

New Phytologist Supporting Information

Article title: Root traits explain rhizosphere fungal community composition among temperate grassland plant species

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Table S1 Species selection with average measured trait values and GenBank accessions used to create the phylogeny.

Species	Root Diameter (mm)	Root Tissue Density (g/cm ³)	Specific Root Length (m/g)	Specific Root Area (cm ² /g)	Root Volume (cm ³)	Root Dry Matter Content (g/g)	Root Nitrogen (mg/g)	Root carbon (mg/g)	Leaf Dry Matter Content (g/g)	Leaf thickness (mm)	Specific Leaf Area (mm ² /g)	Leaf Nitrogen (mg/g)	Leaf Carbon (mg/g)	rbcL	matK
<i>Achillea millefolium</i> L.	0.31	0.20	100.00	890.94	1.51	0.35	21.37	436.43	0.13	0.09	538.85	33.49	446.99	JN892238	JN894883
<i>Achillea ptarmica</i> L.	0.31	0.14	105.42	976.75	1.13	0.22	17.68	432.62	0.21	0.10	418.67	32.28	427.52	JN891887	JN894397
<i>Agrostis capillaris</i> L.	0.21	0.16	227.77	1235.84	1.05	0.33	7.55	448.81	0.33	0.09	413.83	32.35	458.57	JN891522	JN894581
<i>Agrostis stolonifera</i> L.	0.18	0.13	307.83	1710.50	0.73	0.33	7.66	449.75	0.17	0.09	531.56	42.00	444.11	JN891529	JN894586
<i>Anthoxanthum odoratum</i> L.	0.23	0.14	188.20	1324.99	2.97	0.28	7.54	440.71	0.21	0.10	375.47	29.35	445.72	JN891740	JN894743
<i>Centaurea nigra</i> L.	0.37	0.13	77.24	875.69	2.21	0.33	19.47	436.14	0.13	0.17	290.72	31.25	449.46	JN892357	JN895178
<i>Dactylis glomerata</i> L.	0.24	0.18	143.93	1066.10	2.00	0.33	7.63	437.84	0.20	0.09	404.98	31.36	449.34	JN893305	JN895874
<i>Festuca rubra</i> L.	0.23	0.14	210.07	1437.78	1.30	0.29	10.36	442.37	0.24	0.13	209.88	32.44	430.79	JN891470	JN894542
<i>Galium verum</i> L.	0.21	0.16	248.20	1317.85	0.35	0.30	19.05	419.10	0.65	0.04	584.56	36.07	450.17	JN892891	JN895564
<i>Lathyrus pratensis</i> L.	0.41	0.15	61.61	769.67	0.91	0.27	28.99	405.57	0.24	0.07	360.51	35.51	455.62	JN891335	JN894452
<i>Lotus corniculatus</i> L.	0.37	0.11	109.24	1053.51	1.16	0.29	23.25	438.44	0.12	0.10	442.97	38.88	453.89	JN891333	JN894450
<i>Lotus pedunculatus</i> Cav.	0.31	0.16	102.38	1000.44	1.03	0.31	21.09	420.39	0.17	0.10	461.28	37.47	451.23	JN890642	JN893920
<i>Plantago lanceolata</i> L.	0.31	0.13	122.41	1138.17	2.46	0.27	16.61	440.50	0.15	0.17	231.07	28.47	442.64	JN891817	JN894031
<i>Poa pratensis</i> L.	0.19	0.15	259.93	1516.61	0.77	0.29	8.06	443.68	0.23	0.11	334.20	28.70	447.52	JN892398	JN895210
<i>Poa trivialis</i> L.	0.20	0.11	309.15	1882.61	0.73	0.34	11.09	442.09	0.19	0.08	498.47	38.68	420.24	JN892394	JN895206
<i>Ranunculus repens</i> L.	0.35	0.11	101.23	1096.79	1.06	0.24	25.47	417.37	0.16	0.13	371.06	35.63	445.36	JN891519	JN114770
<i>Rumex acetosa</i> L.	0.27	0.66	31.56	261.22	2.04	0.33	13.89	453.04	0.10	0.21	400.99	29.81	458.23	JN892337	JN895163
<i>Trifolium pratense</i> L.	0.26	0.11	190.34	1579.13	0.75	0.37	26.91	448.00	0.18	0.10	390.74	43.79	449.58	JN893083	JN895372
<i>Trifolium repens</i> L.	0.26	0.10	215.92	1687.76	0.91	0.30	23.59	443.33	0.16	0.11	472.66	45.09	445.70	JN891336	JN894453
<i>Vicia cracca</i> L.	0.46	0.09	73.45	1054.82	2.12	0.29	27.17	416.09	0.30	0.05	543.95	35.71	439.21	JN891387	JN894489
<i>Vicia sativa</i> L.	0.33	0.09	142.83	1543.56	1.09	0.37	25.26	427.40	0.16	0.06	600.63	35.39	443.55	JN892351	JN895172

Species authorities were sourced from the EPPO Global Database (<https://gd.eppo.int/>)

Table S2 Results from linear mixed effects models assessing environmental treatment effects on plant trait plasticity.

Trait	Variable	F	Significance	Conditional r^2	Marginal r^2
Root Diameter	Biomass	8.381	<0.001	0.042	0.810
	Treatment	4.074	0.017		
	Biomass : Treatment	0.421	0.652		
Specific Root Length	Biomass	49.70	<0.001	0.204	0.714
	Treatment	28.00	<0.001		
	Biomass : Treatment	8.015	<0.001		
Specific Root Area	Biomass	45.33	<0.001	0.259	0.542
	Treatment	22.70	<0.001		
	Biomass : Treatment	7.689	<0.001		
Root Volume	Biomass	245.6	<0.001	0.565	0.724
	Treatment	0.841	0.432		
	Biomass : Treatment	3.475	0.032		
Root Dry Matter Content	Biomass	0.865	0.352	0.014	0.018
	Treatment	1.107	0.331		
	Biomass : Treatment	1.151	0.317		
Root Tissue Density	Biomass	33.11	<0.001	0.080	0.644
	Treatment	3.860	0.022		
	Biomass : Treatment	6.820	0.001		
Root Carbon	Biomass	0.016	0.897	0.012	0.239
	Treatment	0.285	0.752		
	Biomass : Treatment	0.524	0.592		
Root Nitrogen	Biomass	6.568	0.011	0.010	0.816
	Treatment	1.486	0.228		
	Biomass : Treatment	0.189	0.827		
Specific Leaf Area	Biomass	4.556	0.033	0.167	0.386
	Treatment	<0.001	<0.001		
	Biomass : Treatment	0.610	0.610		
Leaf thickness	Biomass	0.098	0.754	0.011	0.761
	Treatment	0.930	0.395		
	Biomass : Treatment	1.440	0.238		
Leaf Dry Matter Content	Biomass	1.235	0.268	0.015	0.057
	Treatment	1.005	0.367		
	Biomass : Treatment	0.126	0.880		
Leaf Carbon	Biomass	7.082	0.008	0.063	0.252
	Treatment	0.338	0.799		
	Biomass : Treatment	0.597	0.800		
Leaf Nitrogen	Biomass	82.76	<0.001	0.358	0.572
	Treatment	3.776	0.024		
	Biomass : Treatment	1.733	0.178		

Variable refers to the explanatory variables within the model. Biomass refers to total plant biomass. The environmental treatments were whether plants were grown under control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC) conditions. Treatment refers to the environmental treatments. Data were analysed with linear mixed effects models with species and experimental block as random effects. Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (biomass*treatment). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (biomass*treatment) and random (species and experimental block) effects.

Table S3 Phylogenetic structuring of plant functional traits and the calculated trait plasticity index.

Trait	Trait value				Trait Plasticity Index							
	λ	p	K	p	Control vs Shade				Control vs Water Limited			
	λ	p	K	p	λ	p	K	p	λ	p	K	p
Root Diameter	0.998	0.001	0.619	0.001	<0.001	0.999	0.112	0.564	<0.001	0.999	0.112	0.556
Specific Root Length	0.599	0.011	0.337	0.002	<0.001	0.999	0.100	0.525	<0.001	0.999	0.100	0.526
Specific Root Area	0.543	0.128	0.296	0.010	<0.001	0.999	0.087	0.587	0.411	0.027	0.167	0.172
Root Volume	<0.001	0.999	0.181	0.159	<0.001	0.999	0.056	0.812	<0.001	0.999	0.026	0.974
Root Tissue Density	0.974	0.001	0.583	0.143	<0.001	0.999	0.056	0.833	0.230	0.300	0.080	0.721
Root Dry Matter Content	<0.001	0.999	0.028	0.976	<0.001	0.999	0.128	0.427	<0.001	0.999	0.109	0.558
Root Nitrogen	0.920	0.001	0.794	0.001	<0.001	0.999	0.115	0.479	<0.001	0.999	0.169	0.214
Root Carbon	0.913	0.130	0.344	0.009	<0.001	0.999	0.120	0.391	0.279	0.328	0.074	0.734
Leaf Thickness	0.979	0.006	0.481	0.001	<0.001	0.999	0.055	0.847	<0.001	0.999	0.075	0.696
Specific Leaf Area	<0.001	0.999	0.118	0.424	0.060	0.707	0.026	0.939	<0.001	0.999	0.083	0.620
Leaf Dry Matter Content	0.898	0.061	0.241	0.141	<0.001	0.999	0.027	0.961	<0.001	0.999	0.044	0.903
Leaf Nitrogen	0.313	0.237	0.168	0.166	<0.001	0.999	0.103	0.530	<0.001	0.999	0.084	0.636
Leaf Carbon	<0.001	0.999	0.051	0.871	0.070	0.692	0.072	0.710	<0.001	0.999	0.109	0.566

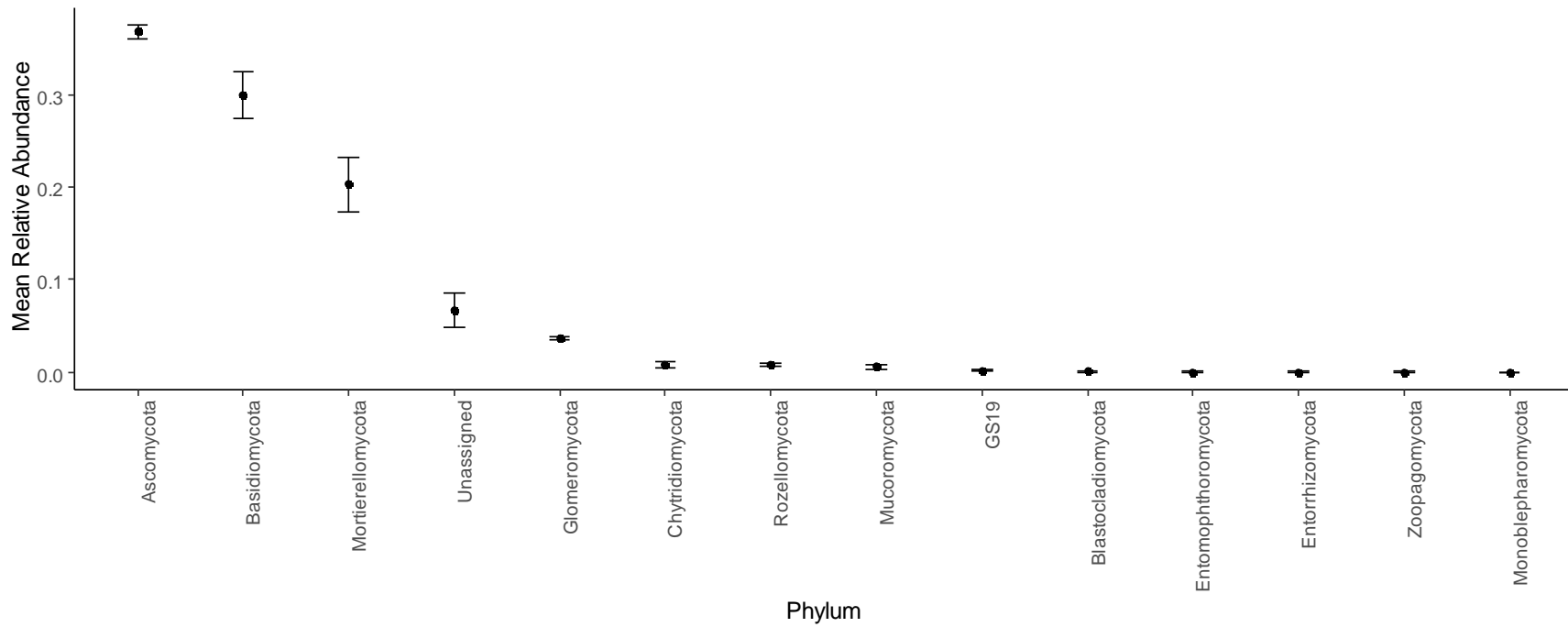


Fig. S1 Mean relative abundance of the phyla identified across all samples in this study. Standard deviation is shown. Relative abundance is measured as the proportion of reads assigned to a phylum relative to the total number of reads within each sample.

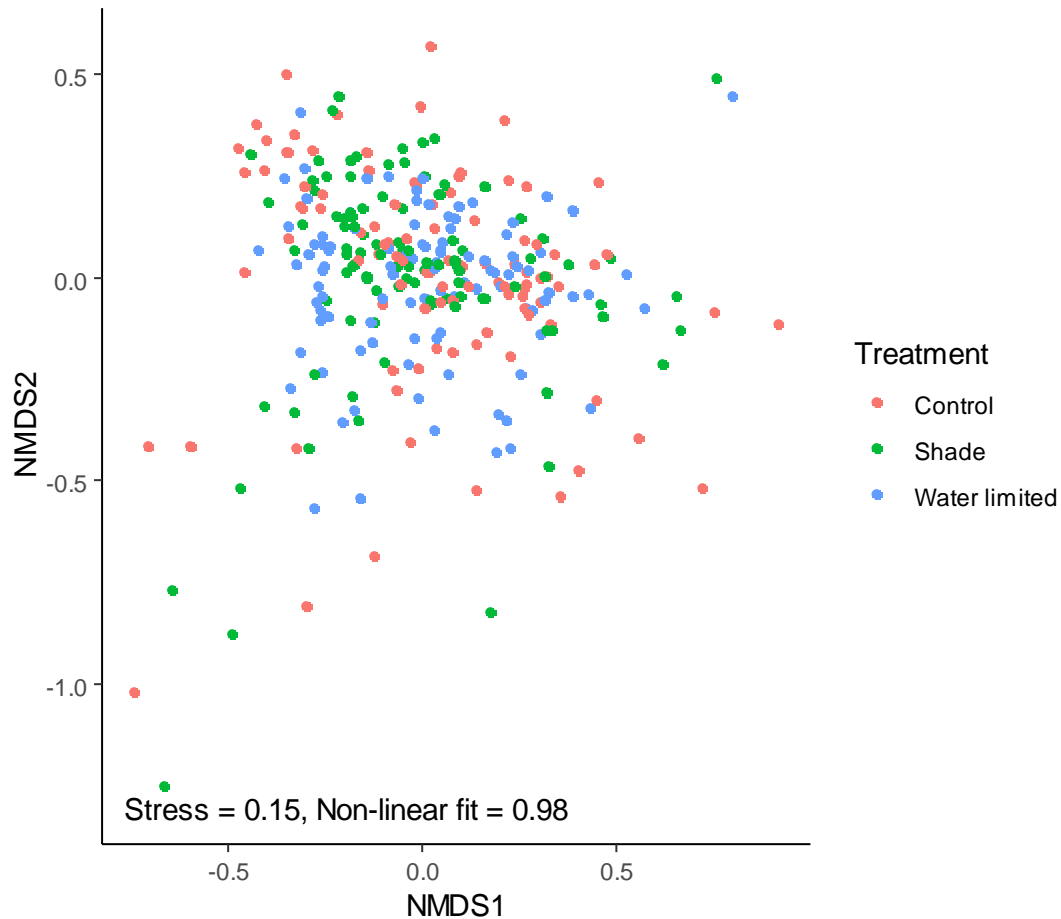


Fig. S2 NMDS ordination of the fungal communities observed in this study. Points are coloured by environment treatment. These were: control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC). NMDS ordination is calculated from a Bray-Curtis dissimilarity matrix of fungal community composition. Centroids of these groups, as calculated by PERMANOVA with 1000 permutations do significantly differ ($P < 0.001$), but environmental treatment explains little variation in fungal community composition ($r^2 = 0.012$).

Table S4 Results from PERMANOVA showing the effect of traits, the environmental treatments and their interactions on the whole fungal community.

Trait	Variable	r^2	Significance
Root Diameter	Treatment	0.018	< 0.001
	Trait	0.019	< 0.001
	Treatment:Trait	0.007	0.199
Specific Root Length	Treatment	0.016	< 0.001
	Trait	0.018	< 0.001
	Treatment:Trait	0.007	0.341
Specific Root Area	Treatment	0.018	< 0.001
	Trait	0.007	0.003
	Treatment:Trait	0.007	0.325
Root Volume	Treatment	0.018	< 0.001
	Trait	0.007	< 0.001
	Treatment:Trait	0.008	0.119
Root Dry Matter Content	Treatment	0.018	< 0.001
	Trait	0.004	0.285
	Treatment:Trait	0.007	0.173
Root Tissue Density	Treatment	0.018	< 0.001
	Trait	0.007	0.007
	Treatment:Trait	0.005	0.879
Root Carbon	Treatment	0.018	< 0.001
	Trait	0.004	0.106
	Treatment:Trait	0.007	0.370
Root Nitrogen	Treatment	0.018	< 0.001
	Trait	0.022	< 0.001
	Treatment:Trait	0.006	0.434
Specific Leaf Area	Treatment	0.018	< 0.001
	Trait	0.003	0.529
	Treatment:Trait	0.005	0.840
Leaf thickness	Treatment	0.018	< 0.001
	Trait	0.004	0.145
	Treatment:Trait	0.004	0.928
Leaf Dry Matter Content	Treatment	0.018	< 0.001
	Trait	0.589	0.589
	Treatment:Trait	0.006	0.430
Leaf Carbon	Treatment	0.018	< 0.001
	Trait	0.005	0.115
	Treatment:Trait	0.005	0.852
Leaf Nitrogen	Treatment	0.018	0.001
	Trait	0.006	0.006
	Treatment:Trait	0.009	0.035

The environmental treatments were whether plants were grown under control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC) conditions. Variable refers to the explanatory variables within the model. Treatment refers to the environmental treatments. Trait refers to the trait in the adjacent 'Trait' column.

Table S5 Mantel tests testing the correlation between plant phylogenetic relatedness and rhizosphere fungal community composition

	Mantel's r	Significance
Pooled	0.383	0.001
Grasses only	0.261	0.062
Forbs only	0.078	0.301
Legumes only	0.173	0.160

Correlations are tested across functional groups (pooled) and by the three functional groups (grasses, forbs and legumes) assessed in this study.

Table S6 Correlations between traits and the trophic guilds identified within the fungal community.

Trait	Assignment	Proportion				Richness			
		Cond r^2	Marg r^2	Estimate	P	Cond r^2	Marg r^2	Estimate	P
Root Diameter	Saprotroph	0.020	0.210	0.204	0.007	<0.001	0.037	0.204	0.820
	Pathotroph	0.002	0.090	-0.098	0.371	0.031	0.031	-0.880	0.001
	AMF	0.339	0.361	1.535	<0.001	0.239	0.301	18.97	<0.001
Specific Root Length	Saprotroph	0.011	0.210	-0.066	0.040	0.003	0.037	-0.132	0.728
	Pathotroph	<0.001	<0.001	-0.002	0.964	0.019	0.019	0.291	0.016
	AMF	0.111	0.142	-0.372	<0.001	0.084	0.121	-4.687	<0.001
Root Nitrogen	Saprotroph	0.015	0.235	0.107	0.015	0.026	0.057	-1.453	0.004
	Pathotroph	0.025	0.107	-0.179	0.004	0.079	0.079	-0.813	<0.001
	AMF	0.211	0.289	0.711	<0.001	0.087	0.109	6.513	<0.001
Specific Root Area	Saprotroph	0.003	0.212	-0.050	0.236	<0.001	0.037	-0.161	0.744
	Pathotroph	<0.001	0.090	-0.033	0.584	0.006	0.006	0.224	0.155
	AMF	0.011	0.066	-0.156	0.060	0.010	0.035	-2.156	0.073
Leaf Carbon	Saprotroph	<0.001	0.209	-0.253	0.623	0.002	0.037	-4.424	0.455
	Pathotroph	<0.001	0.096	-0.281	0.702	<0.001	<0.001	0.048	0.980
	AMF	0.008	0.075	1.582	0.115	0.006	0.031	20.40	0.160

Fungal guilds were assessed by relative abundance (proportion of reads belonging to that guild within a sample) and richness (count). Data were analysed with linear mixed effects models with experimental block as a random effect. Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (the trait). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (trait) and random (experimental block) effects.

Table S7 Results from models explaining the proportion and richness of fungal trophic guilds by plant traits and the environmental conditions the plants were grown under.

Guild	Variable	Significance	Cond r^2	Marg r^2
Proportion AMF	Root Diameter	<0.001	0.382	0.406
	Treatment	0.073		
	Root Diameter:Treatment	0.280		
Proportion AMF	Root Nitrogen	<0.001	0.279	0.360
	Treatment	0.766		
	Root Nitrogen:Treatment	0.758		
Proportion AMF	Specific Root Length	<0.001	0.152	0.186
	Treatment	0.667		
	Specific Root Length:Treatment	0.763		
Proportion Saprotophths	Root Diameter	0.002	0.029	0.220
	Treatment	0.911		
	Root Diameter:Treatment	0.680		
Proportion Saprotophths	Specific Root Length	0.012	0.021	0.222
	Treatment	0.808		
	Specific Root Length:Treatment	0.807		
Proportion Saprotophths	Root Nitrogen	0.024	0.020	0.235
	Treatment	0.617		
	Root Nitrogen:Treatment	0.729		
Proportion Pathotrophs	Root Nitrogen	0.001	0.106	0.190
	Treatment	0.636		
	Root Nitrogen:Treatment	0.993		
Richness AMF	Root Diameter	<0.001	0.286	0.345
	Treatment	0.007		
	Root Diameter:Treatment	0.074		
Richness AMF	Root Nitrogen	<0.001	0.146	0.168
	Treatment	0.854		
	Root Nitrogen:Treatment	0.687		
Richness AMF	Specific Root Length	<0.001	0.119	0.153
	Treatment	0.592		
	Specific Root Length:Treatment	0.874		
Richness Saprotophths	Root Nitrogen	0.004	0.033	0.065
	Treatment	0.613		
	Root Nitrogen:Treatment	0.610		
Richness Pathotrophs	Root Diameter	0.001	0.059	0.059
	Treatment	0.227		
	Root Diameter:Treatment	0.364		
Richness Pathotrophs	Root Nitrogen	<0.001	0.110	0.110
	Treatment	0.362		
	Root Nitrogen:Treatment	0.653		

Models were linear mixed effects models, with experimental block as a random effect. The models in which significant trait-fungal correlations were identified are presented. The absence of a significant interaction term means the effect of the trait on the fungal community was independent of the environmental conditions and the trait plasticity that resulted. Environmental treatments were: control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC). Variable refers to the explanatory variables within the model. Treatment refers to the environmental treatments. Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (the trait). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (trait * treatment) and random (experimental block) effects.

Table S8 The effect of the environmental treatments upon the identified functional guilds of fungi.

	Cond r^2	Marg r^2	Significance	Note
Proportion of Pathotrophs	0.080	0.169	<0.001	Higher in water limited relative to control and shaded
Pathotroph Richness	0.019	0.019	0.051	
Proportion Saprotroph	0.004	0.213	0.439	
Saprotroph Richness	0.003	0.004	0.603	
Proportion AMF	0.080	0.100	<0.001	Lower in shaded compared to control and water limited
AMF Richness	0.067	0.090	<0.001	Lower in shaded compared to control and water limited

Environmental treatments were: control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC). Variable refers to the explanatory variables within the model. Treatment refers to the environmental treatments. Data was analysed using linear mixed effects models with experimental block as a random effect. Cond r^2 refers to the conditional r^2 which represents the fixed effects (treatment) only. Marg r^2 refers to the marginal r^2 which represents the variance explained by both the fixed (treatment) and random (block) effects. Notes detail description of post-hoc analysis using the 'ls_means' function with the argument 'pairwise = TRUE', within the lmerTest package, tested with an alpha of 0.05.

Table S9 Summary of the performance of our random forest modelling and the model validation procedure.

Variable	Model r^2	Model P	Random r^2	Cross validation r^2
Root Diameter	32.63%	< 0.001	-4.2%	35.90%
Specific Root Length	19.99%	< 0.001	-5.5%	22.90%
Root Nitrogen	39.07%	< 0.001	-0.03%	42.12%
Specific Root Area	16.18%	< 0.001	15.81%	17.84%
Leaf Carbon	-3.47%	0.058	-0.07%	< 0.01%

Random r^2 illustrates effect of randomising the trait across the dataframe and reassessing model fit. Note negative r^2 values are possible here. Pseudo R^2 values are reported by package randomForest - pseudo r^2 : $1 - \text{mse} / \text{Var}(y)$. Thus, can be lower than 0 and means that the model has no more predictive power than just using the model estimated mean trait values, therefore showing very poor model performance. Cross validation r^2 refers to the assessment of model performance by 'leave one out cross validation'. A similar value to the observed model fit indicates robust model performance. Significance based on 1000 permutations

Table S10 Summary of the taxonomic and functional depth to which the ASVs identified as important within our random forest modelling were identified.

Trait	Kingdom	Phylum	Class	Order	Family	Genus	Species	Trophic
Root Diameter	100%	93.3%	89.3%	84.0%	50.6%	41.3%	33.3%	64%
Root Nitrogen	100%	91.3%	81.1%	70.0%	45.0%	34.8%	27.5%	46%
Specific Root Length	100%	88.7%	79.2%	77.4%	56.6%	45.2%	30.1%	45%
Specific Root Area	100%	83.1%	77.9%	74.5%	49.1%	40.1%	30.5%	30%

Percentage of ASVs assigned a trophic guild (saprotrophic, pathotrophic or AMF) is also presented, labelled as 'Trophic'.

Table S11 Matrix showing the number of shared ASVs between traits with significant correlations to fungal community structure as determined by random forest regression models.

Variable	Root Diameter	Root Nitrogen	Specific Root Length	Specific Root Area
Root Diameter	-	23 (59)	17 (53)	14 (59)
Root Nitrogen	8	-	17 (53)	13 (59)
Specific Root Length	10	10	-	23 (53)
Specific Root Area	6	6	11	-

Upper diagonal is shared between all identified important ASVs, between pairwise traits. Brackets indicate the maximum number of ASVs that could possibly be shared between 2 traits. Lower diagonal is shared ASVs between the top 20 most important ASVs between pairwise traits

Table S12 Summary of the 9 ASVs that were found to be important across the four significant random forest analyses assessing the fit of traits to the fungal community composition.

ASV_Code	Taxonomy								Samples present	RDIAM		SRL		RN		SRA	
	Kingdom	Phylum	Class	Order	Family	Genus	Species	Trophic Assignment		Coefficient	r ²	Coefficient	r ²	Coefficient	r ²	Coefficient	r ²
ASV_1085	Fungi	Glomeromycota	Archaeosporomycetes	Archaeosporales	-	-	-	-	201	1.43	0.20	-0.51	0.12	0.90	0.21	-0.38	0.03
ASV_1280	Fungi	Glomeromycota	Archaeosporomycetes	Archaeosporales	-	-	-	-	90	1.06	0.18	-0.43	0.15	0.49	0.08	-0.44	0.08
ASV_1187	Fungi	Glomeromycota	Paraglomeromycetes	Paraglomerales	-	-	-	-	89	1.17	0.21	-0.42	0.14	0.49	0.09	-0.39	0.06
ASV_1032	Fungi	Glomeromycota	Paraglomeromycetes	Paraglomerales	-	-	-	-	148	1.28	0.27	-0.55	0.22	0.61	0.22	-0.59	0.11
ASV_1082	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	pratorum	Pathotroph-Saprotroph-Symbiotroph	199	-0.84	0.06	0.26	0.04	-0.51	0.07	0.21	0.01
ASV_1133	Fungi	Mucoromycota	-	-	-	-	-	-	177	1.01	0.06	-0.53	0.09	0.10	0.00	-0.65	0.07
ASV_1299	Fungi	Chytridiomycota	Lobulomycetes	Lobulomycetales	Lobulomycetaceae	-	-	-	26	-0.94	0.02	0.59	0.07	-1.02	0.05	0.89	0.09
ASV_1003	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae	Solicocozyma	terricola	-	305	-0.58	0.10	0.18	0.06	-0.28	0.07	0.13	0.02
ASV_1065	Fungi	Basidiomycota	Tremellomycetes	Filobasidiales	Piskurozymaceae	Solicocozyma	terricola	-	155	-0.39	0.06	0.16	0.05	-0.17	0.03	0.18	0.03

Trophic assignment indicates the assignment using FUNGuild. *Samples* present indicate the number of samples a given ASV was present in, with a potential maximum of 305. *Coefficient* and *r²* is the result of a linear model regressing the relative abundance of the ASV, when it was present in the sample, against the trait, to indicate the direction of the relationship. RDIAM – Root Diameter, SRL – Specific Root Length, RN – Root Nitrogen, SRA – Specific Root Area.

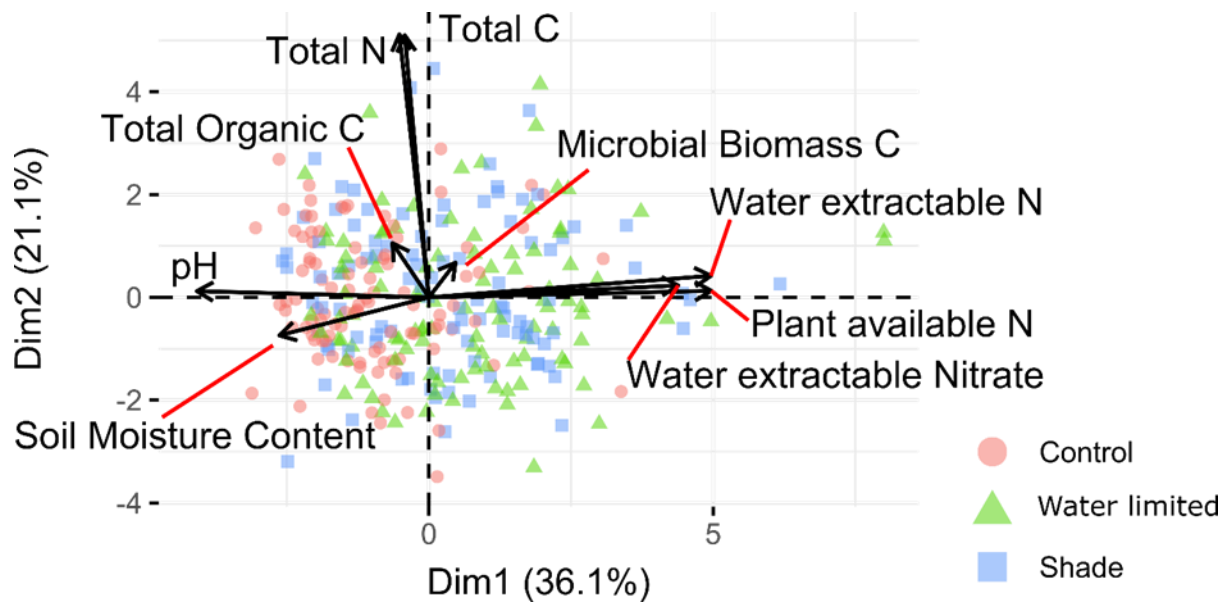


Fig. S3 PCA of soil chemical and biological variables, coloured by environmental treatment.

Table S13 Drivers of variation in principal components derived from soil chemical and biological variables.

Principal Component	Variable	Cond r^2	Marg r^2	Significance
Soil PC1	Plant Species	0.131	0.277	<0.001
	Plant Functional Group	0.003	0.157	0.493
	Treatment	0.159	0.312	<0.001
Soil PC2	Plant Species	0.032	0.056	0.955
	Plant Functional Group	0.003	0.029	0.621
	Treatment	0.004	0.031	0.467

Results from linear mixed effects models with experimental block as a random effect. Environmental treatments were: control (no shade, 60% water holding capacity (WHC)), shaded (55% shade cover, 60% WHC) and water limited (no shade cover, 45% WHC). Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (variable column). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (variable column) and random (experimental block) effects.

Table S14 Fungal guild abundance and richness explained by plant traits and first principal component of soil variables.

Guild	Variable	Significance	Cond r^2	Marg r^2
Proportion AMF	Root Diameter	<0.001	0.352	0.342
	Soil PC1	<0.001		
Proportion AMF	Root Diameter: Soil PC1	<0.001	0.236	0.258
	Root Nitrogen	<0.001		
	Soil PC1	0.298		
Proportion AMF	Root Nitrogen:Soil PC1	0.845	0.144	0.174
	Specific Root Length	0.849		
	Soil PC1	0.065		
Proportion Saprotrophs	Specific Root Length:Soil PC1	0.024	0.020	0.211
	Root Diameter	0.010		
	Soil PC1	0.700		
Proportion Saprotrophs	Root Diameter:Soil PC1	0.765	0.013	0.213
	Specific Root Length	0.048		
	Soil PC1	0.421		
Proportion Saprotrophs	Specific Root Length:Soil PC1	0.438	0.018	0.239
	Root Nitrogen	0.011		
	Soil PC1	0.266		
Proportion Pathotrophs	Root Nitrogen:Soil PC1	0.278	0.054	0.139
	Root Nitrogen	0.003		
	Soil PC1	0.404		
Richness AMF	Root Nitrogen:Soil PC1	0.166	0.255	0.302
	Root Diameter	<0.001		
	Soil PC1	0.159		
Richness AMF	Root Diameter:Soil PC1	0.041	0.151	0.166
	Root Nitrogen	<0.001		
	Soil PC1	0.002		
Richness AMF	Root Nitrogen:Soil PC1	0.072	0.096	0.128
	Specific Root Length	<0.001		
	Soil PC1	0.096		
Richness Saprotrophs	Specific Root Length:Soil PC1	0.128	0.039	0.074
	Root Nitrogen	0.005		
	Soil PC1	0.242		
Richness Pathotrophs	Root Nitrogen:Soil PC1	0.142	0.035	0.035
	Root Diameter	<0.001		
	Soil PC1	0.358		
Richness Pathotrophs	Root Diameter:Soil PC1	0.275	0.080	0.080
	Root Nitrogen	<0.001		
	Soil PC1	0.446		
	Root Nitrogen:Soil PC1	0.440		

Models were linear mixed effects models, with experimental block as a random effect. The models in which significant trait-fungal correlations were identified are presented. The absence of a significant interaction term means the effect of the trait on the fungal community was independent of the soil conditions and any trait plasticity that resulted. Variable refers to the explanatory variables within the model. Treatment refers to the environmental treatments. Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (trait * Soil PC1). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (trait * Soil PC1) and random (experimental block) effects.

Table S15 Fungal guild abundance and richness explained by plant traits and second principal component of soil variables.

Guild	Variable	Significance	Cond r^2	Marg r^2
Proportion AMF	Root Diameter	<0.001	0.342	0.364
	Soil PC2	0.597		
	Root Diameter: Soil PC2	0.409		
Proportion AMF	Root Nitrogen	<0.001	0.211	0.288
	Soil PC2	0.878		
	Root Nitrogen:Soil PC2	0.968		
Proportion AMF	Specific Root Length	<0.001	0.120	0.155
	Soil PC2	0.142		
	Specific Root Length:Soil PC2	0.095		
Proportion Saprotrophs	Root Diameter	0.008	0.021	0.214
	Soil PC2	0.330		
	Root Diameter:Soil PC2	0.353		
Proportion Saprotrophs	Specific Root Length	0.038	0.012	0.212
	Soil PC2	0.479		
	Specific Root Length:Soil PC2	0.508		
Proportion Saprotrophs	Root Nitrogen	0.015	0.022	0.240
	Soil PC2	0.111		
	Root Nitrogen:Soil PC2	0.100		
Proportion Pathotrophs	Root Nitrogen	0.003	0.042	0.125
	Soil PC2	0.186		
	Root Nitrogen:Soil PC2	0.369		
Richness AMF	Root Diameter	<0.001	0.244	0.303
	Soil PC2	0.704		
	Root Diameter:Soil PC2	0.960		
Richness AMF	Root Nitrogen	<0.001	0.090	0.110
	Soil PC2	0.950		
	Root Nitrogen:Soil PC2	0.777		
Richness AMF	Specific Root Length	<0.001	0.091	0.125
	Soil PC2	0.526		
	Specific Root Length:Soil PC2	0.383		
Richness Saprotrophs	Root Nitrogen	0.004	0.029	0.059
	Soil PC2	0.893		
	Root Nitrogen:Soil PC2	0.722		
Richness Pathotrophs	Root Diameter	0.002	0.031	0.031
	Soil PC2	0.802		
	Root Diameter:Soil PC2	0.748		
Richness Pathotrophs	Root Nitrogen	<0.001	0.081	0.081
	Soil PC2	0.326		
	Root Nitrogen:Soil PC2	0.365		

Models were linear mixed effects models, with experimental block as a random effect. The models in which significant trait-fungal correlations were identified are presented. The absence of a significant interaction term means the effect of the trait on the fungal community was independent of the soil conditions and any trait plasticity that resulted. Variable refers to the explanatory variables within the model. Treatment refers to the environmental treatments. Cond r^2 refers to the conditional r^2 , representing the variation explained by the fixed effects (trait * Soil PC2). Marg r^2 shows the marginal r^2 , representing the variation explained by both the fixed (trait * Soil PC2) and random (experimental block) effects.

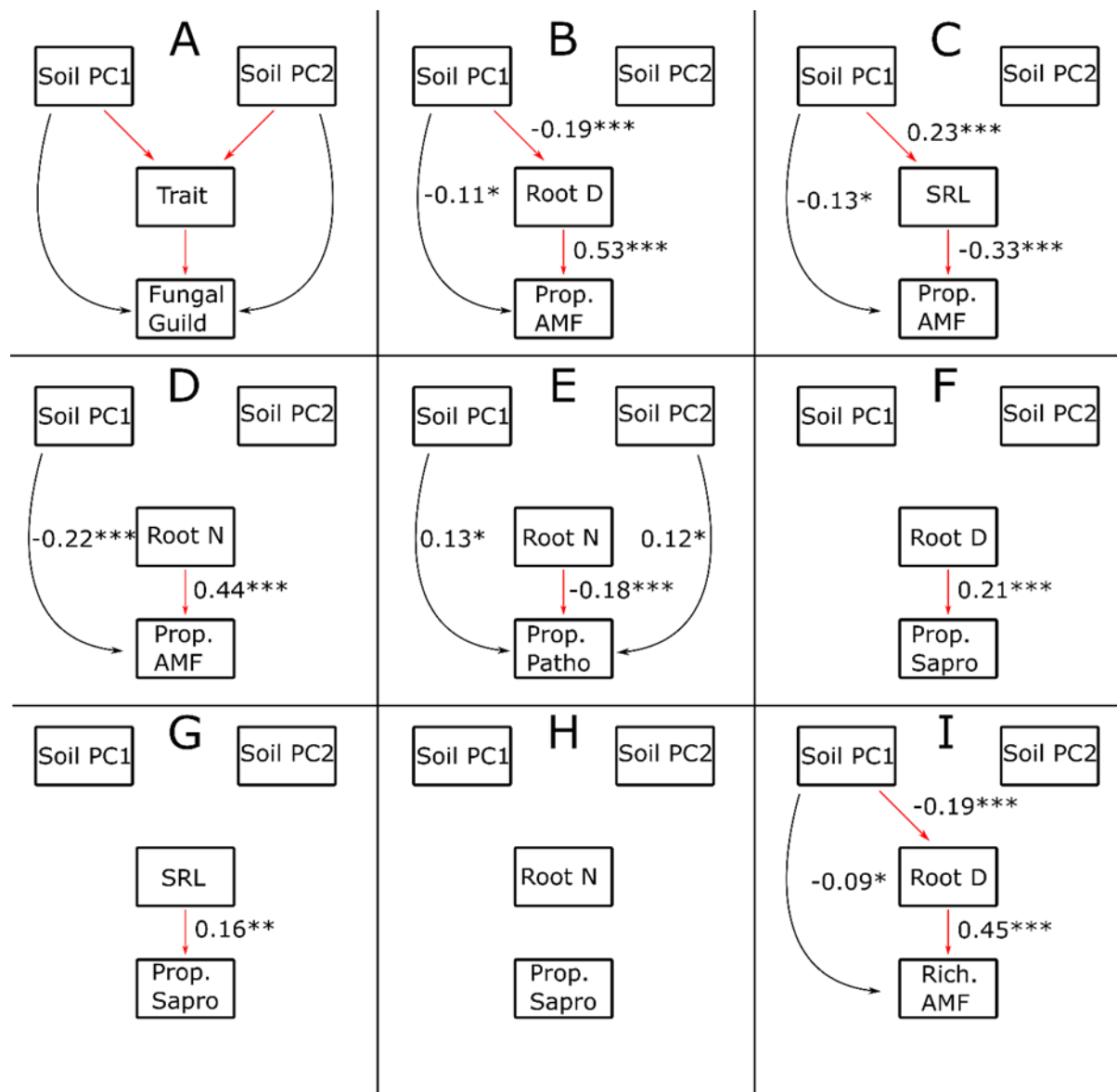


Fig. S4 Path analysis showing the influence of plant traits and soil principal component axes on the relative abundance and richness of fungal guilds. Models are only shown for trait-fungal guilds relationships identified as significant in our correlative analysis. Top left plot indicates the model structure. We examined the direct and indirect influence of Soil PC1 and Soil PC1 on plant traits and the subsequent effects on fungal guild relative abundance. In panel A, we use red arrows to indicate a hypothetical indirect influence of soil principal components on the relative abundance of fungal guilds. Black arrows indirect a direct influence. In the remaining plots, B-I, we use red arrows to indicate either a direct influence of plant traits on fungal guild abundance, or an indirect effect of soil principal components on fungal functional guilds via plant traits. Only significant relationships ($p < 0.05$) are shown and standardised model estimates are included. *** = $P < 0.001$, ** = $P < 0.01$, * $P < 0.05$. In panel H, no arrows are presented as no significant relationships were observed. This is because in the correlative analysis the

relationship between root nitrogen and the proportion of saprotrophs is very weak. Prop. AMF = relative abundance of AMF, Prop. Sapro = relative abundance of saprotrophs, Prop. Patho = relative abundance of pathotrophs, Rich. AMF = AMF richness. Root D = root diameter, SRL = specific root length, Root N = root nitrogen. Methods used in this analysis are presented in methods S2. Only the relationship between richness of AMF and root diameter was affected by the soil principal components, this is the only richness plot presented.

Methods S1 Commercial DNA sequencing methods

DNA was extracted from rhizosphere soil using DNeasy PowerSoil Kits (Qiagen, Germany) and DNA extracts were sequenced commercially (Macrogen, Korea) using an Illumina MiSeq (2 x 300 bp). The ITS2 region was amplified using the ITS3F (5'-GCATCGATGAAGAACGCAGC-3') and ITS4R (5'-TCCTCCGCTTATTGATATGC-3') universal primers (White *et al.*, 1990) with the following PCR conditions: 95 °C for 3 minutes, prior to 25 cycles of 95 °C for 30 s, 55 °C for 30 s and 72 °C for 30 s, before a minute period at 72 °C. Amplicon sizes were verified using a Bioanalyzer DNA 1000 chip (Agilent, California, USA). PCR product was cleaned using AMPure XP beads (Beckman Coulter, California, USA) and a Nextera XT Index Kit used to attach of the Illumina (California, USA) sequencing adaptors. An additional clean up step was performed as described above. Libraries were normalised following quantification on a Bioanalyzer DNA 1000 chip and were used for analysis.

White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and Direct Sequencing of Fungal Ribosomal Rna Genes for Phylogenetics. In: MA Innis, DH Gelfand, JJ Sninsky, and TJ White, eds. *PCR - Protocols and Applications - A Laboratory Manual*. New York: Academic Press. doi: 10.1016/B978-0-12-372180-8.50042-1, 315-322.

Methods S2 Supplementary path analysis in Fig. S4

We used path analysis to examine the direct and indirect influence of principal components capturing variation in soil biological and chemical properties upon soil fungal guilds. We used the 'sem' function in the Lavaan package to fit the models and assessed the underlying relationships using the 'standardizedSolution' function found within the same package. We used standardised model estimates to show the direction and strength of the relationships and only plotted significant relationships ($P < 0.05$).

