Data description

10 worksheets contain five sets of data from each of two experiments.

AMF species Field Inds. = List of the AMF species detected on each experimental plant in the field experiment (total of 135 individuals), along with total richness, Faith’s phylogenetic diversity, and metadata for each individual

AMF species Field means = AMF occurrence data, total AMF richness, and Faith’s phylogenetic diversity averaged across replicates for each combination of *P. pumila* population, field experimental site, and *A. petiolata* weeding treatment. This is the data analyzed in Table 1 and 2 of the article.

AMF VT Field Individual = List of the AMF virtual detected on each experimental plant in the field experiment (total of 135 individuals)

AMF VT Field means = AMF virtual taxa occurrence data averaged across replicates for each combination of *P. pumila* population, field experimental site, and *A. petiolata* weeding treatment.

Raw TRFLP Fragment Data Field = Relative fluorescence of each detected terminal restriction fragment for each individual plant in the field experiment. TRFs are labeled according to the primer (forward, AML1, or reverse, AML2) and restriction enzyme (Tfi or MboI), and the size in base pairs, resulting in four sets of TFs per sample.

AMF species Greenhouse Inds. = List of the AMF species detected on each experimental plant in the greenhouse experiment (total of 141 individuals), along with total richness, Faith’s phylogenetic diversity, and metadata for each individual

AMF species Greenhouse means = AMF occurrence data, total AMF richness, and Faith’s phylogenetic diversity averaged across replicates for each combination of *P. pumila* population and soil inoculum source in the greenhouse experiment. This is the data analyzed in Table 1 and 2 of the article.

AMF VT Greenhouse Individual = List of the AMF virtual detected on each experimental plant in the greenhouse experiment (total of 141 individuals)

AMF VT Greenhouse means = AMF virtual taxa occurrence data averaged across replicates for each combination of *P. pumila* population and soil inoculum source in the greenhouse experiment.

Raw TRFLP Fragment Data Field = Relative fluorescence of each detected terminal restriction fragment for each individual plant in the greenhouse experiment. TRFs are labeled according to the primer (forward, AML1, or reverse, AML2) and restriction enzyme (Tfi or MboI), and the size in base pairs, resulting in four sets of TFs per sample.

Column headings:

Field experiment site = One of five sites in which the field experiment occurred

*P. pumila* population = Source of *P. pumila* seeds (6 total)

*A. petiolata* removal treatment: *A. petiolata* removed (“weeded”) or not (“not weeded”) from 1 m2 plots

Invasion history of field experimental site: Estimated number of years since *A. petiolata* invaded the site in which the *P. pumila* seedlings were planted.

Invasion history of soil inocula: Estimated number of years since *A. petiolata* invaded the site from which soil was sampled for use as inocula in the greenhouse experiment

*P. pumila* Population History of Coexistence with *A. petiolata* = Estimated number of years since *A. petiolata* invaded the site from which the *P. pumila* seeds were collected

Number of Analyzable replicates: Number of replicates (of the original 10 in the field experiment or 5 in the greenhouse experiment) that survived to the end of the experiment and produced an analyzable PCR product

Total Fluorescence: Summed fluorescence of all peaks in the electrophoretic read-out of the PCR for a sample. Used as a covariate to control for differences in PCR efficiency

Initial Seedling Size (number of leaves): Number of leaves present on the *P. pumila* seedling at the time of planting in the field. Used as a covariate to control for possible differences in maternal provisioning.

# of AMF Virtual Taxa: Number of virtual taxa detected in a sample

# of AMF species: Number of recognized AMF species detected in a sample (= richness)

Faith's Phylogenetic Diversity: Summed branch lengths between each pair of AMF species present in a sample

*Paraglomus brasilianum* – *Septoglomus africanum*: AMF species detected in the dataset. For the individual level data, this is either 1 or 0 (presence or absence). For the averaged data, this is the frequency of occurrence among the replicates (between 0 and 1).