Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2019-455-RC1, 2019

Interactive comment on "Reconstructing N_2-fixing cyanobacterial blooms in the Baltic Sea beyond observations using 6- and 7-methylheptadecanes in sediments as specific biomarkers" *by* Jérôme Kaiser et al.

Anonymous Referee #1

Received and published: 17 December 2019

The paper by Kaiser et al. is well written. The authors take a systematic approach to applying 6 and 7-methylheptadecane (6+7Me-C17:0) as a biomarker for Nodularia cyanobacteria. They first analyzed 6+7Me-C17:0 in sediment traps from the Baltic and then in a series of sediment cores from nearby locations. In a core from 1860 – the present day the concentration of 6+7Me-C17:0 correlated well with the Baltic Sea SST at a decadal to multi-decadal timescale and with the AMO.

There are some issues that I believe need to be addressed before this paper can be accepted for publication. Unfortunately I do not agree that the authors have sufficiently shown that the sum of 6 and 7- Me-C17:0 is a "robust semi-quantitative biomarker for cyanobacteria" in the sediment trap samples or in the 1980 – 2015 section of the MSM51-2/20 core. Indeed, there are several mismatches in the sediment trap data and the MSM51-2/20 core data between 6+7Me-C17:0 and the presence of Nodularia. This raised concerns for me as the authors selected the sum of 6- and 7-Me-C17:0 as they were both detected in 4 strains of Nodularia by Bauersachs et al. (2017).

I think it is important to note that Bauersachs et al. report a range of 10 hydrocarbons across 8 species of Baltic Sea cyanobacteria, from the genera Dolichospermum, Aphanizomenon and Nodularia. I feel that it would be more informative to present all the hydrocarbon data from the sediment traps samples, not just 6+7Me-C17:0. Information about the presence/absence of n-C17 and other monomethyl alkanes (MMAs) or dimethyl alkanes (DMAs) would be helpful (and really interesting). This full distribution could be compared (statistically) with a wider range of cell counts of e.g. Dolichospermum, Aphanizomenon and Nodularia species. This would provide a solid base for going forward with 6+7Me-C17:0 as a marker for Nodularia, if the data supports it. For example, I notice that Bauersachs et al. reported that Nodularia was the only genera that also produced DMAs. If those components were also found along with the 6+7Me-C17:0 it would make a much stronger argument for applying 6+7Me-C17:0 as a biomarker for the occurrence of Nodularia in the past Baltic Sea.

Furthermore, it is unfortunate that the separate abundances of 6- and 7- Me-C17:0 were not reported. In the Bauersachs et al. paper the 6 Me-C17:0 to 7- Me-C17:0 ratio was consistently around 0.25 in all 4 Nodularia species. For all the reader knows, the sum in this study could consist primarily of 6-methylheptadecane, which would not correspond to any of the profiles found by Bauersachs et al. Using GC-MS, it should be possible to estimate the proportion of 6 Me-C17:0 and 7- Me-C17:0 by integrating both components from their mass chromatograms. If the 6- and 7-methylheptadecanes come from a different source then a different ratio could be expected.

As I said before, I found the paper well written and interesting but, without a more robust connection between the biomarker and its cyanobacterial source, the extension of the study to the sediment cores carries a high risk. There is too much uncertainty arising from the fact the 6+7Me-C17:0 concentrations only show very low correlation with FCA and the Nodularia and Aphanizomenon biomass data.

Additional points to address:

Abstract Line 10 – Change “time history” to “history”

Line 12 – Change “trap sediments” to “ sediment traps”

Line 19 – Remove “rather”

Introduction

Lines 32 – 34 (and at other points in the manuscript). It does not read well to have a list of items, separated by commas but with multiple cases of “and” as the conjunction. For example, I would write the sentence as: “If diazotrophic cyanobacteria occur in large blooms they contribute to nitrogen-eutrophication, where the massive export and decay of cyanobacterial biomass results in O2 consumption, leading to the spread of bottom water hypoxia and anoxia (Zillen and Conley, 2010; Feistel et al., 2016).”

Line 61 – Change to “considered well suited”

Discussion Line 244 – 246 – Strange wording. I would change to “The 6+7Me-C17:0 content is not significantly positively correlated to the FCA index ($r = 0.08$; $p = 0.71$; $n = 245$ 22), nor to the biomass of Nodularia spumigena ($r = 0.10$; $p = 0.62$; $n = 26$), nor to the biomass of Aphanizomenon sp. ($r = -0.36$; $p = 0.07$; $n = 26$).”

Line 255 – Should be “which may be”

Line 277 – Figure number missing.

Interactive comment on Biogeosciences Discuss., https://doi.org/10.5194/bg-2019-455, 2019.