

Figure S1. Spores of (A) *Rhizophagus irregularis*, (B) *Septoglomus deserticola*, (C) *Claroideoglomus claroideum* and (D) *Claroideoglomus etunicatum*; scale bars = 200 μm

>HG_003_ST1130121_E12

TAACATCGTCTGATTCTAGTCGGCATAGTTTATGGTTAAGACTACGACGGTATCTGATCGTCTTCGAT
 CCCCTAACTTTCGTTCTTGATTAATGAAAACATCCTTGGCAAATGCTTTCGCAGTAGTTAGTCTTCAAT
 AAATCCAAGAATTTACCTCTGACAATTGAATACTAATGCCCCAACTATCCCTATTAATCATTACGGT
 GATCCTAGAAACCAACAAAATAGAATCATGCCGTCCTATTTTATTATTCCATGCTAATGTATTCAAGCA
 AAATGCCTGCTTTAAACACTCTAATTTTTTCAAAGTAAAGGTCCTGGTTCCCCGTGACACCCAATTAAG
 GGCATCGCGGTTCTCCAGAAGGTGAGAAATTGACTACACCAGTTCATACCCCTTAGGGCACGACCGAT
 GTGTCAATCCCGAAAATTCAACTACGAGCTTTTTAACTGCAACAACCTTAATATACGCTATTGGAGCTGG
 AATTACCGCGGCTGCTGGCACCAGACTTGCCCTCCAATTGTTCTCGTTAAGGGATTAAATTGTACTC
 ATTCCAATTACGAGACCCGAAAGAGCCCCGATTGTTATTTATTGTCACCTACCTCCCCGTGTCGGGATT
 GGGTAATTTGCGCGCCTGCTGCCTTCCTTGGATGTGGTAGCCGTTTCTCAGGCTCCCTCTCCGGAATCG
 AACCCTAATTCCCCGTTACCCGTTACCACCATGGTAGGCCTCTATCCT

Accession	Description	Max score	Total score	Query coverage	E-value	Max identity
Y17639	Claroideoglomeraceae Claroideoglomus etunicatum VTX00193	734	734	100.0%	0	99.9%

Figure S2: 18S rRNA sequence data obtained from a single spore isolated from the commercial inoculum expected to contain *C. etunicatum*. The MaarjAM database (<https://maarjam.ut.ee/?action=sBlast&id=132258>) was used to confirm AMF species identity. Quality sequence data (with clear nucleotide peaks) could not be obtained for any other isolates.

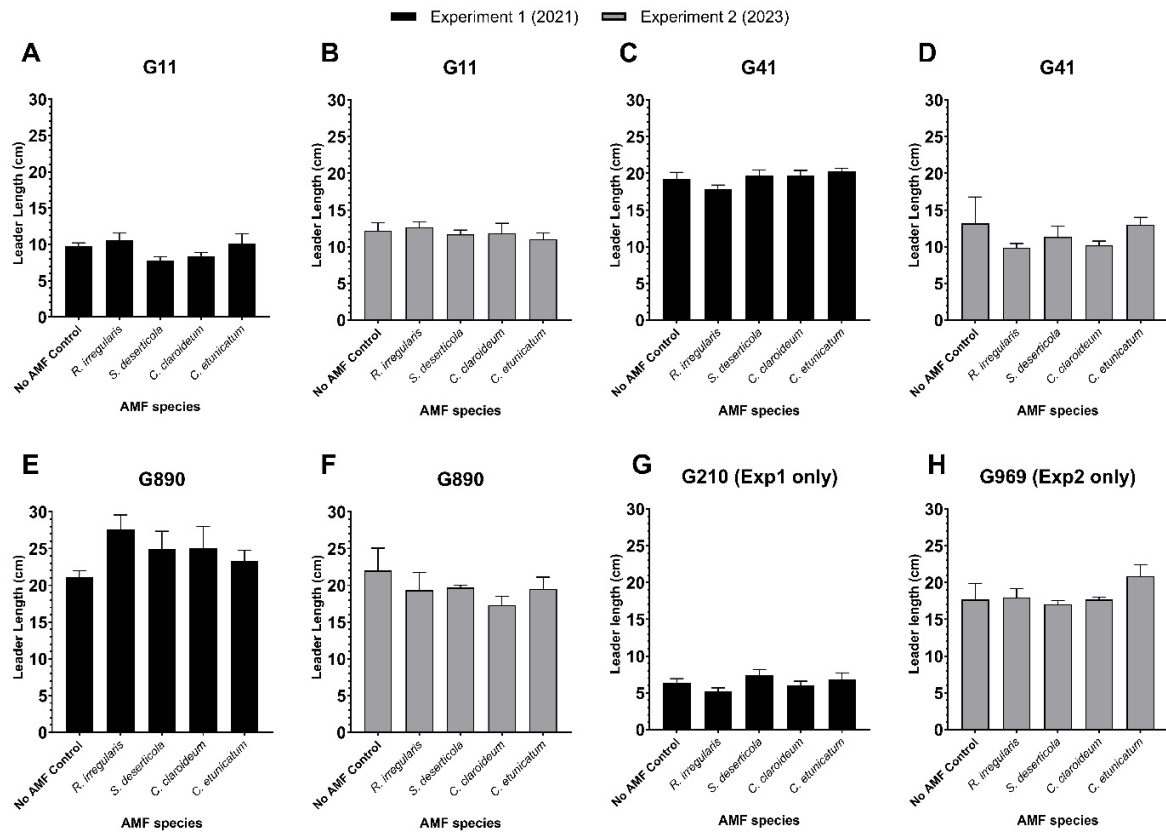


Figure S3: Leader shoot lengths of apple rootstock genotypes inoculated with different species of AMF, 5 weeks after inoculation in Exp 1 (black bars) and Exp 2 (grey bars). Different letters indicate statistically significant differences ($p < 0.05$) in leader length within each rootstock genotype (Two-way ANOVA on transformed ($y=\ln(y)$) data followed by Tukey's multiple comparisons tests). Data represents the mean of 7 replicates (Exp 1) and 3 replicates (Exp 2). Error bars represent the standard error of the mean.

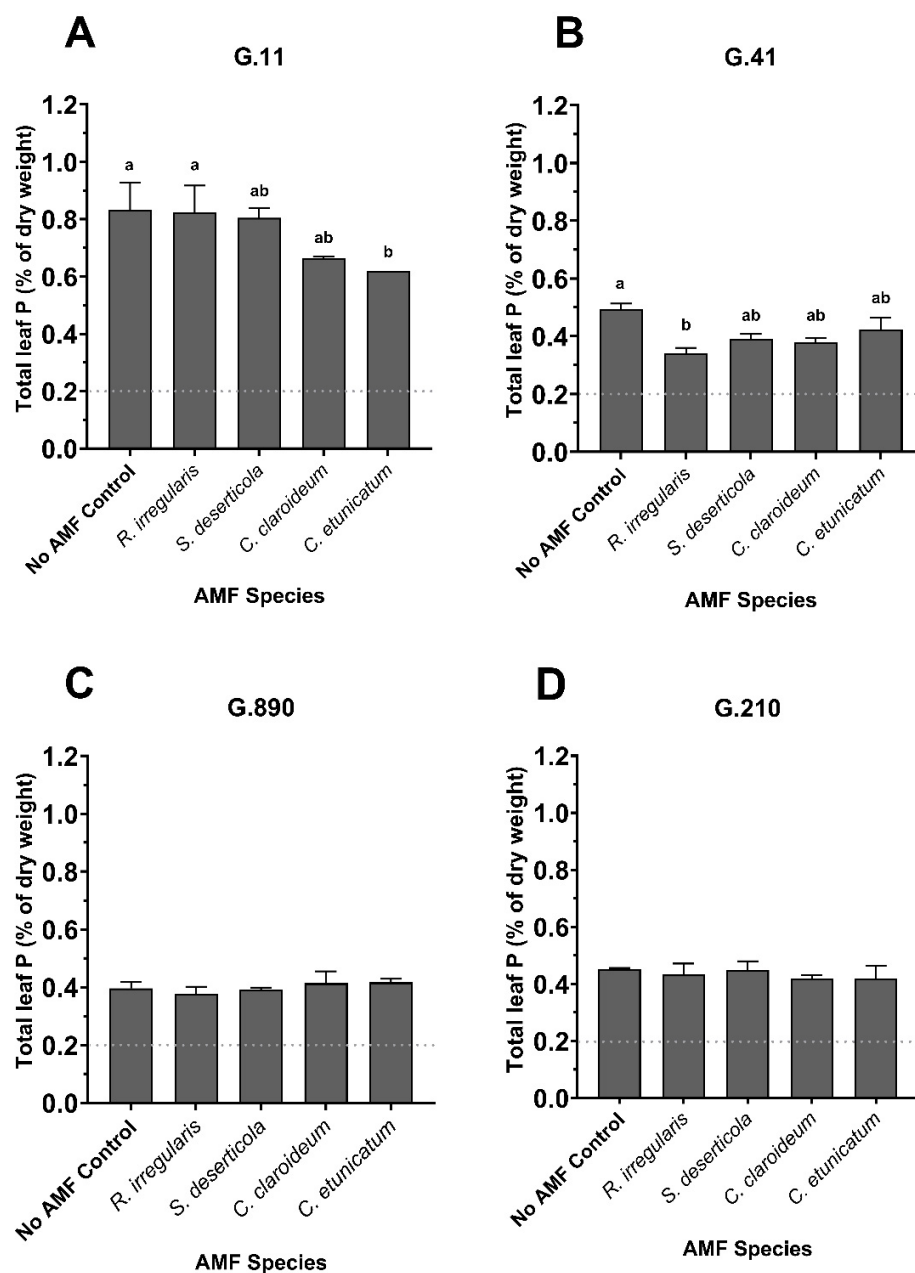


Figure S4: Total leaf foliar P (% of dry weight) in 4 different apple rootstocks inoculated with different species of AMF, 5 weeks after inoculation in Exp 1. Letters indicate statistical differences ($p < 0.05$) in total leaf P (% of dry weight) observed according to two-way ANOVA followed by Tukey's multiple comparisons test. The dashed horizontal line indicates adequate P nutrition ($> 0.2\%$). Data represents the mean of 3 samples pooled from 7 replicate plants.

Table S1: Mean percentage of AMF colonization for each apple rootstock genotype x AMF treatment combination at 5 weeks post-inoculation in Exp1 (2021) and at 2-, 5- and 8-weeks post-inoculation in Exp2 (2023). At each timepoint, data was compared across rootstocks for a given AMF species; rootstocks with the same letter were not significantly different (Dunnett's T3 tests following Welch's ANOVA test). Columns without letters indicate no significant differences. Exp1 values are based on 7 biological replicates per rootstock genotype/AMF treatment combination. Exp2 values are based on 3 biological replicates (x 3 technical replicates each).

Timepoint	Treatment	<i>R. irregularis</i>	<i>S. deserticola</i>	<i>C. claroideum</i>	<i>C. etunicatum</i>
	Genotype				
Exp1 – 5 weeks	G.11	6.29	5	5 ^{ab}	4.29
Exp1 – 5 weeks	G.41	4.57	8.43	6.57 ^{ab}	5.71
Exp1 – 5 weeks	G.210	3.86	4	2.57 ^a	4.71
Exp1 – 5 weeks	G.890	4.43	5.14	7.71 ^b	4.29
Exp2 – 2 weeks	G.11	0.47 ^a	0	0.41	0.2 ^a
Exp2 – 2 weeks	G.41	4.87 ^b	0.17	1.4	1.98 ^b
Exp2 – 2 weeks	G.969	9.56 ^{ab}	0	0.11	9.6 ^c
Exp2 – 2 weeks	G.890	4.82 ^{ab}	1.13	0.77	6.88 ^{abc}
Exp2 – 5 weeks	G.11	10.16	1.07	25.28	40.73 ^a
Exp2 – 5 weeks	G.41	14.31	0.27	12.85	28.86 ^{ab}
Exp2 – 5 weeks	G.969	5.73	0	0	3.74 ^b
Exp2 – 5 weeks	G.890	9.27	0	5.9	7.13 ^b
Exp2 – 8 weeks	G.11	0 ^a	0 ^a	0.36 ^a	0 ^a
Exp2 – 8 weeks	G.969	29.09 ^b	4.59 ^{ab}	33.42 ^b	25.74 ^b
Exp2 – 8 weeks	G.890	4.15 ^b	9.32 ^b	36.66 ^b	42.85 ^b