

Interactive comment on “Microbial dynamics in a High-Arctic glacier forefield: a combined field, laboratory, and modelling approach” by J. A. Bradley et al.

Anonymous Referee #1

Received and published: 16 March 2016

The manuscript, “ Microbial dynamics in a High-Arctic glacier forefield: a combined field, laboratory, and modelling approach,” presents a novel study combining field sampling and numerical modeling (the previously described SHIMMER model) to characterize microbial decomposer dynamics and community composition along a soil chronosequence in a oligotrophic, glacial forefield soil system in Svalbard.

In general, I found the manuscript to be clearly written and the methods/results easy to interpret. Critically, I believe the manuscript could be significantly improved if there were specific hypotheses to guide the study. For example, rather than ‘exploring’ microbial community structure and C cycling dynamics in this recently exposed, High Arctic soil environment, how and why did the authors expect these dynamics to differ along

[Printer-friendly version](#)

[Discussion paper](#)



the soil age chronosequence (0 – 113 years old)? While the integration of the field and modeling efforts are commendable, I was surprised that the work was not guided by more clearly defined hypotheses that the model then tested. I was also interested in seeing a stronger discussion of how this study might compare to other arctic (high and low) and alpine glacial forefield systems.

L. 182, 189, 233, elsewhere. Why was the C content (TOC and inorganic carbonates) of 0 year old soil analyzed, but not the other samples in the chronosequence? Similarly, I was not convinced that by testing the microbial growth rate and respiration for the 113 year old sample only (L 191 – 192); why not explore the growth rate and respiration dynamics for the microbial biomass across the chronosequence, even if biomass is lower in those soil ages?

Paragraph beginning L. 231. For the soil respiration study, why not include a range of temperatures (not just 5 and 25C, which may be beyond the peak metabolic tolerance for this community)? Do you have any data to support these temperature choices?

Paragraph beginning L. 428 This information should be folded into the Results section.

Paragraph beginning L 448. Do you expect the Q 10 to vary seasonally (see Mikan et al. 2002). If so, how would this affect the model interpretation?

L. 538 – 540, elsewhere in the discussion. How would the authors propose to improve our understanding of allochthonous nutrient inputs in this system? Is there plant or lichen biomass at the older sites in the chronosequence? How does this compare to other glacial forefield sites?

Technical corrections

L 183. 'as-collected' is not phrased correctly.

Instead of reporting $P > 0.05$ for non-significant results, report the actual P-value.

L 345. Please report error around mean respiration values presented.

Printer-friendly version

Discussion paper



L 351. Do you mean $P > 0.05$?

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2016-52, 2016.

BGD

Interactive
comment

Printer-friendly version

Discussion paper

