

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.

Anonymous Referee #3

Received and published: 5 May 2011

I cannot support publication of this manuscript in the present form, although the ecological question addressed is really of high interest. I will give some reasons in the following:

1. Assessment of diversity: No information is given on the used primers, on the amplicon length, on the sequencing strategy (unidirectional, vs bidirectional); number of reads per sample (was the same number of reads per sample used for analysis); numbers of OTUs per sample (did the number of OTUs cover diversity ?) How was an OTU defined (how much % similarity); were the sequences submitted to any database ? How were sequencing errors handled etc ?. Without this basic data NO interpretation

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of the results is possible

2. Ecology of litter degradation: Litter degradation is a two step process. In the first phase easily available carbon sources are degraded followed by the degradation of degradation of lignin cellulose and other hardly degradable substances. The corresponding community structure of litter degraders is consequently completely different. Taking the question of the study into account, I think both phases of litter degradation need to be analyzed. Moreover normally soil microbes compete with epiphytes for resources, however in this study litter was just a pure substrate without epiphytic microflora which raises the question of the relevance of this study.

3. Diversity of the used soil: As changes in diversity pattern should be investigated data on the bacterial and fungal community composition of the original soil inoculums is needed.

4. Finally no replicates have been analyzed, which makes a reliable data analysis not possible.

Many minor points like how water content was determined of such different material like litter and soil stays unclear.

Interactive comment on Biogeosciences Discuss., 8, 1643, 2011.

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