

Interactive comment on “Biomarkers in the stratified water column of the Landsort Deep (Baltic Sea)” by C. Berndmeyer et al.

Anonymous Referee #2

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This manuscript describes the distribution of a number of biomarkers in 6 SPM samples of the Baltic Sea, particularly focused on the suboxic zone. In addition, the BHP composition of a surface SPM sample from a cyanobacterial bloom is reported. The biomarker distributions are complemented by selected isotope measurements and their sources are interpreted based on their distribution over the water column.

This is a nice, solid contribution on biomarker assemblages in the water column of the Baltic Sea where few studies have yet been done. The interpretations are fine and consistent with previous studies. The manuscript does seem to be somewhat limited in scope, especially compared to the comprehensive studies done in the Black Sea (Wakeham et al. 2007 being the prime example), to which this system can be roughly compared. It creates, perhaps unintentionally, the impression of a data report rather

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than a focused study (such as with their previous work in the Baltic, focused on the methane cycle). There is nothing wrong with this, it can provide the foundation of future work, but I am not sure if this contribution provides further insights into ‘the distribution of relevant biota’ or ‘biogeochemical processes’ (end of introduction) or ‘POM sources (middle of introduction). I think the metagenome study of Thureborn 2013 does a much more comprehensive job than this biomarker study (a more detailed comparison with this study might be useful, by the way). Rather, I think the aim of this study might be more to see which biomarker lipids in the Baltic Sea are promising to trace certain biogeochemically relevant microbes.

Although the present study is fairly comprehensive method-wise, I could not help thinking that some important biomarkers were not looked at : GDGTs, IPLs, ladderane lipids, carotenoids. For example, Bauersachs et al (2010, PNAS) reported the presence of cyanobacterial glycolipids in Baltic Sea sediments and it would have been great if the authors could have confirmed this in their samples as a good tracer for N₂ fixing cyano’s. Despite this, I do think the data are worthwhile to be published in Biogeosciences provided the abstract and introduction more clearly state what the aim(s) is (are) of this study and some minor comments in the discussion are addressed. Before submitting this review I checked the one published earlier by S. Buhring to avoid overlap in comments.

P 9858 l. 14. Indicate which standards were used.

P 9855, l. 14-25. This part of the introduction is confusing. I do not see the need to mention in situ pumping here. It also jumps back and forth between Baltic Sea and Black Sea. Perhaps this can be rewritten by first saying that comprehensive biomarker water column studies such as those in the Black Sea can tell a lot about biomarker sources followed by a review of biomarker water column studies done in the Baltic Sea.

P. 9860 l. 25., Fig. 3 I note that cholesterol and dinosterol are also present in the

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deepest point at 400 m where it is anoxic. Since the synthesis of sterols requires molecular oxygen (Summons et al, 2006 Phil. Trans.) this must mean that it is not produced in situ and is derived from fossil sinking material. I think you should make a remark on this as a potential complication of interpreting your depth profiles. This also comes back to the point of S. Buring about density layers containing dead material. P 9864 l. 9. I would make it more clear, i.e. phytoplankton and zooplankton.

P. 9866, l. 23-25. Mention Sinninghe Damste et al., 1995, GCA here. I agree with S. Buring that purple sulfur bacteria might also be a good source for tetrahymanol. Were these bacteria detected in the metagenome study of Thureborn et al., 2013 ?

P 9869, l. 18. This is an interesting observation. The maxima of BHT-II would be in agreement with anammox but as stated here, the metagenomic study of Thureborn et al., 2013 does not find hydrazine genes in this zone. A note of caution of course is that this study was done at different time interval. What is noteworthy is that the 10-methyl C16 fatty acid also maximizes at this depth. This PLFA is discussed on the next page but what is not mentioned there is that it is also an important fatty acid in anammox bacteria (eg Sinninghe Damste et al., 2005; FEBS Journal) and has sometimes be used as a tracer for anammox (Schubert et al., 2006, Env Micro). It would be nice if the authors could check for the presence of ladderane fatty acids in their PLFA fractions just to make sure that anammox was really not there. Alternatively, and as also suggested by Rush et al., 2014, the BHT II could be occurring generally in planctomycetes, not only in anammox. Indeed, in the metagenome of Thureborn et al. 2013 they do find sequences belonging to planctomycetes. Could this be the source of BHT II ? Some discussion on this option would be useful.

P 9871 and 9872. The conclusion section is perhaps a bit on the long side. More importantly, I am not sure if I agree with the statements in the last few lines. I think several DNA studies have shed light on biogeochemical processes and the importance of certain microbes in the Baltic Sea. Nuance this statement. Perhaps a more important conclusion would be to further expand the biomarker tool box to see if more tracers are

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available to track important microbes and biogeochemical processes in the Baltic Sea.

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