

# ***Interactive comment on “Hidden biosphere in an oxygen-deficient Atlantic open ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic” by C. R. Löscher et al.***

## **Anonymous Referee #2**

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The manuscript entitled, “Hidden biosphere in an oxygen-deficient Atlantic open ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic,” presents an interesting set of biological and geochemical data from an anticyclonic mode water eddy. The results of the study are placed in appropriate context and reveal how sharp gradients in oxygen may affect microbial community composition.

## General comments

The abstract says that “metagenomic” data are shown, but the molecular markers used

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in this study are for bacterial/archaeal diversity, and a few functional genes. “Meta” suggests that large portions of the community genes are evaluated, which is not the case. It would be more accurate to edit this phrase. Outside of the abstract, this term is not used, so the body of the text is appropriate in scope.

Here the statement is made that enhanced primary productivity fuels enhanced export, but there is little to no primary evidence within the manuscript to support this statement. Is export flux greater within the eddy than in nearby regions, and if so, how is the time-space decoupling of productivity and flux resolved?

The cut-off of 90  $\mu\text{mol/L}$  oxygen concentration to differentiate ‘realm’ effects is not sufficiently supported. Is there evidence in the literature for such a cut-off, for example, are certain microorganisms known to respond differently across this threshold in relation to metabolism/productivity and therefore, it is an ecologically important distinction?

Relating again to the oxygen concentration cut-off – how do communities compare along the oxygen gradient? Does alpha diversity (or total OTU abundance) decrease with decreasing oxygen concentration?

Within the methods section, where volumes are given for reagents within assays, it would be more useful to provide the final concentration.

On several occasions the phrase “of around” is used to mean “approximately.” While generally well written, the manuscript requires some additional editing for increased readability.

Specific comments:

p. 14182 l. 18 – DNA and RNA were quantified fluorometrically using a Nanodrop. This instrument is a spectrophotometer.

p. 14185 Statistics section – intent and readability would be improved for each subsection with an initial sentence about the statistical process and its purpose; especially for those less familiar with the exact procedures.

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p.14188 l. 13-15 What were the depths at which samples were collected that are considered below the euphotic zone?

p. 14188 l. 16-17 How might carbon fixation measurements be affected if total volumes were not filtered for  $\delta^{13}\text{C}$  enrichment? Could primary productivity estimates be over-estimates?

p. 14192 l. 12-16 Are cell counts (microscopy and/or flow cytometry) available to conclude that the qPCR Prochloro/Synechococcus data are representative of relative differences in abundance of cyanobacteria and eukaryotes in- and outside of the eddy or within either chl max layer?

p.14192 l. 17-28 Why might HL-adapted Prochlorococcus ecotypes be abundant below the euphotic zone? This seems counter-intuitive. Suggestions on why this might be would be interesting.

p. 14193 l. 12-13 This paper states that Prochlorococcus could contribute up to 40% of the DOC that could support bacterial production. As written, the statement suggests that Prochlorococcus is responsible for 40% of bacterial production.

p. 14195 l. 20 I am surprised that nifH genes were not quantifiable from the eddy. nifH genes have been retrieved from this region. Assay detection limit? High inorganic dissolved nitrogen concentrations and N:P ratios close to Redfield do not exclude the possibility of diazotrophs and/or biological nitrogen fixation.

## Figures

1. no comments 2. For the oxygen concentrations, can the profile of discrete O<sub>2</sub> concentrations be shown? 3. Figures should be larger for easier readability. 4. Figures should be larger for readability. Greater transparency of the colored bars would make the trends easier to compare across panels. Figure legend reads 'oxygen versus depth,' but this line is oxygen concentration. Colors used for Proteobacteria and Bacteroidetes are very similar. Would be easier to discern with different colors. 5. Dark

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purple and dark blue points are difficult to discern from one another. 6. Check eddy axis labels. Is this correct with 'eddy\_2' on the left? 7. Transparency of bars needs to be greater so data points can be seen. Are these discrete or derived measurements of chl a? Legend edit is required and methods section should include description of chl a measurement methods. Chl a units are missing. 8. Difficult to discern low concentration areas of the plots. Is the number zero copies, or "not detected?" What is the detection limit of the assays? Symbols are difficult to differentiate as plotted. Increase size of plots and/or data points. X axes' labels should be edited to be consistent in format. 9. One symbol could be 'open' so overlapping data can be more clearly seen. Again, what is the detection limit of the assay? Is the data point zero or 'not detected?'

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