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Biodiversity of arbuscular mycorrhizal fungi in the hot-dry valley of the Jinsha River, southwest China

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ABSTRACT

The diversity and community structure of arbuscular mycorrhizal fungi (AMF) in two sites (Pudu and Xiao Rivers) with different vegetation in the hot-dry valley of Jinsha River, southwest China, were investigated. Forty-three morphospecies of AMF were identified. Among them, 28 were in the genus *Glomus*, 7 in *Acaulospora*, 4 in *Scutellospora*, 2 in *Entrophospora* and 2 in *Gigaspora*. The most common and frequent genus was *Glomus*, and several species of *Glomus* and *Gigaspora* were the most common and frequent among the 43 species present in this hot-dry ecosystem. Although Sorenson's coefficient ($C_s = 0.83$) revealed considerable overlap in AM fungal species composition, AMF community structure varied considerably between the two sites. Non-random associations between AMF and host plants were commonly observed in this study and suggest some degree of host preference at the species level. AMF spore density (SD) was positively correlated with species richness (SR), and both were differed significantly between the undisturbed Pudu River site and the disturbed Xiao River site. We suggest that the hot-dry valley of Jinsha River appeared to harbor a high diversity of AMF with an uneven distribution, and that natural disturbance (mud-rock flow and landslides) is important in determining the diversity, density, and distribution of AMF.

1. Introduction

Arbuscular mycorrhizal fungi (AMF) are a major component of rhizosphere soils, and they can form mutualistic associations with the fine roots of approximately 80% of all terrestrial plants. In this symbiosis, the host plant provides the fungus with soluble carbon sources, at the same time the fungus enhances the uptake by plants of certain nutrients, particularly phosphate (Jayachandran and Shetty, 2003), defends plants against pathogens (Rabie, 1998), alleviates environmental stresses on plants (Ruiz-Lozano et al., 2001), improves plant tolerance to drought and polluted environments (Augé, 2001; Vivas et al., 2003), and accelerates plant establishment (Caravaca et al., 2003). At present, AMF are considered as an important component in the restoration and reestablishment of the vegetation in fragile or degraded ecosystems, and in the maintenance of plant biodiversity and ecosystem functioning (van der Heijden et al., 1998; Dhillion and Gardsjord, 2004). The successful restoration and conservation of biodiversity of AMF in natural vegetation has been a topic of long-standing interest to biologists (Requena et al., 2001).

AMF are commonly associated with plants in arid and semiarid regions, and various studies have characterized the distribution and abundance of AMF in these environments (Diallo et al., 1999; Stutz et al., 2000; Pande and Tarafdar, 2004). Previous studies revealed that in arid and semiarid habitat AMF spore production was mainly by *Glomus* species, particularly by small-spored species, and that high numbers of morphological

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species with a patchy distribution were recorded. Furthermore, AMF had been reported to play an important role in the reestablishment of the vegetation in disturbed arid ecosystems (Azcón-Aguilar et al., 2003; Caravaca et al., 2003). It had been demonstrated that establishment of *Retama sphaerocarpa* L. seedlings on a degraded semiarid Mediterranean area was promoted by mycorrhizal inoculation (Del Mar Alguacil et al., 2004), and that indigenous AMF inoculation was more effective than allochthonous AMF (Requena et al., 2001). Inoculation with native AMF had also been reported in promoting the growth of Wyoming big sagebrush (*Artemisia tridentate* ssp. *wyomingensis*) in severely disturbed soil on a mine reclamation site (Frost et al., 2001). This suggested that the diversity and community structure of AMF were important both in sustaining the stability of the plant community and reestablishing vegetation in disturbed arid and semi-arid ecosystems.

The Jinsha River is the upper reach of Yangtze River. The hot-dry valley of the Jinsha River (100°30′E–103°30′, 25°40′N–28°15′), with an elevation <1500 m, winds through Yunnan and Sichuan provinces, southwest China. In this valley, climate is hot and arid with the mean annual temperature ranging from 20 to 27 °C. The annual precipitation is 600–800 mm and distributed unevenly throughout the year: rainfall between June and October accounts for 90% of all the precipitation. The potential evaporation is approximately three to six times as great as the precipitation.

The vegetation is characterized by grasses and shrubs with scattered trees, and is referred to locally as a special type of semi-savanna or savanna of valley-type (Jin and Ou, 2000; Jin, 2002). The most common plant species in the hot-dry valley included *Andropogon yunnanensis*, *Barleria cristata*, *Bothriochloa pertusa*, *Calotropis gigantean*, *Heteropogon contortus*, *Tridax procumbens* and *Ziziphus yunnanensis*.

Arbuscular mycorrhizas (AM) have been considered to be important functional components in this hot-dry valley (Li et al., 2004), but the literature concerning composition and structure of AMF communities in this unique ecosystem is limited (Stutz et al., 2000). The present study was undertaken to determine (1) the biodiversity of AMF in the hot-dry valley, (2) whether similarity existed in the general AMF community structure in sites with different plant communities, (3) whether some degree of host preference existed among AMF in the hot-dry valley and (4) what ecological factors or processes might affect AMF performance in this special ecosystem.

2. Materials and methods

2.1. Sampling sites

Soil samples were collected in two sites with different environments: Pudu River (PR) and Xiao River (XR). PR is located in Luquan County (102°13′E–102°57′, 25°24′N–26°22′), and 43% of the county remains vegetated. XR is situated in Dongchuan County (102°47′E–103°18′, 25°47′N–26°32′). The frequency of natural disturbance is higher in XR due to frequent mud-rock flows and landslides which arise from the unique geologic structure of the area. Interference from human activities such as deforestation, overgrazing, and burning have also accelerated soil degradation and desertification in XR. The vegetation in XR is scattered, and only 20.6% of the area is vegetated. The plant community composition differs strikingly in the two sites, and the only seven plant species common to the two sites are: *A. yunnanensis* (Gramineae), *B. cristata* (Acanthaceae), *Chenopodium ambrosioides* (Polygonaceae), *Cymbopogon distans* (Gramineae), *Rumex hastatus* (Polygonaceae), *Sida szechuensis* (Malvaceae), and *Siegesbeckia orientalis* (Asteraceae).

2.2. Sample collection and treatments

Two plant communities were chosen for sampling in PR and in XR. In total, 56 plant species were sampled from PR and 35 plant species from XR, all during the dry season of 2004.

Approximately 500 g of rhizosphere soil from each plant was collected at a depth of 5–30 cm, air-dried for 2 weeks, placed in sealed plastic bags and stored at 4 °C for up to two months until samples could be treated. Roots connected to each sampled plant were also collected to quantify their arbuscular mycorrhizal status. It was found that 95% of sampled plant species were typically arbuscular mycorrhizal, the exceptions being *C. ambrosioides*, *S. orientalis* at PR and *Abutilon indicum* at XR, and these will not be discussed in this paper.

Spores from the rhizosphere soil samples were isolated through the wet-sieving method described by An et al. (1990). For each soil sample, 20 g soil was independently suspended in 150 ml water, and stirred with a magnetic stirrer for 10 min. We used 76, 105, 150 and 900 μm sieves to collect the spores. The spores on each sieve were filtered onto a filter paper, and placed in a 9 cm Petri dish for examination under a binocular stereomicroscope (7–45×). The intact healthy AMF spores were sorted into groups and counted.

Each spore type was mounted sequentially in polyvinyl lactic acid (PVA) and PVA mixed 1:1 (v/v) with Meltzer's reagent (Morton, 1988) for identification. The identification was based on morphological descriptions published originally and provided by the international collection of vesicular and arbuscular mycorrhizal fungi (http://invam.caf.wvu.edu). AMF species were identified using Olympus CX31 and those with typical taxonomic characters were imaged with Olympus BX51 digital camera. The fixed slides and images were stored as reference collections in our laboratory.

2.3. Statistical analyses

Ecological measures of diversity used to describe the structure of AMF communities included spore density, species richness, relative abundance, isolation frequency, Shannon–Wiener index of diversity, evenness, Simpson's index of dominance, and Sorenson's coefficient (Simpson, 1949; Franke-Snyder et al., 2001; Zhang et al., 2004) (Table 1). Spore density reflected the biomass of AMF species, at least to some extent. Relative abundance was defined as the percentage of spore numbers of a species, which indicated the different sporulation ability of different species of AMF. Isolation frequency was defined as the percentage of soil samples in which a species occurred, which revealed the extent of distribution of a given AMF species in an ecosystem. We determined the dominant AMF species according to relative abundance (RA > 3%) and isolation frequency (IF > 40%). Diversity within AMF community, evenness and the degree of disturbance were reflected by

Table 1 – Diversity measures used to describe AMF communities

Spore density (SD)	The number of spores in 100 g soil
Species richness (SR)	The number of identified AMF species per soil sample
Relative abundance (RA)	$RA = \frac{\text{spore numbers of a species (genus)}}{\text{the total number of identified spore samples}} \times 100\%$
Isolation frequency (IF)	$IF = \frac{\text{the number of soil samples where a species (genus) occurred}}{\text{the total number of soil samples}} \times 100\%$
Shannon–Wiener index of diversity (H')	$H' = -\sum P_i \ln P_i$
Evenness (E)	$E = \frac{H'}{H'_{max}}$
Simpson's index of dominance (D)	$D = \sum[n_i(n_i - 1)/N(N - 1)]$
Sorenson's coefficient (C_s)	$C_s = 2j/(a + b)$

P_i is the relative abundance of each identified species per sampling site and calculated by the following formula: $P_i = n_i/N$, where n_i is the spore numbers of a species and N is the total number of identified spore samples. H'_{max} is the maximal H' and calculated by the following formula: $H' = \ln S$, where S is the total number of identified species per sampling site. a or b was the total number of identified species per sampling site and j was the number of identified species common to both sites.

Shannon–Wiener index of diversity. Sorenson's coefficient was used to compare similarity existing in the general structure of AMF communities and plant communities between the two sites. Since only a few spores of one species were isolated, or the collected spores lacked distinguishable, fine taxonomic characters, these spores could not be identified to species level and were not considered in the statistic analyses, except as part of total spore density.

All data were statistically analyzed of variance (ANOVA) using SPSS (version 11.0). Differences in spore density and species richness between sites with different vegetation were tested using one-way ANOVA. The Pearson correlation coefficient was employed to determine the relationships between spore density and species richness, relative abundance and isolation frequency. In the process of analysis, logarithm transformation of spore density was used to satisfy homogeneity of variance assumptions and normal distribution.

Species accumulation curves were employed to evaluate whether the soil samples collected were satisfactorily representing AMF community structures in the two sites. Using Sigmaplot (version 9.0), we constructed species accumulation curves using the following regression model: $y = a \ln x + b$ (Stout and Vandermeer, 1975), where y is the number of identified species of AMF per sampling site, x the number of soil samples and a is the slope parameter.

3. Results and discussion

3.1. The diversity of arbuscular mycorrhizal fungi

A total of 20,144 spores and sporocarps of AMF were wet-sieved from the 91 rhizosphere soil samples collected, from which 43 AMF species were identified: 35 from PR and 37 from XR (Table 2 and Fig. 1). Seven of these species were in the genus *Acaulospora*, 2 in *Entrophospora*, 28 in *Glomus*, 2 in *Gigaspora* and 4 in *Scutellospora*. In the identified AMF species, 29 AMF species encountered on both sites, 6 species found only in PR (*G. clavispora*, *G. macrocarpum*, *Glomus* sp.2, *Scu. heterogama*, *Scu. verrucosa*, *Scutellospora* sp.1) and 8 species found only in XR (*A. bireticulata*, *G. albidum*, *G. spurcum*, *G. tortuosum*, *G. viscosum*, *Glomus* sp.5, *Glomus* sp.6, *Glomus* sp.7).

The diversity of AMF observed in this hot-dry valley was greater than that (27 AMF species) in the tropical rain forest of Xishuangbanna, southwest China (Zhao et al., 2003) and in arid regions (21 AMF species) of southwestern North America and Namibia, Africa (Stutz et al., 2000). The arid and hot habitat (Stutz and Morton, 1996; Stutz et al., 2000) and the preference of different host plants (He et al., 2002) could be the reasons for relative higher diversity of AMF.

Based on relative abundance and isolation frequency, the 6 dominant species in PR were *G. clariodeum*, *G. clarum*, *G. fasciculatum*, *G. verruculosum*, *Glomus* sp.2 and *Gigaspora* sp.1, whereas there were only two dominant species *G. intraradices* and *G. clariodeum* in XR (Table 2). It was found that there is a significant positive correlation between relative abundance and isolation frequency of AMF species in both sites ($r = 0.567$, $p < 0.001$ and $r = 0.629$, $p < 0.001$, respectively), and it appeared that species producing more spores usually had a wide distribution, while species with small geographic ranges usually produced fewer spores. However, a few AMF species, such as *A. tuberculata* (0.98% of RA, 46.43% of IF), *G. geosporum* (0.97%, 41.07%), *Glomus* sp.1 (1.86%, 57.14%) in PR and *G. clarum* (1.31%, 42.86%), *G. verruculosum* (2.79%, 42.86%) in XR, had low relative abundances but were widely distributed (relative high isolation frequency) (Table 2). In contrast, *G. mosseae* (3.03%, 22.86%), *Glomus* sp.5 (3.28%, 8.57%) in XR were not present at high isolation frequency, but they were dominant in sporulation compared with other species in that site (Table 2). Thus, it is important to considering the spreading and sporulation ability of AMF in determining its dominance in a community.

Glomus was the dominant genus, followed by *Acaulospora* and *Gigaspora* in both sites. The isolation frequency of *Gigaspora* was higher, but its relative abundance was low, and the same trend occurred in *Scutellospora* in PR. It is possible that spores of *Gigaspora* and *Scutellospora* took longer time to form and mature (Hepper, 1984) and that members of the Gigasporaceae typically established an extensive mycelium in soil and produced fewer spores than members of the Acaulosporaceae and Glomaceae (Hart and Reader, 2002; Piotrowski et al., 2004).

The fact that >80% of the total number of spores came from *Glomus* in the two sites was in agreement with the dominance of small spores in *Glomus* in arid regions. In our study, the diameter of most spores (79% in PR, 62% in XR), including those of *Gigaspora* and *Scutellospora* which usually produced relatively large spores, was <105 μm. This predominance of small AMF spores in the hot-dry valley was

Table 2 – Relative abundances (RA) and isolation frequency (IF) of arbuscular mycorrhizal fungi

Sp. no.	Abuscular mycorrhizal fungi	Pudu River (PR)			Xiao River (XR)		
		Spore number	RA (%)	IF (%)	Spore number	RA (%)	IF (%)
	Acaulospora	**240**	**3.38**	**71.43**	**129**	**5.29**	**71.43**
1	*A. bireticulata* Rothwell & Trappe	–	–	–	9	0.37	17.14
2	*A. delicata* Walker, Pfeiffer & Bloss	27	0.38	16.07	48	1.97	14.29
3	*A. denticulate* Sieverding &Toro	30	0.42	23.21	9	0.37	14.29
4	*A. mellea* Spain & Schenck	3	0.04	1.79	2	0.08	5.71
5	*A. scrobiculata* Trappe	83	1.17	26.79	31	1.27	20.00
6	*A. spinosa* Walker & Trappe	12	0.17	14.29	2	0.08	5.71
7	*A. tuberculata* Janos & Trappe	70	0.98	46.43	7	0.29	8.57
	Acaulospora spp.	15	0.21	–	21	0.86	–
	Entrophospora	**2**	**0.03**	**3.57**	**4**	**0.16**	**11.43**
8	*E. infrequens* (Hall) Ames & Schneider	1	0.01	1.79	3	0.12	8.57
9	*E. kentinensis* Wu & Liu	1	0.01	1.79	1	0.04	2.86
	Glomus	**5860**	**82.44**	**100.00**	**2185**	**89.55**	**100.00**
10	*G. aggregatum* Schenck & Smith	26	0.37	12.50	24	0.98	22.86
11	*G. albidum* Walker & Rhodes	–	–	–	5	0.20	2.86
12	*G. clariodeum* Schenck & Smith	1612	22.68	94.64	106	4.34	68.57
13	*G. clarum* Nicolson & Schenck	363	5.11	83.93	32	1.31	42.86
14	*G. clavispora* (Trappe) Almeida & Schenck	11	0.15	3.57	–	–	–
15	*G. constrictum* Trappe	58	0.82	35.71	12	0.49	14.29
16	*G. etunicatum* Becker & Gerd.	1	0.01	1.79	11	0.45	14.29
17	*G. fasciculatum* (Thaxter) Gerd. & Trappe	543	7.64	53.57	1	0.04	2.86
18	*G. geosporum* (Nicol. & Gerd.) Walker	69	0.97	41.07	35	1.43	34.29
19	*G. intraradices* Schenck & Smith	9	0.13	7.14	83	3.40	60.00
20	*G. macrocarpum* Tul. & Tul.	1	0.01	1.79	–	–	–
21	*G. monosporum* Gerd. & Trappe	39	0.55	16.07	18	0.74	17.14
22	*G. mosseae* (Nicol. & Gerd.) Gerd. & Trappe	14	0.20	16.07	74	3.03	22.86
23	*G. multiforum* Blaszkowski & Tadych	81	1.14	17.86	1	0.04	2.86
24	*G. pansihalos* Berch & Koske	20	0.28	12.50	25	1.02	14.29
25	*G. reticulatum* Bhattacharjee & Mukerji	29	0.41	26.79	5	0.20	11.43
26	*G. sinuosa* (Gerd. & Bakshi) Almeida & Schenck	74	1.04	35.71	20	0.82	22.86
27	*G. spurcum* Pfeiffer, Walker & Bloss	–	–	–	23	0.94	28.57
28	*G. tortuosum* Schenck & Smith	–	–	–	5	0.20	2.86
29	*G. verruculosum* Blaszkowski	404	5.68	80.36	68	2.79	42.86
30	*G. viscosum* Nicolson	–	–	–	29	1.19	31.43
31	*Glomus* sp.1	132	1.86	57.14	11	0.45	11.43
32	*Glomus* sp.2	216	3.04	41.07	–	–	–
33	*Glomus* sp.3	40	0.56	7.14	26	1.07	17.14
34	*Glomus* sp.4	137	1.93	37.50	27	1.11	20.00
35	*Glomus* sp.5	–	–	–	80	3.28	8.57
36	*Glomus* sp.6	–	–	–	73	2.99	22.86
37	*Glomus* sp.7	–	–	–	141	5.78	28.57
	Glomus spp.	1981	27.87	–	1250	51.23	–
	Gigaspora	**897**	**12.62**	**91.07**	**111**	**4.55**	**60.00**
38	*Gi. gigantean* (Nicol. & Gerd.) Gerd. & Trappe	174	2.45	62.50	28	1.15	34.29
39	*Gigaspora* sp.1	236	3.32	66.07	7	0.29	11.43
	Gigaspora spp.	487	6.85	–	76	3.11	
	Scutellospora	**109**	**1.53**	**48.21**	**11**	**0.45**	**5.71**
40	*Scu. dipurpurescens* Morton & Koske	32	0.45	10.71	10	0.41	2.86
41	*Scu. heterogama* Walker & Sanders	22	0.31	17.86	–	–	–
42	*Scu. verrucosa* Walker & Sanders	4	0.06	3.57	–	–	–
43	*Scutellospora* sp.1	4	0.06	1.79	–	–	–
	Scutellospora spp.	47	0.66	–	1	0.04	–
Total: AMF = 43 species		**7108**	**100.00**		**2440**	**100.00**	

consistent with previous studies (Li et al., 2004; Li and Zhao, 2005). Furthermore, it has been demonstrated elsewhere that species of *Glomus* are the most common species in soils from the arid or semiarid zones of southwestern North America and Namibia in Africa (Stutz et al., 2000), Rajasthan (Pande and Tarafdar, 2004) and Segegal (Diallo et al., 1999), where water and nutrients are the main constraints even in undisturbed soil. Stutz et al. (2000) reported that small-spored species of *Glomus* that produce greater numbers of spores are selected in arid habitats. It may be that

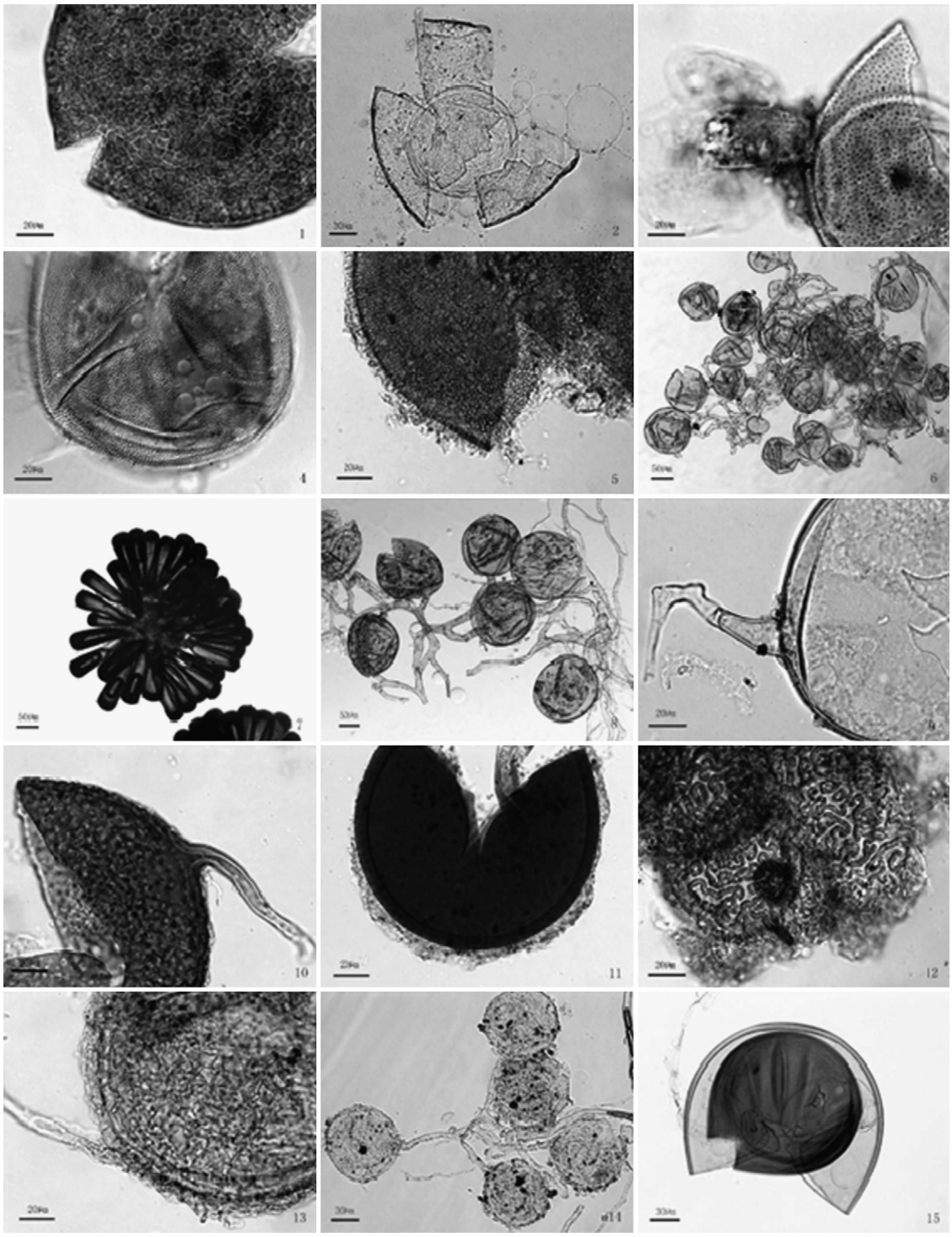

Fig. 1 – Some arbuscular mycorrhizal fungi isolated from hot-dry valley of the Jinsha River, China. (1) *Acaulospora bireticulata*, the double reticulum on outer wall; (2) *Acaulospora delicata*, a crushed spore; (3) *Acaulospora scrobiculata*, the pitted spore wall and soporiferous saccule; (4) *Acaulospora tuberculata* in Melzer's reagent, showing tips on surface of spore wall; (5) *Entrophospora infrequens*, the projections on the outer surface of the inner wall; (6) *Glomus aggregatum* spores in a loose cluster; (7) *Glomus clavispora* in cross-section, with clavated spores formed radially from central plexus of sporocarp; (8) *Glomus intraradices*, showing the multiple walls; (9) *Glomus mosseae*, the funnel-like subtending hypha; (10) *Glomus multiforum*, the funnel-shaped subtending hypha with a curved septum and pits in spore wall; (11) *Glomus pansihalos*, showing the expanded wall; (12) *Glomus sinuosa*, sporocarp showing a peridium composed of thick-walled hyphae covered the spores; (13) *Glomus tortuosum*, spore covered by mantle of convoluted hyphae; (14) *Glomus viscosum* spores in cluster; (15) *Scutellospora dipurpruescens* in Melzer's reagent, showing the germination shield.

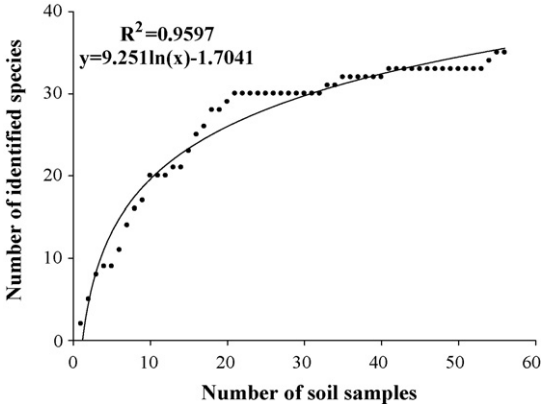

Fig. 2 – AMF species accumulation curve for the Pudu River (PR) site.

small-spored species require less time to produce spores (Hepper, 1984) and are therefore more adaptive in adjusting patterns of sporulation to varied environmental conditions (Stutz et al., 2000). This could be a key to surviving in arid and hot ecosystems.

3.2. *Species accumulation curves of AMF*

Species accumulation curves were employed to estimate the adequacy of the number of soil samples taken from the hot-dry valley. We mapped species accumulation curves of AMF in PR and XR (Figs. 2 and 3), and the strong fit of the actual curves to the model demonstrated that the number of soil sample collected in PR and XR accurately reflected the general structure of the AMF communities in the two plant communities of the hot-dry valley.

3.3. *Spore density, species richness and the distribution of arbuscular mycorrhizal fungi*

Spore density, species richness and the distribution of AMF species in the rhizosphere soil of the 91 plant species are presented in Tables 3 and 4. The average spore density of AMF was significantly higher in PR than in XR. In PR the mean density was 1423 spores/100 g dry soil (range of 85–5315), while the mean density in XR was only 601 spores/100 g dry soil (range of 15–2805). The average species richness showed the same tendency: mean of 9.8 species (range of 2–16) in PR and mean of 7.1 species (range of 1–14) in XR. These results suggest that the distribution of spores was relatively uneven than that of AMF species.

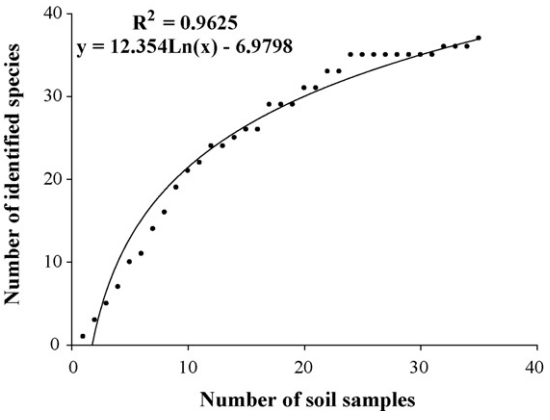

Fig. 3 – AMF species accumulation curve for the Xiao River (XR) site.

Correlation analysis demonstrated that spore density of AMF was positively significantly correlated with species richness in both sites ($r = 0.558$, $p < 0.001$ and $r = 0.683$, $p < 0.001$, respectively). Compared with spore density and species richness found in other ecosystems (Mohammad et al., 2003; Ferrol et al., 2004; Zhang et al., 2004), both in present study were relative high, which was consistent with previous studies in other sites of the arid and hot valley (Li et al., 2004; Li and Zhao, 2005). Rosendahl and Stukenbrock (2004) using LSU rDNA sequences studied the community structure of AMF and found that non-sporulating AM fungal species might be dominant in undisturbed soils, and that moderate disturbance of soil, such as mechanical mixing of soil, could favor the spread and growth of fast-growing sporulating AMF. Therefore, due to selection pressure of the hot and arid climate and the interference by human activities in hot-dry valley, it is possible that these disturbed systems favored sporulating species. Such fast-growing, sporulating species with small spores might easily spread and hence have a better chance to survive.

Though both spore density and species richness of AMF in the hot-dry valley were higher compared with other ecosystems, one-way ANOVA showed that both differed significantly between different plant communities of the valley ($df = 1$, $F = 19.945$, $p < 0.001$ and $df = 1$, $F = 14.159$, $p < 0.001$, respectively). There were also greater diversity, evenness, and dominance indices of AMF in PR than in XR (Table 5). The community diversity was higher and the distribution of AMF species was more uniform in PR ($E = 0.52$) than in XR ($E = 0.48$). In comparing the general AMF community structure in the two plant communities, we found that Sorenson's coefficient of AMF community was 0.81, and the coefficient of plant community was only 0.15. Thus, though plant community composition differed significantly in the two sites, there was a high degree of overlap in fungal species composition between the undisturbed (PR) and disturbed (XR) sites. Furthermore, it was indicated that many of the AMF species identified in our study had broad dispersal and that the environment conditions seemed to be more influential in determining the structure of AMF communities than the vegetation. Similar results were observed by Zhang et al. (2004) who found that there was high AM fungus composition similarity ($C_s = 0.71$) between the deforested land and natural forest, and that the deforestation did not largely influence the AMF species composition in the subtropical region of Dujangyan, southwest China.

Previous studies have demonstrated that the density of spores, species richness and the lengths of extraradical mycelium of AMF can be reduced by soil disturbance (Boddington and Dodd, 2000), and that substrates on eroded sites have significantly lower AM fungal propagule densities (Wu et al., 2002). Ingleby et al. (1997) reported that AMF spores are concentrated in the upper 10 cm of soil, and He et al. (2002)

Table 3 – Distribution, spore density (SD) and species richness (SR) of AMF in the Pudu River (PR) site

Host plant	Arbuscular mycorrhizal fungi	SD	SR
Acanthaceae			
Barleria cristata	10 12 13 15 17 19 25 26 29 31 34 38 41	3675	13
Strobilanthes cusia	12 13 18 25 29 38	190	6
Adiantaceae			
Adiantum diaphanum	3 7 12 13 15 17 26 29 31 34 38 39	4860	12
Amaranthacae			
Achyranthes aspera	3 4 5 12 13 29	710	6
Asclepiadaceae			
Cryptolepis buchananii	3 7 12 13 15 17 26 29 31 34	1190	10
Aspleniaceae			
Sinephropteris delavayi	12 13 23 26 29 31 32 39	1855	8
Asteraceae			
Eupatorium adenophorum	12 13 15 17 21 26 29 31 32 38 39	3200	11
Laggera alata	10 12 13 17 29 31 32 38 39	680	9
Nouelia insignis	2 12 13 17 31 32 38 39	2345	8
Siegesbeckia orientalis	12 13 17 18 32 34 38 39 41	475	9
Bignoniaceae			
Incarvillea arguta	2 19 39	85	3
Chenopodiaceae			
Chenopodium ambrosioides	7 9 12 13 17 26 38 39	475	8
Coriariaceae			
Coriaria sinica	3 5 6 7 10 12 13 21 23 24 29 34 38	370	13
Cruciferae			
Sophora davidii	25 29	140	2
Ebenaceae			
Diospyros mollifolia	5 7 12 13 20 21 22 23 25 29 38 41	5315	12
Equisetaceae			
Equisetum diffusum	3 5 7 12 13 29 34	550	7
Euphorbiaceae			
Euphorbia antiquorum	2 5 7 10 12 13 16 17 23 24 25 26 32 34 38 41	3535	16
Glochidion puberum	7 12 17 25 29 32	3925	6
Gramineae			
Andropogon yunnanensis	7 12 13	405	3
Cymbopogon distans	5 6 12 13 15 17 18 21 29 31 38 39	1480	12
Neyraudia reynaudiana	5 7 12 13 26 29 31 32 39	595	9
Setaria plicata	3 5 12 13 18 26 38 39	465	8
Tripogon bromoides	3 5 6 7 12 13 15 17 18 21 29 31 34 38 39 42	2155	16
Labiatae			
Elsholtzia rugulosa	12 17 18 22 29 31 38 39 41	2205	9
Leonurus heterophyllus	3 6 12 18 25 29 31 34 38 39	535	10
Rabdosia sculponeata	2 5 7 12 13 15 22 26 29 31 32 38 39 41	1350	14
Leguminosae			
Dalbergia yunnanensis	8 12 13 15 18 26 29 31 33 38 39	1040	11
Flemingia strobilifera	7 12 17 18 24 29 32 38 39 40	585	8
Linaceae			
Reinwardtia indica	5 7 12 13 15 17 18 29 31 38 41	985	11
Malvaceae			
Sida szechuensis	12 14 15 18 22 23 29 31 32 34 39	585	11
Urena procumbens	7 12 13 15 17 18 23 24 29 32 34 38 39	2105	13
Moraceae			
Ficus tikoua	6 12 13 21 29 34 38 39	245	8
Oleaceae			
Fraxinus malacophylla	7 13 17 21 31 38 39 43	330	8
Polygonaceae			
Polygonum urophyllum	12 13 15 26 29 38 39 41	545	8

Table 3 (*Continued*)

Host plant	Arbuscular mycorrhizal fungi	SD	SR
Rumex hastatus	7 12 13 15 17 18 22 23 25 26 29 31 32 38 39	2430	15
Pteridaceae			
Onychium lucidum	7 12 13 18 19 24 25 29 34 39	645	10
Pteris henryi	2 3 5 7 12 18 29 31 32 34 39 40	825	12
Pteris vittata	3 5 12 13 17 18 22 29 31 32	1440	10
Rhamnaceae			
Ziziphus yunnanensis	7 12 13 15 17 25 29 34	1260	8
Rosaceae			
Agrimonia nepalensis	5 7 12 13 15 25 29 34 38 39	1090	10
Cotoneaster pannosus	12 13 22 23 31 32 39	160	7
Spiraea martinii	12 13 17 24 29 31 38 39 40	2525	9
Rubhceae			
Emmenopterys henryi	12 13 15 17 18 29 31 34 38 39 40	815	11
Rubia cordifolia	2 7 12 13 15 29 33 38	705	8
Rutaceae			
Boenninghausenia sessilicarpa	5 7 10 12 13 17 25 31 32 34 40	695	11
Scrophulariaceae			
Lindenbergia philippensis	7 10 12 13 17 18 26 29 31 32 33 38 39	1215	13
Selaginellaceae			
Selaginella davidii	3 12 13 15 18 24 26 29 31 32 34 38 39 41 42	2605	15
Solanaceae			
Solanum indicum	2 12 13 15 17 23 26 29 31 32 38 39	1790	12
Solanum verbascifolium	12 13 17 18 23 25 29 31 32 33 34 38 39	700	13
Symplocaceae			
Symplocos racemosa	3 6 12 13 17 18 21 22 25 29 31 32	2920	12
Thymelaeaceae			
Wikstroemia canescens	2 12 13 19 29	295	5
Ulmaceae			
Trema angustifolia	2 7 10 12 13 14 17 18 31 39 40	950	11
Urticaceae			
Debregeasia edulis	12 13 26 29	485	4
Pouzolzia sanguinea	3 6 12 13 17 25 26 29 38 39 41	1045	11
Verbenaceae			
Verbena officinalis	12 13 21 26 29 31 32 34 39	480	9
Vitex negundo	6 7 12 15 17 18 22 26 29 31 38 39	5070	12

Total: soil samples = 56; average spore density = 1423 ± 1310; average species richness = 9.8 ± 3.2. Numbers listed in the column labeled arbuscular mycorrhizal fungi correspond to Table 2.

found the highest spore density at 10–20 cm depth. It is likely that disturbance derived from natural disturbances (e.g. frequent mud-rock flows, landslides) causes the loss of the topsoil that contains most of the spores, resulting in reduced AMF spore abundance and changes in the spatial distribution of AMF species.

Different host plant species in the same plant community and the same host plant species in different plant communities associated with different AMF species with different isolation frequency and relative abundance suggested an uneven distribution of AMF species (Tables 2–4). These significant non-random associations between AMF and host plants might suggest some degree of AMF host preference (Husband et al., 2002). Helgason et al. (2002) investigated the AMF community structure in roots of five woodland plant species, and found that the community structure varied among host plants. They noted that variations in root colonization, symbiotic compatibility, and plant performance within each fungus–plant combination provided evidence of physical and functional selectivity in the plant–AM fungus symbiosis.

Hart and Reader (2002) suggested that the distinct colonizing strategies of various AMF are taxonomically based at the family level, and therefore current AMF taxonomy has a true functional basis. As the studies of Helgason et al. (2002) and Husband et al. (2002) have shown non-random differences in distribution among different AMF species and genera in the field, it is also likely that the preferences of different AMF with different host plants in our study sites might be reflected at the species or family level.

Many factors can influence AMF distribution and community structure, such as climatic and edaphic factors, spatial and temporal variation, vegetation, host-specificity between fungi and plants, disturbance, and differential sporulation ability of AMF taxa (Barni and Siniscalco, 2000; Boddington and Dodd, 2000; Burrows and Pfleger, 2002; Husband et al., 2002;

Table 4 – Distribution, spore density (SD) and species richness (SR) of AMF in the Xiao River (XR) site

Host plant	Arbuscular mycorrhizal fungi	SD	SR
Acanthaceae			
Barleria cristata	2 3 9 21 29 30	305	7
Amaranthacae			
Amaranthus spinosus	12 13 19 22 26 27 38	170	7
Asclepiadaceae			
Calotropis gigantean	12 25 26 39	190	4
Asteraceae			
Artemisia roxburghiana	10 12 13 18 19 24 26 29 33 34 36 38 39	1395	13
Bidens bipinnata	12 13 19 21 30 35 37	910	7
Conyza japonica	4 12 29 30 34 37 38	285	7
Ixeris denticulata	12 22	55	2
Laggera alata	5 12 18 19 24 26 29 38 40	730	9
Laggera pterodonta	12 13 19	50	3
Siegesbeckia orientalis	3 5 12 22 29 30	120	6
Tridax procumbens	10 13 19 27 29 31 37	1375	7
Xanthium sibiricum	1 3 12 18 19 21 25 27 29 36	2805	10
Cactaceae			
Opuntia dillenii	1 12 13 19 24 26 33 34 36 38	1410	10
Chenopodiaceae			
Chenopodium ambrosioides	1 13 16 19 22 28 33 37	445	8
Convolvulaceae			
Porana racemosa	5 12 13 15 18 19 26 30 34 39	990	10
Cyperaceae			
Cyperus rotundus	5 8 13 15 24 27 29 30 34 38	885	10
Eriophorum comosum	13 19 21 25 35 37	300	6
Euphorbiaceae			
Euphorbia hirta	10 12 18 27 33 36	355	6
Gramineae			
Andropogon yunnanensis	3 8 18 21 38	200	5
Arthraxon hispidus	6 19 37	80	3
Bothriochloa pertusa	13 18 19 26	285	4
Chloris virgata	5 7 19 29	50	4
Cymbopogon distans	12 15 19 31 38	420	5
Digitaria cruciata	16	15	1
Heteropogon contortus	2 3 10 12 16 18 22 29 39	1135	9
Labiatae			
Elsholtzia stachyodes	2 7 8 10 12 13 19 26 27 30 35 37 38	830	13
Paraphlomis lancidentata	1 12 13 19 22 27 29 31 34 36 38	590	11
Leguminosae			
Desmodium multiflorum	11 12 15 30 37	130	5
Desmodium multiflorum	11 12 15 30 37	130	5
Indigofera linifolia	12 19 27 29 36	500	5
Malvaceae			
Abutilon indicum	7 12 13 16 18 19 29 30 33 36 38	1750	11
Sida szechuensis	1 4 5 12 17 22 24 25 29 30 34	705	11
Polygonaceae			
Polygonum hydropiper	10 12 30 37	155	4
Rumex hastatus	2 6 10 13 15 18 21 22 23 27 29 31 33 38	1100	14
Solanaceae			
Euphorbia thymifolia	1 2 12 18 19 27 36 37	215	8
Solanum torvum	5 10 12 16 18 19	95	6

Total: soil samples = 35; average spore density = 601 ± 609; average species richness = 7.1 ± 3.4.

Muthukumar and Udaiyan, 2002; Renker et al., 2005). It has been reported that differences in sporulation ability of different AMF species can result in unevenness of spore density (Bever et al., 1996). The population and distribution of AMF varied greatly with different plants and locations (He et al., 2002; Mohammad et al., 2003; Uhlmann et al., 2004). The results of current research suggest therefore that in arid habitats natural disturbance may have a major effect on the

Table 5 – Diversity measurements of AMF communities in the Pudu River (PR) and Xiao River (XR)

Ecological parameters	PR	XR
Shannon–Wiener index of diversity (H')	1.85	1.74
Evenness (E)	0.52	0.48
Simpson's index of dominance (D)	0.067	0.012
Sorenson's coefficient of AMF community (C_s)	0.81	
Sorenson's coefficient of plant community (C'_s)	0.15	

spore density and distribution of AMF, but environmental factors might influence AMF community structure more.

3.4. *Ecological implications of AMF biodiversity*

Kennedy et al. (2002) demonstrated that increasing local biodiversity could act as a barrier to enhance invasion resistance, and the study of McGrady-Steed et al. (1997) showed that biodiversity could regulate ecosystem predictability in terrestrial ecosystems. This suggests that AMF diversity could be used to investigate the function of AMF in maintaining plant biodiversity and ecosystem function during the conservation and restoration of diverse natural ecosystems, especially of the hot-dry ecosystems (van der Heijden et al., 1998; Diallo et al., 1999; Pande and Tarafdar, 2004). Here we suggest that AMF biodiversity and function should be viewed at different hierarchical levels. At the community level, the high AMF community similarity between the two sites with distinct different plant communities suggested that most AMF found in the hot-dry valley could colonize a variety of plant species, and further supported a lack of host specificity among AMF. In contrast, at the species level, the relative abundance and isolation frequency of various AMF species differed significantly between sites (Table 2), and only 11.6% of common AMF species (IF $>$ 30%) coexisted in the two different plant communities. Our study revealed significant non-uniform spatial distributions of the dominant AMF species, and AMF community structure associated with different host plant species varied considerably. Since functional differences in AMF (either inter- or intraspecies) could lead to different levels of plant-fungus compatibility, and since the variation in functional diversity within one AMF species can be greater than differences between different AMF species or even genera (Munkvold et al., 2004), there are clearly opportunities for significant host preference to develop among AMF species. Even species that occurred in both sites often showed different patterns of sporulation and distribution in the two different plant communities, thus reflecting differences in the functional diversity of AMF even where AMF species composition did not vary greatly.

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