

Supplementary materials

An assessment of Urea-Formaldehyde Fertilizer on the Diversity of Bacterial Communities in Onion and Sugar beet

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Supplementary Table 1. Accession numbers for clone libraries used in the present study

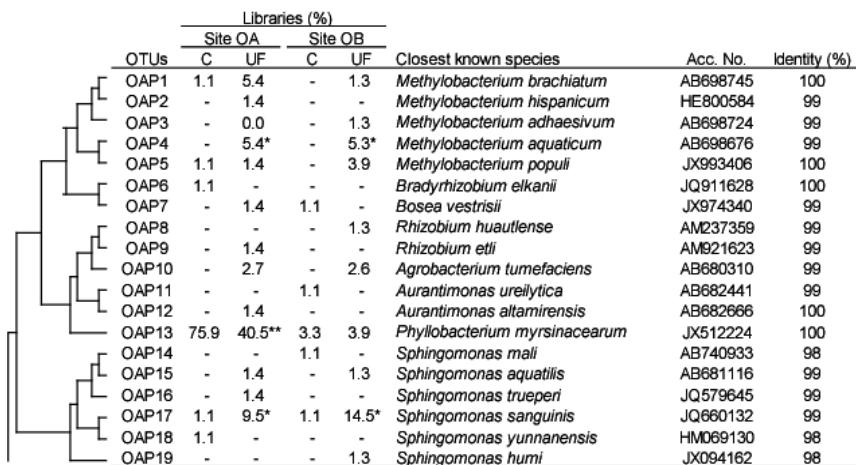
Accession numbers	Libraries
AB810269-AB810355	control library for site OA
AB810356-AB810445	control library for site OB
AB810446-AB810519	UF library for site OA
AB810520-AB810595	UF library for site OB
AB810596-AB810679	control library for site SA
AB810680-AB810759	control library for site SB
AB810760-AB810848	UF library for site SA
AB810849-AB810937	UF library for site SB

Supplementary Table 2. Yields data in the present study

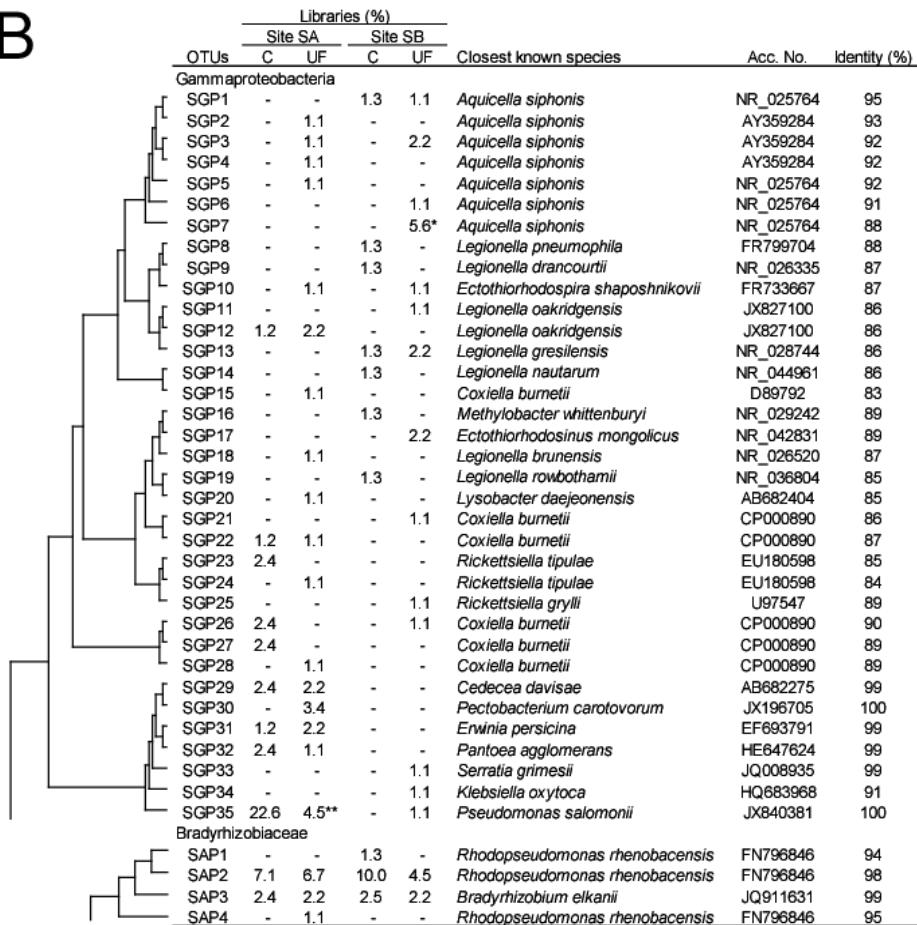
Crops	Locations	Yields (t/ha)	
		C ^a	UF ^a
Onion	OA (Kitami city)	63.6	67.1
Onion	OB (Kunneppucho)	52.9	55.2
Sugar beet	SA (Nakasatsunai village)	57.9	61.4
Sugar beet	SB (Obihiro city)	32.4	38.6

^aC and UF indicate the conventional and UF fertilization, respectively.

A



B



Supplementary Figure 1. The phylogenetic distribution of OTUs based on 16S rRNA gene sequences of the clone libraries for onion- and sugar beet-associated bacteria. The dendrogram indicates the phylogenetic relationships among the representative sequences of OTUs (defined by $\geq 97\%$ identity). The table indicates the relative abundance of clones or isolates belonging to each OTU in each library and the results of a BLAST search using representative sequences. Panel A, Alphaproteobacteria among the onion-associated bacteria; panel B, Alpha- and Gammaproteobacteria among the sugar beet-associated bacteria. * and ** indicate statistical significance calculated using the Fisher's exact test at the 1 and 5% levels ($P < 0.01$ and $P < 0.05$), respectively, between conventional and UF fertilization conditions (C and UF, respectively).