

**Comments to the author:**

Dear Dr Strauss et al,

Thank you for the revised manuscript where you have included the comments/suggestions from both reviewers and your responses.

I am happy with the changes made, so I think this version can be accepted for publication. However, after a second look at the grain size data, I wonder if you need to include a few more details, so I ask you to consider the following additional, very minor comments:

- 1) Consider including the chain-length range of alkanes and fatty acids into Fig S4 or at least into the figure caption?
- 2) Consider splitting n-alkanes into three categories by adding mid-chain n-alkanes (equivalent to fatty acids)?
- 3) Comment on the common observation that higher molecular weight homologues are typically better preserved than short-chain homologues, which, in addition to chain length dominance due to predominant OM sources, would contribute to the pattern that you see in your results. We also know from previous research that organic compounds are enriched in finer material, so this also contributes to what you see here.
- 4) It further looks like Unit 1 has higher fatty acid contributions relative to n-alkanes, whereas you see the opposite in Unit 2. Noting that alkanes are also derived from fatty acid decarboxylation, the OM in Unit 2 could be more degraded?

Thank you for these edits and I look forward to the final version.

Sincerely,

Dr Sebastian Naeher

Dear Editor,

Thank you for your positive feedback. Here we respond to your comments:

- 1) We added the chain length range of the n-alkanes and fatty acids to the figure caption as suggested.
- 2) We will keep the categories we had as we distinguish between different sources between short (e.g. microbial, algal) and long n-alkanes (higher land plants) and short (microbial) and long FAs (higher land plants). Additionally, we chose to make the further distinction in the long FAs as the mid chain FAs C21-C23 could for instance indicate Sphagnum moss species. However, the mid chain FAs are generally low and only increased in two samples when long chain FAs are also increased. Thus, in these samples the mid chain FAs are most likely also contributions from higher land plants. Therefore, we did not focus on the mid chain FAs in the manuscript.
- 3) Following your suggestion, we adapted the sentence in L362: "On top of the preferred decomposition of short chain n-alkanes over the long counterpart (Elias et al., 2007), the stronger negative correlation (even though not significant) between the grain size and the long chain n-alkanes compared to the short chain counterpart could suggest that the latter might be more vulnerable to decomposition or might reflect the different sources of these biomolecules. While long chain n-alkanes derive from higher land plants and enter the soil by deposition, short chain n-alkanes might contain a significant proportion of microbial biomass, which abundance depend on the availability of appropriate substrates."
- 4) In unit II, the long chain FAs still prevail over the long chain n-alkanes, which is also expressed by the HPFA index. We think that you could probably mean that an opposite trend exist in unit III, which seem to be obvious from the long chain FAs and n-alkane data in Figure 3 and is also visible by a decrease in the HPFA (ratio between long chain FA and long chain n-alkanes) data. So yes, this could be an indication that there is an advanced level of OM degradation in the deeper part of the cliff (units III). This might be also supported by the fact that the microbial FAs (iso/anteiso FA) are relative to the long chain fatty acid increased in this interval which suggest a higher microbial activity in this interval. We interpreted that in that way already in section 5.1.2 Line 355-364.

Best regards, Jens Strauss on behalf of the author team