

南極上空大気バイオエアロゾルのこれまでの観測結果と今後の展望

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Future prospects and previous observation results for atmospheric bioaerosols over the Antarctica

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Analyses of ice cores in the Antarctica have been used as a means to reconstruct past environments (Fujii and Motoyama, 2011). The ice cores from the Antarctica could preserve microorganisms from the ancient atmosphere, atmospheric bioaerosols, trapped in the snow and ice of the ice sheet (Segawa *et al.*, 2010). Microorganisms in the Antarctic ice cores could be useful to reconstruct past environments. Atmospheric bioaerosols, may consist of viruses, bacteria, fungi, pollen, plant fibers and are airborne particles that are biological in origin. The bioaerosol over the Antarctica is getting a lot of attention as meteorology, cloud physics, phylogeography, phylogeny, extremophile, environmental medicine, and so on.

Bioaerosols in the atmospheric boundary layer were observed at Syowa Station, Antarctica, during the 54th Japanese Antarctic Research Expedition (2012-2013). We carried out the sampling of bioaerosols using our bioaerosol sampler at C-heliport using a tethered balloon (from December 26, 2013, to January 10, 2014) and at container yard (from January 11 to January 21 and from February 2 to 8, 2014) in Syowa Station. Bioaerosols near to the ground were directly sampled beside the colony of Adélie penguins at the Hukuro Cove. We carried out the sampling using the bioaerosol sampler from 11:06 to 12:06 (LT) and from 16:18 to 17:18 (LT) on January 22, 2013 (Kobayashi *et al.*, 2016). We carried out the sampling using the bioaerosol sampler in the observation room at the top of the icebreaker Shirase. The sampling performed on the outward journey, from November 30 to December 15, 2012, and the return journey, from February 16 to March 16, 2013. The bioaerosols near to the ground were sampled by the bioaerosol sampler at the Yukidori Valley, the Langhovde Glacier from 9:00 to 10:00 and from 16:00 to 17:00 during January 25 and 31, 2013. DNAs were extracted from membrane filter sample and 16S rRNA gene was sequenced using the illumina-MiSeq platform. From these observation results, The 16S rDNA clone library from air over the Antarctica was dominated the class Bacilli, Chloroplast, Alpha-proteobacteria, Beta-proteobacteria, and Gamma-proteobacteria etc.

As future prospects, a focus will be affected the atmospheric bioaerosols over the inland Antarctic Continent. For the study on long-range transportations of microorganisms, it will be necessary to research of the atmospheric bioaerosol in katabatic wind on the inland Antarctic Continent. Furthermore, it will be important the investigation of deposition mechanism of atmospheric bioaerosols to ice because selections of microorganism species in ice core will be clarified. If the selected atmospheric bioaerosol deposited on the ice, it would be doubtful that microorganisms in the Antarctic ice cores could be reconstructed past environments exactly.

References

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