

富士山火山荒原における一次遷移に伴う土壌微生物群集の変化 Successional changes in vegetation and soil microbial community in a volcanic desert on Mount Fuji, Japan

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Lava flows and ash deposits from volcanic eruptions create virgin land surfaces on which ecosystem development processes such as plant colonization and soil formation begin. Such areas affected by volcanic activity are referred to as "volcanic deserts". Volcanic deserts are nutrient-poor ecosystems, and therefore the soil microorganisms function as drivers of carbon and nutrient cycles and soil formation through their role in the decomposition of soil organic matter, and their roles as sources of, and sinks for, labile carbon and nutrients are of great importance. This suggests that successional changes in the microbial community will greatly affect soil C and N pools and cycling in volcanic deserts.

In subalpine volcanic deserts such as those in Japan, we can find isolated island-like plant communities at different developmental stages. The presence of these island-like communities at different successional stages in a small area with the same altitudinal location and initial conditions therefore provides a good opportunity to investigate successional changes in the plant community, soil characteristics, and soil microbial community after a volcanic eruption. However, there is little information about the relationships between the shifts in microbial properties and the development of island-like communities.

In this study, to study the relationship between vegetation development and changes in the soil microbial community during primary succession in a volcanic desert, we examined successional changes in microbial respiration, biomass, and community structure in a volcanic desert on Mount Fuji, Japan.

The study was conducted on the southeastern slope of Mount Fuji between 1500 and 1550 m above sea level. Soil samples were collected from six successional stages, including isolated island-like plant communities. We measured microbial respiration in our laboratory and performed community-level physiological profile (CLPP) analysis, phospholipid fatty acid (PLFA) analysis, and denaturing gradient gel electrophoresis (DGGE) analysis of 16S rDNA amplified by polymerase chain reaction (PCR) to determine the microbial community composition from functional, taxonomic, and genetic perspectives, respectively. Combining these methods should provide a better understanding of soil microbial communities from multiple (functional, taxonomic, and genetic) perspectives.

Microbial biomass (total PLFA content) increased during plant succession and was positively correlated with soil properties including soil water and soil organic matter (SOM) contents. The microbial respiration rate per unit biomass decreased during succession. Nonmetric multidimensional scaling based on the PLFA, DGGE, and CLPP analyses showed a substantial shift in microbial community structure as a result of initial colonization by the pioneer herb *Polygonum cuspidatum* and subsequent colonization by *Larix kaempferi* into central areas of island-like communities. These shifts in microbial community structure probably reflect differences in SOM quality.

Microbial succession in the volcanic desert of Mt. Fuji was initially strongly affected by colonization of the pioneer herbaceous plant (*P. cuspidatum*) associated with substantial changes in the soil environment. Subsequent changes in vegetation, including the invasion of shrubs such as *L. kaempferi*, also affected the microbial community structure.

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