

Supplemental Materials

Table S1 Specific information on the sampling sites

Site	Location	Longitude and Latitude	Altitude (above the sea level)
A	Banan, Chongqing	29°61'N, 106°55'E – 29°65'N, 106°59'E	155 – 175 m
B	Fuling, Chongqing	29°75'N, 107°37'E – 29°79'N, 107°43'E	155 – 175 m
C	Zhongxian, Chongqing	30°32'N, 108°14'E – 30°36'N, 108°22'E	155 – 175 m

Table S2 Relative abundance of arbuscular mycorrhizal fungi (AMF) taxa in the rhizosphere soils of *Cynodon dactylon* in three contrasting land use types along the drawdown zone of the Three Gorges Reservoir

Par1	<i>Paraglomus occultum</i>	-	-	-	4.96	-	-	-	-	0.001	-	-	-	-	-
Par2	<i>Paraglomus</i> sp.	-	0.04	0.001	8.01	0.04	-	-	-	-	-	-	-	-	-
Par3	<i>Paraglomerales</i> sp.	5.28	22.81	2.16	3.65.	12.41	-	-	-	0.001	-	-	-	-	-
	Unkonwn														
Un1	<i>Glomeraceae</i> sp.	0.50	23.36	7.31	7.40	12.36	75.52	14.93	-	6.23	12.26	32.98	25.73	5.88	1.20
Un2	<i>Glomerales</i> sp.	-	0.002	-	-	5.73	-	29.34	36.17	-	31.36	0.15	0.62	3.43	3.62

Abbreviations: NCND, non-cultivated non-disturbed land; DNC, disturbed non-cultivated land; CL, cultivated land. CL1, *Cynodon dactylon* from CL; CL2, *C. dactylon* from CL; CL3, *C. dactylon* from NCL; CL4, *C. dactylon* from NCL; CL5, *C. dactylon* from NCL; DNC1, *C. dactylon* from DNC; DNC2, *C. dactylon* from DNC; DNC3, *C. dactylon* from DNC; DNC4, *C. dactylon* from DNC; NCND1, *C. dactylon* from NCND; NCND2, *C. dactylon* from NCND; NCND3, *C. dactylon* from NCND; NCND4, *C. dactylon* from NCND; NCND5, *C. dactylon* from NCND. ^a DNC5: no hint obtained after the NGS sequencing.

Table S3 Relative abundance (%) of arbuscular mycorrhizal fungi (AMF) taxa in roots associated with *Cynodon dactylon* grown in three contrasting land use types along the drawdown zone of the Three Gorges Reservoir

		Non-cultivated Non-disturbed land (NCND)			Disturbed non-cultivated land (DNC)			Cultivated land (CL)		
		NCND1	NCND2	NCND3	DNC1	DNC2	DNC3	CL1	CL2	CL3
<i>Archaeospora</i>										
Arc1	<i>Archaeosporaceae</i> sp.	–	–	–	82.70	–	–	–	–	0.004
<i>Claroideoglomus</i>										
Cla2	<i>Claroideoglomus walkeri</i>	–	–	–	–	0.65	–	–	–	–
Cla3	<i>Claroideoglomus</i> sp.	–	–	0.003	–	0.10	–	–	–	0.003
Cla4	<i>Claroideoglomeraceae</i> sp.	–	–	–	0.02	–	–	–	–	–
<i>Diversispora</i>										
Div2	<i>Diversispora</i> sp.	–	–	–	–	0.22	–	–	–	–
Div3	<i>Diversporaceae</i> sp.	–	–	–	–	0.21	–	–	–	–
<i>Funneliformis</i>										
Fun1	<i>Funneliformis mosseae</i>	–	0.004	–	–	3.49	–	–	0.05	–
<i>Glomus</i>										
Glo1	<i>Glomus aggregatum</i>	–	–	–	–	–	–	–	–	0.14
Glo2	<i>Glomus cubense</i>	–	–	–	–	–	–	0.61	–	–
Glo3	<i>Glomus indicum</i>	–	–	–	–	–	–	–	–	0.034
Glo5	<i>Glomus microcarpum</i>	–	–	–	–	–	–	–	–	0.20
Glo6	<i>Glomus versiforme</i>	–	–	–	–	–	0.07	–	–	–
Glo7	<i>Glomus</i> sp.	–	–	–	–	–	–	–	1.88	0.08
Glo8	<i>Glomus</i> sp. 7 SUN_2011	12.15	–	–	5.79	–	–	–	–	16.31
Glo9	<i>Glomus</i> sp. 8 SUN_2011	–	15.55	–	–	–	–	20.74	–	0.006

Glo10	<i>Glomus</i> sp. U31	–	0.02	–	–	–	–	–	–	–	0.50
Glo11	<i>Glomus</i> sp. 0502	–	0.07	–	–	–	–	–	–	–	–
<i>Rhizophagus</i>											
Rhi1	<i>Rhizophagus custos</i>						4.07				
Rhi2	<i>Rhizophagus fasciculatus</i>	–	–	–	–	–	–	–	0.85	0.04	
Rhi3	<i>Rhizophagus intraradices</i>	31.98	0.27	85.88	–	28.94	–	–	37.40	3.23	
Rhi4	<i>Rhizophagus irregularis</i>	–	53.28	4.70	–	3.99	23.78	0.38	2.46	1.33	
Rhi5	<i>Rhizophagus</i> sp.	12.55	10.11		–	0.57	65.04	1.83	–	14.18	
<i>Septoglomus</i>											
Sep1	<i>Septoglomus viscosum</i>	–	–	0.02	–	–	–	0.02	0.48	0.50	
<i>Paraglomus</i>											
Par3	<i>Paraglomerales</i> sp.	1.21	0.36	0.09	–	0.001	–	–	0.001	0.006	
Unknown											
Un1	<i>Glomeraceae</i> sp.	2.83	12.97	1.15	11.40	9.38	–	0.96	6.33	37.92	
Un2	<i>Glomerales</i> sp.	–	5.40	–	0.10	–	–	–	–	2.70	

Abbreviations: NCND, non-cultivated non-disturbed land; DNC, disturbed non-cultivated land; CL, cultivated land. CL1, *Cynodon dactylon* from CL; CL2, *C. dactylon* from CL; CL3, *C. dactylon* from NCL; DNC1, *C. dactylon* from DNC; DNC2, *C. dactylon* from DNC; DNC3, *C. dactylon* from DNC; NCND1, *C. dactylon* from NCND; NCND2, *C. dactylon* from NCND; NCND3, *C. dactylon* from NCND.

Table S4 Correlation coefficient between arbuscular mycorrhizal fungi (AMF) community composition and environmental variables (soil chemical characteristics and land-use type) from axes 1 and 2 of ordination

Correlation	Rhizosphere soil		Root	
	R ²	P	R ²	P
AK	0.266	0.181	0.518	0.118
AP	0.130	0.458	0.198	0.510
C/N	0.058	0.732	0.187	0.510
EC	0.032	0.853	0.282	0.383
LU	0.497	0.024	0.608	0.056
pH	0.208	0.277	0.435	0.188
SM	0.389	0.074	0.846	0.005
SOC	0.654	0.005	0.915	0.001
SOM	0.654	0.005	0.915	0.001
TN	0.018	0.923	0.168	0.551

Values in bold indicate significant correlations ($P < 0.05$). Abbreviations: bold data, significant correlation; AK, available potassium; AP, available phosphorus; C/N, carbon and nitrogen ratio; EC, soil electrical conductivity; LU, land-use type; pH, soil pH; SM, soil moisture; SOC, soil organic carbon; SOM, soil organic matter; TN, total nitrogen.

Table S5 Permutational multivariate analysis of variance (PERMANOVA) exploring the differences in arbuscular mycorrhizal fungi (AMF) community structure among contrasting land-use types

	Rhizosphere soil and root			Rhizosphere soil			Root		
Tested factor	Df	Pseudo-F	P (perm)	Df	Pseudo-F	P (perm)	Df	Pseudo-F	P (perm)
Land-use type	1	1.32	0.023	1	2.01	0.001	1	1.14	0.168
PERMDISP		<i>P</i> (perm)			<i>P</i> (perm)			<i>P</i> (perm)	
Land-use type		0.854			0.528			0.817	

Note: Values represent the pseudo-F ratio (F) and the level of significance (*P*).

Table S6 The number of sequencing reads from each fungal phylum detected for all rhizosphere soil or root samples among three contrasting land-use types

	Rhizosphere			Root		
	NCND	DNC	CL	NCND	DNC	CL
<i>Glomeromycota</i>	58553 ± 7508	46590 ± 16495	43472 ± 14969	38182 ± 27702	47062 ± 24950	75794 ± 2989
<i>Chytridiomycota</i>	3928 ± 1346	2 ± 1	40 ± 30	127 ± 117	19 ± 14	49 ± 48
<i>Ascomycota</i>	908 ± 256	664 ± 540	11409± 11221	3181 ± 1212	50305 ± 47002	394 ± 24
<i>Zygomycota</i>	2573 ± 1518	40484 ± 25439	15428 ± 8214	3 ± 3	5258± 5247	5 ± 1
<i>Basidiomycota</i>	1688 ± 594	145 ± 105	961 ± 266	5538 ± 4546	3352 ± 1672	33 ± 13

Data expressed as mean ± SE (n = 5 for rhizosphere, n = 3 for root). NCND, non-cultivated non-disturbed land; DNC, disturbed non-cultivated land; CL, cultivated land. The proportional distributions of the sequences from each fungal phylum detected in all rhizosphere soil and root samples.

Table S7 The PCR primers sequences in this study

The first round PCR primer			
SSUmAf	Nucleotide sequence (5'-3')	LSUmAr	Nucleotide sequence (5'-3')
SSUmAf1	TGGGTAATCTTTGAAACTTYA	LSUmAr1	GCTCACACTCAAATCTATCAA
SSUmAf2	TGGGTAATCTTRTGAAACTTCA	LSUmAr2	GCTCTAACTCAATTCTATCGAT
		LSUmAr3	TGCTCTTACTCAAATCTATCAA
		LSUmAr4	GCTCTTACTCAAACCTATCGA
The second round PCR primer			
	Nucleotide sequence (5'-3')		Nucleotide sequence (5'-3')
ITS70	GTGARTCATCGAACATCTTG-3'	ITS4	TCCTCCGCTTATTGATATGC

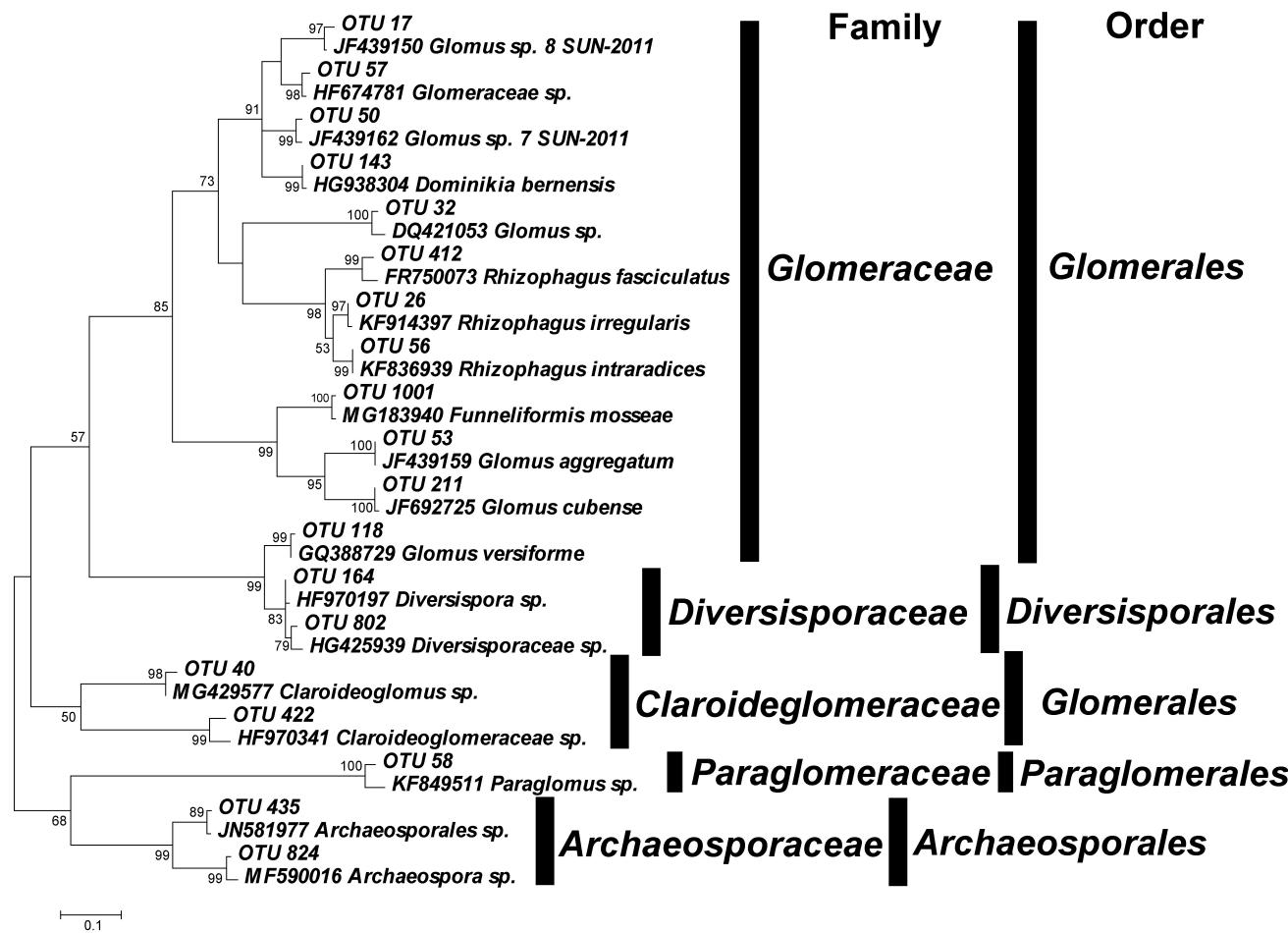


Figure S1 Neighbor-joining phylogenetic tree (Maximum Likelihood method) showing the relationships of the representative sequences of OTUs and the reference sequences from GenBank and UNITE. The DNA fragment of AMF were obtained from *Cynodon dactylon* roots and rhizosphere soils from three contrasting land-use types. The values above the branches are bootstrap values (1,000 replicates).

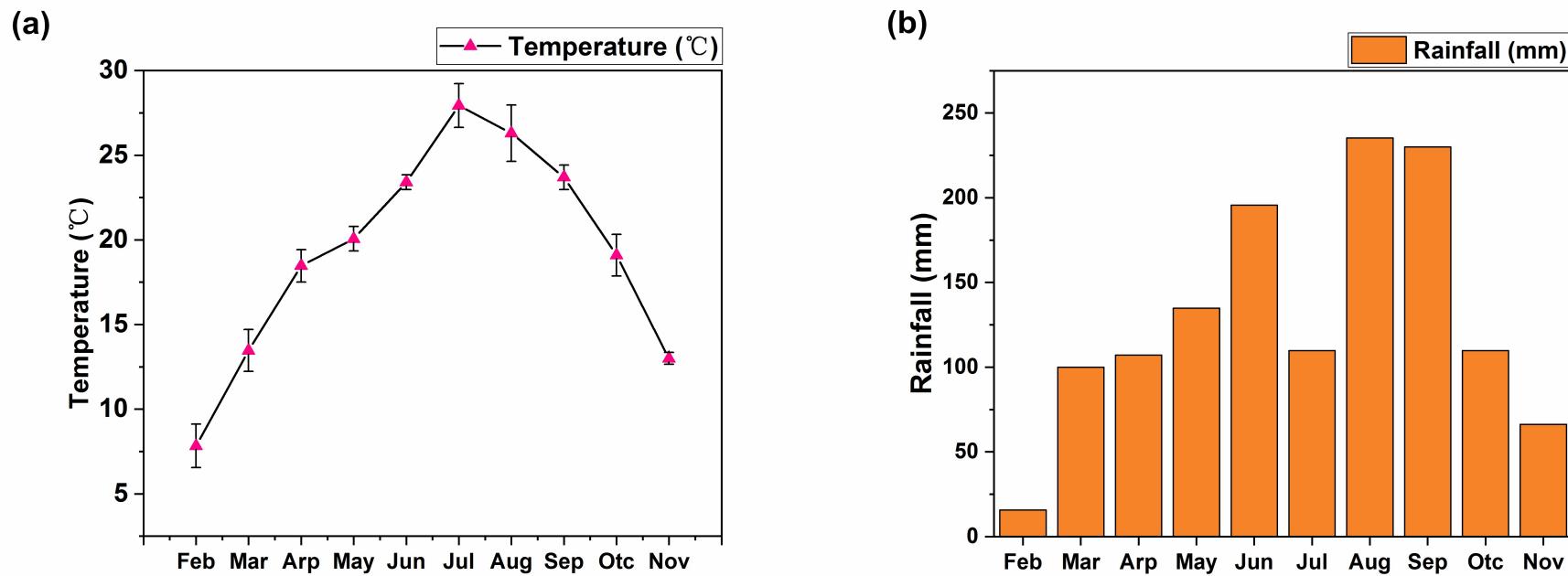


Figure S2 The temperature (a) and rainfall (b) of the sampling sites in the Three Gorges Reservoir from Feb (February) to Nov (November) in 2014.