

## ***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 #1**

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The manuscript '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 Löscher et al. presents interesting differences in microbial community structure in mesoscale eddies in the eastern tropical Atlantic Ocean. The study is comprehensive and presented well, combining biogeochemical and molecular data.

General comments:

I am fairly surprised to not see organisms of the SUP05 clade being present/abundant here as they are normally found in OMZs. Was the amplicon dataset screened for C5820

them?

If the figures are already the size they later should appear in the manuscript, then I would suggest increasing it for the sake of readability. They are really nice, so no need to make them so small.

While the manuscript is generally well written, sometimes complicated sentence structure with multiple subsentences makes reading bothersome. Streamlining this a little could enhance the reading flow significantly.

Specific comments:

p. 14178, l. 10 ff: "...at depth around 40 to 100 m..." sounds weird. Is "...at depths of around 40..." meant?

p. 14180, l. 6-13: Why state the aim and then the ultimate aim? Wouldn't it make more sense to clearly define what the aim was? To identify differences in microbial community structure between eddy and surrounding waters was just a step towards the aim, or?

p. 14190, l. 15: It would be nice to cite the original papers here.

p. 14190, l. 21 ff: It is not clear if the methanogens detected are free living in the water column or are particle associated. Judging from the collection of biomass samples on 0.2  $\mu\text{m}$  filters, both options could be possible. Were free living methanogens detected in OMZs previously?

p. 14192, l. 12-15: To confirm if the upper chl a maximum is caused by eukaryotic phototrophs, it might be an idea to look into the sequences classified as cyanobacterial 16S rRNA and see if 16S genes from plastids were detected and are hidden in there.

p. 14193, l. 23-25: Judging from the phylogenetic information on the metabolisms of the organisms is not always possible, so the statement is fairly strong here. While I think the authors are right I still would word it a little bit more careful.

p. 14194, l. 7: original studies are missing in the references (Morris 2002, Rappe 2002)

p. 14195, l. 4: How do the 3000 copies/L and 100 copies/L compare to the bacterial 16S rRNA gene copy numbers? What part of the population has the capability for denitrification? Because of differences in cell numbers between eddy and the outside the actual difference might not be as high as suggested.

p.14195, l. 12: With similar reasoning as in the comment above, it would make sense to compare the transcripts of the nirS gene to a housekeeping gene.

p. 14197, l. 22: space missing

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Interactive comment on Biogeosciences Discuss., 12, 14175, 2015.