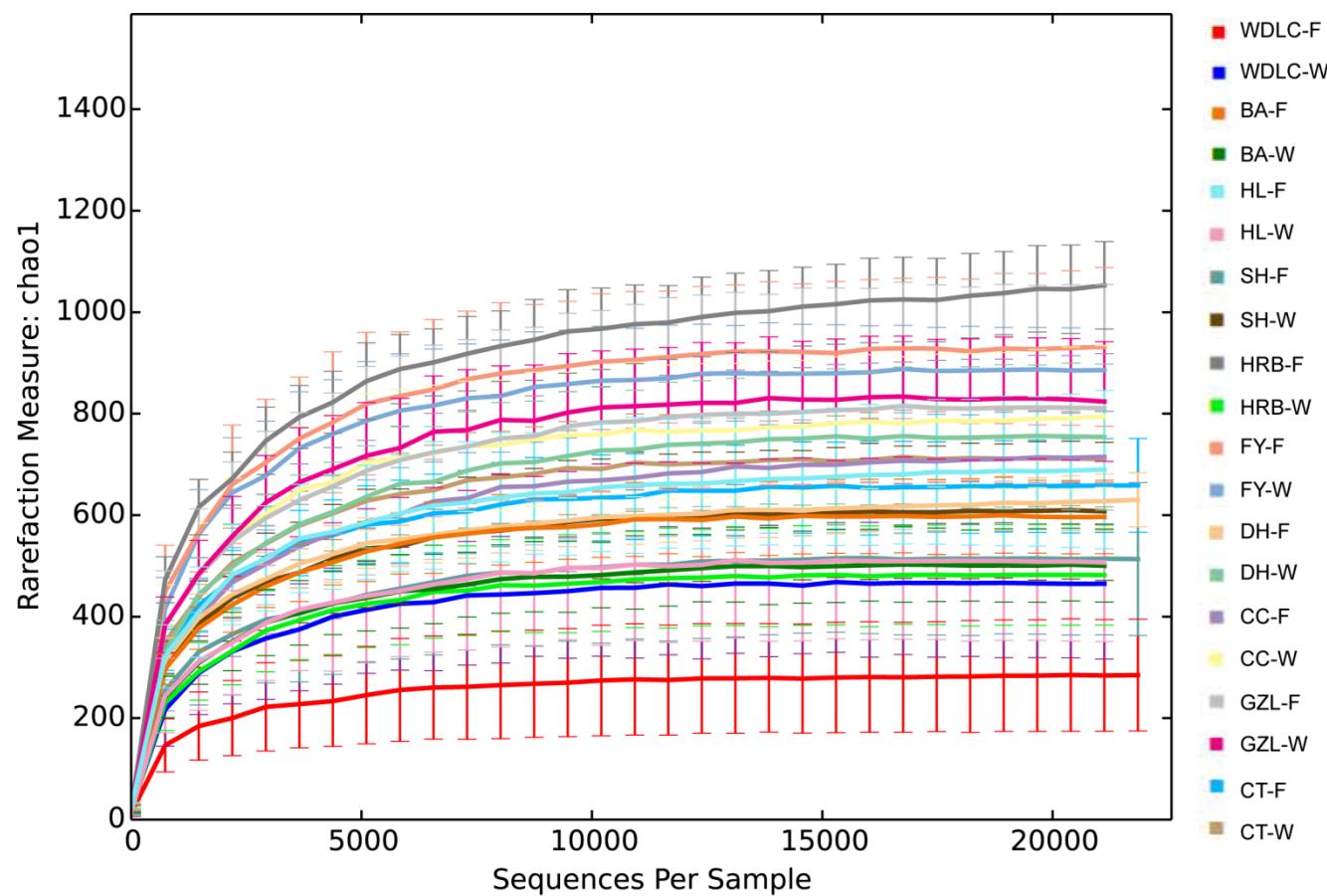


**Comparative analysis of arbuscular mycorrhizal fungal communities between farmland and woodland in the black soil region of northeast China**

**Supplementary figure and tables**



**Figure S1.** Rarefaction curves showing the Chao1 index of different samples. Different colors represent different farmland or woodland sampling sites (WDLC, Wudalianchi; BA, Beian; HL, Hailun; SH, Suihua; HRB, Harbin; FY, Fuyu; DH, Dehui; CC, Changchun; GZL, Gongzhuling; and CT, Changtu). F and W represent farmland and woodland respectively.

**Table S1** Pearson's correlation analysis between soil properties and glomalin-related soil protein (GRSP) in farmland or woodland.

	pH		Total N		Total P		SOC		Urease		Invertase	
	<i>r</i>	<i>P</i>										
Farmland												
Total N	-0.084	0.611										
Total P	-0.713	0.292	<b>0.732**</b>	<0.001								
SOC	-0.070	0.671	<b>0.907**</b>	<0.001	<b>0.787**</b>	<0.001						
Urease	0.149	0.367	<b>0.376*</b>	0.018	0.303	0.060	<b>0.352*</b>	0.028				
Invertase	<b>0.678**</b>	<0.001	-0.042	0.799	-0.152	0.357	-0.005	0.976	-0.045	0.784		
GRSP	<b>-0.367*</b>	0.021	<b>0.350*</b>	0.029	<b>0.506**</b>	0.001	<b>0.461**</b>	0.003	0.024	0.885	<b>-0.326*</b>	0.043
Woodland												
Total N	-0.082	0.618										
Total P	0.113	0.494	<b>0.701**</b>	<0.001								
SOC	-0.009	0.956	<b>0.922**</b>	<0.001	<b>0.734**</b>	<0.001						
Urease	0.270	0.097	<b>0.445**</b>	0.005	<b>0.736**</b>	<0.001	<b>0.449**</b>	0.005				
Invertase	-0.118	0.473	0.094	0.568	0.081	0.624	0.032	0.849	<b>0.418**</b>	0.008		
GRSP	-0.272	0.094	<b>0.682**</b>	<0.001	<b>0.590**</b>	<0.001	<b>0.764**</b>	<0.001	0.241	0.140	-0.044	0.792

SOC, soil organic carbon. Only significant correlations (\*  $P<0.05$ ; \*\*  $P<0.01$  by Turkey's test) were shown in bold number.

**Table S2** Relative abundance of arbuscular mycorrhizal fungal classes, orders, families at 20 sampling sites (WDLC, Wudalianchi; BA, Beian; HL, Hailun; SH, Suihua; HRB, Harbin; FY, Fuyu; DH, Dehui; CC, Changchun; GZL, Gongzhuling; and CT, Changtu). F and W represented farmland and woodland respectively. The value of relative abundance was calculated from mean of 4 samples at each sampling site.

	WDLC		BA		HL		SH		HRB		FY		DH		CC		GZL		CT	
Orders	F	W	F	W	F	W	F	W	F	W	F	W	F	W	F	W	F	W	F	W
Paraglomerales	39.30	52.14	53.97	84.93	23.37	86.16	32.25	52.47	40.71	90.76	42.30	59.08	48.63	78.05	52.69	54.16	53.19	46.78	30.58	44.30
Glomerales	48.11	38.25	37.61	12.99	68.46	10.53	60.52	41.23	51.46	6.39	54.40	37.18	45.52	18.75	35.77	39.43	42.22	47.31	64.92	49.71
Archaeosporales	4.83	4.60	4.18	1.06	2.12	0.90	2.11	1.53	1.31	2.43	1.10	1.61	1.27	0.51	2.83	2.13	1.18	2.12	2.00	2.08
Diversisporales	0.25	0.44	1.46	0.05	0.34	0.21	0.21	0.11	0.31	0.06	0.05	0.10	0.48	0.16	0.14	0.10	0.17	0.17	1.06	0.30
Families																				
Paraglomeraceae	39.30	52.14	53.97	84.93	23.37	86.16	32.25	52.47	40.71	90.76	42.30	59.08	48.63	78.05	52.69	54.16	53.19	46.78	30.58	44.30
Claroideoglomeraceae	40.48	26.42	23.42	10.16	41.37	6.66	47.26	28.96	36.43	2.49	17.07	21.38	32.09	11.89	22.78	20.89	23.56	37.01	16.50	35.41
Glomeraceae	7.63	11.82	14.19	2.83	27.09	3.87	13.26	12.28	15.03	3.90	37.33	15.79	13.43	6.86	12.99	18.54	18.67	10.29	48.41	14.30
Archaeosporaceae	4.51	4.43	3.79	0.23	1.72	0.20	0.69	0.35	0.92	0.13	0.86	1.22	1.09	0.21	2.04	1.53	0.80	1.69	1.77	1.33
Ambisporaceae	0.32	0.17	0.39	0.83	0.40	0.70	1.42	1.18	0.39	2.30	0.24	0.39	0.18	0.30	0.79	0.61	0.38	0.43	0.24	0.75
Gigasporaceae	0.24	0.20	0.34	0.01	0.33	0.20	0.18	0.09	0.24	0.04	0.04	0.08	0.32	0.14	0.12	0.08	0.11	0.15	0.74	0.30
Acaulosporaceae	0.01	0.18	1.01	0.03	0.00	0.01	0.04	0.01	0.02	0	0.00	0.01	0.14	0.01	0.02	0.01	0.05	0.01	0.06	0.00
Diversisporaceae	0	0.05	0.11	0.01	0.01	0	0	0.01	0.05	0.02	0.00	0	0.03	0.01	0.00	0.00	0.01	0.25	0	
Others	7.51	4.57	2.78	0.97	5.71	2.20	4.90	4.66	6.21	0.36	2.15	2.04	4.10	2.53	8.57	4.17	3.24	3.63	1.45	3.62

**Table S3** Pearson's correlation analysis between relative abundance of arbuscular mycorrhizal fungal orders, families, genera and edaphic factors.

	pH		Total N		Total P		SOC		Urease		Invertase		GRSP	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
<b>Orders</b>														
Paraglomerales	<b>0.357**</b>	0.001	<b>0.238*</b>	0.036	-0.057	0.620	0.200	0.081	-0.022	0.849	<b>0.431**</b>	<0.001	0.031	0.787
Glomerales	<b>-0.334**</b>	0.003	<b>-0.279*</b>	0.013	0.018	0.879	<b>-0.234*</b>	0.040	0.001	0.991	<b>-0.432**</b>	<0.001	-0.035	0.759
Archaeosporales	-0.125	0.274	0.175	0.126	<b>0.287*</b>	0.011	0.139	0.228	0.139	0.226	-0.131	0.252	-0.044	0.703
Diversisporales	<b>-0.287*</b>	0.011	-0.091	0.430	0.008	0.943	-0.115	0.319	0.063	0.584	<b>-0.395**</b>	<0.001	-0.170	0.137
<b>Families</b>														
Paraglomeraceae	<b>0.357**</b>	0.01	<b>0.238*</b>	0.036	-0.057	0.620	0.200	0.081	-0.022	0.849	<b>0.431**</b>	<0.001	0.031	0.787
Claroideoglomeraceae	<b>-0.306**</b>	0.006	-0.030	0.795	0.199	0.081	0.030	0.798	0.010	0.933	<b>-0.369**</b>	0.001	0.142	0.213
Glomeraceae	-0.151	0.187	<b>-0.380**</b>	0.001	-0.197	0.083	<b>-0.380**</b>	0.001	-0.009	0.938	<b>-0.225*</b>	0.048	-0.213	0.062
Archaeosporaceae	-0.171	0.134	0.191	0.094	<b>0.304**</b>	0.007	0.151	0.190	0.175	0.126	-0.188	0.100	-0.038	0.741
Ambisporaceae	0.100	0.385	-0.028	0.806	-0.022	0.845	-0.020	0.865	-0.077	0.502	0.126	0.272	-0.018	0.879
Gigasporaceae	<b>-0.349**</b>	0.002	-0.123	0.282	-0.060	0.599	-0.146	0.205	-0.039	0.734	<b>-0.397**</b>	<0.001	-0.064	0.580

Acaulosporaceae	-0.116	0.311	-0.003	0.981	0.085	0.459	-0.022	0.852	0.109	0.340	<b>-0.238*</b>	0.036	-0.151	0.187
Diversisporaceae	-0.199	0.080	-0.139	0.226	-0.084	0.464	-0.145	0.208	0.056	0.624	<b>-0.232*</b>	0.041	-0.197	0.083
Genera														
<i>Paraglomus</i>	<b>0.357**</b>	0.001	<b>0.238*</b>	0.036	-0.057	0.620	0.200	0.081	-0.022	0.849	<b>0.431**</b>	<0.001	0.031	0.787
<i>Claroideoglomus</i>	<b>-0.306**</b>	0.006	-0.030	0.795	0.199	0.081	0.030	0.798	0.010	0.933	<b>-0.369**</b>	0.001	0.142	0.213
<i>Glomus</i>	-0.150	0.191	<b>-0.384**</b>	0.001	-0.200	0.079	<b>-0.385**</b>	0.001	-0.009	0.936	<b>-0.225*</b>	0.047	-0.214	0.060
<i>Archaeospora</i>	-0.171	0.134	0.191	0.094	<b>0.304**</b>	0.007	0.151	0.190	0.175	0.126	-0.188	0.100	-0.038	0.741
<i>Ambispora</i>	0.100	0.385	-0.028	0.806	-0.022	0.845	-0.020	0.865	-0.077	0.502	0.126	0.272	-0.018	0.879
<i>Gigaspora</i>	<b>-0.366**</b>	0.001	-0.087	0.449	-0.028	0.807	-0.146	0.206	0.090	0.433	<b>-0.376**</b>	0.001	-0.196	0.085
<i>Scutellospora</i>	-0.194	0.089	-0.110	0.337	-0.068	0.552	-0.088	0.446	-0.151	0.186	<b>-0.261*</b>	0.021	0.093	0.416
<i>Acaulospora</i>	-0.116	0.311	-0.003	0.981	0.085	0.459	-0.022	0.852	0.109	0.340	<b>-0.238*</b>	0.036	-0.151	0.187
<i>Septoglomus</i>	-0.067	0.559	0.131	0.254	0.089	0.440	0.175	0.127	0.010	0.929	0.001	0.993	0.062	0.589
<i>Diversispora</i>	-0.205	0.072	-0.160	0.162	-0.102	0.373	-0.166	0.150	0.046	0.686	<b>-0.239*</b>	0.035	-0.210	0.065
<i>Redeckera</i>	0.099	0.388	<b>0.391**</b>	<0.001	<b>0.332**</b>	0.003	<b>0.379**</b>	0.001	0.178	0.120	0.119	0.298	<b>0.235*</b>	0.038

SOC, soil organic carbon; GRSP, glomalin-related soil protein. Only significant correlations (\* P<0.05; \*\* P<0.01 by Turkey's test) were shown in bold number.