

Characterization of halotolerant and oligotrophic bacterial communities in Asian desert dust (KOSA) bioaerosol accumulated in layers of snow on Mount Tateyama, Central Japan

著者	Maki Teruya, Aoki Kazuma, Kobayashi Fumihisa, Kakikawa Makiko, Tobo Yutaka, Matsuki Atsushi, Hasegawa Hiroshi, Iwasaka Yasunobu
journal or publication title	Aerobiologia
volume	27
number	4
page range	277-290
year	2011-12-01
URL	<a href="http://hdl.handle.net/2297/26610">http://hdl.handle.net/2297/26610</a>

doi: 10.1007/s10453-011-9196-0

Editorial Manager(tm) for *Aerobiologia*  
Manuscript Draft

Manuscript Number: AERO264R2

Title: Halotolerant and oligotrophic bacterial communities in Asian desert dust (KOSA) bioaerosol accumulated in layers of snow on Mount Tateyama, Central Japan

Article Type: Original paper

Keywords: KOSA, snow cover, bioaerosol, bacteria

Corresponding Author: Teruya Maki

Corresponding Author's Institution:

First Author: Teruya Maki

Order of Authors: Teruya Maki; Kazuma Aoki, Dr.; Fumihisa Kobayashi, Dr.; Makiko Kakikawa, Dr.; Tobo Yutaka, Dr.; Atsushi Matsuki, Dr.; Hiroshi Hasegawa, Dr.; Yasunobu Iwasaka, Dr.

**Abstract:** Microbial particles transported by Asian desert dust (KOSA) possibly impact ecosystems and human health in downwind environments and are commonly called "bioaerosols". The microbial communities associated with KOSA mineral particles (KOSA bioaerosol), which were collected from the snow cover on Mt. Tateyama, were investigated by means of a culture-amendment technique combined with denaturing gradient gel electrophoresis (DGGE) analysis using 16S rRNA genes. After the stratigraphy of the snow layer formed on the walls of a snow pit on Mt. Tateyama, samples were collected from 2 layers which included KOSA particles and one which did not. The snow samples with KOSA particles indicated microbial growth in the 100 and 10<sup>-1</sup> dilution media and in the medium with NaCl below 10 %, while the snow sample without KOSA particles showed no microbial growth in the culture media. The PCR-DGGE analysis revealed that the bacterial compositions in the snow samples including KOSA mineral particles were mainly composed of the members of the phyla Actinobacteria, Firmicutes, and Proteobacteria. In particular, the 2 phylotypes appeared in the microbial cultures were similar to the members of the *B. subtilis* group, which has been detected in bioaerosol samples collected from the atmosphere over KOSA arrival (Suzu City) and source (Dunhuang City) regions. Presumably, halotolerant and oligotrophic bacterial communities are associated with the KOSA particles that descend to the snow cover on Mt. Tateyama.

Suggested Reviewers: Ruprecht Jaenicke  
jaenicke@uni-mainz.de

His research group monitored the abundance of cellular material and proteins in the atmosphere, demonstrating that the bioaerosol would occupy the total amount of aerosol.

Paul J DeMott  
pdemott@lamar.colostate.edu

His research group demonstrated that bioaerosols at high altitudes may act as ice nuclei and cloud condensation nuclei affecting ice-cloud processes, and that the bioaerosols were transported to high altitude and were important factor for establishing the aerosol models.

Kenneth Sassen  
ksassen@gi.alaska.edu

His research group is monitoring the bioaerosol attached on KOSA particles using the LIDAR (Light Detection and Ranging) .

Huey-Jen Su  
hjsu@mail.nck.edu.tw

His research group is investigating the increase of atmospheric microorganisms in Taiwan during the KOSA events.

Heidi Bauer  
heibauer@mail.zserv.tuwien.ac.at

His research group is investigating microbial abundance included in the bioaerosol at a high-elevation site.

Dale W Griffin  
dgriffin@usgs.gov

His research group is investigating the increase of atmospheric microorganisms in Taiwan during the KOSA events.

Response to Reviewers: Response for Reviewer

We thank you for your evaluation for publication of our manuscript. In the revised manuscript, we revised a part of text, and added the information of accession numbers of sequences.

[Q1] Please correct Akio and Watanabe in the text but Aoki and Watanabe in the reference list.

[A1] In the text of revised manuscript, "Akio and Watanabe" was improved to "Aoki and Watanabe" (P6L16).

[Additional improved sections]

The information of accession numbers of 16S rDNA sequences was inserted in the text (P9L8) and Table 2 in the revised manuscript.

Microbial particles transported by Asian desert dust (KOSA) possibly impact ecosystems and human health in downwind environments and are commonly called "bioaerosols". The microbial communities associated with KOSA mineral particles (KOSA bioaerosol), which were collected from the snow cover on Mt. Tateyama, were investigated by means of a culture-amendment technique combined with denaturing gradient gel electrophoresis (DGGE) analysis using 16S rRNA genes. After the stratigraphy of the snow layer formed on the walls of a snow pit on Mt. Tateyama, samples were collected from 2 layers which included KOSA particles and one which did not. The snow samples with KOSA particles indicated microbial growth in the  $10^0$  and  $10^{-1}$  dilution media and in the medium with NaCl below 10 %, while the snow sample without KOSA particles showed no microbial growth in the culture media. The PCR-DGGE analysis revealed that the bacterial compositions in the snow samples including KOSA mineral particles were mainly composed of the members of the phyla *Actinobacteria*, *Firmicutes*, and *Proteobacteria*. In particular, the 2 phlotypes appeared in the microbial cultures were similar to the members of the *B. subtilis* group, which has been detected in bioaerosol samples collected from the atmosphere over KOSA arrival (Suzu City) and source (Dunhuang City) regions. Presumably, halotolerant and oligotrophic bacterial communities are associated with the KOSA particles that descend to the snow cover on Mt. Tateyama.

1 Title:

2 Characterization of halotolerant and oligotrophic bacterial communities in Asian desert dust

3 (KOSA) bioaerosol accumulated in layers of snow on Mount Tateyama, Central Japan

4

5 Authors:

6 Teruya Maki \*<sup>1</sup>, Kazuma Aoki<sup>2</sup>, Fumihisa Kobayashi<sup>1</sup>, Makiko Kakikawa<sup>1</sup>, Toba Yutaka<sup>3</sup>,

7 Atsushi Matsuki<sup>3</sup>, Hiroshi Hasegawa<sup>1</sup>, and Yasunobu Iwasaka<sup>3</sup>

8

9 Affiliation of all authors:

10 1. College of Science and Engineering, Kanazawa University, Kakuma, Kanazawa, Ishikawa,

11 920-1192, Japan.

12 2. Department of Earth Sciences, Faculty of Science, University of Toyama 3190 Gofuku,

13 Toyama 930-8555, Japan.

14 3. Institute of Nature and Environmental Technology, Kanazawa University, Kakuma,

15 Kanazawa, Ishikawa, 920-1192, Japan.

16 4. Frontier Science Organization, Kanazawa University, Kakuma, Kanazawa, Ishikawa,

17 920-1192, Japan.

18

19 \*Corresponding author:

20 Tel: +81-(0) 76-234-4793, Fax: +81-(0) 76-234-4800

21 E-mail:makiteru@t.kanazawa-u.ac.jp

22

1 **Abstract**

2

3 Microbial particles transported by Asian desert dust (KOSA) possibly impact ecosystems and  
4 human health in downwind environments and are commonly called “bioaerosols”. The  
5 microbial communities associated with KOSA mineral particles (KOSA bioaerosol), which  
6 were collected from the snow cover on Mt. Tateyama, were investigated by means of a  
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12 snow sample without KOSA particles showed no microbial growth in the culture media. The  
13 PCR-DGGE analysis revealed that the bacterial compositions in the snow samples including  
14 KOSA mineral particles were mainly composed of the members of the phyla *Actinobacteria*,  
15 *Firmicutes*, and *Proteobacteria*. In particular, the 2 phlotypes appeared in the microbial  
16 cultures were similar to the members of the *B. subtilis* group, which has been detected in  
17 bioaerosol samples collected from the atmosphere over KOSA arrival (Suzu City) and source  
18 (Dunhuang City) regions. Presumably, halotolerant and oligotrophic bacterial communities are  
19 associated with the KOSA particles that descend to the snow cover on Mt. Tateyama.

20

21 Key words: KOSA, snow cover, bioaerosol, bacteria

## 1 **1 Introduction**

2  
3 Asian desert dust (KOSA) occurred from the deserts of northern China, including the Gobi  
4 and Taklamakan Deserts, carry mineral-dust aerosol eastward over the East Sea to Japan and the  
5 Pacific Ocean by the west wind (Duce et al. 1980; Iwasaka et al. 1983). In addition to mineral  
6 dust, the microbial fractions associated with mineral-dust particles, which are commonly called  
7 “bioaerosols” include viruses, bacteria, fungi, and pollen as well as plant and animal debris  
8 (Jones and Harrison 2004; Jaenicke 2005). They potentially impact ecosystems and human  
9 health in the downwind environments (Prospero et al. 2005). Moreover, several species of  
10 microorganisms at high altitudes may act as ice nuclei affecting ice-cloud processes (Bowers et  
11 al. 2009; Pratt et al. 2009), which supports the possibility that wind-blown bioaerosol particles  
12 caught in dust events play an important role in atmospheric radiation transfer and the  
13 geochemical cycle of atmospheric constituents.

14 Recently, microbial cells attached to KOSA mineral particles have been observed with the  
15 use of an epifluorescence microscopic technique (Iwasaka et al. 2009) and the  
16 atmospheric-microbial compositions above the Taklamakan Desert (KOSA source region) were  
17 reported to be made up of several bacterial and fungal species (Kakikawa et al. 2009; Wang et al.  
18 2010). Ground-based studies in KOSA arrival regions have also been undertaken to clarify the  
19 transport of microorganisms by KOSA events, demonstrating that the bioaerosol concentrations  
20 at downwind locations increased when the regions were impacted by airborne desert dust (Yeo  
21 et al. 2002). Our atmospheric studies conducted with balloons that collect samples at altitudes  
22 from 600 to 800 m recovered bacterial populations that were similar to those of the *Bacillus* sp.  
23 between the KOSA source (Dunhuang City) (Kobayashi et al. 2007; Maki et al. 2008) and

1 arrival (Suzu City) regions (Maki et al. 2010). Nevertheless, studies dealing with genetic  
2 diversity, KOSA season dynamics, global distribution, and ecological importance of airborne  
3 bacteria at KOSA arrival regions remain limited because the direct collection of KOSA particles  
4 from atmospheric areas requires a high level of sampling using balloons or aircraft.

5       During the winter and early spring, strong north-westerly winds result in heavy snowfall  
6 on Mt. Tateyama (3015 m above sea level), which faces the East Sea, and the snowfall  
7 sometimes includes KOSA particles from China. The depth of the snow cover on Mt. Tateyama  
8 is approximately 6–10 m in the spring (Aoki and Watanabe 2009). The air temperature, which  
9 rarely exceeds freezing from November to April, maintains the snow cover during the winter.  
10 Moreover, the snow cover prevents windblown contamination of local soil materials on the  
11 ground. Chemical analysis and meteorological correlations demonstrated that the deposition of  
12 KOSA mineral particles causes dusty dirt layers in the snow cover on Mt. Tateyama (Osada et  
13 al. 2004). Therefore, the snow cover is regarded as a product of continuous precipitation during  
14 the KOSA season, and sufficient numbers of atmospheric aerosol samples were obtained from  
15 the snow cover to analyze the microbial community associated with KOSA particles.

16       In the atmosphere, some microorganisms remain viable and are able to withstand low  
17 moisture, extreme temperature, limited oxygen, and extensive UV exposure (Imshenetsky et al.  
18 1978; Alan and Harrison 2004). Halotolerant bacteria are known to tolerate high salinity and be  
19 resistant to stressors, such as high pH, extreme temperatures, and desiccation (Rothschild and  
20 Mancinelli 2001). The NaCl-amendment culture techniques recovered viable halotolerant  
21 bacteria at high altitudes in KOSA source and arrival regions (Maki et al. 2008, 2010).  
22 Halotolerant bacterial communities typify atmospheric microbial transport across hundreds to  
23 thousands of kilometers and at low to extreme altitudes (Okamoto et al. 2004; Echigo et al.



1 2005). On the other hand, since microbial communities under many different terrestrial and  
2 aquatic environments are often exposed to low-nutrient conditions, most environmental bacteria  
3 are assumed to be composed of oligotrophic bacteria, which survive through starvation-survival  
4 responses (Morita 1990). Oligotrophic bacteria produce a physical barrier to minimize  
5 environmental damage, such as extensive UV exposure (Blenkinsopp and Costerton 1991). An  
6 experimental design facilitating the cell activities of halotolerant and oligotrophic bacterial  
7 communities in bioaerosol samples is expected to be useful to investigate viable  
8 microorganisms transported by KOSA events.

9 In this study, snow samples including KOSA particles were collected from the snow cover  
10 on Mt. Tateyama. The viability of halotolerant and oligotrophic bacterial communities in the  
11 snow samples was evaluated with the amendment assay using culture media with different NaCl  
12 concentrations and different dilutions. The compositions of the bacterial species in the microbial  
13 cultures with culture-media amendment and in the genomic DNA of environmental snow  
14 samples were analyzed using denaturing gradient gel electrophoresis (DGGE) analysis of  
15 PCR-amplified bacterial 16S rRNA genes (16S rDNA).

16

## 17 **2. Materials and Methods**

18

### 19 **2.1 Sampling**

20

21 The snow samples were collected at Murododaira (36.57N, 137.60E; 2450 m, MR) on Mt.  
22 Tateyama (Fig. 1). A snow pit was dug, and the walls of the pit were carefully smoothed to leave  
23 the stratigraphy of the snow layer undisturbed. After the surface snow on the wall was removed

1 using a sterilized snow sampler (polycarbonate plates: 3 cm x 20 cm x 0.1 cm), the 10 mL of  
2 snow sample was collected from 10 cm depth from the surface of snow wall using a new  
3 sterilized snow sampler. The snow samples were obtained from the 2 layers including mineral  
4 particles at 558 cm and 540 cm from ground surface (2 samples of Layers A and B,  
5 respectively), and from the single layer without sand particles at 249 cm (1 sample of Layer C)  
6 as a negative-control sample. On the snow wall, the snow layers that showed remarkable  
7 colours, e.g., brown-yellow or dark brown were selected as the layers including mineral  
8 particles. The sampling layers were composed of compacted snow, indicating that the samples  
9 had not melted and, therefore, maintained the records on deposition of aerosol from the  
10 atmosphere. The snow samples were allowed to melt at room temperature in the laboratory.

11

## 12 2.2 Environmental factors

13

14 The snow samples were allowed to melt in a laboratory, and their chemical compositions  
15 (anions and cations) were measured using ion chromatography (HIC-SP: SHIMADZU, Kyoto,  
16 Japan) (Aoki and Watanabe 2009). The values of nns-Ca were calculated from the concentration  
17 ratio of  $\text{Na}^+$  to  $\text{Ca}^{2+}$ . The accuracy of the measured values was around 5%. The solutions of  
18 snow samples were also used for the following experiments.

19 The 500  $\mu\text{L}$  solution of snow samples was fixed with a paraformaldehyde solution at a  
20 final concentration of 1 %. The samples were stained with DAPI (4',6-diamino-2-phenylindole)  
21 at a final concentration of 0.5  $\mu\text{g mL}^{-1}$  for 15 min and filtrated through a 0.22  $\mu\text{m}$  pore-size  
22 polycarbonate filter (Millipore, Tokyo, Japan) stained with Sudan Black (Russell et al. 1974).  
23 After the filter was placed on a slide on top of a drop of low-fluorescence immersion oil, a drop

1 of oil was added and then covered with a cover slide. Slides were examined using an  
2 epifluorescence microscope (Olympus, Tokyo, Japan) with UV excitation system. A filter  
3 transect was scanned, and the particles on the filter transect, which could be discriminated into  
4 water-insoluble particles in two size categories (mineral particles sized  $<5\ \mu\text{m}$  and mineral  
5 particles sized  $>5\ \mu\text{m}$ ) and  $>5\ \mu\text{m}$  water-insoluble particles with microbial-particle attachment  
6 (microbial aggregates sized  $>5\ \mu\text{m}$ ), were counted.

7

### 8 2.3 Physiological experiments

9

10 To investigate the viability of halotolerant bacteria, 1 mL of the solution of snow samples  
11 collected from the 3 snow layers was inoculated to 19 mL of Trypticase Soy Broth  $10^0$  (TS $10^0$ )  
12 media and TS $10^{-1}$  media including NaCl at final concentrations of 0 %, 3 %, 10 %, and 15 %  
13 (w/v). The TS $10^{-1}$  medium was also prepared with a 10-time dilution of the TS $10^0$  medium. The  
14 tryptic-soy-broth (TS) medium was composed of 17 g trypticasepeptone, 5 g phytonepeptone,  
15 2.5 g  $\text{K}_2\text{PO}_4$ , and 2.5 g glucose in 1 L of pure water. A TS medium has been used for detecting  
16 and isolating bacteria from bioaerosol samples (Maki et al. 2008). After the microorganisms in  
17 the bioaerosol samples were cultivated in the media at 20 °C in the dark, the microbial growth  
18 was estimated using 550 nm absorbance every one or two days. After 13 days of incubation, 5  
19 mL of the microbial cultures was used for determining species diversity by PCR-DGGE analysis  
20 targeting bacterial 16S rDNA.

21

### 22 2.4 PCR-DGGE analysis of bacterial 16S rDNA

23

1 Five mL of the solution of snow samples collected from 3 layers and 1 mL of the microbial  
2 cultures with culture-media amendment were used for the extraction of genomic DNAs using  
3 SDS, proteinase K, and lysozyme as described previously (Maki et al. 2008). Furthermore, the  
4 genomic DNAs were purified by phenol-chloroform extraction, chloroform extraction, and  
5 ethanol precipitation. A 16S rDNA region (ca. 550 bp) of the extracted genomic DNAs was  
6 amplified by PCR using the following oligonucleotide primers for PCR-DGGE analysis:  
7 GC-341F, 5'- CGC CCG CCG CGC CCC GCG CCC GTC CCG CCG CCC CCG CCC GCC  
8 TAC GGG AGG CAG CAG-3'; and 907R, 5'-CCG TCA ATT CCT TT[A/G] AGT TT-3'  
9 (Muyzer et al. 1993). For each PCR reaction, 10 ng of the extracted DNAs was added to a PCR  
10 mastermix (20  $\mu$ L) containing 2  $\mu$ mol L<sup>-1</sup> of dNTPs (Takara, Ohtsu, Japan), 2 nmol L<sup>-1</sup> each of  
11 the primers, and 1U of Taq DNA polymerase (Takara, Ohtsu, Japan). Thermal cycling was  
12 performed using a Program Temp Control System PC-700 (ASTECC, Fukuoka, Japan) with a  
13 thermal cycling program. Amplification was verified by agarose gel electrophoresis (1.5 % w v<sup>-1</sup>  
14 agarose gel).

15 The DGGE analysis was performed with 6 % acrylamide gels containing a linear gradient  
16 of denaturant from 40 % to 60 % (100 % denaturant contained 7 mol L<sup>-1</sup> of urea and 40 % (v/v)  
17 formamide). Electrophoresis was carried out at 60 °C and 90 V for 16 h in a 1 x TAE buffer with  
18 an electrophoresis system (AE-6290; ATTA, Tokyo, Japan). After electrophoresis, the gels were  
19 stained with SYBR Gold and scanned in a Printgraph (AE-6933FXCF: ATTA, Tokyo, Japan).  
20 Several bands on the gels were excised for sequencing. The excised gel pieces were transferred  
21 to PCR tubes, and the PCR amplicons (ca.550bp) were purified by phenol-chloroform  
22 extraction and chloroform extraction followed by ethanol precipitation. The nucleotide  
23 sequences were determined using a Dye Deoxy<sup>TM</sup> Terminator Cycle Sequencing Kit (ABI, CA,

1 USA) and a DNA autosequencing system (Model 373A, ABI, CA, USA) according to the  
2 manufacturer's recommended protocol. Primer 341F without a GC clamp or primer 907R was  
3 used as the sequencing primer. The determined sequences were compared with a DDBJ (DNA  
4 Data Bank of Japan) database using the BLAST and FASTA SEARCH programs. A  
5 phylogenetic tree including all sequences was constructed according to the neighbor-joining  
6 algorithmic method using TreeViewPPC (Saitou and Nei 1987). The DDBJ accession numbers  
7 for the partial 16S rRNA gene sequences from TTd-1 to TTd-15 are from AB575959 to  
8 AB575963, and those from TTd-16 to TTd-25 are from AB600636 to AB600643.

9

### 10 **3 Results**

11

#### 12 **3.1 Snow layers**

13

14 The 3 layers on Mt. Tateyama where the samples were obtained were composed of compacted  
15 snow or solid-type depth hoar from which no melted water was detected. Therefore, these snow  
16 layers maintained their original chemical and isotopic compositions at the time of the snowfall.

17 The snow samples of Layers A and B included mineral particles sized  $<5.0 \mu\text{m}$  at particle  
18 densities of more than  $4.00 \times 10^6$  particles  $\text{m L}^{-1}$ , while the mineral particles sized  $<5.0 \mu\text{m}$  of  
19 Layer C decreased to low particle densities of approximately  $1.62 \times 10^4$  particles  $\text{mL}^{-1}$  (Table 1).

20 Furthermore, the mineral particles sized  $>5.0 \mu\text{m}$  were also included in the snow samples of  
21 Layers A and B at particle densities ranging from  $1.48 \times 10^5$  particles  $\text{mL}^{-1}$  to  $3.76 \times 10^5$   
22 particles  $\text{mL}^{-1}$ , and the particles sized  $>5.0 \mu\text{m}$  with microbial aggregates made up  
23 approximately 30 % of the total number of the particles sized  $>5.0 \mu\text{m}$ . In contrast, the large

1 mineral particles sized  $>5.0 \mu\text{m}$  were not observed in the snow samples of Layer C. These  
2 results indicate that the snow samples of Layers A and B included much higher quantities of  
3 mineral particles than those from Layer C (negative control).

4 The solutions of snow samples of Layers A and B contained Ca at significantly high  
5 concentrations of  $164 \mu\text{eq L}^{-1}$  and  $93.8 \mu\text{eq L}^{-1}$ , respectively, while the concentrations of Ca in  
6 Layer C were below the detection limit (Table 1). The 3 layers included  $\text{Na}^+$  at concentrations  
7 ranging from  $5.42 \mu\text{eq L}^{-1}$  to  $59.9 \mu\text{eq L}^{-1}$ . Most Na in the snow on Mt. Tateyama originates  
8 from sea salt. The contribution of sea salt  $\text{Ca}^{2+}$  to the total  $\text{Ca}^{2+}$  content was small (13 % on  
9 average). The solutions of snow samples of Layers A and B contained nns-Ca at high  
10 concentrations of  $161 \mu\text{eq L}^{-1}$  and  $57.6 \mu\text{eq L}^{-1}$ , respectively, while the concentrations of nns-Ca  
11 in Layer C were below the detection limit (Table 1). These results mean that the mineral  
12 particles in the snow layers specifically contained Ca which was tracer of KOSA mineral  
13 particles.

14

### 15 3.2 Physiological culture

16

17 The snow samples of Layers A and B including mineral particles showed microbial growth in  
18 the TS  $10^{-1}$  media containing 0 % NaCl and the TS  $10^0$  media containing 0 %, 3 % or 10 %  
19 NaCl within 13 days of incubation, while the snow sample of Layer C showed no microbial  
20 growth (Fig. 2). Moreover, none of the samples indicated growth in the media containing 15 %  
21 NaCl. In the TS  $10^{-1}$  media with 0 % NaCl, the microbial growth of snow samples of Layers A  
22 and B increased remarkably to more than 30 absorbance (approximately  $10^8 \text{ cells mL}^{-1}$ ) within  
23 the 4 days of incubation, while microbial growth in the TS  $10^{-1}$  media containing 3 %, 10 %, 10

1 and 15 % were not observed during the experimental period. In the TS 10<sup>0</sup> media containing  
2 0 % and 3 % NaCl, the microbial growth of the snow samples of Layers A and B rapidly  
3 increased within 4 days of incubation and fluctuated between 64 and 190 absorbance  
4 (approximately 10<sup>8</sup> - 10<sup>9</sup> cells mL<sup>-1</sup>) during the experimental period. The snow sample of Layer  
5 B in the TS10<sup>0</sup> media containing 10 % NaCl also showed microbial growth from the 6th day of  
6 incubation and maintained low values of absorbance of approximately 10 (approximately 10<sup>7</sup>  
7 cells mL<sup>-1</sup>) during the experimental period.

8

### 9 3.3 DGGE analysis of the bacterial communities

10

11 PCR products amplified from the genomic DNA were directly extracted from the snow samples  
12 of Layers A and B, while PCR amplification was not obtained from the snow sample of Layer C,  
13 suggesting that the microbial biomass in the snow sample of Layer C was undetectable for PCR  
14 amplification. The DGGE analysis using the genomic DNA directly extracted from the snow  
15 samples revealed that the banding patterns were composed of more than 7 bands on each lane  
16 and that the bacterial population structure of Layers A and B was different (Fig. 3). On the other  
17 hand, the DGGE banding patterns of the microbial cultures with culture-medium amendment  
18 showed 1 to 3 bands on each lane. Most single bands (TTd-1, 4, 7, 10, 11, 12, and 14) occurred  
19 in the microbial culture and the genomic DNA directly extracted from snow samples of Layers  
20 A and B, suggesting that the same bacterial species were included in the microbial culture of the  
21 2 snow layers. Two bands of TTd-8 and TTd-9 clearly appeared at each horizontal position in  
22 the microbial cultures with TS10<sup>-1</sup> medium amendment of Layer A, and the bands at the same  
23 horizontal position were detected from the genomic DNA directly extracted from the snow

1 samples of Layers A and B (TTd-2, 3, 5, and 6). The 2 other bands of TTd-13 and TTd-15 were  
2 specifically detected from the 10 % NaCl-amended cultures of Layer A and the 3 %  
3 NaCl-amended cultures of Layer B respectively. These results indicate that some bacterial  
4 species in the microbial cultures amended with the TS10<sup>-1</sup> medium or 3 % and 10 % NaCl were  
5 different among the snow samples of the 2 layers.

6 We excised and sequenced the 25 bands from the DGGE gel. Thirteen phlotypes were  
7 obtained after comparing the sequences with each other and with the bacterial 16S rDNA  
8 databases, and composed of the members of the phyla *Fusobacteria*, *Actinobacteria*, *Firmicutus*,  
9 and *Proteobacteria* and the Plastid DNA (Table 2). Among all 13 phlotypes, 5 phlotypes were  
10 detected from the microbial cultures. A single phlotype of the 5 phlotypes was composed of  
11 the sequences of major bands which were detected from the genomic DNA directly extracted  
12 from the snow samples and the microbial culture of the 2 snow layers (TTd-1, 4, 7, 10, 11, 12,  
13 and 14), supporting the suggestion that the KOSA particles of the 2 snow layers contained the  
14 same bacterial species. Sequences of this phlotype belonged to the *B. subtilis* group and were  
15 identical to those of the *Bacillus* sp. SAd series that was detected at an altitude of 600 m in Suzu  
16 City during KOSA event (Table 2, Fig. 4). Moreover, the 2 other phlotypes, TTd-13 and  
17 TTd-15, which were specific to the microbial cultures with 10% NaCl and 3% NaCl  
18 respectively, also belonged to the genus *Bacillus* and were related with *B. megaterium* and *B.*  
19 *pumilus*, respectively. Among the remaining 2 phlotypes, one phlotype containing TTd-2, -5,  
20 and -8 was included in the beta-proteobacterial division relating to other known bacteria with a  
21 low similarity of below 98 %, and the other phlotype of TTd-3, -6, and -9 was identical to  
22 *Propionibacterium acnes* with a high similarity of 100 %. These 2 phlotypes were specifically  
23 detected from the microbial culture amended with TS10<sup>-1</sup> media (low-nutrient media),



1 suggesting the viability of oligotrophic bacteria in the snow samples.

2 The remaining 8 phylotypes (from TTd-16 to 25) of all 13 phylotypes were detected only  
3 from the genomic DNA directly extracted from the snow samples, and composed of several  
4 microbial species (Table 2, Fig. 4). The phylum *Fusobacteria* group and the plastid DNA  
5 included the sequences of TTd-16 and TTd-22 respectively, and were detected only from the  
6 genomic DNA directly extracted from the snow samples. Furthermore, in the phylum  
7 *Actinobacteria*, the two phylotypes of TTd-20, 21, and 25 belonged to the genus  
8 *Corynebacterium* and the *Nocardioides* group. The 3 phylotypes of TTd-17, 18, 19, 23, and 24  
9 belonging to the beta-proteobacterial subdivision were related to the members of the genus  
10 *Neisseria*, the *Burkholderia* group, and the genus *Acidovorax*. These 8 phylotypes were not  
11 closely related to the other 5 phylotypes detected from the microbial cultures, suggesting that  
12 the some species of bacteria detected from the genomic DNA directly extracted from the snow  
13 samples disappeared in the microbial cultures.

#### 15 **4 Discussion**

16  
17 The KOSA mineral particles in the atmosphere were transported to Japan and accumulated in  
18 the snow cover on Mt. Tateyama from fall to spring (Osada et al. 2004; Aoki and Watanabe  
19 2009). The snow samples of Layers A and B included a significant quantity of mineral particles  
20 sized  $>5 \mu\text{m}$  at higher particle densities of more than  $15.0 \times 10^4$  particles  $\text{mL}^{-1}$  and showed high  
21 concentrations of nns-Ca (Table 1). In contrast, the mineral particles sized  $>5 \mu\text{m}$  and the  
22 nns-Ca in the snow samples of Layer C were below the detection limit. Highly alkaline Ca is a  
23 tracer of mineral dusts from desert and loess in China (Suzuki and Tsunogai 1993). In a previous

1 study, the chemical analysis of the composition of snow samples from Mt. Tateyama indicated  
2 the presence of preserved KOSA mineral particles (Osada et al. 2004). Presumably, the mineral  
3 particles of Layers A and B would be transported from Asian by KOSA events in the spring. The  
4 distribution of microorganisms in snow layers on Mt. Tateyama was of interest for identifying  
5 the bacterial species in the microbial communities associated with KOSA mineral particles.

6 The cell activities and growth of bacteria that survive in snow cover samples were  
7 facilitated using TS 10<sup>0</sup> and TS 10<sup>-1</sup> media containing NaCl concentrations ranging from 0 % to  
8 15 %. Among the samples in the 3 layers, those from Layers A and B included KOSA particles  
9 indicating microbial growth in the 0 %, 3 %, or 10 % NaCl media within 13 days of incubation,  
10 while the samples from Layer C included a few aerosol particles that showed no microbial  
11 growth in any medium (Fig. 2). The KOSA particles in Layers A and B are assumed to include  
12 bacterial cells that are tolerant to NaCl concentrations of up to 10 % and/or low-nutrient  
13 conditions. Bacterial populations which are tolerant to 10 % NaCl concentrations were also  
14 detected from bioaerosol samples collected at high altitudes in Dunhuang City (Maki et al.  
15 2008) and Suzu City (Maki et al. 2010). Since most KOSA particles reaching Japan were mixed  
16 with salt over the East Sea and contained NaCl (Zhang et al. 2006), the microorganisms  
17 attached to KOSA particles in the atmosphere are expected to tolerate high NaCl concentrations.  
18 Echigo et al. (2005) reported that similar members of halotolerant bacteria inhabit non-saline  
19 environments in an area surrounding Tokyo and indicated that they may have been introduced  
20 by KOSA events. Moreover, bacteria that do not form spores or cysts survive under strict  
21 environmental conditions through a series of starvation-survival responses such as a reduction  
22 in cell size (Morita 1990). Starvation-survival appears to be a widespread response, as the  
23 bacteria that inhabit many different aquatic and terrestrial environments have been demonstrated

1 to survive the absence of growth nutrients (Morita 1990). Some oligotrophic bacteria are also  
2 reported to produce a physical barrier to separate adjacent areas of surrounding environments  
3 (Blenkinsopp and Costerton 1991). Such barriers might minimize environmental damage after  
4 exposure to UV irradiance in the atmosphere. Presumably, the halotolerant and oligotrophic  
5 bacteria were associated with KOSA particles and maintained their viability in the atmosphere  
6 and snow cover.

7         The PCR-DGGE analysis using 16S rDNA revealed that the microbial communities in  
8 the snow samples were composed of several bacterial species (Fig. 3). The sequences of bands  
9 on the DGGE gel were classified to the 13 phlotypes, of which 5 were detected from the  
10 microbial cultures (Table 2, Fig. 4). In particular, the 3 phlotypes were detected from the  
11 microbial cultures amended with 0 %, 3 % or 10% NaCl and belonged to the genus *Bacillus* in  
12 the phylum *Firmicutus* (Fig. 4). *Bacillus* sp. is known to form endospores, which are resistant to  
13 environmental stress and enhance their survival in the atmosphere (Riesenman and Nicholson  
14 2000). They have been isolated from aerosol samples in various investigations worldwide as the  
15 most abundant genus (e.g., Prospero et al. 2005). In the *B. subtilis* group, a single phlotype  
16 detected from the major bands (TTd-1, 4, 7, 10, 11, 12, and 14) of both Layers A and B was  
17 closely related to the *Bacillus* sp. SAd series identified in aerosol collected from the atmosphere  
18 in the vicinity of Suzu City during KOSA event (Maki et al. 2010). Other phlotypes of TTd-13  
19 and TTd-15 were similar to the *Bacillus* sp. DAd-1 and -11 in the *B. subtilis* group were  
20 dominant in the atmosphere in the vicinity of Dunhuang City (Maki et al. 2008). Some strains of  
21 *B. subtilis* isolated from the aerosol in Higashi-Hiroshima City (KOSA arrival region) and the  
22 Gobi Desert (KOSA source region) had a similar genetic identity, which supports the hypothesis  
23 of KOSA transport and deposition (Hua et al. 2007). *B. subtilis* have been recovered in the

1 aerosol collected from the northern Caribbean during African dust events (Kellogg et al. 2004).  
2 Moreover, the dominate phylotype of the *B. subtilis* group (TTd-1, 4, 7, 10, 11, 12, and 14)  
3 were detected by means of a culture-amendment technique combined with the PCR-DGGE  
4 analysis (Fig. 4, Table 2). In the previous investigations, when the atmospheric microbial  
5 communities at high altitudes in Suzu City were investigated by the culture-amendment  
6 technique, the viable bacterial species with NaCl amendment were similar to the bacteria  
7 detected from the DNA directly extracted from the bioaerosol samples and the most of bacterial  
8 communities belonged to the genus *Bacillus* (Maki et al. 2010). The findings of this study  
9 support the possibility that the bacterial population of the *B. subtilis* group can maintain its  
10 viability during atmospheric dust transport and extend its habitat toward Mt. Tateyama by  
11 KOSA events.

12 The members of the *B. subtilis* group sometimes cause nosocomial bacteremia by  
13 adsorption of oral preparations containing the bacterial spores (Richard et al. 1988) and are  
14 considered to be a major, primary and potentially serious pathogen infecting clinical patients  
15 (e.g., Velasco et al. 1992). In contrast, the *B. subtilis* group included the antagonists suppressing  
16 pathogenic diseases of plants (Alabouvette et al. 1996) or organic-matter degraders that  
17 contribute to the carbon cycle in terrestrial environments (e.g., Das and Mukherjee 2007). In  
18 addition, some strain types of *B. subtilis* have been used for the production of Japanese health  
19 foods such as *natto* (Ashiuchi and Misono 2002). In fact, the isolates of *B. subtilis* obtained  
20 from the snow samples in this study were demonstrated to produce *natto* (data not shown).  
21 Therefore, the atmospheric transport of the *B. subtilis* group might have negative and positive  
22 influences on humans and environmental ecosystems.

23 Among other 2 phlotypes that were specifically detected from the 2 bands (TTd-8 and

1 -9) of microbial cultures amended with TS10<sup>-1</sup> media (low-nutrient media) of Layer A, one  
2 phylotype was closely related with *Propionibacterium acnes* in the phylum *Actinobacteria*, and  
3 the other phylotype belonged to the beta-proteobacterial subdivision (Fig. 4). The phylotype of  
4 TTd-7 and -10 of the *B. subtilis* group was also detected from the microbial culture amended  
5 with the low-nutrient medium. These bacterial communities of the 3 phylotypes belong to  
6 oligotrophic bacteria, which survive through starvation-survival responses. In particular, the  
7 relative bacterial clusters of the phylotypes of TTd-2, -5, and -8 included *Ultramicrobacteria*  
8 *hongkongensis* and *Pandoraea* sp., which had a diameter of 0.3 µm and were hardly detected  
9 from the environmental samples (Silbaq 2009). Ultramicrobacteria are able to penetrate deeply  
10 into a porous matrix such as sandstone rock (Blenkinsopp and Costerton 1991). The  
11 atmospheric mineral particles might have originated from sandstone rock including  
12 ultramicrobacterial cells from the desert. Furthermore, relative bacterial species such as  
13 *Propionibacterium acnes*, in addition to *B. subtilis*, have been identified in aerosol collected  
14 from the northern Caribbean during African dust events (Griffin et al. 2003; Kellog et al. 2004).  
15 In particular, *P. acnes* is known to survive aerosol transport and is often detected in advanced  
16 noma lesions of humans, causing gangrenous disease in oral cavities (Paster et al. 2002).  
17 Moreover, *P. acnes* in microcomedo contribute to the development of the inflammatory phase of  
18 acne (Eady et al. 2003). Presumably, bacterial communities that did not form spores are  
19 associated with KOSA mineral particles and survive in the atmosphere and snow cover.

20 The remaining 8 phylotypes (from TTd-16 to 25) were detected only from the genomic  
21 DNA directly extracted from the snow samples. The microbial structures of 8 phylotypes were  
22 different from the microbial structures in the amended cultures of the snow samples. The  
23 spectrum of cultured isolates is narrower than that of diverse bacterial lineages detected using

1 culture-independent cloning and sequencing of 16S rDNA directly collected from aerosol  
2 samples (e.g. Maron et al. 2005). In general, 90% to 99% of bacteria in natural environments  
3 could not be cultivated by traditional methods and that many are viable but unculturable (Olsen  
4 et al. 1987). Among the 8 phlotypes, the 5 phlotypes were related to the opportunistic  
5 pathogens such as *Corynebacteirum* species (Feurer et al. 2004), *Neisseria* species (Smith et al.  
6 1999), *Burholderia* species (Hayward et al. 1991) and *Leptorichia* species. (Collins et al. 2001).  
7 The relative bacteria of the 2 phlotypes of TTd-18, -19, and -24 were *Acidovorax* species  
8 (Willems et al. 1990) and *Burholderia* species (Castorena et al. 2006), of which some species  
9 were reported to degrade chemical compounds. The bioaerosols have the possibilities to  
10 implicate the human disease or the chemical-compound cycles in downwind ecosystems. The  
11 detection of plastid DNA of marine phytoplankton indicated that the seawater including  
12 phytoplankton would be mixed into the KOSA mineral particles in the atmospheric areas over  
13 the East Sea. The sequencing of 16S rDNA directly collected from snow samples would also  
14 provide the useful information about bioaerosols transported to Mt. Tateyama, although studies  
15 at the DNA level can not distinguished between viable microorganisms that cannot grow in  
16 culture media and nonviable microorganisms in the snow samples. The combination of the  
17 direct DNA extraction technique and the culture amendment technique is essential for clarifying  
18 the long-range transport of atmospheric bacteria by KOSA events.

19 This study demonstrates that KOSA particles in the snow cover of Mt. Tateyama are  
20 associated with viable halotolerant and oligotrophic bacteria. Halotolerant bacteria were found  
21 to be composed of members of the genus *Bacillus*, and the oligotrophic bacteria belonged to the  
22 genus *Bacillus*, the genus *Propionibacterium* and the beta-proteobacterial subdivision. The  
23 phlotypes of the *B. subtilis* group detected in this study were identical or similar to the

1 atmospheric bacteria collected at high altitudes in the regions of both the KOSA arrival (Suzu  
2 City) and source (Dunhuang City) (Maki et al. 2008, 2010). These results strongly support the  
3 possibility that the bacterial communities of the *B. subtilis* group are transported by the KOSA  
4 events. The sequencing of genetic DNA directly extracted from the snow samples suggested that  
5 the bioaerosol transported by KOSA events included unclturable microbial species, which were  
6 possibly related to opportunistic infection or chemical cycles in downwind ecosystems. The  
7 analytical data of the distribution of microorganisms in the snow layers on Mt. Tateyama have  
8 potential for use in bacterial transport research towards understanding the dynamics of  
9 atmospheric microbial communities during winter and spring, including KOSA events. However,  
10 the atmospheric data were insufficient to identify the accurate dates of KOSA events causing the  
11 accumulation of KOSA particles in the 2 snow layers. In the future, monitoring of the  
12 atmospheric aerosol dynamics in the vicinity of Mt. Tateyama from fall to spring will permit the  
13 identification of the origin of KOSA particles in each snow layer. Moreover, a comparison of the  
14 KOSA bioaerosols in snow cover with the microorganisms collected at high altitudes during the  
15 same KOSA event will clarify the long-range microbial transport from China to Japan by KOSA  
16 events.

17

## 18 **Acknowledgements**

19

20 We thank H. Honoki (Toyama Science Museum) and A. Takahashi (University of Toyama)  
21 for their chemical analysis using ion chromatography. This research was supported by a  
22 Grant-in-Aid for the Encouragement of Young Scientists (22681005) from the Ministry of

1 Education, Science, Sports, and Culture, Japan. The Global Environment Research Fund  
2 (C-091) provided by the Ministry of the Environment, Japan also supported this work.

3

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7

1 Figure Legends

2

3 Fig. 1 Map of Mt. Tateyama in Japan with a sampling site: Murododaira (2450 m, MR).

4

5 Fig. 2 Microbial growth of snow samples collected from Layers A (a, d), B (b, e) and C (c, f) in  
6  $TS10^{-1}$  (from a to c) and  $TS10^0$  (from d to f) media containing NaCl at concentrations of 0 %  
7 (square), 3 % (circle), 10 % (triangle) and 15 % (diamond). All experiments were performed in  
8 tree bottles.

9

10 Fig. 3 DGGE profile (band patterns) of amplified 16S rDNA from the genomic DNA directly  
11 extracted from snow samples of Layers A and B, and from the bacterial cultures of Layers A and  
12 B amended with  $TS10^0$  and  $TS10^{-1}$  media including 0, 3, and 10 % NaCl. A 40 % (upper side) to  
13 60 % (lower side) denaturing gradient was used.

14

15 Fig. 4 Phylogenetic tree including the partial sequences of 16S rDNA amplicons excised from  
16 the DGGE gel shown in Fig. 3. The tree was calculated from a dissimilarity matrix of ca. 342 bp  
17 (*Bacillus subtilis* numbering 455 to 786) alignment using a neighbor-joining algorithm. The  
18 accession number of each reference sequence is also given. Sample information (the microbial  
19 culture amended with  $TS10^0$  and  $TS 10^{-1}$  media including 0, 3 and 10 % NaCl or the genomic  
20 DNA directly extracted from the bioaerosol sample) is shown in parentheses. Bootstrap values  
21 larger than 50 % (after 1,000 resampling) are indicated on the branches.

22

Table 1. Concentrations of mineral particles and ions in the snow layers.

Layer	height	Concentrations of water insoluble particles ( $10^4$ particles/mL)			Concentrations of ions ( $\mu\text{eq L}^{-1}$ )		
		<5 $\mu\text{m}$	>5 $\mu\text{m}$	microbial aggregates (>5 $\mu\text{m}$ )	Na <sup>+</sup>	Ca <sup>2+</sup>	nss-Ca <sup>2+</sup>
A	558	418 $\pm$ 11	21.0 $\pm$ 6.2	3.98 $\pm$ 1.88	59.9	164	161
B	540	444 $\pm$ 15	29.2 $\pm$ 8.4	5.57 $\pm$ 2.32	37.9	93.8	92.1
C	249	1.62 $\pm$ 0.57	N.D*	N.D*	5.42	0	0

\* Particles were not detected under microscopic observation.



Table 2. Phylogenetic affiliation of sequences contained in the DGGE bands.

DGGE band No. <sup>*1</sup>	Sampling location <sup>*2</sup>	Sample condition <sup>*3</sup>	Length (bp)	Category	GenBank accession no.	Closest relative	Similarity (%) <sup>*4</sup>
TTd-1, 4, 7, 10, 11, 12, 14	A, B	TS10 <sup>-1</sup> and TS10 <sup>0</sup> media 0% and 3% NaCl	432	<i>Firmicutes</i>	AB575959	<i>Bacillus</i> sp. SAd serise	100
TTd-2, 5, 8	A, B	TS10 <sup>-1</sup> medium 0% NaCl direct extracted DNA	535	beta-proteobacteria	AB575960	<i>Ultramicrobacter hongkongensis</i>	97.3
TTd-3, 6, 9	A, B	TS10 <sup>-1</sup> medium 0% NaCl direct extracted DNA	449	<i>Actinobacteria</i>	AB575961	<i>Propionibacterium acnes</i>	100
TTd-13	A	TS10 <sup>0</sup> medium 10% NaCl	388	<i>Firmicutes</i>	AB575962	<i>B. pumilus</i>	100
TTd-15	B	TS10 <sup>0</sup> medium 3% NaCl	414	<i>Firmicutes</i>	AB575963	<i>Bacillus</i> sp. B8W22	100
TTd-16	A	direct extracted DNA	464	<i>Fusobacteria</i>	AB600636	<i>Leptotrichia goodfellowii</i>	94.9
TTd-17	A	direct extracted DNA	473	beta-proteobacteria	AB600637	<i>Lautropia</i> sp. TeTO	99.9
TTd-18	A	direct extracted DNA	431	beta-proteobacteria	AB600638	<i>Burkholderia</i> sp. IMP5G	96.4
TTd-19, 24	A, B	direct extracted DNA	511	beta-proteobacteria	AB600639	<i>Acidovorax</i> sp. 01xTSA28A	97.2
TTd-20	A	direct extracted DNA	500	<i>Actinobacteria</i>	AB600640	<i>Corynebacterium tuberculostearicum</i>	99.4
TTd-21, 25	A, B	direct extracted DNA	519	<i>Actinobacteria</i>	AB600641	Actinobacterium OR-82	100.0
TTd-22	B	direct extracted DNA	460	Plastid DNA	AB600642	<i>Chrysochromulina polylepis</i> chloroplast gene	98.7
TTd-23	B	direct extracted DNA	483	beta-proteobacteria	AB600643	<i>Neisseria sicca</i>	99.0

\*1 Numbers of the bands in Fig. 3 refer to the numbering of the TTd series.

\*2 Layer of snow cover.

\*3 Cultures cultivated with NaCl at concentrations of 0%, 3%, and 10%, and genomic DNA directly extracted from the bioaerosol samples.

\*4 Similarity value between each isolate and the closest relative in databases.

line figure

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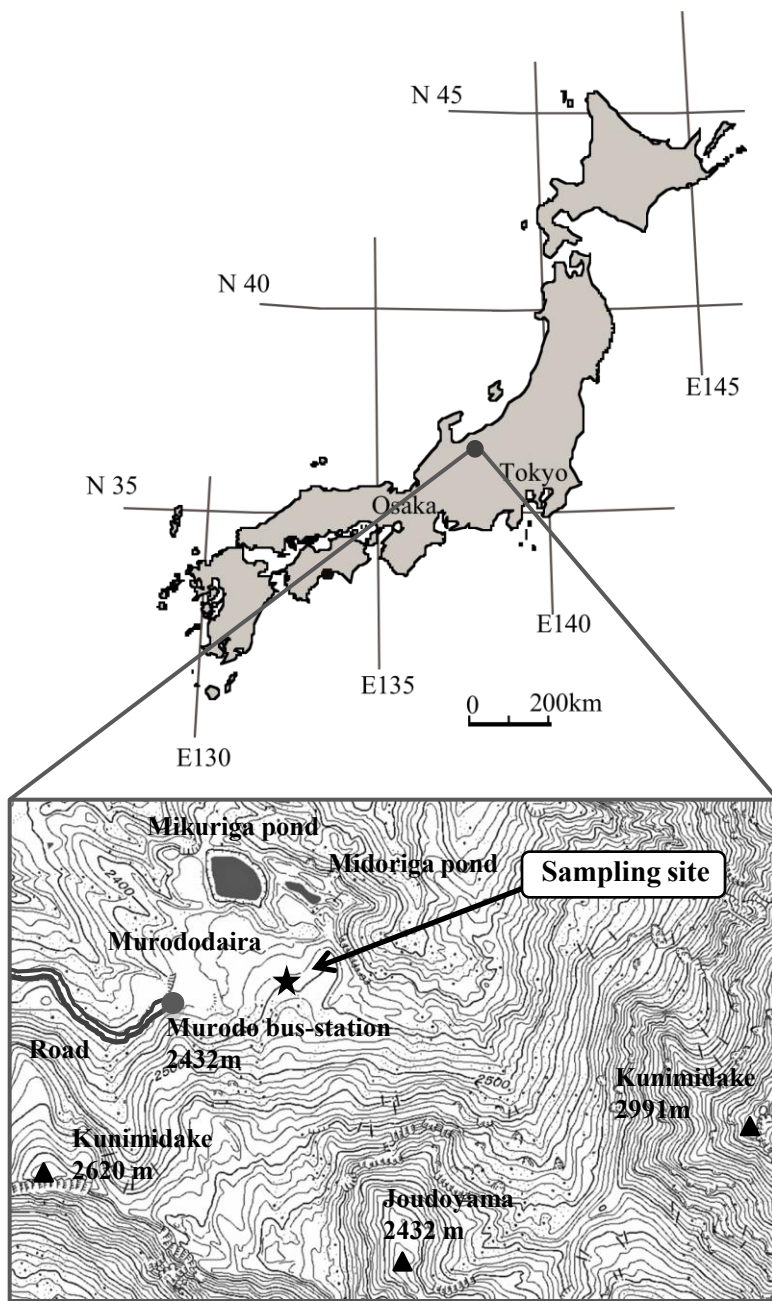


Fig. 1 T.Maki et al.

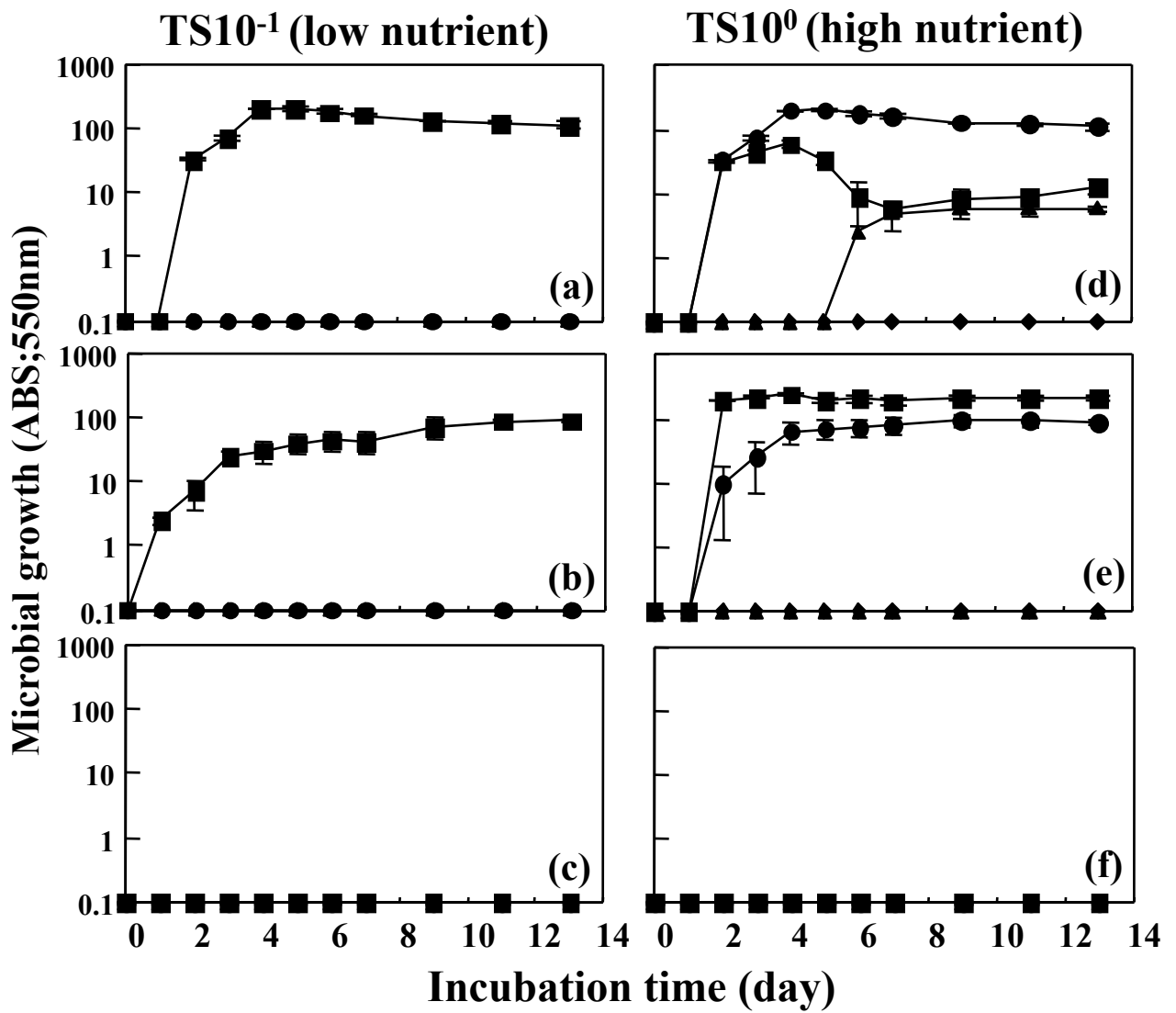


Fig. 2 T.Maki et al.

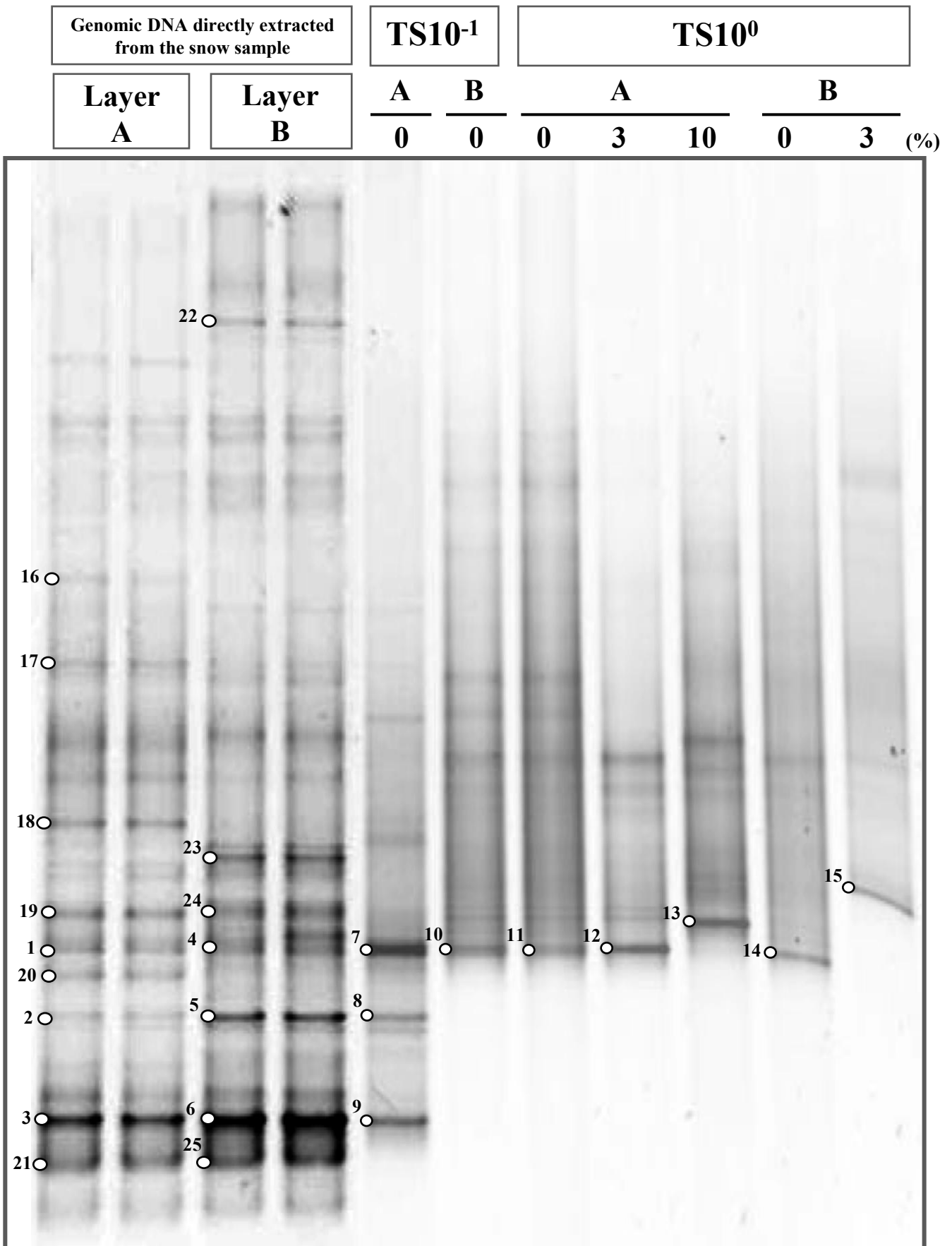


Fig. 3 T.Maki et al.

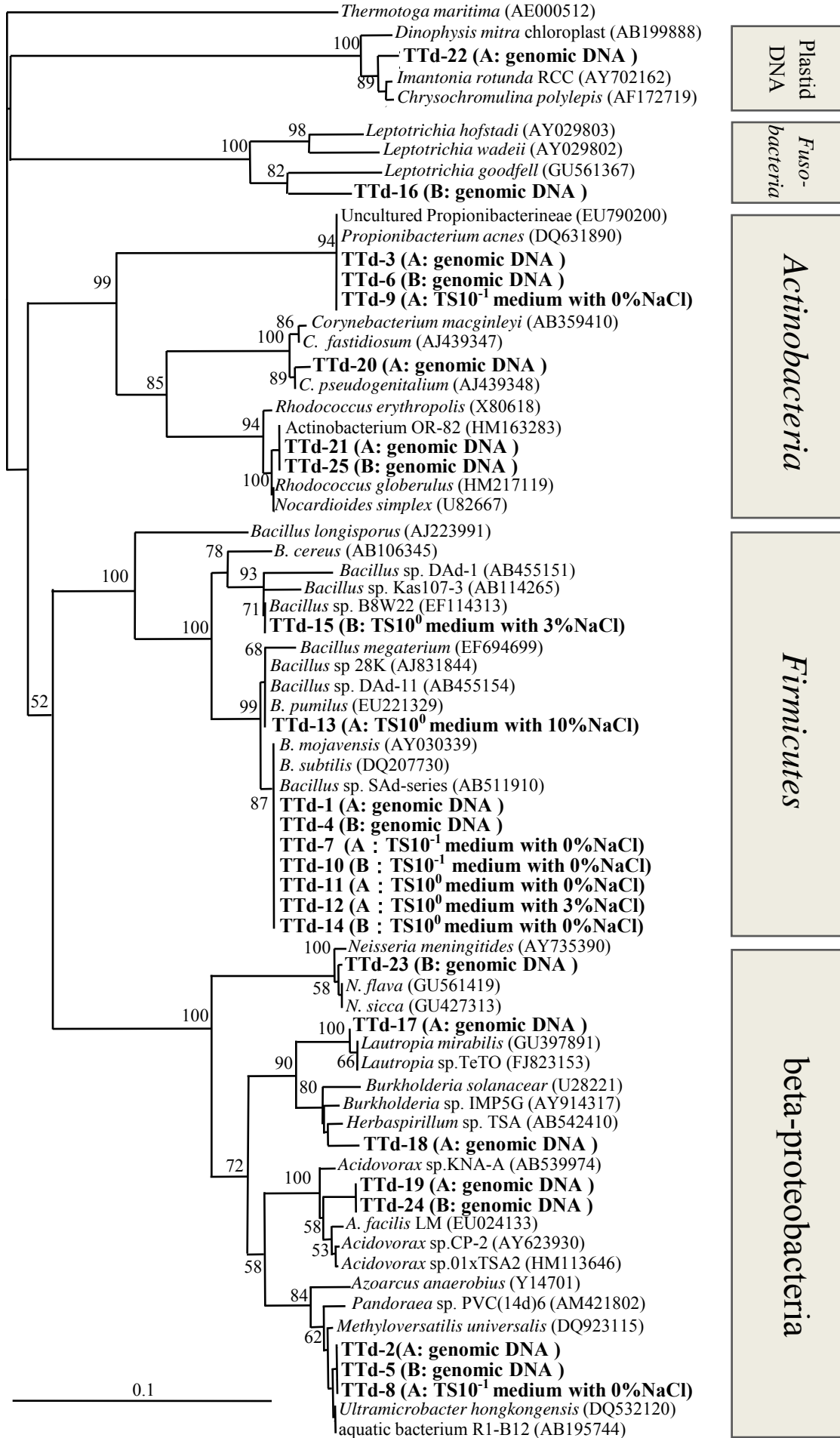


Fig. 3