Supplemental Material

Title: Cadmium Exposure-*Sedum alfredii* Planting Interactions Shape the Bacterial Community in the Hyperaccumulator Plant Rhizosphere

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Summary of the numbers in supplemental material

- The number of pages: 7
- The number of figures: 0
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Table S1 Geochemical properties of the soil used in this study collected from a paddy field located in Shaoxing, Zhejiang province.

Parameter	**Value**
pH	6.58
TOC [g kg^{-1}]	11.10
CEC [cmol kg^{-1}]	8.87
N [g kg^{-1}]	1.35
Cd [mg kg^{-1}]	0.47
Zn [mg kg^{-1}]	91.00
Pb [mg kg^{-1}]	289.11
Cu [mg kg^{-1}]	28.67
Fe [mg g^{-1}]	40.55

Table S2 Three-way analysis of variance (ANOVA) for alpha-diversity metrics (per 16,700 sequences) of bacterial communities across different compartments of two *S. alfredii* ecotypes planted in different Cd-contaminated soils.

Factor	Observed species		Simpson	
	F	*P*	F	*P*
Compartment	19.79	**< 0.001**	81.602	**< 0.001**
Cd	31.483	**< 0.001**	26.602	**< 0.001**
Ecotype	0.348	0.56	36.029	**< 0.001**
Cd : Ecotype	2.396	0.11	14.317	**< 0.001**
Compartment : Ecotype	0.005	0.946	40.385	**< 0.001**
Compartment : Cd	1.116	0.342	10.114	**< 0.001**
Compartment : Cd : Ecotype	1.137	0.335	12.081	**< 0.001**

Bold values represent significant influence of compartment, Cd, ecotype, or their interactions on alpha-diversity metrics ($P < 0.05$).

Table S3 Pearson's correlation coefficients (r) between Cd level and relative abundances of top phylotypes primarily driving bacterial community variation by Cd concentrations at each compartment (n = 9). Only the OTUs with significant coefficients are listed. Contribution: percentages of the contribution of phylotypes to the overall dissimilarity along the Cd gradient calculated by similarity percentage (SIMPER) analysis. Taxonomy of the OTUs was identified in Greengenes database.

OTU ID	**Taxa**	**r**	***P***	**Contribution %**
HE-Rhizosphere				
OTU43111	c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Kaistobacter	0.929	< 0.001	2.19
OTU70716	c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Rhizobium; s_leguminosarum	0.899	0.001	0.36
OTU67423	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.878	0.002	0.69
OTU8159	p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Streptomycetaceae; g_Streptomyces	0.866	0.003	5.90
OTU27802	p_Bacteroidetes; c_Cytophagia; o_Cytophagales; f_Cytophagaceae; g_Dyadobacter	0.859	0.003	0.80
OTU36253	c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Novosphingobium	0.847	0.004	0.30
OTU64559	p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Nocardioidaceae; g_Kribbella	0.840	0.005	0.97
OTU52160	p_TM7; c_TM7-1; o_Unclassified	0.782	0.013	0.57
OTU27835	p_Bacteroidetes; c_[Saprospirae]; o_[Saprospirales]; f_Chitinophagaceae; g_Unclassified	0.769	0.015	0.76
OTU26587	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.759	0.018	0.85
OTU18887	c_Alphaproteobacteria; o_Caulobacterales; f_Caulobacteraceae; g_Asticcacaulis; s_biprosthecium	0.722	0.028	0.35
OTU5499	p_Acidobacteria; c_iii1-8; o_32-20; f_Unclassified	-0.877	0.002	0.26
OTU16416	c_Gammaproteobacteria; o_Xanthomonadales; f_Xanthomonadaceae; g_Lysobacter	-0.796	0.010	0.31
NHE-Rhizosphere				
OTU67423	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.981	< 0.001	1.02

OTU45407	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.956	< 0.001	0.51
OTU22606	c_Alphaproteobacteria; o_Caulobacterales; f_Caulobacteraceae; g_Unclassified	0.948	< 0.001	0.37
OTU26587	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.936	< 0.001	1.97
OTU5860	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.933	< 0.001	0.65
OTU44886	p_Gemmatimonadetes; c_Gemm-1; o_Unclassified	0.917	0.001	0.39
OTU51638	c_Gammaproteobacteria; o_Xanthomonadales; f_Xanthomonadaceae; g_Lysobacter; s_brunescens	0.764	0.016	0.56
OTU67051	c_Betaproteobacteria; o_Ellin6067; f_Unclassified	0.713	0.031	0.38
OTU13447	p_TM7; c_TM7-1; o_Unclassified	-0.828	0.006	0.34
HE-Bulk				
OTU22606	c_Alphaproteobacteria; o_Caulobacterales; f_Caulobacteraceae; g_Unclassified	0.980	< 0.001	0.44
OTU44886	p_Gemmatimonadetes; c_Gemm-1; o_Unclassified	0.943	< 0.001	0.37
OTU67423	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.925	< 0.001	0.91
OTU26587	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.899	0.001	1.47
OTU58630	c_Betaproteobacteria; o_MND1; f_Unclassified	0.888	0.001	0.45
OTU29538	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.895	0.001	0.57
OTU5860	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.849	0.004	0.58
OTU12669	c_Alphaproteobacteria; o_Rhizobiales; f_Hyphomicrobiaceae; g_Rhodoplanes	0.765	0.016	0.34
OTU32799	c_Deltaproteobacteria; o_Myxococcales; f_Haliangiaceae; g_Unclassified	0.763	0.017	0.41
OTU50328	p_Acidobacteria; c_Acidobacteria-6; o_iii1-15; f_Unclassified	-0.851	0.004	0.28
NHE-Bulk				
OTU5860	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.980	< 0.001	0.58
OTU45407	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.943	< 0.001	0.53
OTU58630	c_Betaproteobacteria; o_MND1; f_Unclassified	0.925	< 0.001	0.37
OTU67423	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.899	0.001	0.96
OTU22606	c_Alphaproteobacteria; o_Caulobacterales; f_Caulobacteraceae; g_Unclassified	0.888	0.001	0.49
OTU67051	c_Betaproteobacteria; o_Ellin6067; f_Unclassified	0.895	0.001	0.44
OTU44886	p_Gemmatimonadetes; c_Gemm-1; o_Unclassified	0.849	0.004	0.35

OTU26587	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Ellin5301; g_Unclassified	0.765	0.016	1.65
OTU19426	p_Acidobacteria; c_Acidobacteria-6; o_iii1-15; f_Unclassified	0.763	0.017	0.37
OTU28276	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Ellin5290; f_Unclassified	0.672	0.047	0.37
OTU6487	c_Alphaproteobacteria; o_Rickettsiales; f_mitochondria; g_Unclassified	0.669	0.049	0.39
OTU37719	c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Kaistobacter	-0.756	0.018	0.41
Unplanted soil				
OTU67423	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.918	< 0.001	1.12
OTU5860	p_Gemmatimonadetes; c_Gemmatimonadetes; o_Gemmatimonadales; f_Unclassified	0.949	< 0.001	0.41
OTU22606	c_Alphaproteobacteria; o_Caulobacterales; f_Caulobacteraceae; g_Unclassified	0.941	< 0.001	0.34
OTU51638	c_Gammaproteobacteria; o_Xanthomonadales; f_Xanthomonadaceae; g_Lysobacter; s_brunescens	0.906	0.001	1.11
OTU70479	p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Intrasporangiaceae	0.858	0.003	1.86
OTU51141	p_Actinobacteria; c_Thermoleophilia; o_Solirubrobacterales; f_Unclassified	0.859	0.003	0.43
OTU44886	p_Gemmatimonadetes; c_Gemm-1; o_Unclassified	0.864	0.003	0.39

Table S4 Closest matched type strains of the representative phylotypes associated with the Cd level based on 16S rRNA gene in EzTaxon database.

OTU ID	Length (bp)	Closest match	Similarity (%)	Accession	Taxonomy
Positively correlated group					
OTU8159	445	*Streptomyces lucensis* NBRC 13056^{T}	**99.55**	AB184280	Actinobacteria;Actinobacteria;Streptomycetales;Streptomycetaceae;Streptomyces
OTU43111	440	*Sphingomonas lutea* JS5^{T}	**99.32**	JF922305	Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
OTU26587	457	*Gemmatimonas phototrophica* AP64^{T}	92.78	AUXF01000006	Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas
OTU67423	458	*Gemmatirosa kalamazoonesis* KBS708^{T}	91.68	CP007128	Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa
OTU44886	454	*Gemmatirosa kalamazoonesis* KBS708^{T}	86.78	CP007128	Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa
OTU64559	445	*Kribbella ginsengisoli* Gsoil 001^{T}	**99.55**	AB245391	Actinobacteria;Actinobacteria;Propionibacteriales;Nocardioidaceae;Kribbella
OTU27802	460	*Dyadobacter soli* MJ20^{T}	**99.35**	GQ241324	Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Dyadobacter
OTU27835	460	*Niastella vici* DJ57^{T}	**98.70**	KT388748	Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;Niastella
OTU70716	440	*Rhizobium acidisoli* FH13^{T}	**99.55**	KJ921033	Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobium
OTU36253	440	*Novosphingobium subterraneum* DSM 12447^{T}	**98.64**	JRVC01000007	Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium
OTU52160	441	*Candidatus Saccharimonas aalborgensis*	86.62	CP005957	Saccharibacteria_TM7;Saccharimonas;Saccharimonas;Saccharimonas;Saccharimonas
Negatively correlated group					
OTU50328	464	*Vicinamibacter silvestris* Ac_5_C6^{T}	92.24	KP761690	Acidobacteria;Vicinamibacter;Vicinamibacter;Vicinamibacter;Vicinamibacter
OTU5499	466	*Cystobacter badius* DSM 14723^{T}	84.91	DQ768108	Deltaproteobacteria;Myxococcales;Archangiaceae;Cystobacter
OTU16416	465	*Lysobacter terrae* THG-A13^{T}	**99.57**	KF483861	Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter
OTU37719	440	*Sphingomonas jaspsi* DSM 18422^{T}	**98.18**	KK073876	Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas

Bold values represent similarity > 97%.