*Supplementary material*

Biochar amendment stimulates utilization of plant-derived carbon by soil bacteria in an intercropping system

**Hongkai Liao1,2,3,4 ·Yaying Li1,2,\*· Huaiying Yao1,2,5,\***

1 Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, People’s Republic of China

2 Key Laboratory of Urban Environmental Processes and Pollution Control, Ningbo Urban Environment Observation and Research Station-NUEORS, Chinese Academy of Sciences, Ningbo 315800, People’s Republic of China

3 University of Chinese Academy of Sciences, Beijing 100049, People’s Republic of China

4 Guizhou Provincial Key Laboratory of Mountain Environment, Guizhou Normal University, Guiyang 550001, People’s Republic of China

5 Research Center for Environmental Ecology and Engineering, School of Environmental Ecology and Biological Engineering, Wuhan Institute of Technology, Wuhan 430073, People’s Republic of China

For correspondence. \* E-mail: hyyao@iue.ac.cn; yyli@iue.ac.cn. Tel: +86-0592-6190791; Fax: +86-0592-6190791



**Figure S1** Plants in the pots after 35-day continuous of labeling



**Figure S2** Incorporation of 13C-labelled rhizodeposits into the soils after 35-days of continuous labeling. Bars present means ± SE.



**Figure S3** The relative abundance of rhizosphere bacterial families determined by high-throughput sequencing of the 16S rRNA gene amplicons. Statistically significant differences between group pairs were determined by the *LSD* at *P* < 0.05 level. Bars present means ± SE.



**Figure S4** Effect of the biochar amendment on the alpha diversity of the soil microbial communities. Bars are means ± SE.



**Figure S5** Effect of the biochar amendment on the bacterial richness as estimated by ‘breakaway’ package. Bars are means ± SE.



**Figure S6** Overlap of responsive OTUs between biochar and control treatments

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**Figure S7** Taxonomy of the microbial communities in the light (<1.69 g ml-1) and heavy (>1.70 g ml-1) gradient fractions of the control and biochar treatments.