Diversity and Taxonomy of Endophytic Xylariaceous Fungi from Medicinal Plants of Dendrobium (Orchidaceae)

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Abstract

Dendrobium spp. are traditional Chinese medicinal plants, and the main effective ingredients (polysaccharides and alkaloids) have pharmacological effects on gastritis infection, cancer, and anti-aging. Previously, we confirmed endophytic xylariaceous fungi as the dominant fungi in several Dendrobium species of tropical regions from China. In the present study, the diversity, taxonomy, and distribution of culturable endophytic xylariaceous fungi associated with seven medicinal species of Dendrobium (Orchidaceae) were investigated. Among the 961 endophytes newly isolated, 217 xylariaceous fungi (morphotaxa) were identified using morphological and molecular methods. The phylogenetic tree constructed using nuclear ribosomal internal transcribed spacer (ITS), large subunit of ribosomal DNA (LSU), and beta-tubulin sequences divided these anamorphic xylariaceous isolates into at least 18 operational taxonomic units (OTUs). The diversity of the endophytic xylariaceous fungi in these seven Dendrobium species was estimated using Shannon and evenness indices, with the results indicating that the dominant Xylariaceae taxa in each Dendrobium species were generally different, though common xylariaceous fungi were found in several Dendrobium species. These findings implied that different host plants in the same habitats exhibit a preference and selectivity for their fungal partners. Using culture-dependent approaches, these xylariaceous isolates may be important sources for the future screening of new natural products and drug discovery.

Introduction

Since the discovery of Taxol, an anticancer drug from endophytic fungi, such as Taxomyces andreanae, Pestalotia spp. and Pestalotiopsis spp. [1,2], endophytes as novel sources of phytochemicals and bioactive substances with promising medicinal and agricultural application have attracted much attention from mycologists and chemists worldwide [3–5]. Endophytic fungi can directly enhance plant growth, increase the host plants’ adaptability to such diverse conditions as dry, cold, and high-salt environments, and help to resist pathogen damage [6], as well as being able to alter the community structure [7] and antioxidant activity of the host plants [8]. Recently, based on their good antimicrobial activity, more attention has been given to the potential of exploiting endophytic fungi for novel antibiotics [9–11]. Endophytic fungi are ubiquitous and diverse in plants, and it is estimated that there are approximately 1 million species worldwide [12]; however, only a fraction has been described and explored to date. Although the complex relationship between endophytic fungi and saprophytic and pathogenic fungi has been studied [12–14], their authentic function in ecological systems remains elusive.

Xylariaceae is one of the largest and most widely distributed families of Xylariales (Ascomycota), with approximately 83 genera and at least 1340 species [15]. The members of this family are usually considered to be saprophytic, but some taxa have been described as endophytic or pathogenic [16,17], with a few species being associated with termites [18]. In the past thirty years, a number of studies have reported on the taxonomy, phylogenetic reconstruction, ecology, and relationship between xylariaceous fungal teleomorph and anamorph stages, including work on endophytic xylariaceous fungi [19–28]. Moreover, a series of new compounds have been isolated from Xylariaceae species and demonstrated good antimicrobial or anticancer bioactivity, particularly endophytic Xylaria [29–32]. Endophytic xylariaceous fungi were also recently investigated from many herbs and woody plants, such as liverworts [33], Lepanthes and Dendrobium (Orchidaceae) [34,35], Piper (Piperaceae) [36], Pinus and Picea (Pinaceae) [37] and mangroves [32]. In a previous study, we assessed the diversity of endophytic fungi from Dendrobium (Orchidaceae) and found that xylariaceous fungi were among the dominant taxa in the roots of tropical epiphytic Orchidaceae plants [38]. However, their diversity, taxonomy and the specificity of their relationship with host plants remains unaddressed. In the present study, the culturable endophytic xylariaceous fungi isolated from Dendrobium...
natural products and drug discovery.

were examined for their morphological characters and DNA sequences to reveal their diversity and distribution in their host plants. Using a culture-dependent approach, these xylariaceous isolates will be important sources for the future screening of new natural products and drug discovery.

Results

Fungal Isolation and Identification

A total of 961 culturable endophytic fungi were isolated from seven species of *Dendrobium*. The isolation rate of endophytic fungi in each plant species is listed in Table 1. Most of the isolates were assexual mycelial fungi and rarely produced diagnostically morphological characters, such as conidia or ascospores and basidiospores, thus DNA sequences were selected as the main tool to identify these fungi. Based on morphological and molecular results, 870 strains were identified as belonging to at least 9 orders, 25 genera, and approximately 60 species. The remaining 91 strains cannot be identified to the genus level by DNA sequences because no ITS sequences matching with high similarity in the GenBank database could be found. In the original 961 cultures, the xylariaceous taxa had the highest isolation frequency, 22.58% (217/961), followed by *Fusarium* at 10.71% (103/961), *Colletotrichum* at 6.55% (63/961), and *Phomopsis* at 4.37% (42/961). Thus, xylariaceous fungi as the dominant group were further analyzed.

The morphological examinations of the xylariaceous fungi were performed according to the description of Callan & Rogers [19–21]. Some representative strains were incubated on 2.5% oatmeal agar (OA) at 20°C and 12 h of fluorescent light per day for stromatal and conidial production. The newly isolated 217 xylariaceous strains were divided into at least 13 morphotypes based on their cultural characters (e.g., colony color and surface morphology, stromatal production and conidial and conidiophore morphology) (Table 2, Figure 1), and at least 18 possible morphologies, stromatal production and conidial and conidiophore morphology) (Table 2, Figure 1), and at least 18 possible operational taxonomic units (OTUs) were recognized by phylogenetic analyses (Table 3, Figure 2). The estimation of the Shannon-Weiner diversity index based on the number of OTUs showed that *D. nobile* presented the highest Xylaria species diversity among the seven plant species (1.68), followed by *D. chrysanthum* (1.47) and *D. chrysotoxum* (1.46) (Table 3). Furthermore, *D. nobile* showed a higher evenness index (0.94). The similarity index of the high divergence of the ITS1 region.

Xylariaceous endophytes, 63 strains were closely matched to sequences from the GenBank database, of the 217 newly isolated xylariaceous endophytes, 63 strains were closely matched to sequences from *Nemania* spp., 6 strains were similar to sequences from *Annulohypoxylon* spp., 4 strains were closely related to sequences from *Nodulisporium* spp., and the remaining 144 strains were closely matched to the sequences from members of the *Xylaria* genus (Table 3).

Phylogenetic Analyses

From each morphotype group, we selected 1–3 representative xylariaceous strains to analyze their ITS, nLSU and β-tubulin sequences. We newly acquired 53 ITS, 49 nLSU, and 36 β-tubulin sequences; the GenBank accession numbers are shown in Table S1. Based on the primary ITS and β-tubulin blast results from the GenBank database, of the 217 newly isolated xylariaceous endophytes, 63 strains were closely matched to sequences from *Nemania* spp., 6 strains were similar to sequences from *Annulohypoxylon* spp., 4 strains were closely related to sequences from *Nodulisporium* spp., and the remaining 144 strains were closely matched to the sequences from members of the *Xylaria* genus (Table 3). The 5.8S-ITS2 dataset consisted of 125 aligned sequences, containing 399 characters, and 89 were phylogenetically informative sites. The majority rule tree from the Bayesian analyses is shown in Figure 2. The newly isolated xylariaceous endophytes were clustered into several taxonomic groups of the family, representing at least 18 OTUs (Figure 2). Three OTUs (OTU16–OTU18) belong to members of the *Xylaria* sister genera in *Xylariaceae*, including *Annulohypoxylon*, *Nodulisporium*, and *Daldinia*. The strains identified as *Nemania* were separated into two OTUs (OTU4 and OTU15) in the tree, and the other 13 OTUs mainly represent species of the *Xylaria* genus. The phylogenetic analysis and blast search showed that approximately 19 species of *Xylariaceae* were isolated and that *Nemania diffusa*, *N. bipapillata*, *X. arbuscula*, and *X. grammica* were the most commonly isolated xylariaceous endophytes from the roots of *Dendrobium* from southwestern China. The alignment of the nLSU sequence data, consisting of 93 sequences, contained 780 nucleotides and 133 parsimony-informative sites. The phylogenetic trees generated using Bayesian analyses (BA) and maximum parsimony (MP) analyses have similar topology, thus only the tree from the BA is shown in Figure 3. The tree constructed from the LSU sequences clustered all the newly isolated Xylariaceae fungi into 8 clades, representing 12 OTUs, which correspond to OTUs 1–5, 7, 11–14, 16, and 18 in the ITS tree. OTUs 6, 8, 9, 10, 15, and 17 in the ITS tree do not form a well-supported single group in the nLSU phylogenetic tree. In addition, the members of each OTU in the nLSU tree are similar to those in the 5.8S-ITS2 tree, but their placement is not exactly consistent with that in the 5.8S-ITS2 tree.

### Table 1. The isolation rate of endophytic fungi from each *Dendrobium* species in the study.

| Plant taxa | Abbr. | Plant individual | Root samples | Total root segments | Number of isolated fungi | Isolation rate |
|------------|-------|------------------|--------------|--------------------|--------------------------|--------------|
| *D. nobile* | DNO   | 2                | 7            | 269                | 143                      | 53.1%        |
| *D. fimbriatum* | DFI   | 3                | 8            | 352                | 166                      | 47.1%        |
| *D. chrysanthum* | DCO   | 3                | 7            | 274                | 227                      | 82.8%        |
| *D. feicenerei* | DFA   | 1                | 5            | 170                | 64                       | 37.6%        |
| *D. chrysotoxum* | DCH   | 3                | 6            | 280                | 164                      | 58.5%        |
| *D. aphylum* | DAP   | 2                | 5            | 213                | 59                       | 27.6%        |
| *D. crystallinum* | DCR   | 1                | 4            | 222                | 138                      | 62.1%        |
| **Total**   |       | 7                | 15           | 1780               | 961                      |              |

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The β-tubulin matrix contained 100 aligned sequences, 946 total characters, and 355 parsimony-informative characters. The resulting phylogeny (Figure 4) reveal that all the xylariaceous taxa analyzed formed two large groups, representing members of the Xylaria genus (with Nemania nested in it) and other related genera in Xylariaceae (e.g., Hypoxylon, Annulohypoxylon, and Daldinia). The xylariaceous endophytes formed 9 clades and represented 15 OTUs. We were unable to amplify the β-tubulin region for the taxa of OTU6 and OUT15 in the ITS tree.

Based on the phylogenetic analyses, each Dendrobium species was associated with at least 3 OTUs of xylariaceous endophytes (Table 3 and Figure 2). The endophytic xylariaceous fungi associated with D. nobile are members of 6 OTUs (OTUs 4, 5, 7, 10, 13, and 15), and those associated with D. chrysotoxum are members of 9 OTUs (OTUs 3, 6, 8, 9, 11, 12, and 16–18).
OTU15 (Nemania spp.) was found in four of seven Dendrobium species (D. nobile, D. fimbriatum, D. chrysanthum and D. crystallinum), and X. arbusula (OTU5) and X. grammica (OTU12) were also commonly detected in four to five species of Dendrobium. In addition, xylariaceous OTU7 and OTU13 were restricted to associations with D. nobile, and OTU2 and OTU8–9 were each also restricted to a single Dendrobium species, D. chrysotoxum and D. fimbriatum, respectively.

Although several Dendrobium species were found to share a common Xylaria species in this study, the dominant Xylaria taxa in...
| Morphotype | Representative strains | Culture characters in OA medium | Colony diameter (mm, after two weeks) | Colony colors | Colony surface morphology | Colony margins | Stromatal production and morphology | Anamorph morphology (Conidia and Conidiophores) | Figure |
|------------|------------------------|---------------------------------|--------------------------------------|--------------|--------------------------|---------------|-----------------------------------|-----------------------------------------------|--------|
| Type 1     | 5063, 5100, 5192       |                                 | 5.5                                  | white        | aerial mycelium appressed, abundant | irregular     | absent                            | absent                                        | Figure 1a |
| Type 2     | 5054, 5186             |                                 | 8.5                                  | white, then black in mature | aerial mycelium felty, abundant | conspicuous radial stripe | absent                            | absent                                        | Figure 1b |
| Type 3     | 5055, 5084, 5129       |                                 | 9.0                                  | white, then black in center in mature | aerial mycelium scant to abundant, with dense concentrically zonate | entire        | absent                            | absent                                        | Figure 1c |
| Type 4     | 5268                   |                                 | 9.0                                  | white        | aerial mycelium scant, with star micro-colony | entire        | black stromata submerging in medium | absent                                        | Figure 1d |
| Type 5     | 5071, 5311             |                                 | 9.0                                  | white        | aerial mycelium lanose, abundant | conspicuous radial stripe | white, cylindriform young stromata production | absent                                        | Figure 1e,f |
| Type 6     | 5147                   |                                 | 9.0                                  | white and black-green in center | aerial mycelium appressed abundant | entire        | black, cylindriform stromata production | absent                                        | Figure 1g,h |
| Type 7     | 5165                   |                                 | 5.5                                  | white, then black in mature | aerial mycelium lanose, abundant | entire        | absent                            | absent                                        | Figure 1i,j |
| Type 8     | 5128                   |                                 | 5.0                                  | pale yellow, then black in mature | aerial mycelium lanose, abundant | plumose       | absent                            | absent                                        | Figure 1k,l |
| Type 9     | 5306                   |                                 | 9.0                                  | white, then black in mature | aerial mycelium appressed, abundant | plumose       | absent                            | absent                                        | Figure 1m,n |
| Type 10    | 5083, 5089, 5099, 5125 |                                 | 6.0                                  | white, then black in mature | aerial mycelium lanose, abundant | conspicuous stripe with plumose branch on end | absent                            | absent                                        | Figure 1o,p |
| Type 11    | 5327                   |                                 | 9.0                                  | pale white   | aerial mycelium submerging, scant | entire        | absent                            | absent                                        | Figure 1q |
| Type 12    | 5120                   |                                 | 4.0                                  | brown        | aerial mycelium lanose, abundant | entire        | absent                            | absent                                        | Figure 1r |
| Type 13    | 5341                   |                                 | 9.0                                  | pale yellow, then brown in mature | aerial mycelium lanose, abundant | entire        | absent                            | conidia produced from aerial mycelium.       | Figure 1st |

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Table 3. Distribution of xylariaceous endophytes in the seven *Dendrobium* species in the study.

| Fungal isolate | Closet of Genbank match (ITS sequence) | OTUs | D. nobile | D. fimbriatum | D. chrysotoxum | D. chrysanthum | D. falconeri | D. aphyllum | D. crystallinum | Total |
|----------------|--------------------------------------|------|-----------|---------------|---------------|---------------|-------------|-------------|----------------|-------|
| 5088,5306      | Nemania bipapillata GU292818         | 99   | 9          | 4             | 16            |               |             |             | 24             | 43    |
| 5054,5186      | Xylaria curta GU122444               | 97   | 11         |               |               | 6             |             |             | 17              |      |
| 5146,5151,5128 | Xylaria grammica GU300097           | 97   | 5          |               |               |               |             |             | 5               |      |
| 5084,5091,5055,5228 | Xylaria grammica GU300097 | 99 | OTU12 | 10 | 2 | 2 | 1 | 14 | 29 |
| 5311,5071,5371 | Xylaria fujitae GU322454            | 99   | 2          |               | 2             |               |             |             | 6               |      |
| 5210,5099,5125 | Xylaria apoda GU322437              | 99   | 20         |               |               |               |             |             | 20              |      |
| 5097, 5118     | Xylaria papulis GU300100             | 99   | 14         | 5             |               |               |             |             | 21              |      |
| 5147,5163      | Xylaria arbuscula GU300090           | 98   | 12         |               | 1             | 1             |             |             | 18              |      |
| 5165,5156,5131 | Xylaria venosula GU797434            | 96   | 14         |               |               |               |             |             | 14              |      |
| 5144,5133,5279 | Xylaria amphitele GU300083           | 92   | 3          |               |               | 1             |             |             | 4               |      |
| 5192           | Nemania primoluatea EF026121         | 97   | 15         |               |               | 3             |             |             | 3               |      |
| 5218,5162      | Xylaria venustula GU300091           | 97   | OTU7,8     | 4             |               |               |             |             | 4               |      |
| 5219           | Daldinia eschscholzii AB284189       | 99   | OTU18      |               |               | 1             |             |             | 1               |      |
| 5160,5063,5283 | Xylariaeae AB440120                 | 99   | OTU4       | 7             |               | 3             |             |             | 10              |      |
| 5220,5256,5327 | Xylaria badia GU122446              | 99   | OTU3       | 2             |               | 4             |             |             | 6               |      |
| 5336           | Xylaria multiplex GU300999           | 86   | 1          |               |               |               |             |             | 1               |      |
| 5078,5229      | Nodulisporium sp. GQ334429          | 99   | OTU17      |               |               | 1             |             |             | 1               |      |
| 5341,5241,5250 | Annulohypoxylon sp. FM209456        | 98   | OTU16      | 2             |               | 1             |             |             | 1               | 4     |
| Individual number | 50  | 41  | 26  | 38 | 8 | 13 | 41 | 217 |
| evenness index (E') | 0.94 | 0.83 | 0.75 | 0.82 | 0.85 | 0.86 | 0.66 |
| Shannon Index(H') | 1.68 | 1.33 | 1.46 | 1.47 | 1.37 | 1.38 | 0.92 |
Dendrobium each the reference sequences downloaded from GenBank database sequences often resulted in the wrong naming of taxa and showed that identifying endophytes by blasting with GenBank Xylaria phylogeny studies of endophytic fungi, including endophytic indispensable tools in identification, community diversity, and hyphal strands. Preliminarily grouped into morphotypes by the colony characters study, some xylariaceous strains isolated in our study were verified by ribosomal DNA sequences (ITS) [40]. In the present validity of morphotypes as taxonomic groups was further recognized that colony growth rate, color, and stromatic structure formation as relatively stable diagnostic characters for delimiting European species are dissimilar. Petrini & Petrini (1985) have they are endemic to Asia and the asexual characteristics of the production of their conidia requires more than 6 weeks of incubation time. Another reason is that, although our strains are that the strains we isolated do not form conidiophores or conidia under the currently cultural condition or explains could be that the strains we isolated do not form conidiophores or conidia under the current environmental condition or that the production of their conidia requires more than 6 weeks of incubation time. Another reason is that, although our strains are similar to the species originally described from Europe, possibly, they are endemic to Asia and the asexual characteristics of the European species are dissimilar. Petrińi & Petrińi (1985) have recognized that colony growth rate, color, and stromatic structure formation as relatively stable diagnostic characters for delimiting xylariaceous species at the intragenus level in culture compared to conidiophore morphology and the size and shape of conidia [16]. The validity of morphotypes as taxonomic groups was further verified by ribosomal DNA sequences (ITS) [40]. In the present study, some xylariaceous strains isolated in our study were preliminarily grouped into morphotypes by the colony characters and hyphal strands. Molecular techniques have become the most powerful and indispensable tools in identification, community diversity, and phylogeny studies of endophytic fungi, including endophytic Xylaria species [22–26]. Meanwhile, KoKo et al. (2011) also showed that identifying endophytes by blasting with GenBank sequences often resulted in the wrong naming of taxa and therefore any results must be treated with caution [41]. Thus, the reference sequences downloaded from GenBank database for blasting and conducting phylogenetic tree in this study were mostly published in previous studies [25–27,42]. Among DNA markers, the ITS region is most commonly used for species delimitation. Recently, the ITS region has been confirmed to be applicable as a fungal barcode, and it is able to identify successfully a broad range of fungi (approximately 70%) [43]. However, Hsieh et al. reported that ITS sequences were unsuitable for addressing phylogenetic relationships in Xylariaceae at the genus level [25]. Consistent with the previous study [25], we found that it was difficult to align the ITS sequences of the taxa due to the high variability of the ITS1 region. Thus, only the 5.8S-ITS2 region was selected for phylogenetic tree construction. The intra-group topology of the tree generated using 5.8S-ITS2 was similar to those based on LSU and β-tubulin except for a low intergroup resolution, because there are relatively fewer characters contained in the 5.8S-ITS2 dataset compared to other two datasets. The mycorrhizal specificity of orchids has been reported, and mycorrhizal symbiosis partners were usually found to be fungi belonging to Tulasiellaceae, Ceratobasidiaceae, Sebacinales, and ectomycorrhizal Russulaceae and Tuberaeaceae [44,45]. However, the specificity of non-mycorrhizal endophytes, particularly xylariaceous fungi, in orchid plants is not fully understood. It is difficult to determine the level of specificity in the interaction between host plants and their endophytic fungi because of the endophytic diversity and the limitation of the current research methods [39], though a number of previous studies have demonstrated that endophytic fungi host-specificity was common [46,47]. In the present study, we found that some endophytic Xylariaceae were exclusively detected in specific host plants. For example, OTU7 and OTU13 were uniquely detected in the roots of D. nobile, whereas OTU2 and OTU8-9 were specifically found in the roots of D. chrysotoxum and D. fimbriatum, respectively. Based our limited samples, these findings might imply that non-mycorrhizal endophytic Xylariaceae have host specificity and selectivity to some extent. However, the endophyte community is dynamic, and seasonal changes and host age will likely influence the species composition [48]. Therefore, the endophytic xylariaceous specificity of Orchidaceae should be estimated using both cultural-dependent and culture-independent methods, such as environmental PCR, for a given habitat and growth stage and sample size. Moreover, the present study indicated that the dominant Xylariaceae taxa in each Dendrobium species were different, though several Dendrobium species shared a common Xylaria species. D. fimbriatum and D. crystallinum have a close phylogenetic relationship [49], while in the present study, the two species were colonized by different xylariaceous fungi, indicating that different host plants in the same habitat might have preference and selectivity for their fungal partner.

### Table 4. The similarity index of xylariaceous fungal in seven Dendrobium species.

| Plant species | D. nobile | D. fimbriatum | D. chrysotoxum | D. chrysanthum | D. falconeri | D. aphyllum | D. crystallinum |
|---------------|-----------|---------------|----------------|----------------|--------------|-------------|----------------|
| D. nobile     | 0.18      | 0             | 0.50           | 0.36           | 0.18         | 0.10        |
| D. fimbriatum | 0.33      | 0.55          | 0              | 0.20           | 0.67         |
| D. chrysotoxum| 0.15      | 0.33          | 0.33           | 0.36           |
| D. chrysanthum| 0.18      | 0.55          | 0.60           |
| D. falconeri  | 0.20      | 0.22          |
| D. aphyllum   | 0.22      |

Discussion

Endophytic Xylariaceae have been reported as common, sometimes dominant fungi within the microbiological flora of the roots of tropical Orchidaceae plants [34,35,39]. Our analyses showed that xylariaceous fungi, as non-mycorrhizal fungi, are very abundant and diverse in the roots of Dendrobium species. Morphology is the most reliable way for identification of xylariaceous fungi [27]. However, it is difficult to delimitate endophytes (including endophytic xylariaceous) based on morphology because most of endophytes do not produce sexual states in culture [16]. Rogers [19] and Callan & Rogers [20] have provided a useful method for anamorph production and a key to the identification of certain European xylariaceous species in culture. We attempted to induce the formation of conidia in culture on 2.5% oatmeal agar media (OA) under irregular light, but only a few strains formed stroma after 6 weeks. The possible explains could be that the strains we isolated do not form conidiophores or conidia under the current environmental condition or that the production of their conidia requires more than 6 weeks of incubation time. Another reason is that, although our strains are similar to the species originally described from Europe, possibly, they are endemic to Asia and the asexual characteristics of the European species are dissimilar. Petrini & Petrini (1985) have recognized that colony growth rate, color, and stromatic structure formation as relatively stable diagnostic characters for delimiting xylariaceous species at the intragenus level in culture compared to conidiophore morphology and the size and shape of conidia [16]. The validity of morphotypes as taxonomic groups was further verified by ribosomal DNA sequences (ITS) [40]. In the present study, some xylariaceous strains isolated in our study were preliminarily grouped into morphotypes by the colony characters and hyphal strands.

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Moreover, the present study indicated that the dominant Xylariaceae taxa in each Dendrobium species were different, though several Dendrobium species shared a common Xylaria species. D. fimbriatum and D. crystallinum have a close phylogenetic relationship [49], while in the present study, the two species were colonized by different xylariaceous fungi, indicating that different host plants in the same habitat might have preference and selectivity for their fungal partner.
Xylariaceous fungi are highly abundant in the medicinal plants of *Dendrobium*, but their ecological function has remained unclear to date. Davis et al. [33] have mentioned that xylariaceous fungi in liverworts might be mutualistic with their host, although the association of *Xylaria* as mycorrhizal fungi in orchid plants has yet to be confirmed. Moreover, endophytic fungi play an important...
role in regulating the production of secondary metabolites in their host plants and may increase the concentrations of total alkaloids and polysaccharides in *Dendrobium* [50]. Accordingly, the secondary metabolites of these rich xylariaceous taxa in *Dendrobium* should be widely explored, and the relationship between the endophytic *Xylaria* species and the quality of *Dendrobium* as a medicinal herb need to be extensively investigated.

**Materials and Methods**

**Dendrobium Plants**

Healthy seven *Dendrobium* species, *D. nobile*, *D. fimbriatum*, *D. chrysotoxum*, *D. chrysanthum*, *D. falconeri*, *D. aphyllum* and *D. crystallinum*, were collected from an area of tropical rainforest at the Xishuangbanna, Jinghong City, Yunnan Province, southwestern China in 2009. Plants were identified based on the description of Chen et al [51]. The wild plant samples we studied are very

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**Figure 4. Bayesian 90% majority-rule tree for endophytic Xylariaceae isolated from Dendrobium from beta-tubulin sequences.**

Numbers above branches indicate posterior probabilities (≥90%) and numbers below branches are bootstrap values (≥50%) from 1000 replicates.

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precious medicinal plants and nearly extinct in China. Based on the consideration on the conservation of both the plant and fungal resources, we had to collect only a few individuals per species.

**Fungal Isolation and Identification**

Endophytic fungi were obtained after surface-sterilization of the plant tissues [30]. Symptomless roots of each plant species were rinsed in a sequence distilled water for 1 min, 75% ethanol for 30 s, 3% NaClO for 1 min, and 75% ethanol for 30 s and then rinsed in sterile distilled water three times. Each root was then cut into 2–3 mm sections and placed on potato dextrose agar (PDA). The isolates were subcultured on OA medium for morphological identification and conidial production. The plant samples and fungal isolations are listed in Table 1.

The identification of a representative endophyte culture as a xylariaceous fungus was initially based on the characters of colony and mycelium, according to the description of Petrini & Petrini [16] and Callan & Rogers [20]. These xylariaceous cultures were preliminarily classified into different morphotypes. In addition, internal transcribed spacer region (ITS), large subunit ribosomal RNA (nrLSU), and β-tubulin sequences were employed for identification.

**DNA Extraction, PCR Amplification and Phylogenetic Analyses**

Genomic DNA was extracted from pure mycelia using the E.Z.N.A. Fungal DNA kit (Omega Bio-Tek, Doraville, GA, USA) according to the manufacturer’s protocol. The PCR amplification followed Chen et al. [37]. The primer pairs ITS 1 and ITS 4 for the ITS sequences, primer pairs LROR and LR7 for the nrLSU sequences [52] and primer pairs T1 and T22 for β-tubulin [53] were used. The sequences obtained were blasted against the GenBank database of known members of Xylariaceae, and selected related sequences with high similarity were downloaded for further phylogenetic analyses. The sources for the reference sequences used in the phylogenetic analyses are mostly those reported by Hsieh et al. [25,42], Okane et al. [23,26], and Tang et al. [24]. All the sequences were aligned using Clustal X 1.83 [54]. The phylogenetic analyses were performed using MEGA5 [55] for maximum parsimony analyses (MP) and MrBayes 3.1.2. [56] for Bayesian analyses (BA) on same dataset of 5.8S-ITS2, LSU, and β-tubulin. For the BA analysis, the best-fitted evolutionary model was estimated using MrModeltest version 2.3 [57]. The Bayesian analyses was performed with uniform priors for 2,000,000–5,000,000 generations and sampled every 1000 generations. A probability of 95% was considered significant.

**Data Statistical Analyses**

The isolation ration (F) was calculated by the formula $F = \frac{\text{number of fragments colonized by fungi}}{\text{total number of fragments examined}}$. To compared the specificity and distribution of the xylariaceous species in the seven *Dendrobium* species, the Shannon-Weiner diversity index ($H'$) and evenness index ($E'$) were calculated based on the number of OTUs using the following two formulas, respectively: $H' = \sum (p_i \times \ln p_i)$ and $E' = H'/\ln S$ (S indicates the total number of species) [58].

**Supporting Information**

Table S1 Genbank accession numbers of sequences obtained in our lab (5054–5371) and other sequences used in phylogenetic analysis. (DOC)

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**Author Contributions**

Conceived and designed the experiments: JC SXG. Performed the experiments: JC LCZ YMX DWZ HQL. Analyzed the data: JC SXG. Contributed reagents/materials/analysis tools: JC SXG YQW. Wrote the paper: JC XKX SXG.
Diversity of Endophytic Xylaria from Dendrobium

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