Annexes chapitre IV : Maternal effects and current environmental conditions affect the phenotype and the microbiota assemblage in Aechmea mertensii seedlings
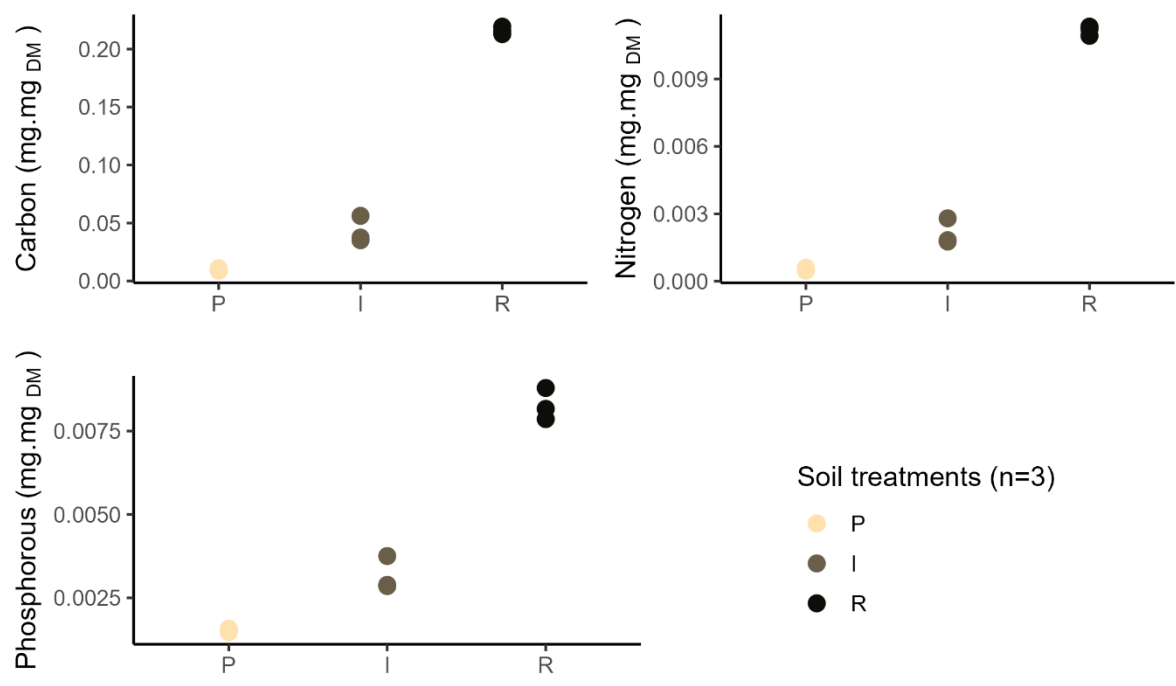
Figure S12: C, N and P content of the three substrates. P – Poor, I – Intermediate and R – Rich.
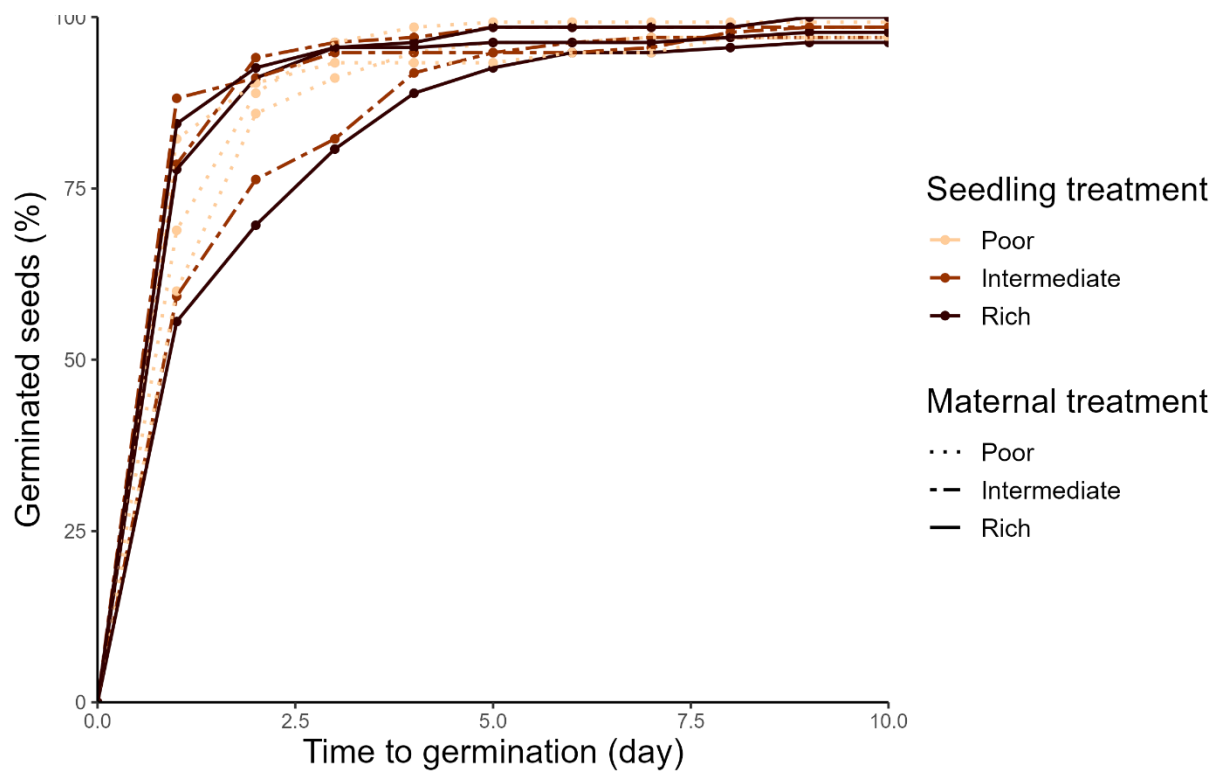
Figure S13: % of germinated seeds of the 10 first day according to maternal and seedling treatment (colour and line type respectively).

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

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 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		

Pairs		Df	Sum of squares	R2	F	Adjusted p value
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 Chi^2 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				
Seedling	Poor	Intermediate	Rich	Poor	Intermediate	Rich	Poor	Intermediate	Rich	KW-chi	P-val
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		
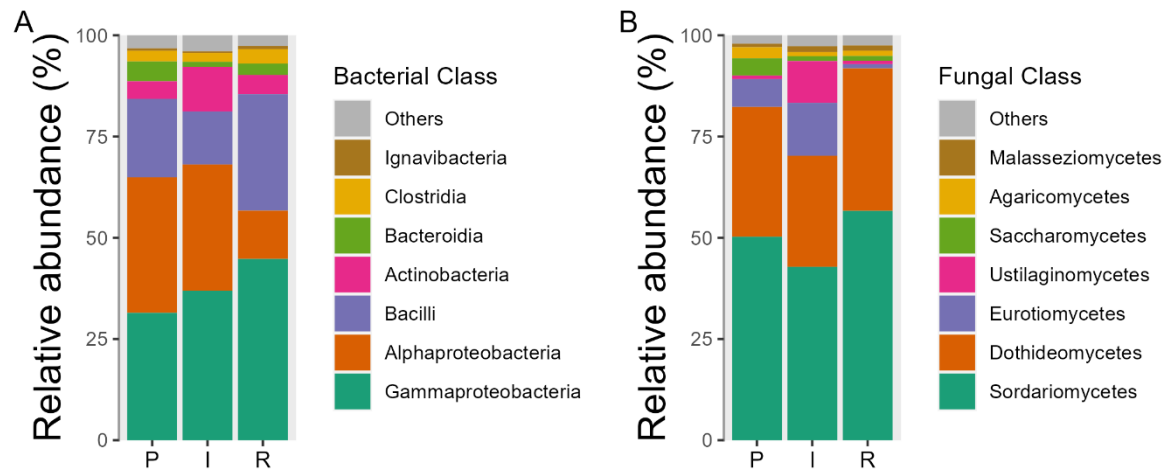
Figure S14: Bacterial (A) and fungal (B) class relative abundance in seed microbiota according to treatments. Only the 7 most abundant classes are displayed. P – Poor, I – Intermediate, R – Rich.
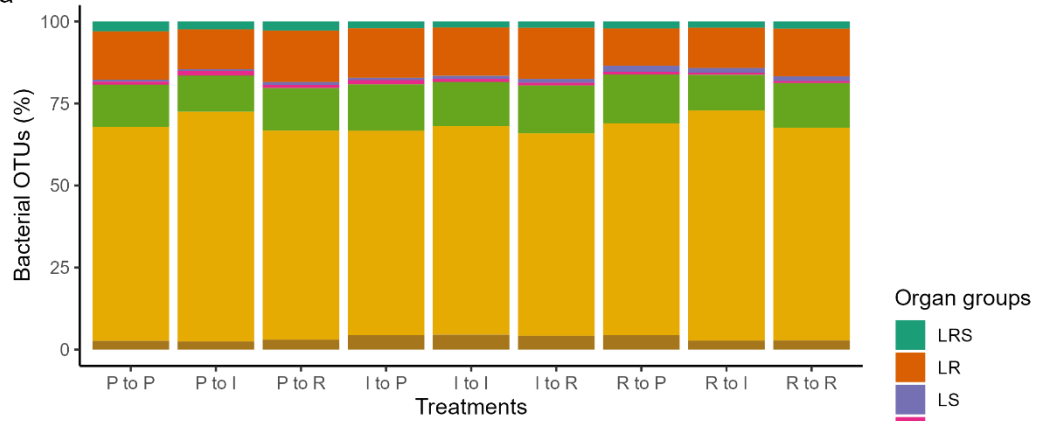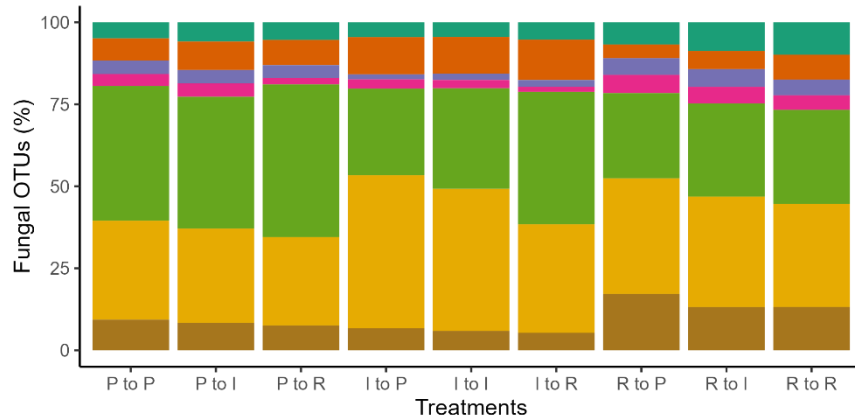
Figure S15: Overall OTUs repartition for each treatment combination between the different organs for (A) bacteria and (B) fungi. L, R and S are the OTUs exclusively found in seedling leaves, seedling roots, or seeds respectively. LRS those found in the three organs and LR, LS and SR those either found 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**
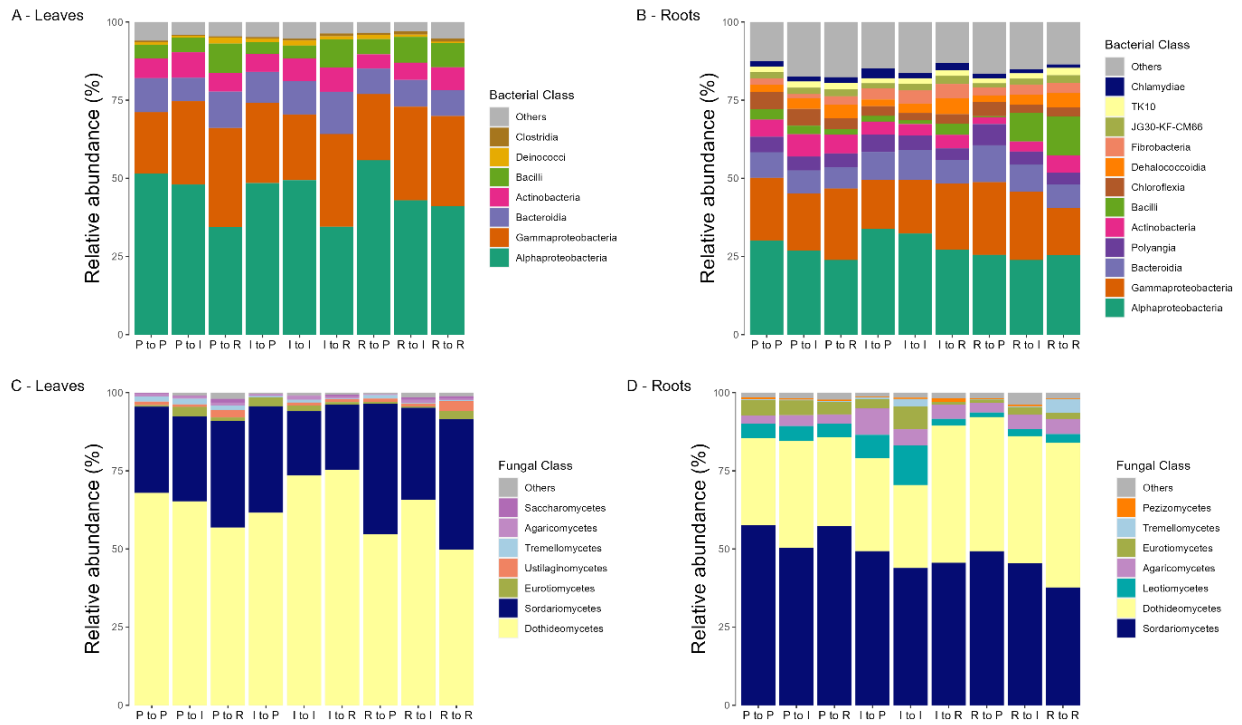
Figure S16: Relative abundance of the dominant bacterial and fungal taxa in leaves (A and C respectively) and roots (B and D). P – Poor, I – Intermediate and R – Rich. Treatments are named as 'Maternal treatment' to 'Seedling treatment'.

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).

|			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		
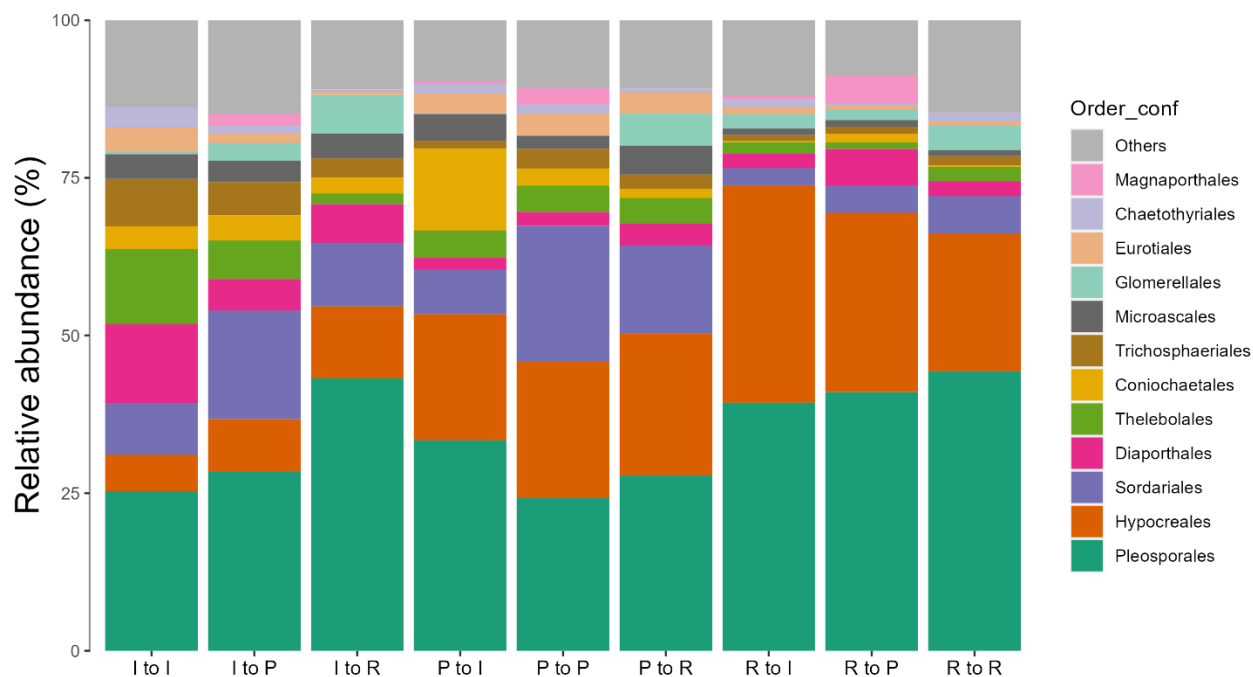
Figure S17: Relative abundance of the dominant fungal orders roots. P – Poor, I – Intermediate and R – Rich. . Treatments are named as 'Maternal treatment' to 'Seedling treatment'.
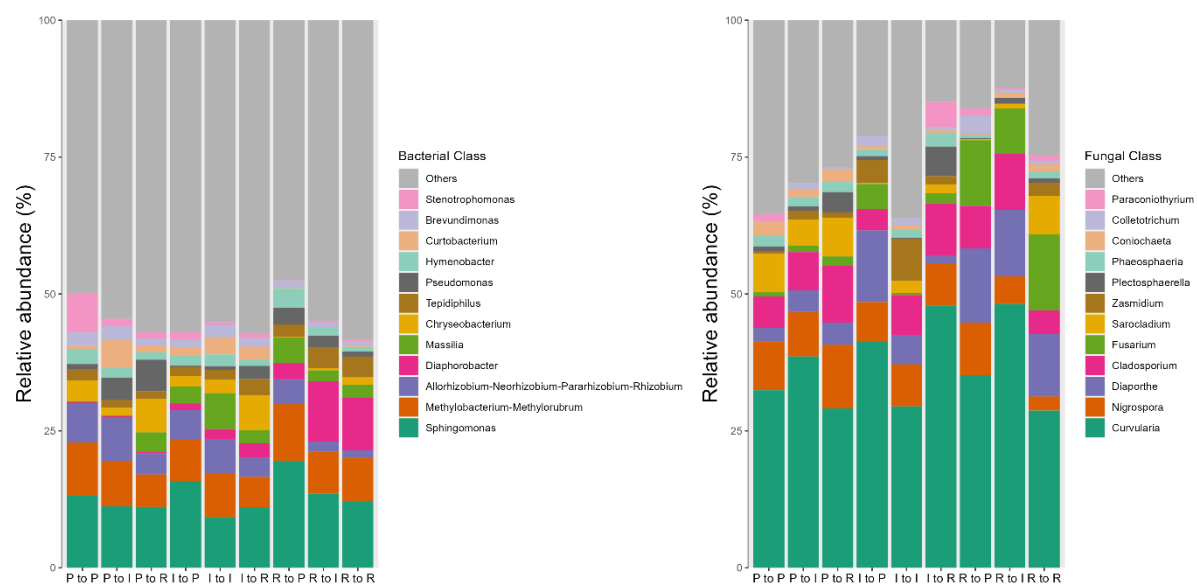
Figure S18: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) class in the leaves of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as 'Maternal treatment' to 'Seedling treatment'.
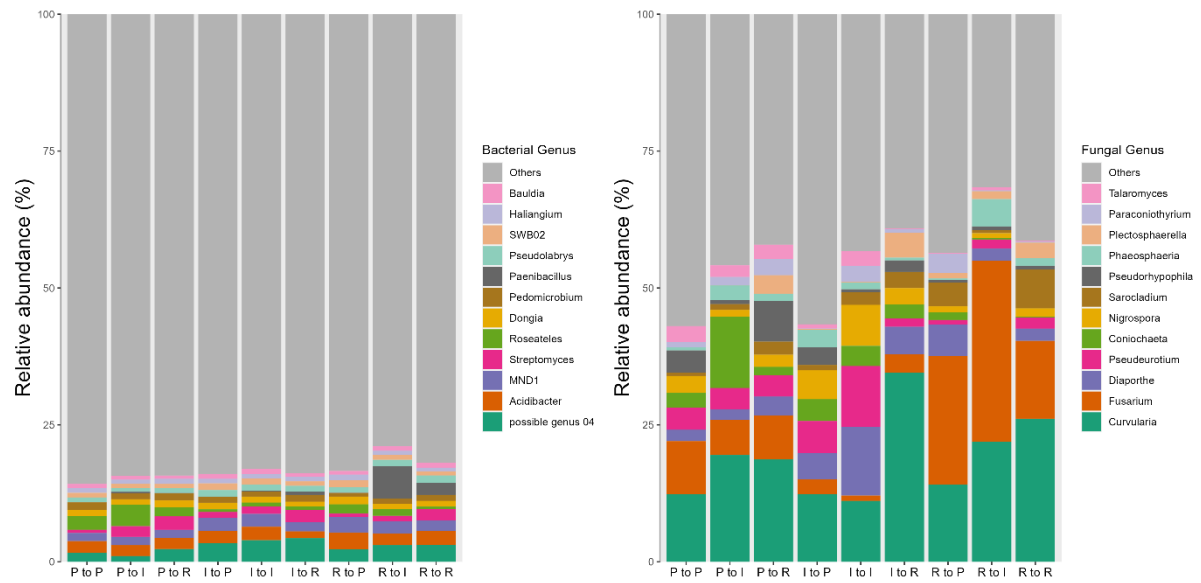
Figure S19: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the roots of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as 'Maternal treatment' to 'Seedling treatment'.
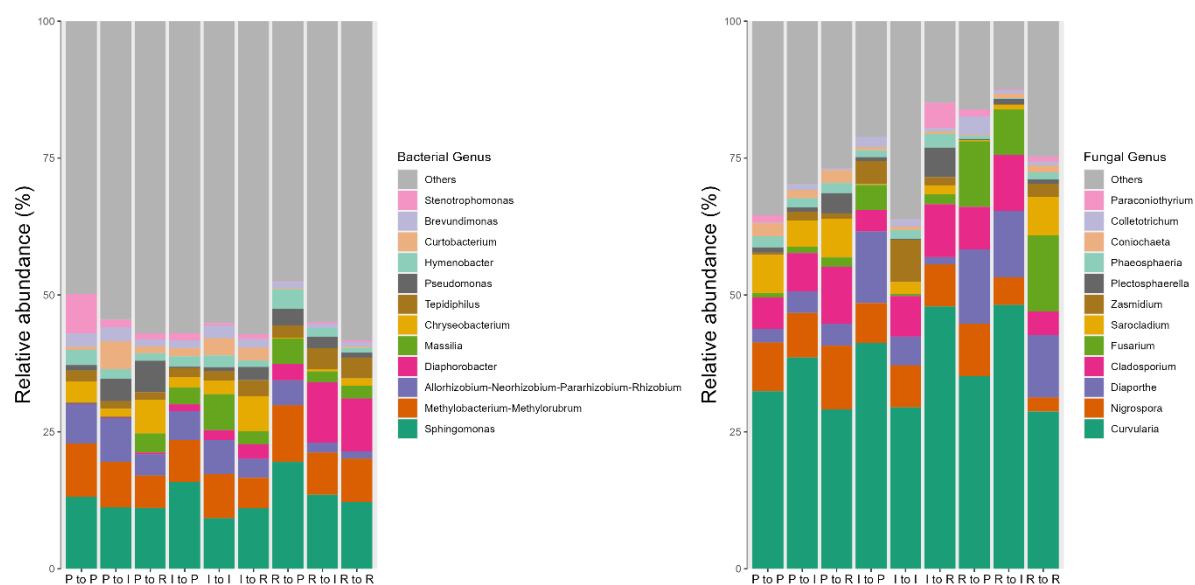
Figure S20: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the leaves of seedlings. P – Poor, I – Intermediate and R – Rich. Treatments are named as 'Maternal treatment' to 'Seedling treatment'.
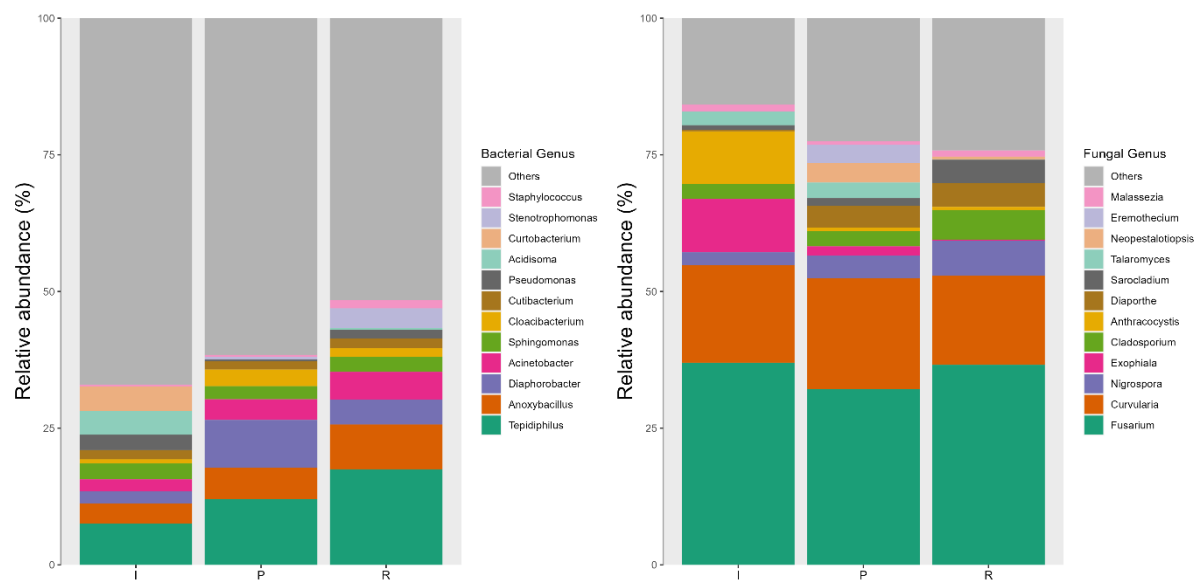
Figure S21: Relative abundance of the dominant bacterial (left panel) and fungal (right panel) genus in the seeds. P – Poor, I – Intermediate and R – Rich.