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Biogeosciences Discussions



# *Interactive comment on* "Biochemical characteristics and bacterial community structure of the sea surface microlayer in the South Pacific Ocean" *by* I. Obernosterer et al.

**Anonymous Referee #2**

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The present paper is well written and presents results of a thoroughly conducted study on biogeochemical and microbiological differences between the sea surface microlayer and the subsurface waters at 5 m depth. The major goal of the study was “to evaluate by two complementary molecular-based techniques” whether the bacterial community differs between the water layers and whether there is a specific relation to major biological and chemical parameters. Although the study has been performed with great care I have the following points of concern:

1) The authors have chosen FISH for detection of particular bacterial groups even though the precise bacterial community structure at the sampling points and dates

remain unknown. The low detection rate of the EUB probe, hence, may have 2 reasons: a) Archaea which are not detected by the EUB probe were also highly abundant? b) methodological reasons, e.g. low hybridization efficiencies due to small and inactive cells and low detection efficiencies when solely using probe EUB and not a mix of probes EUBI-III. Figure 5 shows that percentages of Bacteroidetes, alpha- and gamma-Proteobacteria often exceed those of EUB indicating higher hybridisation efficiencies of the more specific probes.

2) The selected probes have some major biases since they do not detect all known bacteria of the respective group. E.g. probe CF319a miss a high percentage of target sequences when comparing it with the data bases. This needs to be discussed.

3) The CE-SSCP fingerprints do not reveal any information on the phylogeny of particular SSCP-peaks. Hence, the selection of the used FISH probes may have led to a rather low phylogenetic resolution. Bacterial community structure in the sea surface microlayer does not necessarily differ from the subsurface waters at 5 m depth based on the presence and absence of specific SSCP-peaks. Since changes in environmental parameters and the exchange rates between the water layers are high it is more likely that the numbers or activity of specific phylotypes change in relation to the measured parameters. I wonder whether the authors still can determine DNA to RNA ratios by flow cytometry?

4) Although the authors have measured activities for the major bacterial groups (Bacteroidetes, alpha- and gamma-Proteobacteria) differences may be more pronounced for specific phylotypes. This should be at least mentioned in the discussion. Personally, I do not like the statement that all members of the detected bacterial groups do the same. There are many indications in the literature that this is not the case. May be RT-PCR for amplification of RNA would have been more useful?

5) UV radiation is a major environmental variable which –on a short-time scale- can have dramatic effects on activity of specific phylotypes. It is well known that par-



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ticular bacteria are more and others less affected by UV radiation. On the other hand, due to photochemistry more refractory DOC fractions become available for bacteria. This is an important point which should be more intensively discussed by the authors. Are there some data on solar radiation available? If yes, the authors should also try to plot some correlations similar to those for wind speed. I guess wind speed does also effect UV penetration into the water column…

6) I further miss a discussion section on the general importance of the present findings for biogeochemical fluxes and the sea-air gas exchange.

Samples for DOC have been pre-filtered through GF/F filters which have a pore size of ca. 0.7 $\mu$m, thus, some bacteria and other organisms may have passed through the filters. This must be mentioned.

The authors should know that there are more recent papers from Agogue and co-authors. In the 2005 FEMS paper, for instance, they show that also quite some gram-positive bacteria were present. Did the authors check for the presence of these bacteria which would have been missed by the FISH probes…

P2821, line 11: space after chlorophyll a, P2825: line 7, 11, 22, 25: ?? after Reinthaler should be removed, Figure 3: legend is a bit misleading

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Interactive comment on Biogeosciences Discuss., 4, 2809, 2007.