Dear Biogeosciences Editors,

Please find enclosed our revisions along with point-by-point responses to all reviewer comments. We now include an exhaustive list of all parameter values in our online code repository, and the most relevant ecosystem parameters are provided in the main text of the manuscript. We have also conducted simulations testing the sensitivity of our main findings to different assumptions about plankton size and microzooplankton feeding mechanisms. Note that, since our last submission, we updated our code to use a more recent version of the Darwin ecosystem model. None of our main conclusions are qualitatively impacted, but several of the figures have minor aesthetic differences due to small changes in parameter values.

We have also now included more discussion of prior work as it relates to our main conclusions. Overall, we are very grateful to both reviewers for providing thoughtful and constructive comments that we feel have led to deeper understanding of our model simulations that has improved the manuscript.

## Kind regards,

David Talmy, Eric Carr, Selina Våge, Harshana Rajakaruna, and Anne Willem Omta

## **Reviewer 1**

General comments:

Talmy et al. Biogeosci notes

The authors use a simplified N-P-Z-D model to examine the influence of food web structure and mortality closure form on plankton community composition. They found that total phytoplankton biomass and plankton community composition were impacted by food web structure and the form of losses on the microzooplankton grazers. Results demonstrate the quadratic mortality is most consistent with the linear scaling of phytoplankton and microzooplankton biomasses seen in observations and suggest that parallel food webs may be more appropriate for representing the coexistence of small and larger phytoplankton. This simplified experimental design allows for clear understanding of model structure influences ecosystem dynamics and of how much model complexity is required to capture observed biogeochemical properties. The results are bolstered by comparing model results to observed patterns (e.g. the linear scaling of phytoplankton and microzooplankton) rather than individual biomasses alone. I think this would be valuable to the BG readership.

The paper addresses relevant scientific questions within the scope of BG. The concepts, ideas, and tools are not necessarily novel, but their implementation and the comparison with recent observational datasets are. The scientific methods and assumptions are valid and clearly outlined, the results sufficient to support the interpretations and conclusions, and substantial conclusions are reached. The description of experiments and calculations are not sufficiently complete and precise to allow their reproduction by fellow scientists (traceability of results). Additionally, the authors do not give enough credit to related work, though they do clearly indicate their own new contribution. I do not think that the title clearly reflect the contents of the paper, specifically the use of the term "top predator." The abstract provides a concise and complete summary, the overall presentation is well structured and clear, and the language is fluent and precise. All mathematical formulae, symbols, abbreviations, and units are correctly defined and used, though parameter values, which I think are necessary, are not

given. As such, the amount and quality of supplementary material is inappropriate. However, some formulae in appendix can be abbreviated. Finally, the number and quality of references are appropriate.

Thank you for these constructive remarks. We have now provided an exhaustive list of all model parameter values in our online code repository, and a subset of these is provided in the main text. We have also provided results showing additional biogeochemical model predictions in a supplementary file. We respond to each specific comment below.

Specific comments:

#### 1. Title and terminology

I would argue this term is misleading because microzooplankton are rarely considered top predators, even if they are the end of the food chain as modeled in this paper and others. Most people think of a top predator as a carnivore with few or no predators themselves; e.g. L64-65: "higher predation on the top predator" is counterintuitive. "Highest predator," (L136) "highest predator modeled/represented," or "terminal predator" may be better.

# We have changed the title to: "*Killing the predator: impacts of highest predator mortality on global-ocean ecosystem structure*" and used this terminology throughout the manuscript.

#### 2. Take-away message

2a. L19: "importance of parameterizing" Density-dependent mortality on the terminal predator has been included in these models for decades. The closure term was always chosen to get plankton dynamics "correct" (near those observed). I think that L41 may be the more relevant significance of this paper, i.e. understanding "how much model complexity is required to capture biogeochemically relevant properties." Specifically, the underlying drivers of linear scaling between microbial predators and prey are expounded.

We have altered the abstract to emphasize that these biomass scaling relationships can be reproduced with models of low complexity (Lines 20-21, new text underlined):

"Our findings point to the importance of parameterizing mortality of the highest predator for <u>simple food web</u> models to recapitulate trophic structure in the global ocean"

We are reluctant to claim that we can be sure how much complexity is required to capture biogeochemistry, as our study is limited to understanding just one small property of these systems, namely the biomass scaling relationship between microzooplankton predators and their phytoplankton prey.

2b. L44-46, L50-52: I really like the use of relationships/patterns found in observations to inform modeling or to assess models. I think this is an underutilized tool in the field. Such comparisons have been made by Luo et al. (2022) and Petrik et al. (2022), albeit chlorophyll instead of phytoplankton biomass, but they should be cited.

## We have added these citations (Line 45)

#### 3. Comparisons with ESMs

3a. L66-67: I think this statement is false. BGC model developers put a significant amount of effort into calibrating mortality equation structure and parameterization. Often they are trying to capture simple metrics like total NPP or the spatial patterns in the global distribution of chlorophyll, but others go beyond that by calibrating against plankton community composition, Z:P spatial patterns, seasonal plankton biomass patterns, z-ratio, e-ratio, etc. (see Aumont & Bopp 2006, Aumont et al. 2015, Stock & Dunne 2010, Stock et al. 2014, Yool et al. 2013, 2021). Following on this, the authors have shown how phytoplankton community composition can vary based on food web structure and zooplankton mortality

form. Do these choices also influence other important BGC quantities like NPP, export production, and the amount of secondary production available for zooplankton consumers?

We have modified this statement (Lines 67-70):

"The assumptions made here profoundly influence biogeochemical properties such as primary production and chlorophyll distribution (Aumont and Bopp 2006; Stock and Dunne 2010; Yool et al. 2013; Stock et al. 2014; Aumont et al. 2015). However, it is unclear if and how their effects are dependent on choices made about food web structure."

And added maps showing depth integrated primary production, carbon export, and secondary production to the supplementary information (Figs S3-S5)

3b. L95-96, L105, L264: These statements suggest that both parallel and diamond food web models are very prominent in the OBCG component of ESMs. How common is either of these? And is one more common than the other? It would be nice to have more quantitative idea of this. How many global ESMs only have microzooplankton (not one zooplankton that represents both)? And how many of them have parallel vs. diamond feeding? You could focus on just those that participated in CMIP5 or CMIP6. For example in Rohr et al. (2023): 3 with only 1P, 1Z (HAMOCC, CMOC, WOMBAT); 2 diamond (OECO, MARBL); 2 parallel (CanOE, COBALT); 3 hybrid (MEDUSA, PICES, BFM). Or Kearney et al. (2021): 1 with 0P, 0Z (BLING); 4 with 1P, 1Z (CMOC, WOMBAT, MRI, HAMOCC); 3 diamond (OECO, MARBL, NOBM); 2 parallel (CanOE, COBALT); 2 hybrid (MEDUSA, PICES). I don't expect the authors to list all these details in the paper, but suggest at their prevalence (e.g. ~30% of CMIP5 ESMs).

Interestingly, in most cases where there is just one zooplankton, it is usually 'adaptive', intended to represent both micro and meso-zooplankton (see also reviewer 2 comments on this subject). Also, many of the CMIP6 models have elements of both parallel AND diamond feeding (e.g. COBALT and MEDUSA). Therefore, one could argue that in fact none of our models match exactly with any of the CMIP6 models. Nevertheless, parallel feeding and shared predation are components of many of these models, and by evaluating these model properties in isolation, we aspire to inform development of more complex models with other considerations. We have therefore taken this reviewers suggestion but identified all models evaluated by Rohr et al., with diamond (OECO-v2, MARBL, MEDUSA, PISCES, BFM, COBALT) and/or parallel components (CanOE, MEDUSA, PISCES, BFM, COBALT), and rephrased this section, e.g. (Line 99-101):

"Furthermore, parallel feeding was a component of five of ten Earth system models that were part of the most recent Coupled Model Intercomparison project (CMIP6) evaluated by Rohr et al. (2023), making it a useful food-web structure to examine in a global ocean context."

We have also added a paragraph to the discussion recognizing the mismatch between our models and many ESMs (Line 318-326):

"The food-web model structures assumed here are so simple that they exclude many mechanisms already considered in extant Earth system models. For example, many Earth system models contain representations of both microzooplankton and mesozooplankton. In some cases, these are explicitly represented with multiple state variables (Stock et al. 2014; Aumont et al. 2015). In others, a single 'adaptive' zooplankton class mimics the effects of micro- and meso-zooplankton by feeding differently on phytoplankton prey types (Moore et al. 2004; Long et al. 2021). Future studies may evaluate the impact of different closures in the context of these more sophisticated structures. Despite the simplicity of our models, we anticipate that our central conclusions will hold in a more general setting. Specifically, assumptions made about highest predator mortality constrain biomass scaling relationships regardless of model predictions about community composition within a trophic level."

4. Missing information on experiment design and parameters.

4a. L109-110: Are the growth and grazing parameters different by size? Where can I find these?

## Yes, these vary according to allometric scaling relationships that are now provided in Table 3 of the main text

4b. L114: What is the sensitivity of the results to these assumed sizes? I would argue that when ESMs use only one zooplankton type, it is supposed to represent both micro and mesozoo. Similarly, when there are two zoo types, one is micro and one is meso, and the meso preys on the micro, which is missing from the parallel food web here. Also, the "large phytoplankton" here is barely the size of the diatoms in ESMs (10-100 um, "microplankton"), while both the small and large microzooplankton are also at the low end of the microzooplankton (10-200 um in ESMs, 2- 200 um in Sieburth et al. 1978), and when there is only one zooplankton group in ESMs it tends to encompass everything 10-2,000 um. I do not mean to suggest that this study is without value for that reason, but the comparison to global ESMs used for climate change studies is less direct.

Interestingly, there seems to be a great deal of variation regarding what is being described in ESMs. From Rohr et al., 2023: "*it is concerning that some models imply something statistically similar to an ocean filled entirely with very slow-grazing meroplankton larvae (MEDUSA2.1, OECOv2) and others an ocean filled entirely with very rapidly-grazing ciliates (MARBL and CMOC)*." Therefore, our modeled rates of grazing are likely to fall within the envelope of values simulated in ESMs. Nevertheless, we conducted sensitivity simulations modifying phytoplankton and zooplankton size (described in lines 174-179 and lines 282-283) and found that our primary conclusions regarding scaling relationships are insensitive to assumptions about size. These results are shown in Figure S6.

4c. L127-128: Is the linear mortality term included in both versions? Or is it either linear or quadratic mortality? It is rare for ESMs to have either linear or non-linear mortality terms on their zooplankton. The linear loss term in these models usually accounts for metabolic losses while the non-linear term accounts for higher predator mortality (see Kearney et al. 2021, Petrik et al. 2022). This is alluded to on L276-279.

Great question, we did have the linear turned on with the quadratic but have since conducted a sensitivity where we switch it off. Turning off the linear in the quadratic case appears to have negligible impact on the properties we report, indicating that quadratic closure may have an outsized impact on ecosystem properties.

We recognize that both sources of mortality are usually included in ESMs. However, many simpler ecological and biogeochemical models opt for linear closure (excluding quadratic) as these are often algebraically more manageable. We now clarify in the caption of table 2 that these values are switched to zero in simulations where they are not considered

4d. Table 1: Did  $\delta_Z$  and  $\delta_{ZZ}$  have the same values in the parallel and diamond food webs?

Or all the parameters for that matter?

Yes, these are now provided in Table 2 and we clarify that these and all other parameters are held constant unless the entire term is neglected

4e. Figure 2: Are the arrows meant to line up with (phyto $\rightarrow$ PON) and (zoop $\rightarrow$ DOP) or is that just a coincidence?

#### This is just a coincidence

4f. Appendix Equation A34: What are  $g_{max}$  and  $K_{1/2}$  for the two microzoo types? Are all parameters held constant between the model version?

These values are now provided in Tables 2 and 3 of the main text.  $g_{max}$  is determined by allometry but  $K_{1/2}$  is not. Therefore,  $g_{max}$  was different for the two microzooplankton whereas  $K_{1/2}$  was not.

4g. Table A3: The parameter values pertaining to zooplankton mortality and grazing should be given here since that is the focus of the paper. Also, I could not find these parameters on the website listed. Please give the filename and folder/directory with these values.

Tables 2 and 3 provide the relevant mortality and grazing parameter values, and an exhaustive list of parameter values is provided in our online repository (link https://github.com/werdna-spatial/GUD\_closure/tree/main/Paper\_Data).

4h. Table A3. "The large phytoplankton has a faster maximal growth rate and higher nutrient half-saturation constants than the small phytoplankton, representative of differences in growth rate between a eukaryotic algae and a cyanobacteria, respectively (Litchman et al. 2007; Ward et al. 2012)." Is this true of the microzooplankton when there are two size classes?

The larger zooplankton actually has a slower maximal growth rate due to the allometric scaling reported in Table 3

5. Other

5a. L102-104: How do the model results presented in this paper compare to observations in the Pacific (e.g. Follett et al. 2022)? This seems relevant as much of the early literature cited on linear vs. quadratic mortality were trying to capture the difference in the seasonal cycle between the N Pacific and N Atlantic.

We have searched for additional data but have struggled to find a dataset that is suitable. Much of the data used here are from the Atlantic Meridional transects and the English Channel L4 time series. In both cases, total phytoplankton and zooplankton were taxonomically identified and counted. The Hawaii ocean timeseries filters by size but microzooplankton and phytoplankton are within the same size class, making it challenging to separate them. The Follett dataset had abundances of *Prochlorococcus*, *Synechococcus*, and heterotophic bacteria, but we were unable to locate coincident measurements of other phytoplankton and microzooplankton biomass densities. There are some existing compilations of microzooplankton biomass data (e.g.

<u>https://doi.pangaea.de/10.1594/PANGAEA.779970</u>) but it is unclear if these have coincident phytoplankton data. Even if such data existed, biases can be introduced converting from individuals to carbon biomass density and we could not be sure that consistent methodology was used across datasets. We have therefore refrained from evaluating model performance in the Pacific but recognize that this is an important priority for future analyses.

5b. Figure 3 and results: Why just surface biomass? Aren't plankton distributed throughout the euphotic layer? Subsurface biomass could show different patterns. I suggest analyzing and depicting depth-integrated biomass.

All our biomass and productivity maps are now depth integrated

5c. Figure 3 and results: Could you please also show the microzooplankton biomass across the different models? I am curious how much it showed similar patterns to the phytoplankton, which would be expected for the quadratic closure, but not for the linear. This would help understanding the spatial differences that can't be seen in Fig 5.

These results are now shown in Figure S2 and this intuition is exactly correct – the linear closure introduces qualitative differences in spatial distribution of phytoplankton and zooplankton that go away with quadratic closure

5d. L230: Linear mortality resulting in oscillations is known behavior. Please mention in the discussion and refer to the relevant literature (e.g. Steele & Henderson 1992, Fasham 1995, Edwards & Brindley 1999, Edwards & Yool 2000).

We felt it was appropriate to recognize these prior works in the results section, when the behavior is first mentioned (Lines 254-257)

"Consistent with prior analyses (Steele and Henderson 1992; Fasham 1995; Edwards and Brindley 1999; Edwards and Yool 2000) models with linear zooplankton losses predicts oscillations in phytoplankton and microzooplankton biomass."

5e. Figure 6 and results: The statement that "Linear losses on the microzooplankton predict cyclic behavior in the predator-prey relationship that are inconsistent with observations" is not accurate. The slope of (a) and (b) are inconsistent with the global pattern, which are snapshots in time, but it is possible that a similar seasonal pattern exists in the observations. You would need to show those. Given the wealth of data in the English Channel from the CPR, I assume this is possible.

The English Channel data are strikingly linear and have a very high correlation coefficient. We now show these data alongside the model results in Figure 6. None of the models predict regression slopes that exactly match with the regression slope at L4, but of the simulations shown, both models with the quadratic closure are closer to the environmental data. More importantly, the level of correlation between predators and prey is much higher in models with the quadratic closure (r = 0.824 and 0.834 for the parallel and diamond models, respectively) than the linear closure (r = 0.25 and 0.18 for the parallel and diamond models, respectively), and the quadratic closure is much closer to the level of correlation in the L4 data (r=0.693). Predator-prey cycles tend to drive the correlation between predators and prey low, and these cycles are clearly more pronounced in the model with linear closure than the model with quadratic closure. These results are discussed in Lines 251-267.

Technical corrections:

Appendix Equations A1-A10: These are all the same form and don't all need to be shown. You could simply use an "X" or something to denote the nutrient on DOM. Also, A1 has NO3 in the equation, but should be NH4 throughout.

Appendix Equations A11-A14: Again, could just use one example of POM.

We have made these changes – thank you for the helpful suggestions

References cited:

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Petrik, C. M., Luo, J. Y., Heneghan, R. F., Everett, J. D., Harrison, C. S., & Richardson, A. J. (2022). Assessment and constraint of mesozooplankton in CMIP6 Earth system models. Global Biogeochemical Cycles, 36, e2022GB007367. https://doi.org/10.1029/2022GB007367

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Stock, C. A., Dunne, J. P., & John, J. G. (2014). Global-scale carbon and energy flows through the marine planktonic food web: An analysis with a coupled physical-biological model. Progress in Oceanography, 120, 1–28. https://doi.org/10.1016/j.pocean.2013.07.001

Yool, A., Popova, E. E., & Anderson, T. R. (2011). Medusa-1.0: A new intermediate complexity plankton ecosystem model for the global domain. Geoscientific Model Development, 4(2), 381–417. https://doi.org/10.5194/gmd-4-381-2011

Yool, A., Popova, E. E., & Anderson, T. R. (2013). MEDUSA-2.0: An intermediate complexity biogeochemical model of the marine carbon cycle for climate change and ocean acidification studies. Geoscientific Model Development, 6(5), 1767–1811. https://doi.org/10.5194/ gmd-6- 1767-2013

## **Reviewer 2**

Talmy et al. "Killing the predator: impacts of top-predator mortality on global-ocean ecosystem structure"

This is a nice, concise paper analyzing the effects of two variants of a plankton food web structure, with two types of losses (linear and quadratic) for the top predator in the modeled food web. Here, the predators are microzooplankton, but I believe the results are extensible to a case where there is one microzooplankton and one mesozooplankton. In Talmy et al., the authors show that the "diamond" food web structure, where one zooplankton feeds on two phytoplankton, results in a marine ecosystem with less dynamic range between the gyres and the poles in phytoplankton carbon, as well as less co-existence in community composition. Simultaneously, the quadratic losses in the top predators results in a phytoplankton to zooplankton biomass relationship that better represents recent observations. I believe This paper is written in a clear and consise way, but one major criticism is its lack of robust

engagement in other mechanisms that may contribute to variations in community coexistence, Z:P ratio, and phytoplankton carbon. Further, while the authors do cite other publications (Ward et al. 2012, Dutkiewicz et al. 2020) that list parameter values, it was very difficult to evaluate the performance of the model without a list of parameter values.

Thank you for your constructive review. We now provide a subset of parameter values in the main text, as well as a fully exhaustive list in the online code repository. We have also conducted additional simulations exploring the sensitivity of our findings to different mechanisms that contribute to community coexistence and variation in Z:P and planktonic carbon. Of particular interest to us was different assumptions about microzooplankton feeding, which we discuss in detail below and in our revised text.

Therefore, my recommendations are:

• List out in the appendix all the ecosystem-relevant parameter values used in the model

A fully exhaustive list of parameter values is now provided in our online code repository. We have added the most relevant ecosystem parameters to the main text in Tables 2 and 3, and in the Appendix.

• Can the authors engage a bit more robustly in the discussion, other strategies that modelers use to modify zooplankton grazing in a diamond food web structure that may also result in improvements in the two main metrics (dynamic range between gyres and poles in phytoplankton carbon, community co-existence):

We recognize that the suggestion was only to enhance the discussion and not to conduct further analysis / simulation. However, in reading Rohr et al., 2022 and other literature on this topic, we felt it was necessary to consider whether the effect of different grazing formulations (in particular Holling III) might modify our main conclusions about mechanisms contributing to biomass scaling.

1.For example, many biogeochemical models utilize either different maximum grazing rates for zooplankton depending on the prey type, OR use a prey selectivity factor to modulate grazing. For the former, BEC/MARBL (Moore et al. 2004, Long et al. 2021) uses different maximum grazing rates for a single "adaptive" zooplankton to mimic the effect of multiple zooplankton in a single zooplankton class. For the latter, there are multiple examples of this strategy within the biogeochemical models, e.g., PISCES (Aumont et al. 2015), and COBALT (Stock et al. 2014), though those two models also have multiple zooplankton types so it may be slightly harder to compare with a single zooplankton type. However, mathematically, the effect of both these strategies would be similar.

We appreciate drawing our attention to these common structures in ESMs. We have added some text to the discussion identifying these mismatches between our models and the ESMs, Lines 318-326:

"The food-web model structures assumed here are so simple that they exclude many mechanisms already considered in extant Earth system models. For example, many Earth system models contain representations of both microzooplankton and mesozooplankton. In some cases, these are explicitly represented with multiple state-variables (Stock et al. 2014; Aumont et al. 2015). In others, a single 'adaptive' zooplankton class mimics the effects of micro- and meso-zooplankton by feeding differently on phytoplankton prey types (Moore et al. 2004; Long et al. 2021). Future studies may evaluate the impact of different closures in the context of these more sophisticated structures. Despite the simplicity of our models, we anticipate that our central conclusions will hold in a more general setting. Specifically, assumptions made about highest predator mortality constrain biomass scaling relationships regardless of model predictions about community composition within a trophic level."

Here, we have agreed with your assertion (above) that there is good reason to believe our results will extend to these other ecosystem structures. There is prior literature on both the diamond (e.g. Klausmeier and Litchman 2012) and parallel (e.g. Follett et al. 2022) models indicating that, when one or two predators have mismatching grazing rates on different prey, this modifies the abundance of the prey when present, but does not modify the core predictions concerning coexistence and competitive exclusion. We have left the discussion of this topic relatively light to maintain the accessibility of our initial submission.

2.On grazing, values for the zooplankton maximum grazing rates and the grazing half-saturation constant are amongst the least well constrained parameters in food web models, and variations in these parameters have an enormous impact. Rohr et al. 2022 (Progress in Oceanography) shows this quite nicely in a robust analysis, along with evaluating differences in the grazing functional form itself (Holling type II or type III functional responses). It would be nice if the authors could engage a bit more in the discussion regarding whether modelers would be able to compensate for the lack of a second zooplankton (e.g., in the diamond food web model) by modulating maximum grazing rates and grazing half-saturation constants.

We feel that the issue of Holling II vs. III, and the ability of the diamond food-web to compensate for the lack of a second zooplankton with respect to phytoplankton coexistence, are to some extent different questions. In the context of this paper, we have already shown that the impact of the closure holds true regardless of model predictions about phytoplankton community composition. Therefore, even if the adaptive feeding assumed in many ESMs could mimic the effect of a second zooplankton, we would not anticipate that it would impact the biomass scaling relationships predicted by the model. On the other hand, based on Rohr et al., 2022 and other literature, it does seem likely for Holling III to impact our predictions regarding Z vs. P biomass scaling. We expand on both of these issues here but have kept our discussion of these topics in the main text relatively light, to preserve the conciseness that both reviewers commented on.

Regarding the coexistence issue, as we note above, allowing the microzooplankton to be 'adaptive' in the manner assumed in many ESMs by modifying max grazing rates and half-saturation values is unlikely to fully account for a second zooplankton with respect to phytoplankton coexistence, as these grazing parameters modify phytoplankton abundances but do not allow the same degree of coexistence. Interestingly, allowing zooplankton to actively switch prey type based on prey abundance (following Vallina et al., 2014) does provide some degree of coexistence in the phytoplankton but not to the same degree as parallel feeding (compare columns in Figure S7). We report these results in Lines 284-286:

"allowing microzooplankton to switch actively to prey on more abundant phytoplankton allows greater coexistence of phytoplankton in the diamond food web (Figure S7 and Vallina et al. 2014) but unsurprisingly does not qualitatively modify the scaling relationships reported in Figure 5."

We were very interested in the Rohr et al., 2022 study as it pertains to our main predictions about mechanisms driving Z vs. P biomass scaling. Interestingly, when we assume Holling III instead of Holling II, we find significantly more correlation between Z and P for all closures (compare Figure S8 of the SI to Figure 5 of the main text). Even when the linear closure is assumed, Holling III predicts correlation between Z and P that is much closer to the environmental data (Figure S8a,b). Nevertheless, when Holling III is assumed, the quadratic closure still predicts more realistic levels of correlation between Z and P. These new results are explained in Lines 286-292:

"Microzooplankton feeding according to type III functional response leads to far greater correlation between predators and prey across models (Figure S8). These results are consistent with prior studies identifying type III feeding as a stabilizing mechanism on microzooplankton-phytoplankton dynamics (Rohr et al., 2022). Nevertheless, even when a type III response is assumed, the quadratic closure still leads to more realistic correlation between microzooplankton and phytoplankton than the linear closure (Figure S8) pointing to the closure as an important control on trophic structure globally."

Interestingly, the regression slopes with Holling III are all unrealistically steep (figure S8), which we believe is because variance in P is significantly reduced due to the Holling III introducing a refuge in grazing rate at low prey abundance, preventing phytoplankton abundance from reaching very low values. At this junction, we cannot say if the unrealistically steep regression slope introduced by Holling III is an artefact, as it's possible that mesozooplankton predation on microzooplankton also follows a Holling III response, which we anticipate would bring the model slopes back in line with the observational data. This leads to several novel research questions: 1) does mesozooplankton grazing on microzooplankton follow Holling III? 2) if so, does introducing mesozooplankton feeding according to Holling III lead the diamond food-web model to predict realistic biomass scaling when Holling III is also assumed in the microzooplankton-phytoplankton interaction? and 3) can the effects of the mesozooplankton be parameterized with an appropriate microzooplankton closure? We feel these questions are all very interesting but go well beyond the scope of the current study. For parsimony we have limited our revisions to explaining the impact of Holling III on the level of correlation between Z and P (Lines 289-292 and Figure S8) which we anticipate will be a general result that holds true regardless of whether or not mesozooplankton are explicitly resolved.

3.Lastly – prey switching is a major issue that is only mentioned in passing in the discussion. It would be nice to see a more robust discussion – do the authors think that modifications in the switching form would result in substantial changes in the modeled ecosystem, and why? There are a lot of approaches towards switching, as laid out extensively in Gentleman et al. (2003), but models typically use just one or two forms (e.g., Stock et al. 2008 Journal of Marine Systems has addressed this quite nicely in a simple system). In my opinion, a more than cursory treatment of this topic would be important in this paper.

As per our comments above, active switching promotes phytoplankton coexistence (Vallina et al., 2014 and figure S7) but does not modify biomass scaling predictions (explained in lines 284-286). We thank this reviewer for helping to direct our attention to these important questions, as we feel addressing these issues has allowed us to deepen and expand our understanding of the models addressed in this study.

4.Other parameters that may additionally modulate phytoplankton carbon in food web models that aren't addressed include the fraction of phytoplankton and zooplankton losses that go to dissolved organic matter vs. particulate organic matter, which may influence the recycling rate and strength of the microbial loop. Lastly, variations in the relative nutrient uptake rate of the different phytoplankton may also result in more or less differences in the phytoplankton carbon between the gyres and the poles.

We now include sensitivities to phytoplankton size, which modify nutrient affinities (through allometry) but do not modify biomass scaling relationships (lines 282-283). Also, we have conducted sensitives to the POM-DOM partitioning (referred to in our model as an 'export fraction'). Results show that, when modified over a reasonable range, the average predator-prey scaling is sensitive to this number, but the scaling relationship is not. We have opted not to include these results as they go beyond the scope of the present study, which has expanded significantly in response to these helpful reviews.

Other than these points, I found the manuscript written quite clearly, with compelling figures and nice presentation. With a more robust discussion addressing a range of these additional points listed above, this manuscript would make a nice addition to the literature.

We thank this reviewer for the careful reading of our manuscript, and their helpful suggestions. We feel our manuscript has improved significantly as a result.