DMSP degradation, the change of bacterial community structures and their growth response were investigated during incubations of natural seawater, after supplementing DMSP and other organic substrates in the Southern Ocean. Secondly, patterns of DMS emission and bacterial population dynamics are described during mesocosm bloom conditions of diatoms and coccolithophores.

**Methods**

**Southern ocean experiment**

Surface seawater was collected off the Lützow-Holm Bay, St. L12 (67.43S, 37.60E), and off Cape Danley, St. I-4 (66.39S, 64.48E), St. II-5 (67.06S, 68.06E), St. 23 (53.55S, 97.63E) during the cruise of R/V Umitaka-maru, from December 2007 to January 2008. After filtering the seawater with GF/F filters to remove phytoplankton, it was stored for a few days to reduce the ambient DMSP concentration, and then used for on-deck incubations supplemented with 100 nM each of DMSP, leucine and glucose. The concentrations of DMSP and DMS, and...
bacterial abundance, productivity and community structures were monitored up to 6–22 h. Also, bacterial community structures were compared by means of 16S rRNA gene PCR-DGGE analysis after extracting DNA from bacterial cells collected on membrane filters. The identities of actively-growing bacteria were determined by 16S rRNA gene sequences combined with bromodeoxyuridine (BrdU) labeling techniques (Hamasaki et al. 2007).

**Mesocosm experiment**

Seawater was collected in the Otsuchi Bay in June, 2010. The water was filtered through a 100-μm nylon mesh to remove large zooplankton, and received in four 200-L tanks. A half of the water was further filtered through a 10-μm-pore size filter to remove large phytoplankton. Inorganic nutrients (nitrate, phosphate, silicate) were added to each tank. Coccolithophorid algae, *Gephyrocapsa oceanica*, precultured in a laboratory condition were added to two of the four tanks as a seed population. Phytoplankton abundance, bacterial abundance, and DMSP and DMS concentrations were monitored for 11 days.
Results and Discussion

Southern ocean experiment

A decrease of the DMSP concentration was observed in all DMSP amended bottles at all stations (Figs. 1-1, 1-2, 1-3 and 1-4). Also a decrease of the DMSP concentration and subsequent DMS emission was observed in other bottles at high ambient DMSP stations. The ratio of DMS increase/DMSP reduction differed among sampling stations, implying variable activity and community structures of bacteria involving DMSP consumption and DMS emission. A significant reduction of DMS concentration observed in a control bottle, without DMSP addition at St. 1-4 might be due to DMS oxidation which can be another possible pathway of its loss process (Fig. 1-2).

Bacterial community structure analysis by PCR-DGGE showed that a change of organic matters input (DMSP, leucine, glucose) resulted in no difference in the bacterial community structures. DGGE banding patterns were compared among
different stations. Also, the bands including BrdU-labeled ones were excised and sequenced to identify the key species during the experiments (Table 1). The dominant band was identified as originating from bacteria closely related to \textit{Polaribacter irgensii}. Bacteria closely related to \textit{Pseudoalteromonas issachenkonii} appeared at St. L12 and I-4. Since significant amount of DMSP is transformed to DMS especially at the St. L12 and II-5, these bacteria are possible major mediators of DMSP consumption and DMS emission. Also, variable patterns of DMS emission, in spite of similar DGGE banding patterns, may be due to the contribution of minor bacteria missed by PCR-DGGE analysis, which should be clarified in future research.

\textit{Mesocosm experiment}

A rapid increase of chl-a concentration
Bacterial Activity in DMS Emission

A delayed emission of DMS after the peak of chl-a, and a subsequent increase of bacteria, suggested the importance of bacterial activity for determining the dynamics of DMS.

In the other two tanks, containing a seed population of coccolithophorids, the chl-a concentration started to increase at days 3 and 4, and kept increasing until the end of the experiment at day 10 (Figs. 2-2a and 2-2b). The chl-a concentrations caused by the growth of diatoms was observed in two nutrient-enriched tanks of natural seawater (Figs. 2-1a and 2-1b). Peaks of chl-a concentration were shown at days 4 and 5 (29 and 24 mg m$^{-3}$, respectively). Bacterial abundance started to increase after these chl-a peaks and reached a maximum at day 7 (1.6 \times 10^{7} and 1.2 \times 10^{7} cells m$^{-1}$, respectively). DMS concentration showed a significant increase after day 3 and peaks at day 9 (340 and 230 nM, respectively). A delayed emission of DMS after the peak of chl-a, and a subsequent increase of bacteria, suggested the importance of bacterial activity for determining the dynamics of DMS.

In the other two tanks, containing a seed population of coccolithophorids, the chl-a concentration started to increase at days 3 and 4, and kept increasing until the end of the experiment at day 10 (Figs. 2-2a and 2-2b). The chl-a concentrations
were 16 and 18 mg m\(^{-3}\) at the end. Bacterial abundance showed a decrease at first, reached minimum at the day 4 (40.4 \(\times 10^6\) and 0.5 \(\times 10^6\) cells ml\(^{-1}\)) and then increased during the latter half of the experiment. DMS concentration quickly increased at day 2, maintained a high concentration for several days, and then increased again at the end. The rapid increase of DMS may be caused by the degradation of DMSP contained in the seed culture of coccolithophorids added at the start of the experiment. DMSP accumulation, after the peak of DMS, corresponded to the decrease of bacterial abundance. Also, the decrease of DMSP and increase of DMS corresponded well to the increase of bacterial abundance. These results imply a close coupling between bacterial activity and DMS emission during the bloom of the phytoplankton.

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References
