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Biogeosciences
Discussions

Interactive comment on "The effect of resource history on the functioning of soil microbial communities is maintained across time" *by* A. D. Keiser et al.

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The reviewer noted that the ecological question addressed is of high interest. We have responded to the reviewer's four comments individually below.

1. All of the information requested is given in the two references cited in the Methods (Rousk, 2010; Lauber et al., 2009). Given that these are now well-established approaches with the original methods often referenced in published literature (e.g. Fierer et al., 2008; Rousk, 2010), for reasons of conciseness, we did not repeat this information in the text. However, a paragraph with the original methods could be added; we leave this decision to the Editor. For now, we have opted to keep the description in

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the Methods more concise. As for submitting the sequences to a database, there is not currently a publicly-accessible database that accepts pyrosequencing data. This is a problem that researchers are currently trying to address, but it is not trivial. We will certainly provide sequence data to any reader that requests it.

2. There are three aspects to this comment. First, the reviewer suggested that in order to test our hypotheses we needed to assess both phases of litter degradation. We cannot discern from the reviewer's comment the rationale for this but clearly this aspect of the comment is the most pertinent to address because it questions the validity of our experiment to test the hypotheses we pose. In contrast to the reviewer's concern, current theory and empirical data would suggest our test – where we focused on earlier stages of litter decomposition – would be a more conservative test of whether initial functional dissimilarity is maintained across time. Theory suggests that the greater the number of taxa that perform a process, the more likely it is that the process will be buffered against environmental perturbations (e.g. Schimel, 1995; Allison and Martiny, 2008). At the earlier stages of litter decomposition, where more labile compounds are being used, we expect there to be many more taxa that share the ability to degrade a particular compound; with the number of taxa decreasing by orders of magnitude where compounds become more recalcitrant (e.g. Goldfarb et al., 2011). Field data on carbon and nitrogen processes have revealed a role for microbial community composition in more specialized processes (i.e. those performed by far fewer taxa) but not necessarily more general processes such as carbon mineralization (e.g. Balser and Firestone, 2005). Given current theory and empirical data, it would seem our test for functional convergence vs. maintenance of dissimilarity would stack the odds toward favoring convergence – as we focused on a general process (carbon mineralization) at earlier stages of litter decomposition, where the expectation is that labile compounds are most abundant and that many taxa are capable of degrading these materials. However, our data support the counter hypothesis of maintained dissimilarity making our data – if anything – of greater significance in the debate as to whether we have to consider microbial communities when explaining and estimating biogeochemical process rates.

We now summarize these points in the Discussion.

Second, the reviewer suggests litter degradation is a two-step process. This is certainly the textbook definition. We do not address this comment in the manuscript as we do not see that it influences our hypothesis-testing. Further, the textbook idea that carbon degradation of litter is a 2-phase process is being challenged in modeling and experimental papers (see Moorhead and Sinsabaugh, 2006; Klotzbücher et al., in press). If the Editor feels we need to add Discussion about this point we can, but it does not appear to be particularly relevant to our study or our stated hypotheses.

Third, the reviewer discusses whether epiphytic microbes compete with soil microbes. This is an interesting point. The reviewer gave no citations, but in assessing the literature we find that this topic has not received much attention (e.g. Osono, 2007). We could find no evidence that epiphytic microbes should affect functional dissimilarity or similarity across microbial communities. We now cite Osono and Hirose (2011) in the text to note that epiphytic microbes interact with soil microbes and highlight that this might be an interesting avenue for future research into functional dissimilarity.

3. We are unclear from the comment why the reviewer is requesting this information, which is not something we collected. The reason for this is because soil is a distinct microbial habitat from litter and we have no reason to expect that the litter-associated microbial communities would directly reflect the soil-associated communities in our experiment. Instead, the surface soils were the inoculum source. In addition, such community data were not demanded by our hypothesis testing. We only included data for the litter to look at composition in relation to function. This is pertinent to the community composition-function debate and our data interpretation.

4. We state in the manuscript that there are six replicates per inoculum and litter combination for our hypothesis testing related to carbon mineralization (and the main metric in our study). For the supporting information relating to the microbial community data, we now note in the Methods that we pooled replicates as done in Strickland et

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al. (2009). In their analysis, microbial community composition from individual replicates and pooled samples of the same treatment were identical, permitting robust data analysis. Given our community data were supporting information, we followed their approach, and revealed clear patterns in compositional changes across time.

5. We have clarified this methodology in the text.

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