

Supplementary Materials

An Assessment of the Diversity of Culturable Bacteria Associated with Main Roots of Sugar Beet

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Running Title: Main root-associated bacteria in sugar beet

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Table S1. Characteristics of field soil used in the present study

	pH (H ₂ O)	Humid content (%)	Total nitrogen (%)	NO ₃ -N (mg/100g)	NH ₄ -N (mg/100g)	P ₂ O ₅ (mg/100g)	Phosphate absorption coefficient	K ₂ O (mg/100g)	CaO (mg/100g)	MgO (mg/100g)	CEC (me/100g)
2	6.3	6.2	0.32	0.55	0.34	16.5	1786	39.9	441.8	51.1	31.9

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Table S2. Phylogenetic compositions of bacterial isolate collections derived from main roots of sugar beet

Taxa (%) ^a	Bacterial isolate collections			
	R2A		HM	
	SU ^b	CO ^b	SU	CO
Proteobacteria	77.0	75.2	77.2	72.5
Alphaproteobacteria	48.1	52.2	46.7	64.8 [*]
Rhodospirillales	0.0	0.0	1.1	1.1
Rhodospirillaceae	0.0	0.0	1.1	1.1
<i>Inquilinus</i>	0.0	0.0	1.1	1.1
Sphingomonadales	9.6	0.0	9.8	0.0
Sphingomonadaceae	9.1	11.2	9.8	5.5
<i>Sphingobium</i>	0.5	0.6	2.2	0.0
<i>Sphingopyxis</i>	4.3	4.3	1.1	0.0
<i>Novosphingobium</i>	1.1	1.2	4.3	2.2
<i>Sphingomonas</i>	3.2	5.0	2.2	3.3
Erythrobacteraceae	0.5	0.0	0.0	0.0
unclassified Erythrobacteraceae	0.5	0.0	0.0	0.0
Caulobacterales	3.7	1.2	6.5	3.3
Caulobacteraceae	3.7	1.2	6.5	3.3
<i>Brevundimonas</i>	1.1	0.6	1.1	0.0
<i>Caulobacter</i>	2.7	0.6	4.3	3.3
<i>Asticcacaulis</i>	0.0	0.0	1.1	0.0
Rhizobiales	34.8	39.8	28.3	54.9 ^{**†}
Beijerinckiaceae	0.5	0.6	0.0	0.0
<i>Beijerinckia</i>	0.5	0.6	0.0	0.0
Xanthobacteraceae	2.1	4.3	0.0	0.0
<i>Labrys</i>	2.1	4.3	0.0	0.0
Rhizobiaceae	3.2	1.2	6.5	1.1
<i>Rhizobium</i>	3.2	1.2	6.5	1.1
Bradyrhizobiaceae	9.6	14.9	6.5	15.4
<i>Afipia</i>	0.0	0.6	0.0	0.0
<i>Bradyrhizobium</i>	1.6	1.2	0.0	1.1
<i>Bosea</i>	5.3	5.6	6.5	11.0
unclassified Bradyrhizobiaceae	2.7	7.5	0.0	3.3
Phyllobacteriaceae	9.1	6.2	5.4	7.7
<i>Phyllobacterium</i>	0.0	0.6	0.0	0.0
<i>Aminobacter</i>	0.0	0.6	0.0	1.1
<i>Mesorhizobium</i>	8.0	5.0	4.3	6.6
unclassified Phyllobacteriaceae	1.1	0.0	1.1	0.0
Hyphomicrobiaceae	9.1	12.4	6.5	29.7 ^{**††}
<i>Devosia</i>	9.1	12.4	6.5	29.7 ^{**††}
Methylobacteriaceae	0.5	0.0	1.1	0.0
<i>Methylobacterium</i>	0.5	0.0	1.1	0.0
unclassified Rhizobiales	0.5	0.0	2.2	1.1
unclassified Alphaproteobacteria	0.0	0.0	1.1	0.0

Table S2. Continued

Taxa (%) ^a	Bacterial isolate collections			
	R2A		HM	
	SU ^b	CO ^b	SU	CO
Betaproteobacteria	9.6	6.8	20.7 [†]	7.7 [*]
Burkholderiales	9.6	6.8	20.7 [†]	7.7 [*]
Burkholderiales_incertae_sedis	0.0	0.6	0.0	0.0
<i>Aquabacterium</i>	0.0	0.6	0.0	0.0
Burkholderiaceae	0.0	0.0	1.1	0.0
<i>Burkholderia</i>	0.0	0.0	1.1	0.0
Oxalobacteraceae	0.5	0.6	1.1	0.0
<i>Herminiumonas</i>	0.5	0.6	0.0	0.0
<i>Herbaspirillum</i>	0.0	0.0	1.1	0.0
Comamonadaceae	9.1	5.6	18.5 [†]	7.7 [*]
<i>Polaromonas</i>	5.9	1.9	9.8	3.3
<i>Roseateles</i>	0.0	0.0	0.0	1.1
<i>Variovorax</i>	0.5	3.1	7.6 ^{††}	3.3
<i>Acidovorax</i>	1.1	0.0	0.0	0.0
<i>Pelomonas</i>	0.5	0.0	0.0	0.0
<i>Curvibacter</i>	0.5	0.0	0.0	0.0
unclassified Comamonadaceae	0.5	0.6	1.1	0.0
Gammaproteobacteria	18.2	16.1	5.4 ^{††}	0.0 ^{*††}
Pseudomonadales	0.5	0.6	1.1	0.0
Pseudomonadaceae	0.5	0.6	1.1	0.0
<i>Rhizobacter</i>	0.5	0.6	0.0	0.0
<i>Pseudomonas</i>	0.0	0.0	1.1	0.0
Xanthomonadales	17.6	15.5	4.3 ^{††}	0.0 ^{††}
Xanthomonadaceae	17.6	15.5	4.3 ^{††}	0.0 ^{††}
<i>Rhodanobacte</i>	0.5	0.6	1.1	0.0
<i>Lysobacter</i>	5.9	6.2	3.3	0.0 [†]
<i>Dokdonella</i>	1.6	1.9	0.0	0.0
<i>Pseudoxanthomonas</i>	9.1	6.8	0.0 ^{††}	0.0 ^{††}
<i>Stenotrophomonas</i>	0.5	0.0	0.0	0.0
unclassified Proteobacteria	1.1	0.0	4.3	0.0

Table S2. Continued

Taxa (%) ^a	Bacterial isolate collections			
	R2A		HM	
	SU ^b	CO ^b	SU	CO
Actinobacteria	16.6	15.5	9.8	12.1
Actinobacteria	16.6	15.5	9.8	12.1
Actinomycetales	16.6	15.5	9.8	12.1
Streptomycetaceae	0.5	1.2	2.2	0.0
<i>Streptomyces</i>	0.5	1.2	2.2	0.0
Nocardioidaceae	9.6	5.6	0.0 ^{††}	0.0 [†]
<i>Nocardiooides</i>	4.8	1.2	0.0 [†]	0.0
<i>Aeromicrobium</i>	3.2	3.1	0.0	0.0
<i>Kribbella</i>	0.5	0.0	0.0	0.0
<i>Marmoricola</i>	0.5	0.0	0.0	0.0
unclassified Nocardioidaceae	0.5	1.2	0.0	0.0
Microbacteriaceae	2.1	6.2	4.3	4.4
<i>Pseudoclavibacter</i>	0.0	0.0	0.0	1.1
<i>Leifsonia</i>	0.0	0.6	0.0	1.1
<i>Microbacterium</i>	2.1	3.1	4.3	2.2
<i>Salinibacterium</i>	0.0	0.6	0.0	0.0
<i>Agrococcus</i>	0.0	1.9	0.0	0.0
Nocardiaceae	0.0	0.0	0.0	1.1
<i>Nocardia</i>	0.0	0.0	0.0	1.1
Mycobacteriaceae	4.3	2.5	2.2	6.6
<i>Mycobacterium</i>	4.3	2.5	2.2	6.6
Pseudonocardiaceae	0.0	0.0	1.1	0.0
<i>Amycolatopsis</i>	0.0	0.0	1.1	0.0
Bacteroidetes	4.3	5.6	13.0 ^{††}	15.4 ^{††}
Flavobacteria	0.0	0.6	0.0	1.1
Flavobacteriales	0.0	0.6	0.0	1.1
Flavobacteriaceae	0.0	0.6	0.0	1.1
<i>Flavobacterium</i>	0.0	0.6	0.0	1.1
Sphingobacteria	4.3	5.0	13.0 ^{††}	14.3 [†]
Sphingobacteriales	4.3	5.0	13.0 ^{††}	14.3 [†]
Chitinophagaceae	1.6	1.2	3.3	3.3
<i>Sediminibacterium</i>	0.0	0.6	0.0	0.0
<i>Chitinophaga</i>	0.0	0.0	1.1	1.1
<i>Niabella</i>	0.5	0.0	0.0	1.1
<i>Lacibacter</i>	0.5	0.0	1.1	0.0
<i>Niastella</i>	0.0	0.0	1.1	0.0
unclassified Chitinophagaceae	0.5	0.6	0.0	1.1
Sphingobacteriaceae	1.6	2.5	7.6 [†]	3.3
<i>Sphingobacterium</i>	0.0	0.6	0.0	0.0
<i>Muciluginibacter</i>	0.0	0.0	4.3 ^{††}	1.1
<i>Pedobacter</i>	1.6	1.9	3.3	2.2
Cytophagaceae	1.1	1.2	2.2	7.7 ^{††}
<i>Dyadobacter</i>	1.1	1.2	2.2	7.7 ^{††}

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Table S2. Continued

Taxa (%) ^a	Bacterial isolate collections			
	R2A		HM	
	SU ^b	CO ^b	SU	CO
Firmicutes	0.0	3.7 ^{**}	0.0	0.0
Bacilli	0.0	3.7 ^{**}	0.0	0.0
Bacillales	0.0	3.7 ^{**}	0.0	0.0
Bacillaceae 1	0.0	1.9	0.0	0.0
<i>Bacillus</i>	0.0	1.9	0.0	0.0
Paenibacillaceae	0.0	1.9	0.0	0.0
<i>Paenibacillus</i>	0.0	1.9	0.0	0.0
Verrucomicrobia	2.1	0.0	0.0	0.0
Verrucomicrobiae	2.1	0.0	0.0	0.0
Verrucomicrobiales	2.1	0.0	0.0	0.0
Verrucomicrobiaceae	2.1	0.0	0.0	0.0
<i>Haloferula</i>	1.1	0.0	0.0	0.0
<i>Verrucomicrobium</i>	1.1	0.0	0.0	0.0

^aSequences were classified using the Classifier of Ribosomal Database Project II release 10 with a confidence threshold 80%.

^bSU and CO stand for the surface and core parts of main roots of sugar beet, respectively.

* , ** indicate statistical significance examined by the Library Compare of Ribosomal Database Project II at $p < 0.05$ and $p < 0.01$, respectively, between SU and CO in each medium.

†, †† indicate statistical significance examined by the Library Compare of Ribosomal Database Project II at $p < 0.05$ and $p < 0.01$, respectively, between R2A and HM in each part of main roots.

1 **Figure legends**

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3 Fig. S1. Phylogenetic distribution of OTUs at species level for main root-associated
4 bacteria in sugar beet. OTUs (Operational taxonomic units) were defined at 99%
5 sequence identity by using MOTHUR. *Aquifex pyrophilus* (M83548) was used as an out
6 group for the dendrogram. OTUs were expressed as prefixes derived from phylum
7 identity (Symbols; AP, *Alphaproteobacteria*; BP, *Betaproteobacteria*; GP,
8 *Gammaproteobacteria*; B, *Bacteroidetes*; F, *Firmicutes*; A, *Actinobacteria*; V,
9 *Verrucomicrobia*, with consecutive numbers). The table indicates the relative abundance
10 (%) of isolates belonging to each OTU in each collection and the result of BLAST
11 search using representative sequence. SU and CO stand for the surface and core parts of
12 main roots of sugar beet, respectively. *, ** indicate statistical significance examined by
13 Fisher's exact test at $p<0.05$ and $p<0.01$, respectively, between SU and CO in each
14 medium. †, †† indicate statistical significance examined by Fisher's exact test at $p<0.05$
15 and $p<0.01$, respectively, between R2A and HM in each of SU and CO.

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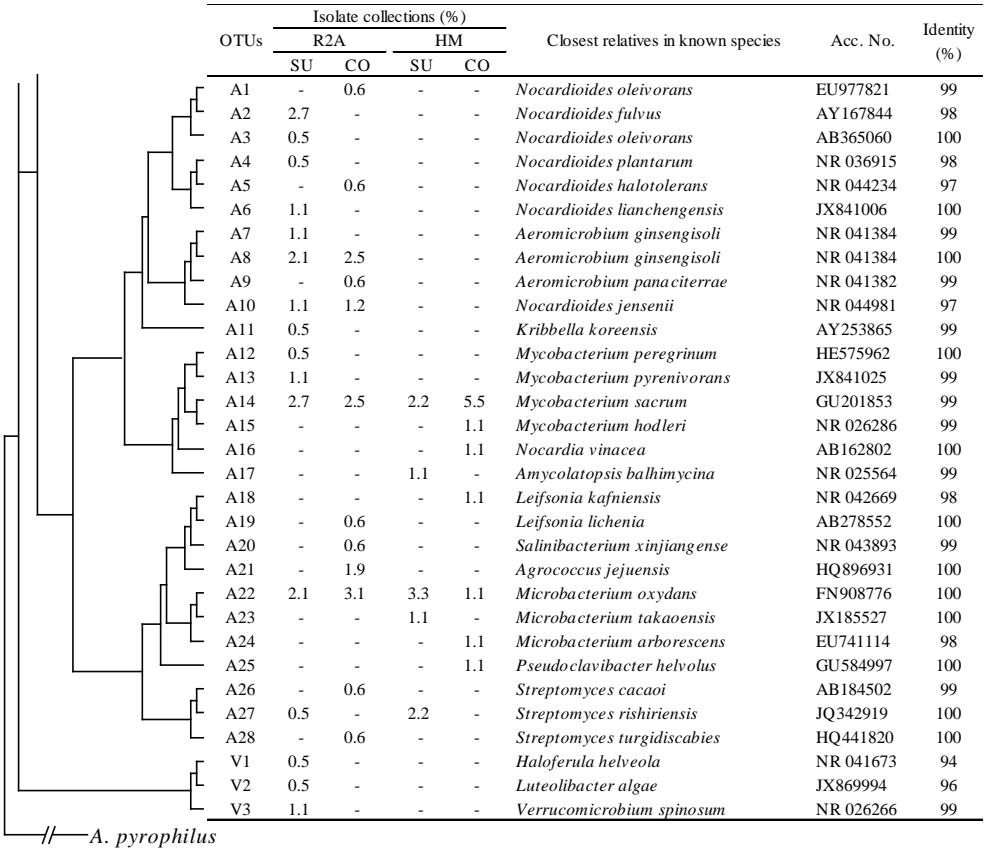
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OTUs	Isolate collections (%)				Closest relatives in known species	Acc. No.	Identity (%)			
	R2A		HM							
	SU	CO	SU	CO						
AP1	-	-	-	1.1	<i>Mesorhizobium loti</i>	FN386773	98			
AP2	-	-	1.1	-	<i>Mesorhizobium ciceri</i>	NR 074211	99			
AP3	3.2	-	-	*	<i>Mesorhizobium loti</i>	FN386773	100			
AP4	1.6	2.5	1.1	-	<i>Mesorhizobium</i> sp.	JX292574	100			
AP5	2.7	2.5	2.2	5.5	<i>Mesorhizobium amorphae</i>	AB741445	100			
AP6	0.5	-	-	-	<i>Mesorhizobium albiziae</i>	NR 043549	98			
AP7	0.5	-	-	-	<i>Mesorhizobium</i> sp.	FJ544261	98			
AP8	-	0.6	-	-	<i>Aminobacter aminovorans</i>	EF473294	95			
AP9	-	-	1.1	-	<i>Aminobacter aminovorans</i>	AM285009	95			
AP10	-	-	-	1.1	<i>Aminobacter aminovorans</i>	EF473294	100			
AP11	-	0.6	-	-	<i>Phyllobacterium myrsinacearum</i>	EU420076	98			
AP12	0.5	-	-	-	<i>Phyllobacterium myrsinacearum</i>	DQ370018	100			
AP13	-	-	-	1.1	<i>Rhizobium radiobacter</i>	KC196495	99			
AP14	0.5	-	-	-	<i>Rhizobium radiobacter</i>	GU826585	99			
AP15	-	0.6	-	-	<i>Rhizobium radiobacter</i>	JX971560	100			
AP16	1.1	0.6	5.4 [†]	-	<i>Rhizobium galegae</i>	Y12360	100			
AP17	0.5	-	-	-	<i>Rhizobium daejeonense</i>	AB681831	99			
AP18	-	-	1.1	-	<i>Rhizobium sullae</i>	FJ785219	100			
AP19	0.5	-	-	-	<i>Rhizobium petrolearium</i>	EU556969	98			
AP20	-	-	1.1	-	<i>Rhizobium giardinii</i>	HQ263115	97			
AP21	0.5	-	-	-	<i>Rhizobium giardinii</i>	HQ263115	99			
AP22	-	-	-	1.1	<i>Devosia insulae</i>	NR 044036	97			
AP23	4.3	3.7	1.1*	7.7	<i>Devosia insulae</i>	NR 044036	99			
AP24	0.5	-	2.2	-	<i>Devosia ginsengisoli</i>	KC676321	100			
AP25	-	-	1.1	-	<i>Devosia insulae</i>	NR 044036	96			
AP26	1.6	3.1	-	2.2	<i>Devosia insulae</i>	NR 044036	99			
AP27	0.5	-	-	-	<i>Devosia insulae</i>	NR 044036	98			
AP28	1.6	5.0	2.2**	19.8 ^{††}	<i>Devosia neptuniae</i>	JX841065	100			
AP29	1.1	-	2.2	-	<i>Devosia limi</i>	NR 042324	99			
AP30	-	0.6	-	-	<i>Devosia subaequiris</i>	NR 042544	98			
AP31	0.5	0.6	-	-	<i>Beijerinckia deryxii</i>	NR 042182	96			
AP32	-	0.6	-	-	<i>Labrys methylaminiphilus</i>	NR 041336	99			
AP33	1.1	3.7	-	-	<i>Labrys methylaminiphilus</i>	NR 041336	100			
AP34	1.1	-	-	-	<i>Labrys methylaminiphilus</i>	NR 041336	98			
AP35	-	0.6	-	1.1	<i>Bradyrhizobium elkanii</i>	KC787046	99			
AP36	-	0.6	-	-	<i>Afipia felis</i>	AY548800	100			
AP37	0.5	-	-	-	<i>Afipia birgiae</i>	NR 025117	99			
AP38	0.5	1.9	-	-	<i>Bradyrhizobium japonicum</i>	AB614498	100			
AP39	1.1	-	-	-	<i>Bradyrhizobium japonicum</i>	JN558795	99			
AP40	-	0.6	-	1.1	<i>Bradyrhizobium japonicum</i>	KC736656	98			
AP41	0.5	-	-	-	<i>Bradyrhizobium elkanii</i>	HQ233241	98			
AP42	1.6	5.6	-	2.2	<i>Rhodopseudomonas rhenobacensis</i>	FN796846	98			
AP43	0.5	0.6	1.1	2.2	<i>Bosea thiooxidans</i>	DQ104985	99			
AP44	4.8	5.0	5.4	8.8	<i>Bosea thiooxidans</i>	JN627995	100			
AP45	0.5	-	1.1	-	<i>Methylobacter adhaesivum</i>	AB698724	100			
AP46	-	-	-	1.1	<i>Caulobacter segnis</i>	NR 074208	99			
AP47	2.7	0.6	4.3	2.2	<i>Caulobacter henricii</i>	NR 025319	99			
AP48	1.1	0.6	1.1	-	<i>Brevundimonas vesicularis</i>	KC494327	100			
AP49	-	-	1.1	-	<i>Asticcacaulis biprosthecum</i>	AJ247193	98			
AP50	-	-	-	1.1	<i>Sphingomonas mali</i>	JN592470	98			
AP51	1.1	0.6	2.2	-	<i>Sphingomonas mali</i>	AB680885	98			
AP52	-	0.6	-	-	<i>Sphingomonas asaccharolytica</i>	AB680883	100			
AP53	2.1	1.9	-	-	<i>Sphingomonas oligophenolica</i>	NR 024685	99			
AP54	-	-	1.1	-	<i>Sphingomonas pituitosa</i>	JF459949	91			
AP55	-	1.9	-	2.2	<i>Sphingomonas azotifigens</i>	JQ579646	98			
AP56	0.5	0.6	2.2	-	<i>Sphingobium aromaticivorans</i>	NR 042479	98			
AP57	-	0.6	-	-	<i>Novosphingobium hassiacum</i>	NR 028962	99			
AP58	0.5	0.6	4.3 [†]	2.2	<i>Novosphingobium subterraneum</i>	JF459977	98			
AP59	0.5	-	-	-	<i>Novosphingobium naphthalenivorans</i>	AB649005	99			
AP60	0.5	-	-	-	<i>Erythrobacter flavus</i>	KC583223	98			
AP61	3.2	4.3	1.1	-	<i>Sphingopyxis panaceterrae</i>	AB245354	99			
AP62	1.1	-	-	-	<i>Sphingopyxis witflariensis</i>	NR 028010	99			
AP63	-	-	1.1	1.1	<i>Inquilinus ginsengisoli</i>	AB245352	100			

1 Fig. S1 K. Okazaki

OTUs	Isolate collections (%)				Closest relatives in known species	Acc. No.	Identity (%)			
	R2A		HM							
	SU	CO	SU	CO						
BP1	-	-	-	1.1	<i>Polaromonas ginsengisoli</i>	AB245355	99			
BP2	5.9	1.9	7.6	2.2	<i>Polaromonas ginsengisoli</i>	AB245355	100			
BP3	-	-	2.2	-	<i>Polaromonas aquatica</i>	NR 042404	99			
BP4	-	-	1.1	-	<i>Curvibacter delicatus</i>	AB680705	97			
BP5	0.5	-	-	-	<i>Curvibacter delicatus</i>	NR 028713	98			
BP6	0.5	0.6	-	-	<i>Albidiferax ferrifreducens</i>	AM265401	98			
BP7	0.5	3.1	7.6 ^{††}	3.3	<i>Variovorax paradoxus</i>	NR 074646	100			
BP8	1.1	-	-	-	<i>Acidovorax radicis</i>	JF915365	100			
BP9	-	-	1.1	-	<i>Rhizobacter fulvus</i>	AB649013	98			
BP10	0.5	0.6	-	-	<i>Rhizobacter fulvus</i>	AB649013	99			
BP11	1.1	-	2.2	-	<i>Rhizobacter fulvus</i>	AB649013	97			
BP12	-	0.6	-	-	<i>Aquabacterium parvum</i>	NR 024874	98			
BP13	-	-	-	1.1	<i>Mitsuaria chitosanitabida</i>	FJ796447	99			
BP14	0.5	-	-	-	<i>Pelomonas soli</i>	EF660749	99			
BP15	-	0.6	-	-	<i>Herminiumonas fonticola</i>	AB512142	99			
BP16	0.5	-	-	-	<i>Herminiumonas saxobsidens</i>	NR 042610	100			
BP17	-	-	1.1	-	<i>Herbaspirillum hiltneri</i>	DQ150563	100			
BP18	-	-	1.1	-	<i>Burkholderia soli</i>	NR 043872	99			
GP1	-	0.6	-	-	<i>Dokdonella fugitiva</i>	NR 042397	97			
GP2	0.5	0.6	-	-	<i>Dokdonella fugitiva</i>	NR 042397	98			
GP3	0.5	0.6	-	-	<i>Dokdonella koreensis</i>	EF589679	95			
GP4	0.5	-	-	-	<i>Dokdonella koreensis</i>	NR 043322	96			
GP5	9.1	6.8	- ^{††}	- ^{††}	<i>Pseudoxanthomonas ginsengisoli</i>	AB245360	100			
GP6	0.5	-	-	-	<i>Stenotrophomonas rhizophila</i>	KC790309	100			
GP7	4.3	-	1.1 ^{**}	-	<i>Lysobacter niastensis</i>	JQ342848	100			
GP8	1.6	6.2	2.2 [*]	- [†]	<i>Lysobacter gumm osus</i>	NR 041005	99			
GP9	-	0.6	1.1	-	<i>Rhodanoba cter ginsenosidimutans</i>	AB682427	98			
GP10	0.5	-	-	-	<i>Rhodanoba cter thiooxydans</i>	AB741464	100			
GP11	-	-	1.1	-	<i>Pseudomonas extremorientalis</i>	NR 025174	100			
B1	-	-	1.1	-	<i>Pedobacter terrae</i>	GU385862	99			
B2	-	-	1.1	-	<i>Pedobacter kribbensis</i>	EF660752	100			
B3	0.5	-	1.1	-	<i>Pedobacter borealis</i>	NR 044381	99			
B4	0.5	-	-	1.1	<i>Pedobacter agri</i>	JX122157	98			
B5	-	0.6	-	1.1	<i>Pedobacter pana citraeae</i>	EF195087	100			
B6	0.5	-	-	-	<i>Pedobacter africanus</i>	NR 028977	99			
B7	-	1.2	-	-	<i>Pedobacter koreensis</i>	NR 043538	99			
B8	-	-	2.2	-	<i>Mucilaginibacter doraji</i>	GU139697	95			
B9	-	-	1.1	-	<i>Mucilaginibacter kameionensis</i>	AB681894	98			
B10	-	-	1.1	-	<i>Mucilaginibacter palidis</i>	NR 042597	97			
B11	-	-	-	1.1	<i>Mucilaginibacter doraji</i>	GU139697	94			
B12	-	0.6	-	-	<i>Sphingobacterium composti</i>	JF731241	93			
B13	-	0.6	-	1.1	<i>Flavobacterium johnsoniae</i>	AM921621	97			
B14	-	-	-	3.3 [†]	<i>Dyadobacter fermentans</i>	NR 074368	98			
B15	1.1	0.6	1.1	2.2	<i>Dyadobacter fermentans</i>	DQ922762	100			
B16	-	0.6	-	2.2	<i>Dyadobacter koreensis</i>	AB681383	97			
B17	-	-	1.1	-	<i>Dyadobacter ginsengisoli</i>	NR 041372	95			
B18	-	-	-	1.1	<i>Niastella populi</i>	EU877262	94			
B19	0.5	-	-	-	<i>Niastella populi</i>	EU877262	93			
B20	-	-	1.1	-	<i>Niastella populi</i>	EU877262	94			
B21	0.5	-	-	1.1	<i>Niabella yanshanensis</i>	FJ457040	98			
B22	-	0.6	-	-	<i>Sediminibacterium salmonicum</i>	NR 044197	93			
B23	-	-	-	1.1	<i>Chitinophaga g insengisegetis</i>	NR 041486	99			
B24	-	-	1.1	-	<i>Chitinophaga g insengisegetis</i>	NR 041486	99			
B25	-	-	1.1	-	<i>Chitinophaga n iabensis</i>	AB682428	86			
B26	0.5	-	-	-	<i>Chitinophaga n iabensis</i>	NR 044559	87			
B27	-	0.6	-	-	<i>Chitinophaga filiformis</i>	JQ659521	88			
F1	-	0.6	-	-	<i>Paenibacillus cineris</i>	EU839659	99			
F2	-	0.6	-	-	<i>Paenibacillus amylolyticus</i>	AM237394	100			
F3	-	0.6	-	-	<i>Paenibacillus alginolyticus</i>	JX464208	98			
F4	-	0.6	-	-	<i>Bacillus ginsengilumi</i>	HQ219843	100			
F5	-	1.2	-	-	<i>Bacillus arbutinivorans</i>	KC315762	100			

1 Fig. S1 Continued K. Okazaki



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