*Supplementary material*

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

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

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

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**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.

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

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

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**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.