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RESEARCH ARTICLE

Diversity and Distribution of Bulb-associated fungi of Fritillaria Cirrhosae Bulbus Source Plants used in Traditional Chinese Medicine

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ABSTRACT

Diversity and community composition of bulb-associated fungi of Fritillaria Cirrhosae Bulbus source plants, which are used in traditional chinese medicine, in the eastern Himalaya–Hengduan Mountains, southwestern China, were estimated based on the internal transcribed spacer rDNA sequence analysis, using host plant species, geographic area, and plant phenology as variables. A total of 1,486 fungal sequences assigned to 251 operational taxonomical units (OTUs) were obtained from the bulbs. Fungal OTUs comprised 96.41% Ascomycotina, 3.52% Basidiomycotina, and 0.07% Zygomycotina. Sordariomycetes, Hypocreales, and Nectriaceae were the most frequent fungal lineages at each taxonomic rank. *Fusarium*, *Ilyonectria*, *Tetracladium*, *Leptodontidium,* and *Tomentella* were the top OTU-rich genera. *Fusarium* sp. 03, *Ilyonectria rufa*, *Fusarium* sp. 08, *Ilyonectria* sp. 03, and *Leptodontidium orchidicola* 03 represented the most frequent OTUs. *Fusarium* spp. were the most frequent general taxa. The distribution of fungal community exhibited preferences for host plant species, geographic area, and plant phenology. These findings are the foundation of our research on culturing and active metabolites of bulb-associated fungi of Fritillaria Cirrhosae Bulbus source plants.

Keywords: Community composition, Eastern Himalaya–Hengduan Mountains, Fungal diversity, ITS rDNA, Medicinal plants

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INTRODUCTION

Fritillaria Cirrhosae Bulbus is an antitussive and expectorant traditional Chinese herbal medicine that has been widely used for more than 2000 years. It is primarily used to treat coughs with less phlegm, sputum with blood, bronchitis with a dry cough, and pulmonary carbuncle [1].

Fritillaria Cirrhosae Bulbus is derived from bulbs of source plant species, including *Fritillaria cirrhosa* D. Don, *F. unibracteata* Hsiao et K. C. Hsia, *F. przewalskii* Maxim., *F. delavayi* Franch., *F. taipaiensis* P. Y.

Li, and *F. unibracteata* Hsiao et K. C. Hsia var. *wabuensis* (S. Y. Tang et S. C. Yue) Z. D. Liu, S. Wang et S. C. Chen [1]. These species are primarily distributed at an altitude of 3,200-4,600 m in alpine shrub and alpine meadow areas in the eastern Himalaya–Hengduan Mountains, Qinghai–Tibet Plateau, and they inhabit a narrow geographic range and restricted habitat [2,3]. Excessive exploitation of Fritillaria Cirrhosae Bulbus source plants and deterioration of the ecological environment have resulted in continuous reduction and gradual depletion of the limited plant resources, and there are difficulties in artificial propagation of these plant species [4,5]. As a result, conflict between exploitation and protection of these plant resources increases.

Endophytic fungi of medicinal plants are generally a significant origin of active ingredients in medicinal plants [6,7], and it was revealed that a few *Fusarium isolates* in bulbs of *F. unibracteata* and *F. unibracteata* wabuensis were able to produce the same imperialine 3β-D-glucoside, peiminine, and peimisine as their host plants [8-11]. Additionally it was reported that the alkaloid content reduced when the diversity of rhizospheric fungi community increased in *F. taipaiensis* [12]. Bulb-associated fungi communities may represent a critical origin of the active alkaloid substances in bulbs of Fritillaria Cirrhosae Bulbus source plants. Thus, increasing conflict between natural resource conservation and demand for Fritillaria Cirrhosae Bulbus source plants as medicinal material may be relieved by the exploitation of their bulb-associated fungi resources in the future.

Previous studies conducted by cultural method revealed diversity of cultured endophytic fungi in bulbs of Fritillaria Cirrhosae Bulbus source plants. Yan et al. [13] isolated 90 fungal species assigned to one class, six orders, and 30 genera from *F. cirrhosa* in four different growth periods, which included *Stachylidium*, *Curvularia*, *Verticillium*, *Cephalosprium*, and *Fusarium* species. Chen [8] and Chen et al. [14,15] cultured fungal species of *Gliocladium*, *Myrothecium*, *Bionectria*, *Nectria*, and *Fusarium* from *F. unibracteata*, *F. przewalskii*, *F. cirrhosa,* and *F. delavayi*. Pan et al. [16] obtained 53 fungal *isolates* of *Fusarium, Plectosphaerella*, *Nectria*, and *Bionectria* from *F. wabuensis.* We acquired 362 fungal *isolates* that belonged to 57 genera in Ascomycotina, Basidiomycotina, and Zygomycotina in bulbs of *Fritillaria cirrhosa*, *F. unibracteata*, *F. przewalskii,* and *F. delavayi* (unpublished data).

The cultural method is commonly used to identify fungal species associated with plants, but alone it cannot systematically reveal the fungal diversity. A combination of cultural and molecular methods may provide more comprehensive results that reveal species diversity of plant-associated fungi, because both culturable and non-culturable fungi can be identified [17]. Additionally, community composition of plant-associated fungi should be influenced by genotype, geographic area and phenology of host plants. As a result, fungal diversity and community composition associated with bulbs of Fritillaria Cirrhosae Bulbus source plants were studied relative to host plant species, primary geographic areas, and crucial plant phenology stages by the internal transcribed spacer (ITS) rDNA sequencing technique in this research, which can provide insight into exploitation of potential fungal resources, and conservation and sustainable development of Fritillaria Cirrhosae Bulbus source plant natural resources in the eastern Himalaya–Hengduan Mountains, Qinghai–Tibet Plateau, China.

MATERIALS AND METHODS

Sampling

Fritillaria cirrhosa (Fc), *F. unibracteata* (Fu), *F. przewalskii* (Fp), and *F. delavayi* (Fd), four representative Fritillaria Cirrhosae Bulbus source plants, were collected in 2014−2016 from the eastern Himalaya-Hengduan Mountains, southwestern China at Weixi (WX), Yunnan (alt. 3,200 m); Songpan (SP), Sichuan (alt. 3,300 m); Yuzhong (YZ), Gansu (alt. 3,500 m), and Kangding (KD), Sichuan (alt. 4,500 m). The average annual temperature is 3°C, the highest temperature is 25.6°C, and the lowest temperature is -25.8°C in these areas; average annual precipitation is 784.9 mm [18,19]. Dominant flora in these areas are north temperate plant communities composed of *Rhododendron*, *Spiraea*, *Sibiraea*, *Saussurea*, *Potentilla*, *Salix*, and *Anaphalis* species [19]. Three populations of each plant species in the same geographic area and at the same plant phenology stage were sampled, and one plant was sampled from each population, which resulted in a total of 24 samples for the four plant species (Supplementary Table S1).

Then, *F. cirrhosa* samples were collected in four geographic areas where it is primarily distributed: WX, Yunnan (alt. 3,200 m); Huadianba (HDB), Yunnan (alt. 3,200 m); Qiaojia (QJ), Yunnan (alt. 3,800 m); and Leiwuqi (LWQ), Xizang (alt. 3,900 m). Three populations of each geographic area at the same plant phenology stage were sampled, and one plant was sampled from each population, which resulted in a total of 24 samples for the four geographic areas (Supplementary Table S1). Among them, *F. cirrhosa* samples from WX were collected at four representative phenology stages with rapid metabolism, which included 2-yr-olds in the mature period (2-MP), 2-yr-olds in the germination period (2-GP), 4-yr-olds in the flowering period (4-FP), and 4-yr-olds in the germination period (4-GP). Plants of each phenology stage were sampled from three constant populations in the same geographic area, and one plant was sampled from each population, which resulted in a total of 12 samples for the four plant phenology stages (Supplementary Table S1). Bulbs of plants were excavated and stored in the original soil at 4°C for further treatment as soon as possible.

Molecular identification of bulb-associated fungi

Bulb samples were surface cleaned before molecular identification, which was based on sequence analysis of the ITS rDNA region. DNA was extracted following the procedures described by Gao and Yang [20]. ITS rDNA was amplified using primer combinations of ITS1F×ITS4, ITS5×ITS4, and ITS1F×LR1 [20]. Amplified products were purified and ligated into TaKaRa pMD18-T plasmids (TaKaRa Bio Inc., Shiga, Japan), the cloned plasmids were transformed into Escherichia coli strain DH5α. For each bulb, about 100 clones were arbitrarily selected for PCR amplification and automatically sequenced with an ABI 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA, USA; Sangon Biotech Co., Ltd., Shanghai, China).

Sequences were sorted into operational taxonomic units (OTUs) at a sequence similarity of ≥97% across ITS rDNA [19] using DOTUR [21]. BLASTn analysis of the representative sequence of each OTU was carried out against the GenBank database for preliminary identification. ITS matches for taxa in National Center for Biotechnology Information's GenBank were defined as corresponding to at least 90% of the sequence length with a sequence similarity of 97-100% and e-values below e-100 at the species level, 90-97% sequence similarity and e-values below e-90 at the genus level, and 80-90% sequence similarity and e-values below e-80 at the order level.

Generated sequences were deposited in GenBank under accession numbers MK405809–MK405831, MK405833–MK406272, MK406275–MK406310, MK406312–MK407528, MK407530–MK407667, MK407669–MK407694, and MK407696–MK408161.

Statistical analysis of fungal diversity and community distribution

The evaluation was conducted on species diversity and community distribution of bulb associated fungi. Rarefaction curve analysis of the number of fungal individuals and fungal OTUs relative to sample size was carried out for the entire fungal community of all plant species from different geographic areas and different plant phenology stages using R (Version 2.15.3, https://www.r-project.org/) [22] with observed index and Chao1 index. OTU frequency was defined as the number of ITS rDNA sequences of the OTU. Diversity measures including Chao1 and ACE estimators, and Shannon and Simpson indexes were calculated for fungal OTUs associated with each host plant species, geographic area, and plant phenology stage using Qiime (Version 1.7.0, http://qiime.org/) [22]. A Kruskal–Wallis (KW) rank-sum test of diversity indexes based on Chao1, Shannon, and Simpson distances, and permutational multivariate analysis of variance (PerMANOVA) of OTU frequency based on Bray–Curtis and Jaccard distances were performed using Mothur (Version 1.43.0, http://www.mothur.org/wiki/Download_mothur/) [22]; diversity indexes and OTU frequency used as dependent variables, and "Host plant species," "Geographic area," and "Plant phenology stage" as independent variables. The significance level was set to p=0.05.

RESULTS

Diversity of bulb-associated fungi of Fritillaria Cirrhosae Bulbus source plants

A total of 1,486 fungal sequences (excluding host plant-contaminated sequences and failed sequences) generated from the four plant species sampled in different geographic areas and at different plant phenology stages were assigned to 251 OTUs and belonged to 12 classes, 32 orders, 51 families, and 99 genera based on primary molecular identification (Supplementary Table S2 and Table S3). Of the OTUs, 33% (84) were preliminarily recognized at the species level, with reference sequences of taxa with ≥97% similarity found in GenBank. Most of the fungal OTUs (96.41%) were Ascomycotina, 3.52% were Basidiomycotina, and 0.07% were Zygomycotina, and were assigned to 90, nine, and three lineages, respectively. OTU richness was high in *Fusarium* (33 OTUs), *Ilyonectria* (17 OTUs), *Tomentella* (14 OTUs), *Tetracladium* (12 OTUs), and *Leptodontidium* (10 OTUs), followed by *Cladosporium* (seven OTUs), *Trichoderma* (six

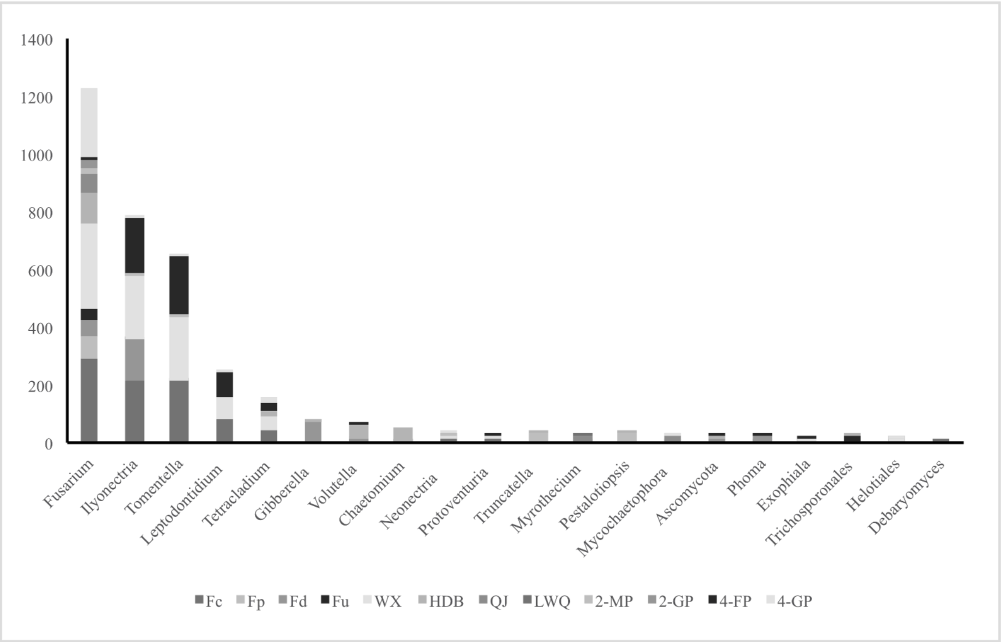

Fig. 1. Operational taxonomical units (OTU) richness of dominant fungal lineages sequenced from bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* collected at four plant phenology stages. Fc, *F. cirrhosa*; Fp, *F. przewalskii*; Fc, *F. cirrhosae*; Fd, *F. delavayi*; Fu, *F. unibracteata*; WX, Weixi; HDB, Huadianba; QJ, Qiaojia; LWQ, Leiwuqi; 2-MP, 2 yr old in mature period; 2-GP, 2 yr old in germination period; 4-FP, 4 yr old in flowering period; 4-GP, 4 yr old in germination period.

OTUs), *Neonectria* (five OTUs), *Gibberella* (four OTUs), and *Phoma* (four OTUs) (Supplementary Table S2 and Table S3). For relative frequency, Sordariomycetes (74.53% of the total sequences) dominated at the class level, Hypocreales (64.88%) dominated at the order level, Nectriaceae (46.21%) dominated at the family level, and *Fusarium* (39.91%) and *Ilyonectria* (14.83%) dominated at the genus level (Fig. 1 and Supplementary Fig. S1); *Fusarium* sp. 03 (frequency = 516), *Ilyonectria rufa* (187), *Fusarium* sp. 08 (222), and *Ilyonectria* sp. 03 (137) were the most frequent OTUs (Fig. 2). The fungal community primarily comprised frequent OTUs and fewer rare OTUs, with 16% of the total OTUs having a cumulative frequency ≥10, 53% having a frequency ≥3, and 39% detected as singletons (Supplementary Table S2 and Table S3). The rarefaction curve did not approach an asymptote with increasing sequencing size, which revealed that a saturated sequencing depth that would cover all fungal OTUs in the samples was not reached (Supplementary Fig. S2); this indicates a need for enhanced sequencing.

Community distribution of bulb-associated fungi of Fritillaria Cirrhosae Bulbus source plants

For the four host plant species, 92 fungal OTUs were detected in Fc, 15 OTUs were unique for this plant, OTU richness was highest in *Tetracladium*, and three *Fusarium* OTUs were the most frequent. Thirty four of the 74 OTUs were unique in Fd, OTU richness was highest in *Fusarium* and one *Ilyonectria* OTU was the most frequent. Two unique OTUs were detected out of 27 in Fp, OTU richness was highest in *Fusarium*,

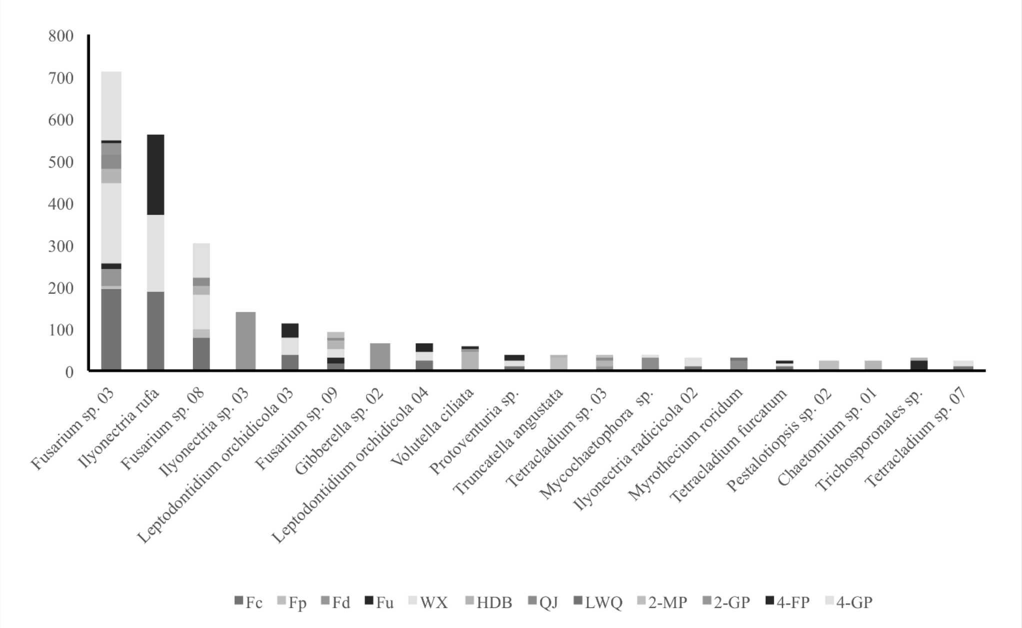

Fig. 2. Frequency of the top frequent fungal operational taxonomical units (OTUs) from bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* collected at four plant phenology stages. Fc, *F. cirrhosa*; Fp, *F. przewalskii*; Fd, *F. delavayi*; Fu, *F. unibracteata*; WX, Weixi; HDB, Huadianba; QJ, Qiaojia; LWQ, Leiwuqi; 2-MP, 2 yr old in mature period; 2-GP, 2 yr old in germination period; 4-FP, 4 yr old in flowering period; 4-GP, 4 yr old in germination period.

and one *Truncatella* OTU was the most frequent. Nine of the 20 OTUs were unique for Fu, OTU richness was highest in *Fusarium*, and two *Fusarium* OTUs were the most frequent (Supplementary Fig. S1 and Table S3). Eight OTUs were shared by two plants, and one *Fusarium* OTU was shared by four plants (Fig. 3 and Supplementary Table S2).

For *F. cirrhosa* collected from four geographic areas, 12 of the 94 detected OTUs were unique for WX, OTU richness was highest in *Tetracladium*, and three *Fusarium* OTUs were the most frequent. Twelve of the 53 OTUs were unique in HDB, OTU richness was highest in *Fusarium*, and one *Volutella* OTU was the most frequent. For 25 common OTUs in QJ, OTU richness was highest in *Fusarium*, and two *Fusarium* OTUs were the most frequent. For seven common OTUs in LWQ, OTU richness was highest in *Colletotrichum*, and one *Debaryomyces* OTU was the most frequent (Supplementary Fig. S1 and Table S3). Twelve OTUs were shared by two sites, and four OTUs were shared by three sites (Fig. 3 and Supplementary Table S2).

For *F. cirrhosa collected* at four plant phenology stages, 10 of the 55 OTUs detected were unique for *4-FP*, OTU richness was highest in *Leptodontidium*, and one *Ilyonectria* OTU was most frequent. Two of the 22 total OTUs were unique in 2-MP, OTU richness was highest in *Ilyonectria*, and one *Fusarium* OTU was the most frequent. In *4-GP*, OTU richness was highest in *Tetracladium*, and two *Fusarium* OTUs were the most frequent. For the two OTUs in *2-GP*, one *Fusarium* OTU was the most frequent (Supplementary Fig. S1 and Table S3). Three OTUs were shared by two phenology stages, and one OTU was shared by

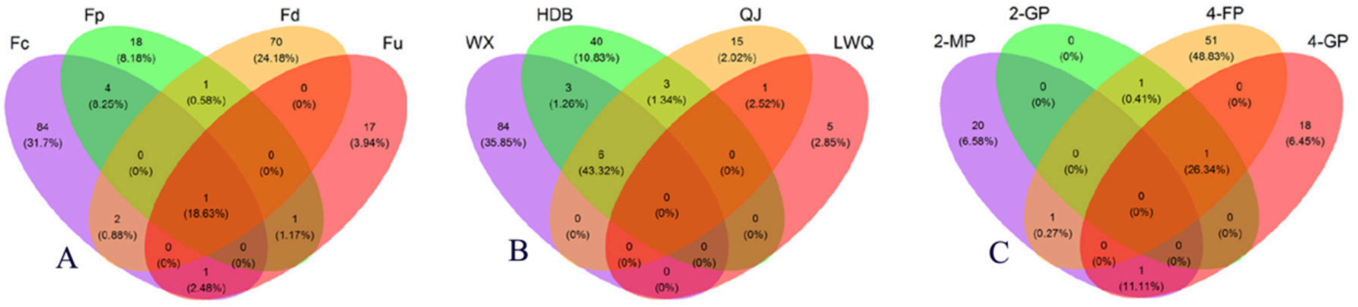

Fig. 3. Venn Diagrams showing the shared fungal operational taxonomical units (OTUs) and exclusive fungal OTUs of bulb samples from four species of Fritillaria Cirrhosae Bulbus source plants (A), *F. cirrhosae* collected in four geographic areas (B), and *F. cirrhosae* collected at four plant phenology stages (C). Percent digits in the parentheses were the sequence percentage of the OTU to the total OTUs in the diagram. Fc, *F. cirrhosa*; Fp, *F. przewalskii*; Fd, *F. delavayi*; Fu, *F. unibracteata*; WX, Weixi; HDB, Huadianba; QJ, Qiaojia; LWQ, Leiwuqi; 2-MP, 2 yr old in mature period; 2-GP, 2 yr old in germination period; 4-FP, 4 yr old in flowering period; 4-GP, 4 yr old in germination period.

three phenology stages (Fig. 3 and Supplementary Table S2).

It should be noted that *Fusarium* and several *Fusarium* OTUs were common fungal lineages and general fungal OTUs associated with Fritillaria Cirrhosae Bulbus source plants in terms of OTU richness and OTU frequency, and they were widely distributed across different host plant species, geographic areas, and plant phenology stages. *Fusarium* displayed high OTU richness in the four host plant species, three geographic areas, and two plant phenology stages. *Fusarium* OTUs were frequent in the four host plant species, three geographic areas, and three plant phenology stages; one *Fusarium* OTU was shared by three plants, three sites, and two phenology stages, and another *Fusarium* OTU was recovered from two plants, three sites, and one phenology stage.

Diversity measures relative to host plant species, geographic area, and plant phenology stage are illustrated in Supplementary Table S4. KW rank-sum test revealed a statistically significant difference in diversity indexes of fungal communities among the four host plant species (Chao1, p=0.0853, >0.05; Shannon, p=0.0188, <0.05; Simpson, p=0.0249, <0.05), among *Fritillaria cirrhosa* in four geographic areas (Chao1, p=0.0156, <0.05; Shannon, p=0.0237, <0.05; Simpson, p=0.0237, <0.05), and among *F. cirrhosa* at four plant phenology stages (Chao1, p=0.0153, <0.05; Shannon, p=0.0156, <0.05; Simpson, p=0.0188, <0.05). PerMANOVA test supported a statistically significant difference in composition of fungal community among the four plants (Bray–Curtis, p=0.002, <0.05; Jaccard, p=0.001, <0.05), among *F. cirrhosa* in four geographic areas (Bray–Curtis, p=0.001, <0.05; Jaccard, p=0.001, <0.05), and among *F. cirrhosa* at four plant phenology stages (Bray–Curtis, p=0.001, <0.05; Jaccard, p=0.001, <0.05). Thus, preferences of fungal communities for host plant species, geographic area, and plant phenology were identified.

DISCUSSION

Fusarium spp. are generally associated with medicinal plants [23,24]. *Fusarium tricinctum*, *F.*

acuminatum, F. sambucinum, and *F. redolens* were isolated from bulbs of Fritillaria Cirrhosae Bulbus source plants [8,14,15,25]. Our study confirmed that *Fusarium* spp. were dominant, general fungal species associated with bulbs of Fritillaria Cirrhosae Bulbus source plants, and were widespread in different source plant species collected from different sites and at different phenology stages. Common *Fusarium* species that have been isolated from Fritillaria Cirrhosae Bulbus source plants, such as *F. acuminatum*, and those that have been found in other medicinal plants, such as *F. solani*, and *F. oxysporum, were detected in our study*. However, unique *Fusarium* species that were also first revealed in this research, such as *F. lateritium, F. proliferatum, F. lateritium, F. penzigii*, and *F. delphinoides*.

It should be noted that many *Fusarium* species are a source of significant bioactive ingredients in valuable medicinal plants [16,25-27]. It was revealed that *Fusarium* isolates from *Fritillaria unibracteata* and *F. unibracteata* wabuensis were able to produce active alkaloid components *of* their host plants [8-10]. Therefore, further research on active metabolites of related *Fusarium* isolates associated with our host plants is needed to exploit potential biopharmaceutical fungi resources, and for resource conservation of valuable Fritillaria Cirrhosae Bulbus source plants in the future.

In the meantime, our results revealed the diversity of bulb-associated fungi of Fritillaria Cirrhosae Bulbus source plants. It was demonstrated that bulbs of the four Fritillaria Cirrhosae Bulbus source plants harbored abundant fungal species distributed across diverse lineages. Endophytic fungi in *Fusarium*, *Penicillium*, *Paraphoma*, *Clonostachys*, *Gibberella*, *Colletotrichum*, *Plectosphaerella*, *Lachnum*, *Volutella*, *Cladosporium*, *Phoma*, *Paraconiothyrium*, *Alternaria*, *Ilyonectria*, *Nectria*, *Myrothecium*, *Rhizoctonia*, *Tomentella*, *Inocybe*, and *Mortierella* (20 taxa, 1/5 of the total taxa identified) have been found in bulbs of Fritillaria Cirrhosae Bulbus source plants using the cultural method [13-16,25]. However, a larger variety of fungal lineages (82 taxa, 4/5 of the total taxa identified) was detected from bulbs of Fritillaria Cirrhosae Bulbus source plants for the first time in this study. Among them, isolations of *Fusariu*m, *Trichoderma*, *Penicillium*, *Epicoccum*, *Chaetomidium*, *Paraphoma*, *Cylindrocarpon*, *Neonectria*, *Plectosphaerella*, *Volutella*, *Chaetomium*, *Colletotrichum*, and *Clonostachys* (13 taxa, 13% of the total taxa identified in this study by molecular method) in bulbs of these plant species have been cultured in our culture tests (unpublished data).

We detected several fungal species that have not been revealed in our or other culture tests [13,16] on Fritillaria Cirrhosae Bulbus source plants by ITS rDNA sequencing in this study. The results are somewhat biased because epiphyte fungi were detected on plant bulbs. However, an integrated molecular and cultural approach is indispensable for more comprehensive identification of fungal diversity associated with medicinal plants.

Besides, community distribution of bulb-associated fungi in terms of host plant species, geographic area, and plant phenology was tested in this study. It was revealed that composition and distribution of fungal community are associated with genotype (species), ecological and environmental conditions (geographic area) and phenology of host plants [6,28,29]. Additionally, it was previously reported that fungal species and quantity are most abundant in 3-yr-old stage *of Fritillaria cirrhosa* [13]. In this research, fungal community composition associated with Fritillaria Cirrhosae Bulbus source plants showed preferences for host plant species, geographic area, and plant phenology. Many fungal lineages and species were unique in specific sampling situations; fungal diversity and specificity were much higher in some plant species (Fc, Fd), some sampling sites (WX, HDB), and one phenology stage (4-FP). This result may be influenced by the small sample size in this study, and sampling-dependent composition of fungal community was indicated; therefore, further research with an increased sample size is needed.

It was revealed that the microbial community of medicinal plants may impact the host metabolome, and thus influence the quality of herbal medicine [30]. Therefore, systematic research that characterizes dynamic correlations between the fungal community and the active metabolites in Fritillaria Cirrhosae Bulbus source plants under different sampling scenarios can provide insight into resource exploitation of critical fungal species related to the production of crucial bioactive compounds, artificial propagation, and conservation of valuable Fritillaria Cirrhosae Bulbus source plants in the future, and also application of key fungal species to improve the quality and medical effectiveness of Fritillaria Cirrhosae Bulbus.

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Supplementary Table S1. Sample list for collected individual plant sources with information regarding host-plant species, geographic area and phenology stage.

Pant species	Phenology stage	Sampling site						
		SP	YZ	KD	WX	HDB	QJ	LWQ
Fc	2- MP				3	3	3	3
	2 -GP				3			
	4-FP				3	3	3	3
	4-GP				3			
Fp	2- MP		3					
	4-FP		3					
Fd	2- MP			3				
	4-FP			3				
Fu	2- MP	3						
	4-FP	3						

Fc: *F. cirrhosae*; Fp: *F. przewalskii*; Fd: *F. delavayi*; Fu: *F. unibracteata*; WX: Weixi; HDB: Huadianba; QJ: Qiaojia; LWQ: Leiwuqi; 2-MP: 2 yr old in mature period; 2-GP: 2 yr old in germination period; 4-FP: 4 yr old in flowering period; 4-GP: 4 yr old in germination period.

Supplementary Table S2. Fungal lineages associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants.

Endophyte lineages	OTU richness	Frequency											
		By host-plant				By sampling site				By growing-physiological period			
		Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP
Ascomycota													
Clavatospora	1	0	0	0	5	0	0	0	0	0	0	0	0
Xylariaceae	1	0	0	0	2	0	0	0	0	0	0	0	0
Podospora	1	0	0	0	1	0	0	0	0	0	0	0	0
Hyalopeziza	1	0	0	0	1	0	0	0	0	0	0	0	0
Paraphoma	2	1	8	0	0	1	0	0	0	0	0	0	1
Pestalotiopsis	3	0	29	0	0	0	2	0	0	0	0	0	0
Mycochaetophora	1	2	1	0	0	2	1	22	0	0	0	0	2
Pleiochaeta	2	1	0	0	0	1	1	0	0	0	0	1	0
Ascomycota	10	3	1	6	0	4	7	1	0	2	0	2	0
Exophiala	3	8	0	0	0	8	0	0	0	0	0	8	0
Pezizomycotina	1	1	0	0	0	1	0	0	0	0	0	1	0
Clonostachys	2	4	0	1	0	4	0	0	0	0	0	0	4
Articulospora	2	0	10	0	0	0	0	0	0	0	0	0	0
Mycocentrospora	1	0	0	0	0	0	1	0	0	0	0	0	0
Cercophora	1	1	0	0	0	1	0	0	0	0	0	1	0
Varicosporium	2	0	0	0	0	0	2	0	0	0	0	0	0
Microdiplodia	1	0	0	0	0	0	4	0	0	0	0	0	0
Davidiella	3	2	0	0	0	2	3	4	0	2	0	0	0
Epicoccum	1	0	0	0	0	0	5	0	0	0	0	0	0
Trichoderma	6	2	0	11	0	3	0	0	0	0	0	1	1
Neonectria	5	10	0	2	0	10	4	0	0	9	0	0	1
Hymenoscyphus	2	2	0	0	0	1	2	0	0	1	0	0	0
Chaetomidium	2	0	0	0	0	0	3	0	0	0	0	0	0
Gibberella	4	0	0	68	1	0	1	0	0	0	0	0	0
Pleospora	4	5	0	1	1	5	0	0	0	0	0	5	0
Protoventuria	1	12	0	0	0	12	0	0	0	0	0	12	0
Pseudogymnoascus	1	0	0	0	0	0	0	1	0	0	0	0	0
Colletotrichum	3	0	0	0	0	0	0	0	14	0	0	0	0
Truncatella	1	0	30	0	0	0	2	0	0	0	0	0	0

Supplementary Table S2. Fungal lineages associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants. (continued)

Endophyte lineages	OTU richness	Frequency											
		By host-plant				By sampling site				By growing-physiological period			
		Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP
Ascomycota													
Helotiaceae	1	0	3	0	0	0	1	0	0	0	0	0	0
Plectosphaerella	1	0	1	0	0	0	0	0	0	0	0	0	0
Cylindrocarpon	1	1	1	0	0	1	0	0	0	1	0	0	0
Lachnum	1	1	0	0	0	1	0	0	0	1	0	0	0
Schizothecium	1	1	0	0	0	1	0	0	0	1	0	0	0
Phaeosphaeria	1	0	0	0	0	0	1	0	0	0	0	0	0
Psiloglonium	1	0	0	0	0	0	1	1	0	0	0	0	0
Monographella	3	0	0	1	0	0	7	2	0	0	0	0	0
Volutella	2	3	0	13	0	3	40	1	0	0	2	1	0
Microdochium	1	0	0	0	0	0	9	0	0	0	0	0	0
Cladosporium	7	1	1	2	0	1	6	1	0	0	0	1	0
Phoma	4	2	0	18	0	2	0	2	0	0	0	2	0
Myrmecridium	1	1	0	0	0	1	0	0	0	0	0	1	0
Paraconiothyrium	1	0	0	0	0	0	5	0	0	0	0	0	0
Hypocrea	1	0	0	0	0	0	2	0	0	0	0	0	0
Leptodontidium	10	81	0	0	0	81	0	0	0	0	0	79	2
Alternaria	2	0	0	0	0	0	0	4	0	0	0	0	0
Rachicladosporium	1	0	0	0	0	0	0	3	0	0	0	0	0
Tetracladium	12	46	0	0	0	43	19	3	0	1	0	26	16
Gloeotinia	2	2	0	0	0	2	0	0	0	0	0	2	0
Troposporella	1	1	0	0	0	1	0	0	0	0	0	1	0
Ochrocladosporium	1	5	0	0	0	5	0	0	0	0	0	5	0
Trichocladium	2	3	0	0	0	3	0	0	0	2	0	1	0
Helotiales	9	7	0	1	0	7	3	0	0	1	0	0	4
Spirosphaera	1	0	0	0	6	0	0	0	0	0	0	0	0
Leptosphaeri	3	2	8	0	1	2	0	0	0	0	0	2	0
Uncultured fungus	3	2	1	0	0	2	0	0	0	0	0	2	0
Thelebolales	1	1	0	0	0	1	0	0	0	0	0	1	0
Ilyonectria	17	217	0	140	1	217	0	1	0	11	0	193	13
Fontanospora	1	0	0	0	0	0	1	0	0	0	0	0	0
Shigella	1	0	0	0	0	0	0	0	2	0	0	0	0
Debaryomyces	1	0	0	0	0	0	0	0	19	0	0	0	0
Curvularia	1	0	0	0	1	0	0	0	0	0	0	0	0
Candida	1	0	0	0	0	0	0	2	0	0	0	0	0
Gryllus	1	0	0	0	0	0	2	0	0	0	0	0	0
Nectria	1	0	0	0	0	0	0	1	0	0	0	0	0
Chaetomium	1	0	0	1	1	0	49	0	0	0	0	0	0
Fusarium	33	296	70	61	35	296	106	69	0	17	27	9	244
Penicillium	3	0	0	9	0	0	0	0	0	0	0	0	0
Mariannaea	1	0	0	2	0	0	0	0	0	0	0	0	0
Nectriaceae	4	0	0	4	0	0	0	0	0	0	0	0	0
Thelonectria	1	0	0	1	0	0	0	0	0	0	0	0	0
Leptosphaeriaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Plectosphaerellaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Hypocreales	3	0	0	3	0	0	0	0	0	0	0	0	0
Fusicolla	1	0	0	1	0	0	0	0	0	0	0	0	0
Hypocreaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Microascaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Clavicipitaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Dothideomycetes	2	0	0	2	0	0	0	0	0	0	0	0	0
Cosmospora	1	0	0	1	0	0	0	0	0	0	0	0	0

Supplementary Table S2. Fungal lineages associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants. (continued)

Endophyte lineages	OTU richness	Frequency											
		By host-plant				By sampling site				By growing-physiological period			
		Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP
Ascomycota													
Kernia	1	0	0	1	0	0	0	0	0	0	0	0	0
Sordariomycetes	2	0	0	2	0	0	0	0	0	0	0	0	0
Myrothecium	2	0	0	1	0	0	0	21	9	0	0	0	0
Acremoniopsis	1	0	0	1	0	0	0	0	0	0	0	0	0
Myceliophthora	1	0	0	1	0	0	0	0	0	0	0	0	0
Chaetomiaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Gypsoplaca	1	0	0	1	0	0	0	0	0	0	0	0	0
Acremonium	1	0	0	1	0	0	0	0	0	0	0	0	0
Hydropisphaera	1	0	0	1	0	0	0	0	0	0	0	0	0
Leotiomycetes	1	0	0	1	0	0	0	0	0	0	0	0	0
Basidiomycota													
Rhizoctonia	2	0	0	0	4	0	0	0	0	0	0	0	0
Cryptococcus	2	1	0	1	0	1	0	0	0	1	0	0	0
Trechispora	1	1	0	0	0	1	0	0	0	0	0	1	0
Tomentella	14	218	0	0	1	218	0	1	0	11	0	194	13
Tremellales	1	0	0	0	0	0	0	0	1	0	0	0	0
Trichosporonales	1	0	0	0	23	0	1	0	0	0	0	0	0
Inocybe	1	0	0	0	2	0	0	0	0	0	0	0	0
Stilbum	1	0	0	0	2	0	0	0	0	0	0	0	0
Cystofilobasidiaceae	1	0	0	1	0	0	0	0	0	0	0	0	0
Zygomycota													
Zygomycota	1	0	0	1	0	0	0	0	0	0	0	0	0
Mortierella	1	0	0	1	0	0	0	0	0	0	0	0	0
Mortierellaceae	1	0	0	1	0	0	0	0	0	0	0	0	0

Fc: *F. cirrhosae*; Fp: *F. przewalskii*; Fd: *F. delavayi*; Fu: *F. unibracteata*; WX: Weixi; HDB: Huadianba; QJ: Qiaojia; LWQ: Leiwuqi; 2-MP: 2 yr old in mature period; 2-GP: 2 yr old in germination period; 4-FP: 4 yr old in flowering period; 4-GP: 4 yr old in germination period.

Supplementary Table S3. Frequency and closed match in Blast result of fungal OTUs associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* in Wei Xi collected at four plant phenology stages.

Endophyte OTUs	By host-plant				By host-plant				By growing-physiological period				Closest match and accession number in GenBank
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP	
Articulospora sp.	0	4	0	0	0	0	0	0	0	0	0	0	*Articulospora* sp. 96, 97% JQ346970.1
Clonostachys rosea 01	0	0	1	0	0	0	0	0	0	0	0	0	*Clonostachys rosea* 100% KY192277.1
Clonostachys rosea 02	4	0	0	0	4	0	0	0	0	0	0	4	*Clonostachys rosea* 99% KT215192.1
Pezizomycotina sp.	1	0	0	0	1	0	0	0	0	0	1	0	*Pezizomycotina* sp. 99% FJ554213.1
Exophiala sp. 01	1	0	0	0	1	0	0	0	0	0	1	0	*Exophiala* sp. 100% HG935705.1
Neonectria sp.	1	0	1	0	1	0	0	0	0	0	0	1	*Neonectria* sp. 99% HG936689.1
Plectosphaerellaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Plectosphaerellaceae sp. 99% KR232522.1
Hypocreaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Hypocreaceae sp. 99% NR_134415.1
Pleiochaeta sp.	0	0	0	0	0	1	0	0	0	0	0	0	*Pleiochaeta* sp. 99% FJ378717.1
Mycochaetophora sp.	2	1	0	0	2	0	0	0	0	0	0	2	*Mycochaetophora* sp. 99% HG936157.1
Pestalotiopsis sp. 01	0	0	0	0	0	2	0	0	0	0	0	0	*Pestalotiopsis* sp. 97% KT963803.1
Pestalotiopsis sp. 02	0	26	0	0	0	0	0	0	0	0	0	0	*Pestalotiopsis* sp. 99, 100% KT963803.1
Pestalotiopsis sp. 03	0	3	0	0	0	0	0	0	0	0	0	0	*Pestalotiopsis* sp. 94% KT963803.1
Paraphoma sp.	1	7	0	0	1	0	0	0	0	0	0	1	*Paraphoma* sp. 99, 100% KT268372.1
Hyalopeziza sp.	0	0	0	1	0	0	0	0	0	0	0	0	*Hyalopeziza* sp. 96% JN033442.1
Podospora ellisiana	0	0	0	1	0	0	0	0	0	0	0	0	*Podospora ellisiana* 98% AY515360.1
Xylariaceae sp.	0	0	0	2	0	0	0	0	0	0	0	0	*Xylariaceae* sp. 97% KT581806.1
Rhizoctonia butinii	0	0	0	3	0	0	0	0	0	0	0	0	*Rhizoctonia butinii* 95% KF386035.1
Clavatospora longibrachiata	0	0	0	5	0	0	0	0	0	0	0	0	*Clavatospora longibrachiata* 94, 95% KF730808.1
Colletotrichum musae 01	0	0	0	0	0	0	0	2	0	0	0	0	*Colletotrichum musae* 90% AJ301904.1
Colletotrichum musae 02	0	0	0	0	0	0	0	8	0	0	0	0	*Colletotrichum musae* 99% AJ301904.1
Colletotrichum musae 03	0	0	0	0	0	0	0	4	0	0	0	0	*Colletotrichum musae* 98, 99% JN121212.1
Neonectria ramulariae	1	0	0	0	1	0	0	0	0	0	0	1	*Neonectria ramulariae* 99% KM249079.1
Pseudogymnoascus sp.	0	0	0	0	0	0	1	0	0	0	0	0	*Pseudogymnoascus* sp. 99% KP902681.1
Protoventuria sp.	12	0	0	0	12	0	0	0	0	0	12	0	*Protoventuria* sp. 99% JQ346991.1
Pleosporales sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	*Pleosporales* sp. 100% KU973713.1
Pleosporales sp. 02	0	0	0	1	0	0	0	0	0	0	0	0	*Pleosporales* sp. 99% HM116749.1
Pleosporales sp. 03	4	0	0	0	4	0	0	0	0	0	4	0	*Pleosporales* sp. 99% FJ553010.1
Pleosporales sp. 04	1	0	0	0	1	0	0	0	0	0	1	0	*Pleosporales* sp. 92% JF449873.1
Myrmecridium schulzeri	1	0	0	0	1	0	0	0	0	0	1	0	*Myrmecridium schulzeri* 86% KP132479.1
Chaetomidium sp.	0	0	0	0	0	1	0	0	0	0	0	0	*Chaetomidium* sp. 99% gb|KM889548.1
Chaetomidium leptoderma	0	0	0	0	0	2	0	0	0	0	0	0	*Chaetomidium leptoderma* 99% JN573176.1
Hymenoscyphus sp.	1	0	0	0	1	0	0	0	1	0	0	0	*Hymenoscyphus* sp. 97% FJ378856.1
Hymenoscyphus ericae complex	0	0	0	0	0	2	0	0	0	0	0	0	*Hymenoscyphus ericae* complex 96% AY394684.1
Neonectria ramulariae	2	0	0	0	2	4	0	0	2	0	0	0	*Neonectria ramulariae* 99% AJ279446.1
Mariannaea elegans	0	0	2	0	0	0	0	0	0	0	0	0	*Mariannaea elegans* 100% AB855778.1
Epicoccum sp.	0	0	0	0	0	5	0	0	0	0	0	0	*Epicoccum* sp. 99, 100% HQ630972.1
Davidiella sp. 01	0	0	0	0	0	2	4	0	0	0	0	0	*Davidiella* sp. 99, 100% HG935309.1
Davidiella sp. 02	0	0	0	0	0	1	0	0	0	0	0	0	*Davidiella* sp. 99% HG935295.1
Microdiplodia hawaiiensis	0	0	0	0	0	4	0	0	0	0	0	0	*Microdiplodia hawaiiensis* 95% DQ885897.1
Varicosporium elodeae	0	0	0	0	0	1	0	0	0	0	0	0	*Varicosporium elodeae* 99% JX981463.1
Cercophora sp.	1	0	0	0	1	0	0	0	0	0	1	0	*Cercophora* sp. 97% HQ631039.1
Mycocentrospora acerina	0	0	0	0	0	1	0	0	0	0	0	0	*Mycocentrospora acerina* 100% KU341519.1
Hypocrea pachybasioides	0	0	0	0	0	2	0	0	0	0	0	0	*Hypocrea pachybasioides* 98% GU934589.1
Paraconiothyrium sp.	0	0	0	0	0	5	0	0	0	0	0	0	*Paraconiothyrium* sp. 94% FN868460.1
Phoma sp. 01	0	0	18	0	0	0	0	0	0	0	0	0	*Phoma* sp. 100% HG935441.1
Phoma sp. 02	0	0	0	0	0	0	2	0	0	0	0	0	*Phoma* sp. 99% AF218789.1
Phoma sp. 03	1	0	0	0	1	0	0	0	0	0	1	0	*Phoma* sp. 99% FN868459.1
Phoma sp. 04	1	0	0	0	1	0	0	0	0	0	1	0	*Phoma* sp. 98% JX010732.1

Supplementary Table S3. Frequency and closed match in Blast result of fungal OTUs associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* in Wei Xi collected at four plant phenology stages. (continued)

Endophyte OTUs	By host-plant				By host-plant				By growing-physiological period				Closest match and accession number in GenBank
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP	
Cladosporium sp. 01	0	0	0	0	0	1	0	0	0	0	0	0	*Cladosporium* sp. 99% KT334734.1
Cladosporium sp. 02	1	0	0	0	1	0	0	0	0	0	1	0	*Cladosporium* sp. 100% HQ211815.1
Cladosporium sp. 03	0	0	1	0	0	2	0	0	0	0	0	0	*Cladosporium* sp. 99, 100% KU366279.1
Cladosporium sp. 04	1	1	0	0	0	1	0	0	0	0	1	0	*Cladosporium* sp. 99% KF367544.1
Cladosporium sp. 05	0	0	0	0	0	2	0	0	0	0	0	0	*Cladosporium* sp. 98% JQ951582.1
Cladosporium sp. 06	0	0	1	0	0	0	0	0	0	0	0	0	*Cladosporium* sp. 100% KY859398.1
Cladosporium tenuissimum	0	0	0	0	0	0	1	0	0	0	0	0	*Cladosporium tenuissimum* 100% AJ300331.1
Monographella nivalis	0	0	1	0	0	0	0	0	0	0	0	0	*Monographella nivalis* 100% KJ780751.1
Monographella lycopodina	0	0	0	0	0	7	1	0	0	0	0	0	*Monographella lycopodina* 99% JF440979.1
Psiloglonium sp.	0	0	0	0	0	1	1	0	0	0	0	0	*Psiloglonium* sp. 99% HG935427.1
Phaeosphaeria sp.	0	0	0	0	0	1	0	0	0	0	0	0	*Phaeosphaeria* sp. 99% EU715675.1
Schizothecium glutinans	1	0	0	0	1	0	0	0	1	0	0	0	*Schizothecium glutinans* 99% AY999116.1
Lachnum sp.	1	0	0	0	1	0	0	0	1	0	0	0	*Lachnum* sp. 100% HQ211775.1
Cylindrocarpon sp.	1	1	0	0	1	0	0	0	1	0	0	0	*Cylindrocarpon* sp. 99% AB725901.1
Plectosphaerella sp.	0	1	0	0	0	0	0	0	0	0	0	0	*Plectosphaerella* sp. 99% HE977552.1
Helotiaceae sp.	0	3	0	0	0	1	0	0	0	0	0	0	Helotiaceae sp. 99% KF359562.1
Truncatella angustata	0	30	0	0	0	2	0	0	0	0	0	0	*Truncatella angustata* 99% GU566260.1
Tetracladium sp. 01	8	0	0	0	8	0	0	0	0	0	0	8	*Tetracladium* sp. 99% HG935221.1
Tetracladium sp. 02	4	0	0	0	4	1	0	0	0	0	0	4	*Tetracladium* sp. 99, 100% HG935228.1
Tetracladium sp. 03	2	0	0	0	2	2	0	0	0	0	0	2	*Tetracladium* sp. 99% HG935220.1
Tetracladium sp. 04	2	0	0	0	2	0	0	0	0	0	0	2	*Tetracladium* sp. 96% HG935203.1
Tetracladium sp. 05	1	0	9	0	1	16	3	0	1	0	0	0	*Tetracladium* sp. 99% HG935225.1
Tetracladium sp. 06	1	0	0	0	1	0	0	0	0	0	1	0	*Tetracladium* sp. 95% EU883433.1
Tetracladium sp. 07	4	0	0	0	4	0	0	0	0	0	4	0	*Tetracladium* sp. 99% KR063520.1
Tetracladium maxilliforme	3	0	0	0	3	0	0	0	0	0	3	0	*Tetracladium maxilliforme* 99% EU883430.1
Tetracladium breve 01	2	0	0	0	2	0	0	0	0	0	2	0	*Tetracladium breve* 99% KC694156.1
Tetracladium breve 02	6	0	0	0	6	0	0	0	0	0	6	0	*Tetracladium breve* 96% EU883431.1
Tetracladium furcatum	9	0	0	0	9	0	0	0	0	0	9	0	*Tetracladium furcatum* 99% EU883432.1
Tetracladium setigerum	1	0	0	0	1	0	0	0	0	0	1	0	*Tetracladium setigerum* 94% EU883427.1
Rachicladosporium sp.	0	0	0	0	0	0	3	0	0	0	0	0	*Rachicladosporium* sp. 99% KC507249.1
Alternaria sp. 01	0	0	0	0	0	0	2	0	0	0	0	0	*Alternaria* sp. 100% JQ346877.1
Alternaria sp. 02	0	0	0	0	0	0	2	0	0	0	0	0	*Alternaria* sp. 99% KR094462.1
Leptodontidium sp.	2	0	0	0	2	0	0	0	0	0	0	2	*Leptodontidium* sp. 99% HQ731635.1
Leptodontidium orchidicola 01	1	0	0	0	1	0	0	0	0	0	1	0	*Leptodontidium orchidicola* 99% AM944357.1
Leptodontidium orchidicola 02	2	0	0	0	2	0	0	0	0	0	2	0	*Leptodontidium orchidicola* 99% FJ665276.1
Leptodontidium orchidicola 03	2	0	0	0	2	0	0	0	0	0	2	0	*Leptodontidium orchidicola* 95% FJ665278.1
Leptodontidium orchidicola 04	22	0	0	0	22	0	0	0	0	0	22	0	*Leptodontidium orchidicola* 99, 100% AF486133.1
Leptodontidium orchidicola 05	38	0	0	0	38	0	0	0	0	0	38	0	*Leptodontidium orchidicola* 99% KF646097.1
Leptodontidium orchidicola 06	1	0	0	0	1	0	0	0	0	0	1	0	*Leptodontidium orchidicola* 99% GQ302678.1
Leptodontidium orchidicola 07	4	0	0	0	4	0	0	0	0	0	4	0	*Leptodontidium orchidicola* 99% GU479910.1
Leptodontidium sp. 01	3	0	0	0	3	0	0	0	0	0	3	0	*Leptodontidium* sp. 99, 100% JF519497.1
Leptodontidium sp. 02	6	0	0	0	6	0	0	0	0	0	6	0	*Leptodontidium* sp. 99% FJ378720.1
Leptosphaeria sp.	0	8	0	0	0	0	0	0	0	0	0	0	*Leptosphaeria* sp. 93% LC150823.1
Articulospora tetracladia	0	6	0	0	0	0	0	0	0	0	0	0	*Articulospora tetracladia* 98% KP234360.1
Spirosphaera beverwijkiana	0	0	0	6	0	0	0	0	0	0	0	0	*Spirosphaera beverwijkiana* 89% HQ696657.1
Rhizoctonia sp.	0	0	0	1	0	0	0	0	0	0	0	0	*Rhizoctonia* sp. 99% AJ242901.1
Trechispora sp.	1	0	0	0	1	0	0	0	0	0	1	0	*Trechispora* sp. 85% JX392832.1
Helotiales sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	Helotiales sp. 100% KT160687.1
Helotiales sp. 02	1	0	0	0	1	0	0	0	0	0	0	1	Helotiales sp. 98% KC785555.1
Helotiales sp. 03	1	0	0	0	1	0	0	0	0	0	0	1	Helotiales sp. 99% KF000642.1
Helotiales sp. 04	1	0	0	0	1	0	0	0	0	0	0	1	Helotiales sp. 99% JF519138.1
Helotiales sp. 05	0	0	0	0	0	1	0	0	0	0	0	0	Helotiales sp. 98% FJ827183.1
Helotiales sp. 06	1	0	0	0	1	0	0	0	1	0	0	0	Helotiales sp. 94% HQ212362.1

Supplementary Table S3. Frequency and closed match in Blast result of fungal OTUs associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* in Wei Xi collected at four plant phenology stages. (continued)

Endophyte OTUs	By host-plant				By host-plant				By growing-physiological period				Closest match and accession number in GenBank
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP	
Helotiales sp. 07	1	0	0	0	1	0	0	0	0	0	0	1	Helotiales sp. 99% KC455335.1
Helotiales sp. 08	2	0	0	0	2	0	0	0	0	0	0	2	Helotiales sp. 97% FJ378851.1
Helotiales sp. 09	0	0	0	0	0	2	0	0	0	0	0	0	Helotiales sp. 96, 97% FJ378848.1
Pleiochaeta ghindensis	1	0	0	0	1	0	0	0	0	0	1	0	*Pleiochaeta ghindensis* 98% EU167561.1
Monographella aff. lycopodina	0	0	0	0	0	0	1	0	0	0	0	0	*Monographella aff. lycopodina* 99% KP714541.1
Fusicolla merismoides	0	0	1	0	0	0	0	0	0	0	0	0	*Fusicolla merismoides* 99% HG936551.1
Exophiala sp. 01	6	0	0	0	6	0	0	0	0	0	6	0	*Exophiala* sp. 95% HQ631063.1
Exophiala salmonis	1	0	0	0	1	0	0	0	0	0	1	0	*Exophiala salmonis* 96% AY213652.1
Trichocladium opacum	1	0	0	0	1	0	0	0	0	0	1	0	*Trichocladium opacum* 100% KF850373.1
Ochrocladosporium	5	0	0	0	5	0	0	0	0	0	5	0	*Ochrocladosporium* 97% JQ346922.1
Gibberella avenacea	0	0	0	1	0	0	0	0	0	0	0	0	*Gibberella avenacea* 99% EU255799.1
Troposporella sp.	1	0	0	0	1	0	0	0	0	0	1	0	*Troposporella* sp. 93% DQ351724.1
Gloeotinia temulenta	1	0	0	0	1	0	0	0	0	0	1	0	*Gloeotinia temulenta* 100% DQ235697.1
Fontanospora eccentrica	0	0	0	0	0	1	0	0	0	0	0	0	*Fontanospora eccentrica* 99% gb|KP234354.1
Gloeotinia temulenta	1	0	0	0	1	0	0	0	0	0	1	0	*Gloeotinia temulenta* 94% KC254110.1
Gibberella sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	*Ilyonectria* sp. 100% KU901549.1
Ilyonectria sp. 02	0	0	137	0	0	0	0	0	0	0	0	0	*Ilyonectria* sp. 100% KU901549.1
Ilyonectria sp. 03	1	0	0	0	1	0	0	0	0	0	1	0	*Ilyonectria* sp. 99% JF735316.1
Ilyonectria sp. 04	1	0	0	0	1	0	0	0	0	0	1	0	*Ilyonectria* sp. 99% JX231161.1
Ilyonectria destructans	0	0	1	0	0	0	0	0	0	0	0	0	*Ilyonectria destructans* 98% KY591577.1
Ilyonectria robusta	0	0	1	0	0	0	0	0	0	0	0	0	*Ilyonectria robusta* 100% KX438333.1
Ilyonectria macrodidyma	1	0	0	0	1	0	0	0	0	0	1	0	*Ilyonectria macrodidyma* 99% JN859418.1
Ilyonectria mors-panacis	3	0	0	0	3	0	0	0	0	0	3	0	*Ilyonectria mors-panacis* 99% JF735280.1
Ilyonectria rufa	187	0	0	0	187	0	0	0	0	0	187	0	*Ilyonectria rufa* 99, 100% JF735278.1
Ilyonectria cyclaminicola 01	1	0	0	0	1	0	0	0	1	0	0	0	*Ilyonectria cyclaminicola* 99% JF735304.1
Ilyonectria cyclaminicola 02	1	0	0	0	1	0	0	0	1	0	0	0	*Ilyonectria cyclaminicola* 99% NR_121495.1
Ilyonectria crassa	3	0	0	0	3	0	0	0	3	0	0	0	*Ilyonectria crassa* 99% JF735275.1
Ilyonectria pseudodestructans	6	0	0	0	6	0	0	0	6	0	0	0	*Ilyonectria pseudodestructans* 99% JF735291.1
Ilyonectria destructans	0	0	0	1	0	0	0	0	0	0	0	0	*Ilyonectria destructans* 98% LC146729.1
Ilyonectria robusta	0	0	0	0	0	0	1	0	0	0	0	0	*Ilyonectria robusta* 99% JF735266.1
Ilyonectria radicicola 01	10	0	0	0	10	0	0	0	0	0	0	10	*Ilyonectria radicicola* 99% KC989075.1
Ilyonectria radicicola 02	3	0	0	0	3	0	0	0	0	0	0	3	*Ilyonectria radicicola* 96% KC989075.1
Tomentella sublilacina	1	0	0	0	1	0	0	0	0	0	1	0	*Tomentella sublilacina* 98% HM189981.1
Thelebolales sp.	1	0	0	0	1	0	0	0	0	0	1	0	Thelebolales sp. 97% HQ207028.1
Uncultured fungus sp. 01	0	1	0	0	0	0	0	0	0	0	0	0	Uncultured fungus sp. 97% JX328350.1
Uncultured fungus sp. 02	1	0	0	0	1	0	0	0	0	0	1	0	Uncultured fungus sp. 85% JQ081775.1
Uncultured fungus sp. 03	1	0	0	0	1	0	0	0	0	0	1	0	Uncultured fungus sp. 85% JQ081780.1
Chaetomium sp. 01	0	0	0	0	0	1	0	0	0	0	0	0	*Chaetomium* sp. 99% HG937119.1
Chaetomium sp. 02	0	0	0	0	0	1	0	0	0	0	0	0	*Chaetomium* sp. 99% KM889527.1
Chaetomium sp. 03	0	0	0	0	0	23	0	0	0	0	0	0	*Chaetomium* sp. 98% EU750691.1
Chaetomium sp. 04	0	0	0	1	0	24	0	0	0	0	0	0	*Chaetomium* sp. 99, 100% KM889548.1
Chaetomium piluliferum	0	0	1	0	0	0	0	0	0	0	0	0	*Chaetomium piluliferum* 100% KU702723.1
Nectria sp.	0	0	0	0	0	0	1	0	0	0	0	0	*Nectria* sp. 99% KM889547.1
Gryllus bimaculatus	0	0	0	0	0	2	0	0	0	0	0	0	*Gryllus bimaculatus* 77% AK281769.1
Candida zeylanoides	0	0	0	0	0	0	2	0	0	0	0	0	*Candida zeylanoides* 99% EF687774.1
Leptosphaeria sp.	2	0	0	0	2	0	0	0	0	0	2	0	*Leptosphaeria* sp. 100% KJ542353.1
Zygomycota sp.	0	0	1	0	0	0	0	0	0	0	0	0	Zygomycota sp. 99% HG935643.1
Curvularia sp.	0	0	0	1	0	0	0	0	0	0	0	0	*Curvularia* sp. 99% HQ631061.1
Stilbum sp.	0	0	0	2	0	0	0	0	0	0	0	0	*Stilbum* sp. 98% HG936801.1
Inocybe ochroalba	0	0	0	2	0	0	0	0	0	0	0	0	*Inocybe ochroalba* 99% EU326165.1
Leptosphaeria sp.	0	0	0	1	0	0	0	0	0	0	0	0	*Leptosphaeria* sp. 99% KT768330.1
Myrothecium gramineum	0	0	1	0	0	0	0	0	0	0	0	0	*Myrothecium gramineum* 100% NR_145068.1
Myrothecium roridum	0	0	0	0	0	0	21	9	0	0	0	0	*Myrothecium roridum* 99% HQ839773.1

Supplementary Table S3. Frequency and closed match in Blast result of fungal OTUs associated with bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* in Wei Xi collected at four plant phenology stages. (continued)

Endophyte OTUs	By host-plant				By host-plant				By growing-physiological period				Closest match and accession number in GenBank
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP	
Debaryomyces subglobosus	0	0	0	0	0	0	0	19	0	0	0	0	*Debaryomyces subglobosus* 99, 100% KP132014.1
Tremellales sp.	0	0	0	0	0	0	0	1	0	0	0	0	Tremellales sp. 99% KF414688.1
Shigella sp.	0	0	0	0	0	0	0	2	0	0	0	0	*Shigella* sp. 100% CP014768.1
Fusarium sp. 01	192	9	42	12	192	33	37	0	0	27	1	164	*Fusidium* sp. 99, 100% JQ347008.1
Fusarium sp. 02	0	0	0	0	0	0	2	0	0	0	0	0	*Fusidium* sp. 100% HG936551.1
Fusarium sp. 03	0	0	0	0	0	0	1	0	0	0	0	0	*Fusidium* sp. 99% AJ179466.1
Fusarium sp. 04	0	0	1	0	0	0	0	0	0	0	0	0	*Fusidium* sp. 100% KX169233.1
Fusarium sp. 05	0	0	1	0	0	0	0	0	0	0	0	0	*Fusidium* sp. 100% KX929306.1
Fusarium sp. 06	0	0	13	0	0	0	0	0	0	0	0	0	*Fusidium* sp. 100% LC228656.1
Fusarium sp. 07	0	0	0	0	0	2	0	0	0	0	0	0	*Fusidium* sp. 99% gb|KT268430.1
Fusarium sp. 08	0	0	0	2	0	2	0	0	0	0	0	0	*Fusidium* sp. 98% GQ280338.1
Fusarium sp. 09	3	0	0	0	3	0	0	0	0	0	3	0	*Fusidium* sp. 99% KF367548.1
Fusarium sp. 10	1	0	0	0	1	0	0	0	0	0	1	0	*Fusidium* sp. 99% HQ630965.1
Fusarium sp. 11	0	0	0	0	0	1	0	0	0	0	0	0	*Fusidium* sp. 99% KC753424.1
Fusarium sp. 12	0	1	0	0	0	8	0	0	0	0	0	0	*Fusidium* sp. 99% DQ421018.1
Fusarium sp. 13	0	0	0	0	0	1	0	0	0	0	0	0	*Fusidium* sp. 99% DQ421011.1
Fusarium sp. 14	1	0	0	0	1	0	0	0	1	0	0	0	*Fusidium* sp. 99% HG935225.1
Fusarium sp. 15	14	0	0	20	14	23	5	0	14	0	0	0	*Fusidium* sp. 99, 100% HG936695.1
Fusarium sp. 16	81	19	0	0	81	23	19	0	1	0	0	80	*Fusidium* sp. 99, 100% JQ347006.1
Fusarium sp. 17	0	2	0	0	0	0	0	0	0	0	0	0	*Fusidium* sp. 99% AJ279478.1
Fusarium sp. 18	0	0	0	0	0	0	2	0	0	0	0	0	*Fusidium* sp. 100% KT963803.1
Fusarium sp. 19	0	15	0	1	0	2	0	0	0	0	0	0	*Fusidium* sp. 99% KT268402.1
Fusarium sp. 20	1	0	0	0	1	0	0	0	0	0	1	0	*Fusidium* sp. 02 89% HG936133.1
Fusarium cf. solani	0	0	0	0	0	0	1	0	0	0	0	0	*Fusarium cf. Solani* 99% JX435194.1
Fusarium lateritium	0	0	0	0	0	1	0	0	0	0	0	0	*Fusarium lateritium* 100% FN397346.1
Fusarium solani 01	0	0	1	0	0	0	0	0	0	0	0	0	*Fusarium solani* 100% LC184262.1
Fusarium solani 02	0	0	1	0	0	0	0	0	0	0	0	0	*Fusarium solani* 100% LC184262.1
Fusarium lateritium 01	0	2	0	0	0	1	0	0	0	0	0	0	*Fusarium lateritium* 99% AF310980.1
Fusarium lateritium 02	0	0	0	0	0	1	0	0	0	0	0	0	*Fusarium lateritium* 100% FN397346.1
Fusarium acuminatum 01	0	13	0	0	0	0	2	0	0	0	0	0	*Fusarium acuminatum* 99% KJ082098.1
Fusarium acuminatum 02	0	8	0	0	0	8	0	0	0	0	0	0	*Fusarium acuminatum* 99% GU566260.1
Fusarium acuminatum 03	0	1	0	0	0	0	0	0	0	0	0	0	*Fusarium acuminatum* 99% gb|KJ019024.1
Fusarium oxysporum	1	0	0	0	1	0	0	0	1	0	1	0	*Fusarium oxysporum* 100% FJ867936.1
Fusarium proliferatum	2	0	0	0	2	0	0	0	0	0	2	0	*Fusarium proliferatum* 99% FN868470.1
Fusarium delphinoides	0	0	1	0	0	0	0	0	0	0	0	0	*Fusarium delphinoides* 100% LC184205.1
Fusarium penzigii	0	0	1	0	0	0	0	0	0	0	0	0	*Fusarium penzigii* 95% NR_137707.1
Leptosphaeriaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Leptosphaeriaceae sp. 100% GU288818.1
Thelonectria veuillotiana	0	0	1	0	0	0	0	0	0	0	0	0	*Thelonectria veuillotiana* 100% EU715669.1
Nectriaceae sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	Nectriaceae sp. 100% KU987906.1
Nectriaceae sp. 02	0	0	1	0	0	0	0	0	0	0	0	0	Nectriaceae sp.100% KT768327.1
Nectriaceae sp. 03	0	0	1	0	0	0	0	0	0	0	0	0	Nectriaceae sp. 100% KX790415.1
Nectriaceae sp. 04	0	0	1	0	0	0	0	0	0	0	0	0	Nectriaceae sp. 100% KR350652.1
Penicillium simplicissimum 01	0	0	1	0	0	0	0	0	0	0	0	0	*Penicillium simplicissimum* 99% KY086229.1
Penicillium simplicissimum 02	0	0	4	0	0	0	0	0	0	0	0	0	*Penicillium simplicissimum* 100% KX148629.1
Penicillium ochrochloron	0	0	7	0	0	0	0	0	0	0	0	0	*Penicillium ochrochloron* 100% HQ850354.1
Neonectria lugdunensis	6	0	0	0	6	0	0	0	6	0	0	0	*Neonectria lugdunensis* 99% KM231762.1
Neonectria westlandica	1	0	0	0	1	0	0	0	1	0	0	0	*Neonectria westlandica* 95% HM484559.1
Neonectria candida	0	0	1	0	0	0	0	0	0	0	0	0	*Neonectria candida* 100% KU516532.1
Gibberella intricans	0	0	1	0	0	0	0	0	0	0	0	0	*Gibberella intricans* 100% KX576658.1
Gibberella sp. 01	0	0	67	0	0	0	0	0	0	0	0	0	*Gibberella* sp.100% KY430581.1
Gibberella sp. 02	0	0	0	0	0	1	0	0	0	0	0	0	*Gibberella* sp. 99% HQ630977.1

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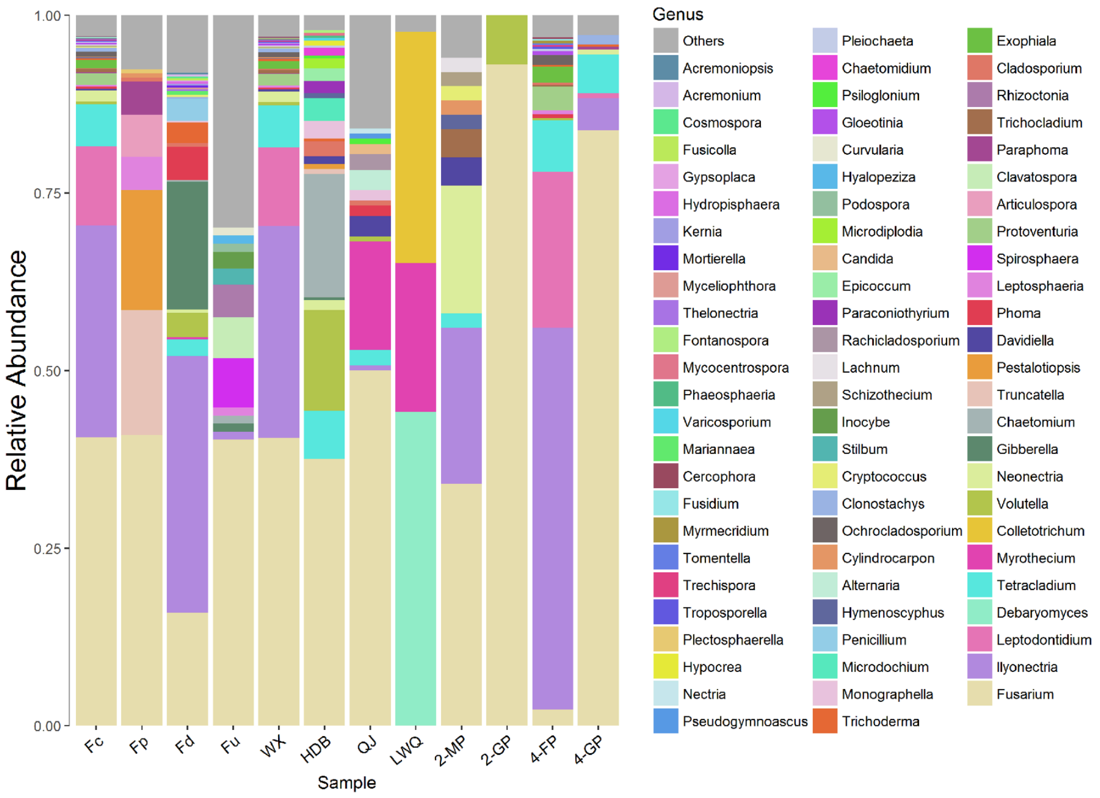
Endophyte OTUs	By host-plant				By host-plant				By growing-physiological period				Closest match and accession number in GenBank
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP	
Trichoderma crassum	0	0	1	0	0	0	0	0	0	0	0	0	*Trichoderma crassum* 100% KP009300.1
Trichoderma longibrachiatum	0	0	1	0	0	0	0	0	0	0	0	0	*Trichoderma longibrachiatum* 99% KP216911.1
Trichoderma sp.	0	0	9	0	0	0	0	0	0	0	0	0	*Trichoderma* sp. 100% KU942400.1
Trichoderma koningiopsis	1	0	0	0	1	0	0	0	0	0	0	1	*Trichoderma koningiopsis* 92% EU718083.1
Trichoderma parapiluliferum	0	0	0	0	0	1	0	0	0	0	0	0	*Trichoderma parapiluliferum* 99% NR_134341.1
Trichoderma gamsii	1	0	0	0	1	0	0	0	0	0	1	0	*Trichoderma gamsii* 99% HM176559.1
Mortierellaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Mortierellaceae sp. 100% KT809098.1
Dothideomycetes sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	Dothideomycetes sp. 90% KT203918.1
Dothideomycetes sp. 02	0	0	1	0	0	0	0	0	0	0	0	0	Dothideomycetes sp. 100% KU204531.1
Clavicipitaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Clavicipitaceae sp. 100% KU141169.1
Microascaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Microascaceae sp. 100% KU702677.1
Volutella gilva	0	0	13	0	0	0	0	0	0	0	0	0	*Volutella gilva* 100% KM231769.1
Hypocreales sp.01	0	0	1	0	0	0	0	0	0	0	0	0	Hypocreales sp.100% HQ631053.1
Hypocreales sp.02	0	0	1	0	0	0	0	0	0	0	0	0	Hypocreales sp.100% KX148716.1
Hypocreales sp.03	0	0	1	0	0	0	0	0	0	0	0	0	Hypocreales sp. 99% KJ807177.1
Cryptococcus aerius	0	0	1	0	0	0	0	0	0	0	0	0	*Cryptococcus aerius* 100% KY105435.1
Cryptococcus sp.	1	0	0	0	1	0	0	0	1	0	0	0	*Cryptococcus* sp. 99% HE977522.1
Davidiella macrospora	2	0	0	0	2	0	0	0	2	0	0	0	*Davidiella macrospora* 100% EU167591.1
Paraphoma sp.	0	1	0	0	0	0	0	0	0	0	0	0	*Paraphoma* sp. 99% KT268373.1
Ascomycota sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 86% HM239833.1
Ascomycota sp. 02	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 100% KX592800.1
Ascomycota sp. 03	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 100% KY412161.1
Ascomycota sp. 04	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 100% KU342071.1
Ascomycota sp. 05	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 99% GU911223.1
Ascomycota sp. 06	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp. 100% KU516597.1
Ascomycota sp. 07	0	0	1	0	0	0	0	0	0	0	0	0	Ascomycota sp.100% KU516526.1
Ascomycota sp. 08	2	0	0	0	2	0	0	0	0	0	2	0	Ascomycota sp. 95% AY969503.1
Ascomycota sp. 09	1	0	0	0	1	0	0	0	1	0	0	0	Ascomycota sp. 94% EU490133.1
Ascomycota sp. 10	0	1	0	0	1	0	0	0	1	0	0	0	Ascomycota sp. 92% KJ735039.1
Ascomycota sp. 11	0	0	0	0	0	7	1	0	0	0	0	0	Ascomycota sp. 99% FJ378864.1
Leotiomycetes sp.	0	0	1	0	0	0	0	0	0	0	0	0	Leotiomycetes sp. 100% JF439476.1
Hydropisphaera erubescens	0	0	1	0	0	0	0	0	0	0	0	0	*Hydropisphaera erubescens* 99% KP269058.1
Volutella ciliata	3	0	0	0	3	40	1	0	0	2	1	0	*Volutella ciliata* 99% AJ301966.1
Acremonium hyalinulum	0	0	1	0	0	0	0	0	0	0	0	0	*Acremonium hyalinulum* 99% NR_131321.1
Gypsoplaca macrophylla	0	0	1	0	0	0	0	0	0	0	0	0	*Gypsoplaca macrophylla* 96% KF650781.1
Microdochium sp.	0	0	0	0	0	9	0	0	0	0	0	0	*Microdochium* sp. 99, 100% AJ279481.1
Chaetomiaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Chaetomiaceae sp. 100% KT768342.1
Myceliophthora similis	0	0	1	0	0	0	0	0	0	0	0	0	*Myceliophthora similis* 99% FJ537093.1
Acremoniopsis suttonii	0	0	1	0	0	0	0	0	0	0	0	0	*Acremoniopsis suttonii* 99% NR_145059.1
Trichosporonales sp.	0	0	0	23	0	1	0	0	0	0	0	0	Trichosporonales sp. 99% EF060462.1
Sordariomycetes sp. 01	0	0	1	0	0	0	0	0	0	0	0	0	Sordariomycetes sp. 100% KX359601.1
Sordariomycetes sp. 02	0	0	1	0	0	0	0	0	0	0	0	0	Sordariomycetes sp. 95% JFJ969800.1
Cystofilobasidiaceae sp.	0	0	1	0	0	0	0	0	0	0	0	0	Cystofilobasidiaceae sp. 100% HG935388.1
Trichocladium sp.	2	0	0	0	2	0	0	0	2	0	0	0	*Trichocladium* sp. 99% JF519272.1
Kernia pachypleura	0	0	1	0	0	0	0	0	0	0	0	0	*Kernia pachypleura* 99% DQ318208.1
Cosmospora consors	0	0	1	0	0	0	0	0	0	0	0	0	*Cosmospora consors* 99% LC224316.1
Mortierella alpina	0	0	1	0	0	0	0	0	0	0	0	0	*Mortierella alpina* 100% HG936566.1

Fc: *F*. cirrhosae; Fp: *F. przewalskii*; Fd: *F. delavayi*; Fu: *F. unibracteata*; WX: Weixi; HDB: Huadianba; QJ: Qiaojia; LWQ: Leiwuqi; 2-MP: 2 yr old in mature period; 2-GP: 2 yr old in germination period; 4-FP: 4 yr old in flowering period; 4-GP: 4 yr old in germination period.

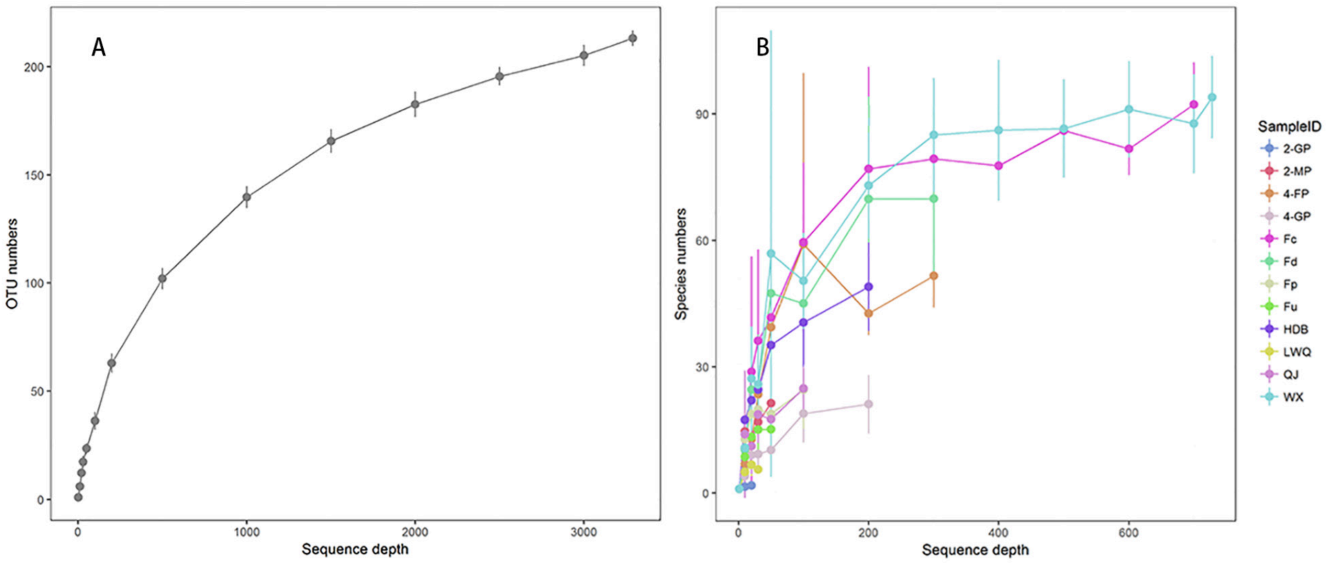
Supplementary Table S4. Diversity measures of bulb associated fungal assemblages by host-plant species, geographic area and plant phenology stage.

Index	Host-plant species				Geographic area				Plant phenology stage			
	Fc	Fp	Fd	Fu	WX	HDB	QJ	LWQ	2-MP	2-GP	4-FP	4-GP
Chao 1	124.140	104.978	126.667	56.694	132.880	103.815	65.611	45.533	56.549	41	103.5	77.810
ACE	130.463	64.659	118.313	59.813	138.761	95.122	66.801	47.305	58.259	43.417	98.917	66.945
Shannon	3.340	3.670	3.417	3.564	3.391	3.838	3.619	3.408	3.561	3.268	3.306	2.936
Simpson	0.906	0.965	0.918	0.965	0.910	0.969	0.962	0.960	0.966	0.951	0.885	0.863

Fc: *F. cirrhosae*; Fp: *F. przewalskii*; Fd: *F. delavayi*; Fu: *F. unibracteata*; WX: Weixi; HDB: Huadianba; QJ: Qiaojia; LWQ: Leiwuqi; 2-MP: 2 yr old in mature period; 2-GP: 2 yr old in germination period; 4-FP: 4 yr old in flowering period; 4-GP: 4 yr old in germination period.



Supplementary Fig. S1. Relative abundance which is a relative percentage of fungal individual in each fungal lineage for fungal lineages detected in bulbs of four species of Fritillaria Cirrhosae Bulbus source plants, *F. cirrhosae* collected in four geographic areas and *F. cirrhosae* collected at four plant phenology stages. Fc, *F. cirrhosae*; Fp, *F. przewalskii*; Fd, *F. delavayi*; Fu, *F. unibracteata*; WX, Weixi; HDB, Huadianba; QJ, Qiaojia; LWQ, Leiwuqi; 2-MP, 2 yr old in mature period; 2-GP, 2 yr old in germination period; 4-FP, 4 yr old in flowering period; 4-GP, 4 yr old in germination period.



Supplementary Fig. S2. Rarefaction Curve between the number of fungal individuals and the number of fungal OTUs for the total bulb associated fungi from all the samples of four species of Fritillaria Cirrhosae Bulbus source plants collected from different geographic areas and different plant phenology stages (A) and samples of four species, four geographic areas and four plant phenology stages respectively (B). Fc, *F. cirrhosae*; Fp, *F. przewalskii*; Fd, *F. delavayi*; Fu, *F. unibracteata*; WX, Weixi; HDB, Huadianba; QJ, Qiaojia; LWQ, Leiwuqi; 2-MP, 2 yr old in mature period; 2-GP, 2 yr old in germination period; 4-FP, 4 yr old in flowering period; 4-GP, 4 yr old in germination period.