

RESEARCH ARTICLE

Fungal Diversity Associated with the Joro Spider *Trichonephila clavata* in Urban Parks and Mountain Forests of Changwon, South Korea

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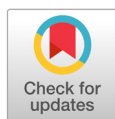
ABSTRACT

Spiders occupy diverse habitats and closely interact with environmental substrates through web construction, locomotion, and prey capture, facilitating frequent contact with fungal propagules. Despite their ecological relevance, fungal communities associated with spiders have received limited attention, and little is known about how habitat context influences spider-associated fungal assemblages. In this study, we investigated the diversity and composition of culturable fungi associated with the Joro spider, *Trichonephila clavata*, a common and ecologically important species in South Korea. Whether fungal communities differed between urban and forest habitats was evaluated. Spider samples were collected from three urban park sites and three mountain forest sites in Changwon, South Korea. A total of 67 fungal strains representing 28 species were recovered. The fungal community was largely composed of ascomycetous fungi, with *Alternaria*, *Cladosporium*, and *Penicillium* frequently isolated, whereas most species occurred at low frequencies. No significant differences were detected between the habitats in terms of alpha diversity indices or community composition. These results suggest limited habitat differentiation in fungal communities associated with *T. clavata*, with host-related factors playing a stronger role than the habitat context.

Keywords: Arthropod, Diversity, Ecology, Fungi, Urban ecology

INTRODUCTION

Spiders are widespread generalist predators that interact continuously with environmental substrates such as vegetation, soil particles, and airborne biological materials through web construction, prey capture, and movement across habitats [1,2]. Through these activities, spiders are persistently exposed to fungal propagules from the surrounding environment, rather than host-specific infection processes [3]. Culture-based studies have shown that living spiders commonly carry diverse fungi on their external surfaces, many of which correspond to environmentally ubiquitous saprotrophic taxa associated with soil, plant debris, and



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phyllosphere habitats [4,5]. These observations suggest that spider-associated fungal assemblages largely reflect passive environmental acquisition and include taxa involved in pathogenic interactions. Nevertheless, research on spider–fungus associations has historically emphasized conspicuous fungal pathogenicity, particularly entomopathogenic infections that are readily detected because of visible symptoms or host mortality [6–8]. Recent reviews have highlighted that this focus leads to a substantial underestimation of non-pathogenic and saprotrophic fungi associated with spiders, which are rarely targeted by traditional surveys [9]. Consequently, most environmentally derived fungi that are incidentally associated with spiders remain poorly documented, limiting our understanding of spiders as ecological interfaces between fungal communities and habitat conditions.

Habitat context is a key determinant of fungal community composition, as vegetation structure, organic matter availability, and microclimatic stability collectively shape the diversity and relative abundance of saprotrophic fungi [10]. Forest ecosystems generally support high fungal diversity owing to continuous litter input and stable moisture regimes [11]. In contrast, urban green spaces, such as city parks, are characterized by managed vegetation, habitat fragmentation, and frequent disturbances, which can reorganize fungal communities rather than uniformly reduce diversity [12,13]. These habitat-driven differences in environmental fungal assemblages are expected to influence fungi incidentally associated with resident arthropods, including spiders, which continuously interact with their surroundings [3,14].

The Joro spider, *Trichonephila clavata*, commonly known as the Mudang spider in South Korea, is a large and conspicuous species native to East Asia, widely distributed across the Korean Peninsula [15]. It occurs across a broad range of habitats from mountain forests to urban green spaces, making it suitable for habitat-comparative studies. Although *T. clavata* has been extensively studied in ecological and molecular contexts, particularly following its introduction to North America [16,17], the fungal diversity associated with this species has received little attention, and no systematic assessment has been conducted in its native range. In this study, the fungal diversity associated with *T. clavata* in Changwon, South Korea, was investigated focusing on culturable fungi isolated from spiders. The aim of the study was to characterize the taxonomic composition of fungi commonly isolated from *T. clavata* and assess whether fungal assemblages differed between mountain forests and urban park habitats. This study establishes baseline information for future investigations by providing basic descriptive data on spider-associated fungi across contrasting environments.

MATERIALS AND METHODS

Sample collection and fungal isolation

This study was conducted in Changwon (South Korea) and focused on two distinct habitat types: urban parks and mountain forests. Three sites were selected for each habitat type, resulting in six sampling sites. The urban park sites were chosen from densely populated areas with moderate human activity, including recreational green spaces characterized by mowed lawns, ornamental plants, and paved paths:

Gaeumjeong-dong Wetland Park (35.231°N, 128.694°E), Seok-dong 2 Park (35.212°N, 128.705°E), and Yongho-dong Yongji Park (35.222°N, 128.681°E). In contrast, mountain forest sites were selected from relatively undisturbed natural woodlands with dense canopy cover, leaf litter, and native vegetation, including broadleaf and coniferous trees, on Mt. Bulmo (35.231°N, 128.748°E), Mt. Cheonjabong (35.224°N, 128.742°E), and Mt. Jeongbyeong (35.244°N, 128.701°E). These forest sites had minimal human intervention and high humidity and soil organic matter content. Sampling was performed during the peak activity period of *T. clavata* (August–September, 2020) to ensure sufficient spider abundance. Spiders were collected from each of the six sites using sterile forceps and plastic containers (50 mL Falcon tubes) to minimize contamination. At each site, 5–8 individuals were captured from the orb webs. Collected spiders were immediately transported to the laboratory in a refrigerator at 4°C.

Before fungal isolation, the spiders were gently washed three times with sterile distilled water to remove external debris and potential transient contaminants from the exoskeleton. Washed spiders were then placed individually in a sterile 50 mL tube and refrigerated at 4°C for 3 days under starvation conditions. This starvation period allowed for complete digestion and excretion of the ingested prey as feces, reducing the risk of isolating gut-derived fungi unrelated to the spider-associated mycobiota. Following starvation, spiders were euthanized by light freezing at –20°C for 5 min, then dissected with sterile scalpels. Each spider was separated into two parts: the cephalothorax and legs. The dissected parts were immediately used for fungal isolation to prevent post-mortem microbial overgrowth. Fungal isolation was performed on potato dextrose agar (PDA; Difco, BD Biosciences, Franklin Lakes, NJ, USA). For each spider part (cephalothorax or legs), the tissue was placed on the surface of the medium (90 mm Petri dishes) and incubated at 25°C in the dark for 2 weeks, with daily monitoring for emerging mycelia. Emerging fungal colonies were subcultured onto fresh 60 mm PDA for pure isolation.

Molecular experiments

DNA extraction and PCR amplification were performed as previously described [18]. Briefly, genomic DNA was extracted using the AccuPrep Genomic DNA Extraction Kit (Bioneer, Daejeon, Korea) and PCR amplification was performed using an AccuPower PCR PreMix (Bioneer) and purified using Expin PCR Purification Kit (GeneAll Biotechnology, Seoul, Korea). The thermal cycling conditions consisted of an initial denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 sec, annealing at 55°C for 30 sec, and extension at 72°C for 40 sec, with a final extension at 72°C for 5 min. PCR amplification was verified using 1% agarose gel electrophoresis before downstream sequencing. All fungal strains were characterized by amplification of the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA using ITS1F and ITS4 [19,20]. After confirming the genus, each sample was further amplified with locus-specific primers for refined identification: beta-tubulin (*BenA*) using bt2a and bt2b [21] and translation elongation factor 1-alpha (*EF1a*) using EF1-728F and EF1-905R [22]. PCR conditions for *BenA* and *EF1a* were similar to those for ITS, with annealing temperatures adjusted to 55°C and 58°C, respectively. Purified amplicons were sequenced by Macrogen Inc. (Seoul, Korea) using an ABI 3730xl sequencer.

Fungal identification and diversity analysis

The raw sequences were assembled and edited using MEGA5 [23]. Initial identification was performed using BLASTn against the NCBI GenBank database. For each identified genus, sequences from the type or authentic strains of related species were downloaded from GenBank. Multiple sequence alignments were generated using MAFFT v7.526 with default settings [24]. Phylogenetic trees were constructed in the MEGA5 software using the neighbor-joining method with the Kimura 2-parameter model, 1,000 bootstrap replicates for node support, and pairwise deletion of gaps. The final species assignments were based on monophyletic clustering with the reference strains. Duplicate species within each sample were removed to create unique species lists for each spider and site for downstream analyses. All sequences generated in this study were deposited in the NCBI GenBank under the accession numbers PX705746–PX705757, PX754293–PX754329, and PX754724–PX754741.

Fungal diversity and community structure were analyzed using R v4.5.1 [25] with vegan and ggplot2 packages [26,27]. Alpha diversity indices were calculated for each site: number of species, Chao1 estimator for unobserved species, Shannon–Wiener diversity index, and Pielou's equitability. Differences in alpha diversity between urban parks and mountain forests were tested using unpaired t-tests, with normality checked via Shapiro–Wilk tests and variance homogeneity by Levene's test. For beta diversity, community dissimilarities were computed using Bray–Curtis dissimilarities. Nonmetric multidimensional scaling (NMDS) ordination was performed with stress values of < 0.2, indicating a reliable representation. A permutational multivariate analysis of variance (PERMANOVA) was conducted using adonis2 to test for significant differences among habitats.

RESULTS

A total of 67 fungal strains were successfully isolated and cultured from the cephalothoraxes and legs of 38 *T. clavata* spiders collected from six sampling sites in Changwon, South Korea. These strains were identified using molecular marker regions, yielding 28 species belonging to three phyla, six classes, 11 orders, 13 families, and 18 genera (Fig. 1). Most strains (65 of 67) belonged to the phylum Ascomycota,

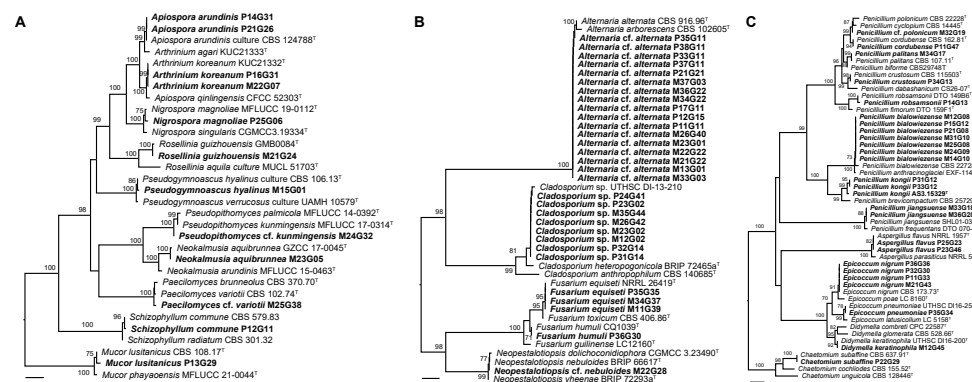


Fig. 1. Phylogenetic trees based on the neighbor-joining method with 1,000 bootstrap replicates for the (A) ITS, (B) *EF1a*, and (C) *BenA* regions. Bootstrap support values $\geq 70\%$ are shown on the branches. Superscript T indicates sequences derived from ex-type strains. The scale bar indicates the number of substitutions per site. Sequences generated in this study are shown in bold. ITS: internal transcribed spacer; *EF1a*: elongation factor 1- α ; *BenA*: beta-tubulin.

highlighting the dominance of Ascomycetes in the fungal communities associated with this spider species. At the class level, Dothideomycetes was the most abundant, comprising 33 strains (49.3%), followed by Eurotiomycetes with 19 strains (27.0%), and Sordariomycetes with 12 strains (17.9%). At the order level, Pleosporales dominated with 25 strains (37.3%), reflecting its common association with environmental molds, followed by Eurotiales with 19 strains (28.4%), and Cladosporiales with 8 strains (11.9%). Family-level analysis revealed Aspergillaceae as the most abundant, with 19 strains (28.4%), closely followed by Alternariaceae with 17 strains (25.4%) and Cladosporiaceae with 8 strains (11.9%). At the genus level, *Alternaria* was the most dominant with 17 strains (25.4%), followed by *Penicillium* (16 strains, 23.9%), *Cladosporium* (8 strains, 11.9%), *Epicoccum* (5 strains, 7.5%), *Apiospora* (4 strains, 6.0%), and *Fusarium* (4 strains, 6.0%). Species identification was performed using phylogenetic analysis, and 28 species were identified. The dominant species was *Alternaria* cf. *alternata* (17 strains), followed by *Cladosporium* sp. (8 strains), and *Penicillium bialowiezense* (7 strains) (Fig. 2). Other notable species included *Epicoccum nigrum* (4 strains), *Fusarium equiseti* (3 strains), *Apiospora arundinis* (2 strains), *Apiospora koreana* (2 strains), *Aspergillus flavus* (2 strains), *Penicillium jiangsuense* (2 strains), and *Penicillium kongii* (2 strains). Of the 28 species, 21 species (75.0%) were found in only one sample. Among these 21 species, 18 were isolated as single strains.

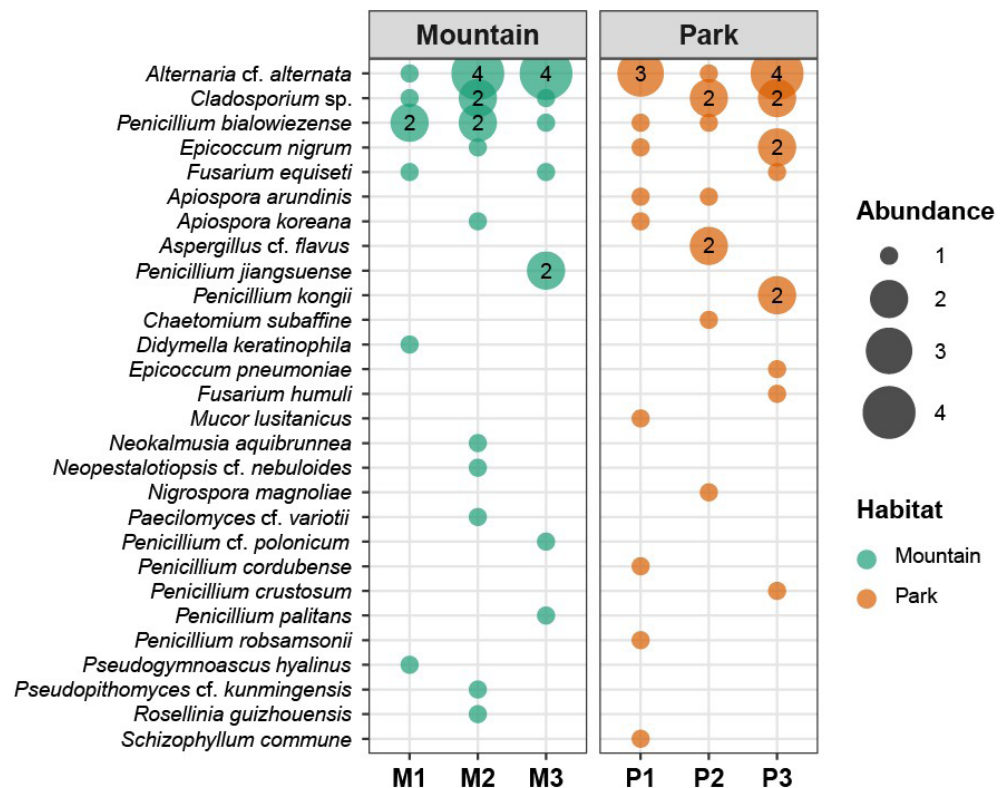


Fig. 2. Bubble plot showing the number of isolates for each species at individual sampling sites. Bubble size represents the abundance of isolates, and numbers ≥ 2 are shown inside the bubbles. Sampling sites are grouped by habitat: mountain (M1–M3) and park (P1–P3).

Alpha diversity analyses were conducted to compare fungal communities between urban parks ($n = 3$ sites, 20 spiders, and 34 strains) and mountain forests ($n = 3$ sites, 18 spiders, and 33 strains) (Fig. 3A). Mean species richness was 8.00 ± 1.00 in urban parks and 7.67 ± 2.08 in mountains, with no significant difference (t -test, $t = -0.25$, $p = 0.82$). The Chao1 estimator showed values of 18.94 ± 15.60 for parks and 13.33 ± 3.21 for mountains ($t = -0.61$, $p = 0.60$). Shannon–Wiener diversity was 2.85 ± 0.16 in parks and 2.73 ± 0.33 in mountains ($t = -0.60$, $p = 0.59$), indicating moderate diversity in both habitats without marked disparities. Pielou’s evenness was similarly comparable at 0.66 ± 0.01 for parks and 0.65 ± 0.02 for mountains ($t = -0.64$, $p = 0.57$). These results indicate that the alpha diversity of the fungal community associated with *T. clavata* did not vary significantly between urban and natural habitats. Beta diversity was assessed using Bray–Curtis dissimilarities, followed by NMDS ordination. The NMDS plot showed overlapping clusters for the urban park and mountain forest communities, with no clear separation along the axes (Fig. 3B). PERMANOVA confirmed the absence of significant differences between habitats ($F = 0.936$, $R^2 = 0.190$, $p = 0.6$). This lack of differentiation may reflect the shared fungal pools in both environments.

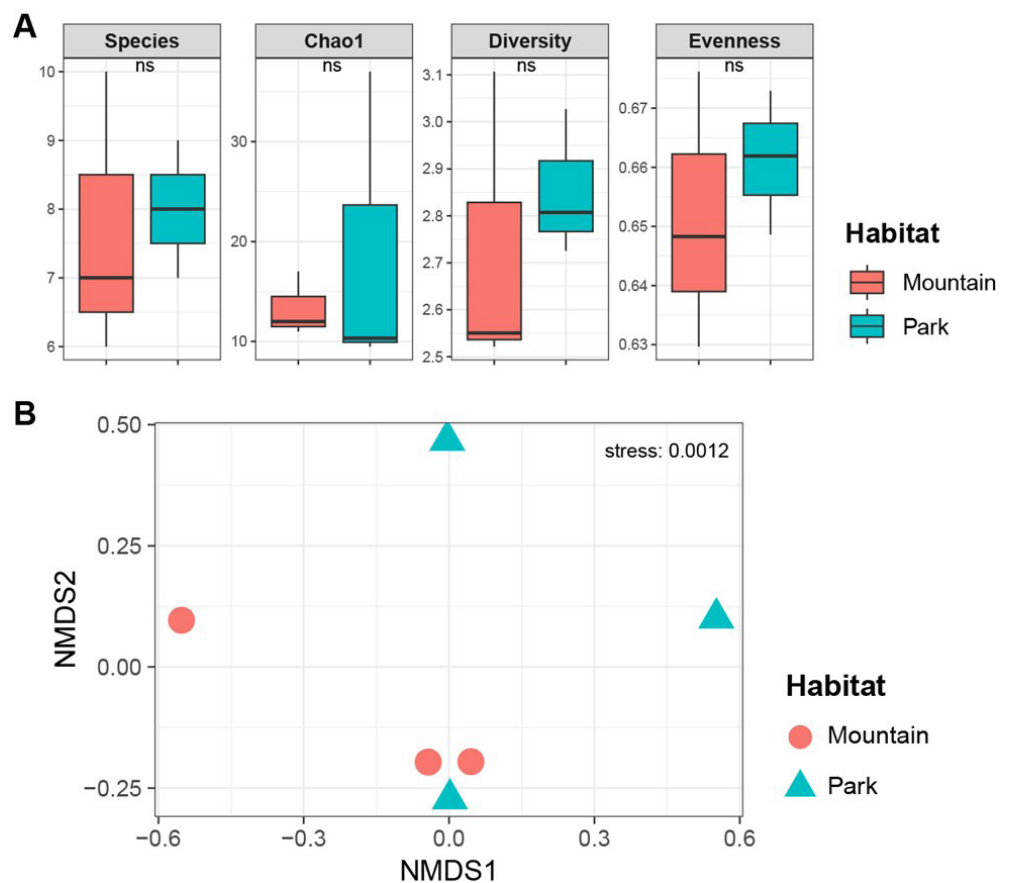


Fig. 3. Diversity analysis comparing habitats. (A) Alpha diversity indices, including Species (number of species), Chao1 (Chao1 richness estimator), Diversity (Shannon–Wiener diversity), and Evenness (Pielou’s evenness). ns indicates statistically not significant differences. (B) Beta diversity based on NMDS ordination using Bray–Curtis dissimilarities. NMDS: nonmetric multidimensional scaling.

However, subtle trends were observed, such as a comparable prevalence of *Alternaria* cf. *alternata* between mountains and parks (nine vs. eight strains) and a higher representation of *Penicillium bialowiezense* in mountains than in parks (five vs. two strains), although these differences were not statistically significant (Fisher's exact test, $p = 0.399$).

DISCUSSION

The fungal communities associated with *T. clavata* in this study were largely composed of genera such as *Alternaria*, *Cladosporium*, and *Penicillium*, which together accounted for more than 60% of the isolated strains, including 17 *Alternaria*, 8 *Cladosporium*, and 16 *Penicillium* strains. This pattern likely reflects a combination of the ecological traits of these fungi and methodological factors related to culture-based isolation. These genera consist mainly of saprophytic or opportunistic fungi that are common in decaying organic matter, soil, and airborne substrates, environments that overlap with habitats frequently contacted by spiders [28–30]. *Alternaria* cf. *alternata*, the most abundant species in this study, is a widely distributed Dematiaceous fungus known for its tolerance to environmental stressors such as ultraviolet radiation and desiccation, which enables persistence on arthropod exoskeletons exposed to outdoor conditions [29,31]. Similarly, *Cladosporium* species are ubiquitous airborne and soil-associated fungi with a high spore-dispersal capacity, facilitating repeated deposition on spider surfaces during web construction and locomotion [30]. *Penicillium* species, including *P. bialowiezense*, are metabolically versatile saprophytes that grow rapidly in nutrient-rich media and tolerate mildly acidic and humid microenvironments that may arise from spider-derived residues or organic deposits [28,32,33].

Previous studies on spider-associated fungi have revealed comparable patterns across different arachnid hosts. For example, a study of *Trichonephila pilipes* from Indian forests reported frequent isolation of *Aspergillus*, *Penicillium*, *Trichoderma*, and *Cladosporium* from spider legs and saliva, with higher fungal loads on the legs attributed to contact with soil and vegetation [34]. Broader surveys of spider-associated fungi worldwide have identified *Alternaria*, *Cladosporium*, and *Penicillium* as common epibionts on spiders, which are typically regarded as ubiquitous environmental fungi rather than specialized arthropod pathogens [5,35]. These genera possess functional traits that allow survival or limited exploitation of the spider environment, including the production of enzymes such as chitinases and proteases that can degrade arthropod cuticles or utilize host-derived nutrients without necessarily inducing disease, consistent with commensal or weakly parasitic interactions [36–39]. In contrast, entomopathogenic specialists such as *Gibellula* and *Beauveria* were rarely recovered, which is consistent with the known biases of culture-based methods that favor fast-growing saprophytes over obligate pathogens [8,40,41].

The absence of significant differences in fungal diversity and community composition between urban parks and mountain forests suggests that habitat-level environmental variations exert a limited influence on host-related filtering processes. Both alpha-diversity indices and beta-diversity analyses indicated

overlapping communities between habitats, despite apparent differences in the surrounding vegetation and land use. This pattern is consistent with a host filtering mechanism, whereby the characteristics of the spider exoskeleton, chemical secretions, and behaviors, such as web maintenance and grooming, constrain fungal colonization and persistence [3,7]. The large body size and orb-weaving lifestyle of *T. clavata* may generate relatively consistent microhabitat conditions, including moist but nutrient-poor surfaces that favor stress-tolerant generalist fungi, such as *Alternaria* and *Penicillium*, regardless of the broader habitat context. Similar host-driven structuring has been documented in other arthropods, where mycobiome composition tends to be more closely associated with host identity than with sampling location, potentially due to antimicrobial compounds or physical barriers present on the cuticle [42–45]. In urban environments, elevated pollution levels may reduce ambient fungal spore densities, but spider mobility and repeated movement among microhabitats may promote the homogenization of associated fungal communities.

A key limitation of this study is its reliance on culture-dependent methods, which are known to bias results toward easily cultivable, fast-growing fungi while underrepresenting slow-growing or unculturable taxa. Isolation of PDA favors mesophilic saprophytes such as *Penicillium* and *Alternaria*, potentially excluding obligate entomopathogens such as *Cordyceps* or *Gibellula*, which may require specialized media or host-specific conditions for growth [8]. Culture-independent approaches, including environmental DNA or metabarcoding analyses of materials recovered from spider surfaces, are likely to reveal additional diversity, including rare or viable but non-culturable taxa. Future studies integrating culture-independent and molecular approaches will provide a more comprehensive understanding of spider-associated fungal assemblages.

In conclusion, this study revealed that *T. clavata* hosts a diverse assemblage of associated fungi with slight variation in community composition between urban and forest habitats. Although taxonomic resolution was limited for some isolates, several species (e.g., *Cladosporium*) may represent previously unrecorded or poorly characterized taxa, warranting further phylogenetic and morphological investigations. These findings highlight spider-associated fungi as underexplored biological resources, particularly given that fungi linked to insects and arachnids can produce antimicrobial compounds, secondary metabolites, and industrially relevant enzymes, such as cellulases and lipases [46,47]. Collectively, these results support the ecological relevance and potential application of arachnid-associated mycobiomes and emphasize the need for expanded surveys to better characterize and utilize these fungal communities.

CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest.

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