Response to Reviewer 1: Dr. Cene Fiser

Manuscript Title: Biogeography and community structure of 1 abyssal scavenging Amphipoda (Crustacea) in the Pacific Ocean.

Ref: bg-2018-347

Journal: BioGeosciences

Dear Dr Fiser,

We would like to thank you very much for your useful feedback on our manuscript.

Below you will find a point by point reply on how we addressed your comments in the revised version of our manuscript. Attached also is a copy of the manuscript with track changes highlighted in blue, to indicate where the grammatical changes and suggested rephrasing of sentences, have been incorporated. Please be advised that all line numbers now refer to the revised PDF attached.

Finally, please see in table 1.0, a summary of comments which have been taken into account, and those requiring a significant revision of the analysis, which will be completed by November 16th.

We thank both you and the journal for the useful comments and opportunity to submit a fully revised manuscript in the very near future.

With Kind Regards, also on behalf of the co-authors,

Tasnim Patel.

Table 1.0 - Summary table showing the status of all comments addressed, and those pending as of **19.10.18.** Comments requiring a revision of the analysis, etc (RC2 and RC3(ii) will be completed by 16th November.

RC1	✓
RC2	TBC
RC3(i)	✓
RC3(ii)	TBC
RC4	✓

RC1: First, I miss details how individual statistical analyses were performed. Please, clarify them.

Our reply: The packages and functions used in R are stated for the rarefaction and NMDS analyses (e.g. Vegan, Bray-Curtis-index and testing of significance with ANOSIM). As suggested, we have now included the version of the Simpson Index equation used to calculate alpha diversity (*D*) in the appendix (4). If further clarification is required please let us know.

RC2: Second, I strongly encourage authors to revise their Catch Per Unit Effort analysis. My feeling is that dependent variable should not be divided by time, and that because of this modification authors miss an important result.

Our reply: We agree with the suggested revision "If you studied a simple relationship x = time, y = catched, I expect you will receive a 'log' shaped curve. From this curve, one could predict optimal time needed for setting the traps".

We plan to implement this new calculation in a revised CPUE plot by November 16th.

RC3 (i): Third, I am not sure that D is best measure of alpha diversity. Please clarify / justify its use.

Our reply: We chose to use the Simpson Index (*D*) to measure alpha biodiversity over e.g. the Shannon-Wiener (*H*) or Sorenson measures, as they are similar, but *D* is more commonly used to express diversity in a location and is based on relative abundances of each species.

Secondly, we noted that we sampled many singletons/doubletons (species occurring at only 1 or 2 stations). The Shannon-Wiener index is more strongly influenced by the occurrence of these "rare" species. Therefore, these smaller numbers (e.g. in contrast to the > 500 individuals of *A. gerulicorbis*), would mean that although they are similar methods, *H* is a less suitable method in this case. This is because *D* gives more weight to the evenness of species relative to the overall sample size. Therefore, it is looking at the basin and sites as a whole. Rather than being skewed by minute diversity changes (which we cannot rule out are an arterfact of undersampling).

The Sorenson index was used, but not included as it is a similarity index which we have already shown using the Bray-Curtis similarity index in the NMDS plot.

RC3 (ii): All indices and relative numbers in this particular manuscript make the ms less intuitive and more complicated.

Our reply: We are unclear about this comment. If it is referring to the naming of sites as D1, D2, D3 etc, we considered to be clearer than SO241-1/33 etc. In figure 1.0, the geographical location of all sites mentioned are shown on a map.

If the comment refers to the Simspon Index as "*(D)*", we are happy to change this throughout to state the full name. We appreciate your clarification.

RC4: I found several small issues, that can be easily solved; they are labelled directly in the PDF.

Our reply: We attach with this reply a revised version of the manuscript. Please find highlighted in blue, the grammatical revisions suggested.

Other questions posed in the manuscript are answered below:

1. Please, state more details on procedure. At present, it is unclear how you constructed them.
   - *Rarefaction curves were constructed using the "rarefy" function of the Vegan package in R.*

2. to compare the beta biodiversity, we estimated the variability of the community compositions per site.
   - *Line 249 now reads – "to compare the beta biodiversity, we estimated the variability of the community compositions between sites."*

3. I am not familiar with technique does it correct also for spatial nonindepndence?

   - *The NMDS ordination is a visualisation of a distance matrix based on the Bray-Curtis index, and correlations cannot be drawn between the points and community dis(similarities) e.g. between the CCZ and DEA. The subsequent ANOSIM is a statistical test to see if these species assemblages show a significant difference between the basins (which they do with p = 0.002).*

     We agree spatial autocorrelation is of importance in statistical tests in which you assume that your data are independent of each other (parametric tests). When they

are spatially autocorrelated they are not independent. No such assumptions are made for NMDS, so spatial autocorrelation issues are not relevant here.

4. I would recommend that you simplify and unify the terminology species-morphospecies - morphotypes through the text.
   - *All four instances of "morphospecies" have been changed to "morphotype".*

5. Please, label color codes (Table 2b)
   - *This has been completed for Table 2b.*

6. Please clarfiy this plot. If I understand your work properly, two questions popup to me:
   1. Is relationship recovered when you analyze the two bioregions separately?
   2. I have concerns with dependent variable, which in your plot implicitly includes also independent variable. High values in the first hours of trapping may be result of low denominator. Levelling of after one day may mean that all individuals in vicinity were attracted, but the catch /hr is low because of high denominator. The number of cathced may increase, but slowly because individuals need time to reach the trap. Calculated per hour it means that time increases faster than individuals, and value is dropping. CPUE may change with respect to nominator and denominator..

   If you studied a simple relationship x = time, y = catched, I expect you will receive a 'log' shaped curve. From this curve, one could predict optimal time needed for setting the traps - and - in my opinion - this would be very useful information for future studies.
   - *The authors intend to revise this plot as per your comment RC2.*

7. Perhaps state "negative exponential correlation"?
   - *This has been changed. Line 335.*

8. This is likely related to previous plot. All D traps were set for a shorter period. If the traps were dropped for longer periods, they would reach the plateau. This is an application from my previous comment: one can expect saturated rarefaction if traps are set for roughly 6 hrs.
   - *The rarefaction analysis is not related to the catch per unit effort. The rarefaction is an analysis of the number of species found (richness), relative to the total number of species found in the two basins. It is a visualisation of whether all species have been recovered or if more sampling would be required. The time of each deployment is not a factor in this analysis. Nonetheless, the residence time of each trap was standardised to approximately 48 hours (as is now shown in table 1).*

9. The interpretation depends on which variation of D you used. It might be a good idea to define to which of many D you relay to. Only then you can state whether high D indicates high biodiversity.
    - *The equation for the Simpson Index is now shown in appendix 4, in this version of the equation, a higher* D *is indicative of higher biodiversity.*

10. I find this division in 2 clusters partially arbitrary, other divisions into eg 3clusters are possible as well. I suggest you make a cluster analysis and check for the numebr of clusters if this is really needed. Otherwise simly cut this part of the sentence.
    - *The authors agree. Line 436 now reads "The NMDS shows that the communities of the two basins are clearly separated (ANOSIM: p = 0.002); Figure 6). The disturbed area in the DEA (D1) is showing a clear difference to the four reference areas (D2 - 5)."*

11. It seems a bit low number? Maybe write over 7000
    - *Line 456 now reads "Over 7000 marine amphipod species have been found below 2000 m."*

12. I would be careful. Why you do not check also row numbers? Playing with indices (individuals / hr, D) is masking the real dynamics
    - *The Simson Index was calculated based on the raw abundances which were simply transformed into relative abundances to show the percentages of each of the species in each basin. This was done, because some stations yielded far more individuals than others. The data was not manipulated to mask the raw numbers. Since the manuscript is not analysing biomass of each station, but biodiversity/assemblage patterns, the data was standardised from absolute abundances into relative abundances.*

13. Please consider also a recent paper in PeerJ, on predatrory amphipods: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5994337/
    - *Thank you, the authors missed this paper. Line 543 now reads "Scavenging amphipods are resilient and dispersive, but most importantly, they are highly mobile (Ingram and Hessler 1983; Lörz et al. 2018)."*

14. As stated above, it is hard to directly compare DEA and CCZ because of different deployment times and different sampling efforts. Rearefactions would be needed for a thorugh comparisons of the two regions.
    - *Clarifications of the deployment times are now provided in table 1. It shows that we tried to standardise the trap residence times, which again, are not related to the overall cruise length. Rarefaction is an estimate of the species richness and not related to the sampling effort and time. As answering to your comment RC2, the plot related to sampling time (CPUE) will be improved in the revised manuscript.*