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

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Dear Editor and Reviewer #1,

First of all, we would like to thank reviewer #1 for the positive feedback and constructive comments on our manuscript; also, we feel highly pleased by the commendation concerning the experimental design. With regard to the specific comments we provide the following answers and suggestions for improving the present study.

1) Considering your query about the ^{13}C distribution among the microbial community structure, both Figures (Fig. 4 and Fig. 5) are based on the same dataset (means of five replicates). A rephrased comment in the statistical section might be helpful for an easier understanding “Principal component analysis was based on mean values ($n=5$)

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of PL and 13C-PL data for each location and time point. The data set for PCA was thus composed of 12 (Fig. 2) and 8 (Fig. 5) average samples". In contrast to Fig. 4, where harvesting time points have been illustrated separately (a and b) to focus on the 13C distribution among the PL structure, Fig. 5 includes both samplings and allows for better visual interpretation of differences along the chronosequence and sampling time points. We decided to present also Fig. 4, because readers frequently like to see the real values and the variability within replicates, indicated as standard deviations. Together with our response, we provide a PCA (Fig. 5-1) based on individual replicates where you will see the treatments overlapping. However we think the average graph is clearer and highly representative of the trends observed with the individual replicates, and thus we prefer using it in the study.

2) Our results show that while the litter derived 13C distribution into the various PLFAs is similar along the chronosequence (Fig. 5), the soil community structure based on PLFAs is different (Fig. 2). This suggests that even though microbial communities in soil might be different between sites, the same organisms are involved in processing the litter material. Therefore the relative distribution of individual PLs is not necessarily related to the relative incorporation of 13C into PLFA groups. In addition, individual microbes might not directly profit from the applied plant litter, but indirectly due to so called "priming effects" (Kuzakov, 2010). This further adds to the divergence of the soil community structure and the incorporation of 13C into PLFA groups. We can additionally present $\delta^{13}\text{C}$ and mol% raw data in Tables in the supplementary material, as also suggested by reviewer #2. An illustration similar to Fig. 4 that includes the relative abundance of the different PLFA groups certainly would be possible but might result in three more figures for 0 (a), 8 (b) and 12 weeks (c).

3) The applied plant litter was relatively low enriched by 13C ($\delta^{13}\text{C}$ = approx. 90‰ vs V-PDB); in atom%, this means the litter consists of around 98.796% 12C and 1.204% 13C (In contrast, non-labelled plant litter is in a range of 98.917% 12C and 1.083% 13C). Stable isotopes allow for subtle differences in the ‰-range and that is why $\delta^{13}\text{C}$

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notation is expressed in “‰” instead of “%”. The majority of C in the total phospholipid content therefore is ^{12}C , and Fig. 1b only states the minor but precisely measurable differences using stable isotopes of the individual litter derived ^{13}C content in the total lipids.

4) In our experiment the main intention was to compare the microbial community structure and litter degrading activity in differently aged soil substrates along the forefield. To minimize the individual rhizosphere effect on the microbial food web, we physically lifted up the vegetation cover between 2 and 5 cm and applied the litter directly on the substrate below the vegetation cover. To ensure an undisturbed system during the experimental period we replaced the vegetation cover after litter application. We will specify this point in the experimental setup in a revised version: “For this purpose the vegetation cover was physically removed and immediately replaced after litter application to ensure undisturbed conditions during the experimental period.”

In order to address the technical comments by the reviewer we suggest including the following revisions in the final version:

P1277 / line 19 We will correct the misspelling of PUFA into PLFA

P1282 / line 18 We will change “applicated” into “applied” as suggested

P1286 / line 17 We accept the suggestion, and suggest rephrasing the sentence to “The total soil PL content increased as ecosystem development progressed with significantly higher values detected at the reference site T4 compared to all other sites ($p < 0.05$, Fig. 1a)”

P1286 / lines 25-27 We suggest providing levels of significance to the text: “Similar to the total PL content, an increasing incorporation of ^{13}C derived from plant litter into total PL was detected at T4 compared to the other sites (Fig. 1b), irrespective of the harvesting time point ($p < 0.05$). Between 8 and 12 weeks a slight decrease in ^{13}C in total PL was observed at T2 and T3 (not significant), whilst a 50% reduction was

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recorded at T4 (Fig. 1b, $p < 0.05$)”

P1287 / line 4 We apologize for the misleading description and will revise the respective lines into “Diversity was lowest at T1, irrespective of treatments ($p < 0.05$). After 8 weeks and after 12 weeks, significantly higher diversity was detected at T4 compared to T1 and T2 ($p < 0.05$).”

P1288 / lines 14-16 We thank the reviewer for his observation. He’s right; incorporation of 13C into the PLEL group in T1 was in general lower than in the other sites. As we mention in the text (lines 6-7, page 1288), incorporation of 13C into phospholipid groups was similar and thus differences between sites were in most cases not significant (Fig. 4). We used the PCA (Fig. 5) to give a clearer picture of the differences between sites/treatments even though these might not always be significant. We suggest rephrasing the paragraph as follows: “Results showed a separation between T1 at 8 and 12 weeks and the rest of the sites along PC1. This component is very similar to that of the total soil microbial community profile (Fig. 2); on average, for T1 there was higher incorporation of 13C into the PUFA group at 8 weeks and less incorporation of 13C into PLEL at both 8 and 12 weeks compared to the other sites. In addition, the average incorporation of 13C into the $-\omega 7$, $-\text{cy}$ and $\text{nor} < 20$ groups after 12 weeks was greater in T1 compared to the other sites. PC2 mainly separates T4 at 12 weeks from the other sites/treatments, which is mainly related to the lack of $>\text{nor} 20$ and $-\omega 5$ PLFAs; hence 13C incorporation into these groups after 12 weeks of litter incubation was negligible. ”

P1303 / Table 3 We apologize for the formatting error. We will include the corrected number for 12 weeks > 700 y in the new version. In addition, we have adjusted the legend together with the table and replaced ages by the defined abbreviations T1-T4.

We hope to have addressed all questions and remarks satisfactorily. We will include these changes and corrections in the revised version to be submitted to Biogeosciences and remain open to any further suggestions that you may consider necessary.

BGD

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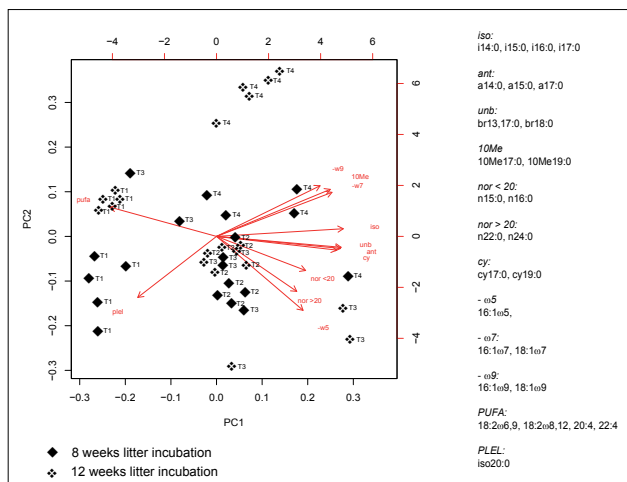


Fig. 1. Illustration of the first (PC1) and the second (PC2) principal component of the principal component analysis (PCA) based on individual replicates of the litter derived ^{13}C distribution ($n=5$)