Differential responses of soil microbial communities to

elevated CO₂ in two root crop radish cultivars

Songmei Shi^{1, 2}, Xue Zhu¹, Xingju Wang¹, Jiajun Song¹, Zhengan Yang¹, Xinhua He^{1, 2, 3*}

1 Key Laboratory of Vegetable Biology in Yunnan, College of Landscape and Horticulture, Yunnan Agricultural University, Kunming 650201, China;

2 Centre of Excellence for Soil Biology, College of Resources and Environment, Southwest University, Chongqing 400716, China;

3 School of Biological Sciences, University of Western Australia, Perth, WA 6009, Australia

*Correspondence: xinhua.he@uwa.edu.au; Tel.: 86-1872328908

In terms of climate change, the increasing atmosphere CO_2 (a CO_2) or elevated CO_2 (e CO_2) concentrations have led to far-reaching impact on the environment and global economy. However, information about such an impact on the plant-soil-microorganism interactions of root crops is limited. We thus studied the impact of eCO_2 (300 ppm higher than current aCO_2) on their yield, soil nutrient and soil microbial community structure of two most widely cultivated radish (Raphanus sativus L. cv. Xinlimei and 501) grown on soil (Eutric Regosol) between November 15, 2021 and March 25, 2022 in environmentally auto-controlled growth chambers. Results showed that aboveground and belowground biomass, and total biomass production of 130-day-old Xinlimei or 501 at harvest were respectively increased by 26%, 29% and 32% or 77%, 22% and 77% under eCO₂ than under aCO₂. eCO₂ also significantly increased enzyme activities of soil sucrase, amylase and phosphatase, but decreased soil NO₃-N and available potassium for both cultivars. Compared to aCO₂, soil bacterial diversity was significantly decreased while fungal diversity was significantly increased under eCO_2 . The community compositions of both soil bacteria and fungi differed between aCO2 and eCO2 for both cultivars. The relative abundances of Proteobacteria, Bacteroidetes and Actinobacteria in bacteria, and Ascomycota and Anthophyta in fungi were changed by eCO₂. Pearson's correlation analysis showed that α -diversity of bacterial and fungal were significantly associated with soil NO3-N, available potassium, activities of amylase, sucrase, protease, and total biomass. Analysis of redundancies revealed that the community composition of bacteria and fungi was significantly affected by soil available phosphorus, available potassium, activities of urease, protease and phosphatase. Results from the present study provide insights into how bacteria and fungi communities in radish soil could be altered under eCO₂, which are valuable for a sustainable root crop production under global CO₂ rising scenarios.

Keywords: Elevated CO₂; Microbial community; Radish; Soil enzyme; Soil nutrients; Yield