**S02-1**

**Succession of microbial ecosystem in fresh volcanic ash deposits on the island of Miyake (Miyake-jima), Japan, revealed by metagenomics**

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**Key word**: volcanic deposit, soil ecosystem, metagenomics, microbial succession

Miyake-jima represents a model ecosystem to examine the soil ecosystem development because of the availability of recent volcanic deposits. Our previous studies showed that chemolithotrophs were the early colonists on the volcanic deposits derived from the Miyake-jima eruption in 2000 and played a role in carbon and nitrogen accumulation in the deposits. In this study, we analyzed the microbial community structures of 3.5, 6.6, and 9.5-years old volcanic deposits after the 2000 eruption through metagenomics. Analyses of 16S rRNA genes derived from 454-pyrosequencing data showed the predominance of domain Bacteria and the absence or trace of Archaea in the deposits. Acidithiobacillus ferrooxidans and Leptospirillum ferroxidans were the dominant bacterial species in the younger deposit and changed over to Acidiphilobacter and Thiobacillus in the older deposits. With respect to nitrogen-fixing bacteria, nifH genes of Acidithiobacillus and Leptospirillum accounted for 42 and 41% of the total nifH, respectively, in the younger deposit, while heterotrophic bacterial sequences accounted for 41-46% in the older deposits. Further investigation is now in progress to provide the information about development of biogeochemical cycles during early ecosystem succession.

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**S02-2**

**Metagenomic and metatranscriptomic analyses of microbial communities in rice paddy soil**

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**Key word**: metagenome, metatranscriptome, paddy soil, denitrification

Rice is one of the important cereal crops in the world. More than 120 million ha of rice paddy fields are located worldwide, 90% of which is localized in Asia. Unlike upland soil, paddy field soil undergoes a drastic change of oxidized / reduced conditions during rice growing season caused by water management. The soil is under anoxic condition during drained periods. After waterlogging, it becomes anoxic and various anaerobic processes proceed sequentially. Response of soil microbial communities on such a changing soil condition is of great interest. We tried to reveal the structure of potential and active microbial communities in rice paddy soil through metagenomic and metatranscriptomic approaches. Two soil DNA samples (before and after waterlogging) and four soil RNA samples (before waterlogging, during waterlogged period 2 samples), and after drainage) were prepared. The GS-FLX pyrosequencing of soil DNA and RNA without any prior PCR amplification generated ca. 3 million sequences in total. Metagenomics and metatranscriptomics revealed detailed structures of microbial communities and functional genes in rice paddy soil. Moreover, we found novel diversity of functional gene sequences involved in denitrification. Based on the sequence information, we isolated and characterized the bacteria that might be a novel nitrous oxide reducer in paddy soil.