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Biogeosciences Discussions

Interactive comment on "Distinctly different bacterial communities in surface and oxygen minimum layers in the Arabian Sea" *by* Mandar Bandekar et al.

Anonymous Referee #2

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The authors have used DNA sequence analysis of environmental 16S rRNA genes and phylogenetic reconstruction to investigate the community diversity of bacteria present at a time-series station in the Arabian Sea. Samples were obtained from the surface mixed layer and from within the oxygen minimum zone (OMZ) on three separate occasions over the course of several months and under contrasting hydrographic conditions. The authors conclude that while there was no distinct seasonal difference in community structure (lines 21-22), greater diversity and community richness were evident within the OMZ when compared to the surface and deep chlorophyll maximum.

While the latter observation is of interest, it is based on a very modest number of sequences from each depth and time point (Table 5) and not that well supported by classi-

cal indices of diversity (Shannon and Simpson indexes). As the authors acknowledge at several points in the manuscript (e.g., Section 3.6, lines 334-335, lines 436-438, etc.) their findings are preliminary because due to the under-sampling of the community they have not captured or analyzed in sufficient depth the far greater diversity evidently present at the station in order to draw robust conclusions.

Where they may be on firmer ground is in reporting that the composition of the surface community was distinct from that of the OMZ (Section 3.5). Much of this difference appears to be explained by the absence of cyanobacteria from the deeper samples (lines 195-198, lines 269-270), however, which is an expected result given their photoautotrophic nature. Indeed, if one ignores the contribution of cyanobacteria to the surface community, the relative percentage contributions of the dominant heterotrophs (alpha and gamma proteobacteria) at all depths would be much less distinct than that shown in Figure 2. Reanalyzing the data (minus cyanobacteria) might proof useful.

Minor points:

Line 13 What does 'Contributions" mean? Numbers, biomass, activity?

Line 84 What is 131 Tris?

Section 2.2 Much more detail of the PCR conditions is required. The reference to the manual of Sambrook (et al.) is insufficient - what were the temperatures, times, cycle numbers, etc.?

Section 2.3 TA cloning is very efficient. What explains the poor numbers of transformants recovered in this study?

Line 103 Manufacturers name and reaction conditions required

Line 104-05 Which primers and reaction conditions were used for sequencing?

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