

## 学 位 論 文 要 旨

### Analysis of Microbial Communities on Recent Volcanic Deposits along a Vegetation Gradient in the Island of Miyake, Japan

植生発達段階の異なる三宅島新生火山灰堆積物における微生物群集の解析

環境資源共生科学専攻 環境保全学大講座

郭 永

New substrates derived from volcanic activities, such as lava, tephra, and volcanic ash, are habitats opening to invasion by microorganisms and the microbial immigration might drive the initial soil genesis and ecosystem formation. Prior to colonization by plants, the pioneer microbes were found to play a significant role in fixation of carbon and nitrogen from the atmosphere, resulting in the input of organic matter to the deposits. Plant colonizers might influence the early microbial community on the new deposits through litter input, root exudates, and dead root tissues. Reciprocally, specific microbes can associate with plants through the root-microbe symbiosis or give a negative effect on plants by microbial interfering actions. Such plant-microbe interaction will accelerate a primary ecosystem succession on the volcanic deposits.

The Island of Miyake (Miyake-jima) is a volcanic island situated on the western rim of Pacific Ocean. The last eruption of Miyake-jima Island from the Mount Oyama in 2000 ejected large amounts of volcanic ash and formed a collapsed crater. About 60% of vegetation on the island was initially influenced by heavy deposition of volcanic ash. After the crater formation, large amount of volcanic gas containing SO<sub>2</sub> and H<sub>2</sub>O have been emitted and caused widespread defoliation, particularly on the leeward side of Mount Oyama. Vegetation has been recovering from the damage at the foothill of mountain and windward sides. The purpose of this study was to characterize the microbial communities on the Miyake-jima volcanic deposits at a windward side where vegetation recovery gradually occurred, and to analyze how the early microbial community responds to the first colonizer plants. To this end, we established three sites along an elevational transect, representing sparsely grass-covered (site IG7), fully grass- and partially shrub-covered (site IG8), and fully grass- and shrub-covered lands (site IG9). The volcanic deposits (C1) and the buried soils (2A) beneath them at each site were sampled in July, 2009 and September, 2011. The investigation was designed to compare bacterial and fungal communities between these deposits by molecular approaches using the T-RFLP, clone library, and PCR-based pyrosequencing methods, as

well as conventional measurements of population density, respiratory activity and substrate utilization profile.

The results showed that all samples of the deposits and the buried soils were acidic [pH (H<sub>2</sub>O), 4.2-4.7], and the deposit samples contained trace of total organic carbon (TOC, 0.2-0.7 g kg<sup>-1</sup>) and total nitrogen (TN, 0.1-0.9 g kg<sup>-1</sup>), which were significantly lower than those in buried soil samples (TOC, 48.9-100.1 g kg<sup>-1</sup>; TN, 4.2-8.3 g kg<sup>-1</sup>). Although the deposit samples contained approx. 100 times low TOC than the buried soil samples, differences in bacterial population density were not as large as the differences in TOC values. Total direct counts (TDC) and plate counts of culturable bacteria of the volcanic deposit sample were range in 1.0-4.0×10<sup>8</sup> cells g<sup>-1</sup> (dry soil) and 0.1-1.2×10<sup>7</sup> CFUs g<sup>-1</sup> (dry soil), respectively. However, no detectable amount of ergosterol and low counts of fungal propagules for the volcanic deposits and buried soil samples indicated that fungi constituted low fractions of their microbial community. Despite the differences in the vegetation cover, the volcanic deposit samples displayed low among-site variation for chemical properties (pH, TOC, and TN) and microbial population densities (TDC and culturable counts).

Statistical analyses of T-RFLP, clone library, and pyrosequencing data reveal that the microbial communities of volcanic deposit samples were phylogenetically diverse, in spite of very low-carbon environmental conditions, and their diversity was comparable to that in the buried soil samples. Comparing with the microbial communities in buried soils, the volcanic deposit communities were characterized by the presence of *Betaproteobacteria* and *Gammaproteobacteria* as the main bacterial classes, *Deinococcus-Thermus* as the minor bacterial phylum, and Ascomycota as the major fungal phylum. Because the volcanic deposit samples display low among-site variation for chemical properties, there is no apparent factor other than the aboveground vegetation cover to explain difference in microbial community among the different site volcanic deposits. Multivariate analysis revealed that a positive correlation of *Oxalobacteraceae*, *Gallionellaceae*, and *Micrococcaceae* with a grass *Carex oshimensis* but a negative correlation of *Xanthobacteraceae* and *Gemmatimonadaceae* with the grass. The presence of *Sphingobacteriaceae*, *Burkholderiaceae*, and *Acetobacteraceae* correlated positively with a tree, *Camellia japonica*. Fungi thriving in the site IG7 volcanic deposits, such as Sordariomycetes, Saccharomycetes, Pezizomycetes, and Lecanoromycetes in the phylum Ascomycota, and Dacrymycetes in the phylum Basidiomycota showed a highly negative relationship with the major plants, *Miscanthus condensatus* and *Alnus sieboldiana*. Agaricomycetes in the phylum Basidiomycota correlated positively but Eurotiomycetes in the phylum Ascomycota negatively with a shrub, *Rubus trifidus*. These results, therefore, suggested that the aboveground vegetation feature significantly influenced the early microbial communities on Miyake-jima volcanic deposits, but their influence on the microbial population was not distinct. In conclusion, these findings give a better understanding of how belowground microbial communities develop and interact with the establishment of the first aboveground plants in newly exposed volcanic deposits.