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Interactive comment on “Microbial food web dynamics along a soil chronosequence of a glacier forefield” by J. Esperschütz et al.

Anonymous Referee #1

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This manuscript describes the analysis of microbial communities present in soil across a receding glacier foreland and their response to the addition of complex organic matter (13C-enriched dried plant material). Specifically, the authors examined the microbial communities in soil present in one of four age classes (10, 60, 100 and 700 years of exposure and development). As observed in previous studies of microbial community structures across glacier forelands, differences were observed in biomass, community structure and diversity, which generally increased with soil age. Using analysis of the phospholipid content and the levels of incorporation of 13C (derived from the plant material), differences in the rates of decomposition of organic matter were observed, but perhaps surprisingly, similar relative patterns of incorporation of 13C into different phospholipid groups were observed in all four age classes, suggesting similar selection of different communities within the soil despite the contrast in the original soil substrate

C592

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and community composition. It is perhaps this aspect which is the novel finding of the work.

The experimental design is well conceived and appears to have been executed to a high standard.

Specific comments

1. I have a query about the analysis of the community structures using the distribution of certain PL groups (e.g figure 4) vs PCA analysis (e.g. figure 5) for comparing community structures and the significance of these differences. While the PCA analysis demonstrates separation of the different samples in terms of community structure, is this based on mean values only? Looking at the data and error bars in figure 4, it would not surprise me if the differences in the ^{13}C incorporation % of individual PL types between the four age classes were not statistically significant in many/most of the cases. Could the authors comment on whether this is taken into account for the PCA analyses?

2. As the relative distribution of ^{13}C into the different PL groups seems to be relatively similar for all age classes (T1-T4), is this reflected by similar community structures based on relative amounts within each PL group? Would it be possible to show this for 0, 8 and 12 weeks somehow? I think it would be nice to see this in addition to the Shannon diversity and evenness measurements.

3. Figure 1. As I am not an expert in the interpretation of isotope ratio signatures, this may not be a sensible question, and I may not be interpreting Figure 1b correctly. Is the majority of the carbon in the litter material ^{13}C , or is it just enriched but mainly ^{12}C ? I ask as where there is large increases in biomass in some sites (e.g. in T4, the phospholipid content approx. doubles from 0 to 8 weeks), this is accompanied by measurable but still only small increases in % ^{13}C content. If the majority of the plant C is ^{13}C , where does the C in the new phospholipids come from?

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4. Just a minor point, but I am a little unclear on the experimental design with regard to the application of litter material below the vegetation cover. Was the vegetation physically removed, litter added, then the plant layer replaced, or was it added at the base of the vegetation layer (i.e. plant/soil interface).

Technical comments

P1277, line 19: typo - I guess PUFA should be PLFA

P1282, line 10: 'applicated' should read 'applied'

P1286, line 17: suggest rephrasing to '.....with significantly higher values ($p < 0.05$) detected.

P1286, lines 24-27: were these observed differences significant?

P1287, line 4: diversity increasing 'concomitantly'. Is this really the case and can a level of significance be applied to this? For the 8 weeks sample, the diversity value at t3 is lower than that of t2 and t4 – and there is no difference between 100 and >700 in diversity in the control samples.

P1288, line 14-16: "for T1 higher incorporation of ^{13}C into the PUFA and PLEL groups and lower incorporation at all other groups compared to the other sites was observed". Is this really the case? At 8 weeks, the PUFU seems to be lowest in T1. Also, are these differences statistically significant?

P1290, line 25-26: "According to Kramer and Gleixner (2008), both Gram-positive and Gram-negative bacteria prefer plant derived C as a C-source." Is this a realistic statement? As both G- and G+ together represents all bacteria, is this not the equivalent to saying all bacteria prefer plant derived C as a C-source?

P1303, Table 3: there seems to be an error in the formatting of the Shannon diversity for 12 weeks, >700 y (number = 21717)

P1303, Table 3: The legend states T1-T4, but the table gives the actual ages. Suggest

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adding T1 to T4 in parentheses beside the ages?

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