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FIG. S1. Phylogenetic analysis of the three AM fungal isolates (*Glomus claroideum* Chomutov, *G. intraradices* Chomutov, *G. mosseae* BEG95) based on sequences of the large subunit of nuclear ribosomal DNA. The most parsimonious tree is presented. Bootstrap values higher than 50% are indicated by the numbers above or below branches. Sequences of *Gigaspora rosea* were used as outgroup. The sequences of the three AMF isolates used in the present study are given in bold. Sequences published by Krak et al. (**Krak K, Janoušková M, Caklová P, Vosátka M, Štorchová H. 2012.** Intraradical Dynamics of Two Coexisting Isolates of the Arbuscular Mycorrhizal Fungus *Glomus intraradices* Sensu Lato as Estimated by Real-Time PCR of Mitochondrial DNA. *Applied and Environmental Microbiology* **78**:3630-3637) are marker by '*'.
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AMF isolate	Primer type	Primer name (primer sequence 5'→3')	Primer concentration (μM)	Ta (°C)	Amplicon size (bp)	Amplification efficiency ^a (SD)	Reference
GI	for	GIX6-F351 (TTCGGGGCTACTTGTCTGAT)	0.3	62	74	99.5 (3.1)	Krak et al. 2012
	for	GIX6-F351b (TTCGGGGCTACCTGTCTGGT)	0.2				
	rev	GIX6-R424 (CCATCGACTTTGATAACCGTAA)	0.5				
GC	for	GCX14-F300 (CTTTAGCGGAATGTGGTGGT)	0.5	58	132	92.4 (2.4)	Present study
	rev	GCX14-R431 (TAGCCTGTTCAAAGGCGAAT)	0.5				
GM	for	GMX2-F1 (CATACCAATGGGAAATCAACC)	0.25	60	112/ 122	93.9 (1.8)	Present study
	for	F2 (CGGGAAATCAACCTTTTGAG)	0.25				
	rev	GMX10-R1 (CGATGTTGACTAACCGTACGAA)	0.25				
	rev	GMX2-R2 (CCGATGTTGACTAACTATACGAAAA)	0.25				

TABLE S1. Parameters of the quantitative PCR assays used for the quantification of nuclear ribosomal DNA copies of three AMF isolates.

GI, *Glomus intraradices* Chomutov; GC, *G. claroideum* Chomutov; GM, *G. mosseae* BEG95; ^a The amplification efficiency was calculated from at least 5 independent dilutions of plasmid templates.

Week	Background	AMF	IP	GM	GI	GC
6	Control	GM	150	72.8 (31.4)	0	0
6	Control	GM	20	44.5 (24.5)	0	0
6	Control	GI	150	0	650 (254)	0
6	Control	GI	400	0	411 (219)	0
6	Control	GC	150	0	0	78.8 (55.0)
6	Control	GC	400	0	0	82.3 (62.7)
12	Control	GM	150	57.7 (16.4)	0	0
12	Control	GM	20	62.3 (35.6)	0	0
12	Control	GI	150	0	786 (188)	0
12	Control	GI	400	0	550 (281)	0
12	Control	GC	150	0	0	50.3 (24.2)
12	Control	GC	400	0	0	17.8 (9.06)
24	Control	GM	150	53.7 (21.6)	0	0
24	Control	GM	20	62.7 (23.2)	0	0
24	Control	GI	150	0	372 (130)	0
24	Control	GI	400	0	461 (154)	0
24	Control	GC	150	0	0	16.2 (10.9)
24	Control	GC	400	0	0	11.2 (5.91)
6	AMF	none	0	1.67 (1.63)	307 (108)	63.7 (30.9)
6	AMF	GM	150	5.17 (4.07)	284 (175)	54.5 (31.2)
6	AMF	GM	20	9.17 (8.38)	258 (146)	57.2 (29.7)
6	AMF	GI	150	0.83 (0.75)	229 (99.7)	99.2 (15.4)
6	AMF	GI	400	2.33 (1.51)	216 (112)	38.3 (18.8)
6	AMF	GC	150	2.50 (1.87)	325 (136)	82.8 (29.8)
6	AMF	GC	400	1.00 (1.1)	140 (46.8)	33.0 (20.2)
12	AMF	none	0	4.33 (4.18)	338 (143)	41.2 (24.2)
12	AMF	GM	150	9.17 (5.19)	357 (217)	36.8 (16.5)
12	AMF	GM	20	12.7 (4.63)	168 (90.5)	22.3 (12.4)
12	AMF	GI	150	3.00 (2.90)	310 (44.1)	27.5 (19.2)
12	AMF	GI	400	3.17 (1.83)	232 (70.7)	20.5 (4.23)
12	AMF	GC	150	3.17 (2.64)	294 (85.6)	33.8 (19.2)
12	AMF	GC	150	3.17 (2.56)	214 (64.8)	18.5 (5.89)
24	AMF	none	0	1.67 (2.16)	300 (132)	8.83 (12.4)
24	AMF	GM	150	2.50 (1.87)	370 (124)	10.5 (7.29)
24	AMF	GM	20	2.00 (2.19)	337 (246)	2.40 (1.67)
24	AMF	GI	150	1.75 (1.50)	356 (170)	20.8 (16.1)
24	AMF	GI	400	2.60 (3.13)	227 (81.3)	7.40 (9.89)
24	AMF	GC	400	2.17 (3.49)	241 (63.6)	2.67 (1.37)
24	AMF	GC	150	2.50 (4.18)	314 (121)	2.83 (1.72)

TABLE S2. Means (SE) of the nuclear ribosomal DNA copies $\times 10^3$ detected of each of the three AMF for each harvest week (Week), background arbuscular mycorrhizal fungal community (Background), isolate inoculated (AMF) and the level of infective propagules at which the isolates were inoculated (IP). For abbreviations of the isolates see Table S1.

	<i>RII inoculation</i>			<i>RII community</i>			
	df	MS (10 ⁻²)	F value	df	MS (10 ⁻²)	F value	
<i>G. mosseae</i>							
Harvest	2	50.2	1.93	Harvest	2	15.7	9.79 ***
AMF	2	310.	11.9 ***	IP level	1	4.99	3.11 †
IP	1	3.42	0.13	Harvest x IP	2	3.36	2.09
Harvest × AMF	4	23.7	0.91	Residual	30	1.61	
Harvest × IP	2	12.5	0.48				
AMF × IP	2	33.6	1.29				
Harvest × AMF × IP	4	21.6	0.83				
Residual	87	26.0					
<i>G. intraradices</i>							
Harvest	2	18.6	4.38 *	Harvest	2	11.6	3.61 *
AMF	2	1.62	0.38	IP level	1	0.12	0.04
IP	1	52.6	12.4 ***	Harvest x IP	2	12.1	3.76 *
Harvest × AMF	4	2.73	0.64	Residual	30	3.22	
Harvest × IP	2	5.85	1.38				
AMF × IP	2	0.51	0.12				
Harvest × AMF × IP	4	10.8	2.55 *				
Residual	86	4.24					
<i>G. claroideum</i>							
Harvest	2	51.0	6.63 **	Harvest	2	99.3	23.0 ***
AMF	2	23.1	3.00 †	IP level	1	1.08	0.25
IP	1	198.	25.7	Harvest x IP	2	42.4	9.85 ***
Harvest × AMF	4	19.1	2.49 *	Residual	30	4.31	
Harvest × IP	2	6.83	0.89				
AMF × IP	2	5.26	0.68				
Harvest × AMF × IP	4	28.0	3.64 **				
Residual	86	7.01					

TABLE S3. ANOVA results for the assessment of variation in the abundance response of the arbuscular mycorrhizal fungal (AMF) isolates to additional AMF inoculation (*RII inoculation*) depending on the harvest, AMF identity, and the IP level at which AMF were inoculated. Also shown are the ANOVA results for the assessment of variation in AMF response to the presence of a background community (*RII community*) depending on the harvest and the IP level at which AMF were inoculated. Full ANOVA results are shown here for discerning the magnitude of the interaction effect. Note, however, non-significant interaction effects were removed to attain the full proportion of variation explained by the main factors when reported in the main text. MS, mean squares; †, $P < 0.1$; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$

Shoot biomass	df	6 weeks		12 weeks		24 weeks	
		MS (10^{-3})	F value	MS (10^{-2})	F value	MS (10^{-1})	F value
<i>G. mosseae</i>							
Background	1	44.4	32.2 ***	280.	193.0 ***	51.7	132. ***
IP level	1	61.0	4.43 *	7.25	5.00 *	1.43	3.64 †
Background × IP	1	< 0.01	< 0.01	1.84	1.27	1.15	2.92
Residual	20	1.38		1.45		0.39	
<i>G. intraradices</i>							
Background	1	60.5	16.3 ***	213.	91.8 ***	16.4	37.6 ***
IP level	1	3.41	0.92	0.42	0.18	1.19	2.73
Background × IP	1	6.67	1.79	9.72	4.19†	0.79	1.81
Residual	20	3.72		2.32		0.44	
<i>G. claroideum</i>							
Background	1	17.4	10.8 **	40.6	19.7 ***	8.50	21.4 ***
IP level	1	6.03	3.76 †	0.05	0.03	1.86	4.73 *
Background × IP	1	4.91	3.06 †	7.81	3.78 †	0.12	0.31
Residual	20	1.60		2.07		0.39	
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Root biomass	df	MS (10^{-3})	F value	MS (10^{-2})	F value	MS (10^{-1})	F value
<i>G. mosseae</i>							
Background	1	17.3	9.41 **	95.9	52.6 ***	33.6	14.8 **
IP level	1	2.09	1.13	4.88	2.68	0.01	0.01
Background × IP	1	6.59	3.58 †	< 0.01	< 0.01	1.92	0.84
Residual	20	1.84		1.83		2.27	
<i>G. intraradices</i>							
Background	1	13.5	6.93 *	83.8	52.9 ***	4.74	4.26 †
IP level	1	3.50	1.80	0.08	0.05	2.06	1.85
Background × IP	1	0.64	0.33	16.9	10.7 **	0.08	0.07
Residual	20	1.94		1.59			
<i>G. claroideum</i>							
Background	1	23.1	14.4 **	1.35	0.56	1.12	0.92
IP level	1	10.6	6.58 *	0.75	0.31	6.20	5.09 *
Background × IP	1	0.59	0.37	1.24	0.51	0.93	0.76
Residual	20	1.60		2.43		1.22	

TABLE S4. ANOVA results for the assessment of variation in plant shoots and roots testing for differences in the level of infective propagules (IP) depending on the arbuscular mycorrhizal fungal background. Full ANOVA results are shown here for discerning the magnitude of the interaction effect. Note, however, non-significant interaction effects were removed to attain the full proportion of variation explained by the main factors IP level and background when reported in the main text. MS, mean squares; †, $P < 0.1$; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$