Diversity and characterization of culturable fungi associated with *Gnetum gnemon* Linn. in organic and conventional farming systems and their potential antagonism against pathogenic fungi

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ABSTRACT: This study compared the diversity and abundance of culturable fungi associated with Gnetum gnemon Linn. grown in separate organic and conventional fields. A total of 236 fungi were isolated from leaves and soil, of which 124 were from organic fields and 112 were from conventional fields. The colonization rates of endophytic fungi ranged from 80% to 93%, and the mean fungal loads of soil fungi ranged from 4.45×10^3 to 5.65×10^3 CFU/g soil. Based on morphological characteristics and ITS sequence analysis, the isolates were identified to 13 orders and 24 genera. The most abundant endophytes were Colletotrichum, Guignardia, Daldinia, and Pestalotiopsis; and the most abundant soil fungi were Aspergillus, Penicillium, and Trichoderma. The fungal communities of G. gnemon were diverse and abundant, as indicated by the species richness and diversity indices. Among them, 23 taxa (55%) were common to both organic and conventional fields; however, the dominant endophytic and soil fungi were dissimilar. In antagonistic assays against the plant pathogenic fungi, Colletotrichum siamense, Colletotrichum gloeosporioides and Pestalotiopsis mangiferae, fungal isolates revealed inhibition percentages of 61% to 100%. Trichoderma hamatum C212, Gliocladium sp. C324, and Daldinia eschscholtzii LM12 showed the strongest antagonistic activities. Aspergillus, Colletotrichum, Daldinia, Talaromyces, and Xylaria showed antimicrobial activities against Micrococcus luteus, Staphylococcus aureus, methicillin-resistant S. aureus (MRSA), Vibrio cholerae, and Candida albicans, with inhibition zones ranging from 12 to 22 mm. We demonstrated for the first time that endophytic and soil fungi associated with G. gnemon have potential as antagonists and antimicrobial agents for biotechnological applications.

KEYWORDS: Gnetum gnemon Linn., fungal diversity, antagonism, antimicrobial activity

INTRODUCTION

Plant-associated fungi are widely distributed in nature. Soil fungi, including root-associated and free-living fungi, make up 10%-30% of the soil rhizosphere, and they are key operators of soil nutrient cycles, acting as main decomposing agents of plant biomass. Most members of soil and root fungal communities are involved in processes that influence plant growth via the saprotrophic decomposition of soil organic residues and the subsequent release of nitrogen, phosphorus, and micronutrients [1, 2]. Similarly, endophytic fungi can be beneficial to their host plants through mutualistic symbiosis; but during certain phases of the growth cycles of hosts, and/or under certain environmental conditions, they can become latent pathogens or saprophytes. Many endophytic fungi can stimulate the production of various compounds and enhance their availability, helping plants to uptake and utilize soil nutrients that have been linked to the promotion of plant growth and development [3]. Endophytic fungi are also capable of improving the resistance of plants to pathogen and insect attacks and their defenses against abiotic stresses [4].

Fungal populations are strongly influenced by the diversity of the topical plant community and soil com-

position. The fungi in return affects plant growth and soil quality [5]. The interactions between plants and associated fungi can also significantly affect the integrity and sustainability of entire agro-ecosystems [6]. Biodiversity in agricultural landscapes, which usually restrict the application of synthetic chemicals and genetically modified products, is greater and species richness was 30% (on average) higher in organic farming systems than in conventional farming systems [7]. Therefore, organic farming could also enhance fungal diversity. On the other hand, the application of fungicides in conventional farming can reduce fungal abundance and diversity. This may have deleterious effects on plant and soil health, and eventually the sustainability of crop production.

Gnetum gnemon Linn. is a medicinal plant indigenous to Southeast Asia and western Pacific Ocean islands. It has been used in folk medicines for treatments of arthritis, bronchitis and asthma [8]. The fruits and leaves of *G. gnemon* are widely consumed and are a relatively rich source of nutrition. Due to its diverse patterns of bioactive compounds, such as flavonoids, saponins and tannins, *G. gnemon* has a broad range of therapeutic uses [9]. Stilbenoids from the species showed moderate antimicrobial activity and lipase and α -amylase activities [10]. *G. gnemon* var. tenerum Markgr. is the main *Gnetum* variety distributed across southern Thailand. This small evergreen shrub (3 m in height) usually grows in shady areas and is resistant to pests and diseases [11]. In Thailand, this plant has been introduced as a co-plant, intercropped with economic perennials, e.g., rubber (*Hevea brasiliensis*) and durian (*Durio zibethinus* L.), to relieve financial difficulties among monocrop farmers during price crises. However, most plantations in Thailand are still operated conventionally and rely on using chemicals to protect crops from pests and microbial diseases [12].

Extensive use of pesticides and fungicides results in widespread environmental contamination of water, edible plants, and the human food chain. As mentioned, the use of chemicals in conventional farming can reduce fungal abundance and diversity, which subsequently affects plant growth and soil quality. As the leaves of the tenerum variety are consumed as a fresh or cooked vegetable in Thailand [12], contamination with agrochemical residues is a real concern. In addition, the overuse or misuse of fungicides can have toxic effects on beneficial organisms, human health, and the environment, and lead to the development of fungicide resistance. For this reason, alternative approaches to crop protection have revealed promising substitutes for chemical fungicides. For example, biocontrol agents are used to increase the diversity of associated microbial communities. Thus, the two interlinked objectives of this study were to investigate the diversity and abundance of culturable fungi associated with G. gnemon grown organically and conventionally, and to characterize biological activities of the fungal isolates as an inhibitor of microbial pathogens. In vitro activities of fungal isolates against the plant pathogenic fungi were examined via dual cultures, and activities against pathogenic microbes were examined via agarwell diffusion assays. The objectives of this study were to prove our hypothesis that the diversity and abundance of foliar endophytic and soil fungi was greater in the organic farm than in the conventional farm, and to observe the inhibitory potentials against microbial pathogens of selected fungal isolates.

MATERIALS AND METHODS

Sample collection and physicochemical analysis of soil

Representative communities of *G. gnemon* Linn. were sampled from conventional and organic farming systems in Phato District, Chumphon Province, Southern Thailand that have been in operation for more than 10 years. The conventional and organic farming sites were located approximately 500 m away from each other, representing the same climate and geographic conditions in each sampling site. Differences in plants and soil morphology were not observed. Plants were sampled separately during the rainy season in October 2021. Fifteen healthy and mature leaves of five

G. gnemon plants growing on each site were randomly collected, making a total of 30 leaf specimens. Leaves were kept in sterile plastic bags and stored at 4 °C. Soil samples were collected from both sites at a depth of 5 to 15 cm. At each site, a 1×1 -m plot was defined from which the samples were collected. All soil samples from each site were pooled in sterile collection bags and processed in the laboratory within 48 h. During sampling, temperature and soil pH were measured using a portable instrument. The *G. gnemon* plants were intercropped with durian (*D. zibethinus* L.) trees. Physicochemical analysis of soil was performed as described by Wingfield et al [13].

Isolation of soil fungi and endophytic fungi

Soil fungi were isolated using the protocol described by Wingfield et al [13] with minor modification. Briefly, a ten-fold serial dilution of soil suspensions was spreadplated onto potato dextrose agar (PDA) supplemented with 100 μ g/ml chloramphenicol. The plates were incubated at 28 °C for 7-21 days. Surface sterilization was carried out to isolate endophytic fungi using a previously described method [14] with minor modification. Briefly, 1.0 cm × 1.0 cm pieces of different parts of leaves (petiole, midrib, vein, and lamina) were immersed in 95% ethanol for 30 s, 5% sodium hypochlorite solution for 5 min, 95% ethanol for 30 s, and sterile distilled water for 3-5 s. The sterilized fragments were placed onto a corn meal agar (CMA) plate containing chloramphenicol (50 µg/ml) and incubated for 7–21 days at 28 °C until the hyphae emerged.

Morphological and molecular identification of fungi

Fungal isolates were initially identified to the genus and species levels based on their macroscopic morphological characteristics. The microscopic appearance of individual fungi was observed using the slide culture technique and the observed mycelial and reproductive structures were used to further identify the fungi. The identification keys described by Wingfield et al [13] were used. Molecular identification of the fungal isolates was performed based on the analysis of DNA sequence of the ITS1-5.8S-ITS2. Genomic DNA was extracted according to a protocol described by Wingfield and Atcharawiriyakul [15]. PCR amplification of fungal ITS regions was carried out using the protocol described by Wingfield et al [13].

Phylogenetic analysis

The closest matched sequences were searched in the National Centre for Biotechnology Information (NCBI) GenBank database using a BLAST search. To confirm the identity of the isolates, phylogenetic and molecular evolutionary analyses were conducted using MEGA version 11 [16]. Multiple sequence alignments were performed using alignments prepared with MUSCLE,

and sequences were manually edited when necessary. The phylogenetic trees were inferred using the maximum-likelihood algorithm. The stability of relationships was evaluated by bootstrap analysis with 1,000 replications. A soil fungus, *Mortierella longigemmata*, was included as an out-group. Sequences were deposited in the GenBank database (OR986518– OR986555).

Diversity and data analysis

The diversity of the fungal isolates was determined by evaluating species richness based on the Menhinick Index (Dmn) [17]. Species diversity was measured by the Shannon (H') Index [18]. The Shannon index was calculated according to the following formula: H' = $\sum_{i=1}^{k} (P_i \times \ln P_i)$, where k is the total number of species at a site, and P_i is the relative abundance of fungal species at a site. The isolation rate (IR) was used to indicate the fungal richness in each sample. It was calculated as the number of fungal isolates obtained from leaf segments divided by the total number of segments tested. The degree of infection by endophytic fungi was evaluated for different leaf tissues by comparing colonization rates (CR), which were calculated as the total number of leaf segments infected by fungi divided by the total number of segments tested. The representation of fungal genera was expressed as relative frequency (RF) calculated as the frequency of a specific genus divided by the total number of fungal isolates. The statistical analysis was conducted using Graph Pad Prism, version 6.0 7.0 (GraphPad Software, La Jolla, CA).

In vitro antagonism assay

Fungal morphotypes were screened for their antagonistic property using in vitro dual culture assays. The fungi grew for the first 5 days on a ¹/₄PDA agar and demonstrated the highest growth radii were selected for antagonism assays with the reference plant pathogenic fungi Colletotrichum siamense LV515 (isolated from infected chili, Capsicum annuum L. var. acuminatum Fingerh), Pestalotiopsis mangiferae LM24 (isolated from infected mango leaves, Mangifera indica Linn.), and C. gloeosporioides (isolated from infected durian leaves, D. zibethinus L.). Seven-day-old cultures were used for all antagonism assays. In each assay, a mycelium disc (6 mm in diameter) of a fungal antagonist and a fungal plant pathogen were placed equidistantly (1 cm from the edge) on a PDA plate (9 cm in diameter). Plates inoculated with a fungal pathogen but not with an antagonist were used as negative controls. The assays were performed in triplicate. Observations were carried out at 28 °C for 7 days to determine the antagonistic capability of each fungus. The mycelial radial growth of the test pathogen was measured on a control plate (R) and in the direction of the antagonistic fungus (r), and the percent inhibition (%I) in mycelial growth was calculated according to the formula % I = $[(R-r)/R] \times 100$. Interactions between fungal antagonists and fungal pathogens were classified according to the following five types of interaction. (1) The two opposing fungi demonstrate similar growth and overlap. (2) The antagonistic fungus outgrows the pathogenic fungus. (3) The pathogenic fungus outgrows the antagonistic fungus. (4) Mutual inhibition of both colonies at a short distance (< 2 mm). (5) Mutual inhibition of both colonies at a longer distance (> 2 mm) (adapted from López et al [19]).

Antimicrobial assays

In vitro antimicrobial activity was tested using the protocol described by Wingfield et al [13] with minor modification. Briefly, fungal isolates were cultivated in a potato dextrose broth (PDB) for 21 days at 28 °C. The culture broths were used for testing antimicrobial activity by agar well diffusion against seven pathogenic bacteria (Micrococcus luteus (ATCC9341), Staphylococcus aureus (ATCC25923), methicillin-resistant S. aureus (MRSA), Escherichia coli (ATCC25922), Pseudomonas aeruginosa (ATCC27853), Salmonella typhi, and Vibrio cholerae) and two pathogenic fungi (Candida albicans (ATCC90028) and Aspergillus fumigatus Af293). Inhibition zones were measured as the mean diameter of the 8 mm wells plus the clearing zone. Assays were performed in triplicates. Vancomycin and gentamicin were used as standard antibacterial agents, and amphotericin B and miconazole were used as standard antifungal agents.

RESULTS

Plant and soil properties

Representative communities of G. gnemon Linn. were sampled from two locations, one a field on a conventional farm, and the other on an organic farm. The genus Gnetum presented in both fields belonged to the variety tenerum (G. gnemon var. tenerum Markgr.). This variety is a green shrub of approximately 3-4 m in height. The leaves were oblong-lanceolate, chartaceous, dark green with an entire margin and netted veins, and typically 10-20 cm long and 4-8 cm wide. The Gnetum shrubs were planted alongside durian (D. zibethinus L.) trees at both locations, and they served as a ground cover crop. At the conventional farm, a herbicide (Glyphosate isopropylammonium, 48% W/V SL) was sprayed four times a month for weed control, and a pesticide (Abamectin, 1.8% W/V EC) once a month for pest control. Details of geographic locations, sampling sites, plant and soil characteristics were shown in Fig. 1. The results of the physicochemical characteristics of soil samples are presented in Table S1. All analyzed parameters of the organic farming soil were much higher than those of the conventional farming soil, except soil pH. Soil samples from



Fig. 1 Plant properties and sampling sites. (A) Geographic location of the sampling sites in Phato District, Chumphon Province, Southern Thailand, and their geographical coordinates were N $10^{\circ} 27' 32.4''$, E $99^{\circ} 24' 10.8''$ (USGS National Map Viewer (http://viewer.nationalmap.gov/viewer)). (B) Characteristics of the sampling sites, Thailand. (C) Characteristics of each stage of *G. gnemon* var. *tenerum* Markgr. leaves.

both sites were mildly alkaline. The organic farming soil was naturally rich in organic matter, minerals and water. On the other hand, the conventional farming soil showed a deficiency in soil components, having total nitrogen, total organic carbon, and organic matter levels lower than the optimal levels reported in the literature [20].

Isolation and colonization of soil fungi and endophytic fungi

From 60 leaf segments (petiole, midrib, vein and lamina) of plants growing in the conventional farming system, a total of 79 endophytic fungi were isolated. From 60 leaf segments of plants growing in the organic farming system, a total of 91 endophytic fungi were isolated (Tables S2 and S3). The overall IR of endophytic fungi was higher in the organic farming system (1.52) than the conventional farming system (1.32; Table 1). This result demonstrated that most of the leaf segments tested contained more than one fungal isolate, indicating a high fungal richness in the G. gnemon leaves. In the organic system, the greatest number of fungal endophytes was isolated from vein (IR, 1.87) and the lowest from petiole (IR, 1.27). In the conventional system, the greatest number of fungal endophytes was isolated from lamina (IR, 1.53) but

the lowest from petiole (IR, 0.93). The total %CR was 91.67 for both sites, but the CRs of different plant tissues were different. The CRs of vein and midrib from the conventional farm (93.33% and 100%, respectively) were significantly higher than those of the vein and midrib from the organic farm (86.67% and 93.33%, respectively). In contrast, the CR of petiole from the conventional farm (80.00%) was significantly lower than the CR of petiole from the organic farm (93.33%). However, the CR of laminas was the same at both sites (93.33%). This result demonstrated a high prevalence of endophytic fungal infection in different tissues of the leaves in both systems. The number of soil fungi isolated from both the conventional and the organic farm soils was the same (33 isolates), giving a total of 66 fungi (Table S2). Mean fungal loads were higher in the soilsoil from the organic farm (Table 1).

Identification of fungi associated with *G. gnemon* Linn.

Based on morphological identification, 236 fungal isolates associated with *G. gnemon* Linn. from the organic and the conventional fields were assigned to 45 representative morphotypes (Fig. 2A). The molecular identification identified 39 fungal species of 24 genera (Table S4 and Fig. 2B) including unidentified



Fig. 2 Morphological and molecular identification of culturable fungi associated with the *G. gnemon* Linn. (A) Representative fungal morphotypes of the isolated fungi. Morphotyping was based on macroscopic and microscopic observations (magnification \times 40). All isolates were grown on PDA plates for 7–14 days at 28 °C. (B) The phylogenetic analysis of isolated fungi produced the above tree generated by the Maximum Likelihood method. The circular phylogenetic tree classifies the isolates at the class, order and genus levels. The inner circle presents orders indicated by different colors, and the outer circle presents classes. Percentages of bootstrap sampling derived from 1000 replications are indicated by the numbers on the tree.

Parameter	Leaf sample											
	Lai	mina	V	/ein	M	idrib	Per	tiole	To	otal		
	IR	%CR	IR	% CR	CFU/g soil							
Conventional farming	1.53	93.33	1.4	93.33	1.4	100	0.93	80.00	1.32	91.67	5.65×10^{3}	
Organic farming	1.60	93.33	1.87	86.67	1.33	93.33	1.27	93.33	1.52	91.67	4.45×10^{3}	

Table 1 Isolation rate (IR) and percentage colonization rate (% CR) of endophytic fungi and mean fungal loads of soil fungi associated with *G. gnemon* Linn.

fungi. The identified isolates belonged to three phyla, seven classes, and thirteen orders. The 24 fungal genera were Apiotrichum, Aspergillus, Auricularia, Cercophora, Colletotrichum, Cutaneotrichosporon, Daldinia, Diaporthe, Gliocladium, Guignardia, Hypocreales, Kalmusia, Leptosphaeria, Meyerozyma, Mucor, Penicillium, Pestalotiopsis, Pseudopestalotiopsis, Purpureocillium, Pyrenochaetopsis, Sporothrix, Talaromyces, Trichoderma, and Xylaria. However, three isolates (C311, CL37 and LL13B representing Purpureocillium, Xylaria and Guignardia, respectively) were potential new taxa because of the low similarities of their ITS sequences. The rDNA ITS sequences of the fungi subjected to molecular identification in this study were deposited in the Genbank (OR986518-OR986555).

Distribution and diversity of fungi associated with *G. gnemon* Linn.

The abundance and the species diversity of fungi in the organic farming were higher than those in the conventional. Of 40 taxa, 32 taxa were obtained from the organic farming system (including 17 from leaves and 14 from soils), whereas 30 taxa were obtained from the conventional farming system (including 13 from leaves and 16 from soils; Table S5). The dominant endophytic fungal genera obtained from the conventional farm were Colletotrichum sp., Daldinia sp. and Guignardia sp., with % RFs of 37.97%, 18.99% and 16.46%, respectively. Similarly, the three endophytic genera were dominant on the organic farm, and their % RFs were 36.27%, 18.68% and 15.38%, respectively (Fig. 3A). The dominant soil fungi from the conventional farm were Aspergillus sp., Penicillium sp. and Trichoderma sp., with % RFs of 36.36%, 21.21% and 15.15% respectively; while the dominant soil fungi from the organic farm were Penicillium sp., Trichoderma sp., Aspergillus sp. and Gliocladium sp., with % RFs of 30.30%, 15.15%, 12.12% and 12.12% respectively.

Among the total fungi associated with *G. gnemon* Linn., the phylum Ascomycota was found to be the most abundant (95.65%) across all the samples analyzed, and the phyla Basidiomycota and Mucoromycota were found to be rare and incidental. Among the endophytic fungi, Xylariales was the most abundant order (RF, 36.48%), followed by Glomerellales (RF, 34.70%) and Diaporthales (RF, 8.82%) (Fig. 3B). Among the soil fungi, Eurotiales was the most abundant order (RF, 54.57%), followed by Hypocreales (RF, 31.83%). Sordariomycetes was the most dominant class among leaf samples, and Eurotiomycetes the most dominant class among soil samples (Fig. 3C). Regardless of the samples analyzed, the numbers of fungal community were equally good on both farms, but fungal isolates from the organic farm were more morphologically diverse. In the analysis of fungal diversity and species richness, the Dmn index of fungi from the organic farming system was slightly higher (2.76) than the index from the conventional farming system (2.74) (Table S5). Shannon's index of species diversity (H') also showed a similar trend; a slightly higher index from the organic farm (2.49) than the conventional farm (2.47).

The endophytic fungal community among leaves from the two sites was clustered together, as was the fungal community among soil samples from the two sites. Among the isolated fungi, regardless of the samples analyzed, 23 taxa (55%) co-existed in G. gnemon Linn. from both farming systems (Fig. S1). However, some endophytic fungi were location-specific. For instance, Auricularia sp. and Cutaneotrichosporon sp. of the phylum Basidiomycota, Colletotrichum siamense and some species of the genus Xylaria (X. allantoidea and X. feejeensis) were only found on the organic farm, while Cercophora sp. was found only on the conventional farm. High specificity was found among soil fungi between the two sites. Mucor sp., Leptosphaeria sp., Pyrenochaetopsis sp. and Hypocreales sp. were specifically found on the organic farm, while Kalmusia sp., Sporothrix sp., some species of the genus Aspergillus (Aspergillus aculeatus and A. sydowii), Penicillium janthinellum and Talaromyces pinophilus were specifically found on the conventional farm.

Antagonism tests against plant pathogenic fungi

Before the antagonism test began, 45 fungal morphotypes were subjected to stressful growth in low nutrient conditions in a 1/3PDA medium. Only fungi that showed to be fast-growing after 5 days (26 isolates) were selected to trial against the plant pathogenic fungi, *C. siamense* IV515, *Pestalotiopsis mangiferae* LM24 and *C. gloeosporioides*. The *Colletotrichum* sp. strain was isolated from infected chili, *Capsicum annuum* L. var. *acuminatum*, presenting anthracnose



Fig. 3 Percentage relative frequency (% RF) of fungi associated with *G. gnemon* Linn. at the genus (A), order (B) and class (C) levels.

Tahl	е2	In vitro	antagonism	data of	selected	funoi	i against i	nlant i	nathoo	r enic f	fiinoi	insing	z a du	al cui	lture	assav
Iavi	C 2	III VIII O	antagoman	uata or	sciected	iungi	agamst	plant	patho	scine i	ungi	using	ς a uu	n cu	nuic	assay.

Isolate name	Plant pathogenic fungi									
	Colletotr	ichum siamense	Pestalotio	opsis mangiferae	Colletotrich	um gloeosporioides				
	Type of interaction	% inhibition growth (%I) \pm SD	Type of interaction	% inhibition growth (%I) \pm SD	Type of interaction	% inhibition growth (%I) \pm SD				
Endophytic fungi										
Auricularia polytricha LP11	4	17.32 ± 1.03	4	23.96 ± 6.52	ND	ND				
Cercophora coprophila CV11	4	18.99 ± 4.97	4	11.87 ± 5.80	2	54.21 ± 3.67				
Colletotrichum sp. LL411	4	21.67 ± 6.40	4	8.99 ± 17.92	ND	ND				
Colletotrichum fructicola CV24	4	14.52 ± 7.07	3	12.67 ± 9.45	ND	ND				
Colletotrichum gloeosporioides CL514	4	17.20 ± 9.34	4	11.64 ± 13.20	4	19.74 ± 10.01				
Colletotrichum gloeosporioides CM19	4	12.98 ± 6.90	4	8.06 ± 10.43	ND	ND				
Colletotrichum siamense LV411	4	17.32 ± 13.55	4	17.05 ± 13.03	4	26.73 ± 1.34				
Daldinia sp. CV515	4	15.48 ± 14.65	2	30.76 ± 1.14	ND	ND				
Daldinia eschscholtzii CM24	4	15.60 ± 4.88	4	17.40 ± 15.80	4	22.05 ± 5.63				
Daldinia eschscholtzii LM12	2	30.65 ± 8.00	2	26.96 ± 5.54	4	26.81 ± 1.75				
Colletotrichum sp. LM513	4	23.57 ± 6.40	5	21.66 ± 13.03	ND	ND				
Diaporthe hongkongensis CP39	2	28.04 ± 12.21	2	33.99 ± 2.44	4	5.63 ± 1.32				
Pestalotiopsis mangiferae LM11	4	22.14 ± 12.46	4	20.97 ± 15.32	4	23.23 ± 6.07				
Xylaria sp. CL37	4	27.20 ± 11.40	5	49.31 ± 3.26	ND	ND				
Soil fungi										
Gliocladium sp. C324	2	100 ± 00	2	64.06 ± 4.56	2	62.12 ± 5.05				
Purpureocillium sp. C311	5	61.07 ± 5.05	5	14.14 ± 1.01	5	18.10 ± 8.89				
Talaromyces pinophilus C323	3	16.01 ± 2.78	3	8.76 ± 1.63	ND	ND				
Talaromyces aculeatus L318	3	13.81 ± 7.41	5	4.38 ± 8.15	ND	ND				
Trichoderma sp. L322	2	58.69 ± 8.42	2	32.30 ± 5.21	ND	ND				
Trichoderma hamatum C212	2	100 ± 00	2	65.44 ± 6.52	ND	ND				

ND refers to not detected.

diseases. The *Pestalotiopsis* sp. strain was isolated from infected mango leaves, *Mangifera indica* Linn., presenting leaf spot disease. The *C. gloeosporioides* was isolated from infected durian leaves, *D. zibethi*- *nus* L., presenting anthracnose disease. When the dual culture tests were completed (after 7 days), some fungi presented a similar mycelial growth and mutual inhibition of a Type 4 interaction. These

fungi were Auricularia polytricha LP11, Cercophora coprophila CV11, Colletotrichum sp. LL411, C. fructicola CV24, C. gloeosporioides CL514 and CM19, and Daldinia eschscholtzii CM24 (Table 2 and Fig. S2). Some tested fungi exhibited a Type 5 interaction, where the opposing fungi demonstrated similar growth but maintained a distance of > 2 mm. These fungi were Colletotrichum sp. LM513, Xylaria sp. CL37, Purpureocillium sp. C311 and Talaromyces aculeatus L318. Fungi exhibiting a Type 2 interaction were D. eschscholtzii LM12, Diaporthe hongkongensis CP39, Gliocladium sp. C324, Trichoderma sp. L322 and T. hamatum C212, where the mycelium of the test fungus outgrew that of the pathogen. This was seen to be most true in Gliocladium sp. and Trichoderma sp. (2++). The inhibition percentage (% I) of each antagonistic fungus against the pathogens revealed different degrees of inhibition (Table 2). Gliocladium sp. C324 and Trichoderma hamatum C212 recorded the highest %I at 100% against C. siamense LV515. Similarly, these two potential antagonists showed the highest %I, up to 65%, against P. mangiferae LM24 and C. gloeosporioides. Purpureocillium sp. C311 showed a good %I of 61.07% against C. siamense LV515, whereas Xylaria sp. CL37 showed an identical % I but against P. mangiferae LM24. Also, over time during the dual culture assay, morphological changes in the test pathogen P. mangiferae were observed. The production of either a yellow or black pigmentation was observed on the fungal colony when co-cultured with Colletotrichum sp., Talaromyces sp. and Xylaria sp. antagonists.

Antimicrobial assay of fungi associated with *G. gnemon* Linn.

Using a culture broth filtrate of 80 µl, 22 out of 52 isolates (42.3%) showed antimicrobial activity against at least one pathogen (Table 3 and Fig. S3). The presence of inhibition zones qualitatively indicated positive antimicrobial activity. Endophytic isolates that exhibited antimicrobial activity were from the genera Colletotrichum sp., Daldinia sp. and Xylaria sp., while soil fungi that exhibited antimicrobial activity were from the genera Aspergillus sp. and Talaromyces sp. In addition, most of the isolates obtained from the conventional farming system showed positive antimicrobial activity against the test pathogens. M. luteus was inhibited by most fungal isolates. However, none of the fungi associated with G. gnemon could inhibit E. coli, P. aeruginosa, S. typhi and A. fumigatus. V. cholerae was the only Gram-negative bacterium that was inhibited by two endophytic fungi: C. siamense LV515 and D. eschscholtzii LM12. The pathogenic yeast C. albicans was inhibited by endophyte Xylaria allantoidea LL13W. In addition, D. eschscholtzii LM12 had positive antimicrobial activity against three bacterial pathogens (S. aureus, M. luteus and V. cholerae).

DISCUSSION

G. gnemon Linn. is a medicinal plant and food in Southeast Asia. In recent years, the biodiversity and pharmacological properties of G. gnemon have been the focus of increasing attention [8-11], but very few attempts have been made to evaluate the diversity of fungi associated with this valuable plant. Two studies have reported fungi associated with Gnetum spp. root tips, revealing the colonization of ectomycorrhizal fungi of the genus Scleroderma and several fungal species from unrelated lineages [21, 22]. These studies thus demonstrated that the roots of *Gnetum* spp. host a narrow range of mycorrhizal symbionts. Here, we investigated the diversity and abundance of culturable fungi associated with G. gnemon Linn. collected from two locations: a conventional farm and an organic farm. In addition, biological activities of the isolated fungi were evaluated. As a result, we discovered some fungi with the potential to inhibit microbial pathogens of plants and humans. We investigated the diversity and abundance of culturable foliar endophytic and soil fungi associated with G. gnemon var. tenerum Markgr. Our study revealed that foliar endophytic and soil fungal communities of G. gnemon were more diverse and abundant than the fungal communities associated with the roots of the species. The fungal communities obtained from both farming systems were dominated by Ascomvcota. The most abundant order of endophytic fungi obtained from leaves was Xylariales (RF, 36.48%), followed by Glomerellales (RF, 34.70%) and Diaporthales (RF, 8.82%), whereas the most abundant order of soil fungi was Eurotiales (RF, 54.57%), followed by Hypocreales (RF, 31.83%). Regarding fungal genera, Colletotrichum sp., Daldinia sp., Guignardia sp. and Pestalotiopsis sp. were dominant in G. gnemon leaves, whereas Penicillium sp., Trichoderma sp., Aspergillus sp. and Gliocladium sp. were dominant in soil. A great number of foliar endophytic fungi have been isolated from leaves of many types of plants (see review by Jia et al [23]. Our findings were similar to those reported in studies of foliar fungal diversity around the world, but different frequencies were observed. This was also true for soil fungi. The dominance of soil fungi by members of the orders Eurotiales and Hypocreales reported by Gaddeyya et al [24] and Rosas-Medina et al [25] was also found in this study. In addition, Tedersoo et al [26] found that Eurotiales and Hypocreales were within the ten most common orders according to data obtained by environmental sequencing.

Differences in soil physicochemical parameters, fungal diversity, and community structure were detected among the sampling sites. Overall, the abundance and species diversity of culturable fungi were slightly higher in the organic farming system than in the conventional farming system. The endophytic fungal community of leaves from both systems was

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Isolate		Zon	e of inhibition (1	nm)		Total
		Bacteria [*]		Ye	ast [*]	no.
	ML	SA	MRSA	VC	CA	
Endophytic fungi						
Colletotrichum sp. CM410	_	_	12.8 ± 0.5	_	-	1
Colletotrichum sp. CV26	18.6 ± 0.2	-	_	_	-	1
Colletotrichum sp. LL411	18.6 ± 0.5	-	_	-	-	1
Colletotrichum fructicola CM39	20.2 ± 0.1	15.6 ± 1.4	_	_	-	2
Colletotrichum fructicola CV24	-	-	12.4 ± 0.1	_	-	1
Colletotrichum siamense LV515	-	19.5 ± 0.5	-	15.2 ± 0.8	-	2
Daldinia eschscholtzii CL411	20.7 ± 0.0	-	-	_	_	1
Daldinia eschscholtzii CM24	-	-	17.6 ± 0.7	-	-	1
Daldinia eschscholtzii CP13	20.4 ± 1.1	_	_	_	_	1
Daldinia eschscholtzii CP25	-	-	14.4 ± 0.4	_	_	1
Daldinia eschscholtzii CP412	_	_	14.9 ± 0.8	_	_	1
Daldinia eschscholtzii LM12	19.4 ± 1.6	15.5 ± 0.3	-	15.9 ± 1.4	_	3
Meyerozyma caribbica CM37	-	12.5 ± 0.0	-	-	-	1
Xylaria sp. LL12	16.4 ± 0.5	14.4 ± 1.0	_	_	_	2
Xylaria allantoidea LL13W	-	-	-	_	16.6 ± 1.5	1
Xylaria feejeensis LP515	18.0 ± 0.3	-	-	-	_	1
Endophytic fungi						
Aspergillus aculeatus C213	16.1 ± 1.4	-	_	-	-	1
Aspergillus unguis LL37	20.3 ± 0.7	-	17.2 ± 0.1	-	-	2
Talaromyces aculeatus C312	19.0 ± 0.9	-	_	-	-	1
Talaromyces aculeatus L318	18.4 ± 1.3	-	12.1 ± 0.1	_	-	2
Talaromyces aculeatus L513	19.3 ± 1.0	-	12.2 ± 0.5	-	-	2
Talaromyces pinophilus C323	19.0 ± 0.8	-	-	-	-	1
Total no.	14	5	8	2	1	
Positive control	ML	SA	MRSA	VC	CA	
Vancomycin (20 µg/ml)	22.6 ± 1.0	18.0 ± 0.1	16.2 ± 0.7	213+05		
Amphotericin B (20 µg/ml)				21.3 ± 0.3	15.2 ± 0.3	

Table 3 Antimicrobial assays of fungi associated with G. gnemon using the agar-well diffusion method.

^{*} ML: *M. luteus* (ATCC9341), SA: *S. aureus* (ATCC25923), MRSA: methicillin-resistant *S. aureus* (MRSA), VC: *V. cholerae*, and CA: *C. albicans* (ATCC90028). The hyphen – indicates no activity.

clustered together, as was the community of the soil from both systems (Fig. S1). These most common fungal genera have been reported to be pioneer colonizers, and their ability to adapt to various environmental conditions leads to their cosmopolitan distribution [25, 27]. Remarkably, our study demonstrated that fungal habitats (plant vs. soil) were strong determinants of fungal communities. Most endophytic fungi inhabiting the G. gnemon leaves were Colletotrichum sp. and Pestalotiopsis sp., which are considered major pathogens in many crops worldwide. In our study, they existed as fungal endophytes without causing any symptoms to G. gnemon. De Silva et al [28] suggested that many species exist as endophytes for part or most of their life cycles in many groups of plants. The differences in lifestyle of these fungal genera might be attributed to their fungal species, the plant species, the physiological maturity of the host and the environmental conditions. Dominant fungi associated with G. gnemon, such as the endophytes Daldinia sp., Diaporthe sp., Colletotrichum sp., Xylaria sp., and soil fungi Aspergillus sp., Penicillium sp. and Trichoderma sp., might be capable of inhibiting other fungal pathogens through different mechanisms. These fungi were reported to produce secondary metabolites that reduce the negative effects from plant pathogenic fungi, including volatile compounds that can suppress pathogen growth [29]. D. eschscholtzii, which was the second most frequently found species in G. gnemon leaves, has been reported to produce 60 compounds that are effective antifungal agents against plant pathogenic fungi Colletotrichum gloeosporoides, C. nymphaeae and C. musae [30]. Therefore, the diverse fungal communities in G. gnemon leaves might provide the plant with a defensive capability against pests and fungal diseases. It was observed by the authors that G. gnemon usually requires minimal fertilizing and no pesticides or fungicides during plantation. Furthermore, microbial diseases of *G. gnemon* are rarely reported. This feature of *G. gnemon* could be attributed to their fungal endophytes.

In conventional farming systems, fungicides and pesticides incur great costs and often cause environmental pollution and reduction of biodiversity. Therefore, biocontrol of plant diseases is an attractive strategy. Fungi have been recognized to contain structurally diverse and biologically active compounds; many of which have been reported to produce a variety of novel bioactive metabolites [13, 23, 24]. Alkaloids, aliphatic compounds, peptides, phenylpropanoids, polyketides, and terpenoids have been isolated from fungi and identified. Here, we demonstrated that fungal endophytes D. eschscholtzii LM12, D. hongkongensis CP39, Gliocladium sp. C324, Trichoderma sp. L322 and T. hamatum C212, successfully inhibited the plant pathogens C. siamense, P. mangiferae and C. gloeosporoides in a dual culture assay. The strong ability of Gliocladium sp. and Trichoderma sp. to out-grow the pathogenic fungi suggested effective competition for nutrients and space for survival. These fungi are among the most common fungi in nature due to their high level of stress tolerance and rapid growth rate [31]. They are known to secrete certain enzymes that are responsible for breaking down the cell walls of pathogen [32]. In addition, Gliocladium sp. C324 and T. hamatum C212 showed inhibition rates of 100% against C. siamense and restricted the growth of *P. mangiferae*. Variations in fungal interactions observed in this study could be influenced by antibiotics produced by the isolates, which could be fungicidal to certain fungi, but fungistatic to others [33]. During the dual culture assay, we observed morphological changes over time of the test pathogen P. mangiferae, which produced either a yellow or black pigmentation in the colony when co-cultured with Colletotrichum sp., Talaromyces sp. and Xylaria sp. These observations were consistent with findings by Hamzah et al [34]. The pigments could include carotenoids, flavins, melanins, quinones, and phenazines [35]; and they might be associated with antibacterial, antifungal, and herbicidal activities [36, 37]

Twenty two out of 52 isolates (42.3%) showed inhibitory activity against at least one human pathogen. Fungal isolates that exhibited antimicrobial activity were from the genera *Aspergillus* sp., *Colletotrichum* sp., *Daldinia* sp., *Talaromyces* sp., and *Xylaria* sp. Among the studied strains, *D. eschscholtzii* LM12 exhibited positive antimicrobial activity against three bacterial pathogens (*S. aureus*, *M. luteus* and *V. cholerae*). *D. eschscholtzii* was previously reported to demonstrate antibacterial activity [24, 38] and antifungal activity [29]. We observed a relatively low level of activity against Gram-negative bacteria from our fungal isolates, which was in accordance with previous studies [13, 14, 39]. Furthermore, most fungal members that showed positive antimicrobial activity against test pathogens, were obtained from the conventional farming system rather than the organic farming system. Renato et al [40] suggested that the chances of discovering new antimicrobial-producing fungal strains were greater if non-mesophilic environments were investigated. Under conditions of nutrient depletion, metal contamination, high salinity or extreme temperatures, fungi must develop survival strategies for growth and reproduction. Besides the exploration of fungal diversity associated with the G. gnemon Linn., our significant findings were the discoveries of three potent fungal strains, D. eschscholtzii LM12, possessing broadrange antimicrobial activity against several microbial pathogens of plants and humans; and Trichoderma and Gliocladium strains showing strong antagonistic activity against fungal pathogens. These properties point to potential biotechnological applications of the three strains.

CONCLUSION

We investigated the diversity and abundance of culturable fungi associated with G. gnemon Linn. grown in organically and conventionally farmed plantations. Our results demonstrated that both farming systems harbored common native fungal communities in both plant and soil samples. Members of fungi isolated from plants and soil were not clustered to the same group, which suggested that the habitat had more influence on the fungal community than the location. However, some fungal strains were location-specific. Dominant fungi associated with G. gnemon were Colletotrichum sp., Daldinia sp., Guignardia sp., Pestalotiopsis sp., Penicillium sp., Trichoderma sp., Aspergillus sp., and Gliocladium sp.; and the fungal communities seemed to be diverse and abundant. The characterization of biological activities of fungal isolates revealed three promising candidates with strong ability to inhibit microbial pathogens; and they could, therefore, be used for biological control. The three candidates were D. eschscholtzii, T. hamatum and Gliocladium strains. Overall, these results suggested that the diversity of fungi associated with G. gnemon could be explored as a potential source of bioactive agents.

Appendix A. Supplementary data

Supplementary data associated with this article can be found at http://dx.doi.org/10.2306/scienceasia1513-1874. 2024.027.

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Appendix A. Supplementary data



Fig. S1 Venn diagram of the culturable fungi associated with *Gnetum gnemon* Linn. from conventional and organic farming systems.



Fig. S2 Dual culture plate assay of test fungi (to the left of plates) against the plant pathogenic fungi (to the right) *Colletotrichum siamense* LV515 (A) and *Pestalotiopsis mangiferae* LM24 (B). The plates were cultivated for 7 days at 27 °C. Radial growths were measured and types of interaction were classified. The asterisks indicate the dual culture after 14 days.



Fig. S3 Antimicrobial activity of fungi associated with Gnetum gnemon Linn. determined by the agar well diffusion method.

Table S1 Physicochemical characteristics of soil samples.

Parameter	Test rest	ılt
	Conventional farming	Organic farming
pH	7.24 ^a	7.16 ^a
Moisture content (%)	13.82 ^a	$17.98^{\rm b}$
Total nitrogen content (% w/w)	0.10^{a}	0.17^{a}
Total organic carbon (% w/w)	0.96 ^a	$1.82^{\rm b}$
Organic matter (% w/w)	1.66 ^a	3.14 ^b

The same superscript letter indicates no significant difference (p > 0.05) between individual parameter from conventional and organic farming.

Table S2 Numbers of soil fungi and endophytic fungi associated with Gnetum gnemon Linn.

Parameter			Leaf sample		Soil sample				
	No	o. of fungal is	solates (No.	es)	No. of	Colony forming units/			
	Lamina	Vein	Midrib	Petiole	Total	isolates	gram soil (CFU/g soil)		
Conventional farming Organic farming	23 (15) 24 (15)	21 (15) 28 (15)	21 (15) 20 (15)	14 (15) 19 (15)	79 (60) 91 (60)	33 33	5.65×10^{3} 4.45×10^{3}		

Table S3 Numbers of infected leaf segments of the Gnetum gnemon Linn.

Parameter		No. of infected leaf segments (Total no. of leaf segments)								
	Lamina	Vein	Midrib	Petiole	Total					
Conventional farming Organic farming	14 (15) 14 (15)	14 (15) 13 (15)	15 (15) 14 (15)	12 (15) 14 (15)	55 (60) 55 (60)					

Nuccomprotes MucconvectesL212.aMuccor circinelloidesKJ588204.199.07Accomycota DohildeonyretesEditation of the circinelloidesSector90.07Accomycota DohildeonyretesC42.2Kalmissia araucaria culture CPC:37475HQ238040.194.64PleosporalesC42.2Kalmissia araucaria culture CPC:37475MH223805.199.81L325Leptospherria sp. strain 1-11-23MH800329.198.65CallAspergillus aculeatus isolate JJGG-66MK644143.198.95CallAspergillus aculeatus isolate JJGG-66MK644143.198.95CallAspergillus aculeatus isolate SURD31MH39223.199.83CallAspergillus avata isolate SURD31MG31922.199.83CallAspergillus avata isolate SURD31MG31922.199.83CallAspergillus unguis arain DUCC VIDMH39273.199.83CallAspergillus unguis arain DUCC VIDMH39273.199.83CallApergillus unguis arain DUCC VIDMK350697.196.83CallParicillum janchindlum strain CNU2050KY06986.197.84CallTalaromyces aculeatus isolare BV023MW760782.199.44SaccharomycetesCallMG90023MW760782.196.64GiomerellalesCY4Collectorichum finction isolare 1NPL2260KY06986.197.84GiomerellalesCY4Collectorichum finction isolare 1NPL2.205.11327.196.55CallMG90004.196.64Collectorichum finction isolare 1NPL2.205.11327.1 <th>Таха</th> <th>Code</th> <th>Closest relative (BLAST)</th> <th>Accession no.</th> <th>Identity (%)</th>	Таха	Code	Closest relative (BLAST)	Accession no.	Identity (%)
Mucronycetes Mucro circinelloides K1588204.1 99.07 Acomycota Dothideomycetes Batyrosphaeriales 11.13B Guignardia mangiferae strain MI26 HQ328040.1 94.64 Pleosoprates C422 Kalmusia araukariae culture CPC/37475 HT223805.1 99.81 Eurotionycetes 131 Pyrenochaetopsis microspora isolate PB147 MK50881.1 96.55 Eurotionycetes C211 Aspergillus flavus strain ASP3 ON365935.1 99.83 C411 Aspergillus flavus strain ASP3 ON365935.1 99.83 C211 Aspergillus grave isolate FBL3.0167 K182807.1 99.49 C312 Aspergillus mytes isolate FBL2.0167 K182807.1 99.49 C313 Apergillus mytes muscles KUDAS1 MK5019722.1 99.43 C314 Pericillinm drysogenum isolate KD023 MW700782.1 99.43 C315 Pericillinm greedpfurms NRL 2687 NK1212601 NK436097.1 98.43 Saccharomycetas C33 MW700782.1 99.43 Talaromyces acutauts tolate B023 MW700782.1 99.43 Sacch	Mucoromycota				
Mucor circhelloides KJ588204.1 99.07 Accomycota Portugingendia Status 99.07 Accomycota Dothidoamycetes Portugingendia 99.07 Botryophaeriales L138 Guignardia mangiferae strain MD26 HQ328040.1 99.61 Eurotionycetes L311 Pyrenochaetapsis microspora isolate PB147 MK508814.1 98.67 Eurotianycetes C213 Aspergillus drus strain ASP3 ON365935.1 99.81 C211 Aspergillus drus strain ASP3 ON365935.1 99.81 C221 Aspergillus orgas isolate JND17 MK3082731.1 99.81 C221 Aspergillus orgas isolate JND271 MK30519722.1 99.83 C333 Panicillium ristain PPRUS2059 WY069843.1 99.79 C314 Panicillium strain PPRUS2059 WY069843.1 99.46 C312 Talaromyces aculatus isolate INC23 MW760782.1 99.46 C323 Talaromyces aculatus isolate INC3 MW760782.1 99.46 C314 Calitorithum functional solate INVE-2 OQ0511327.1 98.43	Mucoromycetes				
Ascomporta Dothideomycets Botryosphaeriales LL13B Guignardia mangiferae strain M26 HQ328040.1 94.64 Pleosporales C42 Kalmusia araucariae culture CPC:37475 MT223805.1 99.81 L325 Leptosphaeria sp. strain 1-11.23 MH800329.1 99.865 Eurotiomycetes C211 Aspergillus faus strain ASP3 ON369935.1 99.83 C211 Aspergillus faus strain ASP3 ON369935.1 99.83 C221 Aspergillus advattis toilate FBKI3.0167 WK32897.1 96.35 C321 Aspergillus davattisolate JAUBD17 MH392731.1 99.83 C313 Persicillum drivagemus toilate KUMBNCBT:79 ON353437.1 97.83 C314 Persicillum grisofulvum strain PVR02659 W059663.1 92.24 C312 Talaromyces aculeatus isolate BO23 MW70782.1 98.46 Sarcharomycetels C337 Talaromyces aculeatus isolate 11-1400 MG01600.1 98.61 Sarcharomycetels CM37 Meyreoyma caribbica isolate 11-140 MW70782.1 99.46 Sarcharomycetels CM37	Mucorales	L212a	Mucor circinelloides	KJ588204.1	99.07
Dothideomycetes Everyosphariales L133B Guignardia mangiferae strain M26 HQ32804.1 94.64 Pleosporales C422 Kalmusia aratacriae culture CPC:37475 MT23805.1 99.81 Eurotionycetes L311 Pyrenochaetopsis microspora isolate PB147 MK508314.1 98.67 Eurotionycetes C213 Aspergillus flows isolate J06C-66 MK44143.1 98.95 C211 Aspergillus flows isolate SWDRj MG519722.1 99.83 C221 Aspergillus orgae isolate SWDRj MG519722.1 99.83 C221 Aspergillus orgae isolate DUDC5719 MT5827591 96.83 C313 Penicillium grisofiluw mistriin PRI22659 WT069863.1 99.24 C325 Penicillium strain pPRI22659 WT069863.1 99.46 C311 Pariacillium strain pPRI22659 WT069782.1 99.46 Saccharomycetes C323 Talaromyces aculatus isolate BD023 MW760782.1 99.46 Saccharomycetes C337 Meyerosyma caribbica isolate 11-1400 MG016004.1 98.61 Sordariomycetes Diaporthe hongkongensis strain TZFH6 <td>Ascomycota</td> <td></td> <td></td> <td></td> <td></td>	Ascomycota				
Botryosphaeriales L1.13B Guignardia magiferae strain M226 HQ328040.1 94.64 Pleosporales L325 Leptosphaeria sp. strain 1-11-23 MH300329.1 99.81 L325 Leptosphaeria sp. strain 1-11-23 MH300329.1 99.81 Eurotiales C213 Aspergillus aculeatus isolate JJGG-66 MK644143.1 98.97 Eurotiales C211 Aspergillus aculeatus isolate FBKJ.0167 KY822897.1 99.83 C411 Aspergillus aculeatus isolate FBKJ.0167 KY822897.1 99.83 C321 Aspergillus unguis strain DVCGS719 MH392731.1 99.83 C314 Penicillium drinogenius isolate MUBND17 MH392731.1 99.83 C314 Penicillium strain DVCGS719 MH392731.1 99.46 C325 Penicillium strain DVCM06C1 MK450697.1 99.46 C314 Penicillium strain CVV000C1 MK450697.1 99.46 C323 Talaromyces aculeatus isolate BO23 MW760782.1 99.46 Saccharomycetes C33 Talaromyces aruleatus isolate BO23 MW760782.1 99.65 C1514	Dothideomycetes				
Pleosporales C422 L32 <i>Kalmusia araucariae</i> culture CPC:37475 MT322305.1 99.81 Eurotiomycetes L311 <i>Pyrenochaetopsis microsport</i> isolate PB147 MK508814.1 98.77 Eurotiales C213 <i>Aspergillus favus strain</i> ASP3 ON365935.1 99.83 C411 <i>Aspergillus favus strain</i> ASP3 ON365935.1 99.83 C422 <i>Aspergillus favus strain</i> ASP3 ON365935.1 99.83 C411 <i>Aspergillus favus strain</i> ASP3 ON365935.1 99.83 C313 <i>Aspergillus favus strain</i> DUCS719 MT582759.1 96.35 C314 <i>Penicillium gisodytivi</i> stoiate FM122659 K7059863.1 99.24 C325 <i>Penicillium strain Strain</i> CMV006C1 MK450697.1 98.65 C312 <i>Talaromyces aculeatus</i> isolate Bf023 MW760782.1 98.46 Gardariomycetes C33 Meyroayme acribica isolate 11-1400 MG016004.1 98.65 Saccharomycetes CM37 <i>Meyeroayma caribica</i> isolate 110-42 OQ511327.1 99.65 Giomerellales CV24 <i>Coletorichum giscoparoidis</i> strain T2H6 MW767083.	Botryosphaeriales	LL13B	Guignardia mangiferae strain MJ26	HQ328040.1	94.64
L325 Leptosphaeria sp. strain 1-11-23 MHS0329.1 98.65 Eurotiales C213 Aspergillus farus isrospora isolate PB147 MK508814.1 98.77 Eurotiales C213 Aspergillus farus isrospora isolate PB147 MK50414.1 98.85 C411 Aspergillus farus isolate FBK13.0167 KK544143.1 98.83 C422 Aspergillus growing isolate FBK13.0167 KK54517.1 99.83 C421 Aspergillus growing isolate SUPDR.j MC50592.1 99.83 C321 Aspergillus growing isolate SUMBNGBT-79 ON533437.1 97.93 C314 Penicillium grisciplurum strain DPR122659 KY069663.1 99.24 C325 Penicillium straits isolate BR023 MW760782.1 98.46 L319 Penicillium grintraits isolate BR023 MW760782.1 99.46 L318 Talaromyces aculaatus isolate BR023 MW760782.1 99.46 C323 Talaromyces aculaatus isolate BR023 MW760782.1 99.46 C311 Talaromyces aculaatus isolate BR023 MW760782.1 99.45 C323 Talaromyces aculaatus isolate BR023	Pleosporales	C422	Kalmusia araucariae culture CPC:37475	MT223805.1	99.81
L311 Pyrenochetopsis microsport isolate PB147 MK608814.1 98.75 Eurotianycetes C213 Aspergillus aculeatus isolate JJGC-66 MK644143.1 98.95 Eurotiales C211 Aspergillus flavus isolate JLGC-66 MK644143.1 98.95 C411 Aspergillus flavus isolate JLGC-66 MK644143.1 98.93 C411 Aspergillus orgate isolate SW-DR-j MC519722.1 99.83 C221 Aspergillus orgate isolate SW-DR-j MC519722.1 99.83 C313 Penicillium grissofubrum strain DUCCS719 MT582759.1 96.35 C313 Penicillium grissofubrum strain DVCCS719 MK4506697.1 98.63 C312 Talaromyces aculeatus isolate BR023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate BR023 MW760782.1 99.46 Saccharomycetels Saccharomycestes		L325	Leptosphaeria sp. strain 1-11-23	MH800329.1	98.65
Eurotiales C213 Aspergillus acukeatus isolate JJGC-66 MK644143.1 98.95 C211 Aspergillus flavus strain ASP3 ON365935.1 99.83 C411 Aspergillus acukeatus isolate FBK13.0167 KV828897.1 99.49 C322 Aspergillus oryzae isolate SW-DR.j MC59722.1 99.83 C421 Aspergillus oryzae isolate SW-DR.j MC59722.1 99.83 C421 Aspergillus acukeatus isolate FBK13.0167 KV828897.1 99.83 C421 Aspergillus acukeatus isolate FBK13.0167 KV828897.1 99.83 C421 Aspergillus unguis strain DVCC5719 MT582759.1 96.35 C421 Penicillium chrysogenum isolate KUMBNOBT-79 ON533437.1 97.93 C414 Penicillium griseofubrum strain DVM06C1 MK450697.1 98.63 C421 Talaromyces acukeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces acukeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces acukeatus isolate Bf023 MW760782.1 99.46 C423 Talaromyces acukeatus isolate Bf023 MW760782.1 99.46 C423 Talaromyces acukeatus isolate Bf023 MW760782.1 99.46 Gondariomycetes Diaporthales C739 Diaporthe hongkongensis strain TZFH6 MW341269.1 98.64 Glomerellales C744 Collectorichum fracticola isolate 11-1400 MG016004.1 98.64 Gondariomycetes Diaporthales C739 Diaporthe hongkongensis strain TZFH6 MW341269.1 99.82 LV411 Collectorichum glocesporioides sinal TKM-52.20 MW332972.1 99.29 LM410 Collectorichum markense isolate 11V1-2 OX73058.1 99.10 LV515 Collectorichum sincense isolate 11V1-2 OX73058.1 99.82 LV411 Collectorichum sincense isolate 11V1-2 OX73058.1 99.82 LV411 Collectorichum sincense isolate 11V1-2 OX73058.1 99.46 C324 Glocadium sp. isolate Bf02290 MH003433.1 98.20 L3110 Phypercellium JLainam strain TVH1-6.65 OV26830.1 93.38 C212 Trichoderma hamatum strain TVH1-65 C7247808.1 99.67 C1212 Trichoderma hamatum strain TVH1-65 C7247808.1 99.69 C1212 Trichoderma hamatum strain TVH1-65 C7247808.1 99.69 C1212 Trichoderma hamatum strain TVH1-65 C7247808.1 99.69 C1213 Daldinia escheolocit		L311	Pyrenochaetopsis microspora isolate PB147	MK508814.1	98.77
Eurotiales C213 Aspergillus acuidatus isolate JJGC-66 MR644143.1 99.95 C411 Aspergillus favus isolate FBRL3.0167 KY828897.1 99.48 C421 Aspergillus godowi isolate JJGCPB MC51972.1 99.83 C421 Aspergillus godowi isolate JJGDPS MC51972.1 99.83 C421 Aspergillus godowi isolate JJGDPS MC52759.1 96.35 C313 Penicillium richtysogenum isolate KUMBNGBT?9 ND533437.1 97.93 C314 Penicillium richtysogenum isolate KUMSNGBT?9 NR120663.1 99.44 C325 Penicillium strain CMV006C1 MK450697.1 98.63 C312 Talaromyces acuidatus isolate Bf023 MW760782.1 99.46 Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas NW760782.1 99.69 Diaporthe hongkongensis strain TZFH6 MW341269.1 98.61 Solatoriomycets Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas Saccharomycetas<	Eurotiomycetes	0010		10000	00.05
C211 Asperglus favas strain ASP3 ON 36535.1 99.83 C322 Asperglus favas strain DASP3 WR 2000 WR 2000 C321 Asperglus grows isolate SW-DR-j MK 3519722.1 99.83 C321 Asperglus grows isolate SW-DR-j MK 3519722.1 99.81 L1.37 Asperglus grows isolate SW-DR-j MK 3519722.1 99.81 C314 Pericillium griscofulum strain DUCC5719 MK 350697.1 99.63 C314 Pericillium griscofulum strain PPR122659 KY 069863.1 99.46 C319 Pericillium griscofulum strain PPR122659 KY 069863.1 99.46 C318 Talaromyces aculeatus isolate Bf023 MW 760782.1 99.46 C323 Talaromyces aculeatus isolate Bf023 MW 760782.1 99.49 Saccharomycetes Saccharomycetes Saccharomycetes Saccharomycetes Saccharomycetes Saccharomycetes C323 Talaromyces are use priorbitus clone OTU49 KY 965441.1 97.83 Sordariomycetes Diaporthe longkongensis train T2FH6 MW 341269.1 98.61 Golamerellales CY24 Colletorrichu	Eurotiales	C213	Aspergillus aculeatus isolate JJGG-66	MK644143.1	98.95
C411 Appergulus juluis Bolate SW-DR-j MG51972.1 99.83 C221 Aspergulus sydowi isolate SW-DR-j MG51972.1 99.83 C211 Aspergulus sydowi isolate SW-DR-j MT58275.1 96.35 C313 Penicillum richysogenum isolate KUMBNGBT79 MT58275.1 96.35 C314 Penicillum richysogenum isolate KUMBNGBT79 NR5868.1 99.24 C325 Penicillum richysogenum isolate KUMSNGBT79 NR 121260.1 98.63 C312 Talaromyces aculeatus isolate BM023 MW760782.1 99.46 C312 Talaromyces aculeatus isolate BM023 MW760782.1 99.46 Saccharomycetes Diaporthe hongkongensis strain TZFH6 MW341269.1 98.61 Glomerellales CV24 Collectorichum fracticola isolate 11N-2.2 OQ511327.1 99.65 Glomerellales CV24 Collectorichum sinense isolate PM2.2 MW760782.1 99.49 LM410 Collectorichum sinense isolate 11N-2.2 MW760782.1 99.69 Saccharomycetales C234 Cletorichum sinense isolate PM2.2 MW760798.1 99.69 Lipotroba </td <td></td> <td>C211</td> <td>Aspergilius flavus strain ASP3</td> <td>UN305935.1</td> <td>99.83</td>		C211	Aspergilius flavus strain ASP3	UN305935.1	99.83
C 322 Apergillus 30/2014 Isolate SV-IN-j MIG5197.22.1. 99-83 C 221 Aspergillus 30/2014 Isolate SV-IN-j MIG5197.22.1. 99.81 L137 Aspergillus 30/2014 Isolate SV-IN-j MIG52759.1. 96.35 C 313 Pericillum griscofulum strain DUCCS719 MITS82759.1. 96.35 C 314 Pericillum griscofulum strain DVCCS719 NT822759.1. 98.63 C 325 Pericillum straitsporum NRL 26877 NR 121260.1. 98.66 C 312 Talaromyces aculeatus isolate Bf023 MW760782.1. 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1. 98.43 C 323 Talaromyces aculeatus isolate Bf023 MW760782.1. 98.64 C 323 Talaromyces aculeatus isolate Bf023 MW760782.1. 98.64 C 323 Talaromyces aculeatus isolate Bf023 MW760782.1. 98.64 Sordariomycetes Saccharomycetes Diaporthales CP39 Diaporthe hongkongensis strain TZFH6 MW341269.1. 98.61 Glomerellales CC24 Collectorichum glocosporioides strain LCM 955.2.02 MN83334.1. 99.82 IV411 C Collectorichum glocosporioides strain LCM 955.2.02 MN83334.1. 99.82 IV411 C Collectorichum siconese isolate 11617.4 MW532972.1. 99.29 IV4110 Collectorichum siconese isolate 12N1-2.0 OM736124.1. 99.29 IV4110 Collectorichum siconese isolate 12N1-2.0 MW767098.1. 99.10 IV515 C alletorichum siconese isolate 12N1-2.0 MW767098.1. 99.10 IV515 C alletorichum siconese isolate 12N1-2.0 MW767084.1. 99.29 LM513 C Olletorichum siconese isolate 12N1-2.0 MW767084.1. 99.29 LM513 C Olletorichum siconese isolate 12N1-2.0 MW767084.1. 99.29 LM513 C Colletorichum sicoleta 12N1-2.0 MW767084.1. 99.47 C 324 Glicolatim sp. isolate BOP2390 MH003433.1. 98.20 L3110 Hypocreales System 40 KX95324.1. 99.67 Ophiostomatales CY11 Cercophora coprophila isolate CTCCSJ-G-H840441 KY764898.1. 99.67 V515 D aldinia eschscholtzii strain KUMCC21-0440 ON426842.1. 99.88 CY15 D aldinia eschscholtzii strain KUMCC21-0440 ON426842.1. 99.88 CY15 D aldinia eschscholtzii strain KUMCC21-0440 ON426842.1. 99.89 CY15 D aldinia eschscholtzii strain KUMCC21-0440 ON426842.1. 99.89 CY15 D aldinia eschscholtzii strain KUMCC21-0440 ON426842.1. 99.89 CY15 D aldinia eschscholtzii strain KUMCC2		C411 C222	Aspergilius flavus isolate FBKL3.010/	KI828897.1 MCE10722.1	99.49
L137 Abge gittus Sydomi Isolate Sitcipi 10 Min532/31.1 97.31 L137 Abge gittus Strain DUCCS719 Min532/31.1 97.93 C313 Penicillium chrysogenum isolate KUMBNGBT-79 ON533437.1 97.93 C314 Penicillium strain DPR122659 KY069863.1 99.24 C325 Penicillium strain CMV006C1 MK450697.1 98.63 L319 Penicillium strain CMV006C1 MK450697.1 98.63 C321 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1 98.64 Saccharomycetales Saccharomycetales G037 Meyerozyma caribbica isolate 11-1400 MG016004.1 98.64 Glomerellales CV24 Collectorichum furtical isolate 17N-2-2 OQ511327.1 99.65 Glomerellales CV24 Collectorichum igloesoporioides strain LCM 955.52.02 MN833334.1 99.82 LV411 Collectorichum simense isolate Ig621 MW760788.1 99.10 LV515 Collectorichum sinemes isolate Ig621 MW767088.1 99.20 <td< td=""><td></td><td>C322</td><td>Aspergillus oryzue isolate SW-DR-J</td><td>MG519/22.1 MH202721 1</td><td>99.63</td></td<>		C322	Aspergillus oryzue isolate SW-DR-J	MG519/22.1 MH202721 1	99.63
Carlo Paper Standard		U221	Aspergillus unquis strain DUCC5710	MT522750 1	99.01
C314 Penicillium grisopialum strain PPRI22659 KY069863.1 99.24 C325 Penicillium grisopialum strain CM006C1 MK450697.1 98.63 C312 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1 98.63 C323 Talaromyces aculeatus isolate Bf023 MW760782.1 98.43 C323 Talaromyces aculeatus isolate Bf023 MW760782.1 98.43 Saccharomycetes Saccharomyces pinophilus clone OTU49 KY965441.1 97.83 Saccharomycetes CM37 Meyerozyma caribbica isolate 11-1400 MG016004.1 98.64 Diaporthe longkongensis strain TZFH6 MW45129.1 99.29 LM410 Colletotrichum fulceosporioides isolate F16T11A MW532972.1 99.29 LM410 Colletotrichum gleocosporioides isolate F16T11A MW763078.1 99.67 LV11 Colletotrichum simense isolate lg621 MW767088.1 99.69 LW411 Colletotrichum simense isolate MF1UCC14-0091 MC792806.1 99.38 LW411 Colletotrichum sinonaterichum sitrain YMF1.665		C313	Denicillium chrysogenum isolate KUMBNGBT-70	ON533437 1	90.33
C325 Penicillum janthinellum strain CMV006C1 MK450697.1 98.63 L319 Penicillum janthinellum strain CMV006C1 MK450697.1 98.63 C312 Tilalaromyces aculeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 Saccharomycetes C323 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 Saccharomycetes Saccharomycetes CM37 Meyerozyma caribbica isolate 11-1400 MG016004.1 98.64 Sordariomycetes CDietorichum fructical isolate 11-1400 MG016004.1 98.64 Giomerellales CV24 Colletorichum gloeosporioides isolate P16T11A MW8312327.1 99.65 CL514 Colletorichum siamense isolate P621 MW767088.1 99.82 LV410 Colletorichum siamense isolate P621 MW767088.1 99.10 LX515 Colletorichum siamense isolate P16214 MW767088.1 99.29 Hypocreales C324 Gioletorichum siamense isolate P16214 MV767088.1 99.67 LX515 Colletorichum siamense isolate CCS1-GHB40441		C314	Penicillium griseofuluum strain PPRI22659	KV069863 1	99.25
L319 Penicillium striatisporum NRRL 26877 NR 121260.1 98.60 C312 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1 98.43 Saccharomycetes Saccharomyces pinophilus clone OTU49 KY965441.1 97.83 Saccharomycetes CM37 Meyerozyma caribbica isolate 11-1400 MG016004.1 98.64 Sordariomycetes Diaporthe hongkongensis strain TZFH6 MW475272.1 99.29 LM410 Colletotrichum fructicola isolate 11N-2-2 OQ511327.1 99.29 LM410 Colletotrichum gleosoporioides isolate F16T11A MW532972.1 99.29 LW410 Colletotrichum siaenes isolate 16T11A MW532972.1 99.29 LW410 Colletotrichum siaenes isolate 16T11A MW75098.1 99.10 LV515 Colletotrichum siaenes isolate 192.1 MW760782.1 99.82 LW410 Colletotrichum siaenes isolate 16T11A MW75298.1 99.29 LM515 Colletotrichum sp. isolate MFLUCC14-0091 MG792806.1 99.29 LM515 Colletotrichum sp. is		C325	Penicillium ianthinellum strain CMV006C1	MK450697 1	98.63
C312 Talaromyces aculeatus isolate Bf023 MW760782.1 99.46 L318 Talaromyces aculeatus isolate Bf023 MW760782.1 98.43 C323 Talaromyces aculeatus isolate Bf023 MW760782.1 98.43 Saccharomycetales C323 Talaromyces prinphilus clone OTU49 KY96541.1 97.83 Saccharomycetales CM37 Meyerozyma caribbica isolate 11-1400 MG016004.1 98.64 Sordariomycetes Diaporthe hongkongensis strain TZFH6 MW341269.1 98.61 Glomerellales CV24 Colletorichum fructicola isolate TISTIHA MW52072.1 99.265 LM410 Colletorichum glocosporioides stolate CM 955.52.02 MN833334.1 99.82 LV411 Colletorichum siamense isolate Ig621 MW760788.1 99.16 LV515 Colletorichum siamense isolate Bf0230 MH003433.1 98.20 LV411 Colletorichum siamense isolate DF1120 MW760788.1 99.67 L3110 Hypocreales C324 Glicodadium sp. isolate MF1UCC14-0091 MG792606.1 99.38 C1212 Trichoderma harzianum isolate CTCSJ-G-HB40441 KY764898.1 99.67		L319	Penicillium striatisporum NBBL 26877	NR 121260 1	98.60
L318Talaromyces aculeatus isolate Bf023MW760782.198.43SaccharomycetesSaccharomycetesSaccharomycetesSaccharomycetesSordariomycetesCM37Meyerozyma caribbica isolate 11-1400MG016004.1GlomerellalesCV24Colletorichum fructicola isolate 1VN-2-2OQ511327.1GlomerellalesCV24Colletorichum gloesoporiodes isolate F16T11AMW532972.1CL514Colletorichum gloesoporiodes isolate F16T11AMW532972.1M410Colletorichum siamense isolate 19621MW767098.1JV411Colletorichum siamense isolate 1971.2OM736124.1SordarialesC324Glicolatinum sp. isolate B0P2390MH003433.1HypocrealesC324Glicolatinum strain YNF1.665OP26830.1GlistSordarialesCV11Erchodram haratanum isolate CTCCS1-G-HB04411KY764898.1OphiostomatalesC316Sporothriz is rain KUMCC21-0440ON426842.199.28KylarialesCV11Cerophora coprophila isolate KNL0C21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM11Parlotiopsis camgligerae isolate MX06-17-LBPEMH179308.198.40SordarialesCV11Cerophora coprophila isolate KNL0C21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28LM11Pseudopestalotiopsis camgligrae isolate MX06-17-LBPEMH179308.198.9		C312	Talaromyces aculeatus isolate Bf023	MW760782.1	99.46
C323Talaromyces pinophilus clone OTU49KY965441.197.83SaccharomycetesCM37Meyerozyma caribbica isolate 11-1400MG016004.198.64SordariomycetesCV24Collectorichum fructicola isolate 11YN-2-2OQ511327.199.65DiaporthalesCV24Collectorichum fructicola isolate 1YN-2-2OQ511327.199.65GlomerellalesCV24Collectorichum fructicola isolate 1YN-2-2OQ511327.199.29LM410Collectorichum gloeosporioides stolate CM 955.52.02MN833334.199.82IV411Collectorichum siamense isolate 1g621MW767098.199.10IV515Collectorichum sp. isolate MFIUCC14-0091MG722806.199.80HypocrealesC324Gilocladium sp. isolate MFIUCC14-0091MG72806.199.80L110Hypocreales sp. strain 40KX953324.199.41C311Purpureocillium iliacinum strain YMF1.665OP268300.193.38C212Trichoderma haraiarum isolate CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporthrix sp. FA1M6LC768714.198.89SordarialesCV11Cercoptora coprophila isolate KoRL1046128MN341349.197.72XylarialesCV11Cercoptora coprophila isolate KoRL104128MN341349.197.82L111Paddinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.89L111Pestudotiopsis mangigreae isolate SUTL0400ON426842.199.89L111<		L318	Talaromyces aculeatus isolate Bf023	MW760782.1	98.43
Saccharomycetes SaccharomycetesCM37Meyerozyma caribbica isolate 11-1400MG016004.198.64Sordariomycetes DiaporthalesCP39Diaporthe hongkongensis strain TZFH6MW341269.198.61GlomerellalesCV24Collectorichum fuccioal isolate 1YN-22OQ511327.199.29LM410Collectorichum glocosporioides strain LCM 955.52.02MN833334.199.82LW411Collectorichum siamense isolate gl621MW767098.199.10LV515Collectorichum siamense isolate gl621MW767098.199.29LM513Collectorichum siamense isolate BG21MW767098.199.80HypocrealesC324Glicoladium sp. isolate MFLUCC14-0091MG792806.199.80L3110Hypocreales sp. strain 40KX953324.199.41C311Purpurcoillium liadinum strain TNi-111-5KC747808.1100.00L212Trichoderma hamatum strain TNi-115.5KC747808.1100.00L212Trichoderma harzianum isolate CTCCSJ-G-HB404411KY764898.199.67OphiostomatalesCV11Cercophora coprophila isolate KORLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.03LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90L111Reudopestalotiopsis strain FO146KU747562.190.32LM11Pestalotiopsis strain BZ4MH72239.199.12LM11Pest		C323	Talaromyces pinophilus clone OTU49	KY965441.1	97.83
Saccharomycetales SordariomycetesCM37Meyerozyma caribbica isolate 11-1400MG016004.198.64SordariomycetesDiaporthe hongkongensis strain TZFH6MW341269.199.65GlomerellalesCV24Collectorichum glocosporioides isolate 1YN-2-2QQ511327.199.65GL514Collectorichum glocosporioides sisolate F16T11AMW532972.199.29LM410Collectorichum glocosporioides strain LCM 955.52.02MN833334.199.82LV11Collectorichum siamense isolate IgS1MW767098.199.10LV515Collectorichum siamense isolate IgS1MW767098.199.80HypocrealesC324Gliocladium sp. isolate BOP2390MH003433.198.20L3110Hyporese sp. strain 40KX953324.199.41C311Purpureocillium lilacinum strain Tri-111-5KC747808.1100.00L212Trichoderma haraiaum strain Tri-111-5KC747808.1100.00L212Trichoderma haraiaum strain Tri-111-5KC747808.199.28SordarialesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesC161Salatinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMC21-0440ON426842.199.89LM11Palatinia eschscholtzii strain KUMC21-0440ON426842.199.89LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LM11Pestalotiopsis mangiferae	Saccharomycetes		5 1 1		
Sordariomycetes Diaporthales Glomerellales CP39 CV24 Diaporthe hongkongensis strain TZFH6 Collectorrichum fructicola isolate 1YN-2-2 Collectorrichum gloeosporioides isolate F16T11A MW341269.1 98.61 98.61 Glomerellales CV24 Collectorrichum gloeosporioides isolate F16T11A MW532972.1 99.29 LM410 Collectorrichum gloeosporioides strain LCM 955.S2.02 MN833334.1 99.82 LV411 Collectorrichum siamense isolate Ig621 MW767098.1 99.10 LV515 Collectorrichum siamense isolate MFLUCC14-0091 MG792806.1 99.80 Hypocreales C324 Gliocladium sp. isolate MFLUCC14-0091 MG792806.1 99.80 L3110 Hypocreales sp. strain 40 KX953324.1 99.41 C311 Purpureocillium lilacinum strain TMF1.655 OP268300.1 93.38 C212 Trichoderma harzianum isolate CTCCSJ-G-HB40441 KY764898.1 99.67 Sordariales CV11 Cercophora coprophila isolate KoRL1046128 MN341349.1 97.72 Xylariales CV11 Cercophora coprophila isolate KoRL1046128 MN341349.1 97.72 Xylariales CV11 Daldinia eschscholtzii strain KUMCC21-0440	Saccharomycetales	CM37	Meyerozyma caribbica isolate 11-1400	MG016004.1	98.64
Diaporthales CP39 Diaporthe kongkongensis strain TZFH6 MW341269.1 98.61 Glomerellales CV24 Colletotrichum fructioola isolate YN-2-2 OQ511327.1 99.65 Glomerellales CV24 Colletotrichum gloeosporioides isolate F16T11A MW352972.1 99.29 LM410 Colletotrichum gloeosporioides isolate F16T11A MW767098.1 99.82 LV411 Colletotrichum siamense isolate Ig621 MW767098.1 99.82 LV515 Colletotrichum siamense isolate P171-2 OM736124.1 99.29 LM513 Colletotrichum sp. isolate B0P2390 MH003433.1 98.20 L3110 Hypocreales sp. strain 40 KX953324.1 99.41 C311 Purpureocillium p1.isolate B0P2390 MH003433.1 98.32 C1212 Trichoderma haarainum stain Tr111-5 KC747808.1 100.00 L212 Trichoderma haarainum isolate CTCCSJ-G-HB40441 KY764898.1 99.67 Sordariales CV11 Cercophora coprophila isolate KORL046128 MN31349.1 97.72 Xylariales CL411 Daldinia eschscholtsii strain KUMCC21-0440 ON426842	Sordariomycetes				
GlomerellalesCV24 CL514Collectorrichum fructicola isolate 1YN-2 Cletotrichum gloeosporioides isolate P16711A MWS32972.199.65 SP.29LM410Collectorrichum gloeosporioides isolate P1671A MWS3334.1MWS32972.1 MWS3334.199.82 SP.29LV411Collectorrichum siamense isolate lg621 UV411MWS32972.1 MWS67098.199.10 MVS155LW515Collectorrichum siamense isolate lg621 Collectorrichum siamense isolate V1Y1-2 MW767098.1MW767098.1 MVS76098.199.10 MVS76098.1HypocrealesC324 Collectorrichum siamense isolate MEUCC14-0091 Hypocreales sp. strain 40 C311 C212MG792806.1 KV953324.199.41 MS20324.1C311 OphiostomatalesC316 C316 C316 C316 C316Sporothrix sp. FA1M6KC747808.1 KC747808.1100.00 MS338 C212 CC515-GHB40441KY764898.1 SordarialesCV11 Cercophora coprophila isolate KORLI046128 CM24 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 ON426842.1 ON426842.1 MV255346.1 MV255346.1 MV255346.1 MV255346.1 MV255346.1 MS319 MI111 Pestalotiopsis camelliae-sinensis NTUCC18-024 MT322040.1 MT322040.1 MT322040.1 MS9.9 MS9.9 CV515 D321dinia eschacholtzii strain KUMCC21-0440 ON426842.1 MV4258346.1 MH712230.1 MS9.9 MI111 Pestalotiopsis camelliae-sinensis NTUCC18-024 MH722304.1 MT3214.1 MT322040.1 MS9.9 MS9.9 MH712230.1 MS9.9 MH712230.1 MS9.9 MH712230.1 MS9.9 MH712230.1 MS9.9 MH712230.1 MS9.9 MH712230.1 MS9.7 MS9.7 MH712230.1 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 MS9.7 <b< td=""><td>Diaporthales</td><td>CP39</td><td>Diaporthe hongkongensis strain TZFH6</td><td>MW341269.1</td><td>98.61</td></b<>	Diaporthales	CP39	Diaporthe hongkongensis strain TZFH6	MW341269.1	98.61
CL514Colletotrichum gloessporioides isolate F16T1IAMWS32972.199.29LM410Colletotrichum gloessporioides strain LCM 955.S2.02MN833334.199.82LW411Colletotrichum siamense isolate Ig621MW767098.199.10LW515Colletotrichum siamense isolate Y1Y1-2OM736124.199.29LM513Colletotrichum sp. isolate MPLUCC14-0091MG792806.199.80HypocrealesC324Gliocladium sp. isolate BOP239OMH003433.198.20L3110Hypocreales sp. strain 40KX953324.199.41C311Purpureocillium Iliacinum strain TMF1.665OP266300.193.38C122Trichoderma hamzianum isolate CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KoRLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08LM11Pestalotiopsis mangiferae isolate MX0C-17-LBPEMH179308.198.90LM11Pestalotiopsis mangiferae isolate MX0C-17-LBPEMH179308.199.02LM11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LM11Pestalotiopsis rangiferae isolate MX0C617-LBPEMH179308.199.02LM11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LL13WXylaria sp. solate SWUF16-11.4 <td>Glomerellales</td> <td>CV24</td> <td>Colletotrichum fructicola isolate 1YN-2-2</td> <td>OQ511327.1</td> <td>99.65</td>	Glomerellales	CV24	Colletotrichum fructicola isolate 1YN-2-2	OQ511327.1	99.65
LM410Colletotrichum gloeosporioides strain LCM 955.52.02MN833334.199.82IV411Colletotrichum siamense isolate lg621MW767098.199.10IV515Colletotrichum siamense isolate YLY1-2OM736124.199.29LM513Colletotrichum sp. isolate MFLUCC14-0091MG792806.199.80HypocrealesC324Gliocladium sp. isolate BOP2390MH1003433.198.20L3110Hypocreales sp. strain 40KX953324.199.41C311Purpureocillium lilacinum strain Tri-111-5KC747808.1100.00L212Trichoderma haratum strain Tri-111-5KC747808.1100.00L212Trichoderma haratum strain Tri-111-5KC747808.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KORLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.90LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.199.02LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.199.02LM11Pestalotiopsis camelliae-sinensis NTUCC18-024MT622776.199.02LM13Xylaria sp. strain B7046MT735141.198.79L113WXylaria allantoida isolate SY00266MT735141.198.79L1		CL514	Colletotrichum gloeosporioides isolate F16T1IA	MW532972.1	99.29
IV411Colletotrichum siamense isolate [g621MW767098.199.10IV515Colletotrichum siamense isolate YLY1-2OM736124.199.29LM513Colletotrichum sp. isolate MFLUCC14-0091MG792806.199.80HypocrealesC324Gliocladium sp. isolate BOP2390MH003433.198.20L3110Hypocreales sp. strain 40KX953324.199.41C311Purprecoillium illicinum strain YMF1.665OP268300.193.38C212Trichoderma hamatum strain Tri-111-5KC747808.1100.00L212Trichoderma harzianum isolate CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporotrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KoRLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.89CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.90LL11Pestalotiopsis anagiferae isolate MX06-17-LBPEMH179308.198.90LL11Pestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LM11Pestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LM11Pestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LM11Pestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LM11Valaria sp. isolate SWUD16-11.4MT622776.199.02<		LM410	Colletotrichum gloeosporioides strain LCM 955.S2.02	MN833334.1	99.82
IV515 Collectorichum siamense isolate YIX1-2 OM736124.1 99.29 Hypocreales LM513 Collectorichum sp. isolate MFLUCC14-0091 MG792806.1 99.80 Hypocreales C324 Gliocladium sp. isolate MFLUCC14-0091 MG792806.1 99.80 L3110 Hypocreales sp. strain 40 KX953324.1 99.41 C311 Purpureocillium lilacinum strain YMF1.665 OP268300.1 93.38 C212 Trichoderma harzianum isolate CTCCSJ-G-HB40441 KY764898.1 99.67 Ophiostomatales C316 Sporothrix sp. FA1M6 LC768714.1 98.40 Sordariales CV11 Cercophora corpophila isolate KoRLI046128 MN341349.1 97.72 Xylariales CL411 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 99.08 CP13 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 98.93 CV515 Daldinia sp. isolate MFLUCC 20-0215 MW255346.1 98.90 LM11 Pestalotiopsis mangiferae isolate MX06-17-LBPE MH179308.1 98.90 99.02 LM11 Pestalotiopsis camelliae-sinensis NTUCC18-024 MT322040		LV411	Colletotrichum siamense isolate lg621	MW767098.1	99.10
LM513 Collectorichum sp. isolate MFLUCC14-0091 MG792806.1 99.80 Hypocreales C324 Gliocladium sp. isolate BOP2390 MH003433.1 98.20 L3110 Hypocreales sp. strain 40 KX953324.1 99.41 C311 Purpureocillium lilacinum strain TNi-165 OP268300.1 93.38 C212 Trichoderma haratum strain TNi-11-5 KC747808.1 100.00 L212 Trichoderma haratum strain TNi-111-5 KC747808.1 100.00 L212 Trichoderma haratum strain TNi-111-5 KC747808.1 100.00 Sordariales C316 Sporothrix sp. FA1M6 LC768714.1 98.40 Sordariales CV11 Cercophora coprophila isolate KRL046128 MN341349.1 97.72 Xylariales CL411 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 99.88 CV515 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 98.93 CV515 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 98.90 LM11 Pseudopestalotiopsis camelliae-sinensis NTUCC18-024 MT322040.1 98.91		LV515	Colletotrichum siamense isolate YLY1-2	OM736124.1	99.29
HypocrealesC324Gliocladium sp. isolate BOP2390MH003433.198.20L3110Hypocreales sp. strain 40KX953324.199.41C311Purpureocillium lilacinum strain YMF1.665OP268300.193.38C212Trichoderma harzianum isolate CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KoRLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia sp. isolate MFLUCC 20-0215MW255346.198.19L111Pestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91CL37Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria sp. Am-NB192LC505079.198.97L133WXylaria sp. Am-NB192LC505079.198.97L133WXylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungusV129		LM513	Colletotrichum sp. isolate MFLUCC14-0091	MG792806.1	99.80
L3110 Hypocreates sp. strain 40 K395324.1 99.41 C311 Purpureocillium lilacinum strain YMF1.665 OP268300.1 93.38 C212 Trichoderma hamatum strain Tri-111.5 KC747808.1 100.00 L212 Trichoderma harzianum isolate CTCCSJ-G-HB40441 KY764898.1 99.67 Ophiostomatales C316 Sporothrix sp. FA1M6 LC768714.1 98.40 Sordariales CV11 Cercophora coprophila isolate KoRLI046128 MN341349.1 97.72 Xylariales CL411 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 99.28 CM24 Daldinia eschscholtzii strain KUMCC21-0440 ON426842.1 99.08 CP13 Daldinia p. isolate MFLUCC 20-0215 MW255346.1 98.93 CV515 Daldinia sp. isolate MX06-17-LBPE MH179308.1 98.90 L111 Pseudopestalotiopsis camelliae-sinensis NTUCC18-024 MT322040.1 98.91 L111 Pseudopestalotiopsis camelliae-sinensis NTUCC18-024 MT322040.1 98.91 L111 Pseudopestalotiopsis camelliae-sinensis NTUCC18-024 MT322040.1 98.91	Hypocreales	C324	Gliocladium sp. isolate BOP2390	MH003433.1	98.20
C311Purpureocilium litacinum strain YMP1.665OP268300.193.38C212Trichoderma hamatum strain Tri-111-5KC747808.1100.00L212Trichoderma harzianum isolate CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KORLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia sp. isolate MFLUCC 20-0215MW255346.198.19LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LL11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91LL11Rylaria sp. strain F0146KU747562.190.32LM38Xylaria sp. strain F0146MT735141.198.87LL25Xylaria lalnoidea isolate XY00266MT735141.198.87LL25Xylaria egeensis strain BZ4MH712239.199.12LV12Unidentified fungusJunidentified fungus98.79TrichosporonalesL212Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		L3110	Hypocreales sp. strain 40	KX953324.1	99.41
C212Incloderma hamatum strain In-111-5RC/4/808.1100.00L212Trichoderma haratanum isola te CTCCSJ-G-HB40441KY764898.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KoRLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LL11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91CL37Xylaria sp. strain F0146KU747562.190.02LP410Xylaria sp. strain F0146KU747562.199.02LP410Xylaria sp. Am-NB192LC505079.198.97LL13WXylaria fejeensis strain BZ4MH712239.199.12LV12Unidentified fungusV1299.12V12V11Auricularia polytrichaLC176783.198.79TremellomycetesL232Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		C311	Purpureocillium lilacinum strain YMF1.665	OP268300.1	93.38
L112Introduction diractatuti mostate CTCCS-G-FiB404411KT/64698.199.67OphiostomatalesC316Sporothrix sp. FA1M6LC768714.198.40SordarialesCV11Cercophora coprophila isolate KoRLI046128MN341349.197.72XylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LL11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91CL37Xylaria sp. strain F0146KU747562.190.32LM38Xylaria sp. Am-NB192LC505079.198.97L113WXylaria allantoidea isolate XY00266MT735141.198.87LL25Xylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungusV1298.79TrichosporonalesL21676783.198.79TremellomycetesIV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.03		C212	Trichoderma namatum strain 1ri-111-5	KC/4/808.1	100.00
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SoldarlatesCV11Celtophola tophola tophola topholaMilotopolaXylarialesCL411Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.28CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.03CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia sp. isolate MFLUCC 20-0215MW255346.198.19LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LL11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91CL37Xylaria sp. strain F0146KU747562.190.32LM38Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria sp. am-NB192LC505079.198.97LL13WXylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungusUnidentified fungus99.12TremellomycetesAuricularialesLP11Auricularia polytrichaLC176783.198.79TremellomycetesIX12Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05	Corderialos	C310	Sporoinirix sp. FAIMO	LG/00/14.1 MN2/12/0 1	96.40
AyianalesChyfinDulainau Eschscholtzii strain KUMCC21-0440ON426842.199.08CM24Daldinia eschscholtzii strain KUMCC21-0440ON426842.199.08CP13Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93CV515Daldinia eschscholtzii strain KUMCC21-0440ON426842.198.93LM11Pestalotiopsis mangiferae isolate MX06-17-LBPEMH179308.198.90LL11Pseudopestalotiopsis camelliae-sinensis NTUCC18-024MT322040.198.91CL37Xylaria sp. strain F0146KU747562.190.32LM38Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria allantoidea isolate XY00266MT735141.198.87LL25Xylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungusUnidentified fungus98.79TremellomycetesTremellomycetesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05	Vulariales	CV11 CL411	Daldinia eschecholtzii strain KIMCC21 0440	ON/268/2 1	97.72
CH12+7Dutatina escisionation and NonCollocation of NonColling and NonColli	Aylallales	CL411 CM24	Daldinia eschecholtzii strain KUMCC21-0440	ON420842.1 ON426842.1	99.20
CV 15Datamin construction and metod for the construction of t		CP13	Daldinia eschscholtzii strain KUMCC21-0440	ON426842.1	99.00
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CL37 Xylaria sp. strain F0146 KU747562.1 90.32 LM38 Xylaria sp. isolate SWUF16-11.4 MT622776.1 99.02 LP410 Xylaria sp. Am-NB192 LC505079.1 98.97 LL13W Xylaria allantoidea isolate XY00266 MT735141.1 98.87 LL25 Xylaria feejeensis strain BZ4 MH712239.1 99.12 LV12 Unidentified fungus MH712239.1 99.12 Basidiomycota Agaricomycetes Auricularia polytricha LC176783.1 98.79 Tremellomycetes Trichosporonales L312 Apiotrichum dehoogii culture CBS:8686 KY101656.1 99.03 LV26P Cutaneotrichosporon debeurmannianum CBS 1896 NR 154752.1 99.05		LL11	Pseudopestalotiopsis camelliae-sinensis NTUCC18-024	MT322040.1	98.91
LM38Xylaria sp. isolate SWUF16-11.4MT622776.199.02LP410Xylaria sp. Am-NB192LC505079.198.97LL13WXylaria allantoidea isolate XY00266MT735141.198.87LL25Xylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungus99.1299.12BasidiomycotaAgaricomycetesAuricularialesLP11Auricularia polytrichaLC176783.198.79TremellomycetesTrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		CL37	Xylaria sp. strain F0146	KU747562.1	90.32
LP410Xylaria sp. Am-NB192LC505079.198.97LL13WXylaria allantoidea isolate XY00266MT735141.198.87LL25Xylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungus99.12BasidiomycotaAgaricomycetesAuricularia polytrichaLC176783.198.79TremellomycetesTrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		LM38	Xylaria sp. isolate SWUF16-11.4	MT622776.1	99.02
LL13WXylaria allantoidea isolate XY00266MT735141.198.87LL25Xylaria feejeensis strain BZ4MH712239.199.12LV12Unidentified fungus99.12BasidiomycotaAgaricomycetesAuricularialesLP11Auricularia polytrichaLC176783.198.79TremellomycetesTrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		LP410	Xylaria sp. Am-NB192	LC505079.1	98.97
LL25 LV12Xylaria feejeensis strain BZ4 Unidentified fungusMH712239.199.12Basidiomycota Agaricomycetes AuricularialesLP11 Auricularia polytrichaLC176783.198.79Tremellomycetes TrichosporonalesL312 LV26PApiotrichum dehoogii culture CBS:8686 Cutaneotrichosporon debeurmannianum CBS 1896KY101656.199.03		LL13W	Xylaria allantoidea isolate XY00266	MT735141.1	98.87
LV12Unidentified fungusBasidiomycota Agaricomycetes AuricularialesLP11Auricularia polytrichaLC176783.198.79Tremellomycetes TrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		LL25	Xylaria feejeensis strain BZ4	MH712239.1	99.12
Basidiomycota Agaricomycetes AuricularialesLP11Auricularia polytrichaLC176783.198.79Tremellomycetes TrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05		LV12	Unidentified fungus		
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AuricularialesLP11Auricularia polytrichaLC176783.198.79TremellomycetesTrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05	Agaricomycetes				
TremellomycetesDistributionTrichosporonalesL312LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05	Auriculariales	LP11	Auricularia polytricha	LC176783.1	98.79
TrichosporonalesL312Apiotrichum dehoogii culture CBS:8686KY101656.199.03LV26PCutaneotrichosporon debeurmannianum CBS 1896NR 154752.199.05	Tremellomycetes			201, 0, 00.1	, , ,
LV26P Cutaneotrichosporon debeurmannianum CBS 1896 NR 154752.1 99.05	Trichosporonales	L312	Apiotrichum dehoogii culture CBS:8686	KY101656.1	99.03
	*	LV26P	Cutaneotrichosporon debeurmannianum CBS 1896	NR 154752.1	99.05

Table S4	BLAST	analysis	results	of the	representative	fungal	morphotypes	associated	with	Gnetum	gnemon	Linn.	and	their
closest rel	atives.													

Таха			%	Relative	frequen	cy (% RI	F)		
	Conve	ntional	arming	Org	anic farr	ning	G	rand tot	al
	Leaf	Soil	Total	Leaf	Soil	Total	Leaf	Soil	Total
Mucoromycota									
Mucoromycetes									
Mucorales									
Mucor circinelloides L212a	0	070	0	6.06	1.61	0	3.03	0.85	
Ascomycota									
Dothideomycetes									
Botryosphaeriales									
Guignardia sp. LL13B	16.46	0	11.61	15.38	0	11.29	15.88	0	11.44
Pleosporales									
Kalmusia araucariae C422	0	3.03	0.89	0	0	0	0	1.52	0.42
Leptosphaeria sp. L325	0	0	0	0	3.03	0.81	0	1.52	0.42
Pyrenochaetopsis microspora L311	0	0	0	0	3.03	0.81	0	1.52	0.42
Eurotiomycetes									
Eurotiales									
Aspergillus aculeatus C213	0	9.09	2.68	0	0	0	0	4.55	1.27
Aspergillus flavus C211, C411	0	15.15	4.46	0	6.06	1.61	0	10.50	2.94
Aspergillus oryzae C322	0	6.06	1.79	0	3.03	0.81	0	4.65	1.30
Aspergillus sydowii C221	0	3.03	0.89	0	0	0	0	1.52	0.42
Aspergillus unguis LL37	0	3.03	0.89	0	3.03	0.81	0	3.03	0.85
Penicillium chrysogenum C313	0	9.09	2.68	0	18.18	4.84	0	13.64	3.81
Penicillium griseofulvum C314	0	6.06	1.79	0	9.09	2.42	0	7.58	2.12
Penicillium janthinellum C325	0	3.03	0.89	0	0	0	0	1.52	0.42
Penicillium striatisporum L319	0	3.03	0.89	0	3.03	0.81	0	3.03	0.85
Talaromyces aculeatus C312, L318	0	3.03	0.89	0	3.03	0.81	0	3.03	0.85
Talaromyces pinophilus C323	0	3.03	0.89	0	0	0	0	1.52	0.42
Saccharomycetes									
Saccharomycetales									
Meyerozyma caribbica CM37	3.80	0	2.68	1.10	0	0.81	2.35	0	1.69
Sordariomycetes									
Diaporthales									
Diaporthe hongkongensis CP39	5.06	0	3.57	5.49	0	5.65	5.29	0	4.66
Glomerellales									
Colletotrichum fructicola CV24	10.13	0	7.14	9.89	0	7.26	10.00	0	7.20
Colletotrichum gloeosporioides LM410, CM19	22.78	0	16.07	20.88	0	15.32	21.76	0	15.68
Colletotrichum siamense LV411, LV515	0	0	0	3.30	0	2.42	1.76	0	1.27
Colletotrichum sp. LM513	5.06	0	3.57	2.20	0	1.61	3.58	0	2.54
Hypocreales									
Gliocladium sp. C324, L222	0	3.03	0.89	0	12.12	3.23	0	7.58	2.12
Hypocreales sp. L3110	0	0	0	0	3.03	0.81	0	1.52	0.42
Purpureocillium sp. C311	0	9.09	2.68	0	6.06	1.61	0	7.58	2.12
Trichoderma hamatum C212	0	9.09	2.68	0	6.06	1.61	0	7.66	2.14
Trichoderma harzianum L212	0	6.06	1.78	0	9.09	2.42	0	7.49	2.10
Ophiostomatales	-			-		-	-		-
Sporothrix sp. C316	0	3.03	0.89	0	0	0	0	1.52	0.42
Sordariales									
Cercophora coprophila CV11	2.17	0	0.89	0	0	0	0.59	0	0.42

 Table S5
 Relative frequency (% RF) and diversity indices of fungi associated with Gnetum gnemon Linn.

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Table S5 Continued ...

Taxa% Relative frequency (% RF)									
	Conve	ntional	farming	Orga	nic far	ming	Gı	and to	tal
	Leaf	Soil	Total	Leaf	Soil	Total	Leaf	Soil	Total
Xylariales									
Daldinia sp. CV515	5.06	0	3.57	3.30	0	2.42	4.12	0	2.97
Daldinia eschscholtzii CL411, CM24, CP13, LM12	13.92	0	9.82	15.38	0	11.29	14.71	0	10.59
Pestalotiopsis mangiferae LM11	10.13	0	7.14	9.89	0	7.26	10.00	0	7.20
Pseudopestalotiopsis camelliae-sinensis LL11	3.80	0	2.68	2.20	0	1.61	2.94	0	2.12
Xylaria sp. CL37	2.53	0	1.79	3.30	0	2.42	2.94	0	2.12
Xylaria sp. LM38	0	0	0	1.10	0	0.81	0.59	0	0.42
Xylaria sp. LP410	0	0	0	1.10	0	0.81	0.59	0	0.42
Xylaria allantoidea LL13W	0	0	0	1.10	0	0.81	0.59	0	0.42
Xylaria feejeensis LL25	0	0	0	2.20	0	1.61	1.18	0	0.85
Unidentified fungus IV12	1.27	0	0.89	1.10	0	0.81	1.18	0	0.85
Basidiomycota									
Agaricomycetes									
Auriculariales									
Auricularia polytricha LP11	0	0	0	1.10	0	0.81	0.59	0	0.42
Tremellomycetes									
Trichosporonales									
Apiotrichum dehoogii L312	0	3.03	0.89	0	6.06	1.61	0	4.55	1.27
Cutaneotrichosporon debeurmannianum LV26P	0	0	0	1.10	0	0.81	0.59	0	0.42
Total %RF	100	100	100	100	100	100	100	100	100
Number of detected species	13	18	31	17	16	33	20	22	42
Menhinick Index (Dmn)	1.46	2.79	2.74 ^a	1.78	2.44	2.76 ^a	1.53	2.46	2.59
Shannon (H') Index	1.77	1.79	2.47 ^b	1.89	2.09	2.49 ^b	1.92	2.07	2.56

The same superscript letter indicates no significant difference (p > 0.05) between individual parameter from conventional and organic farming.