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# *Interactive comment on* "Development of bacterial communities in biological soil crusts along a revegetation chronosequence in the Tengger Desert, northwest China" *by* Lichao Liu et al.

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I would like to thank Referee #1 for good suggestions and valuation to our manuscript. In this study, we analyzed the soil microbial communities related to succession and want to know a link between biocrust development and soil biogeochemical processes. This is also important to interpret ecological theory related to community assembly and biodiversity, and to explain the mechanism of ecosystem stability maintenance. However, the manuscript has some problems that need to be revised. We think these suggestions are very helpful to improve our manuscript, and the modified sentences or words were marked as red in the revised manuscript. Now we discuss these questions

together in the following.

During the experiment and in our writing process, our main goal is to test the hypothesis that bacteria are the main species in C accumulation and soil improvement in early stages of BSC succession. We want to test it by analyzing the bacterial community composition and the potential function of BSCs along a chronosequence in an over 50-year-old revegetation. On lines 64-67, we present three questions in the text. We examined the bacterial community composition, but the other two questions need to be interpreted by existing literature knowledge. Because the bacterial community composition was obtained by high-throughput sequencing, and the experiments to determine concrete functions of each composition could not be realized. So we want to collect the functional information of bacterial community composition at phylum level or genus level to interpret their potential function in the development of soil properties and roles in ecosystem recovery. So the emphasis is in the discussion part. We have added a concluding statement in the discussion part of 'Function of BSC bacteria' (Different compositions of bacterial community play various roles in improving soil properties in different successional stages of BSCs, suggesting their positive potential function in soil biogeochemical cycle and ecosystem process).

On lines 74-75, we hypothesize that bacteria are the key species in C accumulation and soil improvement during BSC succession. In fact, what we really want to say is bacteria have greatest abundance in BSCs compared with other microbial organism such as fungi. So we think they play important roles in C and N accumulation and soil improvement during BSC succession. There was no definite expression in the text and then revised this sentence.

In results of RDA, the referee proposed 2 main concerns. First, the soil biogeochemical data used in the RDA have been collected in 2005. But the data were collected from samples with the same successional stages of our samples in the same experimental site. So we do not think there is a need for repeated analysis of soil physicochemical properties in our samples. The climate of the past 10 years has not changed much and the recovery level of soil and microbe is basically the same in the same development stage. According to the suggestion of “Given likely changes in these soil properties over that 10 year period, the authors need to present this caveat when presenting and discussing their findings”, we present this description to the result part of the text as “Taking into account the likely changes in the soil properties from samples with the same successional stages in the same experimental site, we selected soil biogeochemical data collected from 2005 in the RDA (Table S5).”. Moreover, the soil biogeochemical data were not actually measured in the 5-Year category, but the fitted curves of all indexes of soil biogeochemical properties were made by the authors. So there is no missing the 5-Year properties. Unfortunately, we have not made this point clear in the text, and no fitting data were shown in Table S5. So we added the fitting data of the sand-fixing sites in Table S5, and the instructions are given in Table S5. Second, in order to dealing with the over-fitting in Fig. 9, we selected 9 presentative variables from 18 of the soil biogeochemical data, and made a new RDA figure. Taking into account the high correlation between variables or the relationship between environmental factors and microbial communities, we selected variables including silt + clay content, water holding capacity, Bulk density, pH, Organic C, Total N, Total P, Total K and electric capacity. The new RDA figure and the result were added into the text.

At the end of the Discussion, we want to state that the microorganisms can in turn improve soil texture. Maybe our language is not accurate enough, we also think that it is not safe to say that changes in soil properties in later stages are simply driven by changes in BSC microbes. So the last sentence have been revised as ‘the microorganisms in turn have the positive influence on soil improvement’. Meanwhile, we think the Referee’s statement about the interactions of BSCs and soil biogeochemical properties is fits perfectly at the end of our discussion. So we added directly to our manuscript as part of the prospect or vision for the future work in discussion part.

Please also note the supplement to this comment:
http://www.biogeosciences-discuss.net/bg-2017-139/bg-2017-139-AC1-

supplement.pdf

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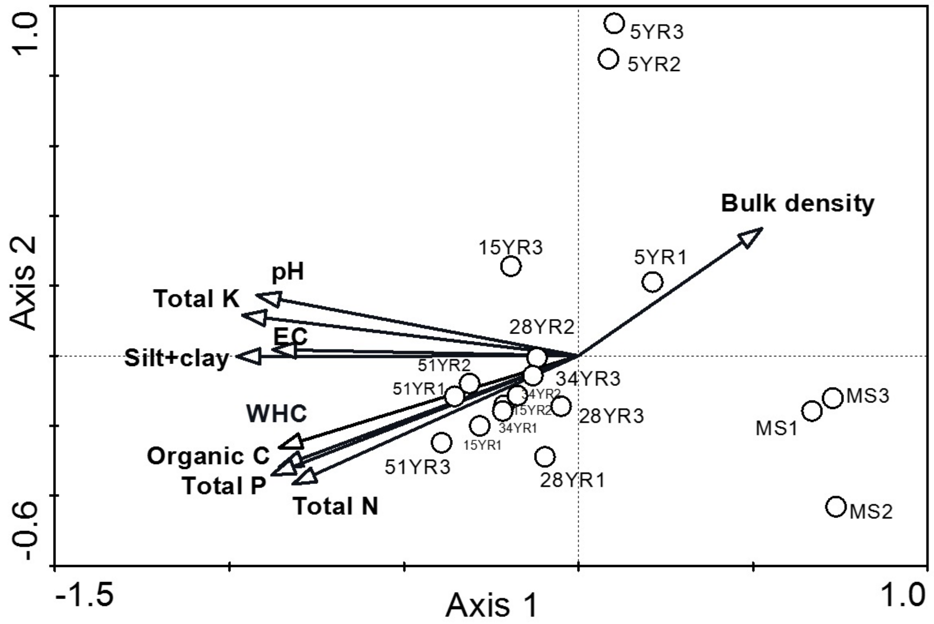
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-0.6
Axis 1
-1.5
1.0
Bulk density
pH
Total K
EC
Silt+clay
WHC
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Total P
Total N
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5YR2
5YR1
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Fig. 1.