

Supplementary materials

An assessment of Urea-Formaldehyde Fertilizer on the Diversity of Bacterial Communities

in Onion and Sugar beet

SEISHI IKEDA<sup>1\*</sup>, KEIJIRO SUZUKI<sup>2,3</sup>, MAKOTO KAWAHARA<sup>4</sup>,

MASAO NOSHIRO<sup>5</sup>, and NAOKAZU TAKAHASHI<sup>4</sup>

<sup>1</sup>*Hokkaido Agricultural Research Center, National Agriculture and Food Research Organization, 9-4 Shinsei-minami, Memuro-cho, Kasai-gun, Hokkaido 082-0081, Japan;* <sup>2</sup>*Kitami Agricultural Experiment Station, Aza Yayoi, Kunneppu, Hokkaido 090-1496, Japan;* <sup>3</sup>*Present address: Central Agricultural Experiment Station, Naganuma, Hokkaido 069-1395, Japan;* <sup>4</sup>*SUN AGRO Co., Ltd., 1470 Shiraoka, Shiraoka, Saitama 349-0218, Japan; and* <sup>5</sup>*HOKKAIDO SUN AGRO Co., Ltd., Sapporo-daiichiseimei-building, Kita 3, Nishi 4, Chuo-ku, Sapporo, Hokkaido 060-0003, Japan*

\*Corresponding author. E-mail: [sikeda67@affrc.go.jp](mailto:sikeda67@affrc.go.jp); Tel: +81-155-62-9276; Fax:

+81-155-61-2127.

Topic of the manuscript: ecology of plant-associated bacteria

Running title: Impacts of a UF fertilizer on plant bacteria

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 <sup>a</sup>	UF <sup>a</sup>
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

<sup>a</sup>C and UF indicate the conventional and UF fertilization, respectively.

**A**

OTUs	Libraries (%)				Closest known species	Acc. No.	Identity (%)
	Site OA		Site OB				
	C	UF	C	UF			
OAP1	1.1	5.4	-	1.3	<i>Methylobacterium brachiatum</i>	AB698745	100
OAP2	-	1.4	-	-	<i>Methylobacterium hispanicum</i>	HE800584	99
OAP3	-	0.0	-	1.3	<i>Methylobacterium adhaesivum</i>	AB698724	99
OAP4	-	5.4*	-	5.3*	<i>Methylobacterium aquaticum</i>	AB698676	99
OAP5	1.1	1.4	-	3.9	<i>Methylobacterium populi</i>	JX993406	100
OAP6	1.1	-	-	-	<i>Bradyrhizobium elkanii</i>	JQ911628	100
OAP7	-	1.4	1.1	-	<i>Bosea vestrisii</i>	JX974340	99
OAP8	-	-	-	1.3	<i>Rhizobium huautlense</i>	AM237359	99
OAP9	-	1.4	-	-	<i>Rhizobium etli</i>	AM921623	99
OAP10	-	2.7	-	2.6	<i>Agrobacterium tumefaciens</i>	AB680310	99
OAP11	-	-	1.1	-	<i>Aurantimonas urelytica</i>	AB682441	99
OAP12	-	1.4	-	-	<i>Aurantimonas altamirensis</i>	AB682666	100
OAP13	75.9	40.5**	3.3	3.9	<i>Phyllobacterium myrsinacearum</i>	JX512224	100
OAP14	-	-	1.1	-	<i>Sphingomonas mali</i>	AB740933	98
OAP15	-	1.4	-	1.3	<i>Sphingomonas aquatilis</i>	AB681116	99
OAP16	-	1.4	-	-	<i>Sphingomonas trueperi</i>	JQ579645	99
OAP17	1.1	9.5*	1.1	14.5*	<i>Sphingomonas sanguinis</i>	JQ660132	99
OAP18	1.1	-	-	-	<i>Sphingomonas yunnanensis</i>	HMD69130	98
OAP19	-	-	-	1.3	<i>Sphingomonas humi</i>	JX094162	98

**B**

OTUs	Libraries (%)				Closest known species	Acc. No.	Identity (%)
	Site SA		Site SB				
	C	UF	C	UF			
<b>Gammaproteobacteria</b>							
SGP1	-	-	1.3	1.1	<i>Aquicella siphonis</i>	NR_025764	95
SGP2	-	1.1	-	-	<i>Aquicella siphonis</i>	AY359284	93
SGP3	-	1.1	-	2.2	<i>Aquicella siphonis</i>	AY359284	92
SGP4	-	1.1	-	-	<i>Aquicella siphonis</i>	AY359284	92
SGP5	-	1.1	-	-	<i>Aquicella siphonis</i>	NR_025764	92
SGP6	-	-	-	1.1	<i>Aquicella siphonis</i>	NR_025764	91
SGP7	-	-	-	5.6*	<i>Aquicella siphonis</i>	NR_025764	88
SGP8	-	-	1.3	-	<i>Legionella pneumophila</i>	FR799704	88
SGP9	-	-	1.3	-	<i>Legionella drancourtii</i>	NR_026335	87
SGP10	-	1.1	-	1.1	<i>Ectothiorhodospira shaposhnikovii</i>	FR733667	87
SGP11	-	-	-	1.1	<i>Legionella oakridgensis</i>	JX827100	86
SGP12	1.2	2.2	-	-	<i>Legionella oakridgensis</i>	JX827100	86
SGP13	-	-	1.3	2.2	<i>Legionella greslensis</i>	NR_028744	86
SGP14	-	-	1.3	-	<i>Legionella nautarum</i>	NR_044961	86
SGP15	-	1.1	-	-	<i>Coxiella burnetii</i>	D89792	83
SGP16	-	-	1.3	-	<i>Methylobacter whittenburyi</i>	NR_029242	89
SGP17	-	-	-	2.2	<i>Ectothiorhodospira mongolicus</i>	NR_042831	89
SGP18	-	1.1	-	-	<i>Legionella brunensis</i>	NR_026520	87
SGP19	-	-	1.3	-	<i>Legionella rowbothamii</i>	NR_036804	85
SGP20	-	1.1	-	-	<i>Lysobacter daejeonensis</i>	AB682404	85
SGP21	-	-	-	1.1	<i>Coxiella burnetii</i>	CP000890	86
SGP22	1.2	1.1	-	-	<i>Coxiella burnetii</i>	CP000890	87
SGP23	2.4	-	-	-	<i>Rickettsiella tipulae</i>	EU180598	85
SGP24	-	1.1	-	-	<i>Rickettsiella tipulae</i>	EU180598	84
SGP25	-	-	-	1.1	<i>Rickettsiella grylli</i>	U97547	89
SGP26	2.4	-	-	1.1	<i>Coxiella burnetii</i>	CP000890	90
SGP27	2.4	-	-	-	<i>Coxiella burnetii</i>	CP000890	89
SGP28	-	1.1	-	-	<i>Coxiella burnetii</i>	CP000890	89
SGP29	2.4	2.2	-	-	<i>Cedecea davisae</i>	AB682275	99
SGP30	-	3.4	-	-	<i>Pectobacterium carotovorum</i>	JX196705	100
SGP31	1.2	2.2	-	-	<i>Ervinia persicina</i>	EF693791	99
SGP32	2.4	1.1	-	-	<i>Pantoea agglomerans</i>	HE647624	99
SGP33	-	-	-	1.1	<i>Serratia grimesii</i>	JQ008935	99
SGP34	-	-	-	1.1	<i>Klebsiella oxytoca</i>	HQ683968	91
SGP35	22.6	4.5**	-	1.1	<i>Pseudomonas salomonii</i>	JXB40381	100
<b>Bradyrhizobiaceae</b>							
SAP1	-	-	1.3	-	<i>Rhodopseudomonas rhenobacensis</i>	FN796846	94
SAP2	7.1	6.7	10.0	4.5	<i>Rhodopseudomonas rhenobacensis</i>	FN796846	98
SAP3	2.4	2.2	2.5	2.2	<i>Bradyrhizobium elkanii</i>	JQ911631	99
SAP4	-	1.1	-	-	<i>Rhodopseudomonas rhenobacensis</i>	FN796846	95

**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).