

Biogeosciences Discuss., referee comment RC2  
<https://doi.org/10.5194/bg-2021-96-RC2>, 2021  
© Author(s) 2021. This work is distributed under  
the Creative Commons Attribution 4.0 License.



## Comment on bg-2021-96

Anonymous Referee #2

---

Referee comment on "Hydrothermal trace metal release and microbial metabolism in the northeastern Lau Basin of the South Pacific Ocean" by Natalie R. Cohen et al.,  
Biogeosciences Discuss., <https://doi.org/10.5194/bg-2021-96-RC2>, 2021

---

In this manuscript, Cohen et al conduct a systematic sampling of different stations in the pelagic ocean along a transect in the south Pacific Ocean to study trace metal distributions and their potential association with microbial physiology. Trace metal concentrations were measured and observed patterns are associated with both ocean scale and local oceanographic and biogeochemical processes. Additional metaproteomic (and 16S/18S rRNA analyses) were conducted to characterize the microbial (eukaryotic and prokaryotic) communities and the proteins. I found the methods to be solid and the paper to be exceptionally well-written and easy to read. I really commend the authors for a very comprehensive piece of work. Overall, in my opinion, this study represents an important piece of work that expands upon the growing body of trace metal studies across the oceans, and specifically contributes to our understanding of the distribution of dissolved metals across ocean depths and regimes, and their association with microbial metabolism.

I do have some concerns/suggestions for improvement that I outline below.

I understand that the authors cannot pinpoint exact sources of trace metals since specific hydrothermal vents were not sampled. This is highlighted in the text very briefly – I think it would be useful to have a map showing the 135 known vents in the NE Lau Basin as they can help the user interpret the data and findings better.

Methods – For the biological analyses are concerned, the only drawback I observe is the Cohen et al 2021 is referred to for most methods. I suggest including some brief additional details here – such as how was the translational metatranscriptome generated? How was the 16S rRNA analyses done?

Figure 1 – I recommend enlarging the maps as the stations are referred to in the manuscript but finding them currently is difficult.

Ln 60 – determined\*

Line 277 – It is unclear to me as to why the Manganese concentrations are so low. Is this unique to this region or is this also observed in other oceanic regions. I ask because Manganese oxidizing bacteria surely also exist in aphotic water columns elsewhere.

Metaproteomics – For the metaproteomics analyses, 20 background samples are used but only a single hydrothermal sample is used. Is there a possibility that more samples could be used? Alternately, could there be some justifications added for this...

Remnant phototrophic metabolism – This is an interesting finding but I do not think it is important or justified enough to be highlighted as a section title. Are the authors confident that this may not have arisen due to any contamination? Are there any studies looking at degradation of proteins from *Prochlorococcus*? To be honest, I do not doubt this finding (I have seen this myself in other aquatic settings) but I am always looking for additional lines of evidence to potentially explain this.