

Endophytic Microorganism From the Endangered Plant *Nervilia Fordii* (Hance) Schltr. In the Southwest Karst Area of China: Isolation, Genetic Diversity and Potential Functional Discovery

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Abstract

The plant *Nervilia fordii* (Hance) Schltr. is known for its antimicrobial and antitumor properties. It is a rare and vulnerable perennial herb of the Orchidaceae family. In this study, 984 isolates were isolated from various tissues of *N. fordii* and were identified through the sequence analyses of the internal transcribed spacer region of the rRNA gene. Except for 12 unidentified fungi, all others were affiliated to at least 39 genera of 14 orders of Ascomycota (72.66%) and Basidiomycota (19.00%). Antimicrobial activity was determined by using the agar diffusion method. Subsequent assays revealed 20 strains of fungal endophytes exhibited antibacterial activity against at least one pathogenic bacterium or fungus. Moreover, the capability of promoting seed germination was evaluated on the basis of the interaction of *Bletilla striata* seeds with the isolates. Results revealed that the three isolates could promote *B. striata* seed germination. After 21 days, the germination rate under treatment with the best strain was 97.89%, which was higher than that under the control treatment (12.68%). Taken together, the present data suggested that various endophytic fungi of *N. fordii* could be exploited as sources of novel natural antimicrobial agents or used for the artificial breeding of rare orchids.

Introduction

Endophytic fungi have been detected in all plant species investigated thus far¹. They inhabit living plant tissues for at least parts of their life cycles without causing any apparent disease or injury to their host² and are ubiquitous in vascular plant species³. All orchids require endophytic fungi. They play a key role in supporting and enhancing plant health and growth^{4,5}, such as produce different plant hormones to enhancing plant growth⁶, protecting the host plant against phytopathogenic microorganisms or pests^{7,8} and so on. In addition, they can influence plant ecology; fitness; the evolution of plant community structures; and the diversity of interacting organisms, including nematodes and insects^{9,10}. Endophytes represent a relatively underexplored and attractive source of natural products that are suitable as novel sources of bioactive metabolites, including metabolites with anticancer, antimicrobial, antimalarial, and other activities, and have thus elicited considerable attention from many researchers^{11,12}. Currently, although many endophytic fungi from various terrestrial plants are gradually being described and explored, they account for less than 10% of the approximately one million known terrestrial endophytes have been investigated¹³.

Nervilia fordii (Hance) Schltr. (Fig. 1 a) is a rare and vulnerable perennial herb of the Orchidaceae family; the whole plant (including rhizome, Fig. 1 b) or the aerial part is used as a traditional Chinese medicine called *Qing Tian Ku*^{14,15}. This plant species is endemic to the southwest karst area of China (Fig. 1 c) and is mainly distributed at altitudes ranging from 220–1,000 m above sea level in sheltered valley or hillside areas^{16,17}. *N. aragoana*, *N. cumberlegii*, *N. fordii*, *N. lanyuensis*, *N. mackinnonii*, *N. plicata* (Andr.) Schltr. var. *plicata*, *N. taiwaniana*, and *N. plicata* (Andr.) Schltr. var. *purpurea* (Hayata) S. S. Ying have been identified as endemic to China in previous studies¹⁸. *N. fordii* is a traditional Chinese medicine that has long been used in Chinese folk medicine for the treatment of various respiratory diseases, such as bronchitis, stomatitis, acute pneumonia, and acute pharyngitis^{19,20}. *N. fordii* has received considerable attention in modern pharmacology research because of its biological behaviors, which include antimicrobial²¹, antitumor²², antiviral²³, and anti-inflammatory²⁴ behaviors.

Therefore, the present work aimed to investigate the species diversity of the culturable endophytic fungi in *N. fordii* collected from Guangxi Provinces, China, via rDNA internal transcribed spacer (ITS) sequences analysis. The endophytic fungi were screened for antimicrobial activities, and their benefit to seed germination was determined. The results of this report are helpful for exploring the potential sources of novel natural antimicrobial and the actual propagation and conservation of orchids.

Materials And Methods

Ethics Committee approval was obtained from the Institutional Ethics Committee of Guangxi University of Chinese Medicine to the commencement of the study. We confirm that all methods were performed in accordance with the relevant guidelines and regulations.

Collection of plant material. In 2020, the samples of *N. fordii* wild plants were collected from Sanhaung Townlet, Guangxi Province, China (109°66'E; 24°94'N). Healthy *N. fordii* plants were selected. Whole plants were dug out and placed in pots with rhizosphere soil and environmental soil, labeled, and transported to the laboratory within 12 h. The plant specimens were identified by Professor Tan and were preserved in the herbarium of the Guangxi Botanical Garden of Medicinal Plants (voucher ID: SHNF20200618).

Fungal isolation and cultivation. Endophytic fungi were isolated from the corms, rhizomes, and leaves of the plant specimens. Procedures for the surface sterilization of plant tissues and the isolation and cultivation of fungi have been previously described by Tan *et al.*^{3,10}. Briefly, roots, rhizomes, and leaves were separated from the plants; washed thoroughly in running tap water to remove dirt; and surface-sterilized sequentially in 70% ethanol (v/v) for 30 s and sodium hypochlorite solution (2.5%, v/v) for 5 min. All tissues were then rinsed three times with sterile distilled water and were surface-dried with sterile filter paper. Subsequently, 0.5 cm × 0.5 cm pieces were excised by using a sterile blade and placed on PDA containing 50 µg·mL⁻¹ oxytetracycline and 50 µg·mL⁻¹ streptomycin. Seven segments were plated per Petri dish (90 mm diameter). The Petri dishes were then wrapped in parafilm and incubated at 25 °C in the dark. They were observed for the growth of fungi from the segments every 2 days for more than 1 week. The colonies were routinely isolated, purified, and maintained in PDA for identification and antimicrobial assays. Pure endophytic fungi were finally photographed and preserved in the Scientific Laboratory Center, Guangxi University of Chinese Medicine.

DNA extraction, PCR amplification, sequencing, and molecular identification. For the production of fungal mycelia, all strains were grown on PDA plates at 25 °C for 1–2 weeks (the diameter of fungal colony was approximately 4 cm, which could meet the requirement of DNA extraction). Mycelia were scraped by using sterile pipette tips and were then freeze-dried, DNA from endophytic fungi was then extracted using by E.Z.N.A.TM Fungal DNA Mini Kits (Omega Bio-tek, Norcross, USA) were utilized in accordance with the manufacturers' instructions for use as templates in polymerase chain reactions (PCR). The primers ITS1

(5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') were constructed for molecular phylogenetic studies and were used to amplify ribosomal internal transcribed spacers (ITS)⁵⁶. The PCR mixture (50 μ L) contained 25 μ L of 2 \times SanTaq PCR Mix (Sangon Biotech, Shanghai), 2 μ L of each primer (5 μ M), and 2–10 μ L of genomic DNA (20–50 ng μ L⁻¹) and brought to a volume of 50 μ L with ddH₂O. PCR was performed on a thermal cycler (BioRAD) as follows: incubation at 94 °C for 3 min; followed by 35 cycles of 94 °C for 30 s, 55 °C for 25 s, 72 °C for 30 s; and then a final extension step at 72 °C for 7 min. Subsequently, PCR products were purified and sequenced at the Shanghai Sangon Biological Engineering Technology & Services Co. Ltd. The sequences were then BLASTed the sequences of known isolates in the NCBI database (<http://www.ncbi.nlm.nih.gov>)⁵⁷. Only those matching previously published sequences with high similarity were used. All identified isolates were categorized at the genus or family levels in accordance with the ownership criterion as follows: species of the same genera had sequence similarity (SS) \geq 95% and those of the same families had SS \leq 95%^{58,59}.

Antimicrobial activity. Three pathogens, including the fungi *C. tropicalis* and bacteria *E. coli* and *S. aureus*, were used to test the antimicrobial activities of all strains. Inhibitory effects were assayed by using the fungus cake method⁶⁰. Streptomycin (20 μ L, 5 mg mL⁻¹) and tetracycline (20 μ L, 5 mg mL⁻¹) were used as positive antimicrobial controls, and PDA agar plugs were used as the negative control. Antimicrobial activities were determined in accordance with the diameters of ZI. Experiments were repeated three times.

Effects of fungal strains on seed germination. All strains were grown on PDA at 25 °C in the dark. After 10 days, five PDA agar plugs (diameter of 2 mm) with active mycelial growth from the colony margin were inoculated into a Petri dish (diameter 9 mm) containing 15 mL of sterile oatmeal agar (2.5 g L⁻¹ oatmeal, 12 g L⁻¹ agar, and pH of 5.2 prior to autoclaving) with five pieces of nylon cloth (1 \times 1 cm), and grown at 25 °C in dark^{61,62}. The seeds of the terrestrial orchid plant *B. striata* were selected as the experimental subject for seasonal reasons. The seeds were surface sterilized with sodium hypochlorite solution for 10 min to remove fungal contamination. After 1 week, approximately 150 axenic seeds of *B. striata* (Fig. 3 a) were sown on the surface of each piece of cloth. Each treatment was replicated on five plates. The treatment without fungi was used as the control. All treatments were placed in a tissue culture chamber under 12 h of light exposure at 25 °C for 70 days. A stereomicroscope (LEICA TL3000 Ergo) was used to assess and record seed germination and protocorm development. Stewart *et al.*⁶³ had divided the seed germination and protocorm development of orchids into six stages (0–5). Three seedling growth stages were added in this study as shown in Table 3 showing as a reference for assessing the percentage of seed germination and protocorm development of *B. striata*.

Statistical analyses. The IR% of the strains were calculated as follows: IR% = (Ni/Nt) \times 100, where Ni represents the number of segments from which the fungal species was isolated, and Nt is the total number of segments incubated⁶⁴. The percentages of seed germination for per stage were calculated by using the following formula⁶¹ :

Percentage of seeds germination

$$= \frac{\text{Number of seeds in per germination stage}}{\text{Total number of viable seeds in the sample}} \times 100.$$

The diversity of fungal species from *N. fordii* was evaluated by using the *H'* and *J* with the following formulas:

$$H' = -\sum (P_i \times \ln P_i) \quad (P_i = n_i / N)$$

$$J = H' / \ln(S)$$

where S represents the total species numbers of endophytic fungi in the community, *n_i* represents the numbers of individuals, and N represents the total number of individuals^{65,66}. All statistical analyses were performed using by SPSS 19.0 (SPSS Inc., Chicago, IL, USA).

Results

Isolation, sequencing data, and diversity of culturable endophytic fungi. In this study, 984 fungal colonies (isolation rate% [IR] = 78.03 %) were isolated from 1261 tissue segments of *N. fordii* plants. The 984 isolates were assigned to 124 strains in accordance with their culture characteristics on potato dextrose agar (PDA) (Fig. 1 d) and ITS rDNA sequence analyses. They included 51 (41.13%), 48 (38.04%), and 76 (61.29%) strains from rhizome, corm, and leaf tissue segments, respectively (Table 1). Except for 12 unidentified fungi without high similarity in the GenBank database, all 112 isolates were categorized at the species, genus, or family level (Table 1).

At least 39 fungal genera were identified in accordance with the diversity and sequence data of the 112 isolates recovered from *N. fordii* plants. Among the 39 genera, 36 were affiliated with phylum Ascomycota and included 715 isolates (72.66%). Three (19.00%) strains were classified as Basidiomycota, comprising *Epulorhiza*, which is affiliated with Tulasnellaceae; and *Phanerochaete* cf., which is affiliated with Phanerochaetaceae.

Further analyses revealed that most isolates belonged to four classes, including Eurotiomycetes, Dothideomycetes, Sordariomycetes, and Leotiomycetes. Further taxonomic analysis showed that most of the isolates (n = 495) from *N. fordii* belonged to class Sordariomycetes. This class was represented by six orders, namely, Sordariales, Glomerellales, Hypocreales, Xylariales, Diaporthales, and Magnaporthales; and 17 genera: *Amesia*, *Chaetomium*, *Colletotrichum*, *Cylindrocarpon*, *Fusarium*, *Ilyonectria*, *Nectria*, *Volutella*, *Corallomycetella*, *Lecanicillium*, *Arthrinium*, *Obolarina*, *Xylaria*, *Daldinia*, *Diaporthe*, *Phomopsis*, *Leptostroma*, and an unknown Magnaporthaceae genus. 181 isolates were assigned to class Dothideomycetes, comprising the five orders of Pleosporales, Cladosporiales, Muyocopronales, Venturiales and Botryosphaerales and 15 genera (*Acrocallymma*, *Letendraea*, *Periconia*, *Ascochyta*, *Epicoccum*, *Phoma*, *Alternaria*, *Bipolaris*, *Exserohilum*, *Sclerostagonospora*, *Torula*, *Dictyosporium*, *Cladosporium*, *Mycoleptodiscus* and *Phyllosticta*). 34 isolates were assigned to

class Eurotiomycetes, and orders Eurotiales and Chaetothyriales, representing the genera *Aspergillus*, *Penicillium*, *Talaromyces*, and *Rhinocladiella*. Finally, five isolates were assigned to class Leotiomycetes and classified as genus *Leptostroma* of the order Rhytismataceae.

The exclusion of 12 unidentified fungi (2.85%) failed to show that the endophytes were widely distributed. The Shannon–Weiner diversity index (H') was estimated on the basis of taxonomic units or morphological characters. ITS sequences showed that the corm segment presented the highest fungal species diversity (2.686), followed by the rhizome (1.923) and leaf (1.976) segments. The corm segment showed a higher Pielou Evenness index (J) (0.835) than the rhizome (0.565) and leaf (0.600) segments (Table 1).

In the present data, endophytic fungi were highly abundant and diverse in the rhizomes of *N. fordii* and that the most ubiquitous phylum of fungi was Ascomycota, which is reportedly among the most prevalent group of eukaryotes globally^{25,26,27}. Eurotiomycetes was the most prevalent class of endophytic fungi, followed by Dothideomycetes. Moreover, 47.87% of endophytic fungi were present in the corm and rhizome of *N. fordii*, and 52.13% of the fungal isolates were found in the leaves of *N. fordii*. The genera of *Epulorhiza*, *Alternaria*, *Phoma*, *Sclerostagonospora*, *Torula*, *Ilyonectria*, *Purpureocillium*, *Amesia*, *Corallomycetella*, and *Daldinia* colonized rhizomes, whereas *Periconia*, *Dictyosporium*, *Volutella*, and *Lecanicillium* were exclusively detected in corms. In addition, *Arthrinium* (26.83%) was the most common fungal genus in *N. fordii* that was abundant in the leaves but was less abundant in corms and rhizomes. The dominant genera of *N. fordii* also included *Colletotrichum* (10.26%, mainly colonizing the leaves) and Tulasnellaceae (16.97%, mainly colonizing the rhizomes).

Antimicrobial activity of culturable endophytic fungi from *N. fordii*. A total of 20 fungal isolates that effectively inhibited pathogen growth were screened out by using the agar diffusion method. The antimicrobial fungi belonged to the genera *Penicillium*, *Aspergillus*, *Epicoccum*, *Alternaria*, *Fusarium*, *Bipolaris*, *Cylindrocarpon*, *Phoma*, *Lecanicillium*, *Amesia*, *Sclerostagonospora*, and *Arthrinium* and included ascomycete and fungal endophyte species (Table 2). Among these fungi, 13 strains (9.33%) showed antibacterial activity against *Escherichia coli*, 14 strains (12.30%) demonstrated activity against *Staphylococcus aureus*, and 2 strains (2.33%) presented activity against *Candida tropicalis*. Notably, *Penicillium* sp. (1151, Fig. 2 a–b) showed the highest activity against all pathogens. The diameter of the inhibition zone (ZI) against *E. coli* was 34.698 mm (Fig. 2 c), which was 1.42 times that against streptomycin and 1.31 times that against tetracycline. The diameter of the ZI against *S. aureus* was 28.478 mm (Fig. 2 d) and was 1.22 and 1.15 times that against the positive control, respectively. However, no activity against *C. tropicalis* was observed. In addition, *Epicoccum* sp. (1243) and *Phoma* sp. (1244, Fig. 1 d) had better antimicrobial effect against *E. coli* (1243 ZI = 18.515 mm; 1244 ZI = 20.690 mm) and *S. aureus* (1243 ZI = 19.540 mm; 1244 ZI = 21.298 mm) than the other strains. Comparison with the positive control group revealed that the antibacterial activities of the strains against the two pathogens exceeded 70%.

Interestingly, the fungi have different antimicrobial activity which isolated from different parts of *N. fordii*. And those that were mainly distributed in the rhizome. However, further studies are required to characterize the dynamic changes in endophytic communities²⁸ and uncultured fungi²⁹ and to confirm fungal tissue specificity³⁰ in *N. fordii*. The results suggested that endophytic fungi from *N. fordii* are potential sources of natural antimicrobial products.

Seed germination trials. This study aimed to obtain isolates with high seed germination activities from *N. fordii* plants. The seeds of the orchid plant *Bletilla striata* were selected as the experimental subject for seasonal reasons.

The results showed that *Arthrinium* sp. (1130 and 1232) and Tulasnellaceae sp. (1217, Fig. 1 d) had higher seed germination activity than the CK group. After 28 days, the germination rate of the seeds treated with the two endophytic *Arthrinium* species increased by 0.37% compared with that of the CK group. After 3 weeks, treatment with the two *Arthrinium* isolates increased the germination of *B. striata* seeds up to the emergence of first leaf by 27.63% and 2.72%, respectively. *Arthrinium* sp. (1130) promoted seed germination up to the elongation of the second leaf stage (0.63%) after 4 weeks, and the dominant seed germination stage was the emergence of the second leaf stage (33.54%). The germination rate during this stage increased by 33.14% compared with that under treatment with the CK. After 4 weeks, *Arthrinium* sp. (1232) promoted seed germination up to the emergence of the second leaf stage (0.39%) and stage 4 was the dominant stage (33.54%). The germination rate in the treatment group increased by 18.90% compared with that in the CK group. After 7 weeks, the two strains of *Arthrinium* promoted seed germination up to the appearance of root stage by 73.17% and 21.05%, respectively. Without symbiotic fungi, seed development of *B. striata* was arrested at stage 7 (Fig. 4. a). The above data indicated that the two *Arthrinium* isolates had a certain capability to promote seed germination.

Tulasnellaceae sp. (1217) had the best germination-promoting activity (Fig. 3 a–f). After 3 weeks, the rate of seed germination under treatment with Tulasnellaceae sp. was 97.89%, which was significantly higher than that under treatment with CK (85.21%). After 7 weeks of sowing, roots appeared in 52.41% of *B. striata* seeds, and the uninoculated control showed a germination rate of zero (Fig. 4 b). *B. striata* seedlings in the experimental group had more roots and larger leaves than the seedlings in other groups. The fresh weight and plant height of the *B. striata* seedlings in the experimental group were 1.22 and 3.34 times higher than those of the seedlings in the control group. Most of the seedlings demonstrated root germination. The total germinated root number and root length of the treated seedlings were 13.55 and 6.07 times those of the control, respectively.

Discussion

Endophytes affect the the quality and quantity of the crude drugs through specific fungus–host interactions^{31,32}. They are widely considered as valuable natural resources with diverse applications in a variety of areas, such as agriculture and biotechnology³³. Most endophytic fungi from wild orchids have been studied. However, studies on endophytic fungi from *Nervilia* plants, particularly studies fungi related to biological activity, have rarely been conducted.

In this study, 112 strains of endophytic fungi belonging to tow phyla, five classes, 16 orders, 28 family and 39 genera were obtained from *N. fordii*. Consistent with the findings of Song *et al.*³⁴, *Arthrinium*, *Colletotrichum*, and Tulasnellaceae were found to be the dominant endophytic fungi of *N. fordii* and accounted for more than 10% of the total endophytes.

The quantities of endophytic fungi varied across different plant tissues from *N. fordii*. The corm of *N. fordii* harbored the highest number of endophytic fungi. The variation in the quantities of endophytic fungi across different plant tissues might be ascribed to environmental differences between the above- and below-ground parts of plants; for example, the roots are highly susceptible to infestation by soil microorganisms due to their long-term presence and close interaction in the soil³⁵. Isolates Ascomycota sp. (1192 and 1299, Fig. 1 d) and Venturiaceae sp. (1300) had darkly pigmented and septate hyphae of thick walls. These strains are often referred to as dark septate fungi (DSE)³⁶ and are isolated from corms. Mandyam & Jumpponen suggested that DSE-plant symbioses are multifunctional and play unique roles in terrestrial ecosystems³⁷. They participate in nutrient acquisition and in the resultant positive host growth responses^{38,39}. The isolation of 20 strains exhibiting strong antimicrobial activity indicated that these plants and their endophytes could be potential sources of novel natural antimicrobials. These strains belonged to 12 genera and one to fungal species, thus illustrating the diversity of the distribution of endophytic fungal genera with antibacterial activity. *Phoma*, *Fusarium* and *Penicillium*, which have been isolated from medicinal orchids, exhibit antibacterial activity. Several endophytic fungi with high antioxidant capacities, such as *Alternaria*, *Fusarium*, *Xylaria*, and *Penicillium*, have been isolated from *Dendrobium*^{40,41}. Similarly, *Lecanicillium*, *Phoma*, and *Ilyonectria* isolated from *Dyosma versipellis* possess antibacterial activity^{3,42}. *Penicillium* sp. (1151) with the best antibacterial activity was screened. The secondary metabolites produced by *Penicillium* sp. have consistently shown good biological activity in antibacterial activities. The well-known antibacterial drugs penicillin and griseofulvin were isolated from *Penicillium chrysogenum*⁴³ and *Penicillium griseofulvum*⁴⁴, which are commonly found in nature. Furthermore, endophytic fungi of *Penicillium* fungal species that have been isolated from some herbal plants, such as *Pogostemon cablin*⁴⁵, *Withania somnifera*⁴⁶, and *Panax ginseng* Meyer⁴⁷ have also been shown to possess a variety of antibacterial activities.

Orchidaceae are typical mycorrhizal plants. Their seeds are tiny, without endosperm and must depend on suitable mycorrhizal fungi to germinate in natural conditions⁴⁸. Symbiotic seed germination has been practically used in orchid recovery projects worldwide and is considered as an effective way for orchid conservation^{49,50}. Seed germination trials confirmed the capability of *Arthrinium* sp. (1130 and 1232) and Tulasnellaceae (1217) to enhance the germination of *B. striata*, among which 1217 had the best seed germination-promoting activity. Previous studies have demonstrated that the majority of orchid mycorrhizal symbionts fall under the broad category of *Rhizoctonia*-like fungi, whose members include Tulasnellaceae, and constitute an important class of symbiotic germinating fungi^{51,52}. Among the reported orchids, fungi of the Tulasnellaceae can promote seed germination in several species of orchids (approximately 40 species), such as *Dendrobium*, *Epidendrum secundum*, *Chiloglottis*, *Dichromanthus* and so on^{53,54,55}.

Endophytic fungi were highly abundant in *N. fordii* plants and exhibited a wide range of biological activities. However, their ecological function, relevant metabolic pathways, and secondary metabolites need extensive investigation. These species are potential viable sources for the exploration of novel natural products and the actual propagation of other orchid species.

Declarations

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Author Contributions

X.-M. T., P. F. and Y.-Q. Z. conceived and designed the experiments. X.-F. Y., X.-M. T., S.-Y. H. and Z.-H. S. performed the experiments. Y.-Q. Z. and X.-F. Y. analyzed the data. X.-M. T. and X.-F. Y. wrote the manuscript. All authors reviewed the manuscript.

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Tables

Table 1. Fungal endophytes from *N. fordii* and their isolation rate (IR%).

Genus (stated in GenBank)	Phylum; Class; Order/Family	Fungal isolate (representative strains number)	Isolate number				IR (%)			
			Leaf	Rhizome	Corn	Total	Leaf	Rhizome	Corn	Total
<i>Aspergillus</i>	Ascomycota; Eurotiomycetes; Eurotiales; Aspergillaceae	1170, 1171, 1179, 1193, 1237, 1238, 1252,	4	9	8	21	0.78%	2.90%	4.97%	2.13
Unknown	Ascomycota; Eurotiomycetes; Eurotiales; Aspergillaceae	1212	1	0	0	1	0.19%	0	0	0.10
<i>Penicillium</i>	Ascomycota; Eurotiomycetes; Eurotiales; Aspergillaceae	1151, 1263	2	4	0	6	0.39%	1.29%	0	0.61
<i>Talaromyces</i>	Ascomycota; Eurotiomycetes; Eurotiales; Trichocomaceae	1270, 1283	1	0	1	2	0.19%	0	0.62%	0.20
Unknown	Ascomycota; Eurotiomycetes; Eurotiales; Trichocomaceae	1295	0	0	1	1	0	0	0.62%	0.10
<i>Rhinochadiella</i>	Ascomycota; Eurotiomycetes; Chaetothyriales; Herpotrichiellaceae	1185	2	1	0	3	0.39%	0.32%	0	0.30
<i>Acrocalymma</i>	Ascomycota; Dothideomycetes; Pleosporales; Massarineae	1186	1	0	6	7	0.19%	0	3.73%	0.71
<i>Letendraea</i>	Ascomycota; Dothideomycetes; Pleosporales; Massarineae	1239	1	0	0	1	0.19%	0	0	0.10
<i>Periconia</i>	Ascomycota; Dothideomycetes; Pleosporales; Massarineae	1207	0	0	1	1	0	0	0.62%	0.10
<i>Ascochyta</i>	Ascomycota; Dothideomycetes; Pleosporales; Didymellaceae	1213, 1235	3	0	15	18	0.58%	0	9.32%	1.83
<i>Epicoccum</i>	Ascomycota; Dothideomycetes; Pleosporales; Didymellaceae	1154	30	17	1	48	5.85%	5.48%	0.62%	4.88
<i>Phoma</i>	Ascomycota; Dothideomycetes; Pleosporales; Didymellaceae	1244, 1254	0	2	0	2	0	0.65%	0	0.20
<i>Alternaria</i>	Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae	1211	0	2	0	2	0	0.65%	0	0.20
<i>Bipolaris</i>	Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae	1198	1	2	0	3	0.19%	0.65%	0	0.30
<i>Exserohilum</i>	Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae	1205	1	1	0	2	0.19%	0.32%	0	0.20
<i>Sclerostagonospora</i>	Ascomycota; Dothideomycetes; Pleosporales; Pleosporaceae	1303	0	1	0	1	0	0.32%	0	0.10
<i>Torula</i>	Ascomycota; Dothideomycetes; Pleosporales; Torulaceae	1315	0	1	0	1	0	0.32%	0	0.10
Unknown	Ascomycota	1192, 1299, 1310, 1312	0	0	11	11	0	0	6.83%	1.12
<i>Dictyosporium</i>	Ascomycota; Dothideomycetes; Pleosporales; Massarineae	1180	0	0	3	3	0	0	1.86%	0.30
Unknown	Ascomycota; Dothideomycetes; Pleosporales; Sporormiaceae	1272	2	0	0	2	0.39%	0	0	0.20
Unknown	Ascomycota; Dothideomycetes; Pleosporales	1233, 1236	0	0	8	8	0	0	4.97%	0.81
<i>Cladosporium</i>	Ascomycota; Dothideomycetes; Cladosporiales; Cladosporiaceae	1135, 1175, 1277, 1280	8	0	4	12	1.56%	0	2.48%	1.22
<i>Mycocleptodiscus</i>	Ascomycota; Dothideomycetes; Muyocopronales; Muyocopronaceae	1292	1	0	0	1	0.19%	0	0	0.10
Unknown	Ascomycota; Dothideomycetes; Venturiales; Venturiaceae	1300	1	0	0	1	0.19%	0	0	0.10
Unknown	Ascomycota; Dothideomycetes; Magnaporthales	1173	4	0	0	4	0.78%	0	0	0.41
<i>Phyllosticta</i>	Ascomycota; Dothideomycetes; Botryosphaerales; Phyllostictaceae	1108, 1144, 1159, 1160	52	1	0	53	10.14%	0.32%	0	5.39

Unknown	Ascomycota; Sordariomycetes; Sordariales	1304	1	0	0	1	0.19%	0	0	0.10
<i>Amesia</i>	Ascomycota; Sordariomycetes; Sordariales; Chaetomiaceae	1260	0	1	0	1	0	0.32%	0	0.10
<i>Chaetomium</i>	Ascomycota; Sordariomycetes; Sordariales; Chaetomiaceae	1201, 1209, 1261	0	3	1	4	0	0.97%	0.62%	0.41
<i>Colletotrichum</i>	Ascomycota; Sordariomycetes; Glomerellales; Glomerellaceae	1101, 1107, 1136, 1139, 1147, 1153, 1188, 1203, 1206, 1215, 1242, 1257, 1284	93	4	4	101	18.13%	1.29%	2.48%	10.2
<i>Cylindrocarpon</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1230	0	9	11	20	0	2.90%	6.83%	2.03
<i>Fusarium</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1119, 1133, 1222, 1225, 1286	17	20	21	58	3.31%	6.45%	13.04%	5.89
<i>Ilyonectria</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1265	0	1	0	1	0	0.32%	0	0.10
<i>Purpureocillium</i>	Ascomycota; Sordariomycetes; Hypocreales; Ophiocordycipitaceae	1314	0	1	0	1	0	0.32%	0	0.10
<i>Nectria</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1288	1	2	1	4	0.19%	0.65%	0.62%	0.41
<i>Volutella</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1251	0	0	2	2	0	0	1.24%	0.20
<i>Corallomyces</i>	Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	1307	0	1	0	1	0	0.32%	0	0.10
<i>Lecanicillium</i>	Ascomycota; Sordariomycetes; Hypocreales; Cordycipitaceae	1262	0	0	1	1	0	0	0.62%	0.10
<i>Arthrinium</i>	Ascomycota; Sordariomycetes; Xylariales; Apiosporaceae	1103, 1105, 1124, 1130, 1163, 1232	202	40	22	264	39.38%	12.90%	13.66%	26.8
<i>Obolarina</i>	Ascomycota; Sordariomycetes; Xylariales; Xylariaceae	1148	11	0	0	11	2.14%	0	0	1.12
<i>Xylaria</i>	Ascomycota; Sordariomycetes; Xylariales; Xylariaceae	1184	1	0	0	1	0.19%	0	0	0.10
<i>Daldinia</i>	Ascomycota; Sordariomycetes; Xylariales; Hypoxylaceae	1200	0	1	0	1	0	0.32%	0.00%	0.10
<i>Diaporthe</i>	Ascomycota; Sordariomycetes; Diaporthales; Diaporthae	1204, 1220	0	3	5	8	0	0.97%	3.11%	0.81
<i>Phomopsis</i>	Ascomycota; Sordariomycetes; Diaporthales; Valsaceae	1202	0	3	3	6	0	0.97%	1.86%	0.61
Unknown	Ascomycota; Sordariomycetes; Magnaporthales; Magnaporthaceae	1104	8	1	0	9	1.56%	0.32%	0	0.91
<i>Leptostroma</i>	Ascomycota; Leotiomycetes; Rhytismatales; Rhytismataceae	1167, 1176	5	0	0	5	0.97%	0	0	0.51
Unknown	Basidiomycota; Agaricomycetes;	1129	0	3	15	18	0	0.97%	9.32%	1.83
<i>Epulorhiza</i>	Basidiomycota; Agaricomycetes; Cantharellales; Tulasnellaceae	1158	0	4	0	4	0	1.29%	0	0.41
Unknown	Basidiomycota; Agaricomycetes; Cantharellales; Tulasnellaceae	1217	1	160	2	163	0.19%	51.61%	1.24%	16.5
<i>Phanerochaete cf.</i>	Basidiomycota; Agaricomycetes; Polyporales; Phanerochaetaceae	1141	2	0	0	2	0.39%	0	0	0.20
Fungal endophyte sp. and fungal sp.		1109, 1120, 1149, 1168, 1172, 1187, 1191, 1228, 1240, 1253, 1255, 1264, 1266, 1278, 1290, 1308, 1305	38	8	8	54	7.41%	2.58%	4.97%	5.49

Unidentified fungi	1106, 1169, 1174, 1183, 1189, 1190, 1195, 1197, 1216, 1229, 1247, 1309	18	4	6	28	3.51%	1.29%	3.73%	2.85
Individual number		513	310	161	984	52.13%	31.50%	16.36%	
Shannon index (<i>H</i>)		1.976	1.923	2.686					
Pielou Evenness index (<i>J</i>)		0.600	0.565	0.835					

Table 2. Antibacterial activity of 33 endophytic fungi isolated from *N. fordii*. Note "–": no activity.

NO.	Plant part	<i>Escherichia coli</i> (inhibitory zone [mm])	<i>Staphylococcus aureus</i> (inhibitory zone [mm])	<i>Candida tropicalis</i> (inhibitory zone [mm])
1151	Leaf, rhizome	34.698	28.478	-
1154	Leaf, rhizome, corm	22.115	15.702	-
1174	leaf	-	9.657	-
1211	rhizome	-	8.673	-
1221	rhizome	-	9.952	12.107
1224	rhizome	15.675	-	-
1230	rhizome	9.958	-	-
1231	rhizome	12.060	12.520	-
1232	leaf	-	8.740	-
1238	leaf	11.592	-	-
1243	rhizome	18.515	19.540	-
1244	rhizome	20.690	21.298	-
1250	rhizome	9.955	-	-
1252	corm	8.515	-	-
1260	rhizome	-	8.730	-
1262	corm	9.142	9.042	-
1266	leaf, rhizome	-	10.580	-
1273	rhizome, corm	11.075	10.270	-
1303	rhizome	11.078	-	9.838
1306	rhizome, corm	-	9.445	-
5 mg·mL ⁻¹ 20 µL streptomycin		24.477	23.336	-
5 mg·mL ⁻¹ 20 µL tetracycline		26.439	24.850	-

Table 3. Seed germination and protocorm development in *N. fordii*⁶³.

Stage	Description
0	No germination, viable embryo
1	Enlarged embryo, production of rhizoid(s) (=germination)
2	Continued embryo enlargement, testa rupture, further rhizoid production
3	Appearance of the protomeristem
4	Emergence of first leaf
5	Elongation of first leaf
6	Emergence of second leaf
7	Elongation of second leaf
8	Appearance of root

Figures

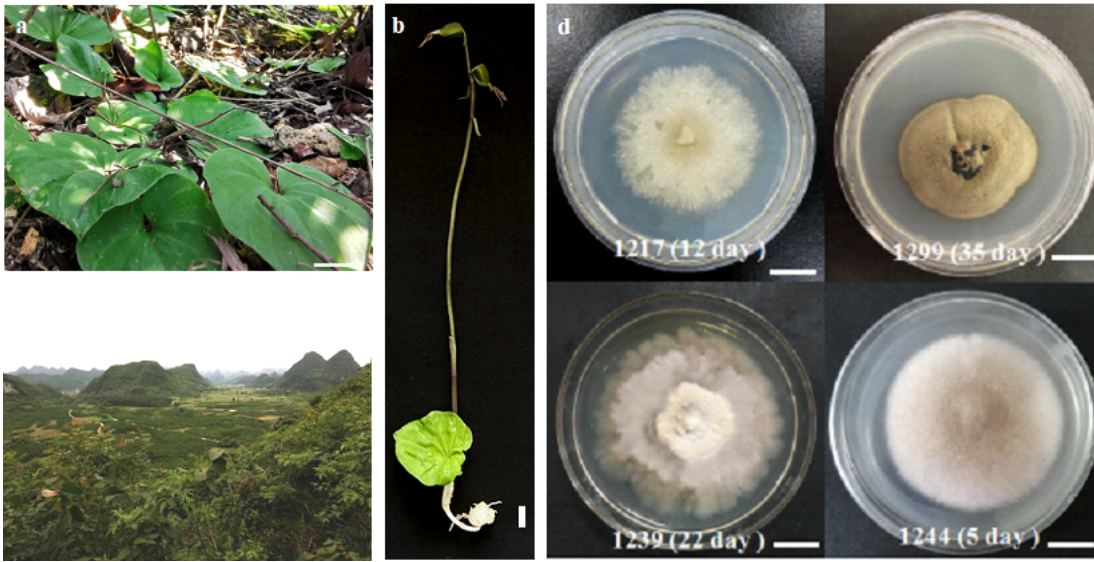


Figure 1

Wild *N. fordii* plant samples and their endophytic fungi. (a) Plants of *N. fordii* growing among on a hillside, bar =1cm; (b) the whole plant (including rhizome), bar =1cm; (c) habitat; (d) representative fungal morphotypes isolated from *N. fordii* grown on potato dextrose agar at 26 °C, bar =0.5cm.

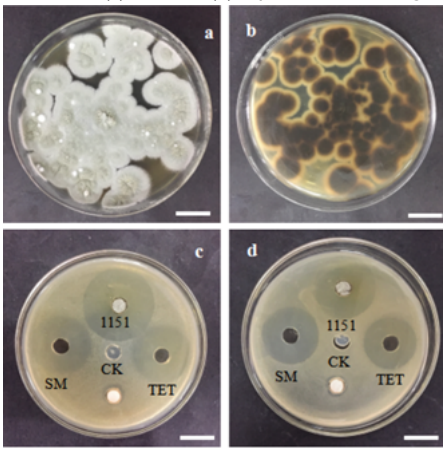


Figure 2

Antimicrobial activity of some strains. (a–b) morphological characteristics of strain 1151; (c) Antibacterial activity of 1151 against *E. coli*; (d) antibacterial activity of 1151 against *S. aureus*. Bar: a–d=1cm.

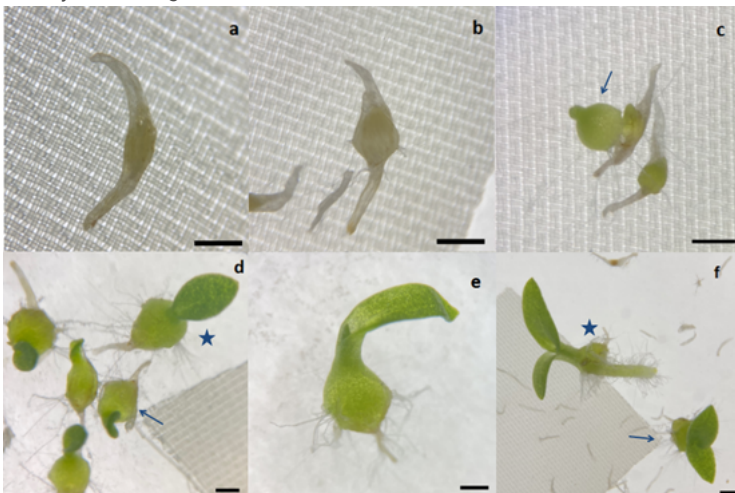


Figure 3

Symbiotic seed germination and protocorm developmental stages of *B.striata* cultured with the mycorrhizal fungal strain 1217 (Tulasnellaceae sp.) cultured on oatmeal agar at 10 weeks after sowing; (a) stage 0; (b) stage 1 (shown by arrow); stage 2 (shown by star); (c) stage 3 (shown by arrow); (d) stage 4 (shown by arrow); stage 5 (shown by star) of protocorm development (note the elongation of the first leaf); (e) stage 6; (f) tage 7 (shown by arrow); and stage 8 (shown by star). Bar: a–f = 500 μ m.

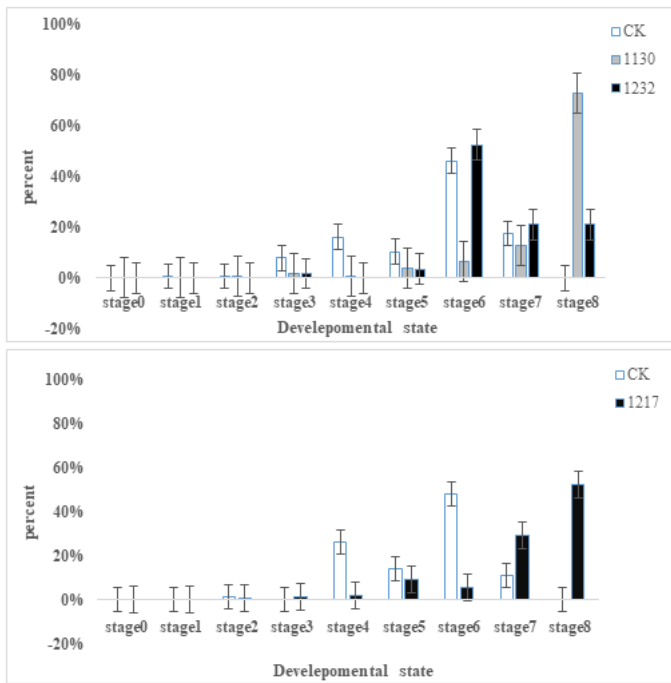


Figure 4
Effects of mycorrhizal fungi on the seed germination of *B.striata* 7 weeks after sowing. (a) *Arthrinium* sp. (1130 and 1232); (b) *Tulasnellaceae* sp. (1217). Note: the results show the mean of three replicates with bars indicating the standard error.