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Research article

Endophytic fungi harbored in *Panax notoginseng*: diversity and potential as biological control agents against host plant pathogens of root-rot disease

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Background: Endophytic fungi play an important role in balancing the ecosystem and boosting host growth. In the present study, we investigated the endophytic fungal diversity of healthy *Panax noto-ginseng* and evaluated its potential antimicrobial activity against five major phytopathogens causing root-rot of *P. notoginseng*.

Methods: A culture-dependent technique, combining morphological and molecular methods, was used to analyze endophytic fungal diversity. A double-layer agar technique was used to challenge the phytopathogens of *P. notoginseng*.

Results: A total of 89 fungi were obtained from the roots, stems, leaves, and seeds of *P. notoginseng*, and 41 isolates representing different morphotypes were selected for taxonomic characterization. The fungal isolates belonged to Ascomycota (96.6%) and Zygomycota (3.4%). All isolates were classified to 23 genera and an unknown taxon belonging to Sordariomycetes. The number of isolates obtained from different tissues ranged from 12 to 42 for leaves and roots, respectively. The selected endophytic fungal isolates were challenged by the root-rot pathogens *Alternaria panax*, *Fusarium oxysporum*, *Fusarium solani*, *Phoma herbarum*, and *Mycocentrospora acerina*. Twenty-six of the 41 isolates (63.4%) exhibited activity against at least one of the pathogens tested.

Conclusion: Our results suggested that *P. notoginseng* harbors diversified endophytic fungi that would provide a basis for the identification of new bioactive compounds, and for effective biocontrol of notoginseng root rot.

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1. Introduction

Panax notoginseng (Burkill) F.H. Chen (Araliaceae) is a perennial herbaceous plant, cultivated mainly in Wenshan, Yunnan, China, and has been historically used as both a medicinal herb and food. Rhizome and roots of *P. notoginseng* are officially recorded as notoginseng in the Chinese Pharmacopoeia [1]. About 61 Chinese patent medicines contain notoginseng, including Yunnan Bai Yao, a famous hemostatic proprietary herbal remedy. The secondary metabolites of this plant include saponins [2,3], flavones [2], amino

acids [4], and polysaccharides [5], with the most emphasis being on saponins. *P. notoginseng* saponins are considered as the major active ingredients in notoginseng. The saponins display multiple pharmacological effects, such as hemostatic [6–9], antioxidant [10,11], neuroprotective [12,13], antitumor [14,15], antidiabetic [16,17], and other activities, and have been extensively used as therapeutic agents in China. The pronounced efficacies of notoginseng saponins have led to the development of several Chinese patent medicines, such as Xuesaitong Capsules/Soft Capsules [18] and Xuesaitong Injection [19].

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In recent years, the demand for notoginseng has been increasing. Unfortunately, the yield and quality of notoginseng are severely limited by replanting obstacles [20], and a number of diseases caused by a plethora of phytopathogens [21]. Among the diseases, the root-rot disease complex is the most destructive one as it results in vield reduction. no harvest, or low content of active ingredients [22]. The reported fungal pathogens causing root rot include Alternaria panax. Alternaria tenuissima. Cvlindrocarpon destructans, Cylindrocarpon didynum, Rhizoctonia solani, Phytophthora cactorum, Phoma herbarum, Fusarium solani, Fusarium oxysporum [21], and Fusarium flocciferum [23]. Although diverse chemical pesticides and some biocontrol methods are used, it is difficult to control the root-rot diseases because of the pathogenic complex. More comprehensive, practical, and ecological methods to eradicate the pathogenic diseases in *P. notoginseng* are urgently needed. Furthermore, specific and nonspecific fungi and bacteria associated with the plant have been found with little information about their ecological functions.

Microbial communities associated with plants play an important role in balancing the ecosystem and boosting host growth. Endophytic fungi, which live in healthy plant tissues for at least a part of their life cycle, without causing any noticeable symptoms of infection or disease, may benefit their host in different ways, such as producing bioactive secondary metabolites, promoting germination and shoot growth, inducing host plants to tolerate to biotic or abiotic stresses [24–27]. In a previous study, Ma et al [28] demonstrated high phylogenetic diversity and biocontrol potential of bacterial endophytes of *P. notoginseng*. However, little is known about the fungal community harbored in *P. notoginseng*.

In this study, the diversity of endophytic fungi isolated from different tissues of healthy *P. notoginseng* was evaluated, and the isolates were screened for their potential antimicrobial activity against five major phytopathogens causing root rot of *P. notoginseng*. To the best of our knowledge, this is the first report of the biodiversity, phylogeny, and assessment of biocontrol potential of endophytic fungi harbored in *P. notoginseng*.

2. Materials and methods

2.1. Isolation of endophytic fungi

Three-year-old healthy *P. notoginseng* plant samples were collected in October 2013, from a plantation in Wenshan, Yunnan, Southwest China. The collected plants were excised into roots, stems, leaves, and seeds, put into plastic bags, transferred to the laboratory within 24 h, and stored at 4°C until the isolation procedure of endophytic fungi was carried out.

The surface sterilization and isolation of fungal endophytes were carried out by following the procedures described by Park et al [29]. The plant samples were washed thoroughly with running tap water to remove soil particles and rinsed six times with distilled water. The separated parts (roots, stems, leaves, and seeds; Fig. 1A) were immersed in 75% ethanol solution for 2–3 min, and subsequently transferred to 5.5% sodium hypochlorite solution for 1–2



Fig. 1. *Panax notoginseng*, endophytic fungi and bioactivities. (A) Different parts of 3-year-old healthy plant of *P. notoginseng*; (B) isolation of endophytic fungi; (C) fermentation; (D) screening of antagonistic endophytic fungi against host phytopathogens of root-rot disease.

min, depending on the different tissues. The surface-sterilized samples were rinsed three times with sterile distilled water and dried with sterile filter paper. Sterile samples were aseptically crumbled into small fragments, evenly placed on Petri dishes containing potato dextrose agar (PDA) with 100 mg/L ampicillin to inhibit bacterial growth. The Petri dishes were incubated at $28 \pm 1^{\circ}$ C until fungal growth started. To confirm that the disinfection process was successful, a 0.1-mL aliquot of the water used for the last washing step was spotted on PDA plates supplemented with 100 mg/L ampicillin, and incubated under the same conditions in parallel. Plates that were not detected as contaminated by cultivable microorganisms were considered as successfully surface disinfected and used for isolation of endophytes [30]. The cultures were monitored every day to monitor the growth of endophytic fungi. Each colony that emerged from the fragments was transferred to antibiotic-free PDA medium (Fig. 1B), for subculture, and brought into pure culture.

The pure cultures were recorded and maintained on PDA in active form for further investigation. For long-term storage, the fungal colonies were stored in 15% (v/v) glycerol at -80° C. All the fungal isolates were deposited in the Yunnan Institute of Microbiology, Yunnan University, Kunming, China.

2.2. Fungal DNA extraction, PCR amplification and sequencing

The pure cultures were used for DNA extraction. DNA was extracted from 0.5–1.0 g mycelia chilled in liquid nitrogen by using the sodium dodecyl sulfate-cetyltrimethyl ammonium bromide method [31]. The internal transcribed spacer (ITS) region was amplified using primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') [32]. The polymerase chain reaction (PCR) was performed in a 50-µL reaction mixture containing 1 µL template DNA, 1 µL forward primer (10µM), 1 µL reverse primer (10 μ M), 5 μ L reaction buffer (10 \times), 4 μ L dNTP (each 2.5 μ M), 0.5 µL Taq DNA Polymerase (5 U/µL), and 37.5 µL sterile doubledistilled water. The PCR cycling protocol consisted of initial denaturation at 94°C for 4 min, followed by 30 cycles of 94°C for 45 s, 55°C for 45 s, and 72°C for 2 min, and a final elongation step of 72°C for 10 min. As a negative control, the template DNA was replaced by sterile double-distilled water. The PCR amplified products were separated by agarose gel electrophoresis, and sequenced on an ABI Prism 3730 sequencer at Sangon Biotech (Shanghai, China).

2.3. Phylogenetic analysis of endophytic fungi

For strain identification, the ITS sequences were compared with those in the NCBI database (http://www.ncbi.nlm.nih.gov/) using the BLAST search program for the final identification of the fungal endophytes program. A phylogenetic tree was constructed by the neighbor-joining method using MEGA version 5.0 software (http:// www.megasoftware.net/), after pairwise alignments using the CLUSTAL X program, version 1.8 (http://www.clustal.org/) [33]. The stability of the internal branches was assessed with 1,000 bootstrap replications. The sequences of this study were deposited in the GenBank database under the accession numbers: KP714353– KP714393 (Table 1).

2.4. Phytopathogens used for antagonistic assays

A. panax, F. oxysporum, F. solani, Phoma herbarum, and Mycocentrospora were isolated from rotten root samples of *P. notoginseng* collected from Wenshan in August, 2012. The identification was performed by morphological and ITS sequencing methods. The pathogenicity was confirmed by experiments with detached roots of healthy notoginseng plants (unpublished data).

2.5. In vitro antagonistic activity against host phytopathogens

Well-grown slant culture of each fungus was used for liquid culture in potato dextrose broth medium (50 mL/250 mL flasks). The flasks were incubated at 28 \pm 1°C on a shaker at 180 rpm (Fig. 1C) for 7 d. The culture broth was filtered through blotting paper and the supernatant was separated. The supernatant was extracted three times with ethyl acetate (EtOAc). The wet mycelium was extracted twice with acetone. After removal of acetone in a rotary vacuum, the aliquot residue was extracted three times with EtOAc. Combined the EtOAc extracts from supernatant and mycelium, the organic phase was dried over Na₂SO₄ (anhydrous). The extracts were then concentrated in a rotary vacuum. The crude extracts were stored at 4°C before usage. The inhibitory effect of the EtOAc extracts obtained from endophytic fungi was tested using the double-layer agar technique [34] (Fig. 1D). The crude extracts were dissolved in 1.0 mL ethanol as stock solution. A 100-µL volume of the ethanol extract suspension was pipetted into each hole. Test plates were incubated at 28 \pm 2°C, and the diameters of the inhibition zones were measured after 24 h. The same volume of ethanol was used as the negative control.

3. Results

3.1. Phylogenetic analysis of endophytic fungi

A total of 89 endophytic fungi were isolated from the roots. stems, leaves, and seeds of healthy notoginseng plants. Forty-one morphotypes were recognizable on the basis of their morphological characteristics. One isolate of each morphotype was selected for classification by phylogenetic analysis. All sequences were BLAST searched in GenBank (NCBI database). The closest matches and the GeneBank accession numbers are listed in Table 1. Only isolate PH30454 revealed at least 98% similarity to known reported sequences. Among 89 endophytic fungi isolates, 86 belonged to phylum Ascomycota, and three to Zygomycota. All isolates were classified to 12 orders (Capnodiales, Chaetothyriales, Diaporthales, Eurotiales, Glomerellales, Helotiales, Hypocreales, Microascales, Mucorales, Pleosporales, Sordariales, Xylariales), 23 genera (Acremonium, Alternaria, Arthrinium, Aspergillus, Botryotinia, Chaetomium, Cladosporium, Colletotrichum, Dictyosporium, Fusarium, Humicola, Ilyonectria, Mucor, Myrothecium, Penicillium, Periconia, Pestalotiopsis, Phialophora, Phoma, Phomopsis, Plectosphaerella, Thielavia, and Trichoderma), in which isolate PH30448 belonging to genus Arthrinium was incertae sedis at order level and isolate PH30402 was an unknown fungus belonging to Sordariomycetes.

The phylogenetic tree (Fig. 2) revealed the relationship between the different species of fungal endophytes obtained from different parts of *P. notoginseng*. The most frequently occurring groups were Hypocreales with 26 isolates (29.2%) and Pleosporales with 19 isolates (21.3%). Hypocreales group included six genera: *Acremonium, Fusarium, Ilyonectria, Myrothecium, Plectosphaerella*, and *Trichoderma*. Pleosporales were integrated by three different genera: *Alternaria, Dictyosporium*, and *Phoma*. The groups Capnodiales, Chaetothyriales, Diaporthales, Glomerellales, Helotiales, Microascales, Mucorales, and Xylariales comprised only one taxon (genus) each (Table 1 and Fig. 2). The results suggested that there were diverse endophytic fungi harbored in the cultivated *P. notoginseng*.

3.2. Fungal distribution analysis

The number of isolates obtained from different tissues of *P. notoginseng* ranged from 12 to 42 for leaves and roots,

Table 1

Analy	/sis	of	89	isolates	from	Panax	notoginsen	y with	the	related	species	and	their	isolation	information
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Phylogenetic group	Representative isolate	Closest species in GenBank	Similarity (%)	Tissues of P. notoginseng				No. of
(genus)	(accession No.)	(accession No.)		Roots	Stems	Leaves	Seeds	isolates
ASCOMYCETES								
Cladosnorium	DU204E0 (VD7142E2)	Cladosporium cladosporioidos (VIZEZOEE)	100				2	0
Ciudosporium	PH30430 (KP714333)	Cladosportum chalosportolaes (KJ767066)	100	2			2	0
	PH30409 (KP714334)	Cladosportum oxysporum (KJ475816)	100	2				
Chaotothurialos	PH50412 (RP714555)	Clauosportani oxysporani (Kj475818)	100	Z				
Dhialophora	DU20402 (VD714256)	Dhialophora mustaa (KE850264)	100	1				1
Diaporthalos	FII30403 (RF714330)	Filulophora musica (Kr850504)	100	1				1
Diaportifiaics	DU20406 (VD714257)	Phomonesis columnaris (VC145992)	100	С				2
Furnitupsis	FII30400 (RF714337)	Filomopsis columnaris (RC145885)	100	2				2
Asporgillus	DU20427 (VD714258)	Aspergillus versicolor (VI152174)	100	1	2			1
Donicillium	PH20444 (VD714250)	Panicillium chrycogonum (LN422541)	100	1	J		2	4
Penicillum	PH30444 (KP714339) PH20424 (VD714260)	Penicillium crustosum (LN482541)	100		2		Z	10
	PH20279 (VD714261)	Penicillium cordubanca (VI101427)	100	2	J			
	PH20200 (KP714301)	Penicillium Ianidosum (VIG76451)	100	ר ר				
Clamanallalas	PH50590 (KP714502)	Penicinium iupidosum (Kj676451)	100	Z				
Colletotrichum	DU20420 (VD714262)	Collatotrichum glogosporioidas (VE864554)	100	С				2
Helotiales	FII30420 (RF714303)	Concrothenant glocosponolaes (K1804554)	100	2				Z
Potruotinia	DU20420 (VD714264)	Potruotinia fuckaliana (VE202200)	100			2		2
Hypocreales	FII30439 (RF714304)	boli yolinia jackenana (Ki 802805)	100			2		Z
Acromonium	DU20454 (VD714265)	Acromonium implicatum (HO014022)	08				1	1
Fusarium	PH20410 (VP714266)	Eusarium acuminatum (VE887007)	50 100	1			1	1
rusunum	PH30410 (KP714300)	Fusarium acuminatum (KF667097)	100	1				0
	PH30360 (KP714307)	Fusarium coloni (KE020488)	100	2		2		
Iluonoctria	PH30430 (KP714308)	Iluonaetria magradiduma (UO702420)	100	2		2		2
пуопестна	PH30396 (KP714369)	llyonectria macroalayma (HQ703420)	100	2				3
Murothacium	PH30396 (KP714370) DH20292 (VD714271)	Murothacium cp. (HO621058)	100	1	1			2
Diactosphaaralla	PH30362 (KP714371) PH20464 (VD714272)	Plactosphaerolla sp. (IV525104)	99 100	2	1		2	5
Pieciosphaerena	PH30404 (KP714372)	Plectosphaerella sp. (JX555104)	100	1	1		2	5
Tui ala a d'anna a	PH30457 (KP714373)	Trichedown a longibuschistum (KIZCZ080)	99	1			I	C
menouermu	PH30433 (KP714374)	Trichodorma koningionaia (KM070602)	100	1	1	1		0
	PH30441 (KP714373)	Trichodorma chiralo (KM079605)	100	Z	1	1		
Microscoloc	PH30432 (RP714576)	Thenouerma spirale (KM079610)	100		1			
Dariconia	DU20429 (VD714277)	Pariconia hystoidas (VC054160)	00		1			1
Placenorales	F1150428 (RF714577)	Fericonia byssolaes (RC954100)	55		1			1
Alternaria	DU20445 (VD714278)	Alternaria cp. (VC771455)	100		1			15
memunu	PH30438 (KP714378)	Alternaria alternata (KM015480)	100		2	5		15
	PH20453 (KF714575)	Alternaria tanuissima (VE20886)	100		2	2	2	
	PH20422 (KF714280)	Alternaria tanuissima (KE208880)	100		1	2	2	
	PH30423 (KF714381) PH30442 (KP714382)	Alternaria alternata (KM015480)	100		1		1	
Dictuosporium	PH30404 (KP714383)	Dictyosporium digitatum (DO018089)	08	1			1	1
Diciyosporium Dhoma	PH30459 (KP714384)	Phoma draconis (CU237795)	100	1			1	3
Thoma	PH30301 (KP71/385)	Phoma radicina (10676200)	00	2			1	5
Sordariales	(KI / 14585)	Thoma Taalema (JQ070200)	55	2				
Chaetomium	PH30461 (KP714386)	Chaetomium globosum (KI728838)	100				1	1
Humicola	PH30417 (KP714387)	Humicola fuscoatra (IN031580)	99	1			1	1
Thielavia	PH30430 (KP714388)	Thielavia arenaria (IX535015)	99	1	1			1
Incertae sedis	11150150 (11711500)	melavia arenana (j.555615)	55		•			
Arthrinium	PH30448 (KP714390)	Arthrinium arundinis (KF850624)	99				2	2
Xvlariales	(UCCFT/IN) 0FF0(U)	And	55				2	2
Pestalotionsis	PH30451 (KP714301)	Pestalotionsis vismiae (IX305715)	100				2	4
i contropoio	PH30414 (KP714301)	Pestalotionsis uvicola (IN198506)	100	2			2	-1
Incertae sedis	PH30402 (KP714380)	Sordariomycetes sp (IX244023)	gq	2				2
ZYGOMYCETES	1150-102 (NI / 14505)	Social configures of an and a second se	55	2				2
Mucorales								
Mucor	PH30392 (KP714393)	Mucor hiemalis (IF299220)	100	3				3
No. of total isolates			100	42	16	12	19	89
								50

respectively (Table 1). Forty-two isolates from roots were assigned to 16 genera and an unknown taxon, and the genera *Fusarium*, *Cladosporium*, and *Penicillium* were the dominant groups. Nineteen isolates from seeds belonged to nine genera. Eight genera fungi (16 isolates) were obtained from stems. The *Alternaria* genus was dominant in seeds and stems. The amount of endophytic fungi from leaves was the least, with only 12 isolates belonging to four genera. In addition, the distribution of endophytic fungi showed significant differences in various organs and showed obvious specificity. For example, the endophytic fungi belonging to *Colletotrichum*, *Ilyonectria*, and *Mucor* were only isolated from roots. 3.3. Antagonism assay of fungal endophytes as potential biocontrol agents

All EtOAc crude extracts of 41 fungal endophyte strains were tested for antagonistic activities against five major fungal pathogens that cause root-rot disease of *P. notoginseng* (Table 2). Twentysix of the 41 isolates (63.4%) exhibited activity against at least one of the pathogens tested. The highest frequency (16 isolates, 39.0%) was against the pathogen *A. panax*, followed by *F. solani* (15 isolates, 36.6%), *F. oxysporum* (14 isolates, 34.1%), *Phoma herbarum* (12 isolates, 29.3%), and *M. acerina* (7 isolates, 17.1%), respectively. Five

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Fig. 2. Phylogenetic tree based on neighbor-joining analysis of the rDNA internal transcribed spacer sequences of the endophytic fungi obtained from different tissues of *Panax notoginseng*. Significant bootstrap values (> 50%) are indicated at the branching points. The tree has been drawn to scale (0.05).

0.05

Table 2	
Endophytic fungal antagonists of root-rot disease p	oathogens

Isolate No.	Antagonistic activity ^{1),2)}							
	Alternaria panax,	Fusarium oxysporum	Fusarium solani	Phoma herbarum	Mycocentrospora acerina			
PH30378	+	_	+	-	_			
PH30382	_	_	-	_	-			
PH30386	+	_	-	_	-			
PH30390	_	_	+	_	-			
PH30391	_	_	_	_	-			
PH30392	+	_	-	_	-			
PH30396	_	_	_	_	-			
PH30398	_	_	_	_	-			
PH30402	_	_	+	_	-			
PH30403	+	+	_	+	-			
PH30404	_	_	+	_	-			
PH30406	_	-	-	_	-			
PH30409	++	+	+++	+	+			
PH30410	-	-	_	-	-			
PH30412	+	++	++	+	+			
PH30414	++	+	+	+++	+			
PH30417	_	-	-	_	-			
PH30420	++	++	+++	_	-			
PH30424	-	+++	++	++	++			
PH30425	-	-	_	+	-			
PH30427	-	+	++	_	-			
PH30428	-	-	-	-	-			
PH30430	-	-	_	-	-			
PH30432	-	++	+	_	-			
PH30435	-	-	-	++	-			
PH30436	_	_	-	_	-			
PH30438	_	_	-	_	-			
PH30439	+	+	+	_	-			
PH30441	++	+++	$^{+++}$	+	+			
PH30442	_	_	-	+	-			
PH30444	++	++	++	+	+			
PH30445	_	_	-	_	-			
PH30448	+	_	-	_	-			
PH30450	+	+	-	+	+			
PH30451	++	_	-	-	-			
PH30452	_	_	-	+	-			
PH30454	+	_	-	-	-			
PH30457	-	+	-	-	-			
PH30459	-	_	-	-	-			
PH30461	++	++	++	-	-			
PH30464	_	_	_	_	_			

 Estimated by measuring the diameter of the clear zone of growth inhibition
 Symbols: -, no activity; +, ++, and +++, weak activity, moderate activity, and strong activity, respectively

isolates, PH30409, PH30412, PH30414, PH30441, and PH30444, were found to inhibit all pathogens tested, implicating they have a broad spectrum of antagonistic activity. Isolates, PH30409, PH30414, PH30420, PH30424, and PH30441 exhibited relatively strong inhibitory effects against the pathogens *F. oxysporum*, *F. solani*, and *Phoma herbarum*. The broad spectrum or strong inhibitory activities of these strains against the host plant pathogens suggest that these endophytic fungi may be potential candidates for the production of bioactive compounds, and have the potential as biological control agents of root-rot disease of *P. notoginseng*. In other virulence tests with detached healthy notoginseng roots, isolates PH30409 and PH30412 were found to be able to cause root rot (unpublished data), although they showed antagonism to tested pathogens.

4. Discussion

Endophytic fungi have been considered as a promising source for the development of biological control agents (BCAs) against phytopathogens, because they exhibit the beneficial functions for host plants [24–27,35,36], and are ubiquitous within almost every tissue type studied [37]. Even so, endophytic fungi are still a poorly investigated group of microorganisms [38], and their complex ecological functions remain to be extensively exploited. *P. notoginseng, Panax ginseng,* and *Panax quinquefolius,* have been widely used for medicinal plants all over the world. There are a few investigations of the endophytic fungi in *Panax* genus, but most of them have been focused on ginseng (*P. ginseng*) [29,39–42] and American ginseng (*P. quinqefolius*) [43]. *P. notoginseng,* an important Chinese medicine plant, has attracted increasing attention in medical and chemical fields because of its active ingredients, but little in ecological and other research areas because of its narrow distribution.

In the present study, the diversity, tissue distribution, and biocontrol potential of cultivable endophytic fungi harbored in P. notoginseng plants were described for the first time. We proposed that the endophytic fungi would exert certain functions to help the host survive in plantation against disastrous root-rot diseases. In the survived and healthy notoginseng plants, the harbored fungal endophytes may give some clue to find effective approaches to control root rot, caused by complex pathogens. Thus, in order to screen for the most promising endophytes, we evaluated the potential of all the endophytic isolates as BCAs by challenging five major root-rot pathogens of the host plant, A. panax, F. oxysporum, F. solani, Phoma herbarum, and M. acerina, whose pathogenicity was confirmed in our previous work. Among the isolates, crude extracts of PH30409 and PH30441 showed strong inhibition on all tested phytopathogens, implicating that the two isolates have the potential to produce active compounds. Other isolates showed selective activity against one or two pathogens. According to the viewpoint by Zhang et al [36], the mechanisms involved in biocontrol of endophytic fungi against phytopathogens include antibiosis, competition for nutrients and space, induction of defense response, and mycoparasitism. The endophytic isolates can be used to screen their antagonistic activity by fermenting in different media in further work. Other mechanisms should also be investigated in the development of BCAs. For instance, Trichoderma spp. widely used in agriculture as biofungicides, have shown many ways against phytopathogens, such as producing active compounds, secreting hydrolytic enzymes, and competing for nutrients [44]. In this study, isolates belonging to Trichoderma were also obtained and tested as active endophytic strains. Endphytic fungus Penicillium chrysogenum showed effects on various plant pathogens [45-47]. García et al [48] reported that the isolate EEZ10 of Penicillium chrysogenum from soil inhibited the growth of Verticillium dahlia in vitro, and is a possible biological control agent for Verticillium disease [48]. The sequence of isolate PH30444 was 100% similar to that of Penicillium chrysogenum, and its crude extract also exhibited inhibition against all tested host phytopathogens. Recently, we found that some endophytic isolates can inhibit pathogens of notoginseng root-rot diseases by mycoparasitism and producing active secondary metabolites and volatile organic compounds [49–54]. These findings showed that endophytic fungi from P. notoginseng are potential BCAs for the host plant.

The culture-based study and molecular identification showed that the total fungal diversity was relatively high, and the overwhelming majority belonged to Ascomycota (96.6% of the total number of isolates). Only a single Zygomycota group was obtained. This finding is consistent with a previous study in *Cannabis sativa* L. [26]. In 12 morphologically distinct groups, Hypocreales (29.2%) and Pleosporales (21.3%) were dominant orders among the endophytic fungi of different tissues of *P. notoginseng*. This result was similar to the previous studies in many medicinal plants [26,55]. The endophytic fungi associated with *P. notoginseng* comprised a number of dominant groups, such as *Alternaria, Fusarium*, and *Penicillium*. All these genera have been previously isolated as endophytes, not only from other *Panax* species [29,39,40,42], but also from a wide range of plant hosts in the temperate and tropical zones [26,56,57]. Although, genera *Alternaria*, *Cladosporium*, *Colletotrichum*, and *Fusarium* were found as endophytes in all three *Panax* species (*P. ginseng*, *P. notoginseng*, and *P. quinquefolium*) [29,39–43], other genera *Arthrinium*, *Botryotinia*, *Chaetomium*, *Dictyosporium*, *Humicola*, *Ilyonectria*, *Mucor*, *Periconia*, *Pestalotiopsis*, and *Thielavia*, have not been obtained from other *Panax* plants, suggesting that *P. notoginseng* harbors specific and diverse fungi due to the unique soil, climatic conditions of Wenshan region and the approaches taken in agro-management.

Some isolated taxa showed preference for specific tissues types. Previous studies in other plants have also indicated that endophytes exhibit tissues specificity [58–60]. As expected, tissue specificity of fungal endophytes was demonstrated in our study. Particular endophytes were only found in one tissue, which suggests that certain species survive within the specific chemistry or texture of different tissues [57]. The diversity and species richness of endophytic fungi were higher in the underground part (roots) than that in the above-ground parts (stems, leaves, and seeds). Some similar results have been reported in the previous studies [55,57]. The possible reasons are that soil-borne fungi are typically more prevalent and diversified than those that infect aerial plant tissues [55], and there are abundant nutriments in roots of P. notoginseng that are suitable for the growth of fungi. The relative abundance of each fungus identified in P. notoginseng reflects an unequal distribution of isolate richness among species. Similar results have been found in other plants, such as Stellera chamaejasme and Taxus globose [55,57].

Plant-endophytic fungus interactions have been extensively investigated. Most of the symbionts may have helped for host plants. It has also been confirmed that the pathogenic-endophytic lifestyles of some fungi are interchangeable [61,62]. These phenomena are caused by many factors, such as environment changes, chemical inducers, and molecular and genetic bases [63,64]. Groups of fungal phytopathogens also contain large numbers of endophytic taxa. In this study, isolates PH30409 and PH30412 caused root-rot symptoms in experimental infection through detached healthy roots of P. notoginseng (unpublished data). Interestingly, crude extracts of them showed antagonistic activities against the tested phytopathogens, and more experimental infections to confirm the pathogenicity of Cladosporium sp. for P. notoginseng in plantation are underway. It is also interesting that some species in Alternaria and Fusarium from soil are pathogenic fungi for P. notoginseng, and these genera were dominant groups in the endophytic isolates. In the cultivation soil, Fusarium was the most isolated genus [65]. Endophytes should originate from the environment in which their host plants live. Therefore, these genera have more opportunities to invade and colonize in the tissues, and evolve as endophytes. Their evolution should be investigated in the further studies.

Nowadays, the notoginseng supply mainly relies on intensive field cultivation under artificial shade structures with fertile and moist soils as the wild-type notoginseng disappeared many years ago [66]. The long shade cultivation, pesticide spray, and chemical fertilizers are widely used in cultivation of notoginseng. To achieve higher yield, the frequencies of pesticide and fertilizer use increase more as the product price increases. These agricultural managements improve the productivity to some degree, but also cause other problems, such as being toxic to humans, animals, and other crops, and development of fungicide-tolerant pathogen strains [67]. At the same time, they affect the structures and functions of microorganisms in bulk soil, rhizosphere soil, and endophytes. The harmful effects should be investigated for further reasonable agroapplications in notoginseng planting. Taken together, our findings revealed that there are diverse endophytic fungi harbored in different tissues of *P. notoginseng* planted in Southwest China. The fungal endophytes serve as great promise not only as BCAs against the known and emerging phytopathogens of *P. notoginseng*, but also as a resource of biologically active novel secondary metabolites [68]. Three endophytic fungal isolates, PH30444, PH30414, and PH30441, are potential BCAs against *A. panax*, *F. oxysporum*, *F. solani*, *Phoma herbarum*, and *M. acerina*, and possibly other pathogens. Further studies are required to clarify the biocontrol active metabolites and the control efficiency of the potential endophytic isolates in both pot and field experiments. A full understanding of endophytic community structure, dynamics, and functions, and the shaping factors will be helpful in selecting pesticide, fertilizer, and other approaches for notoginseng planting.

Conflicts of interest

The authors declare that there are no conflicts of interests.

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