

Supplementary material

Composition and co-occurrence network of the rhizosphere bacterial community of two emergent macrophytes and implications for phytoremediation

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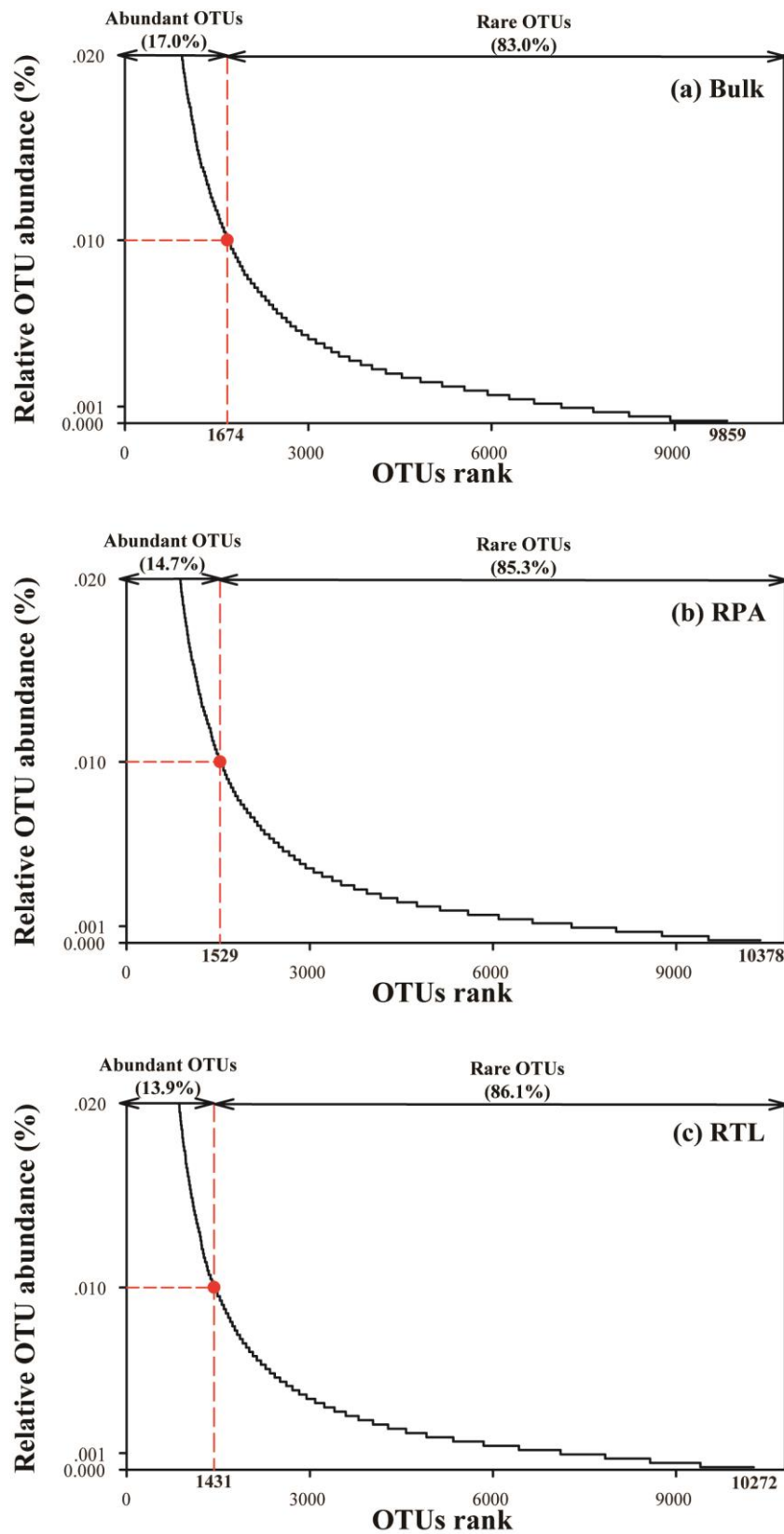


Fig. S1. Rank abundance curve for operating taxonomic units (OTUs) in different groups. The OTUs were defined at the 97% similarity level. (a) Bulk, bulk soil; (b) RPA, rhizosphere of *P. australis*; (c) RTL, rhizosphere of *T. lutarioriparia*.

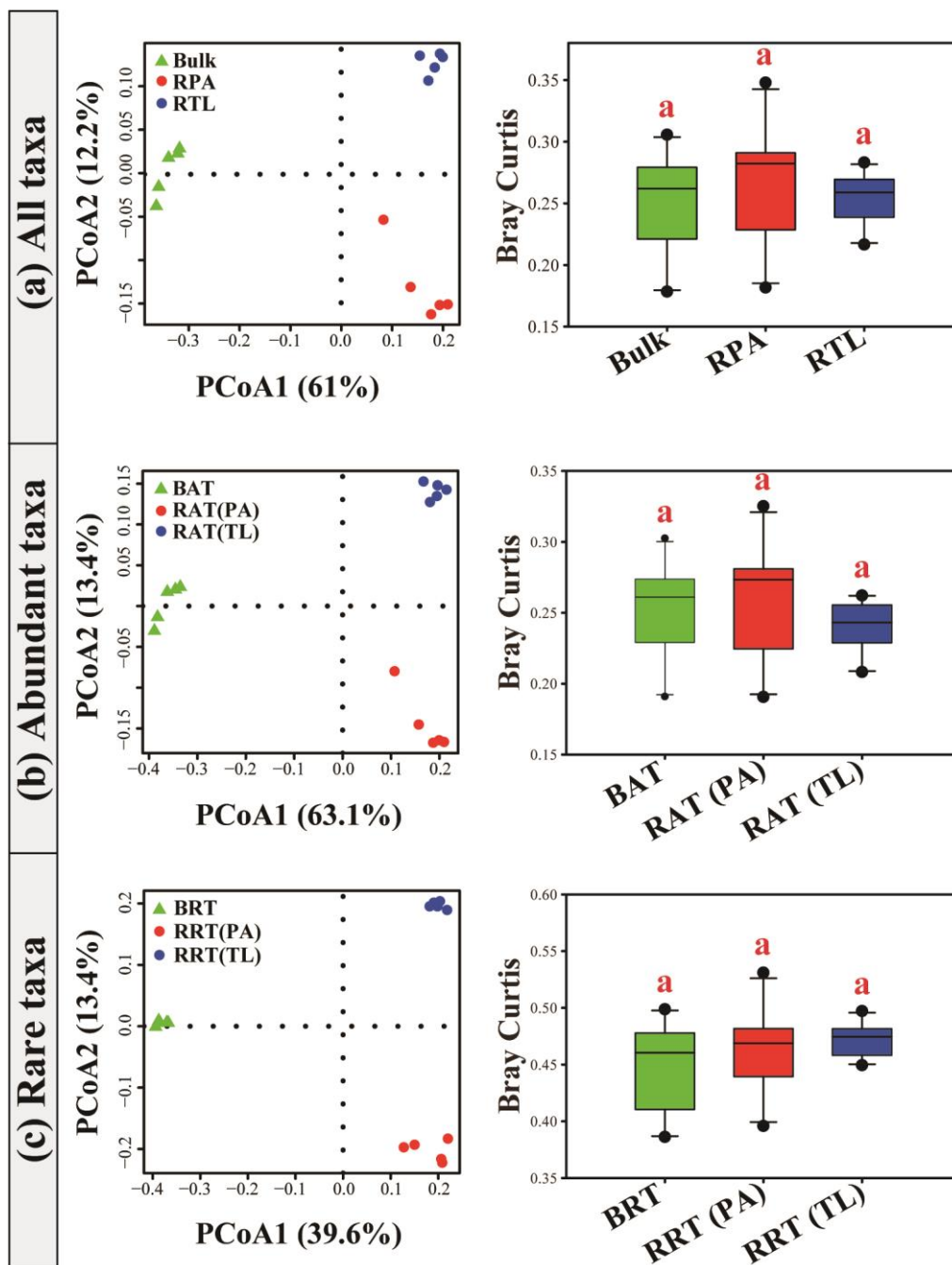


Fig. S2. Comparisons of beta-diversity among different groups. Left, principal coordinate analysis (PCoA) of bacterial communities based on Bray–Curtis distance. Right, box plots showing the dissimilarity of bacterial communities across different samples based on Bray–Curtis distance. Different lowercase letters in bold above boxes represent significant differences in different groups (one-way ANOVA test). (a) All taxa, whole bacterial taxa; (b) Abundant taxa, abundant bacterial taxa; (c) Rare taxa, rare bacterial taxa. BAT, bulk abundant taxa; RAT (PA), rhizosphere abundant taxa of *P. australis*; RAT (TL), rhizosphere abundant taxa of *T. lutariioriparia*; BRT, bulk rare taxa; RRT (PA), rhizosphere rare taxa of *P. australis*; RRT (TL), rhizosphere rare taxa of *T. lutariioriparia*.

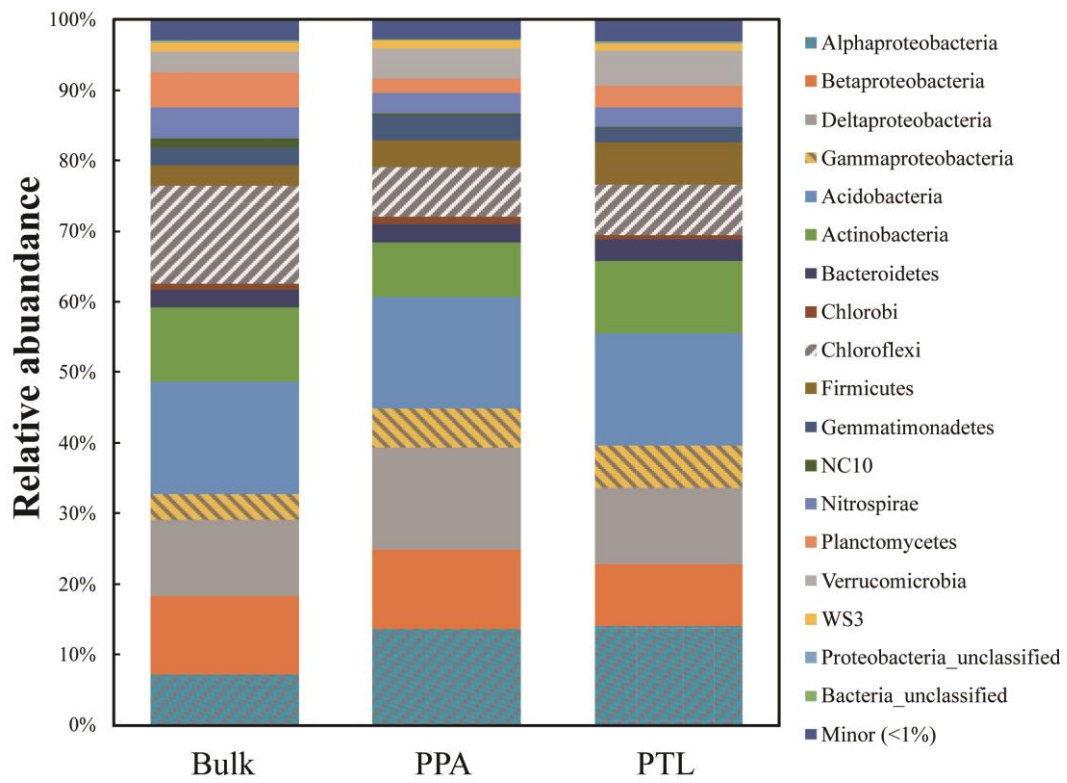


Fig. S3. Relative average abundance of dominant bacterial taxa at the level of phylum or subphylum in different groups. Bulk, bulk soil; RPA, rhizosphere of *P. australis*; RTL, rhizosphere of *T. lutarioriparia*.

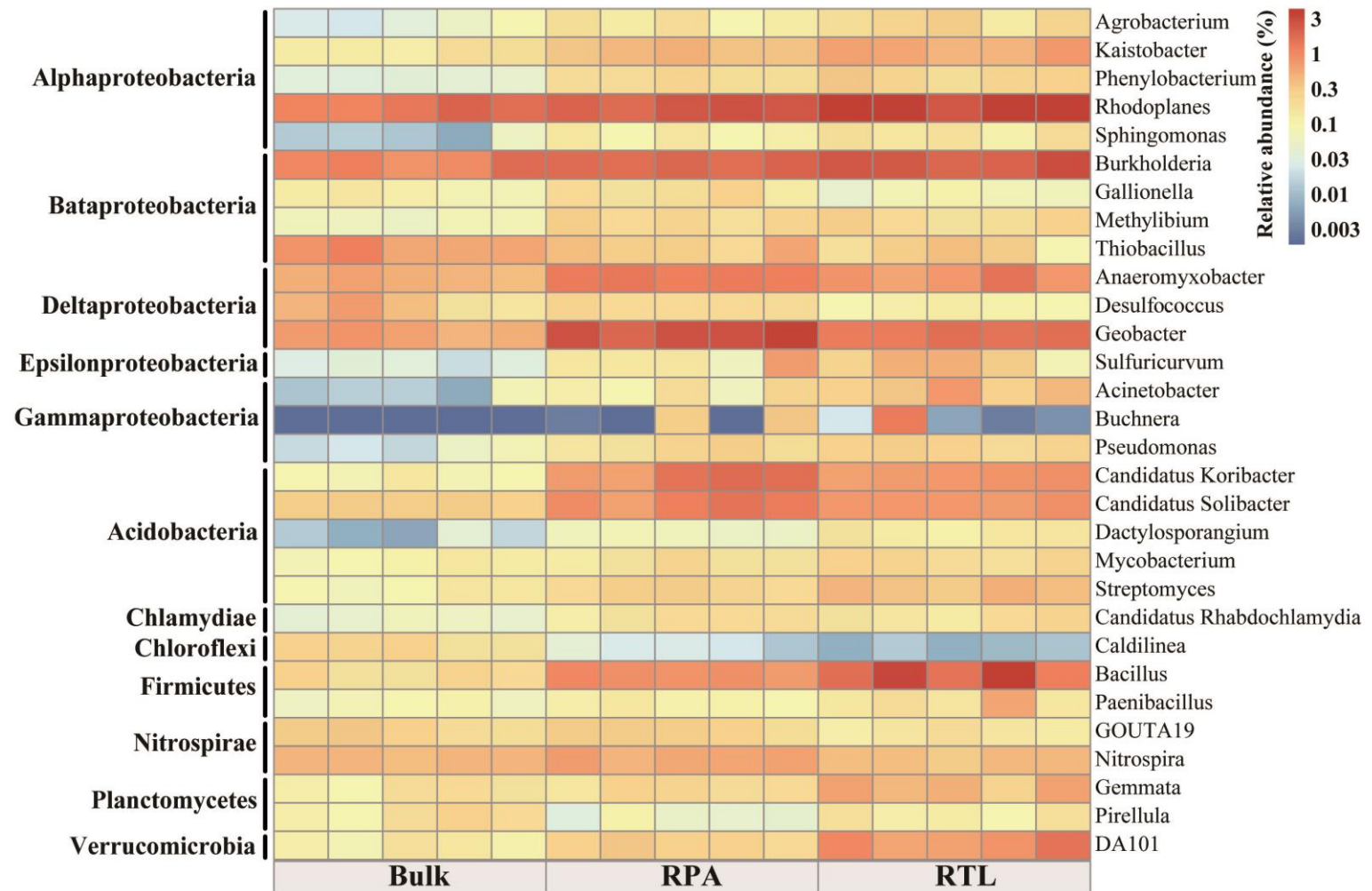


Fig. S4. Heatmap illustrating the distribution of bacterial community at the level of genus in different groups. The right column represents the genus; the left column represents the phylum or subphylum. Bulk, bulk soil; RPA, rhizosphere of *P. australis*; RTL, rhizosphere of *T. lutarioriparia*.

Table S1. The results of analysis of similarities (ANOSIM) and permutational multivariate analysis of variance (PERMANOVA) of pair-wise community comparisons between soil samples based on Bray–Curtis distance matrices

P values < 0.05 in bold. *, *P* < 0.05; **, *P* < 0.01; Bulk, bulk soil; RPA, rhizosphere of *P. australis*; RTL, rhizosphere of *T. lutarioriparia*

Groups	ANOSIM		PERMANOVA	
	<i>R</i>	<i>P</i>	<i>R</i> ²	<i>Pr</i> (> <i>F</i>)
Bulk v. RPA	1	0.017*	0.70644	0.006**
Bulk v. RTL	1	0.007**	0.73368	0.011*
RPA v. RTL	0.956	0.008**	0.37782	0.006**

Table S2. Module hubs and connectors in the species-species co-occurrence networks

p_, c_, o_, f_ and g_ represent phylum, class, order, family and genus respectively

Region	Hubs	Number of nodes	OTU ID	Module	Mean abundance (%)	Phylum	Lowest taxonomic rank
Bulk	Module Hubs	1	OTU141717	Bulk 1	0.05	Betaproteobacteria	f__Rhodocyclaceae
		2	OTU51100	Bulk 2	0.29	Betaproteobacteria	c__Betaproteobacteria
		3	OTU83720	Bulk 3	0.08	Chloroflexi	g__Caldilinea
		4	OTU81121	Bulk 4	0.11	Gemmatimonadetes	c__Gemm-1
	Connectors	5	OTU94274	Bulk 3	0.05	Chloroflexi	o__SJA-15
		6	OTU24647	Bulk 5	0.10	Chloroflexi	o__GCA004
		7	OTU133227	Bulk 5	0.08	Chloroflexi	o__H39
		8	OTU80973	Bulk 6	0.12	Alphaproteobacteria	g__Rhodoplanes
RPA	Module Hubs	9	OTU2414	RPA 1	0.15	Firmicutes	f__Peptostreptococcaceae
		10	OTU33971	RPA 1	0.09	Deltaproteobacteria	g__Desulfobulbus
		11	OTU57412	RPA 2	0.19	Actinobacteria	g__Streptomyces
		12	OTU76368	RPA 2	0.29	Acidobacteria	o__Sva0725
		13	OTU93080	RPA 3	0.10	Deltaproteobacteria	f__JTB36
	Connectors	14	OTU30988	RPA 1	0.13	Betaproteobacteria	f__Rhodocyclaceae
		15	OTU44040	RPA 1	0.09	Chloroflexi	f__A4b
		16	OTU77459	RPA 1	0.26	Alphaproteobacteria	f__Rhodospirillaceae
		17	OTU60944	RPA 3	0.10	Betaproteobacteria	o__IS-44
		18	OTU91107	RPA 3	0.20	Acidobacteria	g__Candidatus Solibacter
		19	OTU99098	RPA 3	0.06	Alphaproteobacteria	f__Acetobacteraceae
		20	OTU118942	RPA 4	0.07	Deltaproteobacteria	o__Myxococcales
		21	OTU17829	RPA 6	0.10	Deltaproteobacteria	o__MBNT15
		22	OTU66336	RPA 6	0.43	Gemmatimonadetes	c__Gemm-1
		23	OTU99327	RPA 6	0.24	Betaproteobacteria	c__Betaproteobacteria
RTL	Module Hubs	24	OTU126352	RTL 2	0.06	Gammaproteobacteria	f__Xanthomonadaceae
	Connectors	25	OTU117406	RTL 1	0.12	Actinobacteria	o__Solirubrobacterales