

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.

Anonymous Referee #1

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Development of bacterial communities in biological soil crusts along a revegetation chronosequence in the Tengger Desert, northwest China.

Liu et al.

This manuscript describes the characterization of bacterial communities in shifting sands and in 6 chronological stages of surface stabilization following intervention to reduce dust and soil movement. The authors found that bacterial biodiversity and biomass increased over time after soils were stabilized, reaching relative high points in the 15-years after stabilization samples and staying relatively high through more advanced stages of stabilization and biocrust development. These substantial changes in bacterial community structure are correlated with changes in soil

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properties—suggesting a link between biocrust development and rates and quality of soil biogeochemical processes.

Overall, this is a reasonably well-written manuscript that is based on strong methods for assessing bacterial community structure. The manuscript is also nicely divided into focal sections making it easy to follow and understand the results. Questions regarding changes in soil microbial communities over time, particularly as related to succession following disturbances, and what this change in community states mean for ecological functions is a longstanding interest in soil biology. More recently, soil microbial communities have become a focus for testing ecological theory related to community assembly and biodiversity. Thus, the current data set is likely to be of interest to a range of ecologists.

Major Comments:

While the paper has clear strengths as noted above, I have a few major concerns at this point I would like the authors to consider and address. In particular, the current manuscript (while based on high-quality methods) is primarily descriptive and neither focuses on testable hypotheses, nor does it present an advance with regard to our understanding of what controls community assembly and structure across succession in soil microbial communities. Given the great interests in this topic and the many available papers reporting relevant findings in other soil bacterial communities, a better investment and framing of the current results within this context would improve the paper.

On lines 64-67, the authors do present 3 general questions, including questions about the role of BSC bacterial communities in the development of soil properties and roles in ecosystem recovery. However, the current manuscript only addresses the simple question of "what changes occur in bacterial community composition?" In addition, on lines 74-75, the authors hypothesize that bacteria are the key species in C accumulation and soil improvement during BSC succession, but there is no explicit, mechanistic test of

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this hypothesis since C accumulation is not parsed among biotic groups and neither is the role of non-BSC soil organisms or simply physical processes in soil improvement.

The authors do a good job of presenting differences in bacterial community structure among successional stages, but the attempt to explain the drivers of these changes is less developed. In particular, Figure 9 shows the results of an RDA which suggest links between soil microbial communities and soil properties. This analysis supports the presence of significant correlations, but it cannot inform readers about what changes first and what is the driver. In other words, we cannot determine to what extent soil properties change and subsequently driver changes in bacterial communities, and to what extent development in bacterial communities drive changes in soil properties. I have 2 main concerns about this section of the manuscript.

First, the soil biogeochemical data used in the RDA appear to have been collected in 2005, 10 years prior to the sampling of the soil bacterial communities. 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. Sampling soil properties in 2005 also make it unclear how soil properties were assessed in the 5-Year category, or how bacterial communities in these samples were compared to soil properties in the RDA behind Figure 9. Where the 5-Year properties gap-filled? A second concern about the RDA approach is the high number of explanatory variables (18) to bacterial samples (21). A key concern in RDA is the potential for 'overdetermination' when a nearly 1:1 ratio of samples to explanatory variables is present. Many of the explanatory variables are sure to be collinear, and over-fitting or over-determining will result. A common method for dealing with this issue is to include an effort to partition the variance explained by each variable in the bacterial community ordinations. It is not uncommon to find that your variables explain >100% of the variation and hence, you are over-fitting the model.

Second, I am concerned about statements made here, and in many other BSC focused papers, about the positive influence of BSCs on soil improvement. At a minimum, con-

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sidering that changes from communities in shifting sands to those in later successional stages rely initially on physical processes that stop the movement of soils to allow development of BSCs, it is not safe to say that changes in soil properties in later stages are simply driven by changes in BSC microbes. While many authors have interpreted correlations among soil properties and BSCs as an indicator that BSCs are drivers of soil fertility and development (Zhang et al. 2010, Chamizo et al. 2012, Delgado-Baquerizo 2013, Chen and Duan 2015, Yu et al. 2016), a number of authors have reported the opposite and suggest a direct influence of soil properties on BSC development (Bowker et al. 2006, Rivera-Aquilar et al. 2006, Bowker and Belnap 2008, Root and McCune 2012, Concostrina-Zubiri et al. 2013, Belnap et al. 2014, Bowker et al. 2016). These are important questions and parsing out the interactions of BSCs and soil biogeochemical properties remains an important frontier in BSC research—however, further work to identify controlled experimental approaches are required to answer this question as field correlations leave us wondering about the directionality of controls over time.

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