

We would like to thank the reviewers for their useful comments and their positive assessment. We have effected the corrections in order to improve the manuscript. Below are the point-by-point answers to all reviewer comments. We hope that the answers are satisfactory. Please note that the line numbers in this letter match the line number of the revised manuscript with a simple markup track change mode.

Abstract:

The results of microbial abundance and diversity, methods of microbial functions prediction, and significance of this study should be added in this section.

Answer: Thank you for your comment. We have added the method of microbial functional prediction method in the revised manuscript. Also, we added results of microbial diversity and abundance.

Abstract(Line 20-29)

Amplicon sequencing for the prokaryotic community and functional prediction with Tax4Fun2 were conducted. Under the CM Simpson's diversity index was higher in soils with common beans than those in other legume treatments. On the other hand, N-cycling genes for ammonia oxidation and nitrite reductase (NO-forming) were more abundant in velvet bean/maize treatment, and this is possibly due to the increased abundance of Thaumarchaeota (6.7%), Chloroflexi (12%), and Planctomycetes (11%). Cowpea/maize treatment had the lowest prokaryotes abundances among legume treatments. Our results suggest that the choice of legume species is important for soil microbial diversity and N-cycling functions in CM applied mixed cropping systems.

Materials and methods:

L116: "four mixed cropping treatments", the description here is not rigorous, there were only three mixed cropping treatments referred to the lines 120-123, please change the expression.

Answer: Thank you, we modified the description as follows.

Method(Line 115-118)

The experimental design, which was completely randomized, included three fertilizer treatments × four plant treatments (three mixed cropping treatments and a single maize treatment) was conducted in triplicate.

L111-139: The Para is so long, it is suggested that this section could be divided into two parts, the first paragraph describes the experimental design, and the other clearly describes the sample collecting methods, especially the methods of soil sampling, such as the depth.

Answer: We thank you for this suggestion. We have added the details of the soil sample collecting method and divided the paragraph into two at Line 136.

Method(Line 136-137)

The soil was sampled from each pot at 0 to 10 cm and passed 2 mm of sieve to homogenize the sample and remove roots and stones.

Result:

L298-303: You can consider summarizing the characteristics of the VM treatment to the abstract.

Answer: Thank you for your comment. I summarized the characteristics of the VM in the abstract as below.

Abstract (Line 26-27)

Cowpea/maize treatment had the lowest prokaryotes abundances among legume treatments.

Discussion:

The core of the title and hypothesis in this paper is the effect of the mixture of different legumes and corn on microorganisms. Therefore, it is suggested to add another section to discuss the reasons for the changes in microbial diversity and community under different intercropping patterns.

Answer: Thank you. We have added another section to explain the reasons behind the effect of legume species on microbial diversity in the intercropping system.

Discussion (Line 432-452)

4.3 Effects of the legume varieties and biochar application on soil microbes

Conclusion:

The conclusion should follow the main idea of the article. please state your major conclusion directly. It's too wordy now.

Answer: Thank you. We have simplified the conclusion to show the main idea directly. We have reduced the words for the conclusion from 199 to 129.

Conclusion(Line 455-466)

Our results demonstrated that the choice of legume species in the intercropping system is an important factor controlling the effect of biochar application on soil microbial diversity, community and functions. The combination of biochar and common bean enhanced microbial diversity with the increase in the abundance of Proteobacteria and Bacteroidetes. On the other hand, biochar combined with velvet bean altered the

soil microbial genes for ammonia oxidation and nitrite reductase (NO-forming), but not the prokaryotic diversities. The increase in the relative abundances of Thaumarchaeota, Planctomycetes, Verrucomicrobia, and Chloroflexi was identified as a potential cause for the alteration of the N-cycling functional genes in velvet bean treatments. These results suggest that consideration of legume species-specific effect is necessary to optimize the positive effect of biochar on microbial diversity and functions.