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Identification of bioaerosols from environmental samples in the AIST, Tsukuba, Japan

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The bioaerosols are the atmosphere particles, mists or dust of μm range, associated with metabolically active or inactive viable particles. They contain living organism's included microorganisms such as viruses, bacteria, and fungi also plant material as well as pollen. Next Generation Sequencing (NGS) is a novel method of DNA sequencing that quickly and efficiently read the underlying sequence of an organism by means of massively parallel sequencing. The aim of this study is identifying organisms which contained in environmental samples by using NGS. This study monitored the environmental sample (bioaerosols) from November 2013 to January 2015 for 50 days using air samples were collected at AIST, Tsukuba, Japan. Samples were bio-analyzed using a next-generation sequencing method. In this study, we used two NGS platform, GS FLX+ (Roche 454 sequencing) and Illumina Misep. The sample was detected plants, eukaryotes and bacteria. The sample was divided into two subgroup subgroups according to the size of its bioaerosols, large subgroup contains bioaerosols whose diameter is bigger than 3.3μm, and small subgroup contains those smaller than 3.3μm.The most abundant bacteria in several samples were of the Actinobacteria (class), Alphaproteobacteria, Bacilli and Clostridia. For the animal detection using internal transcribed spacer 1, only uncultured fungi were detected in more than half of the hits, with a high number of Cladosporium sp. in the samples. For the plant identification, the ITS1 information only matched fungal species. However, targeting of the rbcL region revealed diverse plant information, such as *Medicago papillosa*. In conclusion, traces of bacteria, fungi, and plants could be detected in the bioaerosols, but not of animals using those primers.

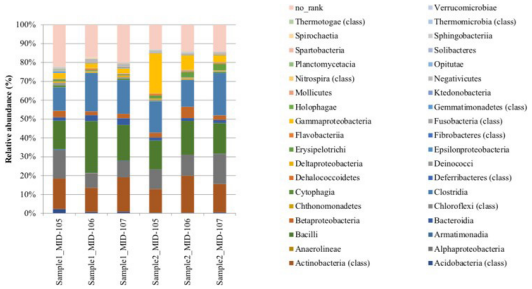

Fig. 1. Identification of bacterial 16S rDNA sequences in bioaerosols at the class level. Sample1: large-sized dust sample; Sample2: small-sized dust sample; MID-107: collection period from November 29, 2013 to December 14, 2013; MID-106: collection period from December 15, 2013 to December 26, 2013; and MID-105: collection period from December 26, 2013 to January 16, 2014.

Recent Publications

1. Choi, Jae-Hoon, Ayaka Kikuchi, Panyapon Pumkaeo, Hirofumi Hirai, Shinji Tokuyama and Hirokazu Kawagishi (2016) Bioconversion of AHX to AOH by resting cells of Burkholderia contaminans CH-1. Bioscience, Biotechnology and Biochemistry 80 (10):2045-2050.
2. Panyapon Pumkaeo. 2018. "Identification of Bacteria from bioaerosl at AIST, Tsukuba, Japan." Proceedings of International Symposium on Animal Production and Consevation for Sustainable Development 2018 UGSAS-GU & BWEL Joint Poster Session on Agricultureal and Basin Water Environmental Sciences 2018:P18.

Biography

Panyapon Pumkaeo has completed his Bachelor's degree from the Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand. Currently, he is pursuing his PhD at United Graduate School of Agricultural Science (UGSAS) in Gifu University, Japan. His research is about "Bioaerosol." He would like to analyze the bioaerosol sample that collected in the atmosphere by using the Next Generation Sequencing (NGS) to know the information of organism present in aerosol where they come from which impact in environment, to avoid bio-invasion. Also, he would like to apply the result from NGS data for developing the primers too easy for identifying the organism in Bioaerosol.

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