Supporting materials

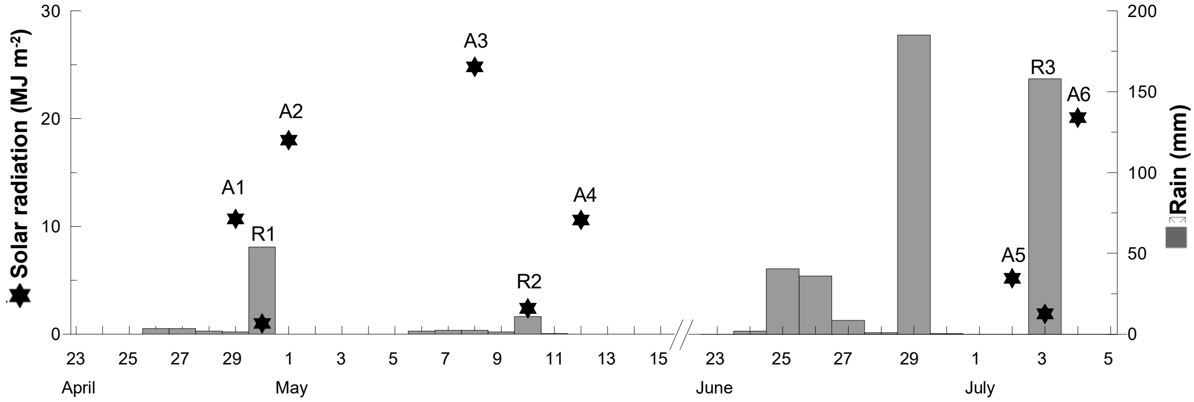
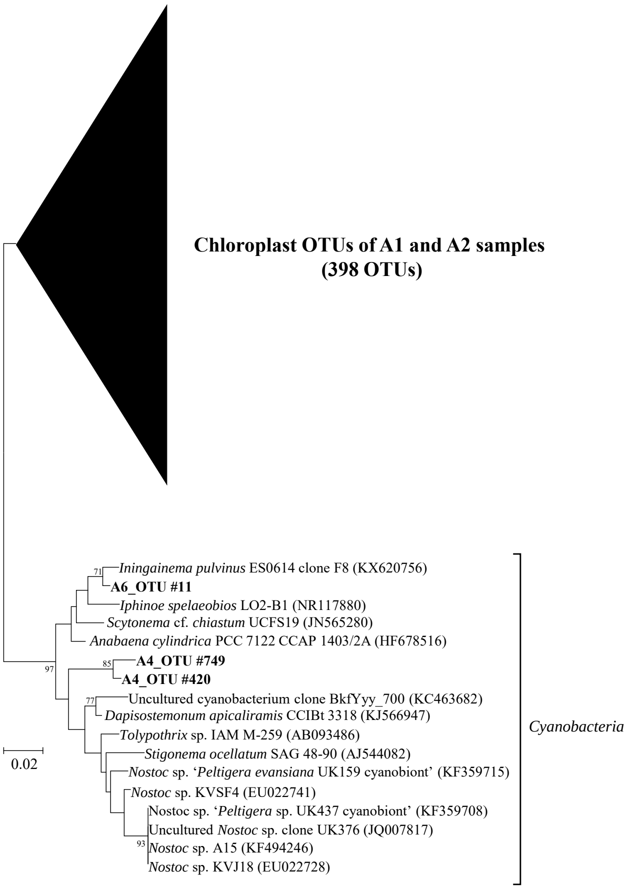
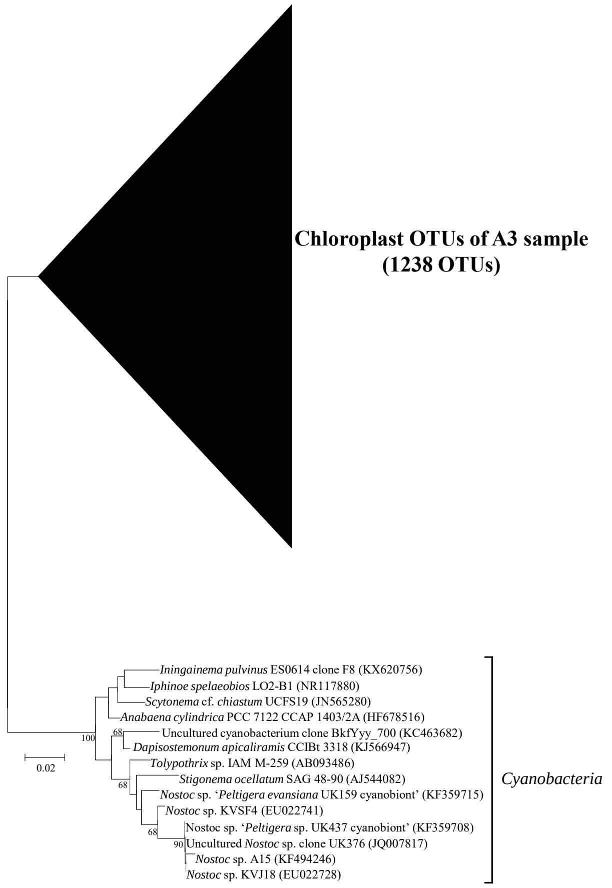


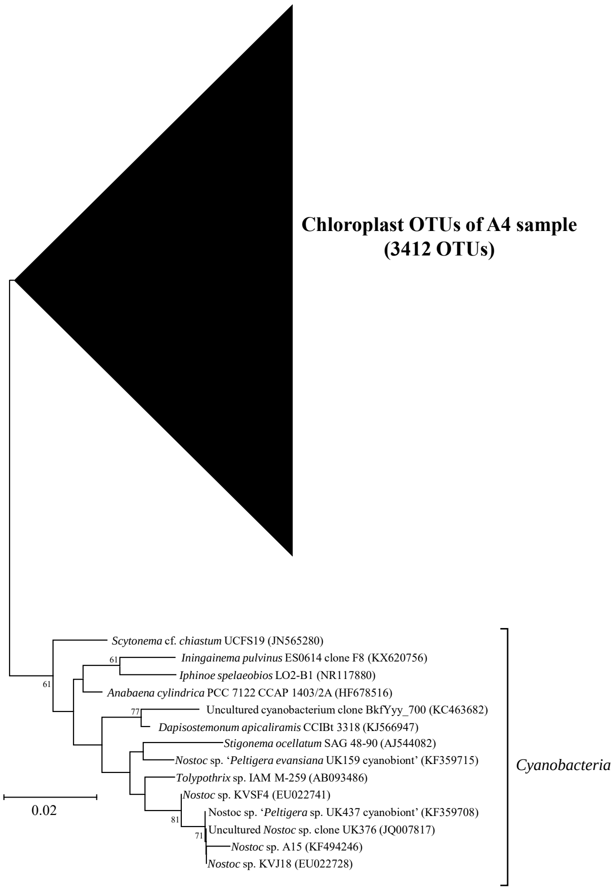
Fig. S1 Temporal variations of solar radiation and precipitation during the sampling period of aerosols and rainwaters. Air collection was from 17:09 h to 19:12 h on April 29 (A1); from 15:09 h to 17:09 h on May 1 (A2); from 12:38 h to 14:39 h on May 8 (A3); from 17:40 h to 19:50 h on May 12 (A4); from 13:25 h to 15:30 h on July 2 (A5) and from 13:28 h to 15:30 h on July 4 (A6). Rain data from April 30 (R1), May 10 (R2), and July 3 (R3) are from a reference [10]; additional rain data are from the Korea Metrological Administration (Sillim-dong, Gwanak-gu, Seoul)


Chloroplast OTUs of A1 and A2 samples
(398 OTUs)
71
Iningainema pulvinus ES0614 clone F8 (KX620756)
A6_OTU #11
Iphinoe spelaeobios LO2-B1 (NR117880)
Scytonema cf. chiastum UCFS19 (JN565280)
Anabaena cylindrica PCC 7122 CCAP 1403/2A (HF678516)
97
85
A4_OTU #749
A4_OTU #420
77
Uncultured cyanobacterium clone BkfYyy_700 (KC463682)
Dapisostemonum apicaliramis CCIBt 3318 (KJ566947)
Tolypothrix sp. IAM M-259 (AB093486)
Stigonema ocellatum SAG 48-90 (AJ544082)
Nostoc sp. 'Peltigera evansiana UK159 cyanobiont' (KF359715)
Nostoc sp. KVSF4 (EU022741)
Nostoc sp. 'Peltigera sp. UK437 cyanobiont' (KF359708)
Uncultured Nostoc sp. clone UK376 (JQ007817)
93
Nostoc sp. A15 (KF494246)
Nostoc sp. KVJ18 (EU022728)
Cyanobacteria
0.02

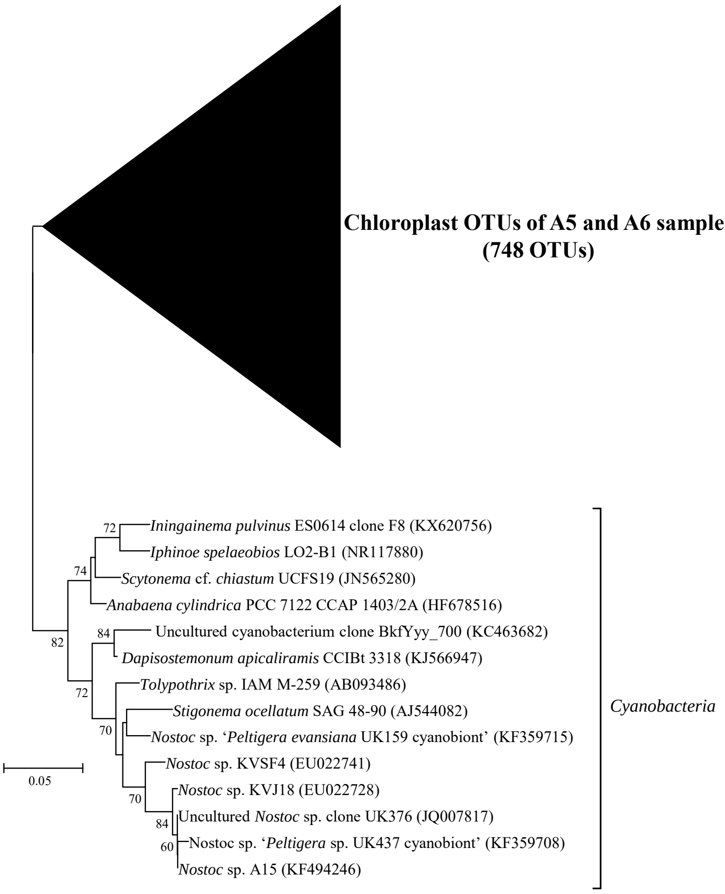
(a)


Chloroplast OTUs of A3 sample
(1238 OTUs)
Iningainema pulvinus ES0614 clone F8 (KX620756)
Iphinoe spelaeobios LO2-B1 (NR117880)
Scytonema cf. chiastum UCFS19 (JN565280)
Anabaena cylindrica PCC 7122 CCAP 1403/2A (HF678516)
68
Uncultured cyanobacterium clone BkfYyy_700 (KC463682)
100
Dapisostemonum apicaliramis CCIBt 3318 (KJ566947)
Tolypothrix sp. IAM M-259 (AB093486)
0.02
Stigonema ocellatum SAG 48-90 (AJ544082)
68
Nostoc sp. 'Peltigera evansiana UK159 cyanobiont' (KF359715)
Nostoc sp. KVSF4 (EU022741)
Nostoc sp. 'Peltigera sp. UK437 cyanobiont' (KF359708)
68
90
Uncultured Nostoc sp. clone UK376 (JQ007817)
Nostoc sp. A15 (KF494246)
Nostoc sp. KVJ18 (EU022728)
Cyanobacteria

(b)


Chloroplast OTUs of A4 sample
(3412 OTUs)
Scytonema cf. *chiastum* UCFS19 (JN565280)
61
Iningainema pulvinus ES0614 clone F8 (KX620756)
61
Iphinoe spelaeobios LO2-B1 (NR117880)
Anabaena cylindrica PCC 7122 CCAP 1403/2A (HF678516)
77
Uncultured cyanobacterium clone BkfYyy_700 (KC463682)
Dapisostemonum apicaliramis CCIBt 3318 (KJ566947)
Stigonema ocellatum SAG 48-90 (AJ544082)
Nostoc sp. ‘*Peltigera evansiana* UK159 cyanobiont’ (KF359715)
Tolypothrix sp. IAM M-259 (AB093486)
0.02
Nostoc sp. KVSF4 (EU022741)
Nostoc sp. ‘*Peltigera* sp. UK437 cyanobiont’ (KF359708)
81
Uncultured *Nostoc* sp. clone UK376 (JQ007817)
71
Nostoc sp. A15 (KF494246)
Nostoc sp. KVJ18 (EU022728)
Cyanobacteria

(c)



(d)

Fig. S2 Neighbor-joining phylogenetic trees based on 16S rRNA gene sequences showing chloroplast and cyanobacteria OTUs from aerosol samples: (a) A1 and A2 samples, (b) A3 sample, (c) A4 sample, and (d) A5 and A6 samples. The numbers at the nodes are bootstrap percentages (based on 1000 resamplings); only values above 60% are shown

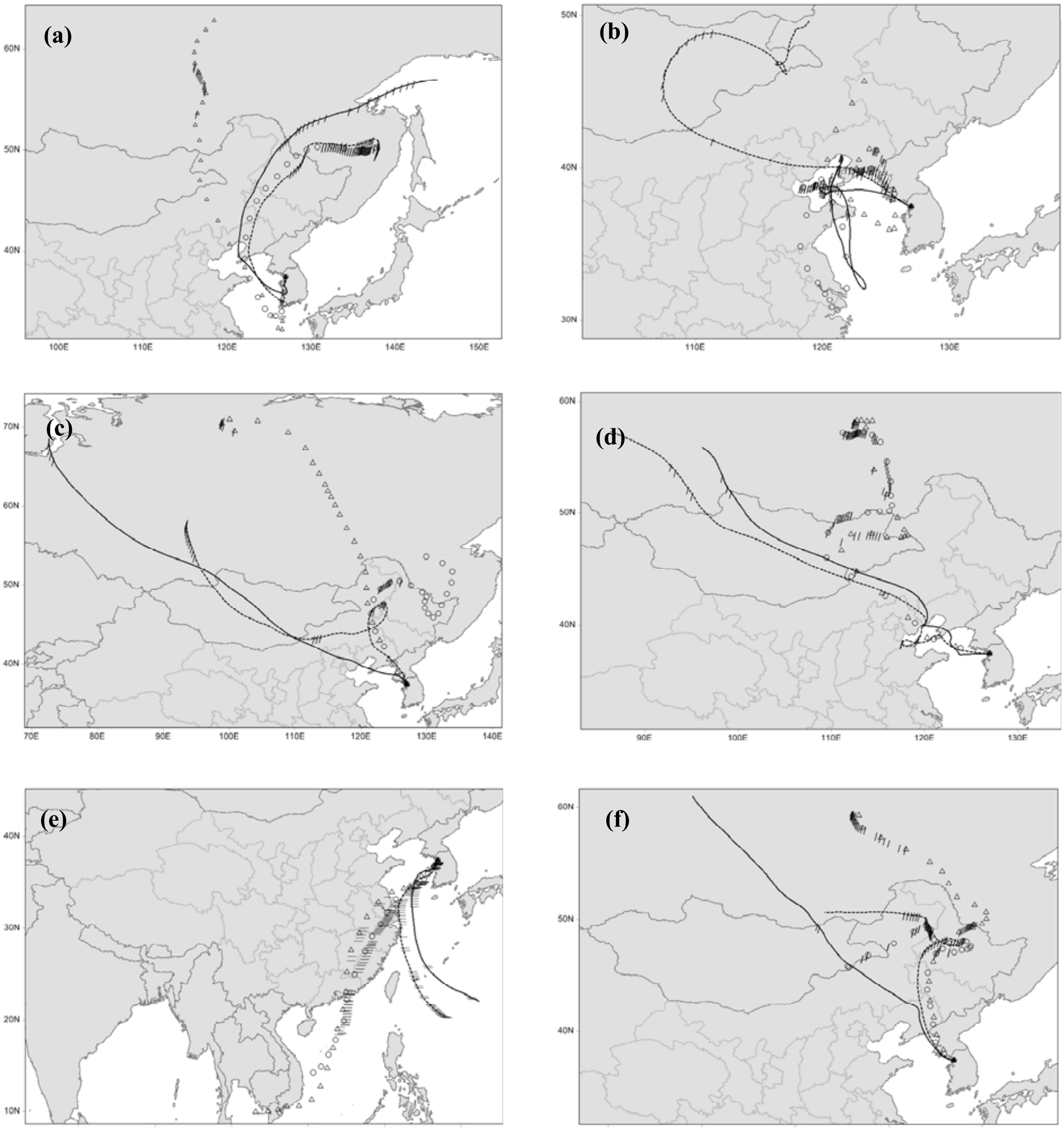


Fig. S3 Air mass backward trajectories at the sampling site on (a) 29 April, (b) 1 May, (c) 8 May, (d) 12 May, (e) 2 July, and (f) 4 July. Each trajectory is indicated by the different heights, 100 m (solid line), 200 m (dashed line), 500 m (circles), and 1000 m (triangles), at which it arrived at the sampling site at 1-day intervals up to 5 days back in time. A slash corresponds to a precipitation period

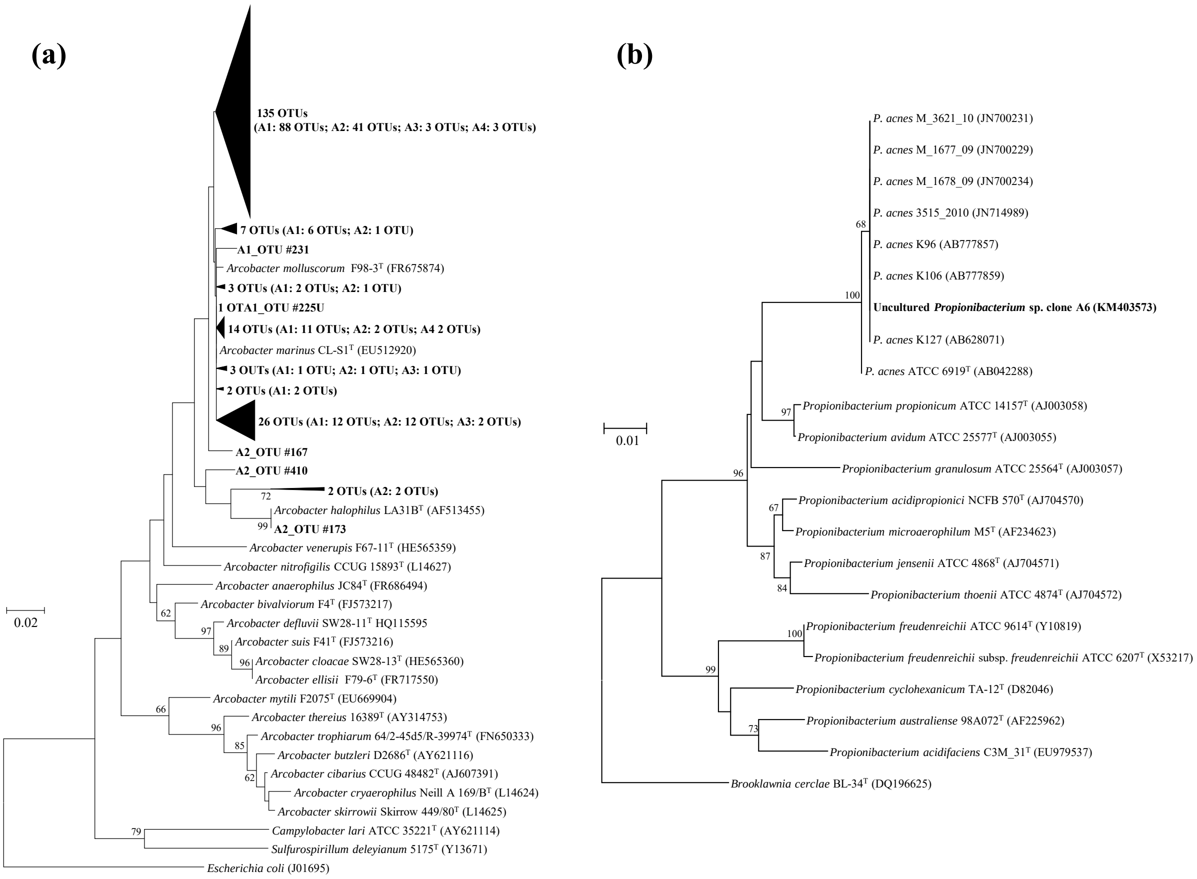


Fig. S4 Neighbor-joining phylogenetic trees based on 16S rRNA gene sequences showing (a) presumable marine bacterial OTUs closest to *Arcobacter* spp. and (b) *Propionibacterium acnes* sequence detected from aerosol sample A6 and sequences closest to *Propionibacterium acnes*. The numbers at the nodes are bootstrap percentages (based on 1000 resamplings); only values above 60% are shown. *Escherichia coli* (J01695) and *Brooklawnia cerclae* BL-34^T (DQ196625) were used, respectively, as the outgroups in (a) and (b). The bar represents 0.02 and 0.01 nucleotide substitutions per site, respectively, in (a) and (b)

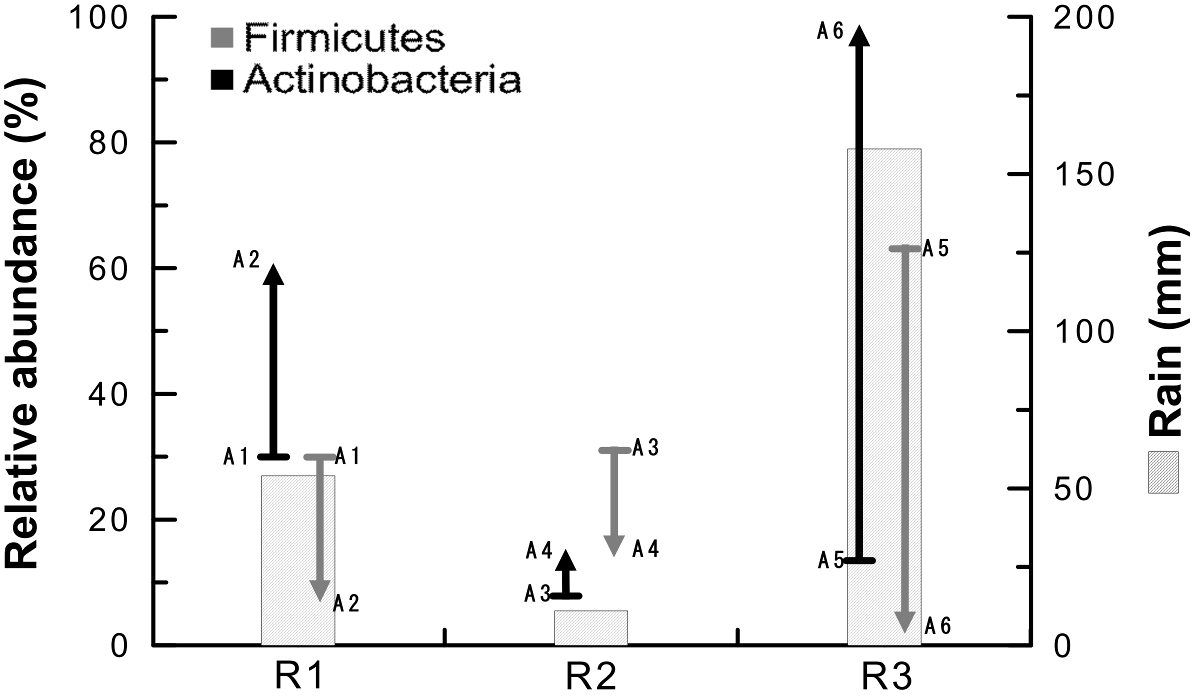


Fig. S5 Variation of relative abundances of *Actinobacteria* (black arrow) and *Firmicutes* (gray arrow) in aerosols samples between before and after rainfall. Rain data from April 30 (R1), May 10 (R2), and July 3 (R3) are from a reference [10]

Table S1 Total number of OTUs (operational taxonomic units) and relative abundances of taxa found in contamination controls for each air sample using the RDP classifier (80% confidence). Phylum or class level classifications are highlighted in bold and the remaining taxa are classified to the level of order or family. –: not detected

Category	**A1**	**A2**	**A3**	**A4**	**A5**	**A6**
Actinobacteria	**–**	**1.6**	**7.5**	**14.7**	**9.3**	**82.6**
Actinomycetales	–	1.6	7.5	14.7	9.3	82.6
Actinomycetales other	–	–	–	–	–	4.3
Propionibacteriaceae	–	1.6	7.5	14.7	9.3	78.3
Bacteroidetes	**–**	**–**	**–**	**–**	**57.4**	**13.0**
Bacteroidetes other	–	–	–	–	5.6	–
Flavobacteriales	–	–	–	–	46.3	13.0
Flavobacteriales other	–	–	–	–	1.9	–
Flavobacteriaceae	–	–	–	–	44.4	13.0
Sphingobacteriales (Chitinophagaceae)	–	–	–	–	5.6	–
Firmicutes	**–**	**–**	**–**	**–**	**1.9**	**–**
Bacillales (Staphylococcaceae)	–	–	–	–	1.9	–
Clostridiales	–	–	–	–	–	–
Proteobacteria	**86.4**	**74.6**	**69.8**	**52.9**	**25.9**	**4.3**
Proteobacteria other	1.7	1.6	1.9	2.9	1.9	–
Gammaproteobacteria	**18.6**	**17.5**	**60.4**	**29.4**	**14.8**	**–**
Gammaproteobacteria other	–	1.6	3.8	–	–	–
Pseudomonadales	3.4	6.3	5.7	2.9	9.3	–
Moraxellaceae	–	–	1.9	–	5.6	–
Pseudomonadaceae	3.4	6.3	3.8	2.9	3.7	–
Enterobacteriales (Enterobacteriaceae)	15.3	9.5	50.9	26.5	3.7	–
Xanthomonadales (Xanthomonadaceae)	–	–	–	–	1.9	–
Betaproteobacteria	**11.9**	**9.5**	**7.5**	**20.6**	**7.4**	**4.3**
Betaproteobacteria other	–	1.6	–	–	–	–
Burkholderiales	11.9	7.9	7.5	20.6	7.4	4.3
Comamonadaceae	11.9	7.9	7.5	20.6	5.6	–
Burkholderiales_incertae_sedis	–	–	–	–	1.9	4.3
Burkholderiaceae	–	–	–	–	–	–
Alphaproteobacteria	**–**	**–**	**–**	**–**	**1.9**	**–**
Sphingomonadales (Sphingomonadaceae)	–	–	–	–	1.9	–
Epsilonproteobacteria	**54.2**	**46.0**	**–**	**–**	**–**	**–**
Campylobacterales (Campylobacteraceae)	54.2	46.0	–	–	–	–
Unclassified Bacteria	**13.6**	**23.8**	**22.6**	**32.4**	**5.6**	**–**

Notes: **Total number of OTUs: A1, 59; A2, 63; A3, 53; A4, 34; A5, 54; A6, 23**

Table S2 Adaptor, sample-specific barcode, and primer sequences used in this study

Sample	Primer name	Adaptor	Barcode	Primer
29 April (A1)	Forward 27F (Bacteria)	CGTATCGCCTCCCTCGCGCCATCAG	AGACGCACTC	GAGTTTGATCMTGGCTCAG
29 April (filter blank)			TCTCTATGCG	
01 May (A2)			AGCACTGTAG	
01 May (filter blank)			TCTCTATGCG	
08 May (A3)			ACGAGTGCGT**	
08 May (filter blank)			CGTGTCTCTA	
12 May (A4)			ACGCTCGACA*	
12 May (filter blank)			CGTGTCTCTA	
02 July (A5)			ACGAGTGCGT**	
02 July (filter blank)			CGTGTCTCTA	
04 July (A6)			ACGCTCGACA*	
04 July (filter blank)			CGTGTCTCTA	
29 April (A1)	Reverse 518R (Bacteria)	CTATGCGCCTTGCCAGCCCGCTCAG	AGACGCACTC	WTTACCGCGGCTGCTGG
29 April (filter blank)			TCTCTATGCG	
01 May (A2)			AGCACTGTAG	
01 May (filter blank)			TCTCTATGCG	
08 May (A3)			ACGAGTGCGT**	
08 May (filter blank)			CGTGTCTCTA	
12 May (A4)			ACGCTCGACA*	
12 May (filter blank)			CGTGTCTCTA	
02 July (A5)			ACGAGTGCGT**	
02 July (filter blank)			CGTGTCTCTA	
04 July (A6)			ACGCTCGACA*	
04 July (filter blank)			CGTGTCTCTA	
29 April (A1)	Forward A20F (Archaea)	CGTATCGCCTCCCTCGCGCCATCAG	ACGAGTGCGT	TTCCGGTTGATCCYGCCRG
29 April (filter blank)			ACGCTCGACA	
01 May (A2)			AGACGCACTC	
01 May (filter blank)			ACGCTCGACA	
08 May (A3)			AGCACTGTAG	
08 May (filter blank)			ATCAGACACG	
12 May (A4)			ATATCGCGAG	
12 May (filter blank)			ATCAGACACG	
02 July (A5)			CGTGTCTCTA	

02 July (filter blank)			CTCGCGTGTC	
04 July (A6)			TCTCTATGCG	
04 July (filter blank)			CTCGCGTGTC	
29 April (A1)	Reverse U519R (Archaea)	CTATGCGCCTTGCCAGCCCGCTCAG	ACGAGTGCGT	GWATTACCGCGGCKGCTG
29 April (filter blank)			ACGCTCGACA	
01 May (A2)			AGACGCACTC	
01 May (filter blank)			ACGCTCGACA	
08 May (A3)			AGCACTGTAG	
08 May (filter blank)			ATCAGACACG	
12 May (A4)			ATATCGCGAG	
12 May (filter blank)			ATCAGACACG	
02 July (A5)			CGTGTCTCTA	
02 July (filter blank)			CTCGCGTGTC	
04 July (A6)			TCTCTATGCG	
04 July (filter blank)			CTCGCGTGTC	

Notes: Samples marked with * or ** were analyzed on different days

Table S3 Occurrences of marine bacteria-like OTUs in aerosol samples. Values are in percentages. –: not detected. For description of samples A1–A6, see Table 1

Class	**Species**	**A1**	**A2**	**A3**	**A4**	**A5**	**A6**
Epsilon-proteobacteria	*Arcobacter* spp.	4.02	0.94	0.57	0.52	–	–
Alpha-proteobacteria	*Sulfitobacter* sp.	0.40	–	–	–	–	–
Alpha-proteobacteria	*Sphingorhabdus* sp.	–	0.47	–	–	–	–
Alpha-proteobacteria	*Sphingobium* sp.	–	–	–	–	0.07	–
Alpha-proteobacteria	*Shimia* sp.	–	–	–	–	0.21	–
Actinobacteria	*Salinibacterium* sp.	–	–	0.11	–	–	–
Bacilli	*Virgibacillus* spp.	–	–	–	0.04	–	–
Bacilli	*Carnobacterium* sp.	–	–	–	–	0.07	–

Table S4 Occurrence of pathogenic bacterial phylotypes in aerosol samples collected at a suburban site in April to July, 2011. Values are in percentages. –: not detected. For description of samples A1–A6, see Table 1

Pathogenic bacterial phylotype	A1	A2	A3	A4	A5	A6
Clavibacter michiganensis subsp. *michiganensis*	17.5	23.2	2.1	1.4	–	–
Bacillus cereus/*anthracis*/*mycoides* clade	–	–	0.1	–	–	–
Staphylococcus epidermidis	0.5	1.0	–	0.04	0.6	–
Staphylococcus cohnii subsp. *cohnii*	–	–	0.2	–	0.7	–
Staphylococcus saprophyticus subsp. *saprophyticus*	–	–	–	–	0.6	–
Staphylococcus saprophyticus subsp. *bovis*	–	–	0.1	–	26.5	–
Propionibacterium acnes	–	1.3	–	–	–	10.7

Table S5 Comparison of estimated absolute abundances of airborne *Actinobacteria*, *Propionibacteriaceae* and *Firmicutes* with- or without chloroplast sequences

		Without chloroplast sequences			**With chloroplast sequences**		
Groups	**Abundances**	**A1 (before Rain)**	**A2 (after Rain)**	**A2/A1 (%)**	**A1 (before Rain)**	**A2 (after Rain)**	**A2/A1 (%)**
Actinobacteria	Bacterial abundance (BA; cells/m^3)	5.3.E + 06	1.3.E + 05	2	5.3.E + 06	1.3.E + 05	2
	Relative abundance (%)	40.3	71.1	176	37	53	144
	Absolute abundance (cells/m^3)	2.1.E + 06	9.2.E + 04	4	1.9.E + 06	6.8.E + 04	4
Propionibacteriaceae	Bacterial abundance (BA; cells/m^3)	5.3.E + 06	1.3.E + 05	2	5.3.E + 06	1.3.E + 05	2
	Relative abundance (%)	–	3.5	> 100	–	3	> 100
	Absolute abundance (cells/m^3)	–	4.6.E + 03	> 100	–	3.4.E + 03	> 100
Firmicutes	Bacterial abundance (BA; cells/m^3)	5.3.E + 06	1.3.E + 05	2	5.3.E + 06	1.3.E + 05	2
	Relative abundance (%)	24.9	2.7	11	22.0	2.0	9
	Absolute abundance (cells/m^3)	1.3.E + 06	3.6.E + 03	0.3	1.2.E + 06	2.6.E + 03	0.2

Groups	**Abundances**	**A3 (before Rain)**	**A4 (after Rain)**	**A4/A3 (%)**	**A3 (before Rain)**	**A4 (after Rain)**	**A4/A3 (%)**
Actinobacteria	Bacterial abundance (BA; cells/m^3)	1.0.E + 04	1.0.E + 04	100	1.0.E + 04	1.0.E + 04	100
	Relative abundance (%)	5.2	12.2	235	3.10	4.90	158
	Absolute abundance (cells/m^3)	5.2.E + 02	1.2.E + 03	235	3.1.E + 02	4.9.E + 02	158
Propionibacteriaceae	Bacterial abundance (BA)	1.0.E + 04	1.0.E + 04	100	1.0.E + 04	1.0.E + 04	100
	Relative abundance (%)	0.03	0.8	2800	0.03	0.31	1033
	Absolute abundance (cells/m^3)	3.0.E + 00	8.4.E + 01	2800	3.0.E + 00	3.1.E + 01	1033
Firmicutes	Bacterial abundance (BA; cells/m^3)	1.0.E + 04	1.0.E + 04	100	1.0.E + 04	1.0.E + 04	100
	Relative abundance (%)	48.1	31.9	66	28.3	13.0	46
	Absolute abundance (cells/m^3)	4.8.E + 03	3.2.E + 03	66	2.8.E + 03	1.3.E + 03	46

Groups	**Abundances**	**A5 (before Rain)**	**A6 (after Rain)**	**A6/A5 (%)**	**A5 (before Rain)**	**A6 (after Rain)**	**A6/A5 (%)**
Actinobacteria	Bacterial abundance (BA; cells/m^3)	4.0.E + 03	1.0.E + 03	25	4.0.E + 03	1.0.E + 03	25
	Relative abundance (%)	5.7	89.9	1577	4.80	72.70	1515
	Absolute abundance (cells/m^3)	2.3.E + 02	9.0.E + 02	394	1.9.E + 02	7.3.E + 02	379
Propionibacteriaceae	Bacterial abundance (BA; cells/m^3)	4.0.E + 03	1.0.E + 03	25	4.0.E + 03	1.0.E + 03	25
	Relative abundance (%)	3.0	83.4	2799	2.0	67.5	3375
	Absolute abundance (cells/m^3)	1.2.E + 02	8.3.E + 02	700	8.0.E + 01	6.8.E + 02	844
Firmicutes	Bacterial abundance (BA; cells/m^3)	4.0.E + 03	1.0.E + 03	25	4.0.E + 03	1.0.E + 03	25
	Relative abundance (%)	61.4	0.6	1	41.8	0.5	1
	Absolute abundance (cells/m^3)	2.5.E + 03	6.1.E + 00	0.2	1.7.E + 03	5.0.E + 00	0.3

Table S6 Marine bacteria-like sequences detected from aerosol samples collected from cities in Texas and Seoul. NAD: Non-Asian Dust, AD: Asian Dust, Alpha: *Alpha-Proteobacteria*, Beta: *Beta-Proteobacteria*, Actino: *Actinobacteria*, Acid: *Acidimicrobiia*, Cyto: *Cytophagia*

Study	**Event**	**Accession #**	**Class**	**Validly published species**	**Similarity (%)**	**Temperature (℃)**	**Salinity (NaCl, %)**	**Pigment**	**Isolation source**	**Remark**	**Reference**
Brodie et al. [1]	–	DQ129634	Alpha	*Roseomonas oryzae*	97.3	4–45 (30)	0–6	Light pink	Paddy rhizosphere soil	Non-spore-forming	[3]
	–	DQ129628	Alpha	*Rhizobium rhizoryzae*	99.9	10–40	1–4	Pearl white	Rice roots	Non-spore-forming	[4]
	–	DQ129625	Alpha	*Paracoccus niistensis*	99.8	10–40 (28–30)	0–7	Vivid orange	Forest soil		[5]
	–	DQ129279	Alpha	*Skermanella aerolata*	98.2	5–35 (25–30)	0–5	Light pink	Air		[6]
Jeon et al. [2]	NAD	HM366528	Alpha	*Marinibacterium profundimaris*	98.7	4–41	0–12	Yellowish	Deep seawater		[7]
	AD	HM366500	Alpha	*Microvirga aerilata*	99.2	10–35	0–3	Pink	Air	Non-spore-forming	[8]
	NAD	HM366536	Beta	*Castellaniella caeni*	99.9	10–37 (30)	0–5	Brownish	Sludge	Non-spore-forming	[9]
	NAD	HM366524	Bacilli	*Staphylococcus pasteuri*	99.7	15–45	5–15	Yellow	Human, animal, food specimens	Nosocomial infections, nonsporulating	[10]
	AD	HM366495	Bacilli	*Sporosarcina contaminans*	98.2	15–50	0–9	Beige	A contaminant from an industrial clean-room floor	Endospore formation	[11]
	AD	HM3664	Baci	*Exiguobacterium*	99.9	20–41	Marine agar	Orange	Brine shrimp	Non-spore-forming	[12]

	93	lli	*mexicanum*							
AD	HM366484	Bacilli	*Oceanobacillus rekensis*	98.1	15–40	5–20	Creamy white	Saline alkali soil samples	Spore-forming	[13]
AD	HM366480	Bacilli	*Chungangia koreensis*	98.8	30–45	0–9.0 (0)	Creamy	Marine sediment	Non-spore-forming	[14]
AD	HM366477	Bacilli	*Bacillus campisalis*	98.9	4–39	0.5–15.0 (2–3)	Light orange–yellow	Marine solar saltern	Endospore-forming	[15]
AD	HM366476	Bacilli	*Oceanobacillus arenosus*	98.7	20–37	0–8 (2)	Creamy	Marine sand	Non-spore-forming	[16]
AD	HM366469	Bacilli	*Lysinibacillus composti*	98.9	10–45 (28)	0–5	Light yellow	Compost	Non-spore-forming	[17]
NAD	HM366530	Actino	*Microbacterium maritypicum*	100	(28, 37)	2–6.5	Light yellow	Seawater, marine mud		[18]
NAD	HM366530	Actino	*Microbacterium liquefaciens*	99.7	4–47 (30)	5, 7	Bright yellow	Dairy products	Non-spore-forming	[19]
AD	HM366514	Actino	*Nocardioides iriomotensis*	98.1	12–37	0–7	Cream yellow	Forest soil	Nonsporulating	[20]
AD	HM366510	Actino	*Kocuria rosea*	99.8	5–25	5	Red	Skin, soil, water	Infective endocarditis	[21]
AD	HM366498	Actino	*Modestobacter marinus*	99.5	4–35	< 5	Orange to red, black	Deep sea sediment	Non-spore-forming	[22]
AD	HM366504	Acid	*Ilumatobacter fluminis*	97.4	26–32	Marine broth	Colorless	Sediment of estuary		[23]
NAD	HM366535	Cyto	*Pontibacter amylolyticus*	97.7	4–40 (35)	0–5 (0–1)	Red	Deep-sea sediment of hydrothermal vent		[24]

References

1. Brodie E L, DeSantis T Z, Parker J P M, Zubietta I X, Piceno Y M, Andersen G L. Urban aerosols harbor diverse and dynamic bacterial populations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104(1): 299–304

2. Jeon E M, Kim H J, Jung K, Kim J H, Kim M Y, Kim Y P, Ka J O. Impact of Asian dust events on airborne bacterial community assessed by molecular analyses. Atmospheric Environment, 2011, 45(25): 4313–4321

3. Ramaprasad E V V, Sasikala Ch, Ramana Ch V. *Roseomonas oryzae* sp. nov., isolated from paddy rhizosphere soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65(10): 3535–3540

4. Zhang X X, Tang X, Sheirdil R A, Sun L, Ma X T. *Rhizobium rhizoryzae* sp. nov., isolated from rice roots. International Journal of Systematic and Evolutionary Microbiology, 2014, 64(4): 1373–1377

5. Dastager S G, Deepa C K, Li W J, Tang S K, Pandey A. *Paracoccus niistensis* sp. nov., isolated from forest soil, India. Antonie van Leeuwenhoek, 2011, 99(3): 501–506

6. Weon H Y, Kim B Y, Hong S B, Joa J H, Nam S S, Lee K H, Kwon S W. *Skermanella aerolata* sp. nov., isolated from air, and emended description of the genus *Skermanella*. International Journal of Systematic and Evolutionary Microbiology, 2007, 57(7): 1539–1542

7. Li G, Lai Q, Du Y, Liu X, Sun F, Shao Z. *Marinibacterium profundimaris* gen. nov., sp. nov., isolated from deep seawater. International Journal of Systematic and Evolutionary Microbiology, 2015, 65(11): 4175–4179

8. Weon H Y, Kwon S W, Son J A, Jo E H, Kim S J, Kim Y S, Kim B Y, Ka J O. Description of *Microvirga aerophila* sp. nov. and *Microvirga aerilata* sp. nov., isolated from air, reclassification of *Balneimonas flocculans* Takeda et al. 2004 as *Microvirga flocculans* comb. nov. and emended description of the genus *Microvirga*. International Journal of Systematic and Evolutionary Microbiology, 2010, 60(11): 2596–2600

9. Liu Q M, Ten L N, Im W T, Lee S T. *Castellaniella caeni* sp. nov., a denitrifying bacterium isolated from sludge of a leachate treatment plant. International Journal of Systematic and Evolutionary Microbiology, 2008, 58(9): 2141–2146

10. Chesneau O, Morvan A, Grimont F, Labischinski H, el Solh N. *Staphylococcus pasteuri* sp. nov., isolated from human, animal, and food specimens. International Journal of Systematic Bacteriology, 1993, 43(2): 237–244

11. Kämpfer P, Falsen E, Lodders N, Schumann P. *Sporosarcina contaminans* sp. nov. and *Sporosarcina thermotolerans* sp. nov., two endospore-forming species. International Journal of Systematic and Evolutionary Microbiology, 2010, 60(6): 1353–1357

12. López-Cortés A, Schumann P, Pukall R, Stackebrandt E. *Exiguobacterium mexicanum* sp. nov. and *Exiguobacterium artemiae* sp. nov., isolated from the brine shrimp *Artemia franciscana*. Systematic and Applied Microbiology, 2006, 29(3): 183–190

13. Long X, Ye R, Zhang S, Liu B, Zhang Y, Zeng Z, Tian Y. *Oceanobacillus damuensis* sp. nov. and *Oceanobacillus rekensis* sp. nov., isolated from saline alkali soil samples. Antonie van Leeuwenhoek, 2015, 108(3): 731–739

14. Kim W, Traiwan J, Park M H, Jung M Y, Oh S J, Yoon J H, Sukhoom A. *Chungangia koreensis* gen. nov., sp. nov., isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2012, 62(8): 1914–1920

15. Kumar R M, Kaur G, Kumar A, Bala M, Singh N K, Kaur N, Kumar N, Mayilraj S. Taxonomic description and genome sequence of *Bacillus campisalis* sp. nov., a member of the genus *Bacillus* isolated from a solar saltern. International Journal of Systematic and Evolutionary Microbiology, 2015, 65(10): 3235–3240

16. Kim W, Siamphan C, Kim J H, Sukhoom A. *Oceanobacillus arenosus* sp. nov., a moderately halophilic bacterium isolated from marine sand. International Journal of Systematic and Evolutionary Microbiology, 2015, 65(9): 2943–2948

17. Hayat R, Ahmed I, Paek J, Sin Y, Ehsan M, Iqbal M, Yokota A, Chang Y H. *Lysinibacillus composti* sp. nov., isolated from compost. Annals of Microbiology, 2014, 64(3): 1081–1088

18. Takeuchi M, Hatano K. Proposal of six new species in the genus *Microbacterium* and transfer of *Flavobacterium marinotypicum* ZoBell and Upham to the genus *Microbacterium* as *Microbacterium maritypicum* comb. nov. International Journal of Systematic Bacteriology, 1998, 48(3): 973–982

19. Suzuki K, Hamada M, Genus I. *Microbacterium* Orla-Jensen 1919, 179AL emend. In: Goodfellow M, Kämpfer P, Busse H J, Trujillo M E, Suzuki K, Ludwig W, Whitman W B, editors. Bergey’s Manual of Systematic Bacteriology. New York: Springer, 2012, vol. 5, 841–852

20. Yamamura H, Ohkubo S Y, Nakagawa Y, Ishida Y, Hamada M, Otoguro M, Tamura T, Hayakawa M. *Nocardioides iriomotensis* sp. nov., an actinobacterium isolated from forest soil. International Journal of Systematic and Evolutionary Microbiology, 2011, 61(9): 2205–2209

21. Shivaji S, Rao N S, Saisree L, Sheth V, Reddy G S N, Bhargava P M. Isolation and identification of *Micrococcus roseus* and *Planococcus* sp. from Schirmacher oasis, Antarctica. Journal of Biosciences, 1988, 13(4): 409–414

22. Xiao J, Luo Y, Xu J, Xie S, Xu J. *Modestobacter marinus* sp. nov., a psychrotolerant actinobacterium from deep-sea sediment, and emended description of the genus *Modestobacter*. International Journal of Systematic and Evolutionary Microbiology, 2011, 61(7): 1710–1714

23. Matsumoto A, Kasai H, Matsuo Y, Omura S, Shizuri Y, Takahashi Y. *Ilumatobacter fluminis* gen. nov., sp. nov., a novel actinobacterium isolated from the sediment of an estuary. The Journal of General and Applied Microbiology, 2009, 55(3): 201–205

24. Wu Y H, Zhou P, Jian S L, Liu Z S, Wang C S, Oren A, Xu X W. *Pontibacter amylolyticus* sp. nov., isolated from a deep-sea sediment hydrothermal vent field. International Journal of Systematic and Evolutionary Microbiology, 2016, 66(4): 1760–1767

Table S7 List of background airborne bacterial operational taxonomic units (OTUs) detected from an aerosol sample in July (A5). OTUs marked with an asterisk are not found in the air samples from April and May. Sequences with < 93.0% similarity were not included. Actino: *Actinobacteria*, Alpha: *Alpha-Proteobacteria*, Beta: *Beta-Proteobacteria*, Gamma: *Gamma-Proteobacteria*

OTUs to closest validly published species				Number of OTUs / reads	Similarity (%)	Habitats**	References
Phylum or Class	Order	Family	Species				
Actino	Actinomycetales	Corynebacteriaceae	Corynebacterium variabile DSM 20132(T)*	1 / 2	98.0	Milk	[1]
		Micrococcaceae	Micrococcus yunnanensis YIM 65004(T)	1 / 1	98.5	Groundwater; Seawater	[2,3]
Bacilli	Bacillales	Bacillaceae	Bacillus stratosphericus 41KF2a(T)*	1 / 2	99.4	Cloud; air; Laminaria saccharina (brown alga)	[4–6]
	Lactobacillales	Carnobacteriaceae	Carnobacterium jeotgali MS3(T)*	1 / 1	97.4	Bovine rumen	[7]
Bacteroidetes	Flavobacteriales	Flavobacteriaceae	Flavobacterium lindanitolerans IP-10(T)*	1 / 2	97.1	River sediment	[8]
Alpha	Rhizobiales	Methylobacteriaceae	Methylobacterium tardum RB677(T)*	1 / 3	98.5	Phyllosphere	[9]
	Rhodobacterales	Rhodobacteraceae	Shimia marina CL-TA03(T)*	1 / 3	97.4	Oil, biofilm	[10,11]
Beta	Burkholderiales	Comamonadaceae	Comamonas testosteroni ATCC 11996(T)*	1 / 1	98.1	Sediments	[12]
			Acidovorax radicis N35(T)	1 / 1	97.6	Wheat roots; Lake water	[13,14]
		Oxalobacteraceae	Janthinobacterium lividum DSM 1522(T)*	1 / 2	97.6	Lake water	[15]
	Methylophilales	Methylophilaceae	Methylophilus luteus Mim(T)*	1 / 2	99.2	Phyllosphere	[16]
Gamma	Pseudomonadales	Pseudomonadaceae	Pseudomonas hibiscicola ATCC 19867(T)	1 / 1	98.3	Gastrointestinal;	[17,18]

						Drinking water	
Actino	Actinomycetales	Intrasporangiaceae	Janibacter limosus DSM 11140(T)*	5 / 5	93.3–96.5	Air	This study
Bacilli	Bacillales	Bacillaceae	Bacillus oceanisediminis H2(T)	1 / 1	96.1	Air	This study
			Bacillus safensis FO-036b(T)*	1 / 2	94.9	Air	This study
			Bacillus altitudinis 41KF2b(T)*	1 / 1	93.4	Air	This study
			Bacillus stratosphericus 41KF2a(T)*	1 / 1	93.1	Air	This study
		Staphylococcaceae	Staphylococcus lugdunensis ATCC 43809(T)*	1 / 1	95.2	Air	This study
	Lactobacillales	Carnobacteriaceae	Desemzia incerta DSM 20581(T)*	5 / 5	93.0–96.6	Air	This study
Bacteroidetes	Flavobacteriales	Flavobacteriaceae	Flavobacterium lindanitolerans IP-10(T)*	1 / 1	95.9	Air	This study
			Flavobacterium tiangeerense 563(T)*	1 / 3	93.7	Air	This study
			Flavobacterium xueshanense Sr22(T)*	1 / 1	93.7	Air	This study
Clostridia	Clostridiales	Clostridiaceae	Clostridium lituseburense ATCC 25759(T)*	4 / 9	95.0–97.0	Air	This study
			Clostridium butyricum ATCC 19398(T)*	1 / 1	94.9	Air	This study
			Clostridium paraputrificum DSM 2630(T)*	2 / 2	93.1–93.3	Air	This study
Alpha	Rhizobiales	Rhizobiaceae	Rhizobium daejeonense KCTC 12121(T)*	1 / 1	95.4	Air	This study
			Rhizobium herbae CCBAU 83011(T)*	1 / 1	93.3	Air	This study
	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium mesophilum MSL-20(T)	2 / 2	94.6–96.0	Air	This study
	Rhodospirillales	Unclassified Rhodospirillales	Reyranella massiliensis URTM1(T)*	1 / 1	96.4	Air	This study
	Sphingomonadales	Erythrobacteraceae	Altererythrobacter aestuarii KYW147(T)	1 / 6	95.7	Air	This study
			Porphyrobacter donghaensis SW-132(T)	1 / 2	95.7	Air	This study
		Sphingomonadaceae	Sphingobium yanoikuyae GIFU 9882(T)*	3 / 4	94.4–96.3	Air	This study
Beta	Burkholderiales	Comamonadaceae	Acidovorax radicis N35(T)	4 / 4	95.1–96.8	Air	This study
			Acidovorax temperans CCUG 11779(T)	1 / 1	93.1	Air	This study
			Acidovorax defluvii BSB411(T)	1 / 1	93.0	Air	This study
			Comamonas aquatica LMG 2370(T)	7 / 8	93.4–96.4	Air	This study
			Comamonas testosteroni ATCC 11996(T)*	2 / 2	93.1–93.3	Air	This study

			Comamonas thiooxydans S23(T)*	1 / 2	93.6	Air	This study
			Delftia lacustris DSM 21246(T)	3 / 3	93.3–94.6	Air	This study
		Incertae sedis	Aquabacterium parvum B6(T)*	1 / 2	95.8	Air	This study
		Oxalobacteraceae	Herbaspirillum autotrophicum IAM	1 / 1	96.9	Air	This study
			Janthinobacterium lividum DSM 1522(T)*	1 / 1	94	Air	This study
Gamma	Enterobacteriales	Enterobacteriaceae	Dickeya chrysanthemi LMG 2804(T)*	1 / 1	96.6	Air	This study
			Escherichia coli O157 EC4115	1 / 1	96.2	Air	This study
			Escherichia coli KCTC 2441(T)	1 / 1	94.3	Air	This study
			Pectobacterium carotovorum subsp.	1 / 1	95.4	Air	This study
			Citrobacter farmeri CDC 2991-81(T)	1 / 1	93.3	Air	This study
	Pseudomonadales	Moraxellaceae	Acinetobacter johnsonii DSM 6963(T)	2 / 2	94.0–95.9	Air	This study
		Pseudomonadaceae	Pseudomonas moorei RW10(T)	1 / 1	95.0	Air	This study
	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas chelatiphaga LPM-5(T)*	1 / 1	93.7	Air	This study

Notes: OTUs indicating human presence were not included in the list of background airborne OTUs. OTUs indicating human presence closest (> 97.3% similarity) to *Clostridium celatum*, *Janibacter limosus*, *Staphylococcus arlettae*, *Staphylococcus epidermidis*, and *Staphylococcus saprophyticus* subsp. *bovis* were found in sample A5. **Habitat was presumed on the basis of reported sources of most similar sequences to each OUT

References

1. Raats D, Offek M, Minz D, Halpern M. Molecular analysis of bacterial communities in raw cow milk and the impact of refrigeration on its structure and dynamics. Food Microbiology, 2011, 28(3): 465–471

2. Tiago I, Chung A P, Veríssimo A. Bacterial diversity in a nonsaline alkaline environment: heterotrophic aerobic populations. Applied and Environmental Microbiology, 2004, 70(12): 7378–7387

3. Kim M, Kwon T H, Jung S M, Cho S H, Jin S Y, Park N H, Kim C G, Kim J S. Antibiotic resistance of bacteria isolated from the internal organs of edible snow crabs. PLoS One, 2013, 8(8): e70887

4. Margesin R, Miteva V. Diversity and ecology of psychrophilic microorganisms. Research in Microbiology, 2011, 162(3): 346–361

5. Maki T, Puspitasari F, Hara K, Yamada M, Kobayashi F, Hasegawa H, Iwasaka Y. Variations in the structure of airborne bacterial communities in a downwind area during an Asian dust (Kosa) event. Science of the Total Environment, 2014, 488–489: 75–84

6. Wiese J, Thiel V, Nagel K, Staufenberger T, Imhoff J F. Diversity of antibiotic-active bacteria associated with the brown alga *Laminaria saccharina* from the Baltic Sea. Marine Biotechnology (New York, N.Y.), 2009, 11(2): 287–300

7. Brulc J M, Antonopoulos D A, Berg Miller M E, Wilson M K, Yannarell A C, Dinsdale E A, Edwards R E, Frank E D, Emerson J B, Wacklin P, Coutinho P M, Henrissat B, Nelson K E, White B A. Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106(6): 1948–1953

8. Branco R, Chung A P, Veríssimo A, Morais P V. Impact of chromium-contaminated wastewaters on the microbial community of a river. FEMS Microbiology Ecology, 2005, 54(1): 35–46

9. Knief C, Frances L, Vorholt J A. Competitiveness of diverse *Methylobacterium* strains in the phyllosphere of *Arabidopsis thaliana* and identification of representative models, including *M. extorquens* PA1. Microbial Ecology, 2010, 60(2): 440–452

10. Redmond M C, Valentine D L. Natural gas and temperature structured a microbial community response to the Deepwater Horizon oil spill. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109(50): 20292–20297

11. Choi D H, Cho B C. *Shimia marina* gen. nov., sp. nov., a novel bacterium of the Roseobacter clade isolated from biofilm in a coastal fish farm. International Journal of Systematic and Evolutionary Microbiology, 2006, 56(8): 1869–1873

12. Li D, Yang M, Li Z, Qi R, He J, Liu H. Change of bacterial communities in sediments along Songhua River in Northeastern China after a nitrobenzene pollution event. FEMS Microbiology Ecology, 2008, 65(3): 494–503

13. Li D, Rothballer M, Schmid M, Esperschütz J, Hartmann A. *Acidovorax radicis* sp. nov., a wheat-root-colonizing bacterium. International Journal of Systematic and Evolutionary Microbiology, 2011, 61(11): 2589–2594

14. Wu L, Ge G, Zhu G, Gong S, Li S, Wan J. Diversity and composition of the bacterial community of Poyang Lake (China) as determined by 16S rRNA gene sequence analysis. World Journal of Microbiology & Biotechnology, 2012, 28(1): 233–244

15. Berg K A, Lyra C, Sivonen K, Paulin L, Suomalainen S, Tuomi P, Rapala J. High diversity of cultivable heterotrophic bacteria in association with cyanobacterial water blooms. The ISME Journal, 2009, 3(3): 314–325

16. Krieger J R, Kourtev P S. Bacterial diversity in three distinct sub-habitats within the pitchers of the northern pitcher plant, *Sarracenia purpurea*. FEMS Microbiology Ecology, 2012, 79(3): 555–567

17. Li E, Hamm C M, Gulati A S, Sartor R B, Chen H, Wu X, Zhang T, Rohlf F J, Zhu W, Gu C, Robertson C E, Pace N R, Boedeker E C, Harpaz N, Yuan J, Weinstock G M, Sodergren E, Frank D N. Inflammatory bowel diseases phenotype, *C. difficile* and NOD2 genotype are associated with shifts in human ileum associated microbial composition. PLoS One, 2012, 7(6): e26284
18. Revetta R P, Gomez-Alvarez V, Gerke T L, Curioso C, Santo Domingo J W, Ashbolt N J. Establishment and early succession of bacterial communities in monochloramine-treated drinking water biofilms. FEMS Microbiology Ecology, 2013, 86(3): 404–414