



Small-scale spatial variability of soil microbial community composition and functional diversity in a mixed forest

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Patterns in the spatial distribution of organisms provide important information about mechanisms that regulate the diversity and complexity of soil ecosystems. Therefore, information on spatial distribution of microbial community composition and functional diversity is urgently necessary. The spatial variability on a 26×36 m plot and vertical distribution (0-10 cm and 10-20 cm) of soil microbial community composition and functional diversity were studied in a natural broad-leaved Korean pine (*Pinus koraiensis*) mixed forest soil in Changbai Mountain. The phospholipid fatty acid (PLFA) pattern was used to characterize the soil microbial community composition and was compared with the community substrate utilization pattern using Biolog. Bacterial biomass dominated and showed higher variability than fungal biomass at all scales examined. The microbial biomass decreased with soil depths increased and showed less variability in lower 10-20 cm soil layer. The Shannon-Weaver index value for microbial functional diversity showed higher variability in upper 0-10 cm than lower 10-20 cm soil layer. Carbohydrates, carboxylic acids, polymers and amino acids are the main carbon sources possessing higher utilization efficiency or utilization intensity. At the same time, the four carbon source types contributed to the differentiation of soil microbial communities. This study suggests the higher diversity and complexity for this mix forest ecosystem. To determine the driving factors that affect this spatial variability of microorganism is the next step for our study.