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Functional Plant Biology

Supplementary Material

Seed bacterial microbiota in post-submergence tolerant and sensitive barley genotypes

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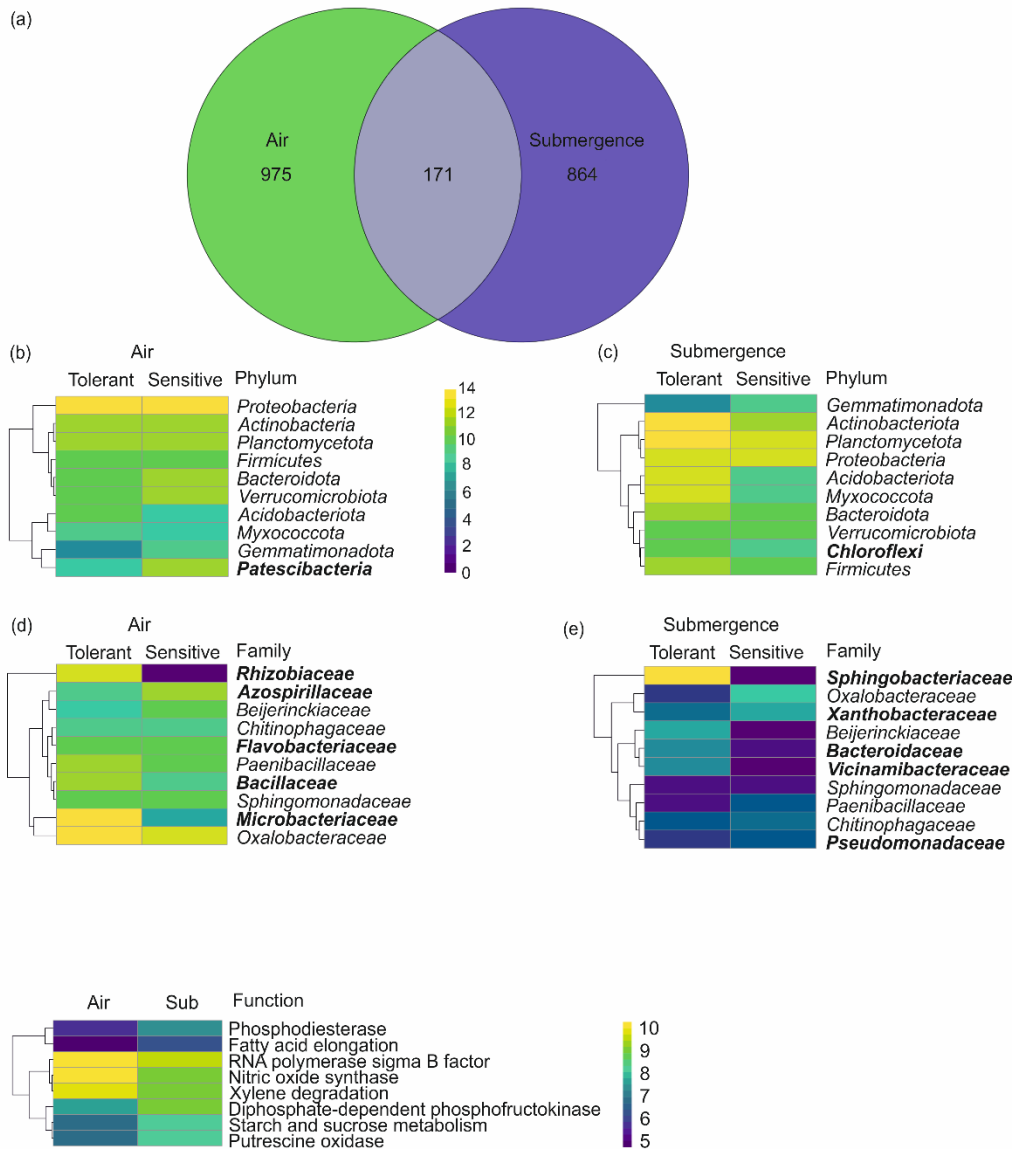
Supplementary Table S1 – Permanova tables. * $p < 0.05$; . $p < 0.1$

Bray-curtis	Df	Sums of squares	Mean squares	F. model	R ²	Pr(>F)
Phenotype	1	0.2699	0.269869	1.61368	0.05222	0.04639 *
Treatment	1	0.1303	0.130287	0.77905	0.02521	0.76405
P X T	1	0.0849	0.084941	0.50790	0.01644	0.99440
Residuals	28	4.6827	0.167238		0.90613	
Total	31	5.1678			1.00000	

Weighted Unifrac	Df	Sums of squares	Mean squares	F. model	R ²	Pr(>F)
Phenotype	1	0.2797	0.27969	1.44076	0.04673	0.06879 .
Treatment	1	0.1383	0.13827	0.71228	0.02310	0.86643
P X T	1	0.1317	0.13170	0.67844	0.02200	0.91542
Residuals	28	5.4356	0.19413		0.90816	
Total	31	5.9853			1.00000	

Jaccard	Df	Sums of squares	Mean squares	F. model	R ²	Pr(>F)
Phenotype	1	0.5649	0.56487	1.28554	0.04153	0.05059 .
Treatment	1	0.3914	0.39136	0.89067	0.02877	0.78124
P X T	1	0.3421	0.34215	0.77867	0.02516	0.98640
Residuals	28	12.3032	0.43940		0.90454	
Total	31	13.6016			1.00000	

Supplementary Figure S1 - a) Venn's diagram performed for the variable treatment. Heatmap of the ten most abundant unique OTUs belonging to air and submergence conditions grouped by Phylum (b, c) and Family (d, e). Unique ASVs for air and submergence are in bold.



Supplementary Figure S2 - Functional analysis performed by MicFunPred tool by using the KEGG ORTHOLOGY (KO) database depending on the treatment variable (FDR, $P < 0.05$).

