



Effects of elevated CO₂ on a temperate forest soil ecosystem

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Increasing atmospheric CO₂ concentrations might indirectly influence soil ecosystem by stimulating plant photosynthesis, belowground allocation of carbon and root exudation. The changed structure and/or function of soil ecosystem are thought to modify the mineralization of organic matter and nutrient transformations, which potentially result in positive or negative feedback to CO₂ enrichment. Microorganisms play a key role in the response of soil ecosystems to the rising pCO₂ as they mineralize organic matter and drive nutrient cycling. To assess the impact of elevated CO₂ concentrations on microbial community and activity in a temperate forest soil developed from old volcano ashes, we conducted an open top chamber (OTC) experiment for growing three species of trees, Korean pine (*Pinus koraiensis* Sieb. et Zucc), Changpai Scotch pine (*Pinus sylvestris* (Takenouchi) T. Wang ex Cheng) and oak (*Quercus mongolica* Fisch) in Changbai mountain forest ecosystems, northeastern China. Soils were collected after 7 years of treatment from elevated (500 $\mu\text{l l}^{-1}$) and ambient (350 $\mu\text{l l}^{-1}$) CO₂ chambers at seven sampling dates from spring 2006 to autumn 2007.

Total organic carbon (TOC) contents in bulk soils of the Korean pine increased significantly ($P < 0.01$) after 9-year exposure to the elevated CO₂, whereas the TOC contents of the soils under the Changpai Scotch pine exposed for 9 years and under oak exposed for 3 years were not significantly influenced by the elevated CO₂ treatment.

Elevated CO₂ affected the activities of soil enzymes such as phosphatase and 1,4- β -acetylglucosaminidase (1,4- β -NAG), which are indicators of nutrient acquisition activity. The activities of 1,4- β -NAG, 1,4- β -xylosidase and phosphatase in bulk soil of Changpai Scotch pine were not affected by elevated CO₂ in 2006, but were reduced in 2007. Elevated CO₂ stimulated average activities of enzyme in soil of oak in summer 2007 ($P < 0.01$). Correlation analysis indicated that soil moisture level was positively correlated with 1,4- α -glucosidase, microbial biomass C (C_{mic}) and N (N_{mic}) across the three species. Peroxidase activity showed strong correlations with N_{mic} ($r = 0.54$, $P < 0.01$) and C_{mic} ($r = 0.81$, $P < 0.01$), phenol oxidase activity showed a high correlation with N_{mic} ($r = 0.48$, $P < 0.01$) and C_{mic} ($r = 0.63$, $P < 0.01$). Our results indicate that soil moisture is an important factor in Changpai mountain forest ecosystem, which affect response of soil microbial enzyme to elevated CO₂, thus a multi-temporal sampling approach is imperative to study temperate forest soil expose to elevated CO₂. Invertase and dehydrogenase activities were significantly enhanced in different degrees under elevated CO₂ than ambient. Nitrifying enzyme activity (NEA) was significantly increased in August 2006 sampling from elevated CO₂ compared to ambient treatment ($P < 0.01$). Dinitrifying enzyme activity (DEA) was marginally significantly decreased by elevated CO₂ treatments in August 2006 ($P < 0.04$) and June 2007 ($P < 0.09$) sampling. β -N-acetylglucosaminidase (β -NAG) activity was increased under elevated CO₂ by 7 % and 25 % in June and August 2006, respectively.

The community genetic structures of bacteria and fungi were strongly modified by seasonal variation; the fungi community composition was affected significantly by enriched atmospheric CO₂ concentrations. Although bacterial community was modified by CO₂ enrichment less than fungus community, the CO₂-induced modification of bacterial population was also detected by PCR-DGGE technique. Sequencing of DGGE bands revealed that the sequence similar to *Calocybe carnea* and *Magmatodrilus obscurus* were predominated in soil under Changpai Scotch pine through the sampling times, and affiliated with *Humicola fuscoatra* and *Candida* sp. were dominant in soil under Korean pine and oak, respectively. The abundance of populations closely related to *Pachyella clypeata*, *Cochlonema euryblastum*, *Lepiota cristata*, *Eimeriidae* sp., *Trichoderma* sp. under Korean pine, and *Candida* sp., *Magmatodrilus obscurus* and *Pachyella clypeata* under oak was significantly enhanced by elevated CO₂, whereas related to *Serendipita vermifera* *Calocybe carnea* were declined.