**Annexes Chapitre III : Water and nutrient resources shape plant traits, their leaf endophytic microbiota, and their relationships**

A graph of different types of minerals

Description automatically generated with medium confidenceFigure S6: C, N and P content of the three substrates. P – Poor, I – Intermediate and R – Rich.

A graph of different colors

Description automatically generated with medium confidenceFigure S7: Number of reads per sample colored according to treatments.

*A comparison of a graph

Description automatically generated*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: Fv/Fm; maximal electron transfer rate: ETRmax (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 (a) | 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** |
| Fv/Fm | 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** |
| ETRmax | 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%) |

A close-up of a graph

Description automatically generatedFigure 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** |

| 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 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.

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 |  |  |

A close-up of a graph

Description automatically generatedFigure 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.

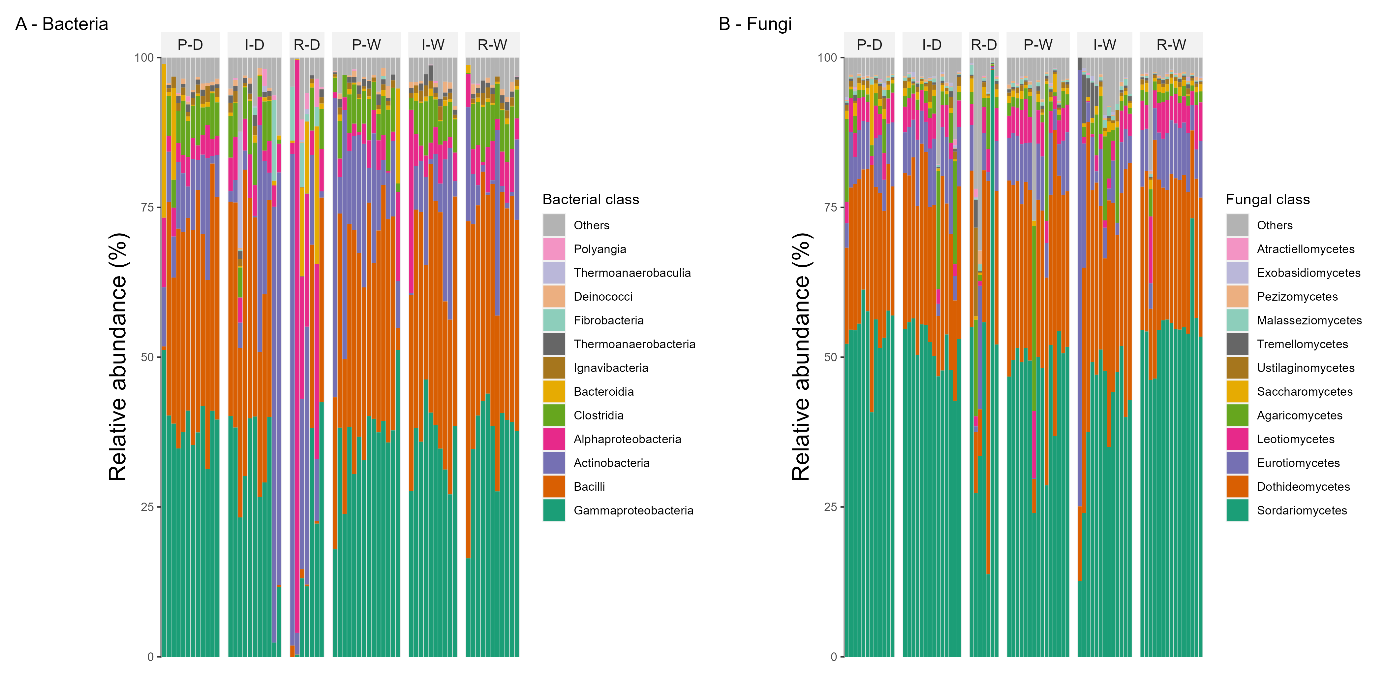


Figure S11: Relative abundance of bacterial (A) and fungal (B) class in the 6 treatments. Treatments are P-D, Poor-Dry; I-D, Intermediate-Dry; R-D, Rich-Dry; P-W, Poor-Wet; I-W, Intermediate-Wet and R-W, Rich-Wet.