**Annexes chapitre IV : Maternal effects and current environmental conditions affect the phenotype and the microbiota assemblage in Aechmea mertensii seedlings**

A graph of different types of minerals

Description automatically generated with medium confidenceFigure S12: C, N and P content of the three substrates. P – Poor, I – Intermediate and R – Rich.

A screen shot of a computer

Description automatically generated

Figure S13: % of germinated seeds of the 10 first day according to maternal and seedling treatment (colour and line type respectively).

| Seedling  Mother | Poor | Intermediate | Rich | Total |
| --- | --- | --- | --- | --- |
| Ecophysiology sampling |  |  |  |  |
| Poor | 41 | 41 | 37 | 119 |
| Intermediate | 43 | 45 | 42 | 130 |
| Rich | 44 | 43 | 43 | 130 |
| Total | 128 | 129 | 122 | 379 |
| Microbiota sampling |  |  |  |  |
| Poor | 45 | 44 | 38 | 127 |
| Intermediate | 41 | 43 | 42 | 126 |
| Rich | 43 | 43 | 44 | 130 |
| Total | 129 | 130 | 124 | 383 |

Table S11: Sample size for the 9 treatments for ecophysiological measurements and microbiota investigation.

Table S12: Results of the perMANOVA performed on seedling traits to test the effects of maternal and seedling treatment as well as their interaction. Bold p-value indicates significance of the tested effect (<0.05).

|  | **Df** | **Sum of squares** | **R2** | **F** | **p value** |
| --- | --- | --- | --- | --- | --- |
| **Maternal treatment** | 2 | 470.676 | 0.116 | 28.262 | **0.001** |
| **Seedling treatment** | 2 | 473.968 | 0.117 | 28.460 | **0.001** |
| **Interaction** | 4 | 105.674 | 0.026 | 3.173 | **0.001** |
| **Residual** | 360 | 2,997.681 | 0.741 |  |  |
| **Total** | 368 | 4,048.000 | 1.000 |  |  |

Table S13: Results of the pairwise permanova performed on Seedling traits to test for pairwise differences between all 9 treatment combinations resulting in 36 comparisons. P-values are Holm’s adjusted and displayed in bold when significant (<0.05).

| **Pairs** |  | **Df** | **Sum of squares** | **R2** | **F** | **Adjusted p value** |
| --- | --- | --- | --- | --- | --- | --- |
| R to R - R to I | Treatment | 1 | 15.431 | 0.031 | 2.596 | 0.051 |
|  | Residual | 80 | 475.542 | 0.969 |  |  |
|  | Total | 81 | 490.972 | 1.000 |  |  |
| R to R - R to P | Treatment | 1 | 129.321 | 0.217 | 21.015 | **0.036** |
|  | Residual | 76 | 467.693 | 0.783 |  |  |
|  | Total | 77 | 597.014 | 1.000 |  |  |
| R to R - I to R | Treatment | 1 | 91.816 | 0.146 | 13.897 | **0.036** |
|  | Residual | 81 | 535.172 | 0.854 |  |  |
|  | Total | 82 | 626.988 | 1.000 |  |  |
| R to R - I to I | Treatment | 1 | 163.184 | 0.210 | 21.469 | **0.036** |
|  | Residual | 81 | 615.667 | 0.790 |  |  |
|  | Total | 82 | 778.851 | 1.000 |  |  |
| R to R - I to P | Treatment | 1 | 295.318 | 0.340 | 41.135 | **0.036** |
|  | Residual | 80 | 574.337 | 0.660 |  |  |
|  | Total | 81 | 869.655 | 1.000 |  |  |
| R to R - P to R | Treatment | 1 | 76.463 | 0.105 | 9.523 | **0.036** |
|  | Residual | 81 | 650.396 | 0.895 |  |  |
|  | Total | 82 | 726.859 | 1.000 |  |  |
| R to R - P to I | Treatment | 1 | 130.566 | 0.138 | 12.932 | **0.036** |
|  | Residual | 81 | 817.813 | 0.862 |  |  |
|  | Total | 82 | 948.378 | 1.000 |  |  |
| R to R - P to P | Treatment | 1 | 299.827 | 0.321 | 37.902 | **0.036** |
|  | Residual | 80 | 632.852 | 0.679 |  |  |
|  | Total | 81 | 932.680 | 1.000 |  |  |
| R to I - R to P | Treatment | 1 | 89.987 | 0.171 | 15.650 | **0.036** |
|  | Residual | 76 | 437.009 | 0.829 |  |  |
|  | Total | 77 | 526.996 | 1.000 |  |  |
| R to I - I to R | Treatment | 1 | 97.424 | 0.162 | 15.642 | **0.036** |
|  | Residual | 81 | 504.488 | 0.838 |  |  |
|  | Total | 82 | 601.912 | 1.000 |  |  |
| R to I - I to I | Treatment | 1 | 186.244 | 0.241 | 25.788 | **0.036** |
|  | Residual | 81 | 584.983 | 0.759 |  |  |
|  | Total | 82 | 771.227 | 1.000 |  |  |
| R to I - I to P | Treatment | 1 | 283.282 | 0.343 | 41.686 | **0.036** |
|  | Residual | 80 | 543.652 | 0.657 |  |  |
|  | Total | 81 | 826.934 | 1.000 |  |  |
| R to I - P to R | Treatment | 1 | 97.612 | 0.136 | 12.758 | **0.036** |
|  | Residual | 81 | 619.712 | 0.864 |  |  |
|  | Total | 82 | 717.324 | 1.000 |  |  |
| R to I - P to I | Treatment | 1 | 141.936 | 0.153 | 14.606 | **0.036** |
|  | Residual | 81 | 787.128 | 0.847 |  |  |
|  | Total | 82 | 929.064 | 1.000 |  |  |
| R to I - P to P | Treatment | 1 | 299.196 | 0.332 | 39.749 | **0.036** |
|  | Residual | 80 | 602.168 | 0.668 |  |  |
|  | Total | 81 | 901.364 | 1.000 |  |  |
| R to P - I to R | Treatment | 1 | 203.585 | 0.291 | 31.564 | **0.036** |
|  | Residual | 77 | 496.639 | 0.709 |  |  |
|  | Total | 78 | 700.225 | 1.000 |  |  |
| R to P - I to I | Treatment | 1 | 154.676 | 0.211 | 20.637 | **0.036** |
|  | Residual | 77 | 577.134 | 0.789 |  |  |
|  | Total | 78 | 731.811 | 1.000 |  |  |
| R to P - I to P | Treatment | 1 | 139.252 | 0.206 | 19.752 | **0.036** |
|  | Residual | 76 | 535.804 | 0.794 |  |  |
|  | Total | 77 | 675.056 | 1.000 |  |  |
| R to P - P to R | Treatment | 1 | 194.947 | 0.242 | 24.533 | **0.036** |
|  | Residual | 77 | 611.863 | 0.758 |  |  |
|  | Total | 78 | 806.810 | 1.000 |  |  |
| R to P - P to I | Treatment | 1 | 126.373 | 0.140 | 12.487 | **0.036** |
|  | Residual | 77 | 779.280 | 0.860 |  |  |
|  | Total | 78 | 905.652 | 1.000 |  |  |
| R to P - P to P | Treatment | 1 | 165.030 | 0.217 | 21.104 | **0.036** |
|  | Residual | 76 | 594.319 | 0.783 |  |  |
|  | Total | 77 | 759.349 | 1.000 |  |  |
| I to R - I to I | Treatment | 1 | 99.374 | 0.134 | 12.641 | **0.036** |
|  | Residual | 82 | 644.614 | 0.866 |  |  |
|  | Total | 83 | 743.988 | 1.000 |  |  |
| I to R - I to P | Treatment | 1 | 213.991 | 0.262 | 28.732 | **0.036** |
|  | Residual | 81 | 603.283 | 0.738 |  |  |
|  | Total | 82 | 817.275 | 1.000 |  |  |
| I to R - P to R | Treatment | 1 | 26.274 | 0.037 | 3.171 | **0.044** |
|  | Residual | 82 | 679.343 | 0.963 |  |  |
|  | Total | 83 | 705.616 | 1.000 |  |  |
| I to R - P to I | Treatment | 1 | 97.550 | 0.103 | 9.447 | **0.036** |
|  | Residual | 82 | 846.759 | 0.897 |  |  |
|  | Total | 83 | 944.309 | 1.000 |  |  |
| I to R - P to P | Treatment | 1 | 201.907 | 0.234 | 24.712 | **0.036** |
|  | Residual | 81 | 661.799 | 0.766 |  |  |
|  | Total | 82 | 863.706 | 1.000 |  |  |
| I to I - I to P | Treatment | 1 | 45.352 | 0.062 | 5.372 | **0.036** |
|  | Residual | 81 | 683.778 | 0.938 |  |  |
|  | Total | 82 | 729.130 | 1.000 |  |  |
| I to I - P to R | Treatment | 1 | 73.081 | 0.088 | 7.887 | **0.036** |
|  | Residual | 82 | 759.838 | 0.912 |  |  |
|  | Total | 83 | 832.919 | 1.000 |  |  |
| I to I - P to I | Treatment | 1 | 26.025 | 0.027 | 2.301 | 0.116 |
|  | Residual | 82 | 927.254 | 0.973 |  |  |
|  | Total | 83 | 953.279 | 1.000 |  |  |
| I to I - P to P | Treatment | 1 | 38.292 | 0.049 | 4.178 | **0.036** |
|  | Residual | 81 | 742.294 | 0.951 |  |  |
|  | Total | 82 | 780.586 | 1.000 |  |  |
| I to P - P to R | Treatment | 1 | 183.817 | 0.204 | 20.722 | **0.036** |
|  | Residual | 81 | 718.507 | 0.796 |  |  |
|  | Total | 82 | 902.325 | 1.000 |  |  |
| I to P - P to I | Treatment | 1 | 67.267 | 0.071 | 6.150 | **0.036** |
|  | Residual | 81 | 885.923 | 0.929 |  |  |
|  | Total | 82 | 953.191 | 1.000 |  |  |
| I to P - P to P | Treatment | 1 | 9.446 | 0.013 | 1.078 | 0.357 |
|  | Residual | 80 | 700.963 | 0.987 |  |  |
|  | Total | 81 | 710.410 | 1.000 |  |  |
| P to R - P to I | Treatment | 1 | 47.228 | 0.047 | 4.026 | **0.036** |
|  | Residual | 82 | 961.983 | 0.953 |  |  |
|  | Total | 83 | 1,009.211 | 1.000 |  |  |
| P to R - P to P | Treatment | 1 | 170.694 | 0.180 | 17.794 | **0.036** |
|  | Residual | 81 | 777.023 | 0.820 |  |  |
|  | Total | 82 | 947.717 | 1.000 |  |  |
| P to I - P to P | Treatment | 1 | 62.047 | 0.062 | 5.322 | **0.036** |
|  | Residual | 81 | 944.439 | 0.938 |  |  |
|  | Total | 82 | 1,006.486 | 1.000 |  |  |

Table S14: Statistical summary table. For each trait the mean ± standard deviation (SD) is displayed for the nine treatments combination (three maternal to three seedling). 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). P – poor substrates, I – intermediate, R – rich. Traits are Number of leaves, Stomatal density (Nb mm-2); Number of roots; Average root diameter (ARD, mm); Leaf Mass Area (LMA, g m-2); Leaf Dry Matter Content (LDMC, g g-1); Relative Water Content (RWC, %); Specific Root Length (SRL, m g-1); Root Tissue Density (RTD, g cm-3); Root to Shoot ratio (RS ratio) and, Relative Growth Rate (RGR, g g-1 month-1).

| Traits | Mean ± SD | | | | | | | | | Significance | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Mother | Poor | | | Intermediate | | | Rich | | | KW-chi | P-val |
| Seedling | Poor | Intermediate | Rich | Poor | Intermediate | Rich | Poor | Intermediate | Rich |
| Number of leaves | 5.5 ± 0.9  (a) | 6.3 ± 1.5  (ab) | 6.9 ± 1.5  (bc) | 5.6 ± 1.3  (a) | 6.6 ± 1.4  (ab) | 7.5 ± 1.3  (cd) | 6.7 ± 1.2  (b) | 8.1 ± 1.2  (d) | 8.2 ± 1.1  (d) | 137.298 | **<0.0001** |
| Stomatal density | 70 ± 10  (abc) | 66 ± 9.8  (abde) | 63 ± 8.7  (d) | 73 ± 9.3  (c) | 69 ± 9.1  (abde) | 66 ± 8.7  (ade) | 72 ± 7.5  (bc) | 66 ± 9.1  (ade) | 64 ± 6.8  (de) | 55.435 | **<0.0001** |
| Number of roots | 3 ± 1.1  (a) | 4.8 ± 2.1  (bc) | 5.8 ± 1.6  (b) | 3.1 ± 1.3  (a) | 3.9 ± 2  (bc) | 5.9 ± 2.1  (b) | 3.7 ± 1.2  (ac) | 5.1 ± 1.6  (b) | 5.1 ± 1.5  (b) | 115.936 | **<0.0001** |
| ARD | 1.2 ± 0.22  (a) | 1.4 ± 0.26  (abcd) | 1.4 ± 0.27  (bcd) | 1.3 ± 0.14  (ab) | 1.3 ± 0.18  (abcd) | 1.3 ± 0.23  (abc) | 1.3 ± 0.16  (abcd) | 1.4 ± 0.22  (cd) | 1.5 ± 0.24  (d) | 43.610 | **<0.0001** |
| LMA | 16 ± 2.9  (ab) | 17 ± 4  (ab) | 18 ± 3.9  (ac) | 16 ± 3  (ab) | 15 ± 3  (ab) | 19 ± 2.4  (cd) | 21 ± 2.7  (de) | 22 ± 2.9  (e) | 20 ± 3.4  (cd) | 125.485 | **<0.0001** |
| LDMC | 0.035 ± 0.0059 (ab) | 0.034 ± 0.0061  (ab) | 0.033 ± 0.0068  (ab) | 0.035 ± 0.0049  (a) | 0.033 ± 0.0041  (ab) | 0.034 ± 0.0034  (ab) | 0.043 ± 0.0044  (c) | 0.038 ± 0.0036  (d) | 0.036 ± 0.0039  (a) | 104.521 | **<0.0001** |
| RWC | 96 ± 2.8  (a) | 94 ± 3.2  (ab) | 94 ± 2.3  (b) | 95 ± 2.4  (ab) | 94 ± 2.7  (ab) | 94 ± 3.5  (b) | 88 ± 3.6  (c) | 88 ± 3.1  (c) | 88 ± 4  (c) | 188.990 | **<0.0001** |
| SRL | 19 ± 7.7  (ab) | 15 ± 8  (acd) | 16 ± 8.8  (abcd) | 19 ± 7.9  (abc) | 17 ± 7  (acd) | 20 ± 7.3  (b) | 15 ± 4.5  (acd) | 14 ± 4.1  (cd) | 13 ± 3.8  (d) | 46.447 | **<0.0001** |
| RTD | 0.0054 ± 0.0025  (ab) | 0.0057 ± 0.0029  (ab) | 0.0047 ± 0.0015  (ab) | 0.0049 ± 0.0019  (ab) | 0.005 ± 0.0023  (ab) | 0.0042 ± 0.0012  (a) | 0.0055 ± 0.0017  (b) | 0.0049 ± 0.00071  (b) | 0.0052 ± 0.0016  (b) | 21.148 | **0.00676** |
| RS ratio | 0.33 ± 0.16 (ab) | 0.33 ± 0.19  (ab) | 0.21 ± 0.12  (cde) | 0.38 ± 0.14  (a) | 0.26 ± 0.12  (ab) | 0.17 ± 0.052  (e) | 0.36 ± 0.12  (a) | 0.25 ± 0.063  (bc) | 0.2 ± 0.086  (de) | 123.029 | **<0.0001** |
| RGR | 0.55 ± 0.37  (a) | 0.95 ± 0.57  (bc) | 1.3 ± 0.26  (bd) | 0.54 ± 0.4  (a) | 0.78 ± 0.5  (bc) | 1.4 ± 0.24  (d) | 0.86 ± 0.23  (c) | 1.4 ± 0.24  (d) | 1.4 ± 0.24  (d) | 188.984 | **<0.0001** |

Table S15: Results of pairwise perMANOVA on seeds fungal communities. P values are Holm’s adjusted and in bold when significant (<0.05).

| **Pairs** |  | **Df** | **Sum of squares** | **R2** | **F** | **Adjusted p value** |
| --- | --- | --- | --- | --- | --- | --- |
| P - PS | Maternal treatment | 1 | 0.482 | 0.040 | 1.050 | 0.141 |
|  | Residual | 25 | 11.471 | 0.960 |  |  |
|  | Total | 26 | 11.953 | 1.000 |  |  |
| P - SP | Maternal treatment | 1 | 0.606 | 0.053 | 1.351 | **0.003** |
|  | Residual | 24 | 10.766 | 0.947 |  |  |
|  | Total | 25 | 11.372 | 1.000 |  |  |
| PS - SP | Maternal treatment | 1 | 0.641 | 0.059 | 1.433 | **0.003** |
|  | Residual | 23 | 10.279 | 0.941 |  |  |
|  | Total | 24 | 10.919 | 1.000 |  |  |

A comparison of different colored bars

Description automatically generatedFigure S14: Bacterial (A) and fungal (B) class relative abundance in seed microbiota according to treatments. Only the 7 most abundant classes are displayed. P – Poor, I – Intermediate, R – Rich.

A screenshot of a computer

Description automatically generatedFigure S15: Overall OTUs repartition for each treatment combination between the different organs for (A) bacteria and (B) fungi. L, R and S are the OTUs exclusively found in seedling leaves, seedling roots, or seeds respectively. LRS those found in the three organs and LR, LS and SR those either found in Leaves and Roots, Leaves and Seeds or Seeds and Roots, respectively. P – Poor, I – Intermediate and R – Rich. Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.

Table S16: Output of the mix linear model testing the effects of seed treatment, seedling treatment and seedling tissue on the average pairwise β diversity between seed and seedling microbiota.

| **Bacteria** | **Estimate** | **Std. Error** | **df** | | **t value** | | **p value** | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Intercept | 1.683 | 0.021 | 43.517 | | 79.635 | | **<0.001** | |
| Seed Intermediate | 0.043 | 0.026 | 27.000 | | 1.621 | | 0.117 | |
| Seed Poor | -0.079 | 0.026 | 27.000 | | -2.998 | | **0.006** | |
| Seedling Intermediate | 0.008 | 0.014 | 147.000 | | 0.599 | | 0.55 | |
| Seedling Poor | 0.027 | 0.014 | 147.000 | | 1.925 | | 0.056 | |
| Roots | 0.255 | 0.011 | 147.000 | | 22.374 | | **<0.001** | |
| **Fungi** |  |  | |  | |  | |  |
| Intercept | 1.669 | 0.028 | | 34.505 | | 60.589 | | **<0.001** |
| Seed Intermediate | 0.103 | 0.037 | | 27.000 | | 2.815 | | **0.009** |
| Seed Poor | -0.017 | 0.037 | | 27.000 | | -0.455 | | 0.653 |
| Seedling Intermediate | 0.020 | 0.013 | | 147.000 | | 1.489 | | 0.139 |
| Seedling Poor | 0.037 | 0.013 | | 147.000 | | 2.745 | | **0.007** |
| Roots | 0.064 | 0.011 | | 147.000 | | 5.929 | | **<0.001** |
|  |  |  |  | |  | |  | |

A screenshot of a computer screen

Description automatically generatedFigure S16: Relative abundance of the dominant bacterial and fungal taxa in leaves (A and C respectively) and roots (B and D). P – Poor, I – Intermediate and R – Rich. Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.

|  |  |  | **Df** | **Sum of squares** | **R2** | **F** | **p value** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Leaves** | Bacteria | Mother treatment | 2 | 1.684 | 0.010 | 1.758 | **0.001** |
|  |  | Seedling treatment | 2 | 1.226 | 0.007 | 1.279 | **0.001** |
|  |  | Mother ID | 27 | 14.203 | 0.085 | 1.098 | **0.001** |
|  |  | Treatments interaction | 4 | 2.121 | 0.013 | 1.107 | **0.001** |
|  |  | Residual | 310 | 148.474 | 0.885 |  |  |
|  |  | Total | 345 | 167.708 | 1.000 |  |  |
|  | Fungi | Mother treatment | 2 | 2.271 | 0.015 | 2.387 | **0.001** |
|  |  | Seedling treatment | 2 | 1.170 | 0.008 | 1.229 | **0.001** |
|  |  | Mother ID | 26 | 14.764 | 0.097 | 1.194 | **0.001** |
|  |  | Treatments interaction | 4 | 2.081 | 0.014 | 1.094 | **0.003** |
|  |  | Residual | 276 | 131.297 | 0.866 |  |  |
|  |  | Total | 310 | 151.582 | 1.000 |  |  |
| **Roots** | Bacteria | Mother treatment | 2 | 1.896 | 0.014 | 2.087 | **0.001** |
|  |  | Seedling treatment | 2 | 1.646 | 0.012 | 1.812 | **0.001** |
|  |  | Mother ID | 27 | 14.358 | 0.103 | 1.171 | **0.001** |
|  |  | Treatments interaction | 4 | 2.227 | 0.016 | 1.226 | **0.001** |
|  |  | Residual | 262 | 119.023 | 0.855 |  |  |
|  |  | Total | 297 | 139.151 | 1.000 |  |  |
|  | Fungi | Mother treatment | 2 | 1.808 | 0.013 | 1.886 | **0.001** |
|  |  | Seedling treatment | 2 | 1.247 | 0.009 | 1.301 | **0.001** |
|  |  | Mother ID | 27 | 14.548 | 0.102 | 1.124 | **0.001** |
|  |  | Treatments interaction | 4 | 2.091 | 0.015 | 1.091 | **0.001** |
|  |  | Residual | 257 | 123.163 | 0.862 |  |  |
|  |  | Total | 292 | 142.857 | 1.000 |  |  |

Table S17: Results of the perMANOVAs performed on leaves and roots bacterial and fungal communities. PerMANOVAs tested for the effect of the mother and seedling treatments as well as their interaction and the mother plant identity (Mother ID). P values in bold indicates a significant effect (p<0.05).

A screenshot of a computer screen

Description automatically generatedFigure S17: Relative abundance of the dominant fungal orders roots. P – Poor, I – Intermediate and R – Rich. . Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.

A close-up of a graph

Description automatically generatedFigure S18: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) class in the leaves of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.

A close-up of a graph

Description automatically generatedFigure S19: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the roots of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.A close-up of a graph

Description automatically generatedFigure S20: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the leaves of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as ‘Maternal treatment’ to ‘Seedling treatment’.

A close-up of a graph

Description automatically generatedFigure S21: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the seeds. P – Poor, I – Intermediate and R – Rich.