Supplementary Materials

Bio-based solutions consisting of arbuscular mycorrhizal fungi (AMF) with contrasting life-history strategies differently affect health-promoting compounds in fruits of field-grown tomato by changing arbuscule occurrence and diversity of AMF in roots

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Table S1 Arbuscular mycorrhizal (AM) fungal species and family, isolate codes, donor, geographical origin and original inoculum supplier

AMF species	AMF family	CCS isolate code[a]	Donor	INVAM isolate code[b]	Geographic orgin	Original isolate supplier
Gigaspora gigantea	Gigasporaceae	MFGS05	Giusto Giovannetti	PA125	Pennsylvania	INVAM, Morgantown, West Virginia
Scutellospora pellucida	Gigasporaceae	MFGS12	Giusto Giovannetti	MN408A	Minnesota	INVAM, Morgantown, West Virginia
Funneliformis mosseae	Glomeraceae	-	Joseph B. Morton	MD118	Maryland	INVAM, Morgantown, West Virginia
Sclerocystis sinuosa	Glomeraceae	MFGS06	Giusto Giovannetti	MD126	Maryland	INVAM, Morgantown, West Virginia

[a] CCS: Centro Colture Sperimentali, Quart (Aosta, Italia)

[b] INVAM: The International Collection of (Vesicular) Arbuscular Mycorrhizal Fungi

Table S2 Mean values ± SE of total phenolic content (TPC), antioxidant activity (ORAC) and lycopene of fruits of plants of *Solanum lycopersicum* var. Pisanello and var. Rio Grande inoculated with four arbuscular mycorrhizal (AM) fungal species: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Samplings at BBCH 89: 22nd July and 1st August 2019 for var. Pisanello, 3rd August and 10th August 2020 for var. Rio Grande

	var. Pisanello[a]		var. Rio Grande	
	1st harvest	2nd harvest	1st harvest	2nd harvest
	TPC			
-M[b]	201.96 ± 4.7	99.60 ± 1.9	60.25 ± 0.2	107.15 ± 11
+M[b]	264.93 ± 5.3	144.61 ± 14	107.48 ± 2.9	144.58 ± 5.9
Giga[c]	263.81 ± 9.5	125.37 ± 5.4	112.94 ± 4.8	134.43 ± 7.9
Glome[c]	266.06 ± 5.8	163.85 ± 26	102.02 ± 1.0	154.74 ± 7.2
G.giga[d]	279.17 ± 14	135.73 ± 5.4	105.22 ± 2.6	146.89 ± 4.8
S.pellu[d]	248.44 ± 3.9	115.00 ± 3.4	120.65 ± 6.9	121.97 ± 12
F.mos[d]	270.79 ± 7.2	161.87 ± 23	102.15 ± 0.7	165.11 ± 12
S.sin[d]	261.33 ± 9.6	165.82 ± 52	101.89 ± 2.1	144.37 ± 1.9
	ORAC			
-M	566.23 ± 4.2	521.09 ± 2.0	292.97 ± 14	242.96 ± 43
+M	557.93 ± 4.2	598.06 ± 53	649.45 ± 58	359.63 ± 59
Giga	554.47 ± 7.5	521.40 ± 2.4	811.14 ± 40	442.37 ± 103
Glome	561.40 ± 4.2	674.72 ± 99	487.77 ± 51	276.90 ± 45
G.giga	569.07 ± 2.2	524.16 ± 4.2	873.02 ± 57	671.35 ± 22
S.pellu	539.86 ± 7.7	518.62 ± 2.0	749.25 ± 30	213.40 ± 13
F.mos	556.54 ± 7.4	648.15 ± 136	494.96 ± 52	218.65 ± 30
S.sin	566.25 ± 3.5	701.29 ± 2.0	480.57 ± 102	335.14 ± 76
	Lycopene			
-M	-	141.67 ± 8.2	-	311.97 ± 82
+M	-	628.69 ± 59	-	780.85 ± 89
Giga	-	593.85 ± 71	-	864.77 ± 88
Glome	-	663.53 ± 99	-	696.93 ± 155
G.giga	-	740.60 ± 58	-	691.93 ± 66
S.pellu	-	447.10 ± 17	-	1037.6 ± 67
F.mos	-	512.80 ± 138	-	438.75 ± 3.2
S.sin	-	814.27 ± 85	-	955.1 ± 230

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (n=3); +M, AM fungal inoculation (n=12)
[c] *Giga* (n=6); *Glome* (n=6)
[d] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S3 *P*-values of linear orthogonal contrasts on total phenolic content (TPC), antioxidant activity (ORAC) and lycopene of fruits of plants of *Solanum lycopersicum* var. Pisanello and var. Rio Grande inoculated with four arbuscular mycorrhizal (AM) fungal species: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Samplings at BBCH 89: 22nd July and 1st August 2019 for var. Pisanello, 3rd August and 10th August 2020 for var. Rio Grande

	var. Pisanello[a]		var. Rio Grande	
	1st harvest	2nd harvest	1st harvest	2nd harvest
	TPC			
-M *vs* +M[b]	**<0.001**[c]	**0.023**	**<0.001**	**0.005**
Giga vs Glome[d]	0.802	0.277	**0.010**	**0.050**
G.giga vs S.pellu[e]	**0.032**	**0.034**	**0.010**	0.085
F.mos vs S.sin[e]	0.462	0.897	0.959	0.142
	ORAC			
-M *vs* +M	0.202	0.503	**<0.001**	**0.034**
Giga vs Glome	0.232	0.152	**<0.001**	**0.003**
G.giga vs S.pellu	0.236	0.712	0.169	**<0.001**
F.mos vs S.sin	**0.004**	0.969	0.866	0.082
	Lycopene			
-M *vs* +M	**-**	**<0.001**	**-**	**0.005**
Giga vs Glome	-	0.390	**-**	0.183
G.giga vs S.pellu	-	**0.023**	**-**	0.064
F.mos vs S.sin	-	**0.021**	**-**	**0.011**

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (n=3); +M, AM fungal inoculation (n=12)
[c] In bold statistically significant values ($P < 0.05$)
[d] *Giga* (n=6); *Glome* (n=6)
[e] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S4 Mean values ± SE of total phenolic content (TPC), antioxidant activity (ORAC) and lycopene of tomato sauce obtained from fruits of plants of *Solanum lycopersicum* var. Pisanello and var. Rio Grande inoculated with four arbuscular mycorrhizal (AM) fungal species: *Gigaspora gigantea* (G.giga) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Fruits used to produce the sauce were sampled at BBCH 89 (2nd harvest): 1st August 2019 for var. Pisanello, 10th August 2020 for var. Rio Grande

	var. Pisanello[a]	var. Rio Grande
	TPC	
-M[b]	11.91 ± 0.3	12.63 ± 0.1
+M[b]	11.35 ± 0.2	12.62 ± 0.2
Giga[c]	11.38 ± 0.1	13.11 ± 0.3
Glome[c]	11.48 ± 0.2	12.13 ± 0.6
G.giga[d]	11.44 ± 0.1	12.46 ± 0.2
S.pellu[d]	11.31 ± 0.1	13.75 ± 0.3
F.mos[d]	11.05 ± 0.1	12.60 ± 0.2
S.sin[d]	11.58 ± 0.2	11.67 ± 0.1
	ORAC	
-M [b]	350.05 ± 3.1	346.45 ± 5.2
+M	352.25 ± 4.6	340.06 ± 3.8
Giga	354.20 ± 7.0	346.95 ± 6.6
Glome	350.29 ± 6.5	333.17 ± 1.3
G.giga	357.57 ± 10	358.58 ± 7.7
S.pellu	350.84 ± 12	335.32 ± 5.1
F.mos	337.3 ± 0.7	334.39 ± 1.0
S.sin	363.3 ± 6.5	331.95 ± 2.6
	Lycopene	
-M [b]	711.25 ± 40	412.30 ± 8.5
+M	665.54 ± 30	372.69 ± 35
Giga	723.03 ± 48	272.68 ± 23
Glome	608.05 ± 15	472.70 ± 20
G.giga	639.65 ± 12	311.50 ± 29
S.pellu	806.40 ± 66	233.85 ± 18
F.mos	620.05 ± 24	472.60 ± 44
S.sin	596.05 ± 21	472.80 ± 10

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (n=3); +M, AM fungal inoculation (n=12)
[c] *Giga* (n=6); *Glome* (n=6)
[d] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S5 *P*-values of linear orthogonal contrasts on total phenolic content (TPC), antioxidant activity (ORAC) and lycopene of tomato sauce obtained from fruits of plants of *Solanum lycopersicum* var. Pisanello and var. Rio Grande inoculated with four arbuscular mycorrhizal (AM) fungal species: *Gigaspora gigantea* (G.giga) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Fruits used to produce the sauce were sampled at BBCH 89 (2nd harvest): 1st August 2019 for var. Pisanello, 10th August 2020 for var. Rio Grande

	var. Pisanello[a]	var. Rio Grande
	TPC	
-M *vs* +M [b]	0.177 [c]	0.959
Giga vs Glome[d]	0.721	**<0.001**
G.giga vs S.pellu[e]	**0.050**	**0.004**
F.mos vs S.sin[e]	0.609	**<0.001**
	ORAC	
-M *vs* +M	0.800	0.271
Giga vs Glome	0.617	**0.018**
G.giga vs S.pellu	0.544	**0.007**
F.mos vs S.sin	**0.036**	0.732
	Lycopene	
-M *vs* +M	0.303	0.214
Giga vs Glome	**0.012**	**<0.001**
G.giga vs S.pellu	**0.011**	0.996
F.mos vs S.sin	0.662	0.067

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (n=3); +M, AM fungal inoculation (n=12)
[c] In bold statistically significant values ($P < 0.05$)
[d] *Giga* (n=6); *Glome* (n=6)
[e] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S6 *P*-values of t-test between total phenolic content (TPC), antioxidant activity (ORAC) and lycopene in fruits and in sauce of tomato (*Solanum lycopersicum* L.) var. Pisanello and var. Rio Grande (i.e., effect of transformation process). Arbuscular mycorrhizal (AM) fungal treatment (five levels) was used as covariate in the analysis. Fruits and sauce were obtained from plants of var. Pisanello and var. Rio Grande inoculated with four AM fungal species

	var. Pisanello[a,b]	var. Rio Grande
TPC	**< 0.001**[c]	**< 0.001**
ORAC	**< 0.001**	0.920
Lycopene	0.066	**0.003**

[a] Fruits were sampled at BBCH 89 (2nd harvest): 1st August 2019 for var. Pisanello, 10th August 2020 for var. Rio Grande. BBCH 89 (fully ripe: all fruits have typical fully ripe color). The sauce was produced from the same fruits

[b] Plants were mock inoculated (control) or inoculated by the following AM fungal species: *Gigaspora gigantea* and *Scutellospora pellucida* belonging to the family Gigasporaceae; *Funneliformis mosseae* and *Sclerocystis sinuosa* belonging to the family Glomeraceae

[c] In bold statistically significant values ($P < 0.05$), (n=15)

Table S7 *P*-values of linear orthogonal contrasts on the richness (S), Shannon index (*H'*) and Simpson index (λ) of arbuscular mycorrhizal (AM) fungal phylotype found within the roots of *Solanum lycopersicum* var. Pisanello and var. Rio Grande. Plants were inoculated with four AM fungal species: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Roots were sampled at BBCH 89 (2nd harvest): 1st August 2019 for var. Pisanello, 10th August 2020 for var. Rio Grande

	var. Pisanello[a]	var. Rio Grande
	S	
-M *vs* +M[b]	**0.007**[c]	**0.010**
Giga vs Glome[d]	**0.002**	**0.001**
G.giga vs S.pellu[e]	**0.038**	-
F.mos vs S.sin[e]	**0.001**	**0.008**
	H'	
-M *vs* +M	**0.001**	**< 0.001**
Giga vs Glome	**<0.001**	**< 0.001**
G.giga vs S.pellu	**<0.001**	**< 0.001**
F.mos vs S.sin	0.335	**0.002**
	λ	
-M *vs* +M	**< 0.001**	**< 0.001**
Giga vs Glome	**< 0.001**	**< 0.001**
G.giga vs S.pellu	**< 0.001**	**< 0.001**
F.mos vs S.sin	**0.006**	**< 0.001**

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (control=3); +M, AM fungal inoculation (n=12)
[c] In bold statistically significant values ($P < 0.05$)
[d] *Giga* (n=6); *Glome* (n=6)
[e] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S8 Mean values ± SE of the richness (S), Shannon index (*H'*) and Simpson index (λ) of arbuscular mycorrhizal fungal (AMF) phylotype found within the roots of *Solanum lycopersicum* var. Pisanello and var. Rio Grande. Plants were inoculated with four arbuscular mycorrhizal (AM) fungal species: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to the family Gigasporaceae (Giga), and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to the family Glomeraceae (Glome). Roots were sampled at BBCH 89 (2nd harvest): 1st August 2019 for var. Pisanello, 10th August 2020 for var. Rio Grande

	var. Pisanello[a]	var. Rio Grande
	S	
-M[b]	6.0 ± 0.3	7.0 ± 0.0
+M[b]	5.0 ± 0.4	6.0 ± 0.9
Giga[c]	4.0 ± 0.4	4.0 ± 0.2
Glome[c]	6.0 ± 0.7	9.0 ± 0.8
G.giga[d]	3.0 ± 0.3	3.0 ± 0.0
S.pellu[d]	5.0 ± 0.3	4.0 ± 0.0
F.mos[d]	7.0 ± 1.0	11.0 ± 0.0
S.sin[d]	4.0 ± 0.3	7.0 ± 0.0
	H'	
-M[b]	0.71 ± 0.01	0.84 ± 0.00
+M	0.62 ± 0.03	0.73 ± 0.06
Giga	0.52 ± 0.03	0.54 ± 0.03
Glome	0.72 ± 0.01	0.92 ± 0.04
G.giga	0.46 ± 0.00	0.48 ± 0.00
S.pellu	0.58 ± 0.01	0.60 ± 0.00
F.mos	0.74 ± 0.01	1.02 ± 0.01
S.sin	0.69 ± 0.00	0.83 ± 0.00
	λ	
-M[b]	0.79 ± 0.01	0.90 ± 0.00
+M	0.74 ± 0.02	0.85 ± 0.02
Giga	0.69 ± 0.02	0.77 ± 0.02
Glome	0.80 ± 0.01	0.92 ± 0.01
G.giga	0.65 ± 0.01	0.73 ± 0.00
S.pellu	0.74 ± 0.01	0.81 ± 0.00
F.mos	0.79 ± 0.01	0.94 ± 0.00
S.sin	0.80 ± 0.00	0.90 ± 0.00

[a] BBCH 89 - Fully ripe: all fruits have typical fully ripe color
[b] -M, mock inoculation (n=3); +M, AM fungal inoculation (n=15)
[c] *Giga* (n=6); *Glome* (n=6)
[d] *G.giga* (n=3); *S.pellu* (n=3); *F.mos* (n=3); *S.sin* (n=3)

Table S9 Rho and *P*-values of BEST analysis using the BioEnv methods (Clark et al. 2008) on the Euclidean resemblance matrix of the square-root transformed and standardized quality parameters of fruits of *Solanum lycopersicum* L. var. Pisanello and Rio Grande with square-root transformed colonization traits and with arbuscular mycorrhizal (AM) fungal community structure. Akaike's information criterion (AICc), P and explained variation out of total variation (%) of the best descriptor/s obtained by Distance-based linear method (DistLM) analysis on the quality parameter matrix with AM fungal colonization traits and with AM fungal community structure. Plants were inoculated with four AM fungal species and mock inoculated. The quality parameters were: total phenolic content, antioxidant activity (ORAC) and lycopene of fruits. The colonization traits data were: AM fungal root colonization and root length containing arbuscules and vesicles. Roots for colonization and AM fungal community assessment and tomato fruits were sampled at BBCH 89

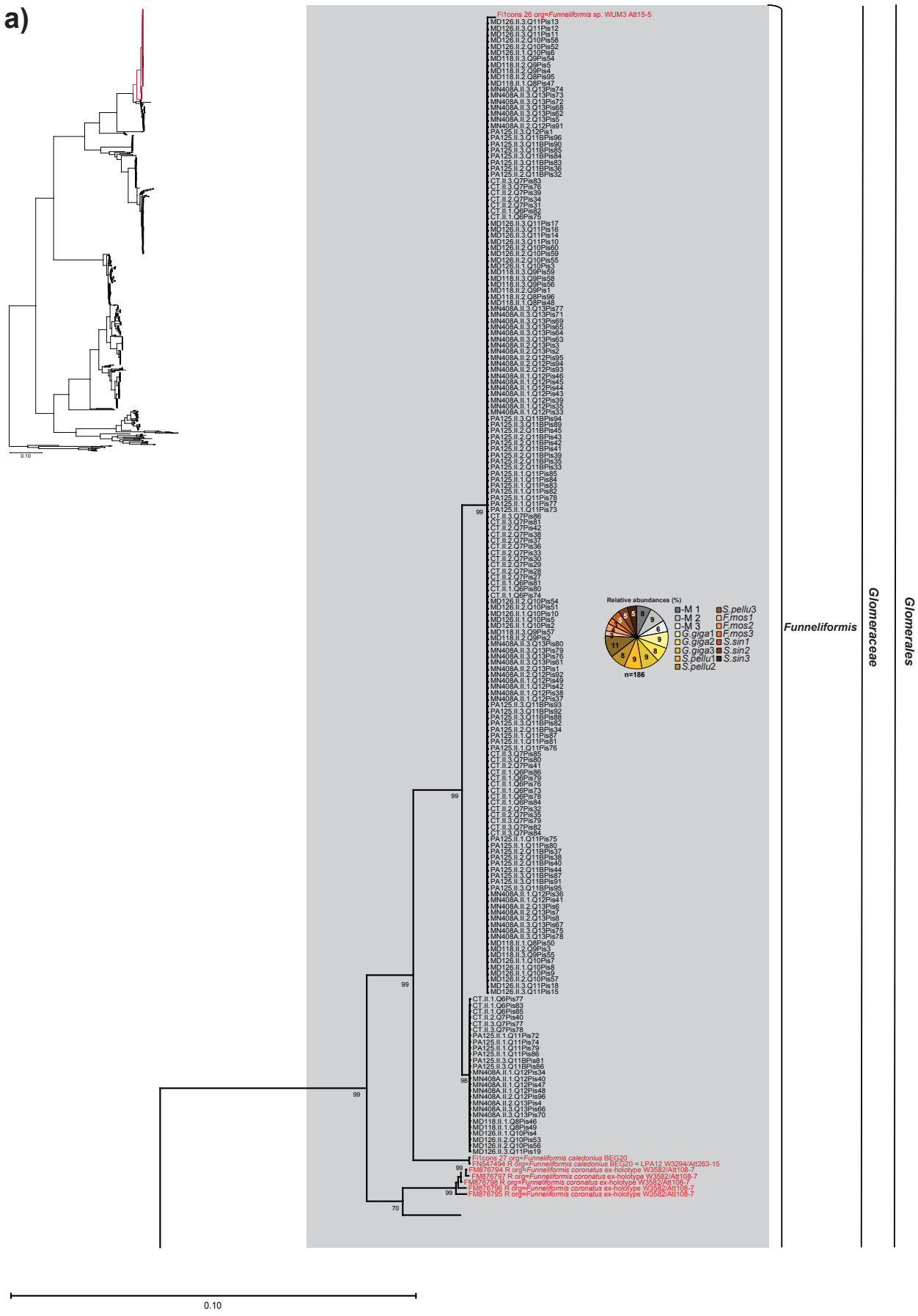
	BEST[a]									
	var. Pisanello[b]					var. Rio Grande				
	Rho		*P*			Rho		*P*		
AM fungal colonization traits	0.343		0.043 [c]			0.256		0.050		
AM fungal community structure	- [d]		-			0.735		0.001		
	DistLM									
	Variable	AICc	*P*	% explained variation out of total variation	Total variation	Variable	AICc	*P*	% explained variation out of total variation	Total variation
AM fungal colonization traits	Arbuscules	96.06	0.013	31.2	31.2	Arbuscules	97.93	0.006	25.97	31.2
	-	-	-	-	-	*Archaespora* sp.	95.16	0.001	38.5	43.71
AM fungal community structure	-	-	-	-	-	*Rhizophagus* sp.	87.08	0.002	32.5	75.6
	-	-	-	-	-	*Rhizophagus fasciculatus*	85.07	0.022	9.3	80.3

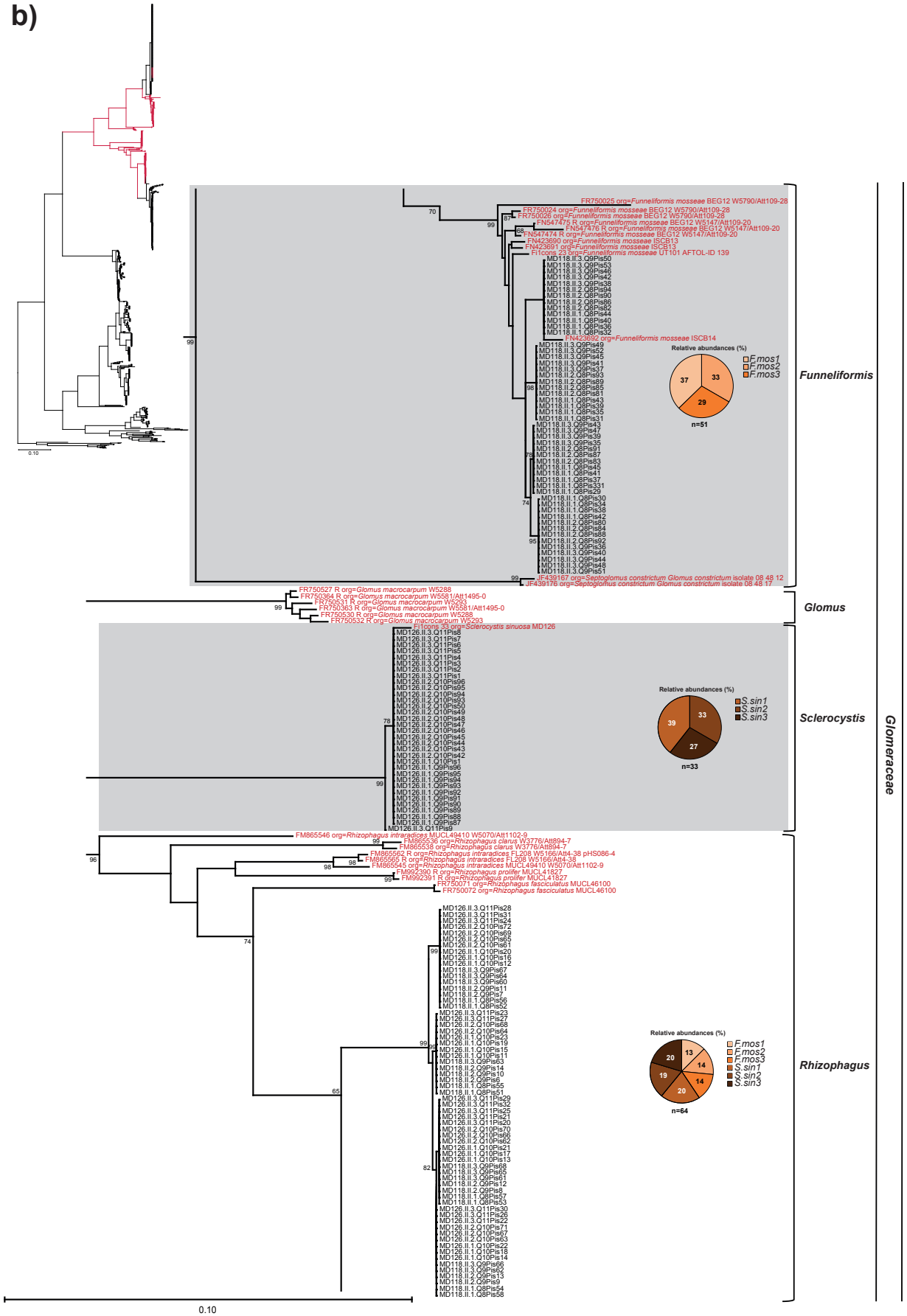
[a] BioEnv methods based on all combinations, Spearman rank and 999 permutations; DistLM using a stepwise selection and Akaike's information criterion (AICc) applied to measure the significance and the variance explained by the best descriptor/s

[b] BBCH 89 - Fully ripe: all fruits have typical fully ripe color

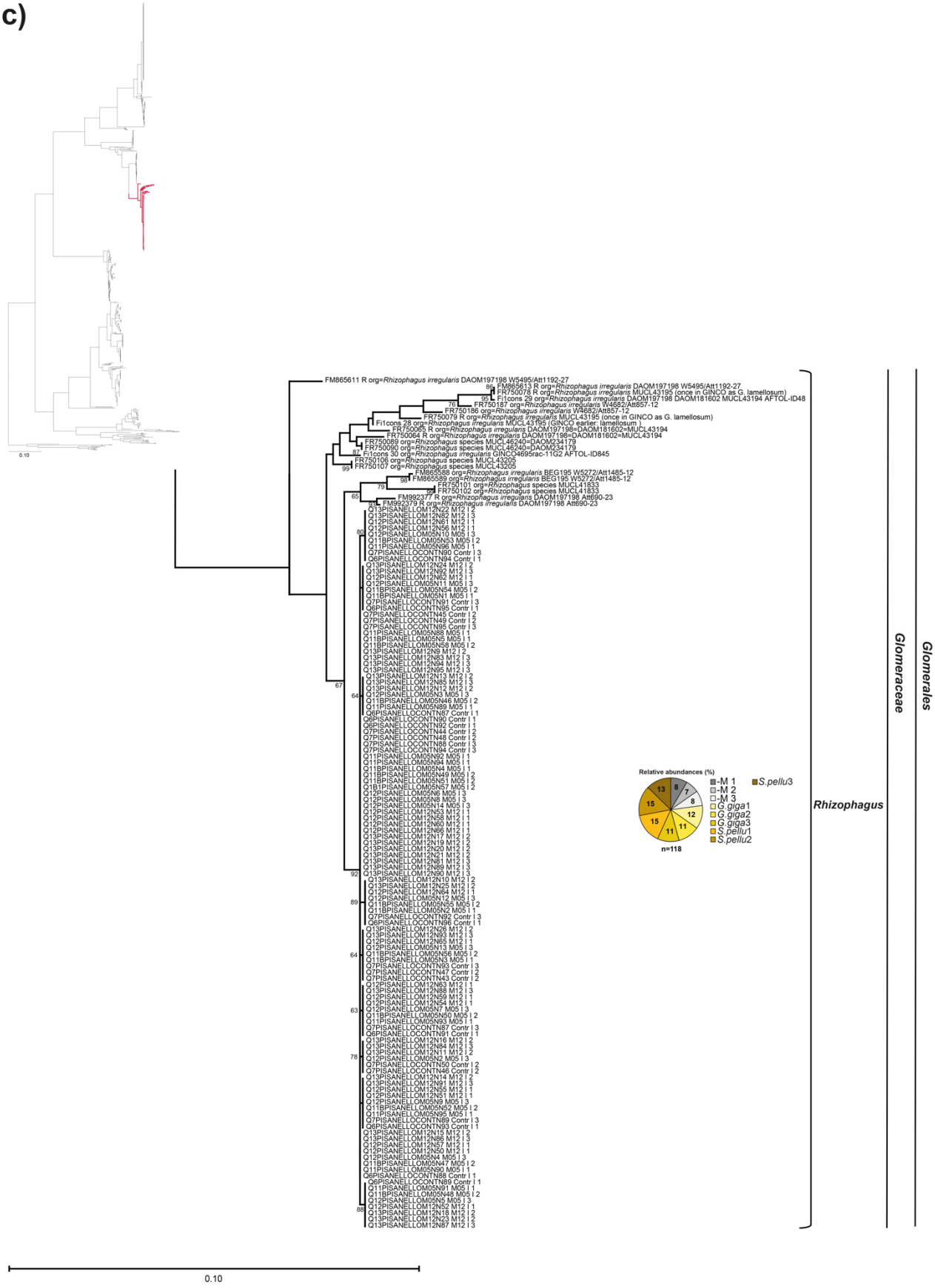
[c] Statical analyses based on 15 replicates

[d] When rho value of the RELATE analysis was non significant, BEST and DistLM analyses were not performed


a)
Fi1cons 26 org=Funneliformis sp. WUM3 Att15-5
Relative abundances (%)
n=186
M 1
M 2
M 3
G.giga1
G.giga2
G.giga3
S.pellu1
S.pellu2
S.pellu3
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
Fi1cons 27 org=Funneliformis caledonius BEG20
FN547494 R org=Funneliformis caledonius BEG20 = LPA12 W3294/Att263-15
FM876794 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876797 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876798 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876796 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876795 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
Funneliformis
Glomeraceae
Glomerales
0.10


b)
FR750025 org=Funneliformis mosseae BEG12 W5790/Att109-28
FR750024 org=Funneliformis mosseae BEG12 W5790/Att109-28
FR750026 org=Funneliformis mosseae BEG12 W5790/Att109-28
FN547475 R org=Funneliformis mosseae BEG12 W5147/Att109-20
FN547476 R org=Funneliformis mosseae BEG12 W5147/Att109-20
FN547474 R org=Funneliformis mosseae BEG12 W5147/Att109-20
FN423690 org=Funneliformis mosseae ISCB13
FN423691 org=Funneliformis mosseae ISCB13
Ftconis 23 org=Funneliformis mosseae UT101 AFTOL-ID 139
FN423692 org=Funneliformis mosseae ISCB14
Relative abundances (%)
F.mos1
F.mos2
F.mos3
37
33
29
n=51
JF439167 org=Septoglomus constrictum Glomus constrictum isolate 08 48 12
JF439176 org=Septoglomus constrictum Glomus constrictum isolate 08 48 17
Funneliformis
FR750527 R org=Glomus macrocarpum W5288
FR750364 R org=Glomus macrocarpum W5581/Att1495-0
FR750531 R org=Glomus macrocarpum W5293
FR750363 R otg=Glomus macrocarpum W5581/Att1495-0
FR750530 R otg=Glomus macrocarpum W5288
FR750532 R org=Glomus macrocarpum W5293
Glomus
Ftconis 33 org=Sclerocystis sinuosa MD126
Relative abundances (%)
S.sin1
S.sin2
S.sin3
39
33
27
n=33
Sclerocystis
FM865546 org=Rhizophagus intraradices MUCL49410 W5070/Att1102-9
FM865536 org=Rhizophagus clarus W3776/Att894-7
FM865538 org=Rhizophagus clarus W3776/Att894-7
FM865562 R org=Rhizophagus intraradices FL208 W5166/Att4-38 pHS086-4
FM865565 R org=Rhizophagus intraradices FL208 W5166/Att4-38
FM865545 org=Rhizophagus intraradices MUCL49410 W5070/Att1102-9
FM992390 R org=Rhizophagus prolifer MUCL41827
FM992391 R otg=Rhizophagus prolifer MUCL41827
FR750071 org=Rhizophagus fasciculatus MUCL46100
FR750072 org=Rhizophagus fasciculatus MUCL46100
Relative abundances (%)
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
20
13
14
19
14
20
n=64
Rhizophagus
Glomeraceae
Glomerales
0.10

c)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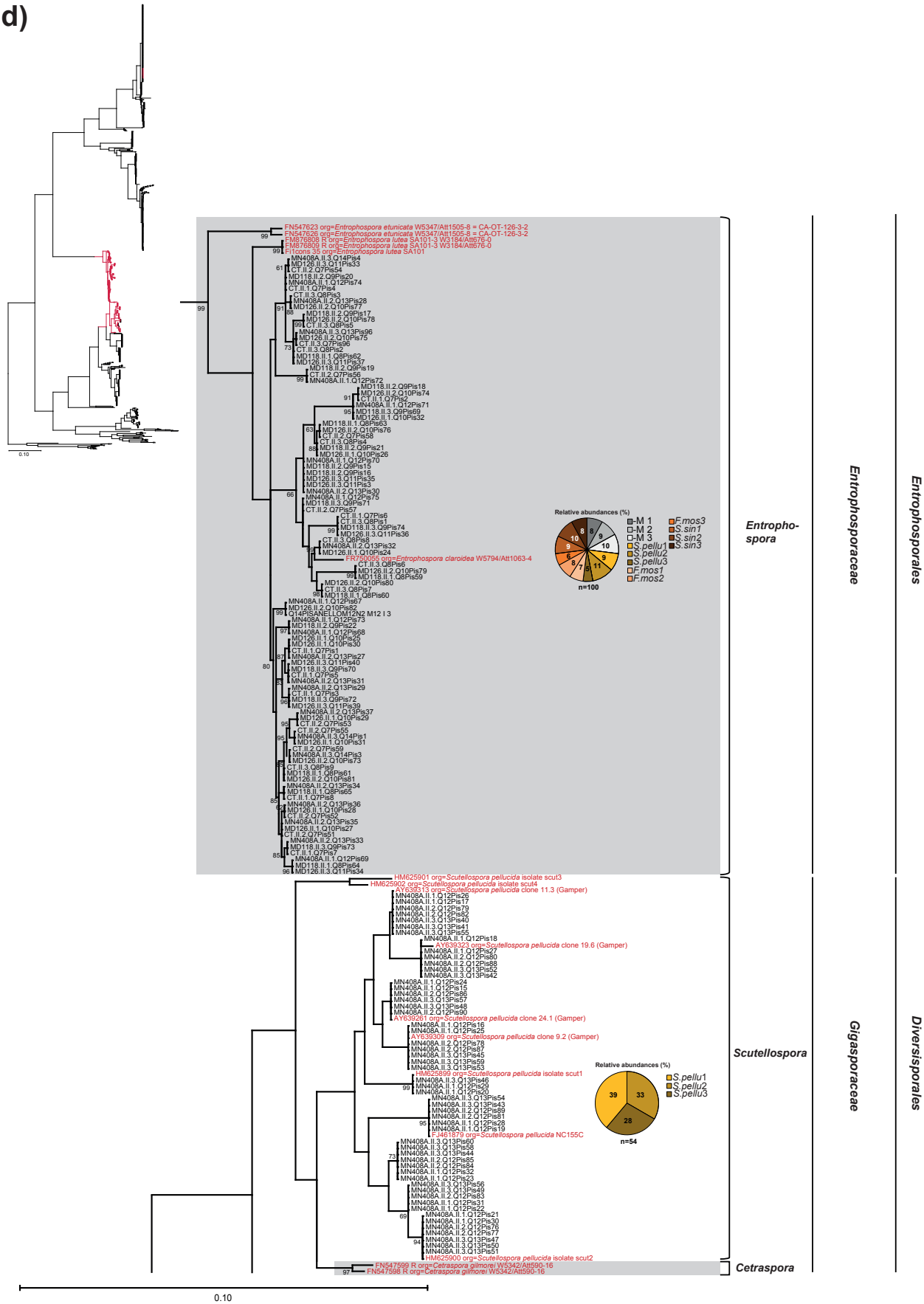
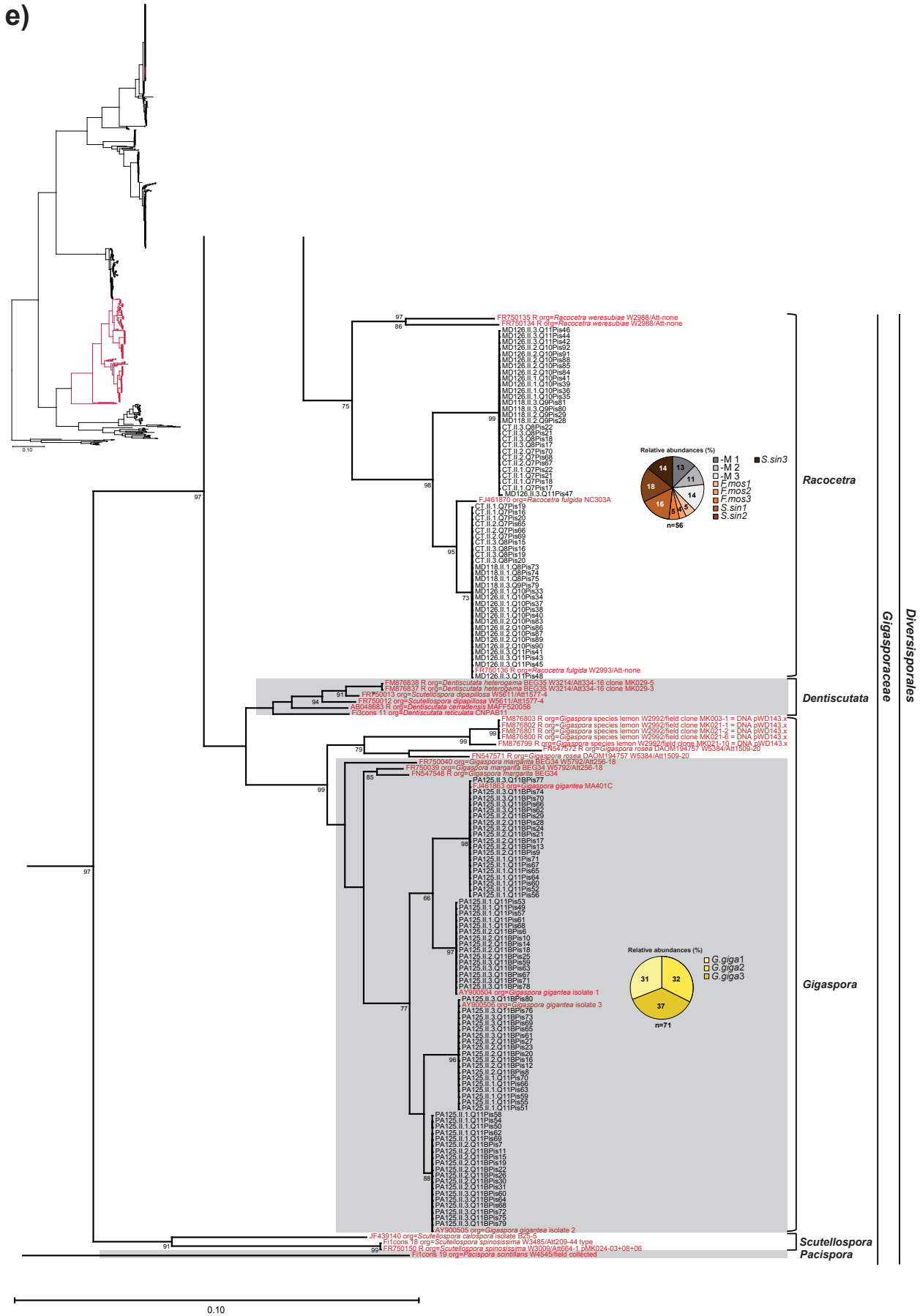
FM865613 R org=Rhizophagus irregularis DAOM197198 W5495/Att1192-27
FR750078 R org=Rhizophagus irregularis MUCL43195 (once in GINCO as G. lamellosum)
Fi1cons 29 org=Rhizophagus irregularis DAOM197198 DAOM181602 MUCL43194 AFTOL-ID48
FR750187 org=Rhizophagus irregularis W4682/Att857-12
FR750186 org=Rhizophagus irregularis W4682/Att857-12
FR750079 R org=Rhizophagus irregularis MUCL43195 (once in GINCO as G. lamellosum)
Fi1cons 28 org=Rhizophagus irregularis MUCL43795 (GINCO earlier: lamellosum
FR750065 R org=Rhizophagus irregularis DAOM197198=DAOM181602=MUCL43194
FR750064 R org=Rhizophagus irregularis DAOM197198=DAOM181602=MUCL43194
FR750089 org=Rhizophagus species MUCL46240=DAOM234179
FR750090 org=Rhizophagus species MUCL46240=DAOM234179
Fi1cons 30 org=Rhizophagus irregularis GINCO4695rac-11G2 AFTOL-ID845
FR750106 org=Rhizophagus species MUCL43205
FR750107 org=Rhizophagus species MUCL43205
FM865588 org=Rhizophagus irregularis BEG195 W5272/Att1485-12
FM865589 org=Rhizophagus irregularis BEG195 W5272/Att1485-12
FR750101 org=Rhizophagus species MUCL41833
FR750102 org=Rhizophagus species MUCL41833
FM992377 R org=Rhizophagus irregularis DAOM197198 Att690-23
FM992379 R org=Rhizophagus irregularis DAOM197198 Att690-23
Relative abundances (%)
-M 1
-M 2
-M 3
G.giga1
G.giga2
G.giga3
S.pellu1
S.pellu2
S.pellu3
n=118
Rhizophagus
Glomeraceae
Glomerales
0.10

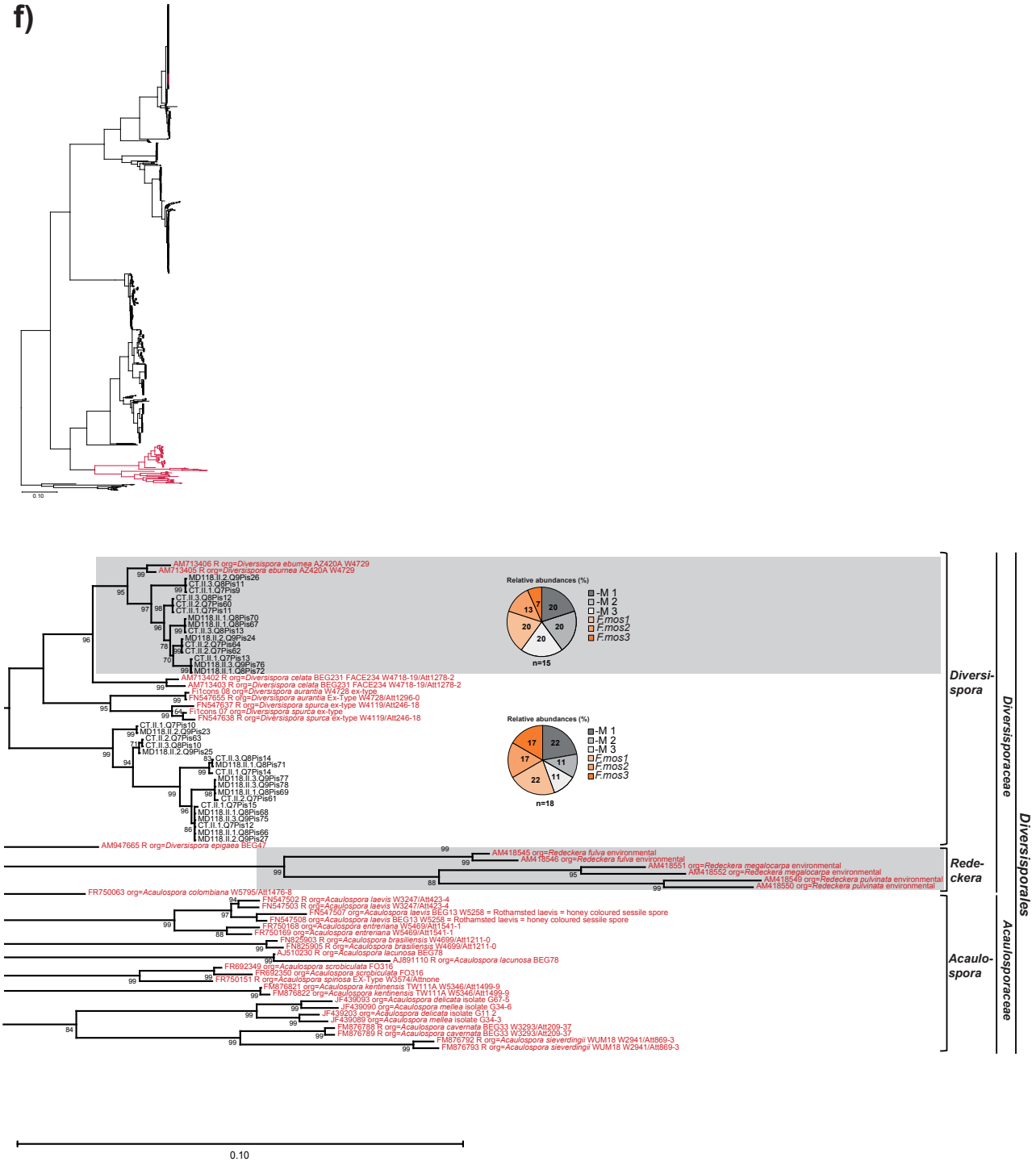
d)



FN547623 org=Entrophospora etunicata W5347/Att1505-8 = CA-OT-126-3-2
FN547626 org=Entrophospora etunicata W5347/Att1505-8 = CA-OT-126-3-2
FM876808 R org=Entrophospora lutea SA101-3 W3184/Att676-0
FM876809 R org=Entrophospora lutea SA101-3 W3184/Att676-0
Fi1cons 35 org=Entrophospora lutea SA101
FR750055 org=Entrophospora claroidea W5794/Att1063-4
Relative abundances (%)
M 1
M 2
M 3
F.mos3
S.sin1
S.sin2
S.sin3
S.pellu1
S.pellu2
S.pellu3
F.mos1
F.mos2
n=100
Entropho-
spora
Entrophosporaceae
Entrophosporales
HM625901 org=Scutellospora pellucida isolate scut3
HM625902 org=Scutellospora pellucida isolate scut4
AY639313 org=Scutellospora pellucida clone 11.3 (Gamper)
AY639323 org=Scutellospora pellucida clone 19.6 (Gamper)
AY639261 org=Scutellospora pellucida clone 24.1 (Gamper)
AY639309 org=Scutellospora pellucida clone 9.2 (Gamper)
HM625899 org=Scutellospora pellucida isolate scut1
F.461879 org=Scutellospora pellucida NC155C
HM625900 org=Scutellospora pellucida isolate scut2
Relative abundances (%)
S.pellu1
S.pellu2
S.pellu3
n=54
Scutellospora
Gigasporaceae
Diversisporales
FN547599 R org=Cetraspora gilmorei W5342/Att590-16
FN547598 R org=Cetraspora gilmorei W5342/Att590-16
Cetraspora
0.10


e)
Racocetra
Dentiscutata
Gigaspora
Scutellospora
Pacispora
Gigasporaceae
Diversisporales
Relative abundances (%)
n=56
n=71
0.10

f)


Relative abundances (%)
-M 1
-M 2
-M 3
F.mos1
F.mos2
F.mos3
n=15
n=18
Diversi-spora
Rede-ckera
Acaulo-spora
Diversisporaceae
Acaulosporaceae
Diversisporales
0.10

g)

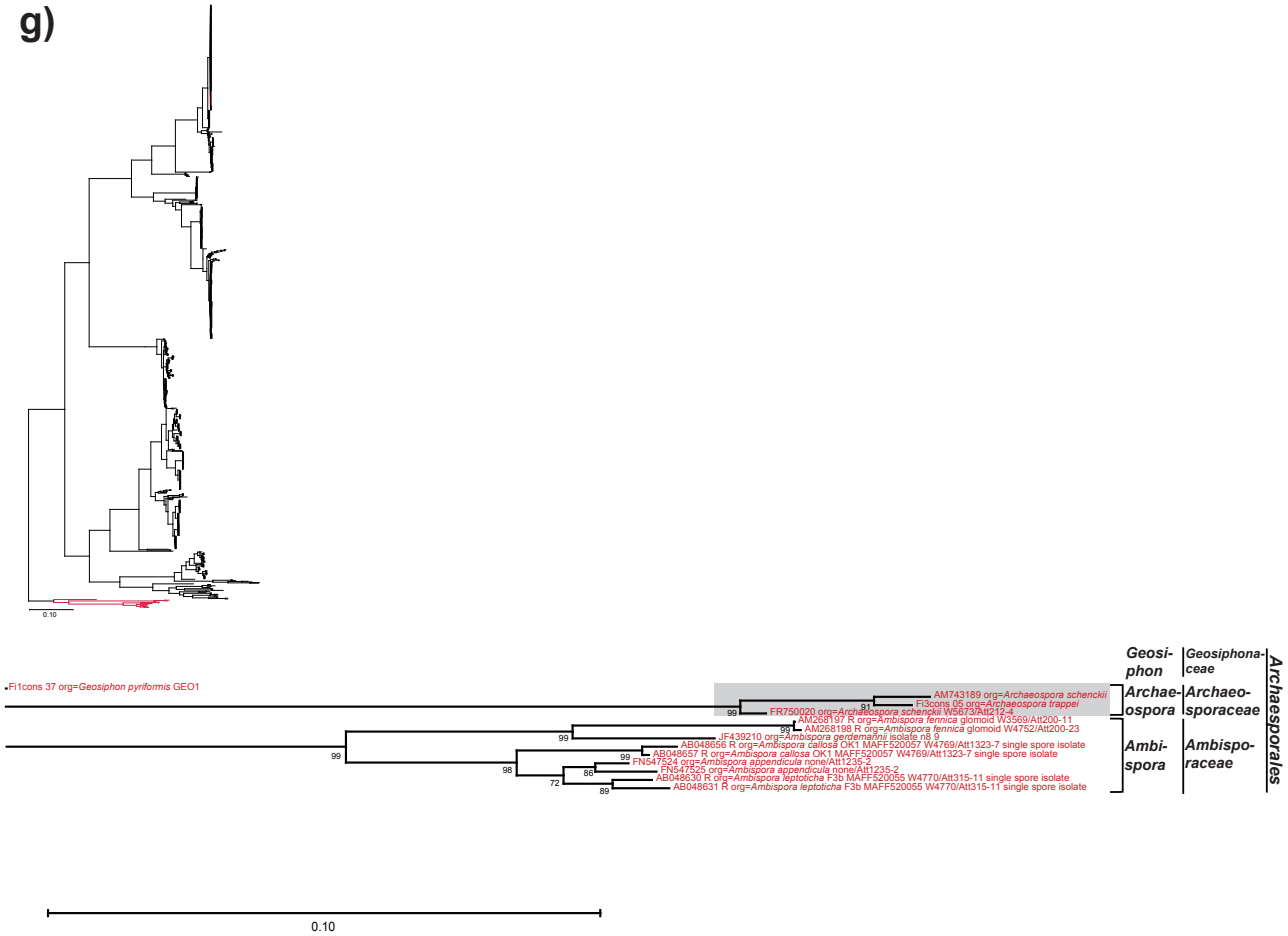
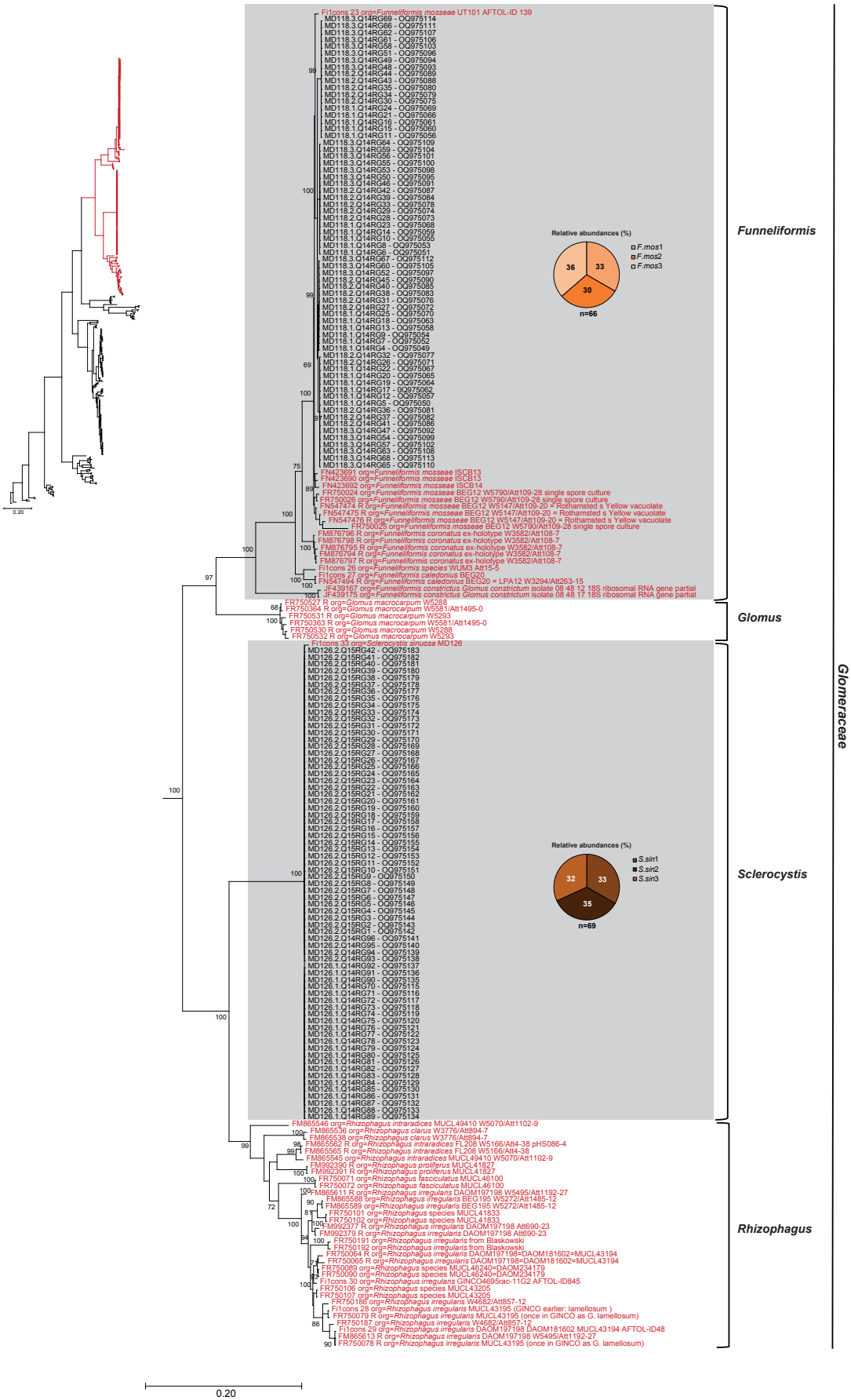
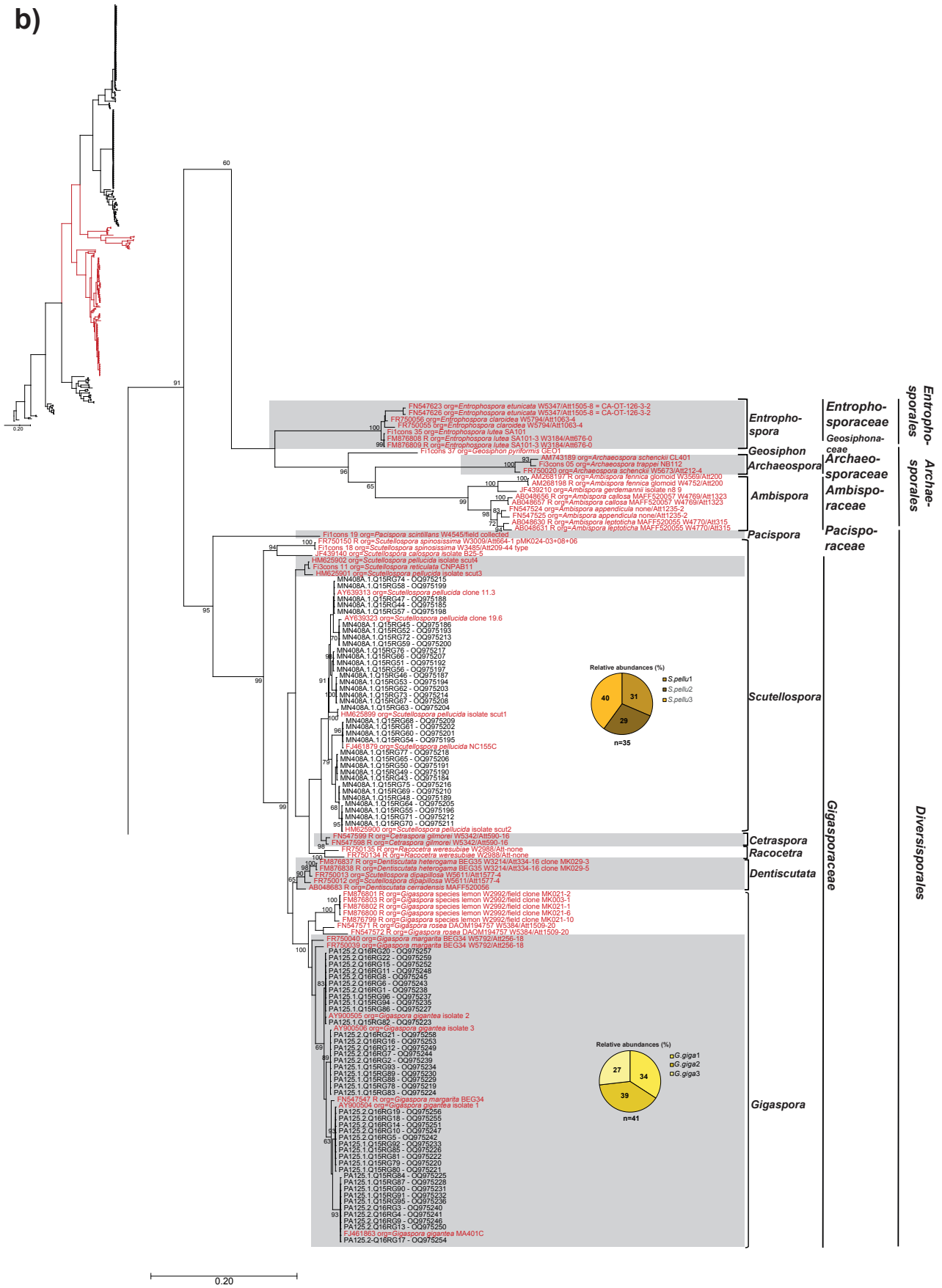

Fi1cons 37 org=Geosiphon pyriformis GEO1
AM743189 org=Archaeospora schenckii
Fi3cons 05 org=Archaeospora trappei
FR750020 org=Archaeospora schenckii W5673/Att212-4
AM268197 R org=Ambispora fennica glomoid W3569/Att200-11
AM268198 R org=Ambispora fennica glomoid W4752/Att200-23
JF439210 org=Ambispora gerdemanniii isolate ri9.9
AB048656 R org=Ambispora callosa OK1 MAFF520057 W4769/Att1323-7 single spore isolate
AB048657 R org=Ambispora callosa OK1 MAFF520057 W4769/Att1323-7 single spore isolate
FN547524 org=Ambispora appendicula none/Att1235-2
FN547525 org=Ambispora appendicula none/Att1235-2
AB048630 R org=Ambispora leptoticha F3b MAFF520055 W4770/Att315-11 single spore isolate
AB048631 R org=Ambispora leptoticha F3b MAFF520055 W4770/Att315-11 single spore isolate
Geosi-phon
Geosiphona-ceae
Archae-ospora
Archaeo-sporaceae
Ambi-spora
Ambispo-raceae
Archaesporales
0.10

Fig. S1 Maximum Likelihood (ML) tree of sequences of arbuscular mycorrhizal fungi (AMF; Glomeromycota) retrieved at 2nd harvest within the roots of tomato (*Solanum lycopersicum* L.) var. Pisanello inoculated with AMF at nursery and mock inoculated (control, -M). Inocula were: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to Gigasporaceae, and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to Glomeraceae. The ML tree is based on sequences obtained from the amplification of part of the SSU, the complete ITS region, and ca. 0.8 kb of the LSU rRNA gene (ca. 1500-bp-long fragment) (Krüger et al. 2009). Fragments were amplified using the primer pair SSUmAf–LSUmAr and then the SSUmCf and LSUmBr as nested primers. The tree is composed by 765 newly generated sequences belonging to 11 phylotypes, plus 161 reference sequences from NCBI. Bootstrap values (based on 1 000 replicates) are shown at the nodes. The Tamura-Nei model was used in the analysis (Tamura and Nei 1993). The scale bar indicates substitutions per site. Portions of the ML tree are shown (a-g). Pie charts represent the percentage of clones of each phylotype in the three replicates of each treatment. The sequences of *Paraglomus occultum* IA702 was used as outgroup. The newly generated sequences are black coloured, while the reference sequences from NCBI are red coloured. The newly generated sequences are named as follows (e.g. MD126.II.3.Q11Pis13): MD126 refers to the AM fungal isolate (see Table S1); II refers to the second harvest; 3 refers to the number of replicate plot; Q11 refers the number of the plate of the Sanger Run; Pis refers to variety Pisanello; 13 refers to the number of the clones within the specific AM fungal treatment and replicate plot. Evolutionary analyses were conducted in MEGA 11 (Stecher et al. 2020; Tamura et al. 2021). All representative newly generated sequences were deposited in the NCBI Sequence Read (SRA) database as SUB13362899.

a)


Relative abundances (%)
F.mos1
F.mos2
F.mos3
36
33
30
n=66
Relative abundances (%)
S.sin1
S.sin2
S.sin3
32
33
35
n=69
Funneliformis
Glomus
Sclerocystis
Rhizophagus
Glomeraceae
Glomerales
0.20


b)
Entrophospora
Geosiphon
Archaeospora
Ambispora
Pacispora
Scutellospora
Cetraspora
Racocetra
Dentiscutata
Gigaspora
Entrophosporaceae
Geosiphonaceae
Archaeosporaceae
Ambisporaceae
Pacisporaceae
Gigasporaceae
Entrophosporales
Archaeosporales
Diversisporales
Relative abundances (%)
S.pellu1
S.pellu2
S.pellu3
40
31
29
n=35
Relative abundances (%)
G.giga1
G.giga2
G.giga3
27
34
39
n=41
0.20

c)

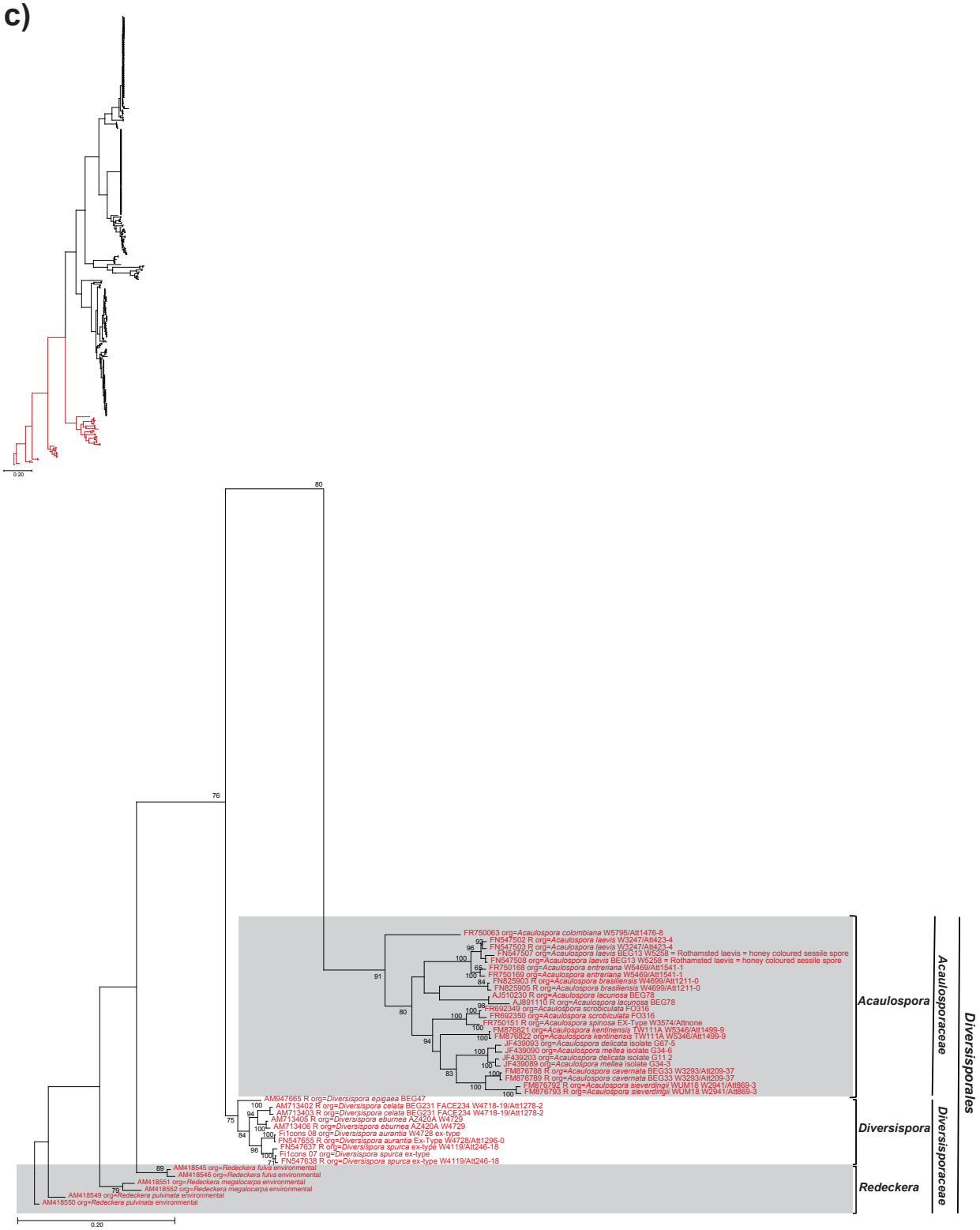

FR750063 org=Acaulospora colombiana W5795/Att1476-8
FN547502 R org=Acaulospora laevis W3247/Att423-4
FN547503 R org=Acaulospora laevis W3247/Att423-4
FN547507 org=Acaulospora laevis BEG13 W5258 = Rothamsted laevis = honey coloured sessile spore
FN547508 org=Acaulospora laevis BEG13 W5258 = Rothamsted laevis = honey coloured sessile spore
FR750168 org=Acaulospora entreriana W5469/Att1541-1
FR750169 org=Acaulospora entreriana W5469/Att1541-1
FN825903 R org=Acaulospora brasiliensis W4699/Att1211-0
FN825905 R org=Acaulospora brasiliensis W4699/Att1211-0
AJ510230 R org=Acaulospora lacunosa BEG78
AJ691110 R org=Acaulospora lacunosa BEG78
FR692349 org=Acaulospora scrobiculata FO316
FR692350 org=Acaulospora scrobiculata FO316
FR750151 R org=Acaulospora spinosa EX-Type W3574/Attnone
FM876821 org=Acaulospora kentinensis TW111A W5346/Att1499-9
FM876822 org=Acaulospora kentinensis TW111A W5346/Att1499-9
JF439093 org=Acaulospora delicata isolate G67-5
JF439090 org=Acaulospora mellea isolate G34-6
JF439203 org=Acaulospora delicata isolate G11 2
JF439089 org=Acaulospora mellea isolate G34-3
FM876788 R org=Acaulospora cavernata BEG33 W3293/Att209-37
FM876789 R org=Acaulospora cavernata BEG33 W3293/Att209-37
FM876792 R org=Acaulospora sieverdingii WUM18 W2941/Att869-3
FM876793 R org=Acaulospora sieverdingii WUM18 W2941/Att869-3
AM947665 R org=Diversispora epigaea BEG47
AM713402 R org=Diversispora celata BEG231 FACE234 W4718-19/Att1278-2
AM713403 R org=Diversispora celata BEG231 FACE234 W4718-19/Att1278-2
AM713405 R org=Diversispora eburnea AZ420A W4729
AM713406 R org=Diversispora eburnea AZ420A W4729
Fi1cons 08 org=Diversispora aurantia W4728 ex-type
FN547655 R org=Diversispora aurantia Ex-Type W4728/Att1296-0
FN547637 R org=Diversispora spurca ex-type W4119/Att246-18
Fi1cons 07 org=Diversispora spurca ex-type
FN547638 R org=Diversispora spurca ex-type W4119/Att246-18
AM418545 org=Redeckera fulva environmental
AM418546 org=Redeckera fulva environmental
AM418551 org=Redeckera megalocarpa environmental
AM418552 org=Redeckera megalocarpa environmental
AM418549 org=Redeckera pulvinata environmental
AM418550 org=Redeckera pulvinata environmental
0.20
Acaulospora
Diversispora
Redeckera
Acaulosporaceae
Diversisporaceae
Diversisporales

Fig. S2 Maximum Likelihood (ML) tree of sequences of AMF (Glomeromycota) retrieved at transplanting within the roots of tomato (*Solanum lycopersicum* L.) var. Rio Grande inoculated with AMF at nursery and mock inoculated (control, -M). Inocula were: *Gigaspora gigantea* (*G.giga*) *and Scutellospora pellucida* (*S.pellu*) belonging to Gigasporaceae, and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to Glomeraceae. The ML tree is based on sequences obtained from the amplification of part of the SSU, the complete ITS region, and ca. 0.8 kb of the LSU rRNA gene (ca. 1500-bp-long fragment) (Krüger et al. 2009). Fragments were amplified using the primer pair SSUmAf–LSUmAr and then the SSUmCf and LSUmBr as nested primers. The tree is composed by 211 newly generated sequences belonging to four phylotypes, plus 158 reference sequences from NCBI. Bootstrap values (based on 1 000 replicates) are shown at the nodes. The Tamura-Nei model was used in the analysis (Tamura and Nei 1993). The scale bar indicates substitutions per site. Portions of the ML tree are shown (a-c). Pie charts represent the percentage of clones of each phylotype in the three replicates of each treatment. The sequences of *Paraglomus occultum* IA702 was used as outgroup. The newly generated sequences are black coloured, while the reference sequences from NCBI are red coloured. The newly generated sequences are named as follows (e.g. MD118.3.Q14RG69): MD118 refers to the AM fungal isolate (see Table S1); 3 refers to the number of replicate plot; Q14 refers the number of the plate of the Sanger Run; RG refers to variety Rio Grande; 69 refers to the number of the clones within the specific AM fungal treatment and replicate plot. Evolutionary analyses were conducted in MEGA 11 (Stecher et al. 2020; Tamura et al. 2021). All representative newly generated sequences were deposited in the NCBI Sequence Read (SRA) database as SUB13324118 and numbers of accession are OQ975049-OQ975259.

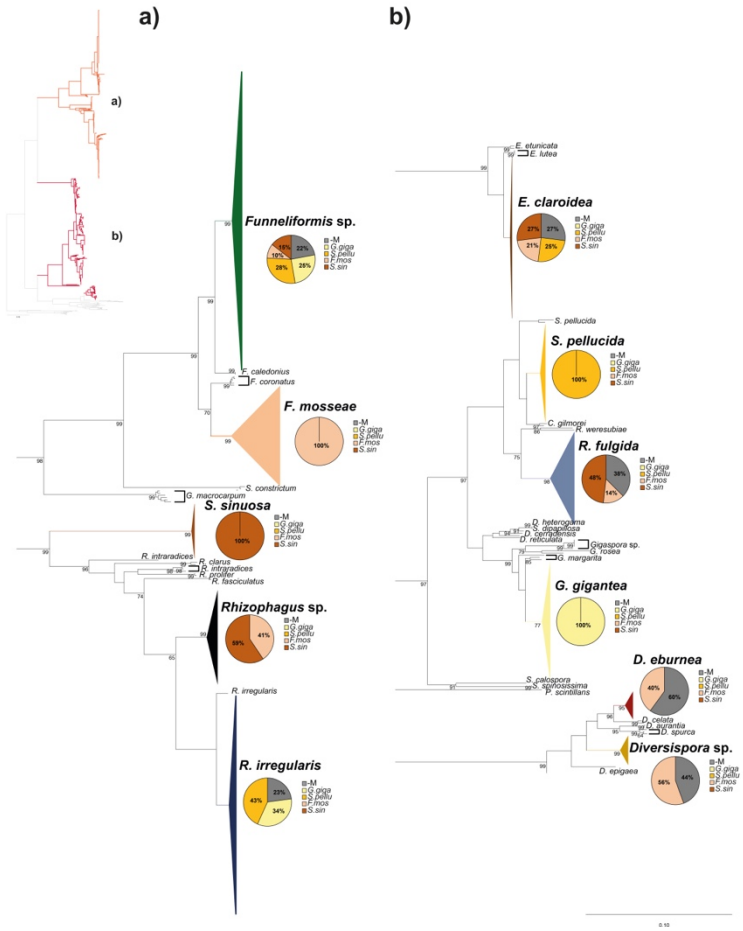
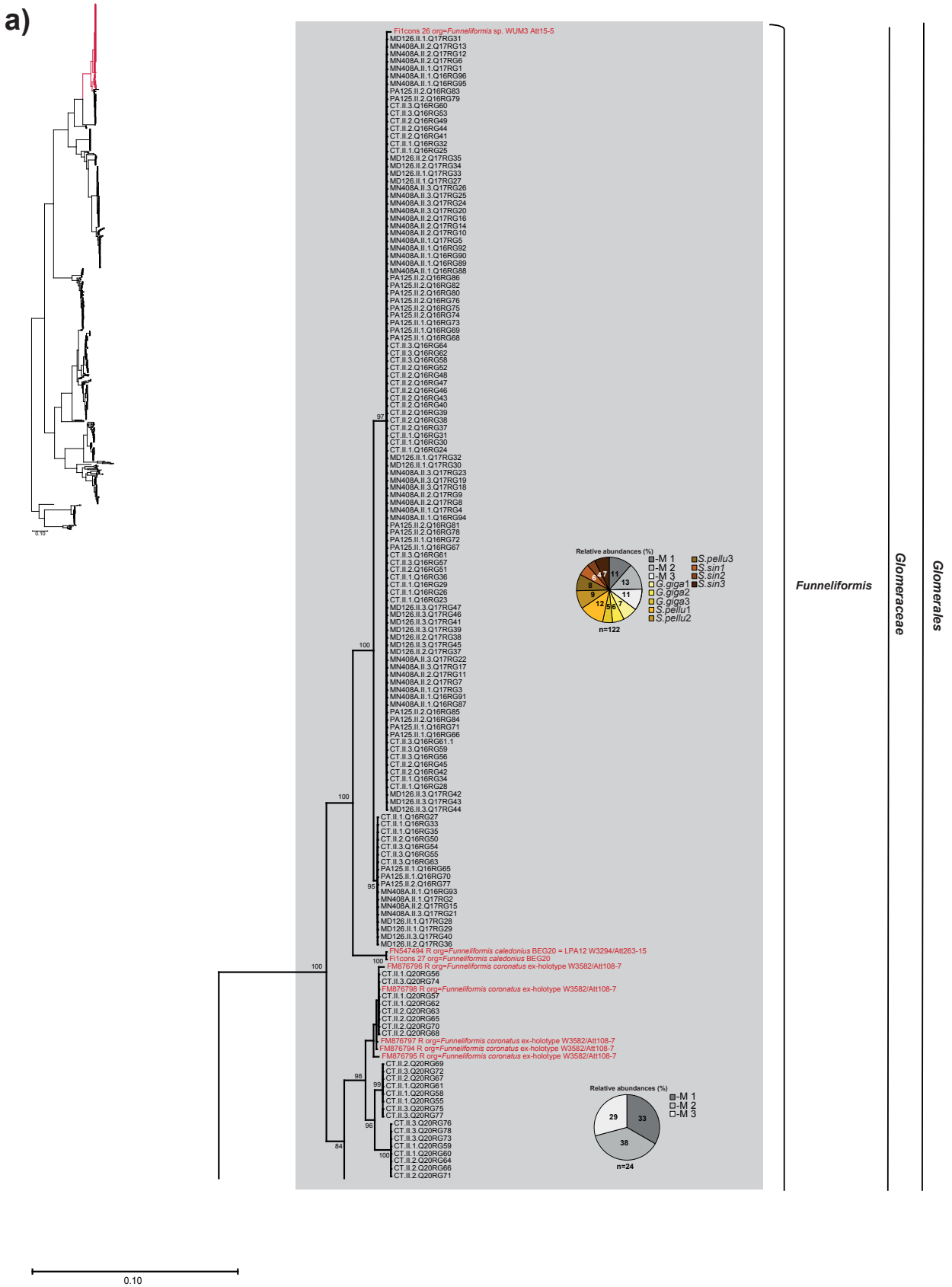
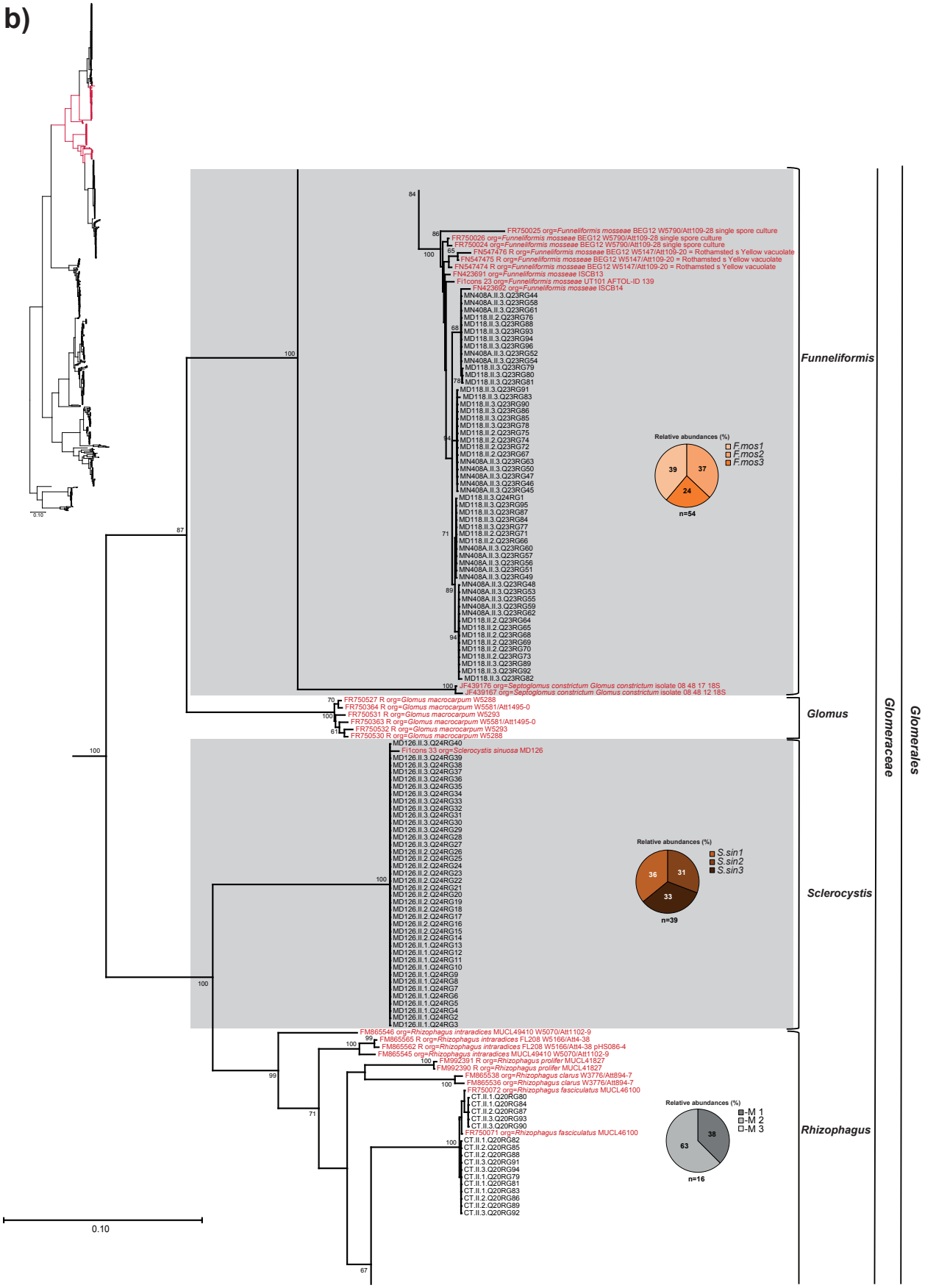
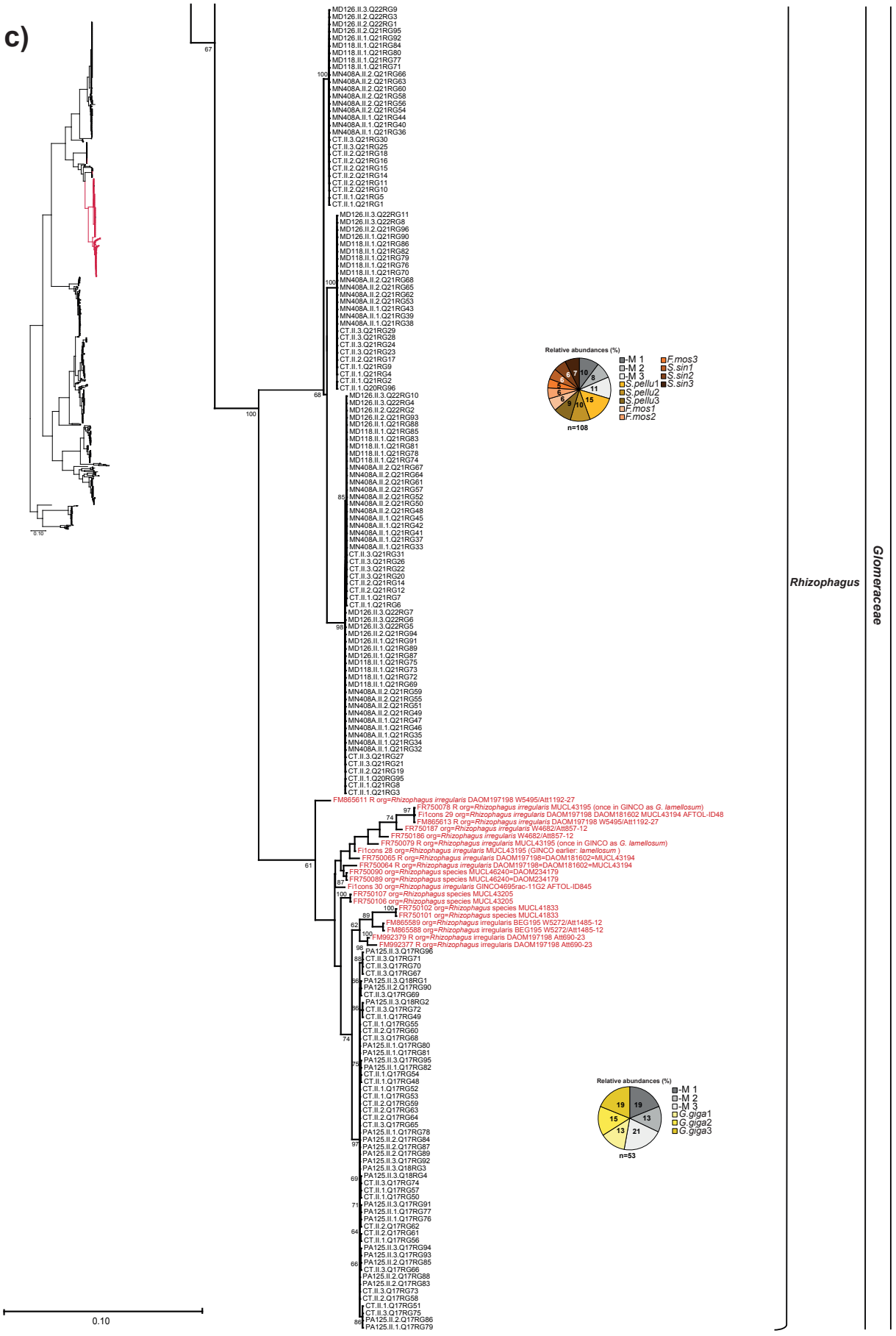
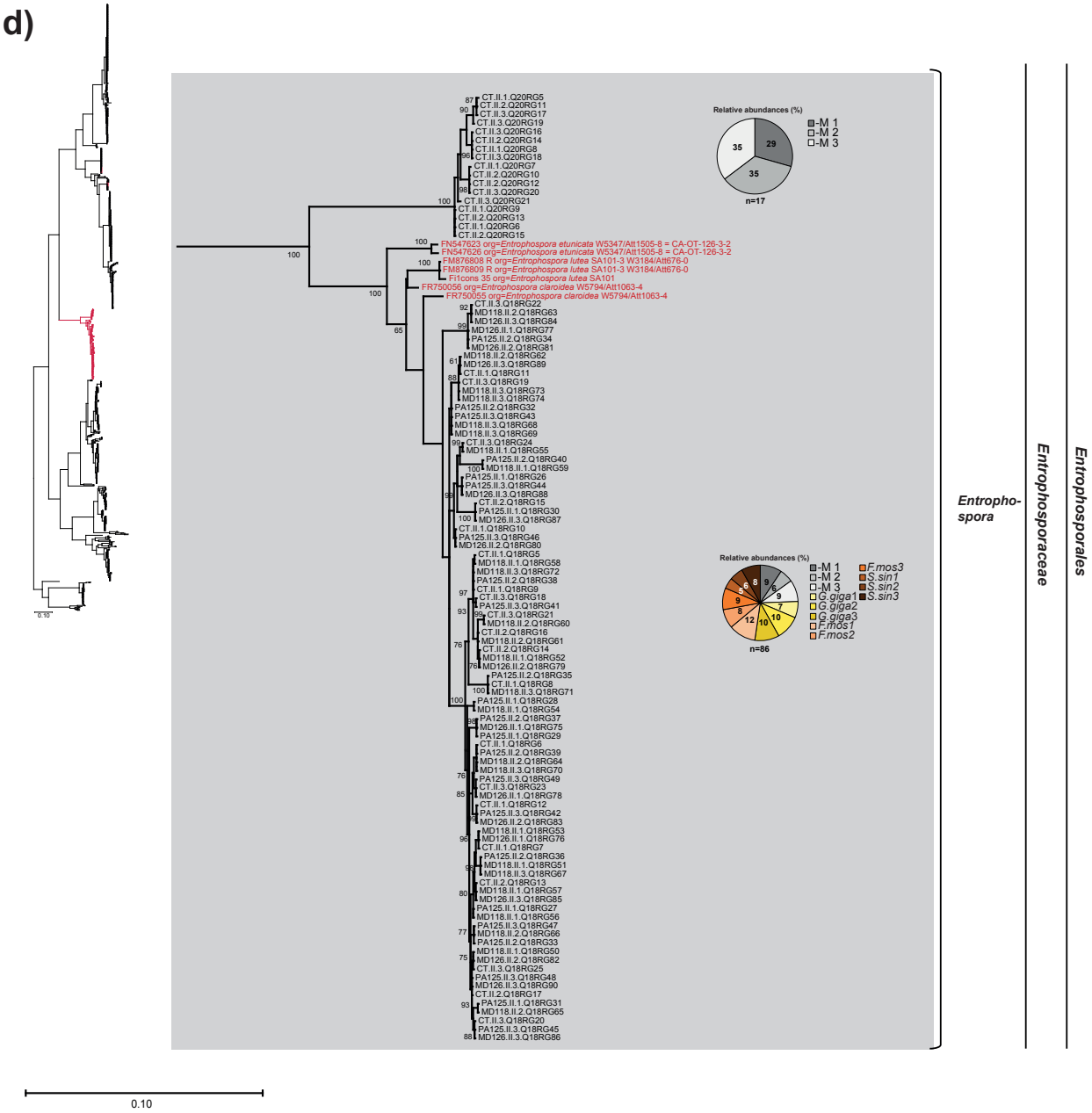


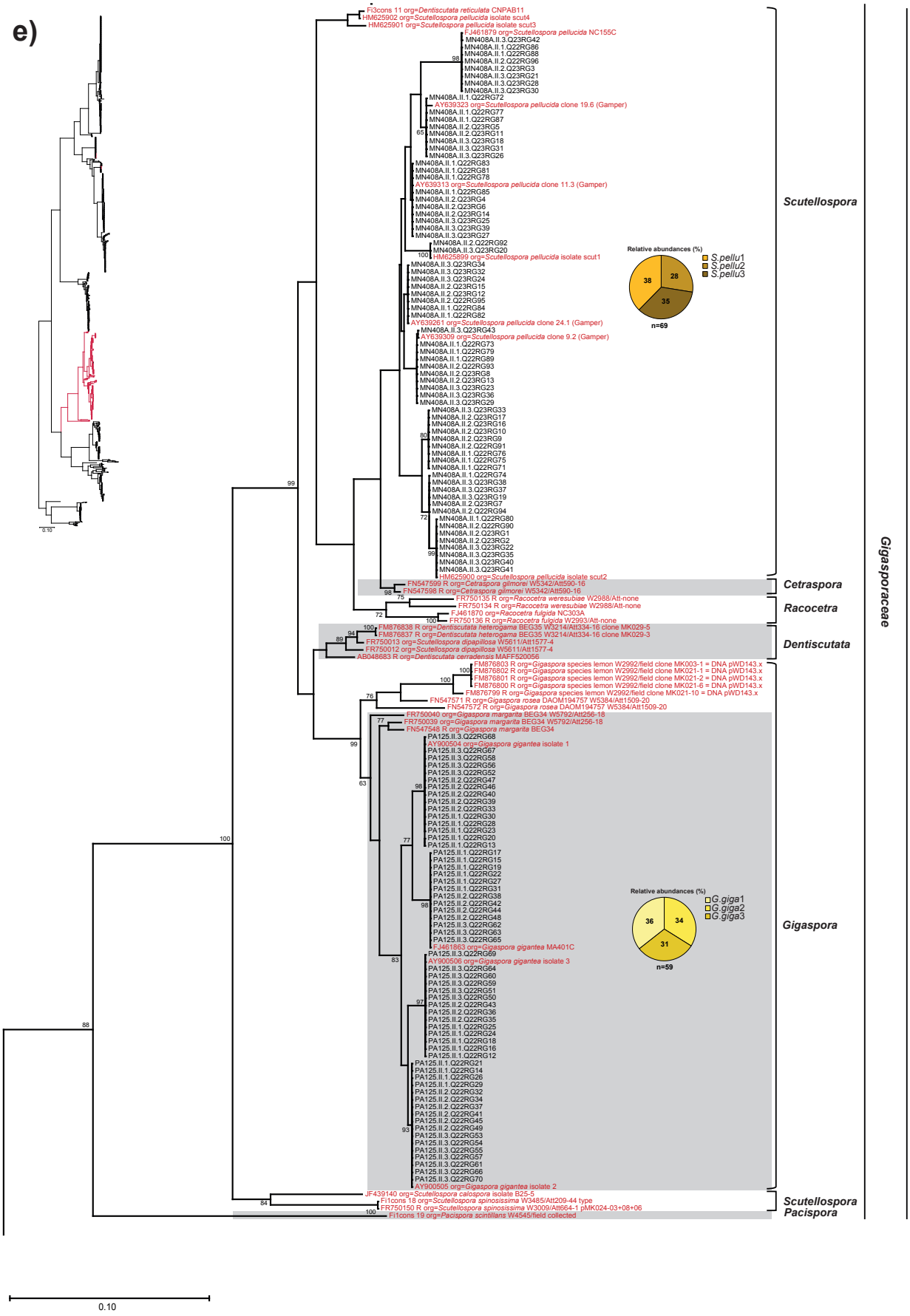
Fig. S3 Collapsed Maximum Likelihood (ML) tree of sequences of AMF (Glomeromycota) retrieved at transplanting within the roots of tomato (*Solanum lycopersicum* L.) var. Rio Grande inoculated with AMF at nursery and mock inoculated (control, -M). Inocula were: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to Gigasporaceae, and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to Glomeraceae. The ML tree is based on sequences obtained from the amplification of part of the SSU, the complete ITS region, and ca. 0.8 kb of the LSU rRNA gene (ca. 1500-bp-long fragment) (Krüger et al. 2009). Fragments were amplified using the primer pair SSUmAf–LSUmAr and then the SSUmCf and LSUmBr as nested primers. The tree is composed by 211 newly generated sequences belonging to four phylotypes, plus 158 reference sequences from NCBI (see Fig. S2 for the whole ML tree including the accession numbers of the newly generated and reference AM fungal sequences). Bootstrap values (based on 1 000 replicates) are shown at the nodes. The Tamura-Nei model was used in the analysis (Tamura and Nei 1993). The scale bar indicates substitutions per site. Portions of the ML tree are shown (a) and (b). Collapsed phylotypes are shown by coloured branches and triangles. Pie charts represent the relative abundances of each phylotypes (calculated as number of clones in each treatment divided by total number of clones of the phylotype and multiplied by 100). The sequences of *Paraglomus occultum* IA702 was used as outgroup. The newly generated sequences are highlighted in boldface, see collapsed branches. Evolutionary analyses were conducted in MEGA 11 (Stecher et al. 2020; Tamura et al. 2021).

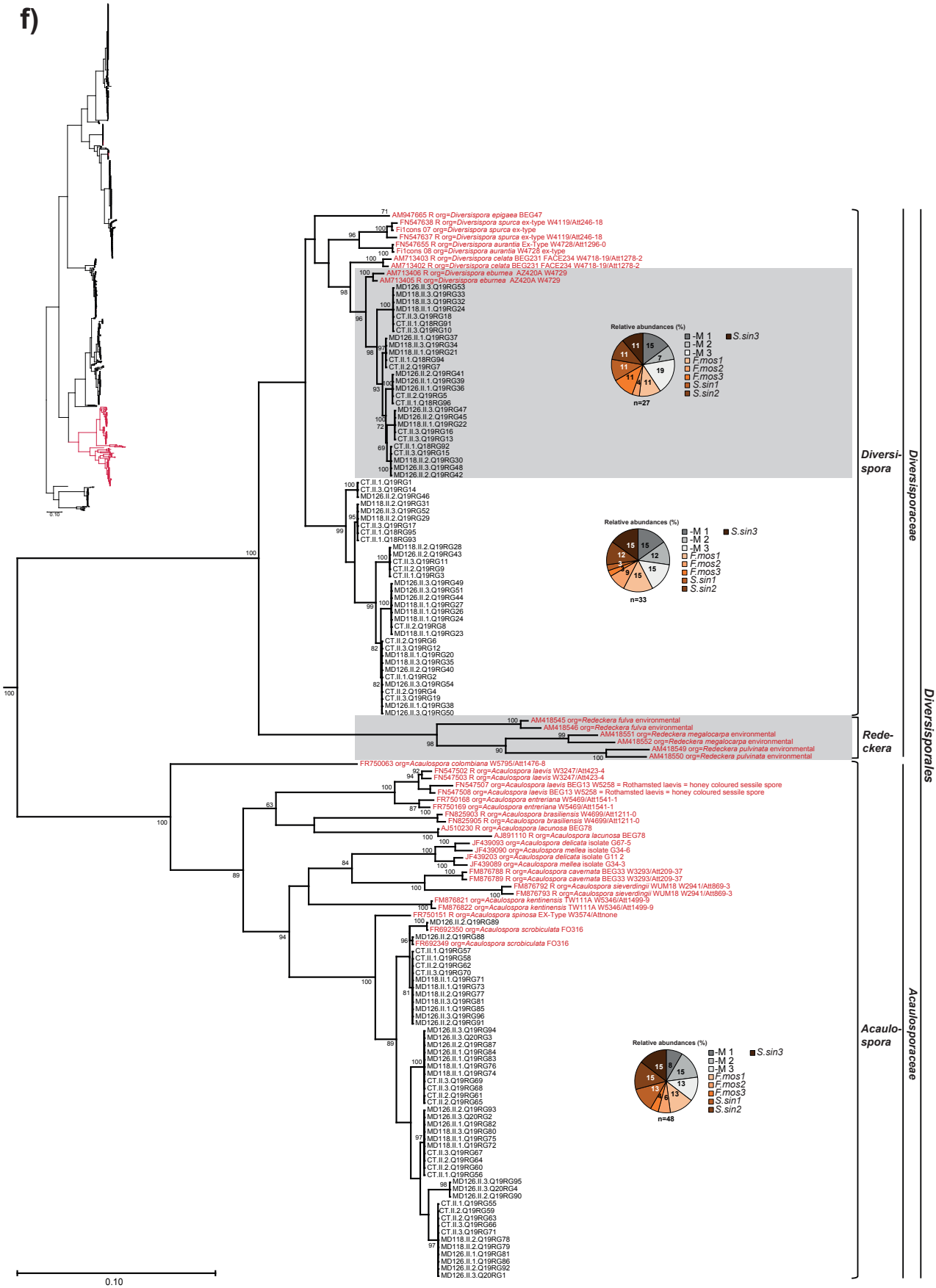

a)
Fi1cons 26 org=Funneliformis sp. WUM3 Att15-5
MD126.II.1.Q17RG31
MN408A.II.2.Q17RG13
MN408A.II.2.Q17RG12
MN408A.II.2.Q17RG6
MN408A.II.1.Q17RG1
MN408A.II.1.Q16RG96
MN408A.II.1.Q16RG95
PA125.II.2.Q16RG83
PA125.II.2.Q16RG79
CT.II.3.Q16RG60
CT.II.3.Q16RG53
CT.II.2.Q16RG49
CT.II.2.Q16RG44
CT.II.2.Q16RG41
CT.II.1.Q16RG32
CT.II.1.Q16RG25
MD126.II.2.Q17RG35
MD126.II.2.Q17RG34
MD126.II.1.Q17RG33
MD126.II.1.Q17RG27
MN408A.II.3.Q17RG26
MN408A.II.3.Q17RG25
MN408A.II.3.Q17RG24
MN408A.II.3.Q17RG20
MN408A.II.2.Q17RG16
MN408A.II.2.Q17RG14
MN408A.II.2.Q17RG10
MN408A.II.1.Q17RG5
MN408A.II.1.Q16RG92
MN408A.II.1.Q16RG90
MN408A.II.1.Q16RG89
MN408A.II.1.Q16RG88
PA125.II.2.Q16RG86
PA125.II.2.Q16RG82
PA125.II.2.Q16RG80
PA125.II.2.Q16RG76
PA125.II.2.Q16RG75
PA125.II.2.Q16RG74
PA125.II.1.Q16RG73
PA125.II.1.Q16RG69
PA125.II.1.Q16RG68
CT.II.3.Q16RG64
CT.II.3.Q16RG62
CT.II.3.Q16RG58
CT.II.2.Q16RG52
CT.II.2.Q16RG48
CT.II.2.Q16RG47
CT.II.2.Q16RG46
CT.II.2.Q16RG43
CT.II.2.Q16RG40
CT.II.2.Q16RG39
CT.II.2.Q16RG38
CT.II.2.Q16RG37
CT.II.1.Q16RG31
CT.II.1.Q16RG30
CT.II.1.Q16RG24
MD126.II.1.Q17RG32
MD126.II.1.Q17RG30
MN408A.II.3.Q17RG23
MN408A.II.3.Q17RG19
MN408A.II.3.Q17RG18
MN408A.II.2.Q17RG9
MN408A.II.2.Q17RG8
MN408A.II.1.Q17RG4
MN408A.II.1.Q16RG94
PA125.II.2.Q16RG81
PA125.II.2.Q16RG78
PA125.II.1.Q16RG72
PA125.II.1.Q16RG67
CT.II.3.Q16RG61
CT.II.3.Q16RG57
CT.II.2.Q16RG51
CT.II.1.Q16RG36
CT.II.1.Q16RG29
CT.II.1.Q16RG26
CT.II.1.Q16RG23
MD126.II.3.Q17RG47
MD126.II.3.Q17RG46
MD126.II.3.Q17RG41
MD126.II.3.Q17RG39
MD126.II.2.Q17RG38
MD126.II.3.Q17RG45
MD126.II.2.Q17RG37
MN408A.II.3.Q17RG22
MN408A.II.3.Q17RG17
MN408A.II.2.Q17RG11
MN408A.II.2.Q17RG7
MN408A.II.1.Q17RG3
MN408A.II.1.Q16RG91
MN408A.II.1.Q16RG87
PA125.II.2.Q16RG85
PA125.II.2.Q16RG84
PA125.II.1.Q16RG71
PA125.II.1.Q16RG66
CT.II.3.Q16RG61.1
CT.II.3.Q16RG59
CT.II.3.Q16RG56
CT.II.2.Q16RG45
CT.II.2.Q16RG42
CT.II.1.Q16RG34
CT.II.1.Q16RG28
MD126.II.3.Q17RG42
MD126.II.3.Q17RG43
MD126.II.3.Q17RG44
CT.II.1.Q16RG27
CT.II.1.Q16RG33
CT.II.1.Q16RG35
CT.II.2.Q16RG50
CT.II.3.Q16RG54
CT.II.3.Q16RG55
CT.II.3.Q16RG63
PA125.II.1.Q16RG65
PA125.II.1.Q16RG70
PA125.II.2.Q16RG77
MN408A.II.1.Q16RG93
MN408A.II.1.Q17RG2
MN408A.II.2.Q17RG15
MN408A.II.3.Q17RG21
MD126.II.1.Q17RG28
MD126.II.1.Q17RG29
MD126.II.3.Q17RG40
MD126.II.2.Q17RG36
FM547494 R org=Funneliformis caledonius BEG20 = LPA12 W3294/Att263-15
Fi1cons 27 org=Funneliformis caledonius BEG20
FM876796 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
CT.II.1.Q20RG56
CT.II.3.Q20RG74
FM876798 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
CT.II.1.Q20RG57
CT.II.1.Q20RG62
CT.II.2.Q20RG63
CT.II.2.Q20RG65
CT.II.2.Q20RG70
CT.II.2.Q20RG68
FM876797 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876794 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
FM876795 R org=Funneliformis coronatus ex-holotype W3582/Att108-7
CT.II.2.Q20RG69
CT.II.3.Q20RG72
CT.II.2.Q20RG67
CT.II.1.Q20RG61
CT.II.1.Q20RG58
CT.II.1.Q20RG55
CT.II.3.Q20RG75
CT.II.3.Q20RG77
CT.II.3.Q20RG76
CT.II.3.Q20RG78
CT.II.3.Q20RG73
CT.II.1.Q20RG59
CT.II.1.Q20RG60
CT.II.2.Q20RG64
CT.II.2.Q20RG66
CT.II.2.Q20RG71
97
100
100
100
95
100
98
99
96
84
100
Relative abundances (%)
-M 1
-M 2
-M 3
G.giga1
G.giga2
G.giga3
S.pellu1
S.pellu2
S.pellu3
S.sin1
S.sin2
S.sin3
11
13
11
7
6
12
9
8
7
n=122
Relative abundances (%)
-M 1
-M 2
-M 3
29
33
38
n=24
Funneliformis
Glomeraceae
Glomerales
0.10
0.10


b)
FR750025 org=Funneliformis mosseae BEG12 W5790/Att109-28 single spore culture
FR750026 org=Funneliformis mosseae BEG12 W5790/Att109-28 single spore culture
FR750024 org=Funneliformis mosseae BEG12 W5790/Att109-28 single spore culture
FN547476 R org=Funneliformis mosseae BEG12 W5147/Att109-20 = Rothamsted s Yellow vacuolate
FN547475 R org=Funneliformis mosseae BEG12 W5147/Att109-20 = Rothamsted s Yellow vacuolate
FN547474 R org=Funneliformis mosseae BEG12 W5147/Att109-20 = Rothamsted s Yellow vacuolate
FM423691 org=Funneliformis mosseae ISCB13
Fi1cons 23 org=Funneliformis mosseae UT101 AFTOL-ID 139
FM423692 org=Funneliformis mosseae ISCB14
MN408A.II.3.Q23RG44
MN408A.II.3.Q23RG58
MN408A.II.3.Q23RG61
MD118.II.2.Q23RG76
MD118.II.3.Q23RG88
MD118.II.3.Q23RG93
MD118.II.3.Q23RG94
MD118.II.3.Q23RG96
MN408A.II.3.Q23RG52
MN408A.II.3.Q23RG54
MD118.II.3.Q23RG79
MD118.II.3.Q23RG80
MD118.II.3.Q23RG81
MD118.II.3.Q23RG91
MD118.II.3.Q23RG83
MD118.II.3.Q23RG90
MD118.II.3.Q23RG86
MD118.II.3.Q23RG85
MD118.II.3.Q23RG78
MD118.II.2.Q23RG75
MD118.II.2.Q23RG74
MD118.II.2.Q23RG72
MD118.II.2.Q23RG67
MN408A.II.3.Q23RG63
MN408A.II.3.Q23RG50
MN408A.II.3.Q23RG47
MN408A.II.3.Q23RG46
MN408A.II.3.Q23RG45
MD118.II.3.Q24RG1
MD118.II.3.Q23RG95
MD118.II.3.Q23RG87
MD118.II.3.Q23RG84
MD118.II.3.Q23RG77
MD118.II.2.Q23RG71
MD118.II.2.Q23RG66
MN408A.II.3.Q23RG60
MN408A.II.3.Q23RG57
MN408A.II.3.Q23RG56
MN408A.II.3.Q23RG51
MN408A.II.3.Q23RG49
MN408A.II.3.Q23RG48
MN408A.II.3.Q23RG53
MN408A.II.3.Q23RG55
MN408A.II.3.Q23RG59
MN408A.II.3.Q23RG62
MD118.II.2.Q23RG64
MD118.II.2.Q23RG65
MD118.II.2.Q23RG68
MD118.II.2.Q23RG69
MD118.II.2.Q23RG70
MD118.II.2.Q23RG73
MD118.II.3.Q23RG89
MD118.II.3.Q23RG92
MD118.II.3.Q23RG82
JF439176 org=Septoglomus constrictum Glomus constrictum isolate 08 48 17 18S
JF439167 org=Septoglomus constrictum Glomus constrictum isolate 08 48 12 18S
Relative abundances (%)
F.mos1
F.mos2
F.mos3
39
37
24
n=54
Funneliformis
FR750527 R org=Glomus macrocarpum W5288
FR750364 R org=Glomus macrocarpum W5581/Att1495-0
FR750531 R org=Glomus macrocarpum W5293
FR750363 R org=Glomus macrocarpum W5581/Att1495-0
FR750532 R org=Glomus macrocarpum W5293
FR750530 R org=Glomus macrocarpum W5288
Glomus
MD126.II.3.Q24RG40
Fi1cons 33 org=Sclerocystis sinuosa MD126
MD126.II.3.Q24RG39
MD126.II.3.Q24RG38
MD126.II.3.Q24RG37
MD126.II.3.Q24RG36
MD126.II.3.Q24RG35
MD126.II.3.Q24RG34
MD126.II.3.Q24RG33
MD126.II.3.Q24RG32
MD126.II.3.Q24RG31
MD126.II.3.Q24RG30
MD126.II.3.Q24RG29
MD126.II.3.Q24RG28
MD126.II.3.Q24RG27
MD126.II.2.Q24RG26
MD126.II.2.Q24RG25
MD126.II.2.Q24RG24
MD126.II.2.Q24RG23
MD126.II.2.Q24RG22
MD126.II.2.Q24RG21
MD126.II.2.Q24RG20
MD126.II.2.Q24RG19
MD126.II.2.Q24RG18
MD126.II.2.Q24RG17
MD126.II.2.Q24RG16
MD126.II.2.Q24RG15
MD126.II.2.Q24RG14
MD126.II.1.Q24RG13
MD126.II.1.Q24RG12
MD126.II.1.Q24RG11
MD126.II.1.Q24RG10
MD126.II.1.Q24RG9
MD126.II.1.Q24RG8
MD126.II.1.Q24RG7
MD126.II.1.Q24RG6
MD126.II.1.Q24RG5
MD126.II.1.Q24RG4
MD126.II.1.Q24RG2
MD126.II.1.Q24RG3
Relative abundances (%)
S.sin1
S.sin2
S.sin3
36
31
33
n=39
Sclerocystis
FM865546 org=Rhizophagus intraradices MUCL49410 W5070/Att1102-9
FM865565 R org=Rhizophagus intraradices FL208 W5166/Att4-38
FM865562 R org=Rhizophagus intraradices FL208 W5166/Att4-38 pHS086-4
FM865545 org=Rhizophagus intraradices MUCL49410 W5070/Att1102-9
FM992391 R org=Rhizophagus prolifer MUCL41827
FM992390 R org=Rhizophagus prolifer MUCL41827
FM865538 org=Rhizophagus clarus W3776/Att894-7
FM865536 org=Rhizophagus clarus W3776/Att894-7
FR750072 org=Rhizophagus fasciculatus MUCL46100
CT.II.1.Q20RG80
CT.II.1.Q20RG84
CT.II.2.Q20RG87
CT.II.3.Q20RG93
CT.II.3.Q20RG90
FR750071 org=Rhizophagus fasciculatus MUCL46100
CT.II.1.Q20RG82
CT.II.2.Q20RG85
CT.II.2.Q20RG88
CT.II.3.Q20RG91
CT.II.3.Q20RG94
CT.II.1.Q20RG79
CT.II.1.Q20RG81
CT.II.1.Q20RG83
CT.II.2.Q20RG86
CT.II.2.Q20RG89
CT.II.3.Q20RG92
Relative abundances (%)
M 1
M 2
M 3
38
63
n=16
Rhizophagus
Glomeraceae
Glomerales
0.10


c)
MD126.II.3.Q22RG9
MD126.II.2.Q22RG3
MD126.II.2.Q22RG1
MD126.II.2.Q21RG95
MD126.II.1.Q21RG92
MD118.II.1.Q21RG84
MD118.II.1.Q21RG80
MD118.II.1.Q21RG77
MD118.II.1.Q21RG71
MN408A.II.2.Q21RG66
MN408A.II.2.Q21RG63
MN408A.II.2.Q21RG60
MN408A.II.2.Q21RG58
MN408A.II.2.Q21RG56
MN408A.II.2.Q21RG54
MN408A.II.1.Q21RG44
MN408A.II.1.Q21RG40
MN408A.II.1.Q21RG36
CT.II.3.Q21RG30
CT.II.3.Q21RG25
CT.II.2.Q21RG18
CT.II.2.Q21RG16
CT.II.2.Q21RG15
CT.II.2.Q21RG14
CT.II.2.Q21RG11
CT.II.2.Q21RG10
CT.II.1.Q21RG5
CT.II.1.Q21RG1
MD126.II.3.Q22RG11
MD126.II.3.Q22RG8
MD126.II.2.Q21RG96
MD126.II.1.Q21RG90
MD118.II.1.Q21RG86
MD118.II.1.Q21RG82
MD118.II.1.Q21RG79
MD118.II.1.Q21RG76
MD118.II.1.Q21RG70
MN408A.II.2.Q21RG68
MN408A.II.2.Q21RG65
MN408A.II.2.Q21RG62
MN408A.II.2.Q21RG53
MN408A.II.1.Q21RG43
MN408A.II.1.Q21RG39
MN408A.II.1.Q21RG38
CT.II.3.Q21RG29
CT.II.3.Q21RG28
CT.II.3.Q21RG24
CT.II.3.Q21RG23
CT.II.2.Q21RG17
CT.II.1.Q21RG9
CT.II.1.Q21RG4
CT.II.1.Q21RG2
CT.II.1.Q20RG96
MD126.II.3.Q22RG10
MD126.II.3.Q22RG4
MD126.II.2.Q22RG2
MD126.II.2.Q21RG93
MD126.II.1.Q21RG88
MD118.II.1.Q21RG85
MD118.II.1.Q21RG83
MD118.II.1.Q21RG81
MD118.II.1.Q21RG78
MD118.II.1.Q21RG74
MN408A.II.2.Q21RG67
MN408A.II.2.Q21RG64
MN408A.II.2.Q21RG61
MN408A.II.2.Q21RG57
MN408A.II.2.Q21RG52
MN408A.II.2.Q21RG50
MN408A.II.2.Q21RG48
MN408A.II.1.Q21RG45
MN408A.II.1.Q21RG42
MN408A.II.1.Q21RG41
MN408A.II.1.Q21RG37
MN408A.II.1.Q21RG33
CT.II.3.Q21RG31
CT.II.3.Q21RG26
CT.II.3.Q21RG22
CT.II.3.Q21RG20
CT.II.2.Q21RG14
CT.II.2.Q21RG12
CT.II.1.Q21RG7
CT.II.1.Q21RG6
MD126.II.3.Q22RG7
MD126.II.3.Q22RG6
MD126.II.3.Q22RG5
MD126.II.2.Q21RG94
MD126.II.1.Q21RG91
MD126.II.1.Q21RG89
MD126.II.1.Q21RG87
MD118.II.1.Q21RG75
MD118.II.1.Q21RG73
MD118.II.1.Q21RG72
MD118.II.1.Q21RG69
MN408A.II.2.Q21RG59
MN408A.II.2.Q21RG55
MN408A.II.2.Q21RG51
MN408A.II.2.Q21RG49
MN408A.II.1.Q21RG47
MN408A.II.1.Q21RG46
MN408A.II.1.Q21RG35
MN408A.II.1.Q21RG34
MN408A.II.1.Q21RG32
CT.II.3.Q21RG27
CT.II.3.Q21RG21
CT.II.2.Q21RG19
CT.II.1.Q20RG95
CT.II.1.Q21RG8
CT.II.1.Q21RG3
FM865611 R org=Rhizophagus irregularis DAOM197198 W5495/Att1192-27
FR750078 R org=Rhizophagus irregularis MUCL43195 (once in GINCO as G. lamellosum)
FI1cons 29 org=Rhizophagus irregularis DAOM197198 DAOM181602 MUCL43194 AFTOL-ID48
FM865613 R org=Rhizophagus irregularis DAOM197198 W5495/Att1192-27
FR750187 org=Rhizophagus irregularis W4682/Att857-12
FR750186 org=Rhizophagus irregularis W4682/Att857-12
FR750079 R org=Rhizophagus irregularis MUCL43195 (once in GINCO as G. lamellosum)
FI1cons 28 org=Rhizophagus irregularis MUCL43195 (GINCO earlier: lamellosum)
FR750065 R org=Rhizophagus irregularis DAOM197198=DAOM181602=MUCL43194
FR750064 R org=Rhizophagus irregularis DAOM197198=DAOM181602=MUCL43194
FR750090 org=Rhizophagus species MUCL46240=DAOM234179
FR750089 org=Rhizophagus species MUCL46240=DAOM234179
FI1cons 30 org=Rhizophagus irregularis GINCO4695rac-11G2 AFTOL-ID845
FR750107 org=Rhizophagus species MUCL43205
FR750106 org=Rhizophagus species MUCL43205
FR750102 org=Rhizophagus species MUCL41833
FR750101 org=Rhizophagus species MUCL41833
FM865589 org=Rhizophagus irregularis BEG195 W5272/Att1485-12
FM865588 org=Rhizophagus irregularis BEG195 W5272/Att1485-12
FM992379 R org=Rhizophagus irregularis DAOM197198 Att690-23
FM992377 R org=Rhizophagus irregularis DAOM197198 Att690-23
PA125.II.3.Q17RG96
CT.II.3.Q17RG71
CT.II.3.Q17RG70
CT.II.3.Q17RG67
PA125.II.3.Q18RG1
PA125.II.2.Q17RG90
CT.II.3.Q17RG69
PA125.II.3.Q18RG2
CT.II.3.Q17RG72
CT.II.1.Q17RG49
CT.II.1.Q17RG55
CT.II.2.Q17RG60
CT.II.3.Q17RG68
PA125.II.1.Q17RG80
PA125.II.1.Q17RG81
PA125.II.3.Q17RG95
PA125.II.1.Q17RG82
CT.II.1.Q17RG54
CT.II.1.Q17RG48
CT.II.1.Q17RG52
CT.II.1.Q17RG53
CT.II.2.Q17RG59
CT.II.2.Q17RG63
CT.II.2.Q17RG64
CT.II.3.Q17RG65
PA125.II.1.Q17RG78
PA125.II.2.Q17RG84
PA125.II.2.Q17RG87
PA125.II.2.Q17RG89
PA125.II.3.Q17RG92
PA125.II.3.Q18RG3
PA125.II.3.Q18RG4
CT.II.3.Q17RG74
CT.II.1.Q17RG57
CT.II.1.Q17RG50
PA125.II.3.Q17RG91
PA125.II.1.Q17RG77
PA125.II.1.Q17RG76
CT.II.2.Q17RG62
CT.II.2.Q17RG61
CT.II.1.Q17RG56
PA125.II.3.Q17RG94
PA125.II.3.Q17RG93
PA125.II.2.Q17RG85
CT.II.3.Q17RG66
PA125.II.2.Q17RG88
PA125.II.2.Q17RG83
CT.II.3.Q17RG73
CT.II.2.Q17RG58
CT.II.1.Q17RG51
CT.II.3.Q17RG75
PA125.II.2.Q17RG86
PA125.II.1.Q17RG79
Relative abundances (%)
-M 1
-M 2
-M 3
S.pellu1
S.pellu2
S.pellu3
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
n=108
Relative abundances (%)
-M 1
-M 2
-M 3
G.giga1
G.giga2
G.giga3
n=53
0.10
Rhizophagus
Glomeraceae
Glomerales


d)
Relative abundances (%)
-M 1
-M 2
-M 3
35
29
35
n=17
Relative abundances (%)
-M 1
-M 2
-M 3
F.mos3
S.sin1
S.sin2
S.sin3
G.giga1
G.giga2
G.giga3
F.mos1
F.mos2
n=86
Entropho-spora
Entrophosporaceae
Entrophosporales
0.10


e)
Fi3cons 11 org=Dentiscutata reticulata CNPAB11
HM625902 org=Scutellospora pellucida isolate scut4
HM625901 org=Scutellospora pellucida isolate scut3
FJ461879 org=Scutellospora pellucida NC155C
AY639323 org=Scutellospora pellucida clone 19.6 (Gamper)
AY639313 org=Scutellospora pellucida clone 11.3 (Gamper)
HM625899 org=Scutellospora pellucida isolate scut1
AY639261 org=Scutellospora pellucida clone 24.1 (Gamper)
AY639309 org=Scutellospora pellucida clone 9.2 (Gamper)
HM625900 org=Scutellospora pellucida isolate scut2
FN547599 R org=Cetraspora gilmorei W5342/Att590-16
FN547598 R org=Cetraspora gilmorei W5342/Att590-16
FR750135 R org=Racocetra weresubiae W2988/Att-none
FR750134 R org=Racocetra weresubiae W2988/Att-none
FJ461870 org=Racocetra fulgida NC303A
FR750136 R org=Racocetra fulgida W2993/Att-none
FM876838 R org=Dentiscutata heterogama BEG35 W3214/Att334-16 clone MK029-5
FM876837 R org=Dentiscutata heterogama BEG35 W3214/Att334-16 clone MK029-3
FR750013 org=Scutellospora dipapillosa W5611/Att1577-4
FR750012 org=Scutellospora dipapillosa W5611/Att1577-4
AB048883 R org=Dentiscutata cerradensis MAFF520056
FM876803 R org=Gigaspora species lemon W2992/field clone MK003-1 = DNA pWD143.x
FM876802 R org=Gigaspora species lemon W2992/field clone MK021-1 = DNA pWD143.x
FM876801 R org=Gigaspora species lemon W2992/field clone MK021-2 = DNA pWD143.x
FM876800 R org=Gigaspora species lemon W2992/field clone MK021-6 = DNA pWD143.x
FM876799 R org=Gigaspora species lemon W2992/field clone MK021-10 = DNA pWD143.x
FN547571 R org=Gigaspora rosea DAOM194757 W5384/Att1509-20
FN547572 R org=Gigaspora rosea DAOM194757 W5384/Att1509-20
FR750040 org=Gigaspora margarita BEG34 W5792/Att256-18
FR750039 org=Gigaspora margarita BEG34 W5792/Att256-18
FN547548 R org=Gigaspora margarita BEG34
AY900504 org=Gigaspora gigantea isolate 1
AY900506 org=Gigaspora gigantea isolate 3
AY900505 org=Gigaspora gigantea isolate 2
JF439140 org=Scutellospora calospora isolate B25-5
Fi1cons 18 org=Scutellospora spinosissima W3485/Att209-44 type
FR750150 R org=Scutellospora spinosissima W3009/Att664-1 pMK024-03+08+06
Fi1cons 19 org=Paraspora scintillans W4545/field collected
Relative abundances (%)
S.pellu1
S.pellu2
S.pellu3
38
28
35
n=69
Relative abundances (%)
G.giga1
G.giga2
G.giga3
36
34
31
n=59
Scutellospora
Cetraspora
Racocetra
Dentiscutata
Gigaspora
Scutellospora
Pacispora
Gigasporaceae
Diversisporales
0.10


f)
AM947665 R org=Diversispora epigaea BEG47
FN547638 R org=Diversispora spurca ex-type W4119/Att246-18
FI1cons 07 org=Diversispora spurca ex-type
FN547637 R org=Diversispora spurca ex-type W4119/Att246-18
FN547655 R org=Diversispora aurantia Ex-Type W4728/Att1296-0
FI1cons 08 org=Diversispora aurantia W4728 ex-type
AM713403 R org=Diversispora celata BEG231 FACE234 W4718-19/Att1278-2
AM713402 R org=Diversispora celata BEG231 FACE234 W4718-19/Att1278-2
AM713406 R org=Diversispora eburnea AZ420A W4729
AM713405 R org=Diversispora eburnea AZ420A W4729
MD126.II.3.Q19RG53
MD118.II.3.Q19RG33
MD118.II.3.Q19RG32
MD118.II.1.Q19RG24
CT.II.3.Q19RG18
CT.II.1.Q18RG91
CT.II.3.Q19RG10
MD126.II.1.Q19RG37
MD118.II.3.Q19RG34
MD118.II.1.Q19RG21
CT.II.1.Q18RG94
CT.II.2.Q19RG7
MD126.II.2.Q19RG41
MD126.II.1.Q19RG39
MD126.II.1.Q19RG36
CT.II.2.Q19RG5
CT.II.1.Q18RG96
MD126.II.3.Q19RG47
MD126.II.2.Q19RG45
MD118.II.1.Q19RG22
CT.II.3.Q19RG16
CT.II.3.Q19RG13
CT.II.1.Q18RG92
CT.II.3.Q19RG15
MD118.II.2.Q19RG30
MD126.II.3.Q19RG48
MD126.II.2.Q19RG42
Relative abundances (%)
-M 1
-M 2
-M 3
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
n=27
CT.II.1.Q19RG1
CT.II.3.Q19RG14
MD126.II.2.Q19RG46
MD118.II.2.Q19RG31
MD126.II.3.Q19RG52
MD118.II.2.Q19RG29
CT.II.3.Q19RG17
CT.II.1.Q18RG95
CT.II.1.Q18RG93
MD118.II.2.Q19RG28
MD126.II.2.Q19RG43
CT.II.3.Q19RG11
CT.II.2.Q19RG9
CT.II.1.Q19RG3
MD126.II.3.Q19RG49
MD126.II.3.Q19RG51
MD126.II.2.Q19RG44
MD118.II.1.Q19RG27
MD118.II.1.Q19RG26
MD118.II.1.Q19RG24
CT.II.2.Q19RG8
MD118.II.1.Q19RG23
CT.II.2.Q19RG6
CT.II.3.Q19RG12
MD118.II.1.Q19RG20
MD118.II.3.Q19RG35
MD126.II.2.Q19RG40
CT.II.1.Q19RG2
MD126.II.3.Q19RG54
CT.II.2.Q19RG4
CT.II.3.Q19RG19
MD126.II.1.Q19RG38
MD126.II.3.Q19RG50
Relative abundances (%)
-M 1
-M 2
-M 3
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
n=33
AM418545 org=Redeckera fulva environmental
AM418546 org=Redeckera fulva environmental
AM418551 org=Redeckera megalocarpa environmental
AM418552 org=Redeckera megalocarpa environmental
AM418549 org=Redeckera pulvinata environmental
AM418550 org=Redeckera pulvinata environmental
FR750063 org=Acaulospora colombiana W5795/Att1476-8
FN547502 R org=Acaulospora laevis W3247/Att423-4
FN547503 R org=Acaulospora laevis W3247/Att423-4
FN547507 org=Acaulospora laevis BEG13 W5258 = Rothamsted laevis = honey coloured sessile spore
FN547508 org=Acaulospora laevis BEG13 W5258 = Rothamsted laevis = honey coloured sessile spore
FR750168 org=Acaulospora entreriana W5469/Att1541-1
FR750169 org=Acaulospora entreriana W5469/Att1541-1
FN825903 R org=Acaulospora brasiliensis W4699/Att1211-0
FN825905 R org=Acaulospora brasiliensis W4699/Att1211-0
AJ510230 R org=Acaulospora lacunosa BEG78
AJ891110 R org=Acaulospora lacunosa BEG78
JF439093 org=Acaulospora delicata isolate G67-5
JF439090 org=Acaulospora mellea isolate G34-6
JF439203 org=Acaulospora delicata isolate G11 2
JF439089 org=Acaulospora mellea isolate G34-3
FM876788 R org=Acaulospora cavernata BEG33 W3293/Att209-37
FM876789 R org=Acaulospora cavernata BEG33 W3293/Att209-37
FM876792 R org=Acaulospora sieverdingii WUM18 W2941/Att869-3
FM876793 R org=Acaulospora sieverdingii WUM18 W2941/Att869-3
FM876821 org=Acaulospora kentinensis TW111A W5346/Att1499-9
FM876822 org=Acaulospora kentinensis TW111A W5346/Att1499-9
FR750151 R org=Acaulospora spinosa EX-Type W3574/Attnone
MD126.II.2.Q19RG89
FR692350 org=Acaulospora scrobiculata FO316
MD126.II.2.Q19RG88
FR692349 org=Acaulospora scrobiculata FO316
CT.II.1.Q19RG57
CT.II.1.Q19RG58
CT.II.2.Q19RG62
CT.II.3.Q19RG70
MD118.II.1.Q19RG71
MD118.II.1.Q19RG73
MD118.II.2.Q19RG77
MD118.II.3.Q19RG81
MD126.II.1.Q19RG85
MD126.II.3.Q19RG96
MD126.II.2.Q19RG91
MD126.II.3.Q19RG94
MD126.II.3.Q20RG3
MD126.II.2.Q19RG87
MD126.II.1.Q19RG84
MD126.II.1.Q19RG83
MD118.II.1.Q19RG76
MD118.II.1.Q19RG74
CT.II.3.Q19RG69
CT.II.3.Q19RG68
CT.II.2.Q19RG61
CT.II.2.Q19RG65
MD126.II.2.Q19RG93
MD126.II.3.Q20RG2
MD126.II.1.Q19RG82
MD118.II.3.Q19RG80
MD118.II.1.Q19RG75
MD118.II.1.Q19RG72
CT.II.3.Q19RG67
CT.II.2.Q19RG64
CT.II.2.Q19RG60
CT.II.1.Q19RG56
MD126.II.3.Q19RG95
MD126.II.3.Q20RG4
MD126.II.2.Q19RG90
CT.II.1.Q19RG55
CT.II.2.Q19RG59
CT.II.2.Q19RG63
CT.II.3.Q19RG66
CT.II.3.Q19RG71
MD118.II.2.Q19RG78
MD118.II.2.Q19RG79
MD126.II.1.Q19RG81
MD126.II.1.Q19RG86
MD126.II.2.Q19RG92
MD126.II.3.Q20RG1
Relative abundances (%)
-M 1
-M 2
-M 3
F.mos1
F.mos2
F.mos3
S.sin1
S.sin2
S.sin3
n=48
0.10
Diversi-spora
Rede-ckera
Acaulo-spora
Diversisporaceae
Acaulosporaceae
Diversisporales

g)

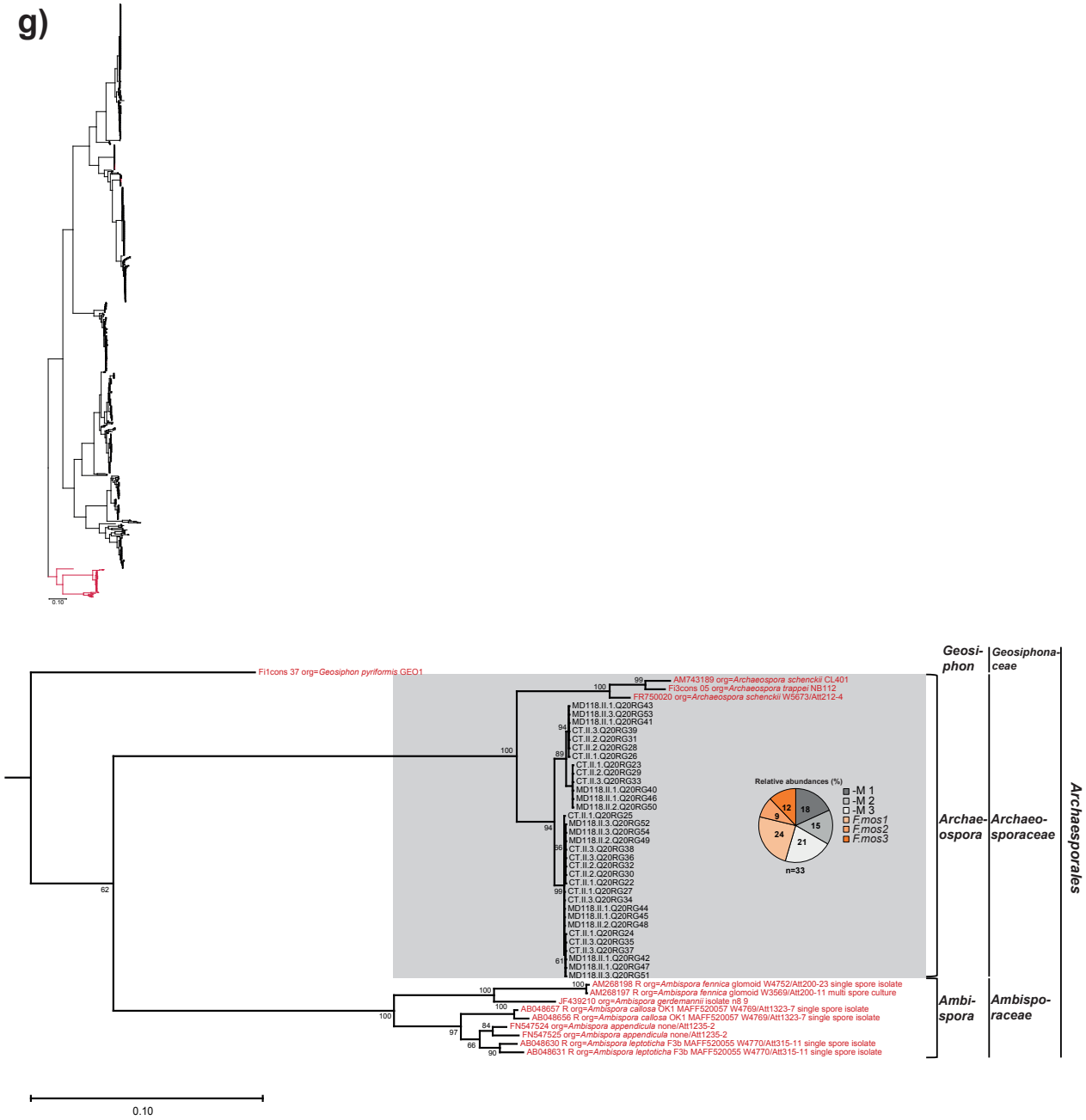

Fi1cons 37 org=Geosiphon pyriformis GEO1
AM743189 org=Archaeospora schenckii CL401
Fi3cons 05 org=Archaeospora trappei NB112
FR750020 org=Archaeospora schenckii W5673/Att212-4
MD118.II.1.Q20RG43
MD118.II.3.Q20RG53
MD118.II.1.Q20RG41
CT.II.3.Q20RG39
CT.II.2.Q20RG31
CT.II.2.Q20RG28
CT.II.1.Q20RG26
CT.II.1.Q20RG23
CT.II.2.Q20RG29
CT.II.3.Q20RG33
MD118.II.1.Q20RG40
MD118.II.1.Q20RG46
MD118.II.2.Q20RG50
CT.II.1.Q20RG25
MD118.II.3.Q20RG52
MD118.II.3.Q20RG54
MD118.II.2.Q20RG49
CT.II.3.Q20RG38
CT.II.3.Q20RG36
CT.II.2.Q20RG32
CT.II.2.Q20RG30
CT.II.1.Q20RG22
CT.II.1.Q20RG27
CT.II.3.Q20RG34
MD118.II.1.Q20RG44
MD118.II.1.Q20RG45
MD118.II.2.Q20RG48
CT.II.1.Q20RG24
CT.II.3.Q20RG35
CT.II.3.Q20RG37
MD118.II.1.Q20RG42
MD118.II.1.Q20RG47
MD118.II.3.Q20RG51
AM268198 R org=Ambispora fennica glomoid W4752/Att200-23 single spore isolate
AM268197 R org=Ambispora fennica glomoid W3569/Att200-11 multi spore culture
JF439210 org=Ambispora gerdemannii isolate n8 9
AB048657 R org=Ambispora callosa OK1 MAFF520057 W4769/Att1323-7 single spore isolate
AB048656 R org=Ambispora callosa OK1 MAFF520057 W4769/Att1323-7 single spore isolate
FN547524 org=Ambispora appendicula none/Att1235-2
FN547525 org=Ambispora appendicula none/Att1235-2
AB048630 R org=Ambispora leptoticha F3b MAFF520055 W4770/Att315-11 single spore isolate
AB048631 R org=Ambispora leptoticha F3b MAFF520055 W4770/Att315-11 single spore isolate
Relative abundances (%)
-M 1
-M 2
-M 3
F.mos1
F.mos2
F.mos3
12
18
9
15
24
21
n=33
Geosi-phon
Archae-ospora
Ambi-spora
Geosiphona-ceae
Archaeo-sporaceae
Ambispo-raceae
Archaesporales
0.10

Fig. S4 Maximum Likelihood (ML) tree of sequences of AMF (Glomeromycota) retrieved at 2nd harvest within the roots of tomato (*Solanum lycopersicum* L.) var. Rio Grande inoculated with AMF at nursery and mock inoculated (control, -M). Inocula were: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to Gigasporaceae, and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to Glomeraceae. The ML tree is based on sequences obtained from the amplification of part of the SSU, the complete ITS region, and ca. 0.8 kb of the LSU rRNA gene (ca. 1500-bp-long fragment) (Krüger et al. 2009). Fragments were amplified using the primer pair SSUmAf–LSUmAr and then the SSUmCf and LSUmBr as nested primers. The tree is composed by 788 newly generated sequences belonging to 15 phylotypes, plus 162 reference sequences from NCBI. Bootstrap values (based on 1 000 replicates) are shown at the nodes. The Tamura-Nei model was used in the analysis (Tamura and Nei 1993). The scale bar indicates substitutions per site. Portions of the ML tree are shown (a-g). Pie charts represent the percentage of clones of each phylotype in the three replicates of each treatment. The sequences of *Paraglomus occultum* IA702 was used as outgroup. The newly generated sequences are black coloured, while the reference sequences from NCBI are red coloured. The newly generated sequences are named as follows (e.g. MD126.II.1.Q17RG31): MD126 refers to the AM fungal isolate (see Table S1); II refers to the second harvest; 1 refers to the number of replicate plot; Q17 refers the number of the plate of the Sanger Run; RG refers to variety Rio Grande; 31 refers to the number of the clones within the specific AM fungal treatment and replicate plot. Evolutionary analyses were conducted in MEGA 11 (Stecher et al. 2020; Tamura et al. 2021). All representative newly generated sequences were deposited in the NCBI Sequence Read (SRA) database as SUB13375274.

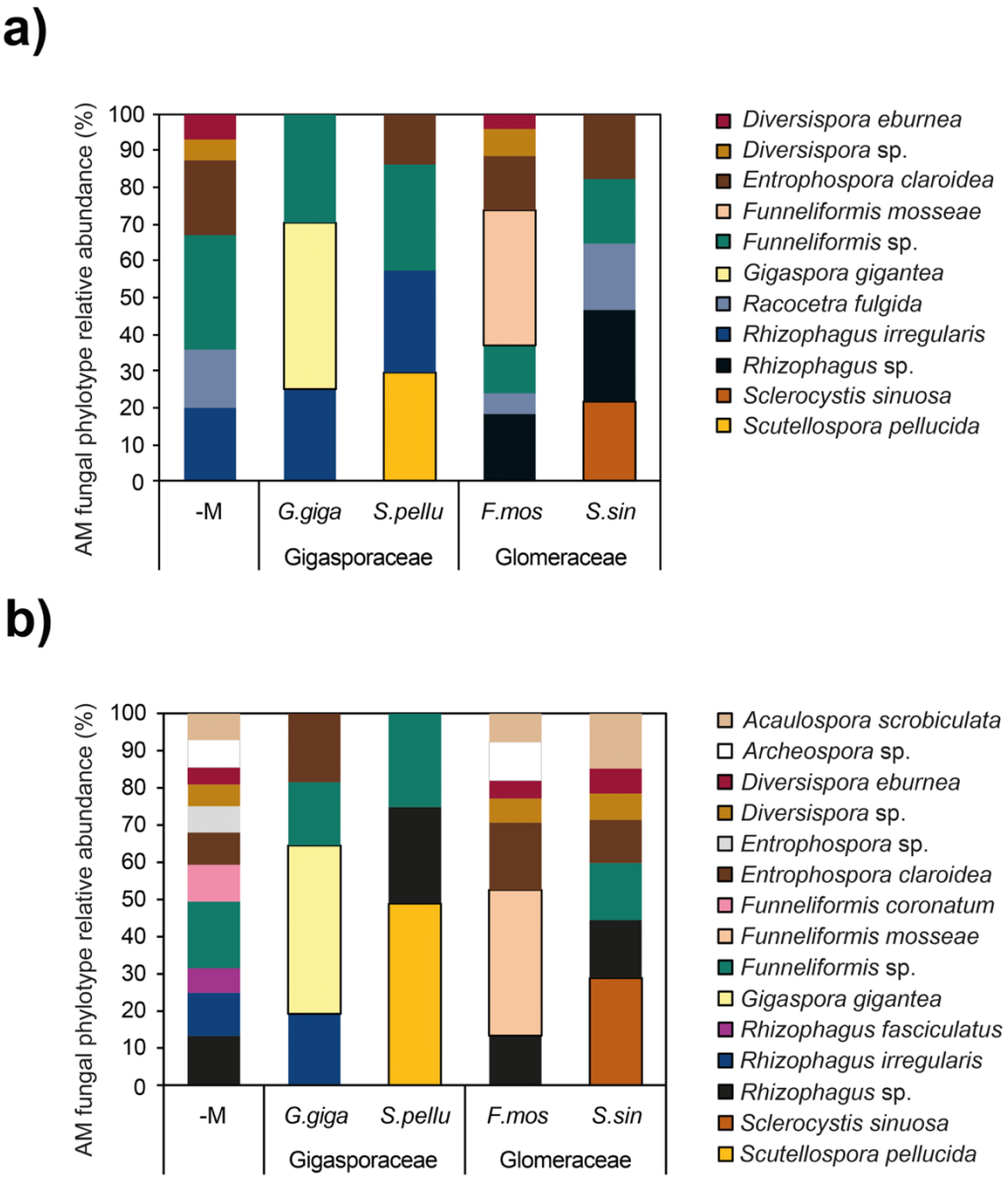


Fig. S5 Effect of AM fungal inoculation on the relative abundance of AMF phylotypes in roots of tomato (*Solanum lycopersicum* L.) var. Pisanello (a) and var. Rio Grande (b). Plants were inoculated with at nursery and mock inoculated (control, -M). Inocula were: *Gigaspora gigantea* (*G.giga*) and *Scutellospora pellucida* (*S.pellu*) belonging to Gigasporaceae, and *Funneliformis mosseae* (*F.mos*) and *Sclerocystis sinuosa* (*S.sin*) belonging to Glomeraceae.

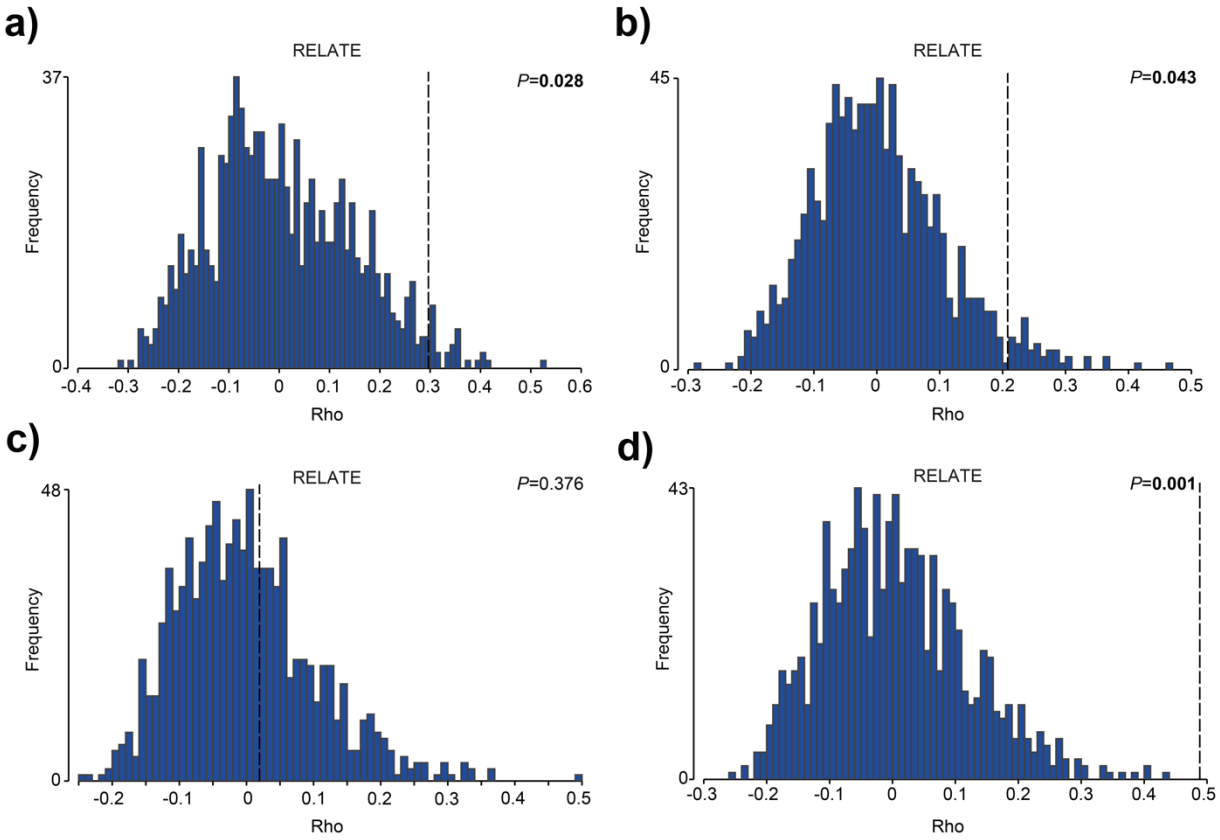


Fig. S6 RELATE analysis based on Spearman rank and 999 permutations for testing the significance of the relationship between the two matrices: the matrix of AM fungal colonisation traits and fruits quality parameters in var. Pisanello (a) and var. Rio Grande (b); the matrix of AMF community structure and fruits quality parameters in var. Pisanello (c) and var. Rio Grande (d) ($\rho = 1$ perfect relationship) (Clarke and Warwick 2001). Significant *P* values are highlighted boldface. The analysis was carried out using PRIMER 7 and PERMANOVA + software (Anderson et al. 2008; Clarke and Gorley 2015).

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