Supplementary Materials

Article

The Composition and Assembly of Bacterial Communities across the Rhizosphere and Phyllosphere Compartments of *Phragmites Australis*

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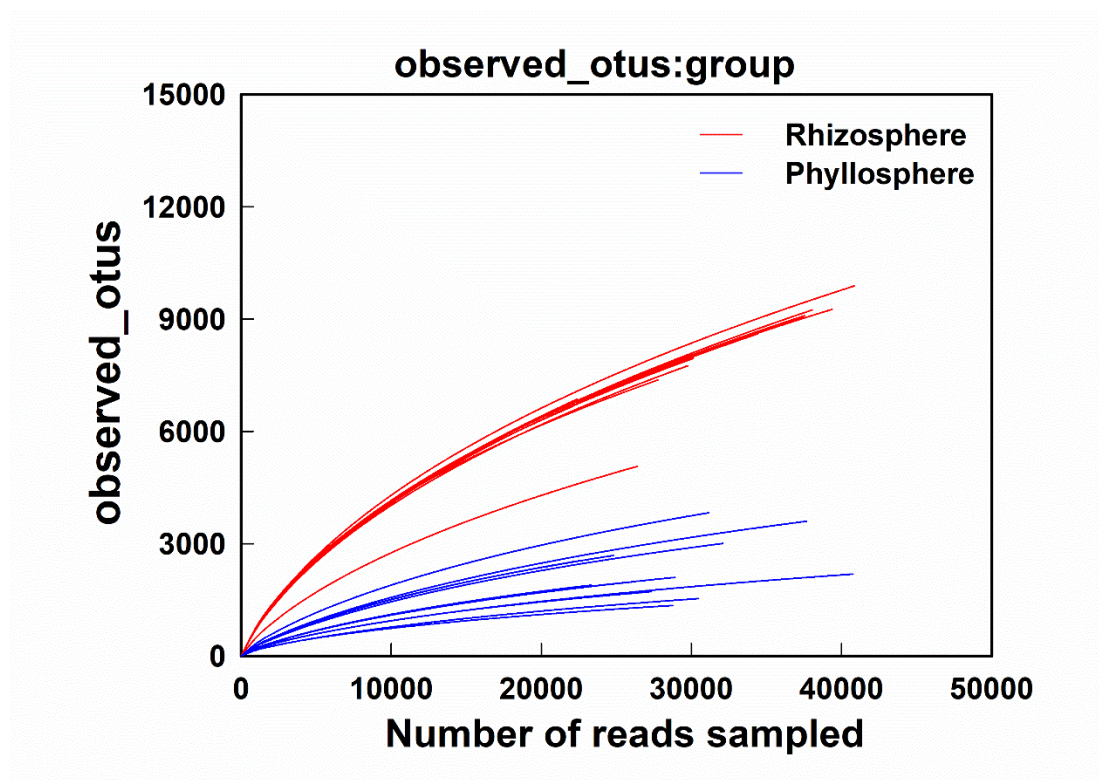* Correspondence: dyzhao@hhu.edu.cn; Tel.: +86-2583787891

Figure S1. Rarefaction curves of observed OTUs in rhizosphere and phyllosphere compartments of *Phragmitas australis*. Curves were determined by average numbers of OTU at the gradient of per 1000

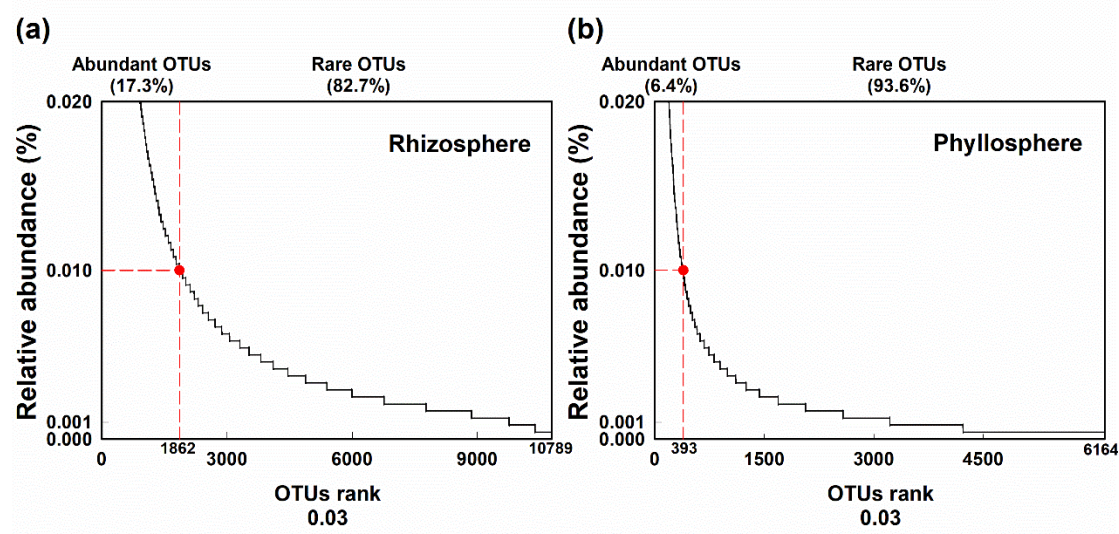reads. The operational taxonomic unit (OTUs) were defined at 3% dissimilarity.

Figure S2. Rank abundance curve for the obtained OTUs. (**a**) Abundant OTUs and rare OTUs in rhizosphere; (**b**) Abundant OTUs and rare OTUs in phyllosphere. The OTUs were defined at 3% dissimilarity.
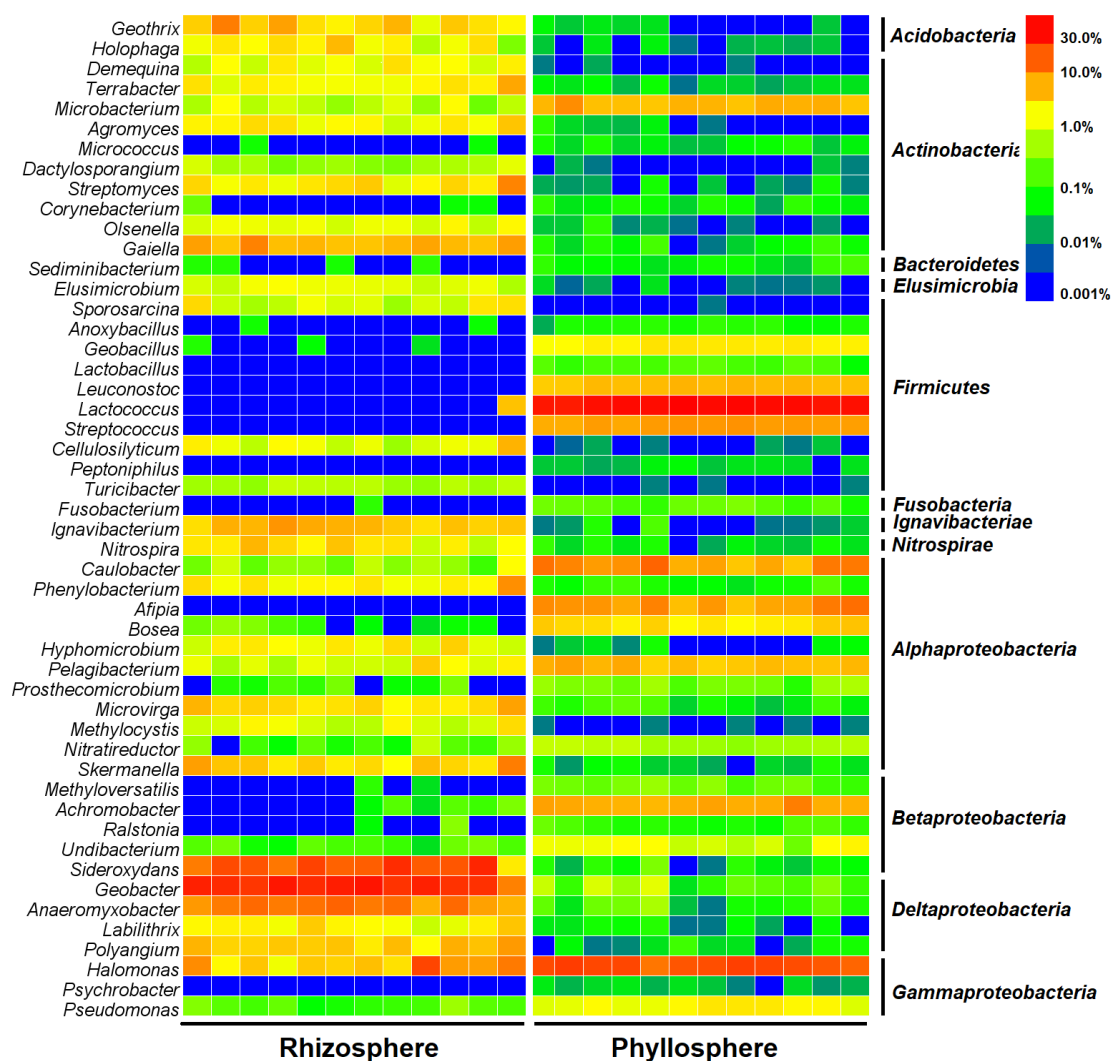
Figure S3. Heatmap show the top 50 most different and abundant genera in different epiphytic compartments. The color bar on the right shows the values of the relative abundance (%) for each genus.

Table S1. List of the physicochemical properties of bulk sediments in this study (n = 5). T, temperature; TN, total nitrogen; NO_3^--N , nitrate nitrogen; NO_2^--N, nitrite nitrogen; TP, total phosphorus.

	T(°C)	pH	TN (g/kg)	NO_3^--N (mg/kg)	NO_2^--N (mg/kg)	TP (g/kg)	Sediment Type
Bulk soil	32	5.67 ± 0.23	0.43 ± 0.21	0.54 ± 0.08	0.18 ± 0.05	0.17 ± 0.04	Silty loam

Table S2. Relative abundance of dominant bacterial phyla/subphyla (relative abundance >1.0 %) in different epiphytic compartments (mean ± SE). Significant differences among different groups (n = 12 for each group) was rendered in Figure 3 according to two-tailed independent-sample *t*-test. Phyla/subphyla with relative abundance < 1.0% were defined as Minor. RAT, rhizosphere abundant taxa; PAT, phyllosphere abundant taxa; RRT, rhizosphere rare taxa; PRT, phyllosphere rare taxa.

Taxon	All		Abundant		Rare	
	Rhizosphere	Phyllosphere	RAT	PAT	RRT	PRT
Acidobacteria	3.24 ± 0.84	0.30 ± 0.20	4.27 ± 0.29	0.00 ± 0.00	5.00 ± 0.59	2.57 ± 1.03
Actinobacteria	12.14 ±2.70	6.65 ± 1.66	13.04 ± 1.46	14.23 ± 0.53	10.32 ± 1.91	14.45 ± 1.92
Bacteroidetes	5.33 ± 1.87	1.50 ± 0.79	6.93 ± 0.68	4.23 ± 0.98	6.67 ± 1.68	7.36 ± 1.42
Chloroflexi	1.11 ± 0.26	0.09 ± 0.07	1.12 ± 0.13	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Firmicutes	13.75 ± 14.21	41.33 ± 7.22	9.07 ± 1.76	27.65 ± 1.72	10.32 ± 4.81	17.57 ± 5.89
Alphaproteobacteria	5.70 ± 1.12	22.64 ± 4.90	6.16 ± 0.22	25.30 ± 1.34	8.41 ± 0.66	15.40 ± 2.05
Betaproteobacteria	11.21 ± 4.48	7.34 ± 1.13	9.36 ± 1.12	10.98 ± 0.88	6.91 ± 1.08	8.95 ± 1.13
Deltaproteobacteria	12.55 ± 3.25	1.83 ± 0.95	14.33 ± 1.08	2.99 ± 0.94	10.16 ± 1.40	7.39 ± 2.17
Gammaproteobacteria	3.33 ± 1.24	14.39 ± 3.49	2.85 ± 0.32	9.26 ± 0.78	2.85 ± 0.72	7.58 ± 1.92
Verrucomicrobia	3.27 ± 1.13	0.25 ± 0.18	0.00 ± 0.00	0.00 ± 0.00	3.62 ± 0.75	1.83 ± 0.84
Bacteria_unclassified	23.16 ± 4.60	1.99 ± 1.08	23.64 ± 0.51	2.08 ± 0.43	27.84 ± 2.28	12.85 ± 3.74
Minor	5.21 ± 1.20	1.67 ± 0.97	9.23 ± 0.25	3.27 ± 0.39	7.91 ± 0.86	4.04 ± 1.14

Table S3: Unweighted UniFrac dissimilarity of bacterial communities among different groups. *P* < 0.001 indicates that the bacterial communities were significantly different among different groups as detected by analysis of ANOSIM and PERMANOVA using the unweighted UniFrac distance.

Distance	Groups		ANOSIM		PERMANOVA		
	group1	group2	R	*P*	F.Model	R²	*P*
unweighted UniFrac	Rhizosphere	Phyllosphere	0.9746	0.001	14.907	0.4039	0.001
	RAT	PAT	1	0.001	293.02	0.93016	0.001
	RRT	RRT	0.9437	0.001	10.701	0.32723	0.001