

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

C. Zindler et al.

czindler@geomar.de

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Response to referee #3 for manuscript bgd-9-C5919-2012

We thank referee #3 for his/her careful work on our ms. The comments and advice were really helpful. We changed the method part and shortened the discussion part as per the suggestions by the referee.

R3: 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

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correlations found may be, the message gets diluted.

Authors: We shortened parts of the Result and Discussion section, tried to focus on important findings and also changed some figures to improve the data presentation. We hope that these changes improved the ms. We are aware that a lot of correlations were discussed, however, we tried to order the correlations in different sections which might help the reader to focus on the certain topics, such as the sulphur cycle by itself or the influence of phytoplankton on the sulphur species. We do not want to delete some correlations because we think it might be interesting and help to understand the complex and dynamic cycle of marine sulphur. We tried to summarize the most important findings of the correlations in the summary section.

R3: 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 methanogenicarchaea could contribute to this, but there are no clear data suggesting this might be the case in the present study.

Authors: We interpreted our results according to the findings and suggestions presented in Damm et al. 2010. They could detect these bacteria types in their experiments conducted with sample water which were taken in the regions where they found relationships between DMSP and methane. They excluded archaea as possible contributors for the methane production. Additionally, we cited papers which presented evidence that alpha-proteobacteria, belonging to the genus of Rhodobacteraceae, are able to degrade DMSP via the demethylation pathway (Moran et al. 2012, 2003, 2007).

R3: 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.

Authors: We deleted this sentence.

Specific comments: R3: P15019, line 2 and further throughout: 'prokaryotic algae', please revise, this expression is incorrect, all algae are eukaryotic. This should be cyanobacteria.

Authors: We changed the expression.

R3: P15020, line25, should be 'as the sole source of DMSO...'

Authors: We changed the word.

R3: P15022 section DMS: DMS must be linked to DMSPp and DMSOp somehow, but with a low r2 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.

Authors: The referee is right that the bacterial degradation of DMSP is also an important source for DMS. We did not mention it in this section because the model did not pinpoint the dissolved fraction of DMSP as correlating with DMS. We decided that we could not list all possible sources and sinks for DMS in this section because it would get too long and it is already indicated by the reviewers that the original discussion can be a bit unwieldy at times.

R3: 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 unlikely, however later on the authors speculate reproduction of methane by aerobic methanogens, which also have not been observed yet.

Authors: The reviewer is right, when defining aerobic methanogenesis exclusively as performed by aerchaaea. However, there are indeed publications which describe CH₄ production by bacteria in aerobic environments (see Karl et al, 2008, Damm et al., 2010). We rephrase the text (see sections Abstract, Discussion, and Conclusion). In addition, we removed the statement regarding direct production of DMSO from DMSP from the text.

R3: P15024, line 6-8: even if bacteria were attached to particles (or were particles
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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

Authors: If the bacteria stay attached on particles (or are particles as suggested by the reviewer) it might be possible that the DMSOd is accumulated in these particles in addition to be part of the dissolved pool. Thus, a mix of particulate and dissolved DMSO is possible. However, this is speculative and not proven by the models.

R3: 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).

Authors: The statistical models we used to identify relationships between sulphur compounds and algae groups cannot explain the fate the sulphur compounds. Thus, all the interpretations we give to explain the relationships we found are speculative. We have no evidence if there is a fast cycle between DMSP, DMS and DMSO or not. However, the referee might be right about the fast cycling by bacterial activities. We thank the referee for this good explanation and changed the statement in the ms concerning the suggestion made by the referee.

R3: 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?

Authors: Indeed, there is no direct evidence of CH₄ production from DMSP. However, the results from a microcosm experiment presented in Damm et al. 2010 point to a production of methane via the DMSP demethylation pathway. A similar pathway was

suggested for sedimentary CH₄ production (albeit at anoxic conditions) via DMSP demethylation by Van der Maarel and Hansen, 1997.

R3: P15031: I do not follow the argument why methane production from methylphosphonates would have to be linked to cyanobacteria. What about heterotrophs?

Authors: We deleted this sentence.

R3: 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.

Authors: We do not agree. Our argumentation is based on the findings of Damm et al., 2010: The bacteria which were mentioned in the ms were identified in microcosm experiments conducted by Damm et al. 2010. These experiments showed enhanced methane concentrations when DMSP was added. Over the course of the experiment the abundance of archaea was negligible and the cited bacteria made up almost 100% of the microbial community. Thus, Damm et al. concluded that microbial degradation of DMSP to methane was conducted by these bacteria (perhaps in connection with N₂ fixation, based on the occurrence of nifH genes over the course of the experiment).

R3: Fig 2 and 3 should be reformatted – perhaps as stacked bar graph. The current presentation is not useful.

Authors: We have changed the figures.

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