Annexes Chapitre III : Water and nutrient resources shape plant traits, their leaf endophytic microbiota, and their relationships
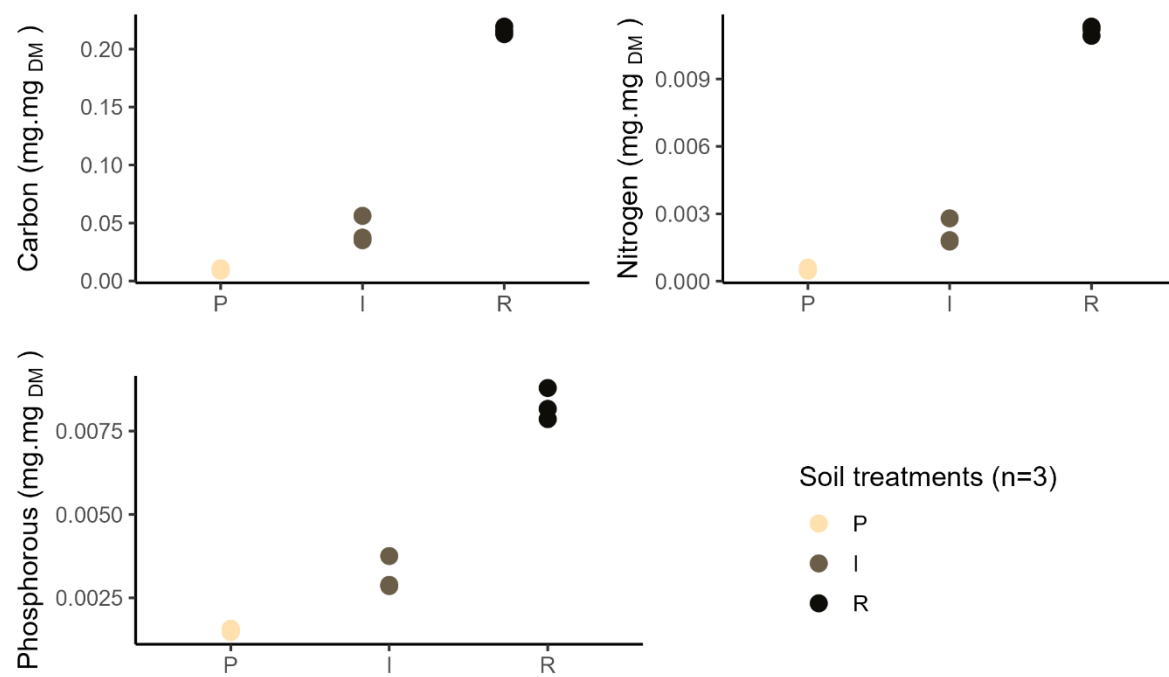
Figure S6: C, N and P content of the three substrates. P – Poor, I – Intermediate and R – Rich.
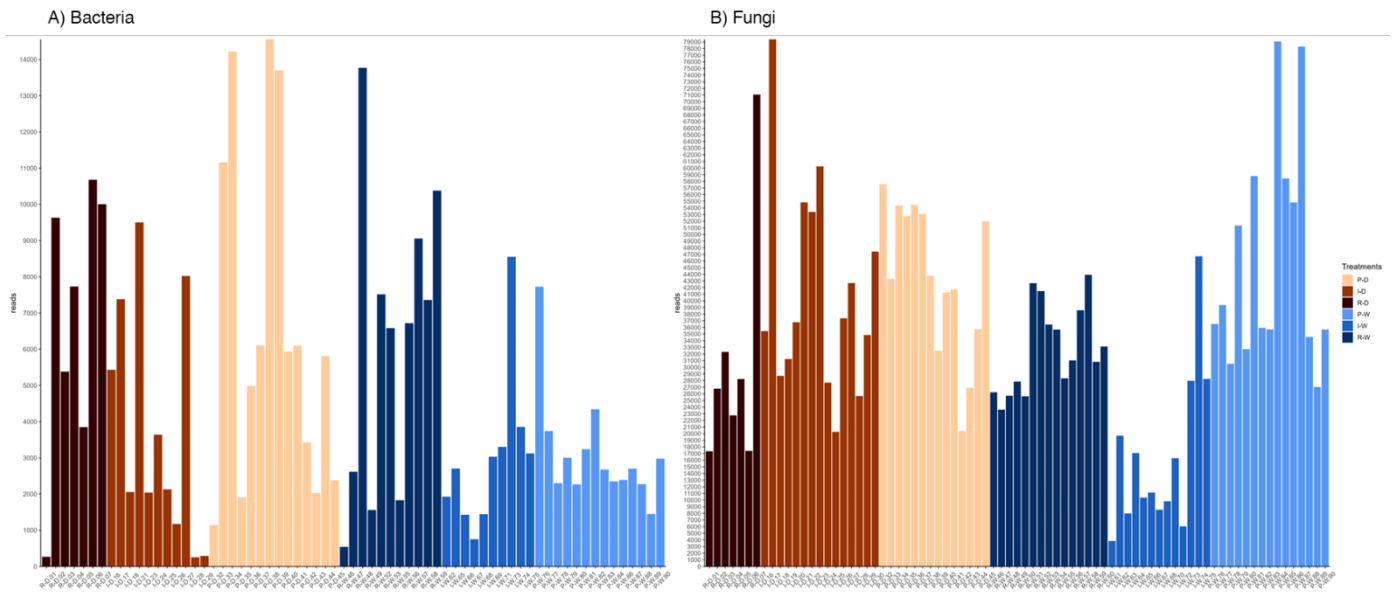
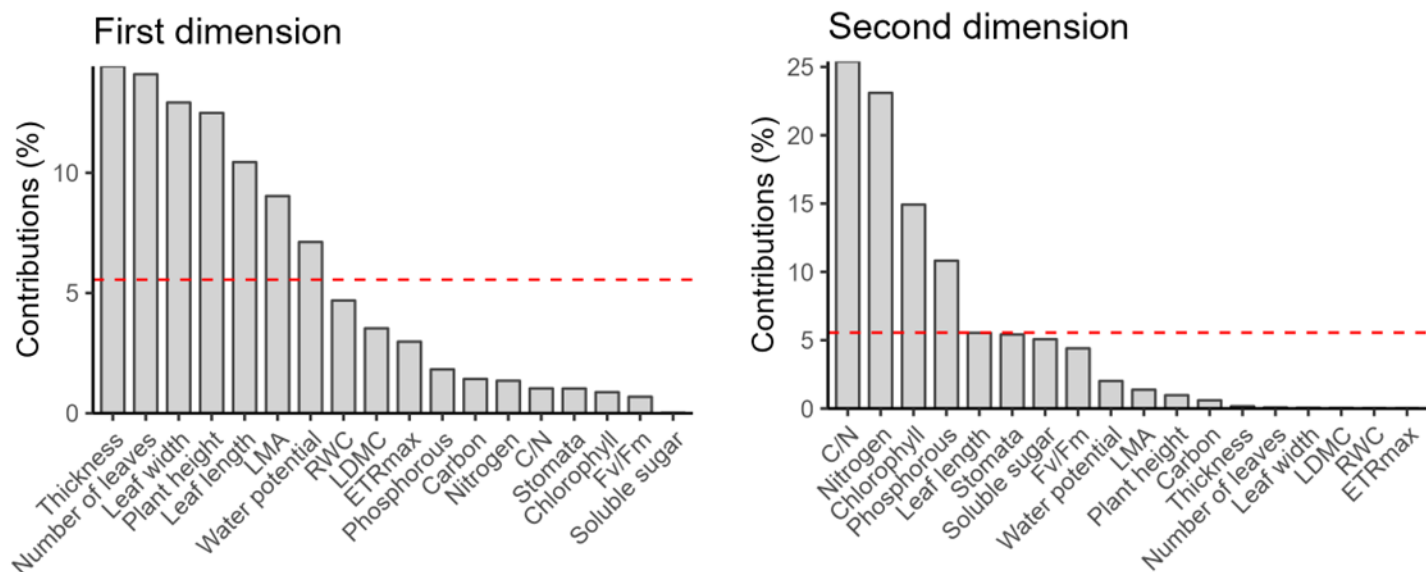Figure S7: Number of reads per sample colored according to treatments.

Figure S8: Contribution of the measured traits to the first (left panel) and second (right panel) dimensions of the PCA performed on leaf traits. The red line indicates the expected equal contribution of all variables (*i.e*, 100%/number of variables, 100/18=5.5).

Table S4: Result table of the pairwise perMANOVA performed on plant traits. Each row is the comparison of a pair of treatments. P.adjusted corresponds to holm's corrected p.values for multiple comparisons and are in bold when significant (<0.05).

Pairs	Df	SumsOfSqs	F.Model	R2	p.value	p.adjusted
R-D vs I-D	1	38.933	2.089	0.095	0.057	0.057
R-D vs P-D	1	72.509	7.636	0.276	0.001	**0.015**
R-D vs R-W	1	199.650	20.495	0.506	0.001	**0.015**
R-D vs I-W	1	171.030	23.320	0.538	0.001	**0.015**
R-D vs P-W	1	170.126	22.511	0.530	0.001	**0.015**
I-D vs P-D	1	52.514	3.683	0.116	0.001	**0.015**
I-D vs R-W	1	282.037	19.538	0.411	0.001	**0.015**
I-D vs I-W	1	207.468	16.316	0.368	0.001	**0.015**
I-D vs P-W	1	193.206	15.006	0.349	0.001	**0.015**
P-D vs R-W	1	252.172	31.901	0.533	0.001	**0.015**
P-D vs I-W	1	119.653	19.345	0.409	0.001	**0.015**
P-D vs P-W	1	78.670	12.399	0.307	0.001	**0.015**
R-W vs I-W	1	79.487	12.496	0.309	0.001	**0.015**
R-W vs P-W	1	181.765	27.875	0.499	0.001	**0.015**
I-W vs P-W	1	68.593	14.287	0.338	0.001	**0.015**

Table S5: Statistical summary table. For each trait the mean ± standard deviation (SD) is displayed for the 6 treatments. The associated Kruskal Wallis Chi² and P-values are shown. Significant P-values (<0.05) are in bold. Letters within brackets indicates significant pairwise differences, Wilcoxon pairwise test (α < 0.05). Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet. Traits are the Number of leaves; Plant height, leaf length and width are in cm; LMA (g. m^{-2}); LDMC (g.g^{-1}); Thickness (mm); Chlorophyll (mg.g^{-1}); PSII quantum yield: F_v/F_m; maximal electron transfer rate: ETR$_{max}$ (µmol.m^{-2}.s^{-1}); Water potential (MPa); RWC (%); C/N ratio; Soluble sugars (µg.mg^{-1}); Carbon, Nitrogen and Phosphorous (mg.g^{-1}).

Traits	Mean ± SD						Significance	
	P-D	I-D	R-D	P-W	I-W	R-W	KW-chi	P-val
Number of leaves	9.6 ± 1.18 (a)	8.47 ± 2.29 (a)	8.86 ± 1.35 (a)	13.1 ± 1.13 (b)	15.9 ± 1.85 (c)	16.1 ± 0.884 (c)	67.172	**<0.0001**
Plant height	9.9 ± 1.67 (ab)	10.2 ± 2.13 (a)	7.79 ± 1.73 (b)	21.9 ± 2.55 (c)	23.6 ± 3.04 (c)	34.3 ± 6.1 (d)	69.984	**<0.0001**
Leaf length	29.1 ± 3.66 (ab)	28.7 ± 3.36 (ab)	25 ± 4.1 (a)	30.4 ± 2.44 (b)	43.5 ± 3.47 (c)	54.5 ± 6.65 (d)	62.499	**<0.0001**
Leaf width	3.01 ± 0.338 (a)	2.99 ± 0.348 (a)	3.27 ± 0.419 (a)	4.26 ± 0.28 (b)	4.3 ± 0.484 (b)	4.47 ± 0.244 (b)	59.898	**<0.0001**
LMA	84 ± 15.9 (a)	76.8 ± 10 (a)	64 ± 21.4 (a)	107 ± 8.82 (b)	101 ± 13 (b)	120 ± 24.6 (b)	47.344	**<0.0001**
LDMC	0.0984 ± 0.0165 (ab)	0.126 ± 0.0571 (ab)	0.0866 ± 0.0297 (ab)	0.103 ± 0.0112 (a)	0.0843 ± 0.0084 (b)	0.0977 ± 0.0161 (ab)	18.730	**0.00216**
Thickness	0.935 ± 0.16 (a)	0.762 ± 0.23 (a)	0.819 ± 0.191 (a)	1.15 ± 0.125 (b)	1.32 ± 0.109 (c)	1.37 ± 0.108 (c)	61.240	**<0.0001**
Stomata	79 ± 13.9 (ab)	93.5 ± 19 (ac)	79.6 ± 17.5 (abc)	71.7 ± 9.08 (b)	98.8 ± 12.1 (c)	94.4 ± 13.3 (ac)	32.448	**<0.0001**
Chlorophyll	2.4 ± 0.784 (ab)	2.84 ± 0.856 (ac)	3.19 ± 1.43 (abc)	1.96 ± 0.42 (b)	3.25 ± 0.596 (c)	4.05 ± 1.66 (c)	36.593	**<0.0001**
F_v/F_m	0.788 ± 0.0683 (a)	0.732 ± 0.128 (a)	0.726 ± 0.0685 (a)	0.795 ± 0.0275 (a)	0.799 ± 0.0194 (a)	0.775 ± 0.0236 (a)	19.413	**0.00161**
ETR$_{max}$	49.2 ± 9.85 (a)	47.7 ± 8.15 (a)	53.6 ± 13.3 (ab)	66 ± 26.1 (ab)	49.2 ± 13.5 (a)	71.7 ± 12.6 (b)	25.648	**0.0001**
Water potential	-0.129 ± 0.306 (ab)	-0.526 ± 0.717 (a)	-0.623 ± 0.653 (a)	-0.0441 ± 0.0894 (bc)	-0.00485 ± 0.0188 (c)	-0.0021 ± 0.00813 (c)	40.170	**<0.0001**
RWC	83.4 ± 4.45 (a)	73.1 ± 21.4 (ab)	72.8 ± 12.6 (a)	89 ± 2.71 (bc)	91.2 ± 2.71 (c)	91.4 ± 2.74 (c)	40.431	**<0.0001**
C/N	58.3 ± 10.5 (a)	40.6 ± 6.45 (b)	26.4 ± 6.38 (c)	80.7 ± 4.77 (d)	62.6 ± 5.57 (a)	37.2 ± 5.91 (b)	69.674	**<0.0001**
Soluble sugar	90.4 ± 37.6 (a)	76.1 ± 25.9 (a)	60.4 ± 19.3 (a)	83.6 ± 17.6 (a)	85.9 ± 24.3 (a)	63 ± 27.3 (a)	13.312	**0.02062**
Carbon	410 ± 7.74 (ab)	416 ± 11.4 (a)	406 ± 12 (abc)	406 ± 6.41 (bc)	402 ± 3.46 (c)	408 ± 5.99 (bc)	22.037	**0.00052**
Nitrogen	7.26 ± 1.41 (a)	10.5 ± 1.76 (b)	16 ± 3.29 (c)	5.05 ± 0.33 (d)	6.48 ± 0.562 (a)	11.2 ± 1.64 (b)	69.499	**<0.0001**
Phosphorous	1.32 ± 0.139 (a)	1.46 ± 0.432 (ab)	1.32 ± 0.145 (a)	1.31 ± 0.172 (a)	1.52 ± 0.266 (ab)	1.77 ± 0.27 (b)	23.105	**0.00032**

Table S6: Relative abundance of the most abundant taxa at the Phylum, Class and Order rank for fungi and bacteria.

| Phylum		Class		Order	
Name	**Otu count**	**Name**	**Otu count**	**Name**	**Otu count**
Fungi					
Aphelidiomycota	1 (0.06%)	Agaricomycetes	222 (13.94%)	Capnodiales	36 (2.26%)
Ascomycota	1034 (64.95%)	Dothideomycetes	281 (17.65%)	Chaetothyriales	24 (1.51%)
Basidiobolomycota	1 (0.06%)	Eurotiomycetes	87 (5.46%)	Diaporthales	36 (2.26%)
Basidiomycota	317 (19.91%)	Leotiomycetes	36 (2.26%)	Glomerellales	21 (1.32%)
Chytridiomycota	16 (1.01%)	Malasseziomycetes	14 (0.88%)	Hypocreales	105 (6.6%)
Entomophthoromycota	1 (0.06%)	Pezizomycetes	13 (0.82%)	Mycosphaerellales	34 (2.14%)
Glomeromycota	7 (0.44%)	Saccharomycetes	28 (1.76%)	Pleosporales	161 (10.11%)
Mortierellomycota	2 (0.13%)	Sordariomycetes	471 (29.59%)	Sordariales	62 (3.89%)
Mucoromycota	12 (0.75%)	Tremellomycetes	25 (1.57%)	Thelebolales	11 (0.69%)
		Ustilaginomycetes	9 (0.57%)	Trichosphaeriales	18 (1.13%)
		others	73 (4.59%)	others	629 (39.51%)
unknown	201 (12.63%)	unknown	333 (20.92%)	unknown	455 (28.58%)
Bacteria					
Acidobacteriota	19 (1.48%)	Actinobacteria	148 (11.55%)	Acetobacterales	18 (1.41%)
Actinobacteriota	206 (16.08%)	Alphaproteobacteria	264 (20.61%)	Bacillales	25 (1.95%)
Bacteroidota	136 (10.62%)	Bacilli	85 (6.64%)	Burkholderiales	74 (5.78%)
Chloroflexi	18 (1.41%)	Bacteroidia	129 (10.07%)	Clostridiales	17 (1.33%)
Deinococcota	9 (0.7%)	Clostridia	59 (4.61%)	Enterobacterales	17 (1.33%)
Fibrobacterota	8 (0.62%)	Deinococci	9 (0.7%)	Lactobacillales	20 (1.56%)
Firmicutes	161 (12.57%)	Gammaproteobacteria	167 (13.04%)	Propionibacteriales	24 (1.87%)
Myxococcota	32 (2.5%)	Ignavibacteria	3 (0.23%)	Pseudomonadales	31 (2.42%)
Patescibacteria	13 (1.01%)	Polyangia	27 (2.11%)	Rhizobiales	101 (7.88%)
Proteobacteria	439 (34.27%)	Thermoanaerobacteria	3 (0.23%)	Sphingomonadales	31 (2.42%)
others	93 (7.26%)	others	217 (16.94%)	others	668 (52.15%)
unknown	147 (11.48%)	unknown	170 (13.27%)	unknown	255 (19.91%)
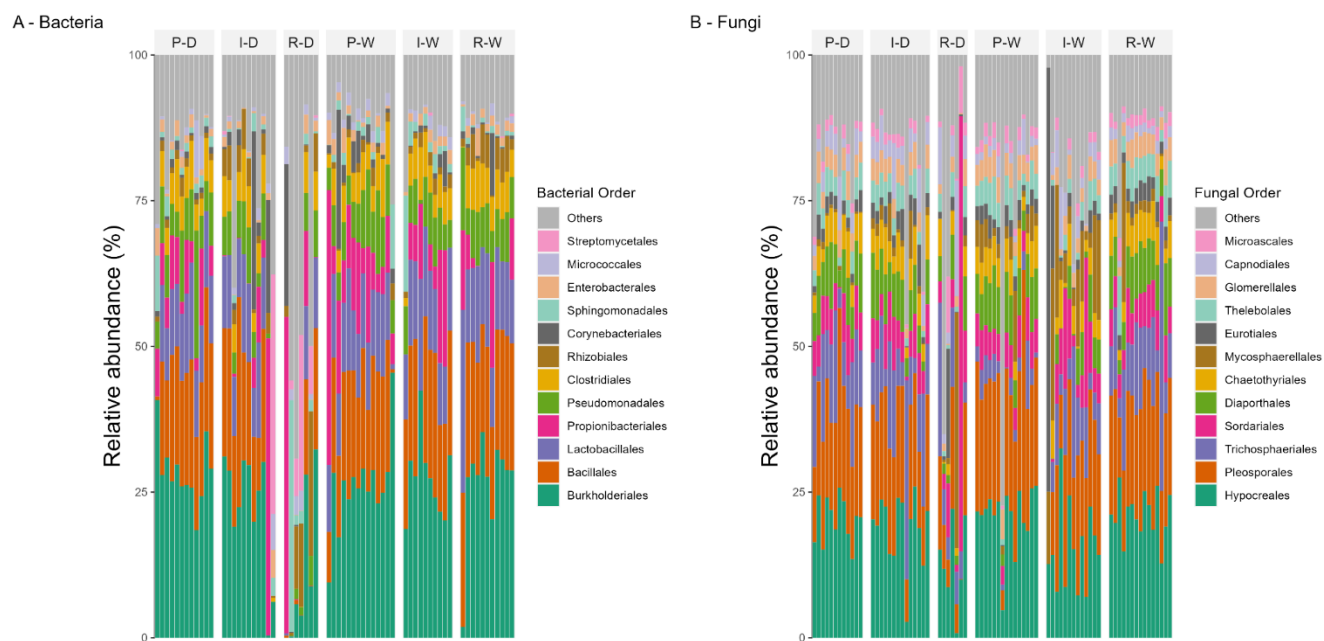
Figure S9: Relative abundance of bacterial (A) and fungal (B) orders in the 6 treatments. Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.

Table S7: Result table of the pairwise perMANOVA performed on the position of bacterial communities in the dbRDA space according to the different treatments. The perMANOVA was conducted on individuals coordinates in the multivariate spaces retrieved from the dbRDA. P.adjusted corresponds to holm's corrected p.values for multiple comparisons and are in bold when significant (<0.05). Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.

Pairs	Df	SumsOfSqs	F.Model	R2	p.value	p.adjusted
R-D vs I-D	1	22.043164	6.507155	0.28911493	0.001	**0.015**
R-D vs P-D	1	30.250818	13.285273	0.43867106	0.001	**0.015**
R-D vs R-W	1	28.817413	10.665847	0.39998155	0.001	**0.015**
R-D vs I-W	1	26.566445	13.548725	0.47458249	0.001	**0.015**
R-D vs P-W	1	31.206621	18.718147	0.49626370	0.001	**0.015**
I-D vs P-D	1	10.640009	4.839587	0.18729350	0.006	**0.015**
I-D vs R-W	1	12.718617	5.018256	0.20058376	0.001	**0.015**
I-D vs I-W	1	12.331108	6.354162	0.25061612	0.001	**0.015**
I-D vs P-W	1	31.051111	18.248338	0.44240177	0.001	**0.015**
P-D vs R-W	1	11.102162	6.623773	0.23978525	0.001	**0.015**
P-D vs I-W	1	4.016283	3.756880	0.15813861	0.004	**0.015**
P-D vs P-W	1	7.825354	7.942722	0.24865515	0.001	**0.015**
R-W vs I-W	1	2.862094	2.099519	0.09950553	0.099	0.099
R-W vs P-W	1	29.404178	24.011527	0.51075829	0.001	**0.015**
I-W vs P-W	1	13.924215	21.349983	0.49250268	0.001	**0.015**

Table S8: Result table of the marginal significance Anova performed on the dbRDA model after variable forward selection for bacterial communities. Bold p value indicates significance of the variable effect (<0.05). Marginal means a different test was performed for each variable in a model containing all the variables.

Variables	Df	SumOfSqs	F	p value
Nitrogen	1	0.651	1.474	**0.001**
C/N	1	0.587	1.328	**0.001**
Water potential	1	0.493	1.116	**0.049**
Chlorophyll	1	0.496	1.122	**0.044**
Residual	59	26.082		

Table S9: Result table of the pairwise perMANOVA performed on the position of fungal communities in the dbRDA space according to the different treatments. The perMANOVA was conducted on individuals coordinates in the multivariate spaces retrieved from the dbRDA. P.adjusted corresponds to holm's corrected p.values for multiple comparisons and are in bold when significant (<0.05). Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.

pairs	Df	SumsOfSqs	F.Model	R2	p.value	p.adjusted
R-D vs I-D	1	20.74934	8.528524	0.3098068	0.001	**0.015**
R-D vs P-D	1	24.90178	12.665446	0.4269427	0.001	**0.015**
R-D vs R-W	1	26.85748	22.315397	0.5273588	0.001	**0.015**
R-D vs I-W	1	46.30076	30.650964	0.6300176	0.001	**0.015**
R-D vs P-W	1	44.40278	19.365529	0.4919413	0.002	**0.015**
I-D vs P-D	1	32.02626	18.266755	0.4321778	0.001	**0.015**
I-D vs R-W	1	52.55523	43.361253	0.6162661	0.001	**0.015**
I-D vs I-W	1	24.88511	17.356285	0.4097688	0.001	**0.015**
I-D vs P-W	1	57.26582	28.364187	0.5123201	0.001	**0.015**
P-D vs R-W	1	58.39346	73.273367	0.7456076	0.001	**0.015**
P-D vs I-W	1	47.55351	47.465177	0.6735976	0.001	**0.015**
P-D vs P-W	1	24.48065	14.673170	0.3698512	0.001	**0.015**
R-W vs I-W	1	54.66178	103.816681	0.7997176	0.001	**0.015**
R-W vs P-W	1	41.40997	35.834331	0.5613646	0.001	**0.015**
I-W vs P-W	1	28.04338	20.552529	0.4414911	0.001	**0.015**

Table S10: Result table of the marginal significance Anova performed on the dbRDA model after variable forward selection for fungal communities. Bold p value indicates significance of the variable effect (<0.05). Marginal means a different test was performed for each variable in a model containing all the variables.

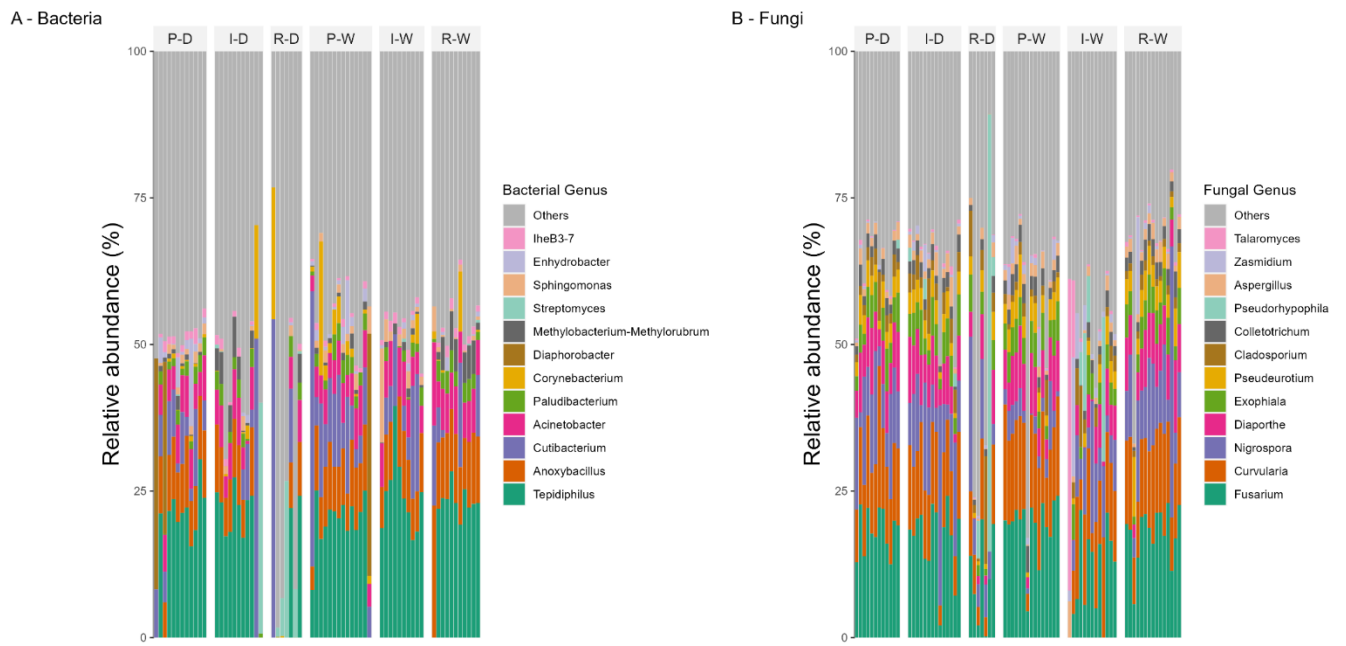| Variables	Df	SumOfSqs	F	p value
Drought	1	0.704	1.695	**0.001**
Substrate	2	0.939	1.131	**0.012**
Residual	71	29.482		

Figure S10: Relative abundance of bacterial (A) and fungal (B) genus in the 6 treatments. Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.
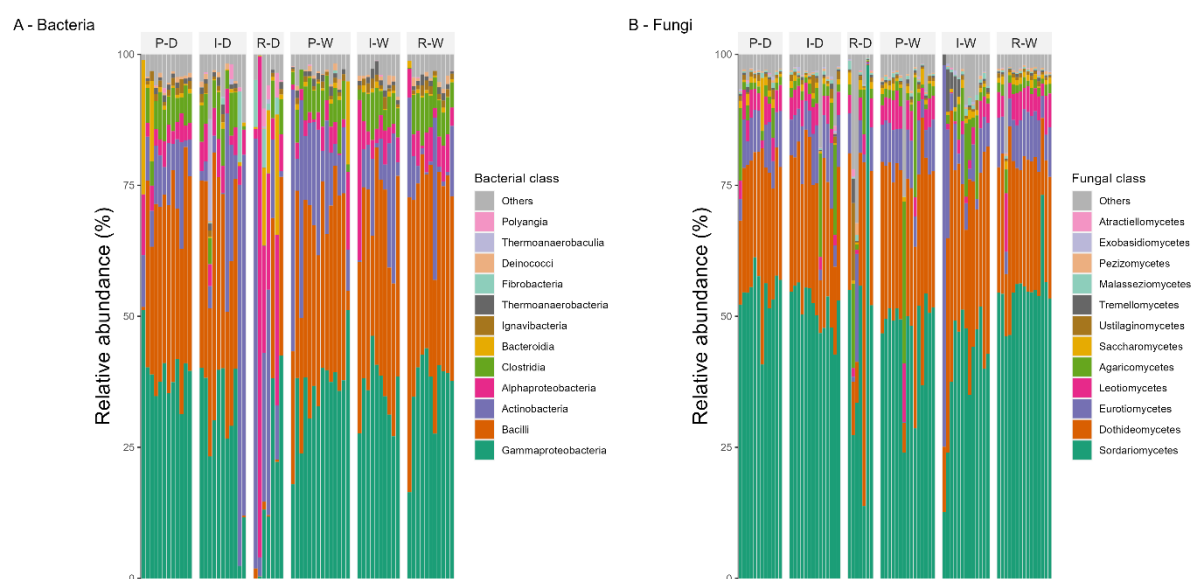
Figure S11: Relative abundance of bacterial (A) and fungal (B) class in the 6 treatments. Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.