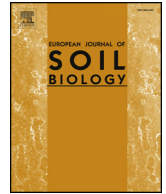




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Spatial heterogeneity of microbial community and enzyme activities in a broad-leaved Korean pine mixed forest

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ABSTRACT

Soil microbial communities support a great belowground biodiversity, but our knowledge regarding their spatial patterns and underlying driving mechanisms in small scale is very limited, especially for forest ecosystems. The spatial distributions of microbial community and enzyme activities depending on soil environmental factors were studied using geostatistical tools. 55 soil samples were collected across a 30 m × 40 m plot in a broad-leaved Korean pine mixed forest in the Changbai Mountains. Abundances of total and bacterial PLFAs had stronger spatial dependence than fungal PLFAs. Gram-positive bacteria had stronger spatial dependence than Gram-negative bacteria, suggesting that Gram-negative bacteria are more susceptible to stochastic factors. The proportions of structural variance for the activities of β -1,4-glucosidase (β G), β -1,4-N-acetylglucosaminidase (NAG) and acid phosphatase (AP) were 0.997, 0.519 and 0.966, respectively, suggesting that β G and AP had high spatial dependence. Cross-variogram analysis showed that root biomass played a critical role in structuring the spatial distributions of total and bacterial PLFAs. Fungi had close spatial connection with total nitrogen (TN), particulate organic carbon and root biomass within the ranges of 8.2–13 m. The β G, NAG and AP activities were closely spatially connected to the soil organic carbon and TN and were all spatially correlated with fungal abundance. Overall, microbial community and enzyme activities were patchily distributed at small spatial scales. Close spatial connections between microbial communities, enzyme activities, and root biomass and soil variables help to understand the main drivers of belowground soil biodiversity in the forest.

1. Introduction

Soil microorganisms play critical roles in biogeochemical processes, such as soil carbon and nitrogen cycling [1–3] and litter decomposition [4]. Patterns of soil microorganisms are strongly connected to the patchy or heterogeneous nature of the soil that occurs at various spatial scales [5]. Therefore, a better understanding of the spatial patterns of microbial community and their driving factors is necessary for understanding the microbial effects on soil biogeochemistry and ecosystem functions.

Spatial scales within individual studies play an important role in understanding microbial distribution [6]. Soil microorganisms follow clear biogeographic trends across a wide variety of landscapes or across

a broad range of spatial scales [7–9]. However, the majority of these studies compared samples at regional or continental scales which reflect substantial variability in environmental conditions, and studies have largely neglected the small spatial scale (e.g. < 10 m) variability among soil microorganisms. A major research topic therefore involves identifying the distances at which the patterns in microbial community structure and activities are manifested, particularly the minimum spatial scales at which spatial patterns can be detected [10]. The spatial autocorrelation of the enzyme activities and microbial biomass was demonstrated to occur at similar scales, typically in the range of tens of centimeters, in *Quercus petraea* forest topsoil [11]. Similarly, a high level of spatial heterogeneity was found in bacterial and fungal abundances and enzymatic activities in temperate mountain forest topsoil at

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