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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)
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

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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>Herminiimonas</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
Nocardioideae	9.6	5.6	0.0 ^{††}	0.0 [†]
<i>Nocardioides</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 Nocardioideae	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>Mucilaginibacter</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. Phylogenic 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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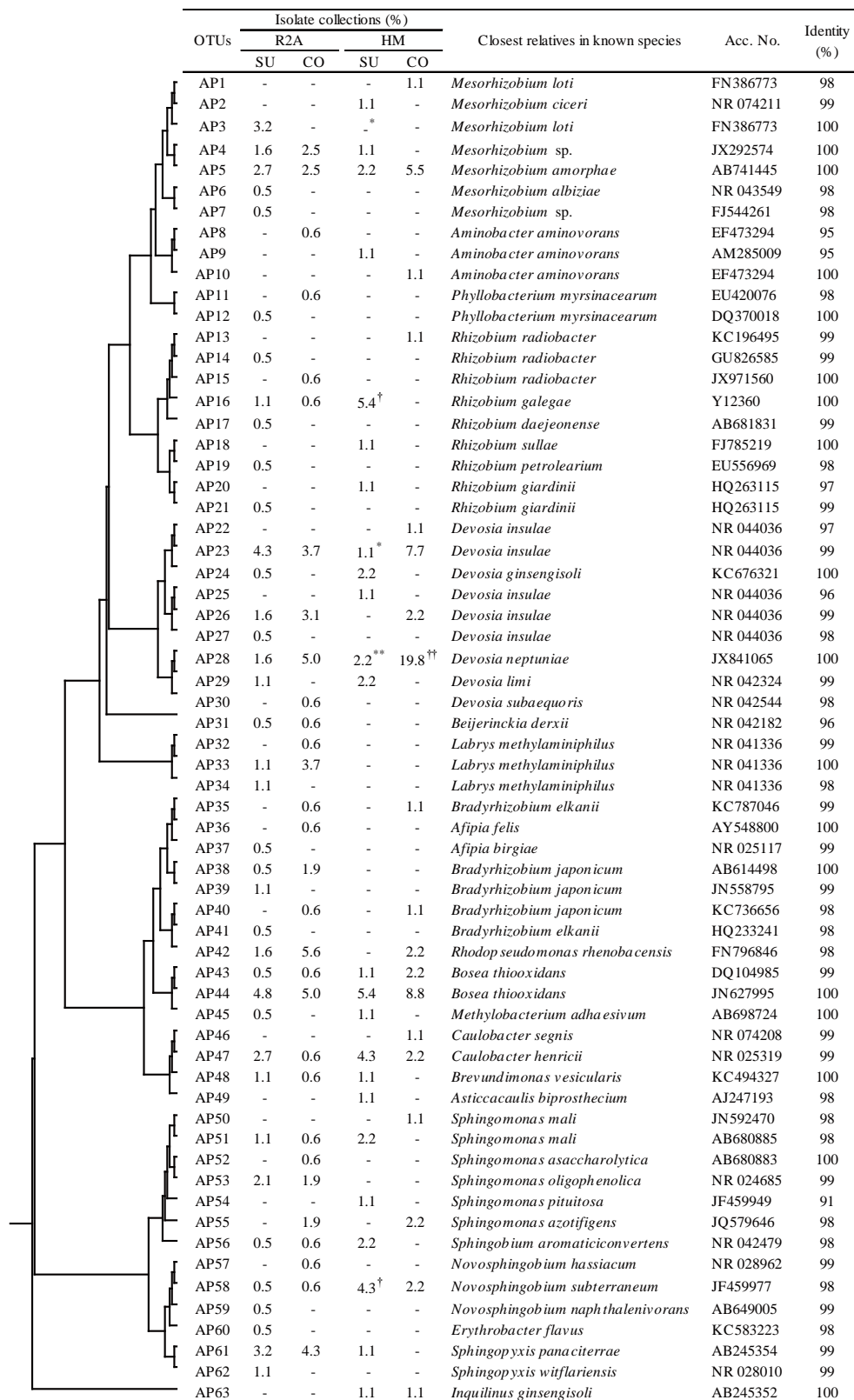
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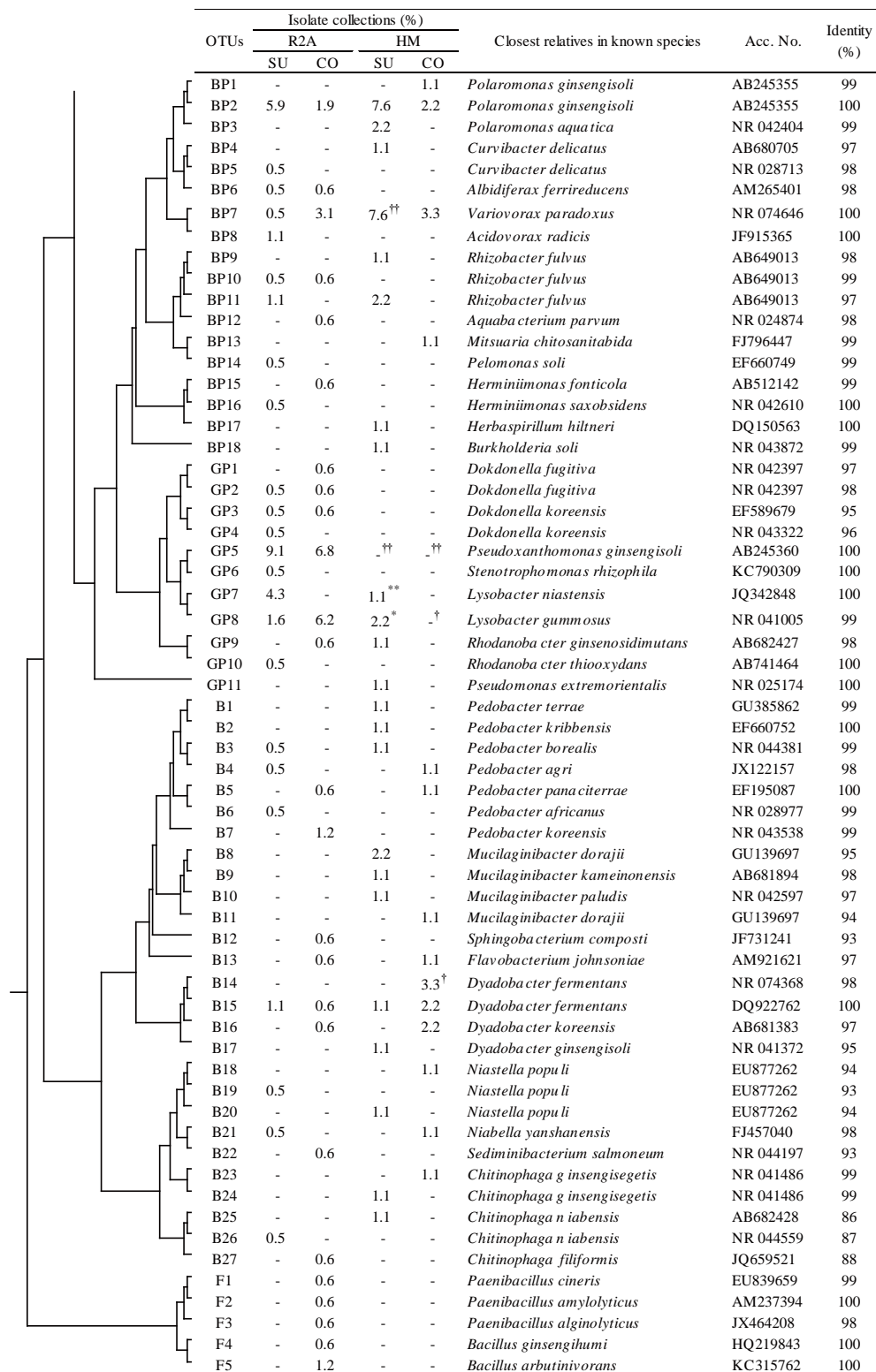
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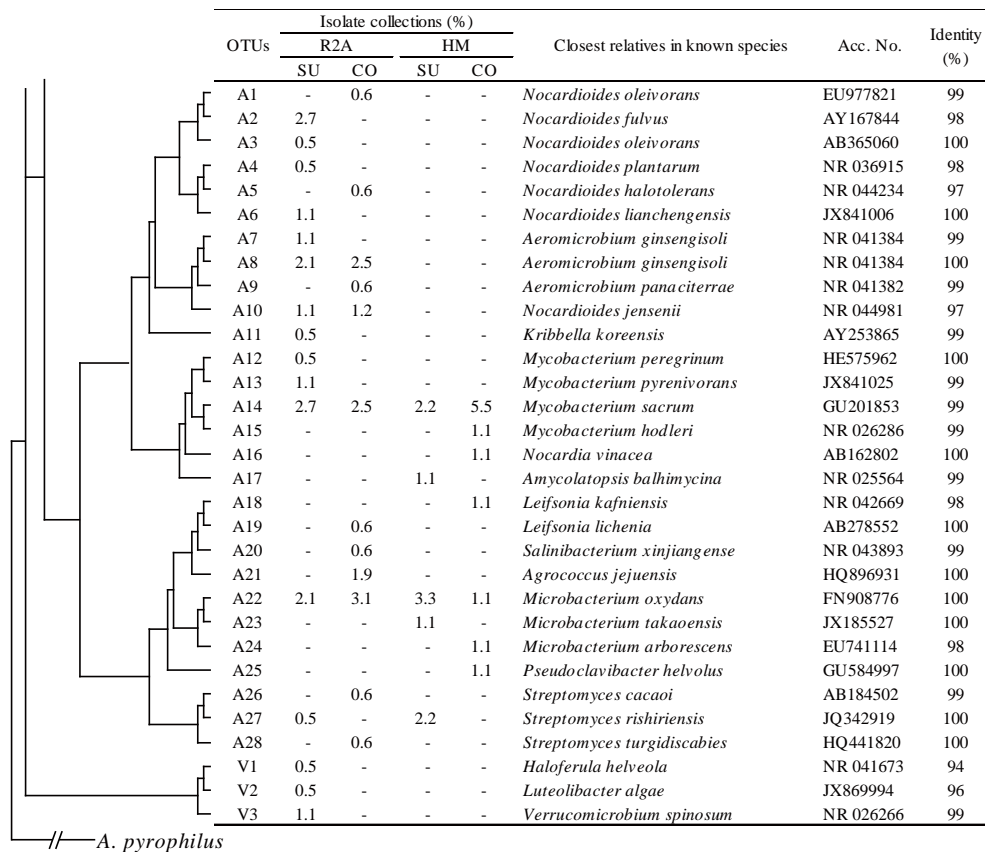


1 Fig. S1 K. Okazaki



1 Fig. S1 Continued K. Okazaki

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1 Fig. S1 Continued K. Okazaki

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