

The Cryosphere Discuss., referee comment RC1
<https://doi.org/10.5194/tc-2022-68-RC1>, 2022
© Author(s) 2022. This work is distributed under
the Creative Commons Attribution 4.0 License.

Comment on tc-2022-68

Anonymous Referee #1

Referee comment on "Variation in bacterial composition, diversity, and activity across different subglacial basal ice types" by Shawn M. Doyle and Brent C. Christner, The Cryosphere Discuss., <https://doi.org/10.5194/tc-2022-68-RC1>, 2022

This is a very well written and presented piece of research, investigating the microbial communities associated with basal ice of different thermal regimes of glacier. The aims are clearly stated, the work rigorous and placing their results within the context of other previously published work in particular a great addition to the literature.

I have some minor comments relating to the wording / writing, and one slightly less minor point about the way in which 16S rRNA sequencing was analysed. In particular, the use of a now out of date SILVA 16S rRNA database. These comments are addressed below in order they arise in the manuscript:

Line 8: "providing a habitat"?

Line 15: This sentence could be clearer to better distinguish between the amplification of the 16S rRNA gene from extracted DNA vs RNA (via cDNA). It took me a few reads of the sentence to see the difference in the current way it is written.

Lines 162-167: If I understand correctly, the coarse and fine sediments were separated to "*facilitate filtration of the large sample sizes*" but surely this would have led to a loss of biomass associated with coarse sediment? Acknowledgement of this would be pertinent.

Line 193: Missing word between "included" and "at 95°C..."

Line 209: One less minor issue I have with this manuscript is the use of SILVA v132 for taxonomic assignment of 16S rRNA gene sequencing data. The more recent version - v138

- is much larger and the associated updated taxonomy has altered lineage assignments to SSU sequencing data, especially at higher taxonomic ranks (e.g. Phylum and Class level). For what reason was v132 chosen over v138? - the former has been available since 2019, and is the norm now for taxonomic assignments. How different would your taxonomic assignments be if you used the newer version?

Line 239-243: It is not clear to me what reference database was used for taxonomic assignments of these previously published datasets, please clarify.

Fig 5 caption: You mention black triangles but do you mean black diamonds? I can't see any triangles on the figure

Line 426: Is this cited reference valid for the whole statement? If so, move to the end of the sentence. Otherwise it seems there are missing references relating to the highly-resistant endospores belonging to *Firmicutes* and *Actinobacteria*

Line 436-7: What data relates to this claim? Link to results if it relates to your study, otherwise cite relevant studies

Line 592: Please swap "(46)" with a citation in a consistent style to the rest of the manuscript