpromma et al., 2018). Therefore, inducing sporulation is a major challenge in the identification of endophytic fungi (Liao et al., 2025). In this study, several isolates failed to produce spores, but were nevertheless described as new record or species based on clear genetic distinctions revealed through DNA sequence comparisons and multi-gene phylogenetic analyses, such as *Tetradiomyces jiangxiensis, Nemania jiangxiensis,* and *Amphisphaeria chenzhouensis.* Their taxonomic placement was achieved solely through multilocus phylogenetic inference, underscoring the growing importance of DNA sequence data in delimiting cryptic and morphologically uninformative taxa. *Tetradiomyces jiangxiensis* further represents a novel lineage within its order, justifying the proposal of *Tetradiomyces* as a new genus. Similarly, several recently described endophytic fungi, such as *Batnamyces globulariicola*, *Cyanodermella asteris*, *Lophiostoma jeollanense*, *Poaceascoma endophyticum, P. koreanum, P. magnum and P. zoysiiradicicola,* were also reported to lack sporulation (Jahn et al., 2017; Liu et al., 2025a; Noumeur et al., 2020).

In addition, we also reported several new species, including *Fusarium jiangxiensis* and *Cyphellophora guangxiensis*, which belong to two ecologically and clinically important genera. *Fusarium* comprises numerous phytopathogenic and mycotoxigenic species (Hyde et al., 2020, 2023; Kvas et al., 2009; Proctor et al., 2013), whereas *Cyphellophora* includes dark septate endophytic (DSE) fungi that occasionally act as opportunistic pathogens (Gao et al., 2015; Grabowski, 2007; Zhuang et al., 2010). The occurrence of these taxa in healthy plant tissues provides new insights and raises questions regarding their ecological roles, whether mutualistic, latent pathogenic, or neutral.

Zasmidium guangxiensis and *Pseudokeissleriella tetradii* expand two genera typically associated with leaf spots or saprobic lifestyles (Thapboualy et al., 2020; Yang et al., 2022b). Their isolation from asymptomatic tissues of *T. ruticarpum* implies potential endophytic adaptation or broader ecological plasticity. Notably, *Pseudokeissleriella tetradii* is the second species in this genus, represents a rare record of this genus from a medicinal host.

The genus *Diaporthe* (Diaporthaceae, Diaporthales) represents a globally distributed group of fungi with diverse ecological strategies, functioning as plant pathogens, endophytes, and saprobes (Dissanayake et al., 2024). In this study, we describe three novel species, *D. jiangxiensis*, *D. hunanensis*, and *D. tetradii* isolated as endophytes from asymptomatic tissues of *Tetradium ruticarpum*. These discoveries not only expand the documented host range of *Diaporthe* but also underscore the genus' significant yet understudied role as a component of endophytic fungal communities in medicinal plants.

This study revealed significant xylariomycetous diversity, with two novel *Amphisphaeria* species (*A. tetradiana* and *A. chenzhouensis*) representing the first reports of this genus from *T. ruticarpum*. Interestingly, we discovered another distinct new species, *Funiliomyces jiangxiensis*, which clusters together with ten species previously assigned to *Dactylaria* as well as *Funiliomyces biseptatu*s, forming a well-supported and independent clade. Based on both phylogenetic analyses and morphological characteristics, we established a new family to accommodate this lineage and recombined ten species, namely *Fun. acaciae*, *Fun. biseptatus*, *Fun. calliandrae*, *Fun. fragilis*, *Fun. hwasunensis*, *Fun. mavisleverae, Fun. monticola*, *Fun. retrophylli*, *Fun. sparsus*, and *Fun. zapatensis*. Additionally, *Nemania jiangxiensis* was described, expanding this traditionally wood-inhabiting genus into the endophytic niche of *T. ruticarpum*. Together, these findings demonstrate the ecological flexibility of

Xylariomycetous fungi, revealing their ability to colonize living plant tissues while maintaining characteristic morphological features of their respective genera (Wang et al., 2023b).

In addition to the novel taxa, three species were identified as new records for *T. ruticarpum*: *Exophiala pisciphila*, a melanized fungus known for metal tolerance and potential biotechnological applications; *Nigrograna jinghongensis*, previously reported only from specific regions in Yunnan; and *Coryneum castaneicola*, previously found on *Castanea* species in the USA and China, and here newly recorded as an endophyte from healthy stems of *T. ruticarpum* in Jiangxi Province. These records broaden the known biogeographic range of the respective taxa and support the notion that tropical and subtropical regions of China represent underdocumented fungal diversity hotspots.

Overall, these taxonomic discoveries highlight the importance of endophytes from *T. ruticarpum* and show that even non-sporulating isolates, which are often overlooked in traditional taxonomy, could represent new evolutionary lineages. The findings emphasize the importance of ongoing integrative taxonomic approaches, especially those incorporating DNA-based phylogenetics, to reveal the hidden diversity and ecological roles of endophytic fungi in medicinal plants.

4.4 Preliminary Screening of Antimicrobial Activities: Potential and Limitations

4.4.1 Overview of Antimicrobial Activities of Endophytic Fungi

Endophytic fungi associated with medicinal plants are increasingly recognized as a reservoir of bioactive secondary metabolites with potential for antimicrobial applications, driven by their long-term co-evolution with host plants and adaptation to complex ecological niches (Jha et al., 2023; Salehi & Safaie, 2024). Up to now, among the limited studies on endophytic fungi associated with *Tetradium ruticarpum*, only one has investigated their antagonistic activity. In that study, the endophytic fungus *Cyanodermella* sp. exhibited varying degrees of antagonistic effects against nine fungal and three bacterial plant pathogens (Ho et al., 2012). The overall antibacterial potential of *T. ruticarpum* endophytic fungi remains largely unexplored. In this study, 35 endophytic fungal strains exhibiting antimicrobial activity, belonging to 12 genera, including *Albifimbria*, *Botryosphaeria*, *Clonostachys*, *Curvularia*, *Diaporthe*, *Epicoccum*, *Fusarium*, *Neosetophoma* ,*Stephanonectria*, *Penicillifer*, *Pestalotiopsis*, and *Pochonia*, were isolated from *T. ruticarpum* (Table 3.12). Endophytes from these genera are well documented for their strong antibacterial activity and, in some cases, for producing the same secondary metabolites as their host plants. For example, *Fusarium* sp. PN8, isolated from *Panax notoginseng*, was found to produce triterpenoid saponins such as ginsenosides Rb1, Rd, and 20(S)-Rg3, which are also present in its host plant. These metabolites exhibited significant antimicrobial activity against several pathogens (Jin et al., 2017). Similarly, *Epicoccum nigrum* from *Hypericum perforatum* produced the same secondary metabolite hypericin as its host, along with emodin, and exhibited strong antibacterial effects (Vigneshwari et al., 2019). However, notable variation was observed in the spectrum and potency of bioactivity among strains and target pathogens, consistent with previous reports that endophytic antimicrobial potential is often strain- and pathogen-specific (Zhang et al., 2022).

4.4.1.1 Antibacterial activity against *Escherichia coli*

For the Gram-negative bacterium *Escherichia coli*, only two *Epicoccum* isolates from *T. ruticarpum* showed inhibitory effects, with inhibition zones of 14.0 mm and 19.0 mm respectively. These values are still considerably lower than that of the positive control ciprofloxacin (63.2 mm) (Table 3.12). These results again underscore the modest antibacterial potency of the tested isolates, but *Epicoccum* spp. have been previously reported to produce polyketide and peptide secondary metabolites with antibacterial properties (Deshmukh et al., 2022), indicating their potential for further chemical investigation. Notably, the root-derived *Epicoccum* isolate exhibited stronger activity than non-root counterparts, hinting at differences in metabolite diversity between plant compartments; this pattern has also been noted in the endophytes of *Artemisia annua* (Alhadrami et al., 2021) and further suggests that tissue-specific sampling may optimize the discovery of active strains.

4.4.1.2 Antibacterial activity against *Xanthomonas campestris*

Xanthomonas campestris, the causal agent of black rot, poses a major threat to the production and quality of Brassicaceae vegetables worldwide. Current management strategies include physical methods such as hot water seed treatment, chemical control using copper-based bactericides, and biological approaches involving antagonistic microbes and plant extracts (Liu et al., 2022b). However, concerns about chemical resistance and environmental safety have driven the search for eco-friendly alternatives. In this study, strains exhibiting strong inhibition against *X. campestris*, including *Epicoccum* sp. 3 (32.7 mm), *Epicoccum* sp. 2 (27.0 mm), and *Epicoccum* sp. 1 (23.0 mm) (Table 3.12), demonstrated substantial inhibition zones that are close to the efficacy of standard bactericides. This significant antibacterial activity highlights the promising potential of these endophytic fungi as biocontrol agents. Supporting this view, previous research has shown that *Epicoccum nigrum* strains possess considerable antimicrobial properties. For example, *Epicoccum nigrum* P16, isolated from sugarcane, was reported by Fávaro et al. (2012) to produce antifungal metabolites and to stimulate root growth, indicating beneficial effects beyond pathogen suppression. Likewise, *Epicoccum nigrum* M13, isolated from seagrass, produced compounds that exhibited notable antibacterial activity against Gram-positive bacteria, with minimum inhibitory concentrations ranging from 2.5 to 20 micrograms per milliliter (Qader et al., 2021). Taken together, these findings reinforce the agricultural potential of Epicoccum species, especially for controlling *X. campestris*, a pathogen that severely impacts crop yields worldwide. Utilizing such endophytic fungi in sustainable crop protection could provide environmentally friendly alternatives to chemical bactericides.

4.4.1.3 Antibacterial activity against *Staphylococcus aureus*

Against the clinically relevant Gram-positive bacterium *Staphylococcus aureus*, only five isolates from *T. ruticarpum* endophytes (affiliated with *Clonostachys*, *Pestalotiopsis*, *Penicillifer*, *Pochonia*, and *Stephanonectria*) exhibited inhibitory activity, with inhibition zones ranging from 10.0 to 14.0 mm, significantly smaller than that of the positive control penicillin (42.0 mm) (Table 3.12). The weak inhibitory effects observed in a few isolates suggest that only a small fraction of endophytic fungi isolated from *T. ruticarpum* possess antibacterial activity against *S. aureus*. In this study, many of the antimicrobial strains, including *Clonostachys* sp., *Pestalotiopsis* sp., *Penicillifer* sp., *Pochonia* sp., and *Stephanonectria* sp., have been reported to exhibit antimicrobial activity, such as *Clonostachys* sp. which has shown activity against *S. aureus*. *Clonostachys rosea*, a widely distributed endophytic fungus with proven biocontrol abilities, has also demonstrated inhibitory activity against *S. aureus*, highlighting its potential as a source of antibacterial agents (Gowrisri & Elango, 2024). Chowdhury et al. (2023) reported that *Pestalotiopsis microspora* (P31), isolated from *Dillenia pentagyna* bark, exhibited significant antimicrobial activity against methicillin-resistant *Staphylococcus aureus* (MRSA), with an MIC of 32 µg/ml. *Stephanonectria* species, especially endophytic strains like *Stephanonectria* PSU-ES172, have demonstrated notable antimicrobial activity, including strong inhibition of *S. aureus* (Supaphon et al., 2013).

4.4.1.4 Antifungal activity against *Aspergillus niger*

Twenty-five endophytic fungal strains of *Tetradium ruticarpum* exhibited antifungal activity against the opportunistic fungus *Aspergillus niger* (Table 3.12). Among them, *Fusarium* strains exhibited strong antifungal activity, with inhibition zones up to 26.7 mm, approaching the positive control Nystatin (30 mm). *Fusarium* species are well-documented producers of antifungal compounds, including enniatins and fusaric acid, supporting the strong activities observed here (Al-Hatmi et al, 2016). *Diaporthe* exhibited moderate antimicrobial activity, consistent with previous reports of *Diaporthe* endophytes isolated from *Mahonia fortunei* (Li et al., 2015). Similarly, *Albifimbria* also exhibited moderate antimicrobial activity. Previous studies have reported that *A. verrucaria* isolate SYE-1 displayed broad-spectrum antifungal effects against *Botrytis cinerea*, *Lasiodiplodia theobromae*, and *Elsinoë ampelina* on grapevine (Li et al., 2020c). Moreover, the principal antifungal compound produced by *A. verrucaria* has been identified as verrucarin A (Gao et al., 2025). A leaf-derived endophytic strain, *Curvularia* sp. 5, from *T. ruticarpum* inhibited *Aspergillus niger* with an inhibition zone of 12.7 ± 2.9 mm, consistent with the known antimicrobial potential of the *Curvularia* genus. Species of *Curvularia* (e.g., *C. lunata*) exhibit broad-spectrum activity against a range of microorganisms, including *Bacillus subtilis*, *Escherichia coli, Saccharomyces cerevisiae*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Aspergillus niger*, and *Candida albicans* (Khiralla et al., 2019, Chukwuemerie et al., 2022). Moreover, crude extracts of *C. lunata* isolated from *Elaeis guineensis* have also demonstrated antimicrobial effects (Nwobodo et al., 2022), further supporting the inherent bioactive potential of this genus. Additionally, six *Clonostachys* sp. 3 strains (ITS comparison suggesting *C. rosea*) isolated from roots in this study exhibited varying degrees of antifungal activity against Aspergillus niger. In contrast, *C. rosea* was previously reported to show no apparent mutual inhibition with *A. niger* under co-culture conditions, where both fungi increased in biomass and metabolic diversity over time (Chatterjee et al., 2016). This discrepancy may result from differences in experimental conditions, as our agar plug assays reflect direct antagonism, whereas co-culture studies emphasize metabolic interactions in shared environments. In this study, a fruit-derived isolate identified as *Neosetophoma* sp. 1 exhibited inhibitory activity against *A. niger* (11.7 ± 0.2 mm). Notably, a strain of this genus, *Neosetophoma samarorum* isolated from sea foam, has been reported to produce metabolites (epolones A and B, pycnidione, coniothyrione) with inhibitory activity against multiple microbial pathogens (Overy et al., 2014). This suggests *Neosetophoma* species, regardless of endophytic or sea foam origin, may share the ability to produce antimicrobial bioactive metabolites. Moreover, in the antifungal assays against *Aspergillus niger*, different strains of the same species (e.g., *Clonostachys* sp. 3) exhibited varying inhibitory effects.The broad range of activity observed suggests substantial inter-strain variability in secondary metabolite biosynthesis, even within the same genus, a well-documented phenomenon in fungal natural product research (Keller, 2019).

4.4.1.5 Antifungal activity against *Candida albicans*

Candida albicans is a clinically important yeast pathogen responsible for opportunistic infections such as candidiasis (Kabir et al., 2012). In the present study, only one endophytic isolate from *Tetradium ruticarpum*, identified as *Botryosphaeria* sp., exhibited antifungal activity against *C. albicans*. This isolate produced a weak inhibition zone of 8.0 mm, which is markedly smaller than that of the positive control Nystatin (21 mm). Endophytic fungi have been shown to exhibit potent anti-*Candida* activity (Weber et al., 2007). For example, Li et al. (2022a) reviewed several endophytic fungi, including *Biatriospora* sp., *Drechmeria* sp., *Phoma* sp., *Stachybotrys chartarum*, and *Xylaria* sp., which exhibited antagonistic activity against *Candida albicans*. In addition, an endophytic *Fusarium* sp. (CR377) isolated from *Selaginella pallescens*, collected in the Guanacaste Conservation Area of Costa Rica, was reported to exhibit potent antifungal activity (Brady & Clardy, 2000). However, in the present study, none of the *Fusarium* endophytes obtained from *T. ruticarpum* exhibited inhibitory effects against *C. albicans*, and only one endophytic strain showed relatively weak antifungal activity. This may be partly due to the limitation of the agar plug diffusion method used, which primarily detects diffusible metabolites. Some endophytes may produce antifungal compounds that are poorly diffusible in agar or require specific induction conditions for biosynthesis, leading to underestimation of their antifungal potential (Yousef et al., 1978, Brakhage, 2013). It has been reported that the endophytic fungus *Clonostachys rosea* B5-2, isolated from mangrove plants, was cultured on solid rice media supplemented with apple juice, which significantly altered its secondary metabolism and induced the production of four previously unreported compounds (Supratman et al., 2021). Therefore, modifying the composition of culture media could be explored as a strategy to enhance the secondary metabolism of endophytic fungi and potentially increase their antimicrobial activity.

4.4.1.6 Antimicrobial potential, chemical investigation, and future applications

As discussed above, genera such as *Fusarium* and *Epicoccum*, which exhibited strong inhibition against *Aspergillus niger* and *Xanthomonas campestris*, respectively, are known producers of diverse secondary metabolites, including polyketides, peptides, and terpenoids (Amuzu et al., 2024; Elkhateeb & Daba, 2019; Toghueo, 2019). For example, *Fusarium lateritium* HU0053, an endophytic strain isolated from corn culture, produces cyclic lipopeptides acuminatums A–F with notable antifungal activity (Zhong et al., 2023). *Epicoccum* sp. CAFTBO from Theobroma cacao produces epicolactone and epicoccolides A and B, potent antifungal polyketides (Talontsi et al., 2013). These results suggest that similar biosynthetic pathways may be active in *T. ruticarpum* strains, meriting further chemical characterization. Meanwhile, considerable variation in antimicrobial activity among isolates within the same genus suggests significant metabolic diversity shaped by ecological and host-related factors (Alhadrami et al., 2021; Liu et al., 2023). Additionally, the presence of both widely studied genera (*Pestalotiopsis*, *Clonostachys*) and less commonly reported genera (*Stephanonectria*, *Penicillifer*) in *T. ruticarpum* points to unique biosynthetic capacities, offering opportunities for discovery of novel compounds. Moreover, these endophytes hold great promise for applications in sustainable agriculture as biocontrol agents against phytopathogens like *Xanthomonas campestris*, potentially reducing reliance on chemical pesticides. Some isolates with activity against clinically relevant pathogens (*Staphylococcus* aureu*s*, *Candida albicans*) may serve as leads for pharmaceutical development, pending further optimization and toxicity evaluation. In summary, *T. ruticarpum* endophytes represent a valuable reservoir of bioactive compounds with potential applications in crop protection and drug discovery, emphasizing the need for continued multidisciplinary research to harness their full potential.

As we know, the observed antimicrobial activities among endophytic fungi from *Tetradium ruticarpum* highlight their potential as promising sources of novel bioactive compounds. Early research by Zhu (2007) isolated an endophytic fungus (*Sclerotium* sp.) from *T. ruticarpum* and identified 44 chemical compounds from this strain. Notably, the metabolites isolated from this endophyte differed from those found in the host plant, suggesting distinct biosynthetic pathways between the fungus and its host. In contrast, subsequent studies by Cao et al. (2011) and Li et al. (2011) reported endophytes capable of producing alkaloid-like secondary metabolites similar to those of their host, indicating possible metabolic convergence or horizontal transfer of biosynthetic traits. The occurrence of secondary metabolites in endophytes from *T. ruticarpum* that are similar to those of the host plant likely reflects a co-evolutionary adaptation. Similar phenomena have been observed in other medicinal plants. For instance, the endophytic fungi associated with *Taxus* species can biosynthesize taxol, a potent anticancer compound originally isolated from the host plant (Stierle et al., 1993; Strobel et al., 1996). It is evident that during long-term cohabitation with host plants, endophytic fungi may be influenced by various biotic and environmental factors, thereby producing secondary metabolites that are either identical to or distinct from those of the host. Additionally, it has been reported that between 2021 and 2024, a total of 132 antibacterial metabolites were produced by endophytic fungi, with medicinal plants serving as their predominant hosts (Ortega et al., 2025). Therefore, the observed antimicrobial properties, along with the extensive diversity of fungal isolates obtained, lay a solid groundwork for elucidating the secondary metabolites driving these bioactivities and assessing their prospective applications.

4.4.2 Interplay of Host and Endophyte Metabolites in Modulating Endophytic Antimicrobial Activity

4.4.2.1 Host metabolic niche: the foundation of endophytic antimicrobial potential

Medicinal plants, as “gold mines” of bioactive secondary metabolites (Kumari et al., 2023), synthesize such metabolites that mainly fall into major categories including phenolics, terpenes, and nitrogen-containing compounds, with specific examples being tannins, alkaloids, volatile oils, and terpenoids (McMurry, 2015). Although these substances do not directly participate in the primary growth and development of plants, they play crucial roles in plants' adaptation to the environment, such as resisting pathogen invasion, attracting pollinators, and transmitting chemical signals. The secondary metabolites of medicinal plants exhibit extensive pharmacological and therapeutic potential, possessing various activities like antimicrobial, anticancer, antioxidant, antiviral, and anti-inflammatory properties (Shafi &Zahoor, 2021). Notably, widely used drugs such as paclitaxel, artemisinin, and vinblastine are derived from medicinal plants and have significantly contributed to the treatment of diseases like cancer and malaria.

The fruit of *Tetradium ruticarpum* is rich in alkaloids (63% of 168 identified constituents), terpenoids, phenolic acids, and flavonoids (Li & Wang, 2020; Xin et al., 2022), creating a distinctive chemical microenvironment. The synthesis of these secondary metabolites is widely recognized as an adaptive response to environmental pressures (Hartmann, 2007). For example, rice plants increase the production of phytoalexins such as sakuranetin in response to pathogen infection and herbivore attack, providing antimicrobial and deterrent effects (Kodama et al., 1992). Meanwhile, abiotic stresses like ultraviolet radiation and drought also induce accumulation of flavonoids and terpenoids, which help mitigate oxidative damage and maintain cellular homeostasis (Agati et al., 2012; Choudhury et al., 2017). In *T. ruticarpum,* abundant indole and quinoline alkaloids likely reflect long-term evolutionary pressures from microbial pathogens and herbivores, serving both direct inhibitory roles and signaling functions to modulate host defense.

The bioactive compounds from *T. ruticarpum* fruit demonstrate diverse therapeutic effects including antitumor, cardiovascular protection, central nervous system regulation, anti-inflammatory, antimicrobial, antioxidant, anti-obesity, and anti-diarrheal activities (Li & Wang, 2020; Shan et al., 2020; Xiao et al., 2023a; Zhao et al., 2019). Some components also have potential for drug interactions and hepatotoxicity (Cai et al., 2014; Singh & Zhao, 2017), and crude extracts exhibit insecticidal and repellent properties (Cao et al., 2018; Fang et al., 2019; Yu et al., 2000).

Together, these multifaceted roles of host secondary metabolites generate a complex chemical environment that shapes the colonization, survival, and metabolic expression of endophytic fungi. A thorough understanding of this chemical milieu is foundational for exploring how endophytes modulate their secondary metabolite profiles in response to host and pathogen-derived signals.

4.4.2.2 Endophytic metabolites: targeted responses to host and pathogen signals

Endophytic fungi associated with *Tetradium ruticarpum* have been sporadically studied. Early research by Zhu (2007) isolated an endophytic fungus (*Sclerotium* sp.) from *T. ruticarpum* and identified 44 chemical compounds from this strain. Notably, the metabolites isolated from this endophyte differed from those found in the host plant, suggesting distinct biosynthetic pathways between the fungus and its host. In contrast, subsequent studies by Cao et al. (2011) and Li et al. (2011) reported endophytes capable of producing alkaloid-like secondary metabolites similar to those of their host, indicating possible metabolic convergence or horizontal transfer of biosynthetic traits. The occurrence of secondary metabolites in endophytes from *T. ruticarpum* that are similar to those of the host plant likely reflects a co-evolutionary adaptation. Similar phenomena have been observed in other medicinal plants. For instance, the endophytic fungi associated with *Taxus* species can biosynthesize taxol, a potent anticancer compound originally isolated from the host plant (Stierle et al., 1993; Strobel et al., 1996). It is evident that during long-term cohabitation with host plants, endophytic fungi may be influenced by various biotic and environmental factors, thereby producing secondary metabolites that are either identical to or distinct from those of the host.

In addition, the endophytic fungus *Cyanodermella* sp., isolated from *T. ruticarpum*, has been demonstrated to exhibit significant antagonistic effects against multiple plant pathogens (Ho et al., 2012). In this study, 35 endophytic fungal strains exhibiting antimicrobial activity were isolated from *T. ruticarpum*, representing 12 genera including *Epicoccum*, *Fusarium*, *Clonostachys*, *Diaporthe*, and others. Endophytes from these genera are well documented for their strong antibacterial activity and, in some cases, for producing the same secondary metabolites as their host plants. For example, *Fusarium* sp. PN8, isolated from Panax notoginseng, was found to produce triterpenoid saponins such as ginsenosides Rb1, Rd, and 20(S)-Rg3, which are also present in its host plant. These metabolites exhibited significant antimicrobial activity against several pathogens (Jin et al., 2017). Similarly, *Epicoccum nigrum* from *Hypericum perforatum* produced the same secondary metabolite hypericin as its host, along with emodin, and exhibited strong antibacterial effects (Vigneshwari et al., 2019). The ability of endophytes to produce bioactive compounds originally derived from the plant likely stems from the complex interactions between endophytic fungi and their host plants. The relationship between an endophyte and its host plant is a complex, evolving interaction shaped by specific adaptations from both organisms and varies depending on the species involved (Verma et al., 2012).

Endophytes can indirectly protect plants by producing bioactive compounds that suppress disease-causing microbes, with these metabolites considered the key factor in this defense process (Omomowo et al., 2023). *Choiromyces aboriginum* isolated from *Phragmites australis* combats soilborne plant pathogens by producing high levels of cell wall-degrading enzymes, enabling effective mycoparasitism (Cao et al., 2009). The endophytic fungal strain *Epicoccum nigrum* ASU11 (Epi) helps control potato blackleg caused by *Pectobacterium carotovora* subsp. *atrosepticum* PHY7 (Pca) by enhancing host antioxidant defenses and reducing disease severity (Khalil Bagy et al., 2019). Additional studies have shown that *Xylaria* has been reported to produce griseofulvin, an antimicrobial compound effective against plant pathogens (Reshma et al., 2019). Similarly, the antibacterial strains screened from endophytic fungi of *T. ruticarpum* are likely to produce secondary metabolites that inhibit pathogens.

This symbiotic relationship enriches secondary metabolite diversity and underscores the complexity of plant–endophyte interactions. Endophytic secondary metabolism is not static but is fine-tuned by both host and pathogen signals, enabling fungi to produce a repertoire of bioactive compounds tailored for symbiotic compatibility and defense. Future studies employing integrated metabolomics, transcriptomics, and functional assays are essential to unravel regulatory mechanisms and exploit endophytic fungi for drug discovery and sustainable agriculture.

4.4.3 Limitations and Future Perspectives

This study provides valuable insights into the antimicrobial properties of endophytic fungi from *Tetradium ruticarpum*, yet several methodological limitations should be acknowledged. The agar plug assay, while efficient for preliminary screening, may underestimate antimicrobial activity due to limited metabolite diffusion and potential interactions with the growth medium (Balouiri et al., 2016). Furthermore, the panel of test microorganisms, though including representative bacterial and fungal pathogens, did not encompass clinically important resistant strains such as extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae* or vancomycin-resistant *Enterococcus* (Angelini, 2024; Bharadwaj et al., 2022). These factors may restrict the broader applicability and clinical relevance of the results.

To address these limitations, future studies should adopt a more comprehensive and integrative approach. Bioassay-guided fractionation combined with advanced analytical techniques such as UHPLC-QTOF-MS and two-dimensional NMR would facilitate detailed chemical characterization of bioactive metabolites. Genomic analyses employing tools like antiSMASH could uncover novel biosynthetic gene clusters, while transcriptomic investigations may elucidate regulatory pathways governing metabolite production (Blin et al., 2013). Expanding antimicrobial screening to include recent clinical isolates, particularly multidrug-resistant strains, alongside the application of advanced infection models such as three-dimensional organoid systems, would enhance the clinical relevance of findings. Collectively, these strategies will help overcome current constraints and accelerate the discovery and development of endophytic fungi as sustainable sources of novel antimicrobial agents.

CHAPTER 5

CONCLUSIONS

5.1 Overall Conclusions

This study systematically investigated the endophytic fungal community of the traditional medicinal plant *Tetradium ruticarpum*, revealing its rich species diversity, ecological distribution characteristics, and potential bioactivities. The findings provide important theoretical foundations and practical references for research on plant-microbe interactions and natural product development. The main conclusions are as follows:

5.1.1 Diversity and Community Structure of Endophytic Fungi Associated with *Tetradium ruticarpum*

Through extensive sampling across tissues, geographic regions, and culture media, a total of 935 fungal isolates were obtained, which belong to three phyla, six classes, 21 orders, 54 families, and 84 genera. Three phyla were observed in the endophytic fungal community of *T. ruticarpum*, namely Ascomycota, Basidiomycota, and Mucoromycota. Ascomycota was dominant (99.5%), with Sordariomycetes (61.9%) and Dothideomycetes (35.4%) being the most abundant classes. At the family level, the five most abundant families were Diaporthaceae (251 isolates, 26.8%), Nectriaceae (111 isolates, 11.9%), Didymellaceae (99 isolates, 10.6%), Glomerellaceae (93 isolates, 9.9%), and Pleosporaceae (70 isolates, 7.5%), collectively accounting for 66.7% of all isolates. At the genus level, *Diaporthe* was the most dominant genus in the endophytic fungal community of *T. ruticarpum*, representing 26.8% of all isolates. Other relatively common genera included *Colletotrichum* (9.9%), *Fusarium* (9.2%), and *Alternaria* (6.1%), whereas the majority of genera (>60%) were rare, displaying a typical “dominant-rare” distribution pattern. Among these genera, 82 were recorded for the first time from *T. ruticarpum*, except for *Hypoxylon* and *Nigrospora*.

5.1.2 Effects of Culture Media, Plant Tissues, and Provinces on Fungal Communities Associated with *Tetradium ruticarpum*

Six different media (PDA, RBA, PCA, MEA, YpSs, and OA) were evaluated to improve the isolation efficiency of endophytic fungi from *Tetradium ruticarpum*. Overall, the isolation success and diversity varied considerably among media. PDA yielded the highest number of isolates and the broadest taxonomic diversity, while RBA also supported a wide range of taxa. Nine genera, including *Alternaria*, *Botryosphaeria*, *Corynespora*, *Epicoccum*, *Neodidymella*, *Clonostachys*, *Colletotrichum*, *Diaporthe*, and *Fusarium*, were consistently recovered from all media, suggesting their adaptability to diverse culture conditions. In contrast, several genera showed clear medium preferences, with PDA containing the largest number of unique genera. These results indicate that the use of multiple media substantially enhances the recovery and diversity representation of endophytic fungi from *T. ruticarpum*.

Four different plant tissues of *T. ruticarpum*, including roots, stems, leaves and fruits, were used to isolate endophytic fungi. Leaves yielded the highest number of isolates (408) and fruits the lowest (80), out of a total of 935 isolates. In terms of genus richness, stems contained the greatest diversity (43 genera), followed by leaves and roots (38 each) and fruits (18). Several genera were recovered from multiple tissues, while many were restricted to a single tissue. Eight genera, including *Botryosphaeria*, *Cladosporium*, *Corynespora*, *Alternaria*, *Curvularia*, *Diaporthe*, *Colletotrichum*, and *Fusarium*, were consistently recovered from all four tissues. These results indicate that tissue type strongly influences the composition of endophytic fungal communities, and that leaves, despite having the highest number of isolates, do not have the highest genus richness, which is observed in stems.

Four provinces in China, namely Jiangxi, Hunan, Anhui, and Guangxi, were surveyed for endophytic fungi associated with *T. ruticarpum*. Jiangxi, the Daodi (authentic) production area, yielded the highest number of isolates (744) and the greatest genus-level diversity (63 genera). The other provinces yielded fewer isolates and lower genus richness, with Hunan contributing 73 isolates across 27 genera, Anhui 63 isolates across 27 genera, and Guangxi 55 isolates across 19 genera. However, because sampling was heavily concentrated in Jiangxi, the lower diversity observed in other provinces may partly reflect limited sampling rather than true absence.

Additionally, several genera were shared by multiple provinces, with six genera (*Clonostachys*, *Botryosphaeria*, *Alternaria*, *Fusarium*, *Colletotrichum*, and *Diaporthe*) common to all four provinces, while others were unique to specific provinces, including five genera in Hunan, thirteen in Anhui, and two in Guangxi. These results suggest that geographic location, local ecological conditions, and the Daodi status partially reflect the composition, richness, and diversity of endophytic fungal communities in *T. ruticarpum*.

5.1.3 Discovery of Novel Taxa and Taxonomic Implications

This study significantly advanced our understanding of fungal diversity in *Tetradium ruticarpum* through the discovery of 12 novel species (e.g., *Diaporthe jiangxiensis*, *Fusarium jiangxiensis*), one new genus (*Tetradiomyces*), one new family (Funiliomycetaceae), and 3 newly recorded species for *Tetradium ruticarpum (Coryneum castaneicola, Nigrograna jinghongensis* and *Exophiala pisciphila*). Notably, several taxa (e.g., *Tetradiomyces jiangxiensis*) were sterile but delineated using multilocus phylogenetics, highlighting the critical role of molecular methods in modern fungal taxonomy. The findings also revealed important ecological adaptations, including: (1) host expansion of typically saprobic/wood-inhabiting genera (*Amphisphaeria*, *Nemania*) into endophytic niches; (2) lifestyle plasticity in clinically relevant genera (*Fusarium*, *Cyphellophora*); and (3) geographic range extensions for metal-tolerant (*Exophiala*) and previously localized taxa (*Nigrograna*).

Our findings reveal that *Tetradium ruticarpum* harbors diverse and cryptic endophytic fungi, underscoring the need for integrative taxonomy that combines morphology and phylogeny. The frequent discovery of novel taxa suggests that medicinal plants contain unique fungal communities worthy of deeper study, particularly regarding their roles in host physiology and potential biotechnological applications.

5.1.4 Antimicrobial Potential of Endophytic Fungi

This study identified 35 bioactive strains (from 12 genera) among 635 endophytic fungal isolates, demonstrating promising antimicrobial properties. Notably, *Epicoccum* spp. exhibited strong anti-phytopathogenic activity against *Xanthomonas campestris* (inhibition zone up to 32.7 mm), highlighting their potential as biocontrol agents. Against clinically relevant pathogens, *Clonostachys* spp. exhibited anti-staphylococcal activity (14.0 mm against *S. aureus*), while *Fusarium* spp. showed antifungal effects against *Aspergillus niger* (26.7 mm), an important opportunistic human pathogen and food spoilage organism. However, limited activity against *Escherichia coli* and *Candida albicans* indicates the need for further optimization through metabolomic profiling or genetic engineering to enhance bioactive compound production. These findings position *T. ruticarpum* endophytes as valuable resources for developing novel antimicrobial agents, particularly for agricultural and biomedical applications.

Overall, this study offers new insights into the diversity, ecological patterns, and bioactive potential of endophytic fungi in *Tetradium ruticarpum*. It emphasizes the need to integrate taxonomic, ecological, and functional perspectives to fully recognize their significance, both as reservoirs of microbial diversity and as sources of novel bioactive compounds.

5.2 Research Advantages

5.2.1 Comprehensive Sampling and Isolation

An advantage of this study is its comprehensive sampling strategy, covering 23 sites across four Chinese provinces and four tissue types (roots, stems, leaves, and fruits). Combined with six different isolation media, this approach enabled a broad recovery of endophytic fungi and represents the first systematic investigation of those associated with *Tetradium ruticarpum*, filling a gap in the current knowledge.

5.2.2 Discovery of Novel Taxa and Hidden Diversity

Another key advantage is the identification of several novel species and genera based on morphological and phylogenetic evidence. These findings highlight the hidden diversity of fungal lineages within *T. ruticarpum* and expand our understanding of endophyte taxonomy in this important medicinal plant.

5.2.3 Bioactive Potential for Antimicrobial Applications

A further advantage lies in the bioactivity screening, which revealed 35 isolates with antimicrobial potential. This not only provides a valuable basis for discovering novel secondary metabolites but also lays the groundwork for future biological control and antimicrobial applications.

5.3 Challenges and Perspectives

5.3.1 Uneven Sampling Limits Comprehensive Diversity Assessment

Although the present study collected *Tetradium ruticarpum* samples from 23 locations across four provinces in China, sampling was not fully balanced among tissue types and regions. For instance, fruit tissues were underrepresented due to seasonal constraints or limited availability in certain sites. This spatial and tissue-level heterogeneity restricts the ability to make robust statistical comparisons and may result in biased diversity estimates. As such, current results can only offer a preliminary view of the endophytic fungal diversity in *T. ruticarpum*, and more representative sampling is essential for conclusive ecological insights.

5.3.2 Non-sporulating Isolates Challenge Species Identification

A major taxonomic challenge encountered in this study is the identification of non-sporulating fungal isolates. Many potentially novel strains did not produce reproductive structures under standard culture conditions, hindering traditional morphological classification. While multilocus phylogenetic analyses combined with hyphal morphology were used to infer species boundaries, the lack of conidia or other diagnostic features prevents the completion of formal descriptions. This issue underscores the broader difficulty of working with sterile mycelia in endophyte research and emphasizes the need for optimized sporulation protocols.

5.3.3 Limitations of Preliminary Antimicrobial Screening

The antimicrobial activity observed in 35 fungal isolates suggests potential for therapeutic applications, but current screening remains at a preliminary level. The agar plug assay employed here, while suitable for initial detection, provides only rough estimations of bioactivity and may not reflect the full potential of secondary metabolite production. Factors such as nutrient composition, culture duration, and incubation conditions can significantly influence metabolite expression. Furthermore, without metabolite extraction or chemical profiling, the specific compounds responsible for the observed activity remain unidentified, limiting further pharmacological evaluation.

5.4 Future Research Directions

5.4.1 Expanding Sampling Across Broader Geographic and Ecological Ranges

Given the wide distribution of *T. ruticarpum* across China, future studies should aim to include additional sampling sites that represent diverse climates, altitudes, and soil types. In particular, systematic sampling of all major tissue types, including those currently underrepresented, will provide a more holistic understanding of endophyte-host interactions and their ecological determinants. Such data will also help uncover geographic patterns in fungal diversity and identify region-specific taxa.

5.4.2 Investigating Other Microfungi Groups Associated with *Tetradium ruticarpum*

Endophytic fungi are the main focus of this study. In contrast, other microfungi, such as saprobic and pathogenic species associated with *Tetradium ruticarpum*, remain relatively undocumented and represent promising directions for future research. Further investigations into these fungal groups will contribute to a more comprehensive understanding of the microfungal community associated with this medicinal plant.

5.4.3 Inducing Sporulation in Endophytic Isolates

Inducing sporulation remains a key bottleneck in the taxonomy of endophytic fungi, as many isolates fail to develop reproductive structures under standard laboratory conditions. Even when exposed to various induction treatments, spore production is often absent. This limitation hampers the acquisition of complete morphological data, which is essential for the accurate identification and description of new species. Future research should explore alternative culture media, environmental triggers (e.g., light, temperature), and co-culture techniques to enhance sporulation and facilitate comprehensive morphological characterization.

5.4.4 Chemical Characterization of Antimicrobial Metabolites

In this study, the agar plug method was used for the preliminary screening of isolates exhibiting antimicrobial activity. While 35 isolates showed inhibitory effects, the specific active compounds responsible have not yet been isolated or structurally elucidated. Therefore, future research should focus on the extraction and purification of these bioactive metabolites using advanced techniques such as HPLC and LC-MS to identify the active components.

Understanding and characterizing these antimicrobial compounds is of great significance, as it may lead to the discovery of novel bioactive molecules with potential pharmaceutical applications. Given the rising threat of antibiotic resistance, exploring endophytic fungi derived from medicinal plants like *Tetradium ruticarpum* provides a promising avenue for sourcing new antimicrobial agents. Furthermore, detailed chemical and structural analyses combined with genomic insights can illuminate the biosynthetic pathways involved, guiding the development of effective and sustainable therapeutics. This integrated approach not only enriches our knowledge of fungal secondary metabolism but also enhances the potential for practical applications in medicine and agriculture.

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APPENDIX A

THE DETAILED INFORMATION OF METABOLITES FROM *TETRADIUM RUTICARPUM*

Table A1 Metabolites from *Tetradium ruticarpum*

Classification	No.	Name	Molecular formula	Molecular weight	References
Alkaloids					
Indoles	1	Evodiamine	$C_{19}H_{17}N_3O$	303.4	(Li & Wang, 2020)
	2	10-Hydroxyevodiamine	$C_{19}H_{17}N_3O_2$	319.4	(Li & Wang, 2020)
	3	Carboxyevodiamine	$C_{20}H_{17}N_3O_3$	347.4	(Li & Wang, 2020)
	4	Acetonylevodiamine	$C_{22}H_{21}N_3O_2$	359.4	(Li & Wang, 2020)
	5	Dihydrorutaecarpine	$C_{18}H_{15}N_3O$	289.3	(Li & Wang, 2020)
	6	14-Formyldihydrorutaecarpine	$C_{20}H_{18}N_2O_2$	318.4	(Wang et al., 2010)
	7	13b-Hydroxymethylevodiamine	$C_{20}H_{19}N_3O_2$	333.4	(Li & Wang, 2020)
	8	13b-Hydroxyevodiamine	$C_{19}H_{17}N_3O_2$	319.4	(Li & Wang, 2020)
	9	Rutaecarpine	$C_{18}H_{13}N_3O$	287.3	(Li & Wang, 2020)
	10	1-Hydroxyrutaecarpine	$C_{18}H_{13}N_3O_2$	303.3	(Li & Wang, 2020)
	11	3-Hydoxyrutaecarpine	$C_{18}H_{13}N_3O$	303.3	(Li & Wang, 2020)
	12	7β-Hydroxyrutaecarpine	$C_{18}H_{13}N_3O$	303.3	(Li & Wang, 2020)
	13	10-Hydroxyrutaecarpine	$C_{18}H_{13}N_3O$	303.3	(Li & Wang, 2020)
	14	(7R,8S)-7,8-hydroxyrutaecarpine	$C_{18}H_{13}N_3O_3$	319.3	(He et al., 2024)
	15	(7R,8S)-7-Hydroxy-8-methoxy-rutaecarpine	$C_{19}H_{15}N_3O_3$	333.3	(Li & Wang, 2020)
	16	(7R,8S)-7-Hydroxy-8-ethoxy-rutaecarpine	$C_{20}H_{17}N_3O_3$	347.4	(Li & Wang, 2020)
	17	Hortiacine	$C_{19}H_{15}N_3O_2$	317.3	(Zhao et al., 2015a)
	18	Rutaecarpine-10-O-β-D-glucopyranoside	$C_{24}H_{23}N_3O_7$	465.5	(Li & Wang, 2020)
	19	Rutaecarpine-10-O-rutinoside	$C_{30}H_{33}N_3O$	451.6	(Li & Wang, 2020)
	20	Dehydroevodiamine	$C_{19}H_{15}N_3O$	301.3	(Li & Wang, 2020)
	21	Evodiamide	$C_{19}H_{21}N_3O$	307.3	(Li & Wang, 2020)
	22	N-(2-methylaminobenzoyl)tryptamine	$C_{18}H_{19}N_3O$	293.37	(Zhao et al., 2015a)
	23	Evodianinine	$C_{19}H_{13}N_3O$	299.3	(Li & Wang, 2020)
	24	Dievodiamine	$C_{38}H_{30}N_6O_2$	602.7	(Li & Wang, 2020)
	25	Rhetsinine	$C_{19}H_{17}N_3O_2$	319.4	(Li & Wang, 2020)
	26	Goshuyuamide I	$C_{19}H_{19}N_3O$	305.4	(Li & Wang, 2020)
	27	Goshuyuamide II	$C_{19}H_{17}N_3O_2$	319.36	(Li & Wang, 2020)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	28	10-Methoxygoshuyuamide-II	$C_{20}H_{19}N_3O_3$	349.4	(Li & Wang, 2020)
	29	Wuchuyuamide I	$C_{19}H_{17}N_3O_4$	351.4	(Li & Wang, 2020)
	30	Wuchuyuamide II	$C_{19}H_{17}N_3O_3$	335.4	(Zuo et al., 2000)
	31	Wuzhuyurutine A	$C_{17}H_{11}N_3O_2$	289.29	(Li & Wang, 2020)
	32	Wuzhuyurutine B	$C_{17}H_{11}N_3O_3$	305.29	(Li & Wang, 2020)
	33	Wuzhuyurutine C	$C_{18}H_{13}N_3O_3$	319.3	(Li & Wang, 2020)
	34	Wuzhuyurutine D	$C_{17}H_{11}N_3O_3$	305.29	(Li & Wang, 2020)
	35	Bouchardatine	$C_{17}H_{11}N_3O_2$	289.29	(Li & Wang, 2020)
	36	Evollionine A	$C_{19}H_{15}N_3O_2$	317.3	(Li & Wang, 2020)
	37	Evollionine B	$C_{20}H_{19}N_3O_5$	381.4	(Li & Wang, 2020)
	38	β-Carboline	$C_{11}H_8N_2$	168.19	(Xiao et al., 2023)
	39	1,2,3,4-Tetrahydro-1-oxo-carboline	$C_{11}H_{10}N_2O$	186.21	(Xiao et al., 2023)
	40	6-Methoxy-N-methyl-1,2,3,4-tetrahydro-β-carboline	$C_{13}H_{16}N_2O$	216.28	(Li & Wang, 2020)
	41	Evodiagenine	$C_{19}H_{13}N_3O$	299.3	(Wang et al., 2010)
	42	(-)-Evodiakine	$C_{19}H_{17}N_3O_3$	335.4	(Li & Wang, 2020)
	43	(+)-Evodiakine	$C_{19}H_{17}N_3O_3$	335.4	(Li & Wang, 2020)
	44	3-Hydroxyacetylindole	$C_{10}H_9NO_2$	175.18	(Xiao et al., 2023)
	45	N-methyltryptamine	$C_{11}H_{14}N_2$	174.24	(Xiao et al., 2023)
	46	5-Methoxy-N-methyltryptamine	$C_{12}H_{16}N_2O$	204.27	(Li & Wang, 2020)
	47	N, N-Dimethyltryptamine	$C_{12}H_{16}N_2$	218.29	(Xiao et al., 2023)
	48	5-Methoxy-N, N-dimethyltryptamine	$C_{13}H_{18}N_2O$	218.29	(Li & Wang, 2020)
	49	(S)-7-Hydroxysecorutaecarpine	$C_{18}H_{15}N_3O_3$	321.3	(Li & Wang, 2020)
	50	Evodamide A	$C_{19}H_{15}N_3O_2$	318.12	(Li et al., 2020a)
	51	13,14-Dihydrorutecarpine	$C_{18}H_{15}N_3O$	289.3	(Li et al., 2020a)
	52	N-formyldihydrorutaecarpine	$C_{19}H_{15}N_3O_2$	317.3	(Li & Wang, 2020)
	53	Hortiamine	$C_{20}H_{17}N_3O_2$	331.4	(Li & Wang, 2020)
	54	2-Hydroxy-1-(1H-indol-3-yl)-ethanone	$C_{10}H_9NO_2$	175.18	(He et al., 2024)
	55	13-Methyl-13H-indolo[2',3':3,4]pyrido[2,1-b]quinazolin-5-one	$C_{19}H_{13}N_3O$	299.3	(Li & Wang, 2020)
	56	Rutaecarpine-1-O-β-D-glucopyranoside	$C_{24}H_{23}N_3O_7$	465.5	(Li & Wang, 2020)
	57	1-Hydroxymethyl goshuyuamide II	$C_{20}H_{19}N_3O_3$	372.13	(Qin et al., 2021a)
	58	10-methoxygoshuyuamide-II	$C_{20}H_{19}N_3O_3$	349.39	(Li et al., 2020a)
	59	13-hydroxymethyl goshuyuamide-II	$C_{20}H_{19}N_3O_3$	349.39	(Qin, 2015)
	60	N14-formyl dihydrorutaecarpine	$C_{19}H_{15}N_3O_2$	317.35	(Yang et al., 2008)
	61	1-O-β-D-glucopyranosylrutaecarpine	$C_{24}H_{23}N_3O_7$	466.16	(Xia et al., 2016)
	62	7,8-dehydrorutaecarpine	$C_{18}H_{11}N_3O$	285.31	(Xia et al., 2016)
	63	Hydroxyevodiamine	$C_{19}H_{17}N_3O_2$	319.36	(Zuo et al., 2003)

Table A1 (continued)

Classification	**No.**	**Name**	**Molecular formula**	**Molecular weight**	**References**
	64	Nb-demethylevodiamide	$C_{18}H_{19}N_3O$	294.16	(Li et al., 2016c)
Quinolones	65	Evollionine C (Methyl 5-(1,4-dihydro-1-methyl-4-oxoquinolin-2-yl) pentanoate)	$C_{16}H_{19}NO_3$	273.33	(Li et al., 2014)
	66	1-Methyl-2-ethyl-4(1H)-quinolone	$C_{12}H_{13}NO$	187.24	(Wang et al., 2013a)
	67	1-Methyl-2-(2-cyclopentylethyl)-4(1H)-quinolinone	$C_{17}H_{21}NO$	255.35	(Xiao et al., 2023)
	68	1-Methyl-2-pentyl-4-(1H)-quinolone	$C_{15}H_{19}NO$	229.32	(Li & Wang, 2020)
	69	1-Methyl-2-heptyl-4(1H)-quinolone	$C_{17}H_{23}NO$	257.37	(Li & Wang, 2020)
	70	1-Methyl-2-octyl-4(1H)-quinolone	$C_{18}H_{25}NO$	271.4	(Li & Wang, 2020)
	71	1-Methyl-2-nonyl-4(1H)-quinolone	$C_{19}H_{27}NO$	285.4	(Li & Wang, 2020)
	72	1-Methyl-2-[(Z)-4-nonenyl]-4(1H)-quinolone	$C_{19}H_{25}NO$	283.4	(Xiao et al., 2023)
	73	1-Methyl-2-decyl-4(1H)-quinolone	$C_{20}H_{29}NO$	299.4	(Li & Wang, 2020)
	74	1-Methyl-2-undecyl-4(1H)-quinolone	$C_{21}H_{31}NO$	313.5	(Li & Wang, 2020)
	75	1-Methyl-2-[(Z)-1-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO$	311.5	(Xiao et al., 2023)
	76	1-Methyl-2-[(E)-1-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO$	311.5	(Li & Wang, 2020)
	77	1-Methyl-2-[(Z)-5-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO$	311.5	(Li & Wang, 2020)
	78	1-Methyl-2-[(Z)-6-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO$	311.5	(Li & Wang, 2020)
	79	1-Methyl-2-[(1E,5Z)-1,5-undecadienyl]-4(1H)-quinolone	$C_{21}H_{27}NO$	309.4	(Li & Wang, 2020)
	80	1-Methyl-2-[6-carbonyl-(E)-4-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO_2$	327.5	(Li & Wang, 2020)
	81	1-Methyl-2-[7-hydroxy-(Z)-8-tridecenyl]-4-(1H)-quinolone	$C_{23}H_{34}NO_2$	356.259	(Matsuo et al., 2024)
	82	1-Methyl-2-[8-hydroxy-(E)-9-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO_2$	355.51	(Matsuo et al., 2024)
	83	1-Methyl-2-[10-hydroxy-(Z)-8-tridecenyl]-4(1H)-quinolone	$C_{23}H_{34}NO_2$	356.259	(Matsuo et al., 2024)
	84	1-Methyl-2-undecanone-10'-4(1H)-quinolone	$C_{21}H_{31}NO_2$	329.5	(Xiao et al., 2023)
	85	1-Methyl-2-dodecyl-4-(1H)-quinolone	$C_{22}H_{33}NO$	327.5	(Li & Wang, 2020)
	86	1-Methyl-2-[(Z)-5'-dodecenyl]-4(1H)-quinolone	$C_{22}H_{31}NO$	325.5	(Li & Wang, 2020)
	87	Dihydroevocarpine	$C_{23}H_{35}NO$	341.5	(Li & Wang, 2020)
	88	Evocarpine	$C_{22}H_{33}NO$	327.5	(Li & Wang, 2020)
	89	Euocarpine A	$C_{21}H_{27}NO_2$	325.4	(Li & Wang, 2020)
	90	Euocarpine B	$C_{21}H_{27}NO_2$	325.4	(Li & Wang, 2020)
	91	Euocarpine C	$C_{23}H_{31}NO_2$	353.5	(Li & Wang, 2020)
	92	Euocarpine D	$C_{23}H_{31}NO_2$	353.5	(Li & Wang, 2020)
	93	Euocarpine E	$C_{19}H_{28}NO$	286.4	(Li & Wang, 2020)
	94	1-Methyl-2-[(Z)-4-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO$	339.5	(Li & Wang, 2020)
	95	1-Methyl-2-[(Z)-7-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO$	339.5	(Li & Wang, 2020)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	96	1-Methyl-2-[(Z)-8-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO$	339.5	(Xiao et al., 2023)
	97	1-Methyl-2-[12-tridecenyl]-4(1H)-quinolone	$C_{22}H_{33}NO$	339.5	(Li & Wang, 2020)
	98	1-Methyl-2-[(4Z,7Z)-4,7-tridecadienyl]-4(1H)-quinolone	$C_{23}H_{31}NO$	337.5	(Li & Wang, 2020)
	99	1-Methyl-2-[6-carbonyl-(E)-7-tridecenyl]-4(1H)-quinolone	$C_{23}H_{31}NO_2$	353.5	(Zhao et al., 2015a)
	100	1-Methyl-2-[7-carbonyl-(E)-9-tridecenyl]-4(1H)-quinolone	$C_{23}H_{31}NO_2$	353.5	(Li & Wang, 2020)
	101	1-Methyl-2-[7-hydroxy-(E)-9-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO_2$	355.5	(Xiao et al., 2023)
	102	1-Methyl-2-[12-hydroxy-tridecyl]-4(1H)-quinolone	$C_{23}H_{35}NO_2$	357.5	(Li & Wang, 2020)
	103	1-Methyl-2-[13-hydroxyl-tridecenyl]-4(1H)-quinolone	$C_{23}H_{35}NO_2$	357.5	(Li & Wang, 2020)
	104	1-Methyl-2-tetradecyl-4-(1H)-quinolone	$C_{24}H_{37}NO$	355.6	(Li & Wang, 2020)
	105	1-Methyl-2-[13-tetradecenyl]-4-(1H)-quinolone	$C_{24}H_{35}NO$	353.6	(Li & Wang, 2020)
	106	1-Methyl-2-pentadecyl-4(1H)-quinolone	$C_{25}H_{39}NO$	369.6	(Li & Wang, 2020)
	107	1-Methyl-2-[(Z)-5'-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{37}NO$	367.6	(Li & Wang, 2020)
	108	1-Methyl-2-[(Z)-6-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{37}NO$	367.6	(Li & Wang, 2020)
	109	1-Methyl-2-[(Z)-9-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{37}NO$	367.6	(Li & Wang, 2020)
	110	1-Methyl-2-[(Z)-10-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{37}NO$	367.6	(Li & Wang, 2020)
	111	1-Methyl-2-[(6Z,9Z)-6,9-pentadecadienyl]-4(1H)-quinolone	$C_{25}H_{35}NO$	365.6	(Li & Wang, 2020)
	112	1-Methyl-2-[(9E,13E)-heptadecadienyl]-4(1H)-quinolone	$C_{25}H_{35}NO$	365.6	(Xiao et al., 2023)
	113	1-Methyl-2-[(6Z,9Z,12Z)-6,9,12-pentadecatriene]-4(1H)-quinolone	$C_{25}H_{33}NO$	363.6	(Xiao et al., 2023)
	114	1-Methyl-2-[(6Z,9Z,12E)-pentadecatriene]-4(1H)-quinolone	$C_{25}H_{33}NO$	363.6	(Li & Wang, 2020)
	115	1-Methyl-2-[15-hydroxyl-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{39}NO_2$	385.6	(Qin et al., 2021b)
	116	1-Methyl-2-hexadecylol-4-(1H)-quinolone	$C_{26}H_{41}NO$	383.6	(Li & Wang, 2020)
	117	1-Methyl-2-[7-hydroxy-(E)-9-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO_2$	327.5	(Zhao et al., 2021b)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	118	1-Methyl-2-[7-hydroxy-undecyl]-4(1H)-quinolone	$C_{21}H_{31}NO_2$	329.5	(Zhao et al., 2021b)
	119	1-Methyl-2-[(3E,6Z,9Z)-3.6,9-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{33}NO$	363.6	(Zhao et al., 2021b)
	120	1-Methyl-3-[(7E,9E,12Z)-7,9,12-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{33}NO$	363.6	(Qin et al., 2021b)
	121	1-Methyl-3-[(7E,9E,11E)-7,9,11-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{33}NO$	363.6	(Qin et al., 2021b)
	122	1-Methyl-2-[(3E,6Z,9Z,12E)-3,6,9,12-pentadecenyl]-4(1H)-quinolone	$C_{25}H_{31}NO$	361.6	(Zhao et al., 2021b)
	123	1-Methyl-2-[(4Z,7Z,10E-4,7,10-tridecenyl]-4(1H)-quinolone	$C_{23}H_{29}NO$	335.5	(Zhao et al., 2021b)
	124	1-Methyl-2-[(1E,4Z,7Z,10E)-1,4,7,10-tridecenyl]-4(1H)-quinolone	$C_{23}H_{27}NO$	333.5	(Zhao et al., 2021b)
	125	1-Methyl-2-[7,9-dihydroxy-(Z)-8-tridecenyl]-4(1H)-quinolone	$C_{23}H_{33}NO_3$	339.5	(Zhao et al., 2021b)
	126	1-Methyl-2-[(9E,13E)-9,13-heptadecadienyl]-4(1H)-quinolone	$C_{27}H_{39}NO$	393.6	(Li & Wang, 2020)
	127	1-Methyl-2-[15-hydroxyl-pentadecyl]-4(1H)-quinolinone	$C_{25}H_{39}NO_2$	369.6	(Li & Wang, 2020)
	128	1-Methyl-2-[(Z)-8-undecenyl]-4(1H)-quinolone	$C_{21}H_{29}NO$	311.5	(Ma et al., 2021)
	129	1-Methyl-2-[(1E,4Z,7Z)-1,4,7-undecenyl]-4(1H)-quinolone	$C_{21}H_{25}NO$	307.5	(Zhao et al., 2021b)
	130	2-Nonyl-4(1H)-quinolone	$C_{18}H_{25}NO$	271.4	(Xiao et al., 2023)
	131	2-Undecyl-4(1H)-quinolone	$C_{20}H_{29}NO$	299.4	(Li & Wang, 2020)
	132	2-Undecanone-10'-4(1H)-quinolone	$C_{20}H_{27}NO_2$	313.4	(Li & Wang, 2020)
	133	2-Tridecyl-4(1H)-quinolone	$C_{22}H_{31}NO$	325.5	(Xiao et al., 2023)
	134	2-[(6Z,9Z)-Pentadeca-6,9-dienyl]-quinolin-4(1H)-one	$C_{24}H_{31}NO$	349.5	(Xiao et al., 2023)
	135	2-Hydroxy-4-methoxy-3(3'-methyl-2'-butenyl)-quinolin	$C_{15}H_{17}NO_2$	243.3	(Xiao et al., 2023)
	136	8-Hydroxy-4-methoxy-3-(3-methylbut-2-en-1-yl)quinolin-2(1H)-one	$C_{15}H_{17}NO_3$	259.32	(Li et al., 2020a)
	137	evoxoidine	$C_{18}H_{19}NO_5$	329.35	(Su et al., 2017)
	138	Atanine	$C_{15}H_{17}NO_2$	243.3	(Li & Wang, 2020)
	139	3-(3-Hydroxy-3-methylbutyl)-4-methoxyquinolin-2(1H)-one	$C_{15}H_{19}NO_3$	261.32	(He et al., 2024)
	140	4-Hydroxy-3-(3-hydroxy-3-methylbutyl)quinolin-2(1H)-one	$C_{15}H_{19}NO_3$	261.32	(He et al., 2024)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	141	(S)-3-(2-Hydroxy-3-methylbut-3-en-1-yl)-4-methoxyquinolin-2(1H)-one	$C_{15}H_{17}NO_3$	259.32	(Li et al., 2020a)
	142	ruticarponine B （3-(3-hydroxy-3-methylbutyl)-4-methoxy-2(1H)-quinolinone）	$C_{15}H_{19}NO_3$	284.12	(Tan et al., 2025)
	143	ruticarponine A 8-hydroxy-3-(3-hydroxy-3-methylbutyl)-4-methoxy-2(1H)-quinolinone	$C_{15}H_{19}NO_4$	300.12	(Tan et al., 2025)
	144	1-methyl-2-(13-hydroxy-tridecenyl)-4(1H)-quinolone	$C_{23}H_{35}NO_2$	357.54	(Zhao et al., 2015a)
	145	1-methyl-2-(15-hydroxy-pentadecenyl)-4(1H)-quinolone	$C_{25}H_{39}NO_2$	385.59	(Zhao et al., 2015a)
	146	1-methyl-2-dodecyl-4(1H)-quinolone	$C_{22}H_{33}NO$	327.51	(Wang et al., 2013)
	147	1-methyl-2-hexadecylol-4(1H)-quinolone	$C_{26}H_{41}NO$	384.32	(Ling et al., 2016)
	148	2-ethyl-1-methyl-4(1H)-quinolone	$C_{12}H_{13}NO$	187.24	(Wang et al., 2013)
	149	Quinolone A methyl-3-[1-methyl-4(1H)-quinolone-yl]	$C_{14}H_{16}NO_3$	246.11	(Li et al., 2019)
	150	Quinolone B 4-methoxy-3-(3-methylbut-2-en-1-yl)-2-quinolone-8-O-β-D-glucopyranoside	$C_{21}H_{27}NO_8$	422.18	(Li et al., 2019)
Quinolines	151	Skimmianine	$C_{14}H_{13}NO_4$	259.26	(Li & Wang, 2020)
	152	Dictamnine	$C_{12}H_9NO_2$	199.2	(Xiao et al., 2023)
	153	Evolitrine	$C_{13}H_{11}NO_3$	229.23	(Xiao et al., 2023)
	154	6-Methoxydictamnine	$C_{13}H_{11}NO_3$	229.23	(Xiao et al., 2023)
	155	Evodine	$C_{18}H_{19}NO_5$	329.3	(Xiao et al., 2023)
	156	Ribalinine	$C_{15}H_{17}NO_3$	259.3	(Xiao et al., 2023)
Indole quinazoline	157	7-(R)-O-β-D-glucopyranosylrutaecarpine	$C_{24}H_{23}N_3NaO_7$	488.143	(Li et al., 2024)
	158	7-(S)-O-β-D-glucopyranosylrutaecarpine	$C_{24}H_{23}N_3NaO_7$	488.143	(Li et al., 2024)
	159	Wuzhuyuluckid A	$C_{20}H_{22}N_3O_4$	352.166	(Li et al., 2024)
	160	Wuzhuyuluckid B	$C_{19}H_{19}N_4O$	319.155	(Li et al., 2024)
	161	Wuzhuyuluckid C	$C_{29}H_{27}N_3NaO_6$	536.179	(Li et al., 2024)
Organic amines	162	Evodiamide A	$C_{20}H_{19}N_3O_5$	381.4	(Li & Wang, 2020)
	163	Evodiamide B	$C_{19}H_{16}N_4O_2$	332.4	(Li & Wang, 2020)
	164	Evodiamide C	$C_{37}H_{32}N_6O_6$	656.7	(Xiao et al., 2023)
	165	Evodiaxinine	$C_{20}H_{15}N_3O$	313.4	(Li & Wang, 2020)
	166	Synephrine	$C_9H_{13}NO_2$	167.2	(Li & Wang, 2020)
	167	N-(trans-p-Coumaroyl)-tyramine	$C_{17}H_{17}NO_3$	283.32	(Xiao et al., 2023)
	168	N-(cis-p-Coumaroyl)-tyramine	$C_{17}H_{17}NO_3$	283.32	(Xiao et al., 2023)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	169	Wuchuyuamide III	$C_{18}H_{17}NO_3$	295.3	(Li & Wang, 2020)
	170	Wuchuyuamide IV	$C_{19}H_{17}NO_4$	323.3	(Li & Wang, 2020)
	171	Evodileptin B	$C_{17}H_{17}NO_4$	299.32	(Kim et al., 2022b)
	172	2-Methylamino-benzamide	$C_8H_{10}N_2O$	150.18	(Li & Wang, 2020)
Acridons	173	Melicopidine	$C_{17}H_{15}NO_5$	313.3	(He et al., 2024)
Purines	174	Caffeine	$C_8H_{10}N_4O_2$	194.19	(He et al., 2024)
Terpenoids					
Limonoids	175	Limonin	$C_{26}H_{30}O_8$	470.5	(Li & Wang, 2020)
	176	12α-Hydroxylimonin	$C_{26}H_{30}O_9$	486.5	(Li & Wang, 2020)
	177	Dehydrolimonin	$C_{26}H_{30}O_8$	470.5	(Li & Wang, 2020)
	178	Limonin 17-β-D-glucopyranoside	$C_{32}H_{42}O_{14}$	650.7	(Xiao et al., 2023)
	179	Rutaevin	$C_{26}H_{30}O_9$	486.5	(Li & Wang, 2020)
	180	Rutaevin acetate	$C_{28}H_{32}O_{10}$	528.5	(Li & Wang, 2020)
	181	12α-Hydroxyrutaevin	$C_{26}H_{30}O_{10}$	502.5	(Li & Wang, 2020)
	182	Evodol (I)	$C_{26}H_{28}O_9$	484.5	(Li & Wang, 2020)
	183	12α-Hydroxyevodol	$C_{26}H_{28}O_{10}$	500.5	(Li & Wang, 2020)
	184	6α-Acetoxyl-12α-hydroxyevodol	$C_{28}H_{32}O_{11}$	544.5	(He et al., 2024)
	185	Limonin diosphenol 17-β-D-glucopyranoside	$C_{32}H_{40}O_{15}$	664.6	(Zhao et al., 2015a)
	186	Jangomolide	$C_{26}H_{28}O_8$	468.5	(Li & Wang, 2020)
	187	6α-Acetoxy-5-epilimonin	$C_{28}H_{32}O_{10}$	528.5	(Li & Wang, 2020)
	188	6β-Acetoxy-5-epilimonin	$C_{28}H_{32}O_{10}$	528.5	(Li & Wang, 2020)
	189	6β-Hydroxy-5-epilimonin-17-β-D-glucopyranoside	$C_{32}H_{42}O_{15}$	666.7	(Li & Wang, 2020)
	190	Evorubodinin	$C_{27}H_{32}O_{10}$	516.5	(Xiao et al., 2023)
	191	Shihulimonin A	$C_{26}H_{30}O_{10}$	502.5	(Li & Wang, 2020)
	192	Evolimorutanin	$C_{28}H_{36}O_{11}$	548.6	(Xiao et al., 2023)
	193	Evodirutaenin	$C_{26}H_{28}O_{11}$	516.5	(Li & Wang, 2020)
	194	Isolimonexic acid	$C_{26}H_{30}O_{11}$	518.5	(He et al., 2024)
	195	Obacunonsaeure	$C_{26}H_{32}O_8$	472.5	(He et al., 2024)
	196	Obacunone	$C_{26}H_{30}O_7$	454.5	(Li & Wang, 2020)
	197	7-Deacetylproceranone	$C_{26}H_{31}O_5$	423.5	(Xiao et al., 2023)
	198	Nomilin	$C_{28}H_{34}O_9$	514.6	(Li & Wang, 2020)
	199	Isoobacunoic acid	$C_{26}H_{32}O_8$	472.5	(He et al., 2024)
	200	7β-Acetoxy-5-epilimonin	$C_{28}H_{32}O_{10}$	528.5	(Qin et al., 2021b)
	201	Clauemargine L	$C_{26}H_{30}O_8$	470.5	(Qin et al., 2021b)
	202	Euodirutaecin A	$C_{26}H_{28}O_{11}$	516.5	(Qian et al., 2014)
	203	Euodirutaecin B	$C_{26}H_{28}O_{11}$	516.5	(Qian et al., 2014)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	204	19-Hydroxy methyl isoobacunoate diospheno	$C_{27}H_{32}O_{10}$	516.5	(Qin et al., 2021b)
	205	7α-Obacunyl acetate	$C_{28}H_{34}O_{9}$	514.6	(Lacroix et al., 2011)
	206	19-hydroxy methyl isoobacunoate diosphenol	$C_{28}H_{36}O_{10}$	532.59	(Qin et al., 2021b)
	207	9α-methoxyl dictamdiol	$C_{16}H_{20}O_{5}$	292.33	(Qin et al., 2021b)
Others	208	Taraxerone	$C_{30}H_{48}O$	424.7	(Xiao et al., 2023)
	209	Oleanolicacid	$C_{30}H_{48}O_{3}$	456.7	(Li & Wang, 2020)
	210	Evoditrilone A	$C_{29}H_{44}O$	408.7	(Li & Wang, 2020)
	211	Evoditrilone B	$C_{29}H_{44}O$	408.7	(Li & Wang, 2020)
	212	1β,4β-Dihydroxyeudesman-11-ene	$C_{15}H_{26}O_{2}$	238.37	(Xiao et al., 2023)
	213	Evolide A	$C_{12}H_{16}O_{4}$	224.1	(Zhang et al., 2020)
	214	Evolide B	$C_{11}H_{14}O_{4}$	210.23	(Zhang et al., 2020)
Flavonoids					
Flavonols	215	Isorhamnetin	$C_{16}H_{12}O_{7}$	316.26	(Li & Wang, 2020)
	216	Isorhamnetin-3-O-β-D-galactoside	$C_{22}H_{12}O_{12}$	468.3	(Li & Wang, 2020)
	217	Isorhamnetin-3-O-β-D-glucopyranoside	$C_{22}H_{12}O_{12}$	468.3	(Li & Wang, 2020)
	218	Isorhamnetin-3-O-rutinoside	$C_{28}H_{32}O_{16}$	624.5	(Xiao et al., 2023)
	219	Isorhamnetin-3-O-β-D-xylopyranosyl(1 → 2)-β-D-glucopyranoside	$C_{27}H_{30}O_{16}$	610.5	(Li & Wang, 2020)
	220	Quercetin	$C_{15}H_{10}O_{7}$	302.23	(Li & Wang, 2020)
	221	Quercetin-3-O-β-D-galactoside (hyperoside)	$C_{21}H_{20}O_{12}$	464.4	(Xiao et al., 2023)
	222	Isorhamnetin-3-O[2-O-β-D-xylopyranosyl-6-O-α-L-rhamnopyranosyl]-β-D-glucopyranoside	$C_{33}H_{40}O_{20}$	756.7	(Xiao et al., 2023)
	223	Isoquercitrin	$C_{21}H_{20}O_{12}$	464.4	(Li & Wang, 2020)
	224	Quercetin-3-O-β-D-xylopyranosyl(1 → 2)-β-D-glucopyranoside	$C_{26}H_{38}O_{17}$	622.6	(Li & Wang, 2020)
	225	Limocitrin-3-O-β-D-glucopyranoside	$C_{23}H_{24}O_{13}$	508.4	(Li & Wang, 2020)
	226	Limocitrin-3-O-rutinoside	$C_{29}H_{34}O_{17}$	654.6	(Li & Wang, 2020)
	227	Limocitrin-3-O-β-D-xylopyranosyl (1 → 2)-β-D-glucopyranoside	$C_{28}H_{32}O_{17}$	640.5	(Li & Wang, 2020)
	228	Limocitrin-3-O[2-O-β-D-xylopyranosyl-6-O-α-L-rhamnopyranosyl]-β-D-glucopyranoside	$C_{34}H_{42}O_{21}$	786.7	(Xiao et al., 2023)
	229	Isorhamnetin-3-rutinoside-4'-glucoside	$C_{34}H_{42}O_{21}$	786.7	(Zhao et al., 2015a)
	230	Isorhamnetin-3-O-sambubioside	$C_{27}H_{30}O_{16}$	610.5	(Li & Wang, 2020)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	231	Quercetin-3-O-α-D-arabinopyranoside	$C_{20}H_{18}O_{11}$	434.3	(Zhao et al., 2015a)
	232	Quercetin-3-O-sambubioside	$C_{26}H_{28}O_{16}$	596.5	(Li & Wang, 2020)
	233	Rutin	$C_{27}H_{30}O_{16}$	610.5	(He et al., 2024)
	234	Quercetin-3-O-β-D-ghucoside-7-O-α-L-thammanoside	$C_{27}H_{30}O_{16}$	610.5	(Zhao et al., 2015a)
	235	Phellodensin F	$C_{26}H_{30}O_{10}$	502.5	(Xiao et al., 2023)
	236	Epimedoside C	$C_{26}H_{28}O_{11}$	516.5	(Xiao et al., 2023)
Flavonoids	237	Tricin-7-O-β-D-glucopyranoside	$C_{23}H_{24}O_{12}$	492.4	(He et al., 2024)
	238	Diosmetin-7-O-β-D-glucopyranoside	$C_{22}H_{22}O_{11}$	462.4	(Li & Wang, 2020)
	239	Diosmin	$C_{28}H_{32}O_{15}$	608.5	(Li & Wang, 2020)
	240	Chrysoeriol-7-O-rutinoside	$C_{28}H_{32}O_{15}$	608.5	(Li & Wang, 2020)
Flavonones	241	Evodioside B	$C_{32}H_{40}O_{15}$	664.6	(Xiao et al., 2023)
	242	Hesperidin	$C_{28}H_{34}O_{15}$	610.6	(Xiao et al., 2023)
Flavanols	243	Catechin	$C_{15}H_{14}O_{6}$	290.27	(Xiao et al., 2023)
Volatile oils					
Monoterpenoids	244	3-Carene	$C_{10}H_{16}$	136.23	(He et al., 2024)
	245	(Z)-carveol	$C_{10}H_{16}O$	152.23	(He et al., 2024)
	246	Cosmene	$C_{10}H_{14}$	134.22	(He et al., 2024)
	247	Isocarveol	$C_{10}H_{16}O$	152.23	(He et al., 2024)
	248	Limonene dioxide	$C_{10}H_{16}O_{2}$	168.23	(He et al., 2024)
	249	Linalool	$C_{10}H_{18}O$	154.25	(He et al., 2024)
	250	Myrcene	$C_{10}H_{16}$	136.23	(He et al., 2024)
	251	(E)-ocimene	$C_{10}H_{16}$	136.23	(Xiao et al., 2023)
	252	(Z)-ocimene	$C_{10}H_{16}$	136.23	(Xiao et al., 2023)
	253	Phellandra	$C_{10}H_{16}O$	152.23	(He et al., 2024)
	254	α-Pinene	$C_{10}H_{16}$	136.23	(He et al., 2024)
	255	β-Terpinene	$C_{10}H_{16}$	136.23	(He et al., 2024)
	256	g-Terpinene	$C_{10}H_{16}$	136.23	(He et al., 2024)
Sesquiterpenes	257	(+)-α-Bisabolol	$C_{15}H_{26}O$	222.37	(He et al., 2024)
	258	γ-Cadinene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	259	δ-Cadinene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	260	α-Caryophyllene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	261	β-Caryophyllene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	262	Caryophyllene oxide	$C_{15}H_{24}O$	220.35	(He et al., 2024)
	263	Cubebene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	264	β-Elemene	$C_{15}H_{24}$	204.35	(He et al., 2024)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	265	δ-Elemene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	266	Elixene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	267	3,7(11)-Eudesmadiene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	268	β-Eudesmene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	269	α-Farnesene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	270	Farnesyl alcohol	$C_{15}H_{26}O$	222.37	(He et al., 2024)
	271	1,2,3,4,4a,7-Hexahydro-1,6-dimethyl-4-(1-methylethyl)-naphthalene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	272	α-Selinene	$C_{15}H_{24}$	204.35	(He et al., 2024)
	273	Spathulenol	$C_{15}H_{24}O$	220.35	(He et al., 2024)
	274	Viridiflorol	$C_{15}H_{26}O$	222.37	(He et al., 2024)
Aliphaties	275	3,4-Dimethyl-2,4.6-octatriene	$C_{10}H_{14}$	134.22	(He et al., 2024)
	276	2-Dodecen-1-ylsuccinic-anhydride	$C_{16}H_{26}O_3$	266.38	(He et al., 2024)
	277	2-Hendecanone	$C_{11}H_{22}O$	170.29	(He et al., 2024)
	278	6-Methylhepta-3,5-dien-2-one	$C_8H_{12}O$	124.18	(He et al., 2024)
	279	Methylpalmitate	$C_{17}H_{34}O_2$	270.5	(He et al., 2024)
	280	2.4,6-Octatrienal	$C_8H_{10}O$	122.16	(He et al., 2024)
	281	2-Pentadecanone	$C_{15}H_{30}O$	226.4	(He et al., 2024)
	282	Santolina triene	$C_{10}H_{16}$	136.23	(He et al., 2024)
	283	1,2,4,4-Tetramethyl-1-cyclopentene	C_9H_{16}	124.22	(He et al., 2024)
	284	2-Tridecanone	$C_{13}H_{26}O$	198.34	(He et al., 2024)
	285	2,5-Dimethylacetophenone	$C_{10}H_{12}O$	148.2	(He et al., 2024)
	286	2,2'-Methylenebis(4-methyl-6-tert-butylphenol)	$C_{23}H_{33}O_2$	341.5	(He et al., 2024)
	287	O-cymene	$C_{10}H_{14}$	134.22	(He et al., 2024)
Organic acids					
Organic acids	288	Neochlorogenic acid	$C_{16}H_{18}O_9$	354.31	(He et al., 2024)
	289	Chlorogenic acid	$C_{16}H_{18}O_9$	354.31	(Zhao et al., 2015a)
	290	Caffeic acid	$C_9H_8O_4$	180.16	(He et al., 2024)
	291	Ferulic acid	$C_{10}H_{10}O_4$	194.18	(He et al., 2024)
	292	p-Hydroxycinnamic acid	$C_9H_8O_3$	164.16	(Li & Wang, 2020)
	293	2-O-trans-caffeoylgluconic acid	$C_{15}H_{18}O_{10}$	358.3	(Li & Wang, 2020)
	294	3-O-trans-caffeoylgluconic acid	$C_{15}H_{18}O_{10}$	358.3	(Li & Wang, 2020)
	295	4-O-trans-caffeoylgluconic acid	$C_{15}H_{18}O_{10}$	358.3	(Li & Wang, 2020)
	296	5-O-trans-caffeoylgluconic acid	$C_{15}H_{18}O_{10}$	358.3	(Li & Wang, 2020)
	297	6-O-trans-caffeoylgluconic acid	$C_{15}H_{18}O_{10}$	358.3	(Li & Wang, 2020)

Table A1 (continued)

Classification	No.	Name	Molecular formula	Molecular weight	References
	298	trans-Caffeoyl-6-O-D-gluconic acid methyl ester	$C_{16}H_{20}O_{10}$	372.32	(Li & Wang, 2020)
	299	trans-Caffeoyl-6-O-D-glucono-γ-lactone	$C_{15}H_{16}O_9$	340.28	(Li & Wang, 2020)
	300	Citric acid	$C_6H_8O_7$	192.12	(Li & Wang, 2020)
	301	Caffeic acid methyl ester	$C_{10}H_{10}O_4$	194.18	(Li & Wang, 2020)
	302	1-O-caffeoyl-D-glucoside	$C_{15}H_{18}O_9$	342.3	(Li & Wang, 2020)
	303	Cryptochlorogenic acid	$C_{16}H_{18}O_9$	354.31	(Zhao et al., 2015a)
	304	Ethylparaben	$C_9H_{10}O_3$	166.17	(Li & Wang, 2020)
	305	trans-Feruloylgluconic acid	$C_{16}H_{20}O_{10}$	372.32	(Zhao et al., 2015a)
	306	3-O-Feruloylquinic acid	$C_{17}H_{20}O_9$	368.3	(Zhao et al., 2015a)
	307	4-O-Feruloylquinic acid	$C_{17}H_{20}O_9$	368.3	(Zhao et al., 2015a)
	308	5-O-Feruloylquinic acid	$C_{17}H_{20}O_9$	368.3	(Zhao et al., 2015a)
	309	Floribundic acid	$C_{20}H_{24}O_5$	344.4	(Zhao et al., 2015a)
	310	trans-4-Hydroxycinnamic acid methyl ester	$C_{10}H_{10}O_3$	178.18	(Xiao et al., 2023)
	311	Isocitric acid	$C_6H_8O_7$	192.12	(He et al., 2024)
	312	Methyl-3-O-feruloylquinate	$C_{18}H_{22}O_9$	382.4	(Zhao et al., 2015a)
	313	Protocatechuic acid	$C_7H_6O_4$	154.12	(He et al., 2024)
Other categories					
Anthraquinones	314	Chrysophanol	$C_{15}H_{10}O_4$	254.24	(Li & Wang, 2020)
	315	Emodin	$C_{15}H_{10}O_5$	270.24	(Li & Wang, 2020)
	316	Physcion	$C_{16}H_{12}O_5$	284.26	(Li & Wang, 2020)
Steroid	317	β-Daucosterol	$C_{35}H_{60}O_6$	576.8	(Li & Wang, 2020)
	318	β-Sitosterol	$C_{25}H_{50}O$	366.7	(Li & Wang, 2020)
	319	β-Stigmasterol	$C_{29}H_{48}O$	412.7	(Li & Wang, 2020)
Others	320	Calodendrolide	$C_{15}H_{16}O_4$	260.28	(Li & Wang, 2020)
	321	Catechol	$C_6H_6O_2$	110.11	(He et al., 2024)
	322	Cinchonain	$C_{24}H_{20}O_9$	452.4	(He et al., 2024)
	323	Coniferin	$C_{16}H_{22}O_8$	342.34	(Li & Wang, 2020)
	324	Hiiranlactone E	$C_{16}H_{28}O_2$	252.39	(Xiao et al., 2023)
	325	7-Hydroxycoumarin	$C_9H_6O_3$	162.14	(He et al., 2024)
	326	myo-Inositol	$C_6H_{12}O_6$	180.16	(He et al., 2024)
	327	4-Methoxybenzyl alcohol	$C_8H_{10}O_2$	138.16	(He et al., 2024)
	328	9α-Methoxyl dictamdio	$C_{16}H_{20}O_5$	292.33	(Qin et al., 2021b)
	329	Syringin	$C_{17}H_{24}O_9$	372.4	(Li & Wang, 2020)

APPENDIX B

THE DETAILED INFORMATION OF PHYLOGENETIC ANALYSES

Table B1 GenBank accession numbers of the *Zasmidium* used in the phylogenetic analyses in this study

Species	Strain Number	Status	LSU	ITS	RPB2
Nothopericoniella perseamacranthae	CBS 122097		GU452682	MF951354	MF951583
Zasmidium angulare	CBS 132094	T	JQ622096	JQ622088	MF951690
Zasmidium anthuriicola	CBS 118742	T	FJ839662	FJ839626	MF951691
Zasmidium aporosae	P210X	T	OR143827	OR143787	
Zasmidium arcuatum	CBS 113477	T	EU041836	EU041779	MF951692
Zasmidium aucklandicum	CPC 13569		MF951280	MF951409	MF951733
Zasmidium biverticillatum	CBS 335.36		EU041853	EU041796	
Zasmidium cellare	CBS 146.36N	T	EU041878	EU041821	MF951693
Zasmidium cerophillum	CBS 103.59	T	GU214485	EU041798	MF951694
Zasmidium citri-griseum	CBS 122455		KF902151	KF901792	MF951695
Zasmidium commune	CBS 142530	T	KY979820.1	NR_156003	
Zasmidium corymbiae	CBS 145047	T	NG_066279	NR_161118	MK047534
Zasmidium cyatheae	COAD:1425	T	KT037571	KT037530	
Zasmidium dalbergiae	P550	T		KC677913	
Zasmidium dasypogonis	CBS 143397	T	NG_058514	NR_156662	
Zasmidium daviesiae	CBS 116002		FJ839669	FJ839633	MF951698
Zasmidium ducassei	BRIP 53367	T		NR_164517	
Zasmidium elaeocarpi	CBS 142187	T	MF951263	MF951398	MF951699
Zasmidium eucalypticola	CBS 142186	T	MF951265	MF951400	MF951701
Zasmidium eucalyptigenum	CBS 138860	T	KP004486	KP004458	
Zasmidium eucalyptorum	CBS 118500	T	MF951266	KF901652	MF951702
Zasmidium faygaleae	BRIP 72890b		OR673899	OR673894	
Zasmidium fructicola	CBS 139625	T	KP895922	KP896052	MF951703
Zasmidium fructigenum	CBS 139626	T	KP895926	KP896056	MF951704
Zasmidium gahniicola	CBS:143422	T	MG386103	MG386050	
Zasmidium grevilleae	CBS 124107	T	FJ839670	FJ839634	MF951705
Zasmidium guangxiensis	**JAUCC 7351**			**PV587090**	
Zasmidium guangxiensis	**JAUCC 6594**	**T**		**PV587002**	
Zasmidium gupoyu	CBS 122099		MF951267	MF951401	MF951706
Zasmidium hakeae	CBS 142185	T	MF951268	MF951402	MF951707

Table B1 (continued)

Species	Strain Number	Status	LSU	ITS	RPB2
Zasmidium hakeicola	CBS 144590)	T	NG_066335	NR_163384	MK442687
Zasmidium indonesianum	CBS 139627	T	KF902086	KF901739	MF951710
Zasmidium iteae	CBS 113094	T	MF951271	MF951405	MF951711
Zasmidium johnsoniae	BRIP 72385e	T		OP256852	OP289001
Zasmidium liboense	GUCC 1720.2		MT712180	MT683373	MT700486
Zasmidium lonicericola	CBS 125008	T	KF251787	KF251283	MF951712
Zasmidium macluricola	BRIP 52143	T		NR_137739	
Zasmidium mangiferae	MFLUCC 24–0391	T	PQ638521	PQ639273	
Zasmidium mangrovei	PREM:41457	T	MW046214		
Zasmidium morrisoniae	BRIP 70485a	T	PP707924	PP707907	PP712796
Zasmidium musae	CBS 121384		MF951272	EU514292	MF951713
Zasmidium musae-banksii	CBS 121710	T	EU041852	EU041795	MF951716
Zasmidium musicola	CBS 122479	T	MF951275	EU514294	MF951717
Zasmidium musigenum	CBS 190.63		EU041857	EU041800	MF951718
Zasmidium nancybirdwaltoniae	BRIP 72888b	T		OR290131	
Zasmidium nocoxi	CBS 125009	T	KF251788	KF251284	MF951719
Zasmidium pearceae	BRIP 72388b	T		OP023117	OP021641
Zasmidium phormii	ICMP 25677			PQ380928	
Zasmidium phormii	JAC15565			OL653017	
Zasmidium pitospori	CBS 122274		MF951276	MF951406	MF951720
Zasmidium podocarpi	CBS 142529		KY979821	NR_156004	
Zasmidium proteacearum	CBS 116003		FJ839671	FJ839635	MF951721
Zasmidium pseudoparkii	CBS 110999	T	JF700965	DQ303023	MF951723
Zasmidium pseudotsugae	rapssd		EF114704	EF114687	
Zasmidium pseudovespa	CBS 121159	T	KF901836	MF951407	MF951724
Zasmidium queenslandicum	CBS 122475	T	MF951277	EU514295	MF951725
Zasmidium rothmanniae	CBS 137983	T	NG_064291	NR_157438	
Zasmidium scaevolicola	CBS 127009	T	KF251789	KF251285	MF951726
Zasmidium schini	CBS 142188	T	MF951278	MF951408	MF951727
Zasmidium sp.	CBS 118494		MF951279	DQ303039	MF951728
Zasmidium strelitziae	CBS 121711	T	EU041860	EU041803	MF951729
Zasmidium suregadae	P36		KC677939	KC677914	
Zasmidium syzygii	CBS 133580	T	KC005798	KC005777	MF951730
Zasmidium thailandicum	CBS 145027	T	NG_066342	NR_164463	
Zasmidium tsugae	ratstk		EF114705	EF114688	
Zasmidium velutinum	CBS 101948	T	EU041838	EU041781	MF951731
Zasmidium xenoparkii	CBS 111185	T	JF700966	DQ303028	MF951732

Table B2 GenBank accession numbers of isolates used in the phylogenetic analyses of *Tetradiomyces* and related taxa

Species	Strain Number	Status	LSU	ITS
Falciformispora senegalensis	CBS 196.79	T	KF015631	KF015673
Falciformispora tompkinsii	CBS 200.79	T	KF015625	KF015670
Latorua caligans	CBS 576.65		KR873266	KR873232
Latorua grootfonteinensis	CBS 369.72		KR873267	
Longipedicellata aptrootii	MFLUCC 10-0297		KU238894	KU238893
Longipedicellata aptrootii	MFLUCC 16-0384		KY066738	
Longipedicellata aptrootii	MFLUCC 16-0244		KY066739	
Matsushimamyces bohaniensis	CBEC001	T	KR350633	KP765516
Multiverruca sinensis	CGMCC 3.20956	T	ON230021	ON230024
Multiverruca sinensis	GZUIFR 22.040		ON230022	ON230025
Multiverruca sinensis	GZUIFR 22.041		ON230023	ON230026
Polyschema congolensis	CBS 542.73		EF204502	
Polyschema larviformis	ILLS00171087		MH472659	MH472659
Polyschema larviformis	CBS 463.88		EF204503	
Polyschema sclerotigenum	UTHSC DI14-305		KP769976	KP769975
Polyschema terricola	CBS 301.65		EF204504	
Pseudoasteromassaria fagi	KT3432 = HHUF 30472		LC061590	LC061595
Pseudoasteromassaria spadicea	MFLUCC 15-0973		KY522724	KY522726
Pseudoxylomyces elegans	HHUF 30139		AB807598	LC014593
Tetradiomyces jiangxiensis	**JAUCC 7347**	**T**		**PV587086**
Tetradiomyces jiangxiensis	**JAUCC 7348**			**PV587087**
Tetradiomyces jiangxiensis	**JAUCC 7349**			**PV587088**
Triseptata sexualis	MFLUCC 11-0002		MN977833	MN977832
Verrucohypha endophytica	COAD 3604		PP913764	PP913763

Table B3 GenBank accession numbers of isolates used in the phylogenetic analyses of *Pseudokeissleriella* and related taxa

Species	Strain Number	Status	SSU	ITS	LSU	TEF1
Bambusicola bambusae	MFLUCC 11-0614	T	JX442039	NR_121546	JX442035	KP761722
Bambusicola irregulispora	MFLUCC 11-0437	T	JX442040	NR_121547	JX442036	KP761723
Bimuria novae-zelandiae	CBS 107.79	T	AY016338	NA	AY016356	DQ471087
Crassoascoma potentillae	UESTCC 21.0010		OK161233	OK161237	OK161254	OK181165
Crassoascoma potentillae	UESTCC 21.0011		OK161234	OK161238	OK161255	OK181166
Crassoascoma potentillae	CGMCC 3.20483	T	OK161236	OK161240	OK161257	OK181168
Darksidea alpha	CBS 135650	T	KP184049	KP183998	KP184019	KP184166
Darksidea beta	CBS 135637	T	KP184074	KP183978	KP184023	KP184189
Darksidea delta	CBS 135638	T	KP184069	KP183981	KP184024	KP184184
Darksidea epsilon	CBS 135658	T	KP184070	KP183983	KP184029	KP184186
Darksidea gamma	CBS 135634	T	KP184073	KP183985	KP184028	KP184188
Darksidea zeta	CBS 135640	T	KP184071	KP183979	KP184013	KP184191
Didymosphaeria rubi-ulmifolii	MFLUCC 14-0023	T	KJ436588	NA	KJ436586	NA
Groenewaldia indica	NFCCI 5439	T	OQ379189	OQ379185	OQ379187	OQ361689
Groenewaldia indica	NFCCI 5440		OQ379190	OQ379186	OQ379188	OQ361690
Halobyssothecium carbonneanum	CBS 144076	T	NA	MH062991	MH069699	NA
Halobyssothecium estuariae	MFLUCC 19-0386	T	MN598868	MN598890	MN598871	MN597050
Halobyssothecium kunmingense	KUMCC 19-0101	T	MT864313	MT627715	MN913732	NA
Halobyssothecium obiones	MFLUCC 15-0381	T	MH376745	MH377060	MH376744	MH376746
Helminthosporium velutinum	MAFF 243854	T	AB797240	LC014556	AB807530	AB808505
Katumotoa bambusicola	KT1517a	T	AB524454	LC014560	AB524595	AB539108
Keissleriella breviasca	KT649	T	AB797298	AB811455	AB807588	AB808567
Keissleriella caraganae	KUMCC 18-0164	T	MK359444	MK359434	MK359439	MK359073
Keissleriella cladophila	CBS 104.55	T	GU296155	NA	GU301822	GU349043
Keissleriella culmifida	KT2642	T	AB797302	LC014562	AB807592	AB808571
Keissleriella genistae	CBS 113798	T	GU205242	NA	GU205222	NA
Keissleriella gloeospora	KT829	T	AB797299	LC014563	AB807589	AB808568
Keissleriella poagena	CBS136767	T	NA	KJ869112	KJ869170	NA
Keissleriella quadriseptata	KT2292	T	AB797303	AB811456	AB807593	AB808572
Keissleriella taminensis	KT571	T	AB797305	LC014564	AB807595	AB808574
Keissleriella trichophoricola	CBS 136770	T	NA	KJ869113	KJ869171	NA
Keissleriella yonaguniensis	KT 2604	T	AB797304	AB811457	AB807594	AB808573
Lentithecium clioninum	KT1149A	T	AB797250	LC014566	AB807540	AB808515
Lentithecium fluviatile	CBS 122367		GU296158	NA	GU301825	GU349074
Lentithecium pseudoclioninum	KT1113	T	AB797255	AB809633	AB807545	AB808521

Table B3 (continued)

Species	Strain Number	Status	SSU	ITS	LSU	TEF1
Magnicamarosporium iriomotense	KT2822	T	NA	AB809640	AB807509	AB808485
Massarina eburnea	CBS 473.64		GU296170	NA	GU301840	GU349040
Montagnula opulenta	CBS 168.34		AF164370	NA	DQ678086	NA
Murilentithecium clematidis	MFLUCC 14-0562	T	KM408761	KM408757	KM408759	KM454445
Murilentithecium rosae	MFLUCC 15-0044	T	MG829137	MG828920	MG829030	NA
Neobambusicola strelitziae	CBS 138869	T	NA	NA	KP004495	NA
Neoophiosphaerella sasicola	KT1706	T	AB524458	LC014577	AB524599	AB539111
Phragmocamarosporium platani	MFLUCC 14-1191	T	KP842919	NA	KP842916	NA
Phragmocamarosporium rosae	MFLUCC 17-0797	T	MG829156	NA	MG829051	MG829225
Pleurophoma italica	MFLU:15-1254		KY501122	KY496754	KY496734	KY514398
Pleurophoma pleurospora	TASM 6115	T	MG829159	MG828944	MG829054	MG829226
Poaceascoma aquaticum	MFLUCC 14-0048	T	KT324691	NA	KT324690	NA
Poaceascoma filiforme	CBS 146689	T	NA	MT373362	MT373345	NA
Poaceascoma halophila	MFLUCC 15-0949	T	MF615400	NA	MF615399	NA
Poaceascoma helicoides	MFLUCC 11-0136	T	KP998463	KP998459	KP998462	KP998461
Poaceascoma taiwanense	MFLU 18-0083	T	MG831568	MG831569	MG831567	NA
Pseudokeissleriella bambusicola	CGMCC 3.20950	T	ON614096	ON614135	ON614138	ON639623
Pseudokeissleriella bambusicola	UESTCC 22.0028	T	ON614095	ON614134	ON614137	ON639622
Pseudokeissleriella tetradii	**JAUCC 6570**	**T**	**PV330325**	**PV330322**	**PV330328**	**PV324745**
Pseudokeissleriella tetradii	**JAUCC 6578**		**PV330326**	**PV330323**	**PV330329**	**PV324746**
Pseudokeissleriella tetradii	**JAUCC 6586**		**PV330327**	**PV330324**	**PV330330**	**PV324747**
Setoseptoria arundelensis	MFLUCC 17-0759	T	MG829173	MG828962	MG829073	NA
Setoseptoria arundinacea	KT600		AB797285	LC014595	AB807575	AB808551
Setoseptoria englandensis	MFLUCC 17-0778	T	MG829174	MG828963	MG829074	NA
Setoseptoria macropycnidia	CBS114202		GU296198	NA	GU301873	GU349026
Setoseptoria magniarundinacea	KT1174	T	AB797286	LC014596	AB807576	AB808552
Setoseptoria phragmitis	CBS 114802	T	NA	KF251249	KF251752	NA
Setoseptoria scirpi	MFUCC 14-0811	T	KY770980	MF939637	KY770982	KY770981
Spegazzinia deightonii	MAFF 243876		AB797291	NA	AB807581	AB808557
Sulcatispora acerina	KT 2982	T	LC014605	LC014597	LC014610	LC014615
Sulcatispora berchemiae	KT 1607	T	AB797244	AB809635	AB807534	AB808509
Tingoldiago clavata	MFLUCC 19-0496	T	MN857186	MN857182	MN857178	NA
Tingoldiago graminicola	KH68	T	AB521726	LC014598	AB521743	AB808561
Tingoldiago hydei	MFLUCC 19-0499	T	NA	MN857181	MN857177	NA
Towyspora aestuari	MFLUCC 15-1274	T	KU248853	KU248851	KU248852	NA
Wettsteinina lacustris	CBS 618.86		DQ678023	AF250831	NA	DQ677919

Table B4 GenBank accession numbers of the *Nigrograna* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	LSU	SSU	TEF1	RPB2
Nigrograna acericola	CGMCC 3.24957	T	OR253153	OR253312	NA	OR263572	NA
Nigrograna antibiotica	CCF 4378	T	JX570932	KF925327	KF925328	JX570934	LN626661
Nigrograna antibiotica	CCF 4998		LT221894	LT221895	NA	NA	NA
Nigrograna aquatica	MFLUCC 14-1178		MF399065	MF415392	MF415394	MF498582	NA
Nigrograna aquatica	MFLUCC 17-2318	T	MT627705	MN913705	NA	NA	NA
Nigrograna asexualis	ZHKUCC 22-0214	T	OP450965	OP450971	OP450979	OP432245	OP432241
Nigrograna asexualis	ZHKUCC 22-0215		OP450966	OP450972	OP450980	OP432246	OP432242
Nigrograna cangshanensis	MFLUCC 15-0253	T	KY511063	KY511064	KY511065	NA	NA
Nigrograna carollii	CCF 4484	T	LN626657	LN626682	LN626674	LN626668	LN626662
Nigrograna chromolaenae	MFLUCC 17-1437	T	MT214379	MT214473	NA	MT235801	NA
Nigrograna coffeae	ZHKUCC 22-0210	T	OP450967	OP450973	OP450981	OP432247	OP432243
Nigrograna coffeae	ZHKUCC 22-0211		OP450968	OP450974	OP450982	OP432248	OP432244
Nigrograna fuscidula	CBS 141556	T	KX650550	NA	NA	KX650525	NA
Nigrograna fuscidula	CBS 141476		KX650547	NA	KX650509	KX650522	KX650576
Nigrograna heveae	ZHKUCC 22-0284	T	OP584490	OP584488	OP584492	OP750372	OP750374
Nigrograna heveae	ZHKUCC 22-0285		OP584491	OP584489	OP584493	OP750373	OP750375
Nigrograna hydei	MFLU 18-2073	T	MN387225	MN387227	NA	MN389249	NA
Nigrograna impatientis	GZCC 19-0042	T	MN387226	MN387228	NA	MN389250	NA
Nigrograna italica	MFLU 23-0139	T	OR538590	OR538591	NA	OR531366	OR531365
Nigrograna jinghongensis	KUMUCC 21-0035	T	MZ493303	MZ493317	MZ493289	MZ508412	MZ508421
Nigrograna jinghongensis	KUMUCC 21-0036		MZ493304	MZ493318	MZ493290	MZ508413	MZ508422
Nigrograna jinghongensis	**JAUCC 6868**		**PQ895912**	**PQ901855**	**PQ932044**	**PV008164**	**PV008162**
Nigrograna jinghongensis	**JAUCC 6582**		**PQ895913**	**PQ901856**	**PQ932045**	**PV008165**	**PV008163**
Nigrograna kunmingensis	ZHKUCC 22-0242	T	OP456214	OP456379	OP456382	OP471608	NA
Nigrograna kunmingensis	ZHKUCC 22-0243		OP484334	OP456380	OP456383	OP471609	NA
Nigrograna lincangensis	ZHKUCC 23-0798	T	OR853099	OR922323	OR941079	OR966282	OR966280
Nigrograna lincangensis	ZHKUCC 23-0799		OR853100	OR922324	OR941080	OR966283	OR966281
Nigrograna locuta-pollinis	CGMCC 3.18784	T	MF939601	MF939583	NA	MF939613	MF939610
Nigrograna locuta-pollinis	LC11690		MF939603	MF939584	NA	MF939614	MF939611
Nigrograna mackinnonii	CBS 674.75	T	KF015654	KF015612	GQ387552	KF407986	KF015703
Nigrograna mackinnonii	E5202H		JX264157	KJ605422	JX264155	JX264154	JX264156
Nigrograna magnoliae	MFLUCC 20-0020	T	MT159628	MT159622	MT159634	MT159605	MT159611
Nigrograna magnoliae	MFLUCC 20-0021		MT159629	MT159623	MT159635	MT159606	MT159612
Nigrograna mycophila	CBS 141478	T	KX650553	NA	NA	KX650526	NA
Nigrograna mycophila	CBS 141483		KX650555	NA	KX650510	KX650528	KX650577
Nigrograna norvegica	CBS 141485	T	KX650556	NA	KX650511	NA	KX650578
Nigrograna obliqua	CBS 141477	T	KX650560	NA	NA	KX650531	KX650580
Nigrograna obliqua	CBS 141475		KX650558	NA	KX650512	KX650530	KX650579
Nigrograna obliqua	MRP		KX650561	NA	NA	KX650532	KX650581
Nigrograna oleae	CGMCC:3.24423	T	OR253080	OR253232	NA	OR262140	NA

Table B4 (continued)

Species	Strain Number	Status	ITS	LSU	SSU	TEF1	RPB2
Nigrograna peruviensis	CCF 4485	T	LN626658	LN626683	LN626677	LN626671	LN626665
Nigrograna puerensis	ZHKUCC 22-0212	T	OP450969	OP450975	OP450983	OP432249	NA
Nigrograna puerensis	ZHKUCC 22-0213		OP450970	OP450976	OP450984	OP432250	NA
Nigrograna rhizophorae	MFLUCC 18-0397	T	MN047085	NA	NA	MN077064	MN431489
Nigrograna rhizophorae	MFLU 19-1234		NA	MN017845	NA	MN077063	MN431490
Nigrograna rubescens	DAOMC 252610	T	OQ400924	OQ400934	NA	OQ413077	OQ413082
Nigrograna samueliana	NFCCI-4383	T	MK358817	MK358812	MK358810	MK330937	MK330939
Nigrograna schinifolii	GMB0498	T	OR120434	NA	NA	OR150022	NA
Nigrograna schinifolii	GMB0504		OR120441	NA	NA	OR150023	NA
Nigrograna lincangensis	ZHKUCC 23-0798	T	OR853099	OR922323	OR941079	OR966282	OR966280
Nigrograna lincangensis	ZHKUCC 23-0799		OR853100	OR922324	OR941080	OR966283	OR966281
Nigrograna locuta-pollinis	CGMCC 3.18784	T	MF939601	MF939583	NA	MF939613	MF939610
Nigrograna locuta-pollinis	LC11690		MF939603	MF939584	NA	MF939614	MF939611
Nigrograna mackinnonii	CBS 674.75	T	KF015654	KF015612	GQ387552	KF407986	KF015703
Nigrograna mackinnonii	E5202H		JX264157	KJ605422	JX264155	JX264154	JX264156
Nigrograna magnoliae	MFLUCC 20-0020	T	MT159628	MT159622	MT159634	MT159605	MT159611
Nigrograna magnoliae	MFLUCC 20-0021		MT159629	MT159623	MT159635	MT159606	MT159612
Nigrograna mycophila	CBS 141478	T	KX650553	NA	NA	KX650526	NA
Nigrograna mycophila	CBS 141483		KX650555	NA	KX650510	KX650528	KX650577
Nigrograna norvegica	CBS 141485	T	KX650556	NA	KX650511	NA	KX650578
Nigrograna obliqua	CBS 141477	T	KX650560	NA	NA	KX650531	KX650580
Nigrograna obliqua	CBS 141475		KX650558	NA	KX650512	KX650530	KX650579
Nigrograna obliqua	MRP		KX650561	NA	NA	KX650532	KX650581
Nigrograna oleae	CGMCC:3.24423	T	OR253080	OR253232	NA	OR262140	NA
Nigrograna peruviensis	CCF 4485	T	LN626658	LN626683	LN626677	LN626671	LN626665
Nigrograna mycophila	CBS 141478	T	KX650553	NA	NA	KX650526	NA
Nigrograna puerensis	ZHKUCC 22-0212	T	OP450969	OP450975	OP450983	OP432249	NA
Nigrograna puerensis	ZHKUCC 22-0213		OP450970	OP450976	OP450984	OP432250	NA
Nigrograna rhizophorae	MFLUCC 18-0397	T	MN047085	NA	NA	MN077064	MN431489
Nigrograna rhizophorae	MFLU 19-1234		NA	MN017845	NA	MN077063	MN431490
Nigrograna rubescens	DAOMC 252610	T	OQ400924	OQ400934	NA	OQ413077	OQ413082
Nigrograna samueliana	NFCCI-4383	T	MK358817	MK358812	MK358810	MK330937	MK330939
Nigrograna schinifolii	GMB0498	T	OR120434	NA	NA	OR150022	NA
Nigrograna schinifolii	GMB0504		OR120441	NA	NA	OR150023	NA
Nigrograna sichuanensis	CGMCC 3.24424		OR253096	OR253248	NA	OR251058	NA
Nigrograna thailandica	MFLUCC 17-2663		MK762709	MK762716	MK762704	NA	NA
Nigrograna thymi	MFLUCC 17-0497	T	KY775576	KY775573	KY775574	KY775578	NA
Nigrograna trachycarpi	GMB0499	T	OR120437	NA	NA	OR150024	NA
Nigrograna trachycarpi	GMB0505		OR120440	NA	NA	OR150025	NA
Nigrograna verniciae	CGMCC:3.24425	T	OR253116	OR253275	NA	OR251168	NA
Nigrograna wuhanensis	ZHKUCC 22-0329	T	OP941389	OP941390	OQ061465	OP947079	NA

Table B4 (continued)

Species	Strain Number	Status	ITS	LSU	SSU	TEF1	RPB2
Nigrograna yasuniana	YU.101026	T	HQ108005	LN626684	LN626676	LN626670	LN626664
Occultibambusa bambusae	MFLUCC 13-0855	T	KU940123	KU863112	NA	KU940193	KU940170
Occultibambusa fusispora	MFLUCC 11-0127	T	MZ329036	MZ329032	MZ329028	MZ325466	MZ325469
Occultibambusa pustula	MFLUCC 11-0502	T	KU940126	KU863115	NA	NA	NA

Table B5 GenBank accession numbers of the *Cyphellophora* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	LSU	TUB2
Cyphellophora aestiva	CBS 227.86		JQ766425	JQ766474	JQ766331
Cyphellophora aestiva	CBS:497.80	T	MH861291	MH873056	MW297547
Cyphellophora ambigua	CMRP2859	T	MT075638	-	-
Cyphellophora americana	CCF 6569	T	PP431575	PP431637	-
Cyphellophora artocarpi	CHCJHBJBLM	T	KP010367	KP122930	KP122925
Cyphellophora attinorum	CBS 131958	T	KF928463	KF928527	KF928591
Cyphellophora botryosa	CGMCC 3.19239	T	MK116369	MK116380	-
Cyphellophora capiguarae	CBS 132767	T	KF928464	KF928528	KF928592
Cyphellophora catalaunica	FMR 3992	T	HG003670	HG003673	-
Cyphellophora chlamydospora	CBS 127581（FMR 10878）	T	HG003674	HG003675	-
Cyphellophora clematidis	CBS 144983	T	MK442577	MK442519	MK442730
Cyphellophora deltoidea	CBS 263.77	T	KX447684	KX447683	-
Cyphellophora denticulata	COAD 3772	T	PQ236737	PQ236741	-
Cyphellophora denticulata	COAD 3773		PQ236733	PQ236745	-
Cyphellophora deltoidea	CBS 263.77	T	PQ236737	PQ236741	
Cyphellophora deltoidea	COAD 3772		PQ236733	PQ236745	
Cyphellophora endoradicis	CBS 148862	T	KT268871	OM527235	OM574614
Cyphellophora eucalypti	CBS 124764	T	KC455238	KC455254	KF928601
Cyphellophora europaea	CBS 101466	T	KC455246	KC455259	KC455229
Cyphellophora filicis	DP002A		MK404056	MK404052	-
Cyphellophora filicis	DP002B	T	MK404057	MK404053	-
Cyphellophora fusarioides	CBS 130291		JQ766439	JQ766486	JQ766363
Cyphellophora fusarioides	MUCL 44033	T	KC455239	KC455252	KC455224
Cyphellophora gamsii	CPC 25867	T	KX228255	NG_067308	KX228381
Cyphellophora goniomatis	CBS 146077	T	MN562133	MN567640	MN556842
Cyphellophora guangxiensis	JAUCC6546	T	PV082617	PV082619	PV155492
Cyphellophora guangxiensis	JAUCC6547		PV082616	PV082618	PV155491
Cyphellophora guizhouensis	CGMCC 3.19234	T	MK116364	MK116375	-
Cyphellophora guyanensis	MUCL 43737	T	KC455240	KC455253	KC455223
Cyphellophora hongheensis	KUMCC 21-0455	T	OM001338	OM001335	-
Cyphellophora jingdongensis	IFRDCC 2659	T	MF285234	MF285236	-
Cyphellophora laciniata	CBS 190.61	T	JQ766423	JQ766472	JQ766329
Cyphellophora livistonae	CPC 19433	T	NR_111824	NG_042752	-
Cyphellophora ludoviensis	CMRP1317	T	KX434722	KX583708	KX583749
Cyphellophora musae	GLZJXJ41	T	-	KP122932	KP122927
Cyphellophora neerlandica	CBS 149512	T	OQ990089	OQ990043	OQ989252
Cyphellophora neerlandica	CPC42641		OQ990090	OQ990044	OQ989253
Cyphellophora olivacea	CBS 123.74	T	KC455248	KC455261	KC455231
Cyphellophora oxyspora	CBS 698.73	T	KC455249	KC455262	KC455232

Table B5 (continued)

Species	Strain Number	Status	ITS	LSU	TUB2
Cyphellophora panamaensis	CPC 46528	T	PQ498949	PQ498998	PQ497778
Cyphellophora pauciseptata	CBS 284.85	T	MH861880	MH873568	JQ922031
Cyphellophora phyllostachydis	HLHNZWYZZ08	T	KP010371	KP122933	KP122929
Cyphellophora pluriseptata	CBS 286.85	T	KC455242	KC455255	KC455225
Cyphellophora reptans	CBS 113.85	T	JQ766445	JQ766493	JQ766370
Cyphellophora sambuci	CPC 39957	T	OK664711	OK663750	OK651206
Cyphellophora sessilis	CBS 243.85	T	MH861875	MH873561	KC455234
Cyphellophora spiralis	FMR 18548	T	ON009850	ON009930	ON667784
Cyphellophora suttonii	CBS 449.91	T	KC455243	KC455256	KC455226
Cyphellophora vermispora	CBS 228.86	T	KC455244	KC455257	KC455227
Cyphellophora vietnamensis	CBS 146924	T	LR814107	LR814108	LR814116
Exophiala bergeri	CBS 353.52	T	EF551462	NG_059199	EF551497
Exophiala clavispora	CGMCC 3.17517	T	KP347942	KP347964	KP347932
Exophiala salmonis	CBS 157.67	T	MH858932	MH870616	JN112499

Table B6 GenBank accession numbers of the *Exophiala* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	LSU	SSU	TUB2
Cyphellophora eucalypti	CBS 124764	T	KC455238	KC455254	KC455297	KF928601
Cyphellophora fusarioides	MUCL 44033	T	KC455239	KC455252	KC455298	KC455224
Exephiala yuxiensis	YMF1.07354		OL863155	OL863154	OM149370	OL944581
Exophiala abietophila	CBS 145038	T	MK442581	NG_066323		
Exophiala alcalophila	CBS 520.82	T	JF747041	AF361051	JN856010	JN112423
Exophiala angulospora	CBS 482.92	T	JF747046	KF155190	JN856011	JN112426
Exophiala aquamarina	CBS 119918	T	JF747054		JN856012	JN112434
Exophiala arunalokei	NCCPF106033		MW724320			
Exophiala asiatica	CBS 122847	T	EU910265			
Exophiala atacamensis	CCCT:19.114		MT137540	MT137544		
Exophiala attenuata	F10685		KT013095	KT013094		
Exophiala bergeri	CBS 353.52	T	EF551462	FJ358240	FJ358308	EF551497
Exophiala bonariae	CBS 139957	T	JX681046	KR781083		
Exophiala brunnea	CBS 587.66	T	JF747062	KX712342	JN856013	JN112442
Exophiala caementiphila	APSM 2022a		OX380499	OX380504		OX380502
Exophiala calicioides	JCM9765				AB007686	
Exophiala campbellii	NCPF 2274		LT594703	LT594760		
Exophiala cancerae	CBS 120420	T	JF747064			JN112444
Exophiala candelabrata	FMR 18336	T	ON009851	ON009931		ON491591
Exophiala capensis	CBS 128771	T	JF499841	MH876538		
Exophiala castellanii	CBS 158.58	T	JF747070	KF928522	JN856014	KF928586
Exophiala chapopotensis	EXF-16016		MT268970	OQ996257	OR035765	
Exophiala cinerea	CGMCC 3.18778	T	MG012695	MG197820	MG012724	MG012745
Exophiala clavispora	CGMCC 3.17512		KP347940	MG197829	MG012733	KP347931
Exophiala crusticola	CBS 119970	T	AM048755	KF155180	KF155199	
Exophiala dehoogii	FMR 19001		ON009858	ON009938		ON491588
Exophiala dermatitidis	CBS 207.35	T	KF928444	KF928508		KF928572
Exophiala dopicola	CBS:537.94	T	MH862483			
Exophiala ellipsoidea	CGMCC 3.17348	T	KP347955	KP347956	KP347965	KP347921
Exophiala embothrii	CBS 146558	T	MW045817	MW045821		MW055976
Exophiala encephalarti	CBS:128210		HQ599588	HQ599589		
Exophiala equina	CBS 119.23	T	JF747094		JN856017	JN112462
Exophiala eucalypti	CBS 142069		KY173411	KY173502		
Exophiala eucalypticola	CBS:143412	T	MH107891	MH107938		MH108039
Exophiala eucalyptigena	CBS 148273	T	ON811493	ON811552		ON803590
Exophiala eucalyptorum	CBS 121638	T	NR_132882	KC455258	KC455302	KC455228
Exophiala exophialae	CBS 668.76	T	AY156973	KX822326	KX822287	EF551499
Exophiala frigidotolerans	CBS 146539	T	LR699566	LR699567		
Exophiala gregii	BRIP 76064a	T	PP081661	PP081668		
Exophiala halophila	CBS 121512	T	JF747108		JN856015	JN112473

Table B6 (continued)

Species	Strain Number	Status	ITS	LSU	SSU	TUB2
Exophiala heteromorpha	CBS 232.33	T	MH855419	MH866871		
Exophiala hongkongensis	CBS 131511		JN625231			JN625236
Exophiala italica	MFLUCC 16-0245	T	KY496744	KY496723	KY501114	
Exophiala jeanselmei	CBS 507.90	T	AY156963	FJ358242	FJ358310	EF551501
Exophiala lacus	FMR 3995		KU705830	KU705847		
Exophiala lamphunensis	SDBR-CMU404	T	ON555798		ON555813	
Exophiala lapidea	SDBR-CMU409	T	ON555803		ON555818	
Exophiala lavatrina	NCPF 7893		LT594696	LT594755		
Exophiala lecanii-corni	CBS 123.33	T	AY857528	FJ358243	FJ358311	
Exophiala lichenicola	CPC 43306		OR680762	OR717018		
Exophiala lignicola	CBS 144622	T	MK442582	MK442524		
Exophiala macquariensis	CBS 144232	T	MF619956			MH297438
Exophiala mali	CBS 146791	T	MW175341	MW175381		
Exophiala mansonii	CBS 101.67	T	AF050247	AY004338	X79318	
Exophiala mesophila	CBS 402.95	T	JF747111	KX712349	JN856016	JN112476
Exophiala moniliae	CBS 520.76	T	KF881967	KJ930162		
Exophiala multiformis	FMR 18809	T	OU624180	OU624179		OU624443
Exophiala nagquensis	CGMCC 3.17284		KP347947	MG197838	MG012742	KP347922
Exophiala nidicola	FMR 3889		MG701055	MG701056		
Exophiala nigra	CBS 535.94	T	KY115191	KX712353		
Exophiala nishimurae	CBS 101538	T	AY163560	KX822327	KX822288	JX482552
Exophiala oligosperma	CBS 725.88	T	AY163551	KF928486	FJ358313	EF551508
Exophiala opportunistica	CBS 109811	T	KF928437	KF928501		KF928565
Exophiala palmae	CMRP 1196	T	KY680434	KY570929		KY689829
Exophiala phaeomuriformis	CBS 131.88	T	AJ244259			
Exophiala pisciphila	CBS 119914		JF747133			JN112495
Exophiala pisciphila	CBS 121505		JF747129			JN112491
Exophiala pisciphila	CBS 537.73	T	NR_121269	MH872483	NG_013192	JN112493
Exophiala pisciphila	CCF 4488		LT604105			
Exophiala pisciphila	SK48		MN811694			
Exophiala pisciphila	AFTOL-ID 669		DQ826739	DQ823101	DQ823108	
Exophiala pisciphila	CCF 5283		LT604107			
Exophiala pisciphila	FMR_18640		ON009854	ON009934		ON667790
Exophiala pisciphila	**JAUCC 6544**		**PV586960**			
Exophiala placitae	CBS 121716	T	MH863143	MH874694		
Exophiala polymorpha	CBS 138920	T	KP070763	KP070764		
Exophiala prostantherae	CBS 146794	T	MW175344	MW175384		
Exophiala prototropha	CBS:534.94		OR371992			
Exophiala pseudooligosperma	YMF 1.6741		MW616557	MW616559	MW616558	MZ127830
Exophiala psychrophila	CBS 191.87	T	JF747135		JN856019	JN112497

Table A6 (continued)

Species	Strain Number	Status	ITS	LSU	SSU	TUB2
Exophiala quercina	CPC 33408		MT223797	MT223892		
Exophiala radicis	P2772		KT099203	KT723447	KT723452	KT723462
Exophiala ramosa	FMR_18632	T	ON009853	ON009933		ON667786
Exophiala sacchari	CMRP3436	T	MZ132100	MW881154		
Exophiala salmonis	CBS 157.67	T	AF050274	AY213702	JN856020	JN112499
Exophiala saxicola	SDBR-CMU415	T	ON555809		ON555824	
Exophiala siamensis	SDBR-CMU417	T	ON555811		ON555826	
Exophiala sideris	CBS 121818	T	HQ452311		HQ441174	HQ535833
Exophiala spartinae	CBS 147266	T	MW473723			
Exophiala spinifera	CBS 899.68	T	AY156976			EF551516
Exophiala tremulae	CBS 129355	T	FJ665274		KT894147	KT894148
Exophiala verticillata	FMR_18551	T	ON009859	ON009939		ON667785
Exophiala viscosa	JF 03-3F	T	OR088060			
Exophiala wilsonii	CCF 5674		OR552118	OR555859	OR555748	
Exophiala xenobiotica	CBS 128104		MH864829	MH876272		
Exophiala yunnanensis	YMF1.06739		MZ779226	MZ779229	MZ781222	OM095379

Table B7 GenBank accession numbers of the *Fusarium* used in the phylogenetic analyses in this study

Species	Strain Number	Status	RPB1	RPB2	TEF1
Fusarium abutilonis	NRRL 66737	T	OM160825	OM160846	OM160867
Fusarium aconidiale	CBS 147772		MZ078192	MZ078218	MZ078246
Fusarium algeriense	CBS 142638	T	MF120488	MF120499	MF120510
Fusarium anguioides	LC7240		MW024433	MW474388	MW580442
Fusarium anguioides	NRRL 25385		JX171511	JX171624	MH742689
Fusarium atrovinosum	CBS 445.67	T	MN120713	MW928822	MN120752
Fusarium atrovinosum	CBS 130394		MN120714	MN120734	MN120753
Fusarium atrovinosum	NRRL 13444		JX171454	JX171568	GQ505403
Fusarium atrovinosum	NRRL 34013			GQ505472	GQ505408
Fusarium atrovinosum	NRRL 34016		HM347170	GQ505475	GQ505411
Fusarium austroafricanum	NRRL 66741	T	MH742537	MH742616	MH742687
Fusarium austroafricanum	NRRL 66742		MH742538	MH742617	MH742688
Fusarium aywerte	NRRL 25410	T	JX171513	JX171626	
Fusarium bambusarum	CGMCC 3.20820	T	MW024434	MW474389	MW580443
Fusarium bambusarum	LC7187		MW024435	MW474390	MW580444
Fusarium beomiforme	CBS 100160	T	MF120485	MF120496	MF120507
Fusarium buharicum	CBS 178.35	T	KX302920	KX302928	KX302912
Fusarium buharicum	CBS 796.70		JX171449	JX171563	
Fusarium burgessii	CBS 125537	T	MT409440	HQ646393	HQ667148
Fusarium camptoceras	CBS 193.65	T	MW928800	MN170383	AB820706
Fusarium celädicola	MFLUCC 16-0526	T	MH576579	ON759296	ON745620
Fusarium chlamydosporum	CBS 145.25	T	MN120715	MN120735	MN120754
Fusarium chlamydosporum	CBS 615.87		JX171526	GQ505469	GQ505405
Fusarium chlamydosporum	CBS 677.77		MN120716	GQ505486	GQ505422
Fusarium chlamydosporum	NRRL 34019			GQ505478	GQ505414
Fusarium chlamydosporum	NRRL 43633			GQ505493	GQ505429
Fusarium citricola	CBS 142421	T	LT746290	LT746310	LT746197
Fusarium citricola	CPC 27067		LT746287	LT746307	LT746194
Fusarium concolor	CBS 183.34	T	MH742492	MH742569	MH742650
Fusarium concolor	CBS 677.94		MH742503	MH742580	MH742660
Fusarium continuum	CBS 140841	T	KM520387	KM236782	KM236722
Fusarium convolutans	CBS 144207	T	LT996193	LT996141	LT996094
Fusarium convolutans	CBS 144208		LT996194	LT996142	LT996095
Fusarium guadeloupense	NRRL36125		OM160833	OM160854	OM160875
Fusarium guadeloupense	NRRL 66743		OM160832	OM160853	OM160874
Fusarium humicola	CBS 124.73	T	MN120718	MN120738	MN120757
Fusarium jiangxiensis	JAUCC 4303	T	submitted	submitted	submitted
Fusarium jiangxiensis	JAUCC 4841		submitted	submitted	submitted
Fusarium juglandicola	CBS 147773	T	MZ078190	MZ078215	MZ078243
Fusarium juglandicola	CBS 147775		MZ078191	MZ078217	MK034341

Table B7 (continued)

Species	Strain Number	Status	RPB1	RPB2	TEF1
Fusarium kotabaruense	Inacc F963	T	LS479875	LS479859	LS479445
Fusarium lateritium	NRRL 13622		JX171457	JX171571	
Fusarium microconidium	CBS 119843		MN120721		MN120759
Fusarium nelsonii	CBS 119876	T	MN120722	MN120740	MN120760
Fusarium nelsonii	CBS 119877		MN120723	MN120741	MN120761
Fusarium neosemitectum	CBS 189.60	T		MN170422	MN170489
Fusarium neosemitectum	CBS 190.60			MN170423	MN170490
Fusarium peruvianum	CBS 511.75	T	MN120728	MN120746	MN120767
Fusarium salinense	CBS 142420	T	LT746286	LT746306	LT746193
Fusarium salinense	CPC 26403		LT746284	LT746304	LT746191
Fusarium sp.	NRRL 13338		JX171447	JX171561	GQ505402
Fusarium sp. 1	NRRL 66179		KX302921	KX302929	KX302913
Fusarium sp. 1	NRRL 66180		KX302922	KX302930	KX302914
Fusarium sp. 1	NRRL 66181		KX302923	KX302931	KX302915
Fusarium sp. 1	NRRL 66182		KX302924	KX302932	KX302916
Fusarium sp. 1	NRRL 66183		KX302925	KX302933	KX302917
Fusarium sp. 1	NRRL 66184		KX302926	KX302934	KX302918
Fusarium spinosum	CBS 122438	T	MN120729	MN120747	MN120768
Fusarium spinosum	NRRL 43631		HM347187	GQ505491	GQ505427
Fusarium sporodochiale	CBS 220.61	T	MN120731	MN120749	MN120770
Fusarium stilboides	NRRL 20429		JX171468	JX171582	
Fusarium sublunatum	CBS 189.34	T	JX171451	JX171565	
Fusarium sublunatum	CBS 190.34		KX302927	KX302935	KX302919
Fusarium tjaynera	NRRL 66246	T	KP083268	KP083279	EF107152
Fusarium torreyae	CBS 133858	T	JX171548	JX171660	HM068337
Fusarium zanthoxyli	NRRL 66285	T	OM160837	OM160858	OM160879

Table B8 GenBank accession numbers of the *Coryneum* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	LSU	TEF1	RPB2
Coryneum arausiacum	MFLU 14-0796	T	MF190121	MF190067	MF377575	MF377609
Coryneum castaneicola	CFCC 52315	T	MH683559	MH683551	MH685731	MH685723
Coryneum castaneicola	CFCC 52316		MH683560	MH683552	MH685732	MH685724
Coryneum depressum	D202		MH674330	MH674330	MH674338	MH674334
Coryneum fagi	BJFC-S1782	T	MW144761	MW144953	NA	NA
Coryneum fagi	BJFC-S1783		MW144762	MW144954	NA	NA
Coryneum gigasporum	CFCC 52319	T	MH683565	MH683557	MH685737	MH685729
Coryneum gigasporum	CFCC 52320		MH683566	MH683558	MH685738	MH685730
Coryneum heveanum	MFLUCC 17-0369	T	MH778707	MH778703	NA	NA
Coryneum heveanum	MFLUCC 17-0376		MH778708	MH778704	NA	NA
Coryneum ilicis	CFCC 52994	T	MK799948	MK799935	NA	NA
Coryneum ilicis	CFCC 52995		MK799949	MK799936	NA	NA
Coryneum ilicis	CFCC 52996		MK799950	MK799937	NA	NA
Coryneum jiangxiensis	JAUCC4408	T	PV586546			
Coryneum jiangxiensis	JAUCC5057	T	PV586734			
Coryneum lanciforme	D215		MH674332	MH674332	MH674340	MH674336
Coryneum modonium	D203		MH674331	MH674331	MH674339	MH674335
Coryneum perniciosum	CBS 130.25		MH854812	MH866313	NA	NA
Coryneum septemseptatum	GMB0393		OQ540748	OQ540743	OQ540767	
Coryneum septemseptatum	GMB0392	T	OQ560328	OQ560329		
Coryneum sinense	CFCC 52452	T	MH683561	MH683553	MH685733	MH685725
Coryneum sinense	CFCC 52453		MH683562	MH683554	MH685734	MH685726
Coryneum songshanense	CFCC 52997	T	MK799946	MK799933	MK799822	MK799812
Coryneum songshanense	CFCC 52998		MK799947	MK799934	MK799823	MK799813
Coryneum suttonii	CFCC 52317		MH683563	MH683555	MH685735	MH685727
Coryneum suttonii	CFCC 52318		MH683564	MH683556	MH685736	MH685728
Coryneum umbonatum	D201		MH674329	MH674329	MH674337	MH674333
Stegonsporium pyriforme	CBS120522		NR_172969	MH682182	EU040003	MH682183
Stilbospora macrosperma	CBS115073		NR_145278	NG_063951	EU039999	KF570195

Table B9 GenBank accession numbers of the *Diaporthe* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	TEF1	TUB2	CAL	HIS
Diaporthe acardii	CBS 720.97	T	KC343024	KC343750	KC343992	KC343266	KC343508
Diaporthe acardii	BRIP 66526		N/A	MN696527	MN696538	N/A	N/A
Diaporthe acardii	Phom240		KY511315	MH708543	KY511346	N/A	N/A
Diaporthe acardii	PMM1681		KY511337	MH708552	KY511369	N/A	N/A
Diaporthe acardii	CAA817		MK792305	MK828076	MN000351	MK883831	MK871445
Diaporthe acardii	CAA818		MK792307	MK828078	MN000352	MK883833	MK871447
Diaporthe acardii	CPC 34247		MH063905	MH063911	MH063917	MH063893	MH063899
Diaporthe acardii	CPC 34248		MH063906	MH063912	MH063918	MH063894	MH063900
Diaporthe acardii	CGMCC3.18286		KX986790	KX999182	KX999223	N/A	KX999261
Diaporthe acardii	LC4419		KX986789	KX999181	KX999222	KX999286	KX999260
Diaporthe acardii	CGMCC3.28206		PQ288777	PQ296167	PQ296218	PQ296273	PQ303515
Diaporthe acardii	CGMCC3.28220		PQ288774	PQ296164	PQ296215	PQ296270	PQ303512
Diaporthe acardii	SAUCC5560		PQ288775	PQ296165	PQ296216	PQ296271	PQ303513
Diaporthe acardii	SAUCC5603		PQ288776	PQ296166	PQ296217	PQ296272	PQ303514
Diaporthe acutispora	CGMCC3.18285	T	KX986764	KX999155	KX999195	KX999274	KX999235
Diaporthe biconispora	ZJUD62	T	KJ490597	KJ490476	KJ490418	MT898460	KJ490539
Diaporthe biconispora	ZJUD61		KJ490596	KJ490475	KJ490417	N/A	KJ490538
Diaporthe biconispora	ZHKUCC 22-0058		ON322887	ON315044	ON315076	N/A	ON315017
Diaporthe biconispora	ZHKUCC 22-0059		ON322888	ON315045	ON315077	N/A	ON315018
Diaporthe biconispora	SAUCC 194.72		MT822600	MT855912	MT855797	MT855679	MT855568
Diaporthe biconispora	NFCCI 4385		MN061372	N/A	MN431500	N/A	N/A
Diaporthe biconispora	BCKSKMP-8		MG049670	N/A	N/A	N/A	N/A
Diaporthe biconispora	FS441		MK592793	N/A	N/A	N/A	N/A
Diaporthe biconispora	CGMCC3.25976		PQ288782	PQ296172	PQ296223	PQ296278	PQ303520
Diaporthe biconispora	SAUCC0078		PQ288783	PQ296173	PQ296224	PQ296279	PQ303521
Diaporthe chamaeropis	CBS 454.81	T	KC343048	KC343774	KC344016	KC343290	KC343532
Diaporthe chamaeropis	CBS 753.70		KC343049	KC343775	KC344017	KC343291	KC343533
Diaporthe chamaeropis	AR5149		KC843309	KC843118	KC843223	KC843143	N/A
Diaporthe chamaeropis	FAU 461		KC843307	KC843116	KC843221	KC843141	N/A
Diaporthe cinerascens	CBS 719.96		KC343050	KC343776	KC344018	KC343292	KC343534
Diaporthe corylicola	CFCC 53986	T	MW839880	MW815894	MW883977	MW836684	MW836717
Diaporthe decedens	CBS 109772		KC343059	KC343785	KC344027	KC343301	KC343543
Diaporthe decedens	CBS 114281		KC343060	KC343786	KC344028	KC343302	KC343544
Diaporthe donglingensis	CFCC 56581	T	OM956090	ON157986	ON158021	N/A	ON157951
Diaporthe donglingensis	CFCC 57432		OM956091	ON157987	ON158022	N/A	ON157952
Diaporthe foeniculina	CBS 111553	T	KC343101	KC343827	KC344069	KC343343	KC343585
Diaporthe foeniculina	AR5151		KC843303	KC843112	KC843217	KC843137	N/A
Diaporthe foeniculina	CBS 123208		KC343104	KC343830	KC344072	KC343346	KC343588
Diaporthe foeniculina	FAU 460		KC843304	KC843113	KC843218	KC843138	N/A
Diaporthe foeniculina	ICMP 12285		KC145853	KC145937	N/A	N/A	N/A

Table B9 (continued)

Species	Strain Number	Status	ITS	TEF1	TUB2	CAL	HIS
Diaporthe foeniculina	CBS 136971		KJ160564	KJ160596	N/A	N/A	N/A
Diaporthe foeniculina	CBS 136972		KJ160565	KJ160597	MF418509	MG281695	MF418264
Diaporthe foeniculina	JZBH320170		MN653009	MN892277	MN887113	N/A	N/A
Diaporthe foeniculina	MFLUCC 17-1029		KY964191	KY964147	KY964075	N/A	N/A
Diaporthe foeniculina	CPC 18191		JF951146	N/A	N/A	N/A	N/A
Diaporthe foeniculina	JZB320006		MK066126	MK078545	MK078546	N/A	N/A
Diaporthe foeniculina	MFLUCC 18-0739		MH846233	N/A	MK049555	N/A	N/A
Diaporthe foeniculina	PSCG 031		MK626922	MK654855	MK691245	N/A	MK726207
Diaporthe foeniculina	PSCG 032		MK626923	MK654856	MK691246	N/A	MK726208
Diaporthe foeniculina	CGMCC3.28226		PQ288779	PQ296169	PQ296220	PQ296275	PQ303517
Diaporthe foeniculina	SAUCC1102		PQ288780	PQ296170	PQ296221	PQ296276	PQ303518
Diaporthe forlicesenica	MFLUCC 17-1015	T	KY964215	KY964171	KY964099	N/A	N/A
Diaporthe hsinchuensis	NTUPPMCC 18-153-1	T	MZ268409	MZ268472	MZ268430	MZ268451	MZ268493
Diaporthe hsinchuensis	NTUPPMCC 18-153-2		MZ268410	MZ268473	MZ268431	MZ268452	MZ268494
Diaporthe hunanensis	**JAUCC 7359**		**PV587098**				
Diaporthe hunanensis	**JAUCC 6903**	**T**	**PV587080**				
Diaporthe jiangxiensis	**JAUCC 4738**		**PV586605**				
Diaporthe jiangxiensis	**JAUCC 5242**		**PV586813**				
Diaporthe jiangxiensis	**JAUCC 5575**		**PV586908**				
Diaporthe jiangxiensis	**JAUCC 3940**	**T**	**PV586346**				
Diaporthe jiangxiensis	**JAUCC 5228**		**PV586799**				
Diaporthe jiangxiensis	**JAUCC 5225**		**PV586796**				
Diaporthe jiangxiensis	**JAUCC 5545**		**PV586878**				
Diaporthe jiangxiensis	**JAUCC 5224**		**PV586795**				
Diaporthe jiangxiensis	**JAUCC 5244**		**PV586815**				
Diaporthe multiguttulata	CFCC 53095	T	MK432645	MK578121	MK578048	MK442967	KJ490575
Diaporthe multiguttulata	CFCC 53099		MK573958	MK574633	MK574653	MK574593	MK574613
Diaporthe parvae	PSCG034	T	MK626919	MK654858	MK691248	N/A	MK726210
Diaporthe pterocarpi	MFLUCC 10-0575		JQ619901	JX275418	JX275462	JX197453	N/A
Diaporthe pterocarpi	CBS 133813		KC343123	KC343849	KC344091	KC343365	KC343607
Diaporthe pterocarpi	LGMF922		KC343124	KC343850	KC344092	KC343366	KC343608
Diaporthe pterocarpi	SAUCC194.36		MT822564	MT855877	MT855761	MT855647	MT855533
Diaporthe pterocarpi	URM 7873		MH122535	MH122530	MH122521	MH122525	MH122518
Diaporthe pterocarpi	URM 7874		MH122538	MH122533	MH122524	MH122528	MH122517
Diaporthe pungensis	SAUCC194.112	T	MT822640	MT855952	MT855837	MT855719	MT855607
Diaporthe pungensis	SAUCC 194.89		MT822617	MT855929	MT855814	MT855696	MT855585
Diaporthe tetradii	JAUCC 7358		PV587097				
Diaporthe tetradii	JAUCC 6904	T	PV587081				
Diaporthe undulata	CGMCC3.18293	T	KX986798	KX999190	KX999230	N/A	KX999269

Table B10 GenBank accession numbers of the *Amphisphaeria* used in the phylogenetic analyses in this study

Species	Strain Number	Status	ITS	LSU	RPB2	TUB2
Amphisphaeria acericola	MFLUCC 14-0842	T	MF614128	MF614131	N/A	N/A
Amphisphaeria acericola	MFLU 16-2479		MK640423	MK640424	N/A	N/A
Amphisphaeria ailaoshanensis	HKAS 130266	T	PP584673	PP584770		
Amphisphaeria ailaoshanensis	HKAS 130267		PP584674	PP584771		
Amphisphaeria camelliae	HKAS 107021	T	MT756621	MT756615	MT789850	MT774368
Amphisphaeria camelliae	MFLUCC 20-0122		MT756622	MT756616	MT789851	MT774369
Amphisphaeria chenzhouensis	**JAUCC5233**	**T**	**PV586804**			
Amphisphaeria chenzhouensis	**JAUCC6862**		**PV587040**			
Amphisphaeria chiangmaiensis	CMUB 40017	T	OR507139	OR507152	OR504416	N/A
Amphisphaeria chiangmaiensis	MFLU 23-0411		OR507140	OR507153	N/A	N/A
Amphisphaeria curvaticonidia	HKAS 102288	T	MT756624	MT756618	MT789853	N/A
Amphisphaeria curvaticonidia	MFLUCC 18-0620		MT756623	MT756617	MT789852	N/A
Amphisphaeria flava	MFLUCC 18-0361	T	MH971224	MH971234	N/A	MK033638
Amphisphaeria fuckelii	CBS 140409	T	KT949902	KT949902	MH554918	MH554677
Amphisphaeria fuckelii	WU 33555		KT949903	KT949903	N/A	N/A
Amphisphaeria guttulata	MFLU 22-0078	T	OQ101582	OQ101583		
Amphisphaeria hibiscicola	HKAS 136910	T	PQ570847	PQ570865		
Amphisphaeria hongheensis	MHZU 24-0515		PQ165968	PQ166524	PQ249401	PQ249399
Amphisphaeria hongheensis	GMB1135T	T	PQ165969	PQ166525	PQ249402	PQ249400
Amphisphaeria hydei	CMUB 40016	T	OR507141	OR507154	OR504417	OR519975
Amphisphaeria karsti	GZAAS 20-0147	T	OR224991	OR209622	N/A	N/A
Amphisphaeria karsti	GZAAS 20-0148		OR224992	OR209623	N/A	N/A
Amphisphaeria kunmingensis	KUNCC 23-15522	T	PP584675	PP584772		PQ046051
Amphisphaeria magna	HKAS 130270 T	T	PP584677	PP584774		
Amphisphaeria magna	HKAS 130271		PP584678	PP584775		
Amphisphaeria mangrovei	NFCCI 4247	T	MG844283	MG844275	N/A	N/A
Amphisphaeria micheliae	HKAS 107012	T	MT756625	MT756619	MT789854	MT774370
Amphisphaeria micheliae	MFLUCC 20-0121		MT756626	MT756620	MT789855	MT774371
Amphisphaeria neoaquatica	MFLUCC 14-0045	T	MK828607	MK835805	N/A	N/A
Amphisphaeria oleae	CGMCC 3.24959	T	OR253156	OR253313	OR253756	OR266102
Amphisphaeria oleae	UESTCC 23.0120		OR253157	OR253314	OR253757	OR266103
Amphisphaeria orixae	GZCC 22-2031	T	OQ064541	OQ064543	N/A	N/A
Amphisphaeria orixae	GZCC 22-2032		OQ064542	OQ064544	N/A	N/A
Amphisphaeria parvispora	MFLU 18-0767		MW240644	MW240574	MW658631	MW775601
Amphisphaeria qujingensis	KUMCC 19-0187	T	MN477033	MN556316	N/A	N/A
Amphisphaeria qujingensis	KUMCC 19-0186		MN707568	MN707566	N/A	N/A
Amphisphaeria sambuci	CBS 131707	T	KT949904	KT949904	MH554911	MH704632
Amphisphaeria sambuci	WU 33557		KT949905	KT949905	N/A	N/A
Amphisphaeria shangrilaensis	HKAS 130272	T	PP584679	PP584776		
Amphisphaeria sorbi	MFLUCC 13-0721	T	KR092797	KP744475	N/A	N/A

Table B10 (continued)

Species	Strain Number	Status	ITS	LSU	RPB2	TUB2
Amphisphaeria tetradiana	**JAUCC3992**		**PV586391**			
Amphisphaeria tetradiana	**JAUCC4298**		**PV586483**			
Amphisphaeria tetradiana	**JAUCC4299**		**PV586484**			
Amphisphaeria tetradiana	**JAUCC4374**		**PV586514**			
Amphisphaeria tetradiana	**JAUCC4432**		**PV586570**			
Amphisphaeria tetradiana	**JAUCC4843**		**PV586707**			
Amphisphaeria tetradiana	**JAUCC4860**		**PV586723**			
Amphisphaeria tetradiana	**JAUCC5139**		**PV586750**			
Amphisphaeria tetradiana	**JAUCC5616**	**T**	**PV586949**			
Amphisphaeria thailandica	MFLU 18-0794	T	MH971225	MH971235	MK033640	MK033639
Amphisphaeria umbrina	AFTOL-ID 1229		N/A	AF452029	N/A	N/A
Amphisphaeria uniseptata	CBS 114967	T	N/A	MH554197	MH554878	MH554638
Amphisphaeria verniciae	UESTCC 23.0122		OR253155	OR253270	OR251140	OR266103
Amphisphaeria verniciae	CGMCC 3.24960	T	OR253154	OR253269	OR251139	OR266100
Amphisphaeria xishuangbannaensis	KUNCC 23-15524	T	PP584681	PP584778		
Amphisphaeria yunnanensis	KUMCC 19-0188	T	MN477177	MN556306	N/A	N/A
Amphisphaeria yunnanensis	KUMCC 19-0189		MN550997	MN550992	N/A	N/A
Beltraniopsis longiconidiophora	MRC 6-1	T	MF580249	MF580256	N/A	N/A
Beltraniopsis neolitseae	CBS:137974	T	KJ869126	KJ869183	N/A	N/A

Table B11 GenBank accession numbers of the *Funiliomyces* used in the phylogenetic analyses in this study

Speceies	**Strain Number**	**Status**	**LSU**	**ITS**	**RPB2**
Achaetomium macrosporum	CBS 532.94		KX976699	KX976574	KX976797
Amphisphaeria fuckelii	CBS 140409	T	KT949902	KT949902	MH554918
Amphisphaeria thailandica	MFLU 18-0794	T	MH971235	MH971225	MK033640
Anungitiomyces stellenboschiensis	CPC 34726	T	MK876415	MK876376	NA
Appendicospora hongkongensis	HKAS 107015		MW240581	MW240651	MW658638
Arthrinium hysterinum	ICMP 6889		MK014841	MK014874	DQ368649
Arthrinium pseudoparenchymaticum	SICAUCC 18-0008		MK346321	MK346319	MK359207
Beltrania pseudorhombica	CBS 138003	T	KJ869215	MH554124	MH555032
Beltraniopsis neolitseae	CBS 137974	T	KJ869183	KJ869126	NA
Brachiampulla verticillata	ICMP 15993		MW144403	MW144419	NA
Castanediella acaciae	CBS 139896	T	MH878661	KR476728	NA
Castanediella cagnizarii	MUCL 41095		KC775707	KC775732	NA
Castanediella ramosa	MUCL 39857		KC775711	KC775736	NA
Chaetomium elatum	CBS 374.66		MH870466	KC109758	KF001820
Clypeophysalospora latitans	CBS 141463	T	KX820261	KX820250	NA
Cylindrium elongatum	CBS 115974		KM231733	KM231853	KM232429
Cylindrium grande	CBS 145578		MK876426	MK876385	MK876482
Funiliomyces acaciae	**CPC 29771**		**KY173493**	**KY173400**	**NA**
Funiliomyces bisepatus	**CBS 475.94**		**EU107288**	**NA**	**NA**
Funiliomyces biseptatus	CBS 100373	T	NG_067443	NR_159862	NA
Funiliomyces calliandrae	**CPC 48004**		**PV664963**	**PV664937**	**PV664022**
Funiliomyces fragilis	**P057**		**EU107290**	**NA**	**NA**
Funiliomyces hwasunensis	**CMML 20-35**		**PQ741487**	**PQ741486**	**NA**
Funiliomyces hwasunensis	**CMML 20-88**		**PQ741488**	**NA**	**NA**
Funiliomyces jiangxiensis	**JAUCC 5298**	T	**OQ869216**	**OQ869213**	**OR046688**
Funiliomyces jiangxiensis	**JAUCC 4255**		**OQ869214**	**OQ869215**	**OR046687**
Funiliomyces mavisleverae	**BRIP 76362a**		**PQ431199**	**PQ431206**	**NA**
Funiliomyces monticola	**CBS 188.95**		**EU107289**	**NA**	**NA**
Funiliomyces retrophylli	**CBS:148271**		**ON811548**	**ON811489**	**NA**
Funiliomyces sparsa	**P055**		**EU107291**	**NA**	**NA**
Funiliomyces zapatensis	**CBS 429.93**		**EU107287**	**NA**	**NA**
Hyponectria buxi	UME 31430		AY083834	NA	NA
Iodosphaeria honghensis	MFLU 19-0719	T	MK722172	MK737501	MK791287
Iodosphaeria tongrenensis	MFLU 15-0393		KR095283	KR095282	NA
Leiosphaerella praeclara	CBS 125586		JF440976	JF440976	NA
Melogramma campylosporum	MFLU 17-0348		MW240575	MW240645	MW658632
Melogramma campylosporum	MFLU 18-0778		MW240576	MW240646	MW658633
Neoamphisphaeria hyalinospora	MFLU 19-2131	T	MW240579	MW240649	MW658636

Table B11 (continued)

Speceies	Strain Number	Status	LSU	ITS	RPB2
Neoamphisphaeria shangrilaensis	HKAS:130274		PP584800	PP584703	NA
Neophysalospora eucalypti	CBS 138864	T	KP004490	KP004462	NA
Nothodactylaria comitabilis	CPC 45173		PQ498974	PQ498925	NA
Nothodactylaria fusiformis	KUNCC 23–13961	T	PQ671162	PQ671242	PQ662509
Nothodactylaria guizhouensis	KUNCC 23–14080	T	PQ671163	PQ671243	PQ662510
Nothodactylaria nephrolepidis	CPC:37028		MN567639	MN562132	MN556809
Nothodactylaria nephrolepidis	CBS:146078^{T}	T	NG_068668	NR_166331	NA
Nothodactylaria polyblastis	KUNCC 23–13922	T	PQ671164	PQ671244	PQ662511
Nothodactylaria woodwardiae	KUNCC 23–13927	T	PQ671165	PQ671245	PQ662512
Nothodactylaria woodwardiae	KUNCC 23–13886		PQ671166	PQ671246	PQ662513
Nothodactylaria woodwardiae	KUNCC 23–14045		PQ671167	PQ671247	PQ662514
Nothodactylaria woodwardiae	KUNCC 23–13954		PQ671168	PQ671248	NA
Nothodactylaria woodwardiae	KUNCC23–14006		PQ671169	PQ671249	NA
Oxydothis metroxyli	MFLUCC 15-0283		KY206764	KY206775	NA
Oxydothis metroxylonicola	MFLUCC 15-0281	T	KY206763	KY206774	KY206781
Oxydothis palmicola	MFLUCC 15-0806	T	KY206765	KY206776	KY206782
Phlogicylindrium eucalypti	CBS 120080	T	DQ923534	DQ923534	MH554893
Phlogicylindrium uniforme	CBS 131312	T	JQ044445	JQ044426	NA
Polyscytalum eucalyptorum	CPC 17207	T	KJ869176	KJ869118	NA
Pseudapiospora corni	CBS 140736	T	KT949907	KT949907	NA
Pseudomassaria chondrospora	CBS 125600		JF440981	JF440981	NA
Pseudosporidesmium knawiae	CBS:123529	T	MH874823	MH863299	NA
Pseudosporidesmium lambertiae	CBS 143169	T	MG386087	MG386034	NA
Pseudotruncatella arezzoensis	MFLUCC 14-0988	T	MG192317	MG192320	NA
Pseudotruncatella bolusanthi	CBS 145532	T	MK876448	MK876407	NA
Robillarda sessilis	CBS 114312	T	KR873284	KR873256	NA
Seiridium marginatum	CBS 140403	T	KT949914	KT949914	MK523301
Sordaria fimicola	CBS 723.96			MH862606	
Strelitziomyces knysnanus	CBS 146056	T	MN567642	MN562135	MN556810
Subsessila turbinata	MFLUCC 15-0831	T	KX762289	KX762288	NA
Vialaea insculpta	DAOM 240257		JX139726	JX139726	NA
Vialaea minutella	BRIP 56959		KC181924	KC181926	NA
Xyladictyochaeta lusitanica	CBS 142290	T	KY853543	KY853479	NA

Table B12 GenBank accession numbers of the *Nemania* used in the phylogenetic analyses in this study

Speceies	Strain Number	Status	ITS	LSU	RPB2	TUB2
Daldinia bambusicola	CBS 122872	T	KY610385	KY610431	KU684287	KU684127
Hypoxylon pulicicidum	CBS 122622		JX183076	KY610492	KY624280	JX183074
Nemania abortiva	BISH 467	T	GU292816		GQ844768	GQ470219
Nemania aenea	CBS680.86		AJ390427			
Nemania aquilariae	KUMCC 20-0268	T	MW729422	MW729420	MW717891	MW881142
Nemania bannaensis	GMB0731	T	PP153355		PP198079	PP197666
Nemania beaumontii	HAST 405		GU292819		GQ844772	GQ470222
Nemania bipapillata	HAST 90080610		GU292818		GQ844771	GQ470221
Nemania buxi	GMB0735	T	PP153356		PP198081	PP197664
Nemania camelliae	GMB0067		MW851888	MW851871	MW836056	MW836030
Nemania camelliae	GMB0068	T	MW851889	MW851872	MW836055	MW836029
Nemania caries	GMB0070	T	MW851874	MW851857	MW836071	MW836036
Nemania caries	GMB0069		MW851873	MW851856	MW836069	MW836035
Nemania changningensis	GMB0057		MW851876	MW851859	MW836062	MW836028
Nemania changningensis	GMB0056	T	MW851875	MW851858	MW836061	MW836027
Nemania chestersii	JF 04024			DQ840072	DQ631949	DQ840089
Nemania colliculosa	TROM:129	T	OP289676			
Nemania confluens	ZT-Myc-64253		MW489543			
Nemania cyclobalanopsina	GMB0062	T	MW851883	MW851866	MW836057	MW836025
Nemania cyclobalanopsina	GMB0061		MW851882	MW851865	MW836058	MW836026
Nemania delonicis	MFLU 19-2124	T	MW240613	MW240542	MW342617	MW775574
Nemania dendrobii	MFLUCC 18-1213	T	MZ463138	MZ463181	MZ970708	MZ998957
Nemania diffusa	GMB0071		MW851877	MW851860	MW836067	MW836031
Nemania diffusa	GMB0072		MW851878	MW851861	MW836068	MW836032
Nemania diffusa	HAST 91020401		GU292817		GQ844769	GQ470220
Nemania ethancrensonii	CBS 148337	T	ON869311	ON869311	ON808489	ON808533
Nemania feicuiensis	GMB0058		MW851879	MW851862	MW836064	MW836024
Nemania feicuiensis	GMB0059	T	MW851880	MW851863	MW836063	MW836023
Nemania fusoidispora	GZUH0098	T	MW851881	MW851864	MW836070	MW836037
Nemania geijerae	BRIP 67055a	T	PV074483			
Nemania guangdongensis	ZHKUCC 22-0136	T	OR164916		OR166293	
Nemania huangjingensis	GMB0747		PQ884663	PQ885375		PQ893575
Nemania huangjingensis	GMB0746	T	PQ884662	PQ885374		PQ893574
Nemania hydei	MFLU 23-0381	T	OR492027	OR492028	OR496292	OR496293
Nemania hyrcana	MUCL 57704		OP359332	OP359329	OP359598	OP359603
Nemania hyrcana	MUCL 57703		OP359333	OP359330	OP359599	OP359604
Nemania illita	YMJ 236		EF026122		GQ844770	EF025608
Nemania jiangxiensis	**JAUCC 4404**	**T**	**PV586542**			
Nemania jiangxiensis	**JAUCC 5100**		**PV586746**			
Nemania landingshanensis	GMB0791	T	PP153358		PP198083	PP197685

Table B12 (continued)

Speceies	Strain Number	Status	ITS	LSU	RPB2	TUB2
Nemania lasiocarpae	PP153360	T	PP153360		PP198085	PP197687
Nemania leigongshanensis	GMB0743	T	PP153362		PP198087	PP197689
Nemania leishanensis	GMB0768		PP584764	PP584837		PP951421
Nemania lishuicola	GMB0065	T	MW851886	MW851869	MW836065	MW836033
Nemania longipedicellata	MFLU 18-0819	T	MW240612	MW240541	MW342616	MW775573
Nemania macrocarpa	WSP 265	T	GU292823	MH874423	GQ844776	GQ470226
Nemania maritima	HAST 89120401	T	GU292822		GQ844775	GQ470225
Nemania mengmanensis	GMB0793	T	PP153365			PP197692
Nemania palmarum	MFLU:24-0159		PP592423	PP621048		
Nemania paraphysata	MFLU 19-2121	T	MW240609	NG_081491	MW342613	
Nemania phetchaburiensis	MFLU 16-1185	T	MN047124	MN017888		
Nemania plumbea	JF TH-04-01		DQ641634	DQ840071	DQ631952	DQ840084
Nemania plumbea	6540		JQ846087			
Nemania pouzarii	ATCC 2612		KC477228			
Nemania prava	TROM 104	T	OP289674			
Nemania primolutea	YMJ 91102001	T	EF026121		GQ844767	EF025607
Nemania queenslandica	BRIP 67056a	T	PV074484			
Nemania rubi	GMB0064	T	MW851885	MW851868	MW836059	MW836021
Nemania serpens	MUCL 57702		OP359334	OP359331	OP359600	OP359605
Nemania serpens	HAST 235		GU292820		GQ844773	GQ470223
Nemania sphaeriostoma	JDR 261		GU292821		GQ844774	GQ470224
Nemania subchangningensis	GMB0749	T	PP153366			PP197693
Nemania thailandensis	MFLU 19-2122		MW240610	MW240539	MW342614	MW775571
Nemania thailandensis	MFLU 19-2117	T	MW240611	NG_081492	MW342615	MW775572
Nemania uda	CBS 148422		ON869312	ON869312	ON808488	ON808532
Nemania viridis	MFLU 17-2600	T	MN047123	MN017887		
Nemania yunnanensis	KUMCC 20-0267		MW729423	MW729421	MW717892	MW881141

APPENDIX C

ESTIMATES OF EVOLUTIONARY DIVERGENCE OVER SEQUENCE PAIRS BETWEEN GROUPS

Estimates of evolutionary divergence in ITS rDNA and LSU rDNA sequences of the genus *Tetradiomyces.*

Table C1 The number of base substitutions per site between genera based on ITS sequences

	Latorua	***Matsushimamyces***	***Polyschema***	***Pseudoasteromassaria***	***Triseptata***	***Verrucohypha***	***Multiverruca***
Matsushimamyces	0.1800						
Polyschema	0.1414	0.1918					
Pseudoasteromassaria	0.2273	0.2823	0.2209				
Triseptata	0.1377	0.1998	0.1566	0.1822			
Verrucohypha	0.1583	0.1379	0.1358	0.2402	0.1757		
Multiverruca	0.0819	0.1569	0.0987	0.1990	0.1451	0.1035	
Tetradiomyces	0.1329	0.1841	0.1443	0.2392	0.1681	0.1239	0.1080

Table C2 The number of base substitutions per site between genera based on LSU sequences

	Latorua	***Matsushimamyces***	***Polyschema***	***Pseudoasteromassaria***	***Triseptata***	***Verrucohypha***	***Multiverruca***
Matsushimamyces	0.0274						
Polyschema	0.0300	0.0359					
Pseudoasteromassaria	0.0296	0.0376	0.0380				
Triseptata	0.0396	0.0387	0.0326	0.0314			
Verrucohypha	0.0259	0.0386	0.0286	0.0326	0.0439		
Multiverruca	0.0132	0.0191	0.0256	0.0282	0.0319	0.0266	
Tetradiomyces	0.0330	0.0372	0.0326	0.0374	0.0399	0.0141	0.0292

Estimates of evolutionary divergence in ITS rDNA, LSU rDNA, SSU rDNA, and TEF1 sequences of the *Pseudokeissleriella*.

Table C3 The number of base substitutions per site between genera based on SSU sequences

	Darksidea	*Crassoascoma*	*Groenewaldia*	*Halobyssothecium*	*Katumotoa*	*Keissleriella*	*Lentithecium*	*Murilentithecium*	*Neobambusicola*	*Phragmocamarosporium*	*Pleurophoma*	*Poaceascoma*	*Setoseptoria*	*Tingoldiago*	*Towyspora*	*Wettsteinina*	*Pseudokeissleriella*
Crassoascoma	0.0427																
Groenewaldia	0.0166	0.0220															
Halobyssothecium	0.0100	0.0121	0.0172														
Katumotoa	0.0120	0.0154	0.0217	0.0100													
Keissleriella	0.0166	0.0207	0.0213	0.0123	0.0147												
Lentithecium	0.0076	0.0106	0.0169	0.0072	0.0068	0.0104											
Murilentithecium	0.0051	0.0113	0.0161	0.0053	0.0077	0.0100	0.0028										
Neobambusicola	0.0109	0.0123	0.0206	0.0124	0.0092	0.0158	0.0092	0.0087									
Phragmocamarosporium	0.0061	0.0123	0.0154	0.0072	0.0097	0.0098	0.0048	0.0051	0.0107								
Pleurophoma	0.0041	0.0083	0.0163	0.0064	0.0093	0.0066	0.0026	0.0033	0.0105	0.0034							
Poaceascoma	0.0094	0.0113	0.0164	0.0081	0.0120	0.0112	0.0064	0.0065	0.0131	0.0071	0.0064						
Setoseptoria	0.0055	0.0088	0.0154	0.0057	0.0080	0.0083	0.0031	0.0014	0.0087	0.0034	0.0020	0.0053					
Tingoldiago	0.0054	0.0068	0.0143	0.0046	0.0079	0.0082	0.0016	0.0010	0.0090	0.0031	0.0017	0.0043	0.0012				
Towyspora	0.0056	0.0089	0.0150	0.0063	0.0082	0.0082	0.0027	0.0015	0.0092	0.0035	0.0023	0.0046	0.0018	0.0016			
Wettsteinina	0.0084	0.0098	0.0176	0.0058	0.0109	0.0106	0.0043	0.0027	0.0098	0.0049	0.0049	0.0055	0.0033	0.0038	0.0033		
Pseudokeissleriella	0.0119	0.0153	0.0216	0.0104	0.0020	0.0147	0.0086	0.0076	0.0092	0.0097	0.0093	0.0120	0.0080	0.0079	0.0082	0.0109	
Pseudokeissleriella tetradii	0.0118	0.0151	0.0214	0.0111	0.0020	0.0145	0.0093	0.0075	0.0092	0.0096	0.0092	0.0119	0.0079	0.0079	0.0081	0.0109	0.0000

Table C4 The number of base substitutions per site between genera based on LSU sequences

	Darksidea	***Crassoascoma***	***Groenewaldia***	***Halobyssothecium***	***Katumotoa***	***Keissleriella***	***Lentithecium***	***Murilentithecium***	***Neoophiosphaerella***	***Phragmocamarosporium***	***Pleurophoma***	***Poaceascoma***	***Setoseptoria***	***Tingoldiago***	***Towyspora***	***Pseudokeissleriella***
Crassoascoma	0.0191															
Groenewaldia	0.0295	0.0393														
Halobyssothecium	0.0288	0.0270	0.0410													
Katumotoa	0.0210	0.0255	0.0264	0.0248												
Keissleriella	0.0292	0.0249	0.0319	0.0272	0.0164											
Lentithecium	0.0293	0.0260	0.0315	0.0142	0.0181	0.0214										
Murilentithecium	0.0327	0.0252	0.0373	0.0244	0.0170	0.0148	0.0219									
Neoophiosphaerella	0.0275	0.0218	0.0297	0.0280	0.0166	0.0202	0.0206	0.0282								
Phragmocamarosporium	0.0224	0.0252	0.0374	0.0250	0.0164	0.0154	0.0237	0.0053	0.0270							
Pleurophoma	0.0216	0.0214	0.0342	0.0256	0.0176	0.0115	0.0237	0.0119	0.0220	0.0119						
Poaceascoma	0.0396	0.0284	0.0386	0.0346	0.0303	0.0305	0.0305	0.0335	0.0281	0.0332	0.0287					
Setoseptoria	0.0346	0.0288	0.0367	0.0341	0.0276	0.0251	0.0296	0.0318	0.0250	0.0309	0.0225	0.0227				
Tingoldiago	0.0179	0.0247	0.0319	0.0246	0.0125	0.0159	0.0207	0.0122	0.0260	0.0131	0.0125	0.0328	0.0280			
Towyspora	0.0185	0.0307	0.0377	0.0301	0.0219	0.0284	0.0277	0.0266	0.0243	0.0260	0.0247	0.0353	0.0338	0.0186		
Pseudokeissleriella	0.0246	0.0200	0.0403	0.0260	0.0136	0.0168	0.0205	0.0191	0.0161	0.0186	0.0129	0.0232	0.0190	0.0171	0.0236	
Pseudokeissleriella tetradii	0.0333	0.0216	0.0406	0.0278	0.0096	0.0187	0.0260	0.0220	0.0169	0.0208	0.0148	0.0261	0.0239	0.0156	0.0275	0.0066

Table C5 The number of base substitutions per site between genera based on ITS sequences

	Darksidea	*Groenewaldia*	*Halobyssothecium*	*Katumotoa*	*Keissleriella*	*Lentithecium*	*Murilentithecium*	*Neoophiosphaerella*	*Pleurophoma*	*Poaceascoma*	*Setoseptoria*	*Tingoldiago*	*Towyspora*	*Wettsteinina*	*Pseudokeissleriella*
Crassoascoma	0.1810														
Groenewaldia	0.3236														
Halobyssothecium	0.1424	0.3203													
Katumotoa	0.2246	0.4122	0.1805												
Keissleriella	0.1770	0.3031	0.1806	0.2160											
Lentithecium	0.1689	0.3292	0.1249	0.1847	0.1680										
Murilentithecium	0.2052	0.3964	0.1829	0.1910	0.1667	0.1025									
Neoophiosphaerella	0.1642	0.3754	0.2001	0.1436	0.2048	0.1729	0.1803								
Pleurophoma	0.1853	0.3084	0.2021	0.2055	0.1481	0.2012	0.2294	0.2010							
Poaceascoma	0.2602	0.3749	0.2742	0.2783	0.2580	0.3009	0.3134	0.2316	0.2737						
Setoseptoria	0.2677	0.4300	0.2547	0.2198	0.2230	0.2445	0.2743	0.2072	0.2688	0.2710					
Tingoldiago	0.2173	0.3940	0.2081	0.1864	0.2176	0.2143	0.2378	0.1798	0.2395	0.2912	0.2353				
Towyspora	0.1923	0.3965	0.2005	0.1470	0.2099	0.2025	0.1993	0.1640	0.2178	0.2801	0.1891	0.1255			
Wettsteinina	0.2534	0.4511	0.2259	0.2091	0.2208	0.2304	0.2448	0.1903	0.2668	0.2568	0.1329	0.2415	0.2079		
Pseudokeissleriella	0.1308	0.2984	0.1709	0.0839	0.1661	0.1611	0.1861	0.1165	0.1714	0.2307	0.1962	0.1724	0.1218	0.1763	
Pseudokeissleriella tetradii	0.1639	0.3224	0.1554	0.0557	0.1748	0.1406	0.1545	0.1458	0.1837	0.2182	0.1752	0.1511	0.1026	0.1400	0.0201

Table C6 The number of base substitutions per site between genera based on TEF1 sequences

	Darksidea	***Groenewaldia***	***Halobyssothecium***	***Katumotoa***	***Keissleriella***	***Lentithecium***	***Murilentithecium***	***Neoophiosphaerella***	***Phragmocamarosporium***	***Pleurophoma***	***Poaceascoma***	***Setoseptoria***	***Tingoldiago***	***Wettsteinina***	***Pseudokeissleriella***
Crassoascoma	0.0622														
Groenewaldia	0.0855														
Halobyssothecium	0.0739	0.0884													
Katumotoa	0.0881	0.0940	0.0652												
Keissleriella	0.0658	0.0934	0.0787	0.0768											
Lentithecium	0.0468	0.0848	0.0568	0.0650	0.0731										
Murilentithecium	0.0665	0.0973	0.0807	0.0793	0.0487	0.0733									
Neoophiosphaerella	0.0705	0.0886	0.0584	0.0416	0.0703	0.0553	0.0727								
Phragmocamarosporium	0.0722	0.0917	0.0718	0.0733	0.0481	0.0668	0.0373	0.0609							
Pleurophoma	0.1036	0.0947	0.0839	0.0869	0.0501	0.0789	0.0435	0.0786	0.0542						
Poaceascoma	0.0846	0.0998	0.0824	0.0775	0.0760	0.0757	0.0734	0.0688	0.0720	0.0912					
Setoseptoria	0.0746	0.0975	0.0680	0.0628	0.0718	0.0706	0.0765	0.0541	0.0654	0.0860	0.0711				
Tingoldiago	0.0968	0.1049	0.0910	0.0717	0.0960	0.0856	0.1024	0.0634	0.0935	0.1042	0.0919	0.0749			
Wettsteinina	0.0674	0.0832	0.0723	0.0548	0.0650	0.0602	0.0611	0.0488	0.0575	0.0712	0.0714	0.0525	0.0651		
Pseudokeissleriella	0.0768	0.0864	0.0586	0.0221	0.0671	0.0559	0.0710	0.0346	0.0594	0.0783	0.0732	0.0509	0.0599	0.0421	
Pseudokeissleriella tetradii	0.0732	0.0835	0.0594	0.0286	0.0622	0.0523	0.0685	0.0335	0.0598	0.0750	0.0691	0.0502	0.0523	0.0398	0.0128

Estimates of evolutionary divergence in ITS rDNA, LSU rDN, and RPB2 sequences of the Funiliomycetaceae.

Table C7 The number of base substitutions per site between genera based on ITS sequences

	Beltraniaceae	**Castanediellaceae**	**Clypeohpysalosporaceae**	**Amphisphaeriaceae**	**Sporocadaceae**	**Pseudomassariaceae**	**Phlogicylindriaceae**	**Xyladictyochaetaceae**	**Cylindriaceae**	**Vialaeaceae**	**Nothodactylariaceae**	**Funiliomycetaceae**	**Pseudotruncatellaceae**	**Melogrammataceae**	**Appendicosporaceae**	**Apiosporaceae**	**Oxydothiaceae**	**Anungitiomycetaceae**	**Pseudosporidesmiaceae**
Castanediellaceae	0.110																		
Clypeohpysalosporaceae	0.181	0.168																	
Amphisphaeriaceae	0.145	0.157	0.217																
Sporocadaceae	0.125	0.119	0.144	0.167															
Pseudomassariaceae	0.187	0.185	0.166	0.209	0.157														
Phlogicylindriaceae	0.150	0.145	0.185	0.178	0.145	0.186													
Xyladictyochaetaceae	0.137	0.122	0.189	0.162	0.128	0.173	0.136												
Cylindriaceae	0.140	0.132	0.130	0.150	0.152	0.150	0.136	0.121											
Vialaeaceae	0.240	0.239	0.228	0.255	0.225	0.213	0.238	0.259	0.242										
Nothodactylariaceae	0.250	0.233	0.237	0.270	0.223	0.183	0.223	0.244	0.195	0.238									
Funiliomycetaceae	0.230	0.229	0.230	0.264	0.217	0.182	0.223	0.229	0.209	0.231	0.156								
Pseudotruncatellaceae	0.178	0.154	0.147	0.179	0.130	0.158	0.181	0.159	0.167	0.212	0.206	0.219							
Melogrammataceae	0.227	0.214	0.209	0.255	0.159	0.179	0.204	0.202	0.180	0.240	0.213	0.221	0.145						

Table C7 (continued)

	Beltraniaceae	Castanediellaceae	Clypeohpysalosporaceae	Amphisphaeriaceae	Sporocadaceae	Pseudomassariaceae	Phlogicylindriaceae	Xyladictyochaetaceae	Cylindriaceae	Vialaeaceae	Nothodactylariaceae	Funiliomycetaceae	Pseudotruncatellaceae	Melogrammataceae	Appendicosporaceae	Apiosporaceae	Oxydothiaceae	Anungitiomycetaceae	Pseudosporidesmiaceae
Appendicosporaceae	0.286	0.290	0.308	0.339	0.270	0.219	0.292	0.279	0.229	0.258	0.262	0.255	0.223	0.241					
Apiosporaceae	0.235	0.232	0.278	0.306	0.256	0.198	0.269	0.233	0.196	0.264	0.273	0.272	0.204	0.207	0.253				
Oxydothiaceae	0.288	0.272	0.298	0.324	0.233	0.253	0.281	0.284	0.214	0.262	0.297	0.299	0.221	0.275	0.281	0.282			
Anungitiomycetaceae	0.310	0.282	0.293	0.339	0.276	0.233	0.293	0.298	0.245	0.282	0.286	0.280	0.218	0.225	0.300	0.302	0.297		
Pseudosporidesmiaceae	0.316	0.314	0.308	0.335	0.302	0.265	0.292	0.321	0.280	0.263	0.257	0.258	0.298	0.293	0.297	0.313	0.318	0.269	
Iodosphaeriaceae	0.356	0.329	0.363	0.369	0.348	0.275	0.333	0.318	0.298	0.270	0.321	0.306	0.252	0.271	0.341	0.330	0.320	0.316	0.258

Table C8 The number of base substitutions per site between genera based on LSU sequences

	Beltraniaceae	Amphisphaeriaceae	Castanediellaceae	Phlogicylindriaceae	Xyladictyochaetaceae	Funiliomycetaceae	Cylindriaceae	Nothodactylariaceae	Pseudotruncatellaceae	Oxydothiaceae	Anungitiomycetaceae	Hyponectriaceae	Sporocadacea	Clypeohpysalosporaceae	Melogrammataceae	Apiosporaceae	Pseudomassariaceae	Appendicosporaceae	Pseudosporidesmiaceae	Iodosphaeriaceae
Amphisphaeriaceae	0.047																			
Castanediellaceae	0.041	0.058																		
Phlogicylindriaceae	0.055	0.056	0.050																	
Xyladictyochaetaceae	0.049	0.055	0.040	0.032																
Funiliomycetaceae	0.059	0.061	0.044	0.050	0.042															
Cylindriaceae	0.057	0.053	0.048	0.051	0.044	0.053														
Nothodactylariaceae	0.064	0.067	0.055	0.052	0.040	0.040	0.047													
Pseudotruncatellaceae	0.060	0.062	0.051	0.053	0.039	0.036	0.053	0.038												
Oxydothiaceae	0.056	0.051	0.051	0.051	0.044	0.038	0.053	0.047	0.037											
Anungitiomycetaceae	0.072	0.069	0.070	0.076	0.064	0.057	0.059	0.065	0.053	0.052										
Hyponectriaceae	0.077	0.080	0.076	0.076	0.065	0.058	0.059	0.054	0.045	0.058	0.059									
Sporocadacea	0.061	0.062	0.062	0.053	0.058	0.066	0.058	0.056	0.070	0.060	0.080	0.083								
Clypeohpysalosporaceae	0.062	0.054	0.063	0.070	0.063	0.069	0.050	0.062	0.064	0.058	0.072	0.071	0.065							
Melogrammataceae	0.060	0.056	0.059	0.047	0.037	0.044	0.046	0.044	0.045	0.036	0.054	0.058	0.055	0.053						
Apiosporaceae	0.065	0.064	0.063	0.062	0.062	0.056	0.056	0.057	0.052	0.049	0.060	0.069	0.070	0.065	0.047					
Pseudomassariaceae	0.067	0.068	0.064	0.071	0.063	0.065	0.063	0.065	0.065	0.062	0.080	0.076	0.073	0.068	0.065	0.073				
Appendicosporaceae	0.076	0.077	0.083	0.083	0.078	0.065	0.070	0.069	0.063	0.057	0.056	0.057	0.081	0.077	0.060	0.066	0.082			

Table C8 (continued)

	Beltraniaceae	Amphisphaeriaceae	Castanediellaceae	Phlogicylindriaceae	Xyladictyochaetaceae	Funiliomycetaceae	Cylindriaceae	Nothodactylariaceae	Pseudotruncatellaceae	Oxydothiaceae	Anungitiomycetaceae	Hyponectriaceae	Sporocadacea	Clypeohpysalosporaceae	Melogrammataceae	Apiosporaceae	Pseudomassariaceae	Appendicosporaceae	Pseudosporidesmiaceae	Iodosphaeriaceae
Pseudosporidesmiaceae	0.088	0.093	0.098	0.097	0.086	0.078	0.092	0.086	0.077	0.066	0.066	0.080	0.100	0.092	0.073	0.079	0.102	0.053		
Iodosphaeriaceae	0.087	0.091	0.098	0.102	0.096	0.084	0.104	0.100	0.087	0.073	0.074	0.089	0.110	0.098	0.084	0.089	0.106	0.067	0.051	
Vialaeaceae	0.076	0.075	0.066	0.073	0.067	0.057	0.083	0.072	0.061	0.058	0.074	0.077	0.084	0.086	0.062	0.070	0.085	0.069	0.081	0.089

Table C9 The number of base substitutions per site between genera based on RPB2 sequences

	Beltraniaceae	Melogrammataceae	Cylindriaceae	Sporocadaceae	Nothodactylariaceae	Funiliomycetaceae	Amphisphaeriaceae	Phlogicylindriaceae	Apiosporaceae	Iodosphaeriaceae	Appendicosporaceae	Oxydothiaceae
Melogrammataceae	0.208											
Cylindriaceae	0.251	0.215										
Sporocadaceae	0.234	0.241	0.286									
Nothodactylariaceae	0.273	0.256	0.293	0.285								
Funiliomycetaceae	0.252	0.259	0.270	0.309	0.262							
Amphisphaeriaceae	0.259	0.247	0.285	0.256	0.303	0.304						
Phlogicylindriaceae	0.262	0.229	0.271	0.296	0.296	0.309	0.313					
Apiosporaceae	0.280	0.286	0.280	0.299	0.298	0.298	0.296	0.301				
Iodosphaeriaceae	0.238	0.262	0.319	0.308	0.307	0.311	0.311	0.293	0.340			
Appendicosporaceae	0.276	0.282	0.344	0.312	0.315	0.316	0.349	0.323	0.353	0.285		
Oxydothiaceae	0.326	0.305	0.315	0.315	0.338	0.324	0.367	0.298	0.342	0.349	0.375	
Anungitiomycetaceae	0.376	0.392	0.420	0.418	0.392	0.426	0.433	0.399	0.440	0.366	0.397	0.446

Note The number of base substitutions per site between family is shown.

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PUBLICATION

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