

Effects of changes in microbial activities on the decomposition processes of fine roots

Tonghua Li^{2,3} and Xuefeng Li^{1,2}

¹Chinese Academy of Sciences, China

²Northeast Forestry University, China

³Heilongjiang Vocational College of Biology Science and Technology, China

The relationships between soil microbial properties and fine-root decomposition processes under elevated CO₂ are poorly understood. To address this question, we determined soil microbial biomass carbon (SMB-C) and nitrogen (SMB-N), enzymes related to soil carbon (C) and nitrogen (N) cycling, the abundance of cultivable N-fixing bacteria and cellulolytic fungi, fine root organic matter, lignin and holocellulose decomposition, and N mineralization for two years in a oak (*Quercus mongolica* Fischer ex Ledebour) ecosystem in northeastern China. The experiment consisted of three treatments: elevated CO₂ chambers, ambient CO₂ chambers, and chamberless plots. Fine roots had significantly greater organic matter decomposition rates under elevated CO₂. This corresponded with significantly greater SMB-C. Changes in the activities of protease and phenol oxidase under elevated CO₂ could not explain the changes in fine root N release and lignin decomposition rates, respectively, while holocellulose decomposition rate had the same response to experimental treatments as did cellulase activity. Changes in cultivable N-fixing bacterial and cellulolytic fungal abundances in response to experimental treatments were identical to those of N mineralization and lignin decomposition rates, respectively, suggesting that the two indices were closely related to fine root N mineralization and lignin decomposition. Our results showed that the increased fine root organic matter, lignin and holocellulose decomposition, and N mineralization rates under elevated CO₂ could be explained by shifts in SMB-C and the abundance of cellulolytic fungi and N-fixing bacteria. Enzyme activities are not reliable for the assessment of fine root decomposition and more attention should be given to the measurement of specific bacterial and fungal communities.