



The elevational pattern of microbial community and enzyme activity along the northern slope of Changbai Mountain

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we present a comprehensive analysis of soil microbial community structure, enzyme activities and their role in soil organic matter mineralization along six elevations representing five typical vegetation types from forest to alpine tundra in Changbai Mountain, China. The results showed that the microbial PLFAs presented hump-shaped patterns along the elevation with the total microbial PLFAs highest in Ermans birch forest soil. The fungi to bacteria and gram positive to negative bacteria ratios increased along the elevation with the lowest values in Broad leaved forest and Dark-coniferous spruce-fir forest soil, respectively. The soil microbial community structures showed a biogeography distribution pattern in vertical direction with microbial community structures in Broad leaved forest and Mixed coniferous broad leaved forest different from other four sites. The soil enzyme activities in Broad leaved forest and Mixed coniferous broad leaved forest were significantly higher than in other four elevations. Principal component analysis (PCA) revealed substantial differences in soil microbial community composition among study sites, appeared to be driven primarily by MAT, MAP, soil temperature and content of silt & clay on the first principal component (PC1) which accounted for 87.1 % of the total sample variance. However, soil nutrients mainly responsible for the variation of soil enzyme activities. The soil organic matter mineralization rates tended to be highest in Ermans birch forest site and lowest in Dark-coniferous spruce-fir forest site and showed positive relationship with total microbial, bacterial and actinomycetes PLFAs. These findings could be used to facilitate interpretation of soil microbial community and ecological function in latitude forests ecosystem especially in volcanic forest ecosystem.