

Interactive comment on “Prominent bacterial heterotrophy and sources of ^{13}C -depleted fatty acids to the interior Canada Basin” by S. R. Shah et al.

Anonymous Referee #2

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The paper presents a detailed analysis of fatty acids and their stable isotopic composition, from two stations in the Canada basin, one from an ice free region and one that is ice covered. They investigated how the FA abundances and ^{13}C values change with depth, in order to assess sources of organic matter in the Canadian Arctic. Overall the paper is well written, contains new and interesting data and provides a detailed enough argumentation and discussion to come to valid conclusions. The length of the paper is rather long. I deem the paper relevant for the scope of GB. I have the following remarks that may improve the manuscript:

Page 6700 top part: Most of this part belongs in fact to the materials and methods section. 6701 / line 11 - 15 (difference discussion). It is not clear why this is in the
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results section and in any case hard to follow if one does not have the numbers of these other settings at hand. 6701, l 18 what is the blank value? specify or refer to a table. 6702 l. 3 The referral to the work of Honjo et al fits better as part of the discussion and is on top of that not constructed well. The whole top part of page 6702 (the end of 3.2) already contains quite some discussion mixed with pure results. The same is the case for 3.3, where already quite some interpretations instead of pure observations, are made. 6703. l. 11. Define what BFAs are; l. 24, define what SFAs are. (i.e. write them out in full the first time you mention them). paragraph 4.1 The last concluding sentence states first that the source of FA on the blank filters is ambiguous, yet the authors suddenly conclude, in the somewhat cryptic second part of the sentence, that it can be assumed that FAs found on filters represent that of bacteria living at the filtered depth - at least this is what I make out to be the meaning of the last sentence. It is not clear how they come to this conclusion. What would be useful to know is a conclusion about the contribution of the blank to the total - in other words first discuss amounts, then the possible sources and estimate of the most important one(s), and then in the end conclude how much it may influence the finally observed FA patterns and ^{13}C values at the various depths. From the results or discussion it is also not clear how the blank correction was in fact made. What the authors have not considered in this discussion, or least this does not become clear, is that DOC and POC is a mix of compounds with different characteristics - some being more prone to adsorption (partially hydrophobic) than others. This is especially true for FAs, which likely behave different than total POC or DOC. Thus, to evaluate possible sources of blank FA's, one needs to compare like with like - i.e. FA's present at various depth, not bulk POC or DOC.

Section 4.5. One of the possible sources of FA the authors define, is a combination of suspended heterotrophic or chemo-autotrophic bacterial cells. It may be fine to lump together these different bacterial sources from a FA type perspective, however this is not true from an isotopic perspective. chemoautotrophs use not only a different C source (e.g. ^{13}C -depleted DIC) but may also fractionate quite differently.

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In the introduction and discussion emphasis is placed on the difference in sea-ice covered and ice-free regions, and the study was also (in part) set up like this. However, the conclusion that the FAs reflect contrasting ecological conditions is a very vague one, hopefully the authors can come to some more specific conclusions, they do spend quite some text about this topic in the discussion.

Table 1. It is impossible to assess what the relative contribution is of the blank without knowing how many liters seawater was pumped over the filters, or the absolute amounts on the filters. Please include this data.

Figures: Include a map with locations of the stations.

In figure 1a two depth ranges shown but it is not clear from where they are - make them separate and indicate stations. However, consider making a graph where the minor FA's are also visible. There are too many FA stacked on top with too similar colors. At the moment one might as well present only the FAs with >5% abundance. Fig 1a is only mentioned in the text after referral has been made to 1b and 2 and 3. Consider to make a separate figure. 1b could be combined with Figs 2 and 3.

Fig 2. A: Not all plots show well on the same axis. Consider using multiple x-axes. B: The black line at 3 ng/ug is odd until one realizes the scale changes. better indicate on the scale only with e.g. //. Same for fig 3.

Fig. 4. Indicate for what area+depth the calculations were performed. Change 'TO' into 'to'. Consider changing 4B to figure 5, because A and B are not really related. B is hard to understand when read just by itself. Consider to mention that f-bacteria is 0.8.

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