

論文の内容の要旨

森林科学 専攻
平成 28 年度博士課程 入学
氏 名 執行 宣彦
指導教員 平尾 聡秀

論文題目 Spatio-temporal variability of soil microbial communities and their identity for litter decomposition in cool-temperate montane forests

(冷温帯林の土壌微生物群集の時空間変動性と落葉分解に対する固有性)

Microbial ecologists have long sought to understand what factors govern soil fungal and bacterial communities. Climate and soil conditions have been regarded as the main factors determining soil microbial communities. However, based on a number of observations that plant community structures also drive forest ecosystems, plant-soil linkages may affect soil fungal and bacterial communities. The interactions between plants and soil microbial communities show a direct pathway through plant roots and indirect pathway through soil food webs. Although the direct pathway has strong specificity, idiosyncratic relationships between soil microbial communities and plants are not fully clarified in the indirect pathway.

In forest ecosystems, one idiosyncratic relationship that is particularly relevant for litter decomposition has been identified as home-field advantage (HFA). Namely, soil microbial communities may become specialized in breaking down litter that they are associated with, resulting litter decomposing more rapidly in its ‘home’ environment than in an ‘away’ environment. Clarifying the mechanism of HFA can fully explain variations

of litter decomposition and solve the problem of biogeochemical models. However, it is not clear how these idiosyncratic microbial communities are positioned in the whole community and how it responds to environmental changes.

This thesis aims to verify how soil microbial communities exhibit spatio-temporal variability and identity to litter decomposition. Chapter two clarifies the importance of relationships between plant communities and soil properties along elevational gradients. The following chapters also focus on two major spatio-temporal scales where aboveground ecosystem components mainly influence soil microbial communities. The first is elevational change, which is covered in chapter three. The second is seasonal change, which is handled in chapter four. Chapter five deals with the relationships between HFA for litter decomposition and soil microbial identity. This thesis consists of the general introduction (Chapter 1), four chapters presenting the main research of the doctoral thesis (Chapters 2-5), and the general discussion of the key findings (Chapter 6).

Chapter two examined the direct and indirect roles of environmental factors in forming elevational diversity gradients (EDGs) of forest understory vegetation. EDGs of vegetation can be shaped by the evolutionary histories of plants as well as by ecological factors. However, few studies of EDGs have focused on the roles of phylogenetic constraints and the associations with complicated interactions among environmental factors. In this research, taxonomic and phylogenetic diversities of tree seedlings increased monotonically with elevation, and the same pattern was found for the taxonomic diversity of herbs. Structural equation modeling indicated that both the taxonomic and phylogenetic diversity of tree seedlings were most associated with soil properties, although the phylogenetic diversity of herbs was related to light conditions. These results highlight the importance of environmental filtering by soil properties in shaping EDGs of tree seedlings. This research implies that phylogenetic constraints in adaptation to soil properties should be considered when predicting changes in EDGs under environmental fluctuations.

Chapter three examined how plant functional diversity, soil properties and soil temperature affect EDGs of soil bacteria and fungi at different soil depths. Elevational gradients also represent model systems for understanding the relationships between soil microbial communities and environmental factors, but the multiple influences of plant-soil linkages and the climate on EDGs of soil microbes have never been explored. In this

research, the diversity of bacteria decreased with elevation in surface soils but showed no relationship with elevation in deep soils. Structural equation modeling showed that soil bacterial diversity across elevational gradients was directly affected by plant functional diversity, especially where leaf C:N ratio diversity had stronger effects than soil properties. Chapter three found that EDGs of soil bacteria as a consequence of the total effect of elevation were determined by the degree of negative indirect effects of soil temperature, via plant functional diversity and soil properties, against a positive direct effect of soil temperature on bacterial diversity. These findings demonstrate that community assembly of soil microbes is causally linked with the climate, plant functional diversity and soil properties, which determine EDGs.

Chapter four aimed to evaluate the importance of seasonality, elevation, and soil depth in determining soil fungal and bacterial communities, given the influence of climate conditions, soil properties, and plant traits. Both aboveground and belowground properties operate over seasonal timescale in forest ecosystems at the mid-to-high latitude, but the seasonality of soil fungal and bacterial communities in this area has not been fully understood. Seasonal diversity and abundance patterns did not match between fungi and bacteria, where the peak of fungal diversity and bacterial abundance was observed in April, but those of bacterial diversity occurred in January. Model-based clustering found taxonomic groups associating carbon and biogeographical cycles that were paralleled with seasonality, implying that they are indispensable taxa driving ecosystem processes in temperate forests. Furthermore, bacterial communities were profoundly explained by both spatial and seasonal changes in soil water contents, while many taxonomic groups of soil fungi were related to plant traits along elevational gradients. These findings suggest that the contribution of the seasonal variability of climate conditions, soil properties, and plant traits are equal to or greater than those of spatial changes for microbial communities in forest soils at mid-to-high latitudes.

Chapter five aimed to understand the relationships between HFA for litter decomposition and soil microbial communities. Given the “community-by-environment” interaction in microbial ecology, it is assumed that both soil and climate affinity strongly influenced litter decomposition, but this hypothesis was not supported. Rather, HFA effects of litter decomposition highly depended on the source soil via fungal and bacterial identity. Although a home-climate advantage for litter was significant in the early stage of decomposition, it was not a strong limiting factor as compared with a soil advantage.

These suggest that litter decomposition in temperate forests was explained by microbial communities that are not functionally redundant, but these relationships may have the robustness to climate change. As mentioned in chapter one, HFA for litter decomposition plays an essential role in understanding overall decomposition processes that have implications for global climate and biogeochemical models. These findings contribute to an understanding of the impacts of global climate changes on belowground ecosystem processes and the role of microbial communities in biogeochemical cycles of forest ecosystems. Chapter five also implies that ignoring home-soil advantages for litter decomposition could lead to misinform biogeochemical models and potential cascading consequences for forest management.

Chapter six recaptures and discusses the results obtained in the main researches of the doctoral thesis (Chapters 2-5) and combines these findings. This thesis found that: (1) plant-soil linkages were significant along elevational gradients in cool-temperate montane forests; (2) Community assembly of soil fungi and bacteria was linked with the climate, plant traits, and soil properties, which determine elevational and seasonal diversity patterns; (3) Identity of soil microbial communities for litter decomposition has the robustness to climate change. The findings of the doctoral thesis highlight that soil microbial communities have spatio-temporal variability in response to environmental changes, but their identity for litter decomposition has the robustness to environmental perturbations, which explained by plant-soil linkages in forest ecosystems. The further elucidation of the linkages between microbial identity and forest ecosystem functionings may simplify an understanding of the manner how plant-soil linkages shape ecosystem processes.