

## Study of the Bioaerosols on the Yukidori Valley, Langhovde, East Antarctic

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Recently, study of microorganism in the atmosphere (bioaerosol) has attracted much attention for many problems, such as trans-boundary of destructive fungus and environmental pollutants. However, study of the bioaerosol on Antarctic is not well-researched since it is difficult to execute the research. In this study, we investigated the bioaerosols on Antarctic for new possibilities and further development of various fields, such as ecology, meteorology, environment and atmospheric circulation, of Antarctic microorganism.

Bioaerosol samples on membrane filters were obtained by the 54<sup>th</sup> Japanese Antarctic Research Expedition (JARE54) on the Yukidori Valley (from 26 January 2013 to 30 January 2013), the hilltop (29 January 2013) and the end of Langhovde glacier (30 January 2013), East Antarctic. DNAs extracted from the bioaerosol samples were identified 16S rDNA of microorganism using Next Generation Sequencing Analysis. As a result, daily variation of family level Microbial diversity with regard to Yukidori Valley showed that microorganism changed, the reason for various meteorology factor, such as wind direction and weather (fig. 1). In case of the hilltop, microbial diversity was increased in family *Bacillaceae*, this microorganism is known as resistant to drying and also exist in the atmosphere. <sup>1)</sup> On the other hand, microbial diversity in the end of Langhovde glacier was decreased in family *Bacillaceae* and increased in class *beta-proteobacteria* and class *gamma-proteobacteria*. These results will be useful not only for monitoring an ecosystem of Antarctic, but also environment and atmospheric circulation of the Antarctic, and other ecosystem monitoring of the world. <sup>2)</sup> In additional, these results might indicate that there is a possible of long distance transport of bioaerosols by atmospheric circulation.

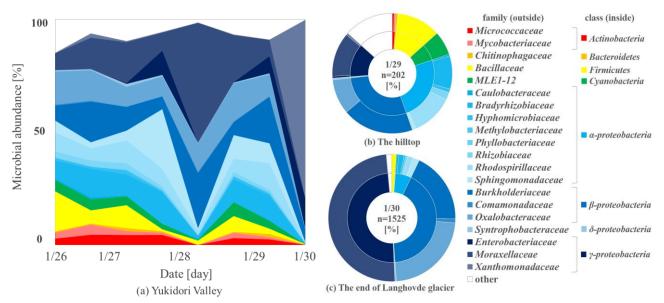


Fig. 1 Family level distribution of bioaerosol on (a) the Yukidori Valley, (b) the hilltop and (c) the end of Langhovde glacier

## References

- 1) Kobayashi, F., *et al.*, Study on Atmospheric Diffusion of Bioaerosols in a KOSA Source Region, Earozoru Kenkyu, 22 (3), 218-227, 2007.
- 2) Kanda H., *et al.*, Biological Studies on Ecosystems in the Yukidori Valley, Langhovde, East Antarctica, Antarctic Record, 34 (1), 76-93, 1990