

Interactive comment on “Sulphur compounds, methane, and phytoplankton: interactions along a north-south transit in the western Pacific Ocean” by C. Zindler et al.

Anonymous Referee #3

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This study is a major effort of a carefully and, to my mind well executed, sampling campaign of the Western Pacific that has resulted in a large dataset comprising phytoplankton pigment data, and measurements of dissolved and particulate DMSP and DMSO, and DMS and methane. The principal aim of the study is to try and correlate the measured concentrations of DMSPd, DMSPp, DMSOd, DMSOp, DMS and methane in order to delineate whether there are (i) specific algal groups contributing to DMSP and derived sulfur compounds, and (ii) processes governing cycling of different sulfur compounds and (iii) whether there are links between DMSP, DMS, DMSO and methane production.

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The authors use statistical approaches to cluster the different provinces encountered during the cruise transect (Japan to Australia) based on pigment data from some 100 plus sampling stations with further qualification of these clusters according to absence or presence of specific pigments.

Overall I would suggest that the manuscript lacks focus and could be shortened and made more concise, the presentation of data could also be improved. The authors spend a lot of time discussing correlations of nearly everything that was measured to one another and for the reader that makes it difficult to follow what the really interesting correlations found may be, the message gets diluted. Finally, the section dealing with suggesting methane production from DMSP by particular metabolic pathways (DMSP demethylation) and types of aerobic DMSP degrading proteobacteria is inadequate interpretation of literature data; actually there are no data anywhere that have shown either. Perhaps it might be possible that methanogenic archaea could contribute to this, but there are no clear data suggesting this might be the case in the present study. Finally, it is argued that methylphosphonate degradation is unlikely to contribute to methane production here, but no convincing arguments are made that would allow to disregard this pathway.

Specific comments:

P15019, line 2 and further throughout: ‘prokaryotic algae’, please revise, this expression is incorrect, all algae are eukaryotic. This should be cyanobacteria.

P15020, line25, should be ‘as the sole source of DMSO...’

P15022 section re DMS: DMS must be linked to DMSPp and DMSOp somehow, but with a low r^2 it is clear that the potential antioxidant cascade this is just one of the processes contributing to its production, for instance bacterial degradation of DMSPd.

P15023 line 5: the authors exclude direct production of DMSO from DMSP since ‘this pathway has not been observed yet’, which might indeed make it somewhat un-

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likely, however later on the authors speculate re production of methane by aerobic methanogens, which also have not been observed yet.

P15024, line 6-8: even if bacteria were attached to particles (or were particles in their own right), the production of DMSO from DMSPd (via DMS, I assume) would release DMSO into the dissolved phase, thus this would be unlikely to explain the DMSOp pool

P15025 line 23-24: if this is an oligotrophic system, it may be very likely that most DMS might be used as an additional energy source by bacteria and so there could be quick turnover of DMS to DMSO (see Green et al 2011, *Appl Environ Microbiol* 77, 3137; Boden et al 2011, *FEMS Micro Letters* 322, 188), hence the argument that only a minor part of DMSP is cycled via DMS is not logical, especially as it is unclear how it could end up in DMSO otherwise (see point about direct DMSP to DMSO conversion made earlier).

P15030 line 5: I am unaware of any publications demonstrating production of methane from DMSP by the demethylation pathway? Could this be misinterpretation of the literature?

P15031: I do not follow the argument why methane production from methylphosphonates would have to be linked to cyanobacteria. What about heterotrophs?

P15031 line 5-12: none of the bacteria mentioned here has ever been shown to produce methane, this entire chain of arguments is therefore wrong and unjustified.

Fig 2 and 3 should be reformatted – perhaps as stacked bar graph. The current presentation is not useful.

Interactive comment on *Biogeosciences Discuss.*, 9, 15011, 2012.