Response to both reviewers

Thank you very much for your constructive comments and suggestions on our manuscript. Please note four major elements as our effort to fully address your and other reviewer's concerns together, which served as the basis for updated results in the revised manuscript as well as our response to each comment in this file. After these major changes summarized below, most of the results remain similar and the main conclusions of the revised version remain the same compared to the previous version: 1) significant associations of the observed bacterial mode with the modelled NPP, POC flux, and BCD; 2) significant associations of the observed *f*HNA with the modelled NPP, POC flux, and BCD 3) larger increases of HNA stocks and functions under climate change conditions than those of LNA cells; and 4) larger cell-specific BP and SDOC uptake rates of HNA cells than those of LNA cells. This suggests the robustness of our model study.

In response to the reviews, we made a number of substantial revisions to the modeling study and manuscript:

1) **Modification of modeling framework:** We re-built, re-optimized, and re-analyzed the model by completely changing the previous version's 0-D (fixed surface layer) formulation to a 1-D (vertical profile) framework.

2) **Additional data assimilation:** We added diatom and cryptophyte Chl observations for 2010-2011, 2012-2013, and 2013-2014 in that data assimilation; this new data became available for use during the period of revision.

3) **Model equations and GMD manuscript:** We included a complete set of model equations (line 90-103, Appendix A) and other details about the model set-up (Text S1-4), as well as attached our Geoscientific Model Development (GMD) manuscript on the original WAP model that served as the basis for our study's bacteria-oriented model (Kim, H. H., Luo, Y.-W., Ducklow, H. W., Schofield, O. M., Steinberg, D. K., and Doney, S. C.: WAP-1D-VAR v1.0: Development and Evaluation of a One-Dimensional Variational Data Assimilation Model for the Marine Ecosystem Along the West Antarctic Peninsula, *Geosci. Model Dev. Discuss*. [preprint], https://doi.org/10.5194/gmd-2020-375, in review, 2021).

4) **Climate change simulations:** We updated error estimates in the climate change experiments (Results 3.4) after fixing an error in the Monte Carlo simulation code. Temperature and sea-ice perturbations were also replaced by +0.5ºC and +1.0ºC of warming and 5% and 10% of melting, from +1.0ºC and +2.0ºC of warming and 10% and 20% of melting in the previous version, in order to reflect better the trends and changes relevant to the WAP.

5) **Others:** We 1) added the summary of the climatological model optimization in Table 2 (missing in the previous version), 2) combined the 4-modelled years together (Figure 3a;

each year presented in the previous version) and included the Taylor diagram of the climatological model (Figure 3b; missing in the previous version) for model skill assessment, 3) removed discussion on microzooplankton model fits from Table 2 for consistency (presented in Table 2 in the previous version but never discussed), and 4) removed the discussion on the fate of BCD as it did not add new information to the study.

In particular, modification of the modeling framework to 1-D vertical profile and additional data assimilation were both labor-intensive and time-consuming, which caused a long delay in providing our Final Author's comments. Thank you again for your patience and for willingness to re-review the revised manuscript in advance. Below are our responses to each of your specific comments that are highlighted throughout the revised manuscript file.

Response to the referee #1

Please see the **"response to both reviewers"** above for the major changes to the previous version.

This ms presents a bacteria-oriented ecosystem model, calibrated with a data assimilation scheme, with two explicit bacteria types, fast growing (HNA) and slow growing (LNA). The authors find that properties of the bacterial community are strong predictors of bacterial carbon (C) demand, primary production (PP), and export (EP). The calibrated model is used to make predictions for a warming ocean. At first I was quite intrigued by the approach of this study. But after going through the ms, it now appears fraught with too many problems to make it worthwhile. The problems start already with the title. I consider "microbial diversity-informed modelling..." a gross overstatement of the authors' approach, which is more correctly describes in the abstract as "bacteria-oriented". Below I will outline why I consider this a failed attempt and how it might be modified into a useful contribution. Because I have the strong impression that essential information about the model and the data-assimilation method is missing, I will not go into much detail, though.

Thank you very much for your comments. We hope that the GMD manuscript and added details about the model in the revised version clear up these concerns. We agree with your assessment on the title of the study. With only part of the microbial diversity data directly informing the model (bacterial physiology data) we modified the title to "Modelling polar marine ecosystem functions guided by bacterial physiological and taxonomic traits" in the revised version.

My first major problem was understanding the design of the model. The authors refer to one published work (Luo et al., 2010) regarding the model equations (besides unpublished manuscripts, which may or may not eventually be published), and present only the equations for the two bacteria groups. The model of Luo et al. (2010) is much more complex, totalling 30 state variables, than this one (with 12 states), so this reference does not really help much. Without access to the model

equations, any attempt to understand the model code will be futile. In consequence, it also remains unclear what the model currency is. According to Fig. 1 and the description in the text (which is not very clear in this respect, except that the number of states is 12) the model employs a fixed stoichiometry approach but it remains unclear whether the fluxes are based on nitrogen (N) or phosphorus (P). Also according to Fig. 1, it appears that inorganic nutrient have no effect on and are not utilised by phytoplankton, leaving open the question what drives PP in this model. Since only very little information about the model is provided in the text of the ms and the supplement, the model design remains very much opaque. From what little information is presented I can see clearly only that the model is 0-D and employs a rather simplistic physiology (fixed stoichiometry).

It is correct that the model was applied as a 0-D framework in the previous version (i.e., a 0-D box model of the surface layer at 10 m), but as mentioned above, the revised version is now based on the new model results from a 1-D vertical profile framework (line 126-129).

The model tracks and simulates C, N, and P stocks as concentrations in different inorganic and organic pools (e.g., C, N, P for all living model groups, N for nitrate and ammonium, and P for phosphate). The model has flexible stoichiometry, in which phytoplankton store more C under high light and nutrient-depleted conditions and more N and P under low light conditions. If the N or P cellular quota is lower than the predefined reference (Redfield) ratio, plankton excrete DOM to adjust their stoichiometry close to the reference ratio. To make these points clear, we 1) revised Figure 1 to show N and P uptake by phytoplankton and 2) added a section demonstrating the model's variable stoichiometry (Text S1, line 221-227).

The model PP is driven by photosynthetic active radiation and nutrient uptake by phytoplankton, but given the abundance of NO_3, PO_4, and SiO_3 (Kim et al., 2016, doi: 10.1002/2015JG003311) and iron (Annett et al., 2017, doi: 10.1016/j.marchem.2017.06.004) at the study site, it is the light level that primarily limits PP. To make this point clear, we added the model coupled ordinary differential equations (line 90-102, Appendix A) and other details (Text S1-4).

The model has 84 parameters, of which 22 (inferred from l. 219 of the ms) are calibrated via data assimilation. What is missing here is a description of how these 22 parameters have been selected in the first place. For example, was the selection based on a preliminary sensitivity analysis or a-priori knowledge or assumptions of the model equations? Also, 22 is, in my experience, a very large number of parameters to constrain given the kinds and amount of data employed here. Thus, it is not very surprising that only a subset of 7–10 of these could be constrained well.

We revised the Material and Methods 2.3 to demonstrate how we chose an initial subset of model parameters submitted to optimization (line 156-165).

With regard to your concern on too many optimized parameters, the number of optimized parameters (optimized with high uncertainties, by definition) changed from 12-15 in the previous version to 3-6 in the revised version, while the number of constrained (optimized with low

uncertainties, by definition) parameters changed from 7-10 in the previous version to 5-7 in the revised version, therefore, the revised version has a larger fraction of well-constrained parameters.

Related to this, the next problem is the description regarding overfitting and portability. I agree that these are essential concepts all too often neglected in modelling studies and so was happy to see that these are addressed here. Nevertheless, I question the quantification of overfitting (lines 175–179) by comparing the residual error with the (undefined in the ms) "target error" of the observations. Overfitting has very little to do with the noisiness of the observations. It is a consequence of the fact that every model is a simplification of the system it describes, and it is also tightly related to portability. The connection is that overfitting can compromise portability, and this is a good way of assessing overfitting. Overfitting often results from attempting to constrain too many parameters, which is revealed here by several parameters being not well constrained (Tables S2–S6). The different estimates of portability for the different year are another indication of overfitting.

This is an excellent point. The portability analysis showed that the optimized model parameter set for 2012-13 was most portable while the parameter set for 2011-12 was least portable (Table 2), in which the most (n = 7 out of total 11) and the least numbers (n = 5 out of total 11) of parameters were constrained (i.e., optimized with low uncertainties), respectively (Tables S3-4). The other two years exhibited intermediate levels of portability, with similar portability index values characterized by the same number of constrained parameters (n = 6 out of total 10 for 2010-11 and n = 6 out of total 12 for 2013-14; Tables S2, S5). In other words, it was the number of well-constrained parameters that mattered most in driving high model portability, suggesting the connection between overfitting and portability of optimized models, as you suggested. It is commonly thought that more tuned parameters indicate a higher possibility of overfitting and less portability. However, our analysis showed that if the tuned parameters were well-constrained by observations, they would not compromise portability. We added these points in Discussion 4.1 (line 370-376).

However, it is our understanding that a reduced chi-square estimate of model fit is a reasonable metric for assessing overfitting of data (Glover et al., 2011, doi: 10.1017/CBO9780511975721). Target errors in our study reflect both the observational errors and seasonal and interannual variations of the observations (which has been intensively defined and discussed in Section 2.5), and larger target errors compared to model-observation misfits, or the noisiness of the observations, would be an indication of overfitting.

I must admit that the concept of the bacterial modes was new to me, so I was happy to see the clear definition in Section 2.2 (first para). However, I could not figure out the main characteristic of these modes, since only very cursory information is presented in the text and Fig. 6. A table listing the modes and their properties and composition might be very helpful here. As it stands, the concept remains rather confusing. For example, the authors state that (l. 276) each mode is dominated by unique bacterial taxa. But considering Fig. 6, it appears that Candidatus Pelagibacter

dominates both modes 6 and 1, although it appears that mode 1 is supposed to be dominated by Candidatus Thioglobus.

Thank you for this comment. The modes are entirely taxonomic, although they can be related statistically to different physiological or ecophysiological parameters. A complete discussion of the modes is given in Bowman et al. (2017; Bowman, J., Amaral-Zettler, L., J Rich, J. *et al*. Bacterial community segmentation facilitates the prediction of ecosystem function along the coast of the western Antarctic Peninsula. *ISME J* 11, 1460–1471, doi: 10.1038/ismej.2016.204). Because of this we have opted not to give a more in-depth description here, but have modified the caption for Fig. 6 to try and make this concept more clear. In direct response to your question Mode 6 is dominated by P. ubique (comprising over 50 % of the community for some map units in Mode 6) while Mode 1 is dominated by T. singularis (also reaching over 50 % of the community).

The above may be viewed as more technical problems, which could possibly be dealt with by, e.g., a detailed model description with all equations, or a recalibration of the model etc. However, I also see a major conceptual problem regarding the design of the study. The problem lies in the way the authors use the model to make predictions for a warmer ocean. The main assumption behind the presented approach is that bacterial community composition is strongly correlated ("strong predictor", Abstract) to PP and EP. The functional bacterial community composition is represented in the model and its calibration by assigning higher growth rates to HNA than LNA. Nevertheless, bacteria process the DOM produced during PP, so the behaviour of the bacterial community must be viewed as a response, not a driver, of PP. If bacterial community composition is in fact strongly correlated with PP and EP, that is in itself a very significant finding and I would very much like to see this substantiated. It could become a very useful diagnostic tool. However, here the authors treat the bacteria as the driving force determining PP and EP, which is wrong for several reasons. First, it reverses the cause-effect relation between bacterial activity and PP. Second, even if the cause-effect relation was OK, the data do not cover sufficient interannual temperature variability to allow predicting the response to a warmer ocean.

Thank you for this insightful comment. It is well understood that there can be significant feedback between bacteria and PP, in particular in systems where large PP rates are supported by fast/efficient recycling of nutrients by bacterial remineralization of organic matter to inorganic nutrients. By contrast, the fact that macro- and micronutrients are abundant at the study site (Kim et al., 2016, doi: 10.1002/2015JG003311; Annett et al., 2017, doi: 10.1016/j.marchem.2017.06.004) makes the limitation of light, not of nutrients (Eq. A.2.4-5, B.2.4-5), determine PP rates (Eq. A.2.7, B.2.7). PP rates are also proportional to phytoplankton biomass that is grazed by microzooplankton, which follows preferential selection on phytoplankton (i.e., g_{DA}, g_{CR}) versus bacterial food sources (i.e., g_{HNA}, g_{LNA}) as well as bacterial biomass (Eq. A.2.33, A.3.33). This step-wise, indirect connection makes the bacterial-microzooplankton grazing influence on PP rather remote compared to nutrient recycling by bacteria. The same applies to EP. Thus, we agree with your argument that bacteria should be

regarded as a responder, rather than a driver, of PP and EP, and therefore changed the wording from "predict/predictor" to "indicate/indicator", "respond", "reflect", or "associated" in the revised version.

Regarding your second comment, our climate change experiments identified functional relationships between modeled processes and temperature. Although the real response may not follow the same functions when temperature increases beyond the existing observed range, this is best we can do for future projections as in other modeling studies. In our experiments, the "climate change" condition is equivalent to simultaneous warming and melting, which have more solid physical basis as well as more profound impacts on bacterial processes than the warming alone condition does. Nevertheless, we reduced the range of warming to +0.5ºC and +1.0ºC, which is relatively minor increases that are not expected to cause much different trends from the existing observed patterns.

Response to the referee #2

Please see the **"response to both reviewers"** above for the major changes to the previous version.

General

The manuscript provides an analysis of the bacteria dynamics and ecosystem functioning in the surface ocean layer of the coastal West Antarctic Peninsula, based on in situ measurements and an ecosystem model. The authors develop and validate an existing model and apply it in a 0-dimensional configuration to analyze the bacteria dynamics and the link between the bacterial characteristics and the ecosystem functions. To investigate the impact of climate change on the ecosystem, they use the model to assess changes on bacteria fluxes and ecosystem functions under temperature increase and sea-ice melting conditions. The manuscript makes novel contribution with respect to ecosystem modelling, in which bacteria are often under-studied despite the fact that they play a crucial role in the ecosystem. The manuscript is well written and organized. However I have the following main concerns that should be addressed before I can recommend its publication: some aspects on the description of the model and its specific implementation for this study should be justified and clarified; the authors carried out a validation effort but, as the validation performed in the study of Kim et al. (in review) is not accessible and the specific implementation is unclear, this effort should be fleshed out to gain additional confidence in the model results; also discussions on model performance, on limitations and weaknesses of the modelling should be included.

Thank you very much for your comments. We hope that the GMD manuscript and added details about the model in the revised version clear up these concerns. For other significant issues that you listed, please see our response below specific to each of your comments.

Main comments

1/ Description of the ecosystem model and its implementation for this study

One of the objectives of the work is to extend an existing model (Luo et al., 2010) applied by Kim et al. (in review) in the study area, by refining the bacteria compartment of this model. The fact that the manuscript of Kim et al. (In review) is not yet accessible makes it difficult to understand the extension and the specific implementation (period, 1-d/0-d, boundary conditions) performed for the study presented here. The modelling is 0-dimensional. The authors should justify the choice of the 0-dimensional study instead of a 1-dimensional study as performed by Luo et al. (2010) and that is usually done for ecosystem modelling at a water column measurement station. Is 0-dimensional (and even 1-dimensional) modelling appropriate for this coastal site? Is there a significant influence of lateral transport of organic carbon or nutrients on the ecosystem in this region? If a 0-dimensional is justified here the limitations of this 0-d modelling should be clearly discussed.

The model was applied as a 0-D framework in the previous version (i.e., a 0-D box model of the surface layer at 10 m), but as mentioned above, the revised version is now based on the new model results from a 1-D profile simulation (line 126-129). We also added the justification for the 1-D modeling of the WAP study site (line 129-133).

In the Supplementary Material, the authors specified the boundary conditions of the model during the growth season for the nutrient and dissolved organic matter: "The boundary conditions of nitrate, phosphate, SDOC, SDON, and SDOP are set to 30.9 mmol m-3, 2.4 mmol m-3, 6.5 mmol m-3, 0.6 mmol m-3, and 0.03 mmol m-3, respectively". I find unclear the description of the boundary conditions for this 0-dimensional modelling. What are the boundary conditions for phytoplankton, zooplankton and particulate organic carbon? Are the given conditions at the base of the 10m depth layer? A constant concentration of variables over time at 10m depth does not seem appropriate for representing a seasonal cycle of the ecosystem. The vertical fluxes of the different model variables at the base of the modelled layer should be better specified in the case when the MLD is greater than 10m or at least references to a similar 0-dimensional study describing this should be included (Luo et al. (2010) study is a 1-dimensional modelling study). The authors should clarify and justify the forcing and boundary conditions of the modelled surface layer and specify the depths of the euphotic and mixed layer here.

We appreciate your concern about several issues regarding the 0-D modeling of the system in the previous version. As mentioned above, the revised version is now based on the new model results from 1-D modeling, whose framework is directly comparable to the 1-D models in Luo et al. (2010; Luo, Y.W., Friedrichs, M.A., Doney, S.C., Church, M.J. and Ducklow, H.W., 2010. Oceanic heterotrophic bacterial nutrition by semilabile DOM as revealed by data assimilative modeling. *Aquatic Microbial Ecology*, *60*(3), pp.273-287. doi: 10.3354/ame01427) and in the attached GMD manuscript (Kim et al., 2021). In these two studies climatological observations of

the deep water values were used for bottom boundary conditions of NO_3, PO_4, and SDOM, while bottom boundary conditions of other variables (i.e., C, N, and P components of bacteria, phytoplankton, zooplankton, LDOM, and detritus as well as NH_4) were set as zero – an approach valid for the vertical domain down to the deep, (near) bottom depth of the study sites.

For this particular bacteria-oriented study, however, we think it is best to minimize the number of depth levels that do not have bacterial traits observations, yet to include an adequate number of depth levels required for simulating seasonally-varying MLD and light impacts (mostly < 20 m of MLD and ~ 25 ± 8 m of euphotic zone depth using hydro-light data for 2010-2011 and 2013-2014 at the study site). Thus, we chose to model 0, 10, and 20 m, which required non-zero bottom boundary values from 20 m, because of high biological and biogeochemical activities there. There are, however, no available observations of HNA, LNA, LDOM, microzooplankton, and krill biomass, LDOM, detritus, and NH_4 at 20 m at the study site. Instead, we 1) estimated the climatological (2010-2013) HNA and LNA biomass at 20 m using the ratio of bacterial production to group-specific biomass observations at 10 and 20 m, 2) extracted the climatological (2002-2011) modelled values of microzooplankton, krill, detritus, LDOM, and NH_4 at 20 m from our GMD manuscript (Kim et al., 2021), and 3) used the climatological (2010-2013) observations of diatom- and cryptophyte biomass at 20 m for their bottom boundary conditions. We revised the section detailing these procedures (Text S3, line 342-348).

2/ Data assimilation

The authors show that data assimilation and parameter optimization can reduce model/observation errors, especially for bacterial stocks and flows. However, the simultaneous assimilation of climatological data and data corresponding to the given year raises questions, notably given the strong link between nutrients and phytoplankton time evolutions (Kim et al 2016) and the possibility of a time lag in phytoplankton growth from one year to another. The authors should justify the choice to assimilate climatological data for Chl and microzooplankton instead of not assimilating these data if they were not measured in the simulated year as is done for nitrate and POC? Does this choice lead to some inconsistencies?

In the previous version, the decision of assimilating the climatological Chl data had been made based upon our initial attempt of model optimization without assimilating Chl data type at all. However, model cost functions had failed to reach local minima, suggesting the necessity of the Chl data type to constrain key model parameters sensitive to lowering total cost functions (e.g., Θ). Similarly, the single-year observation of microzooplankton data had been assimilated to better constrain grazing loss terms of phytoplankton and bacteria, which otherwise also led to failed optimization. We had not encountered the same issue when not assimilating nitrate and POM.

In the revised version, thanks to the updated data sets we were able to assimilate diatom- and cryptophyte-specific Chl for 2010-2011, 2012-2013, and 2013-2014, resolving your concern about the potential mismatch between the time evolutions of Chl and of nutrients (or PP, also) in those years. However, Chl data were still missing in 2011-12, for which we assimilated the

climatological observation due to above reasons. We revised the Results 2.4. section to include these points (line 176-182).

3/ Validation of the model results

The authors present a comparison of the model results with the available in situ data. First, the description and discussion of these comparisons should be a little more substantial. For instance the error on primary production appears significant in some years (e.g. 2012-2013) and data assimilation does not seem to bring an improvement in modelled primary production for all periods and years (e.g. January/February 2012) (Figures S1-S5). Also, a negative correlation is obtained in some years for phosphate. The authors should mention and discuss these points. Second, a description with a figure of the comparison of the modelled and observed climatological or 4-year seasonal cycles of nutrients, phytoplankton, zooplankton and bacteria (in addition to the error that is presented) in the main text or in the Supplementary Material would increase confidence in the capacity of the model to represent the seasonal cycle of the ecosystem.

We updated the Results 3.1 on model skill assessment based on the new 1-D model results and mentioned several data types whose correlations were negative and variability was not well captured (line 255-259). We also included the seasonal cycle of the ecosystem, as suggested, and included it in the discussion of model fits (Figure S7).

The authors use their model to explore the impact of an increase in temperature and a decrease in sea ice concentration, predicted as a result of climate change, on the WAP ecosystem, in particular on bacterial fluxes, primary production and POC export flux. A validation of the model's capacity to reproduce the already observed climate trends of the ecosystem as mentioned in the introduction L49-52, over a longer period for some of the model's variables (POC, Chl), fluxes (primary production) and/or indicators (for instance time and magnitude of the maximum concentration of bacteria, phytoplankton, DOM or POM or primary production or annual averages) would strengthen confidence in the model for the study of the impact of future changes. This is perhaps presented in the study by Kim et al (in review) but could be redone with this new version of the model and added in this manuscript, perhaps in the Supplementary Material. Another possibility would be to compare the interannual variability obtained with a modelling without data assimilation and with the climatological model parameter set of the 4 simulated years (2010-2011 to 2013-2014) to the observed interannual variability (by specifying the potential anomaly in temperature and sea-ice concentration for those years).

This is a great suggestion. As suggested, we conducted a modified set of the cross-validation analysis to examine the climatological model's capacity to reproduce the observed climate trends of the WAP ecosystem variables. In this analysis, we compared the observed interannual variability to the modelled interannual variability using the climatological parameter set and each year's forcing (without further data assimilation). The climatological model yielded overestimated BP and HNA biomass in 2011-12 and underestimated PP in 2012-13 and 2013-14, compared to

other variables whose interannual variability was captured comparatively well compared to their observed interannual variability (Table S7). Notably, 2011-12 was characterized by the negative temperature anomaly (-0.13 ± 0.83ºC versus 0.03 ± 0.84ºC for the 4-year climatology) and the positive sea-ice anomaly (24 ± 38% versus 21 ± 29% for the 4-year climatology), with significantly lower temperature and higher sea-ice cover than other three years (all $p < 0.05$, two-sample *t*-test). This coldest year had the lowest values of BP, HNA biomass, and PP observations (Table S7), consistent with increases in the modelled BP, HNA biomass, and PP under the combined warming/melting scenario, adding confidence in using the climatological model for the climate change experiments. We revised the Results 4.4 to discuss these points (line 461-474) and added a supplementary figure (Table S7).

4/ Interannual variability

The following comment is in line with the previous one. The ecosystem model is applied to 4 consecutive years, 2010-11 to 2013-14. The results show interannual variability in bacterial carbon stocks and fluxes. As the changes of primary production and POC export flux are analyzed under varying temperature and sea-ice concentration conditions, those fluxes could also be presented (in Figure 4) and discussed for the 4 modeled years. The authors do not discuss the link between the interannual variability of bacterial C flux and that of meteorological and physical forcing. The authors should consider adding a short description of the meteorological and physical forcing for these 4 years. A figure of the forcing in the Supplementary Material would also be helpful. The authors could specify the potential anomaly in temperature and sea-ice concentration for these 4 years and consider adding a discussion on the interannual variability in ecosystem functioning and in particular bacteria dynamics in response to the interannual variability of forcing.

We added a figure summarizing each year's physical forcing (Figure S1) and discussed the interannual variability of the ecosystem variables in relation to the interannual variability of temperature and sea ice (line 474-477), in addition to our response above under section 3/ validation of the model results (line 461-474). We also added the modelled PP and POC sinking flux in Figure 4 and added a supplementary table summarizing the annual maximum and minimum values of the modelled variables in different sets of temperature/sea ice anomalies (Table S7).

5/ Discussion on modelling limitations and results

Section 4 should be flushed out with discussions on weaknesses and limitations of the model such as 0-dimensional modelling, short duration of the simulation to explore impact of climate change, errors in some variables or fluxes, data assimilation. The authors mention a "microzooplankton model-observation misfits" in their model outputs (L 163). A discussion on the potential impact of this discrepancy on major results of the study, for instance on distribution of loss terms (including grazing) of the BCD presented in 3.2 and discussed in 4.1, seems to me to be necessary. The authors refine the bacterial compartment of the model.

Thank you for reminding us to discuss the weakness and limitations of the study that were poorly demonstrated in the previous version. As suggested, we added the discussions on the duration of the climate change experiments (line 461-464) and error/mismatch of zooplankton variables in data assimilation aspects (line 401-408). As mentioned, we no longer include the fate of the BCD as it does not add new information to the findings and discussion points of the study.

It would be interesting that the authors specify if they have compared the results of this new version with those of the basic version and if so, if they obtain a significant improvement of the modeling of bacteria concentration and production, primary production and POC stock with this new version. It would be relevant to know the potential positive contributions of this complexification of the ecosystem model to guide future works on ecosystem modelling.

As suggested, we added a paragraph to discuss the suggested points and contributions to WAP ecosystem modeling brought by our bacteria-oriented modeling (line 478-490).

The use of the term "POC export flux" for the calculated sinking flux of particulate organic matter at 10m depth does not necessarily seem appropriate to me. The term POC export generally refers to POC export under the euphotic layer or the mixed layer. What are the depths of the mixed layer and the euphotic layer in this region? This term could be replaced by a more appropriate term at least in the introduction, discussion and abstract sections.

As suggested, POC, C, or particle export flux was replaced by POC, C, or particle "sinking flux" throughout.

Minor comments / technical corrections

L55-58: Could you be more specific and indicate the growth of what, the depth of the Palmer Station, the period of comparisons with observations? Revised (line 56-69)

L118-119: Could you specify the depth of the site modelling? Added (line 122)

L 299-301: The authors should justify the choice of perturbations applied on temperature and sea-ice concentration by citing previous studies on climate change in the study area. Added (line 438-445)

L 406: Replace "phytoplankton account" by "POM production by phytoplankton accounts"? This sentence was deleted as no longer valid.

L 415: "experiments" seems more appropriate than "scenarios" considering the duration of the simulation. Replaced by "experiments", "simulations", or "conditions" throughout

L 418, 431: Warming temperature/ temperature warming : Remove temperature or replace warming by increasing. Fixed

Figure 4: black titles written over blue colours are difficult to read in Figure 4b, the values in the colour bar overlap. The comparison of HNA and LNA bacteria biomass and fluxes would be easier with an identical range in the colour bar of both panels. We tried, but the figure was illegible due to significant intergroup variability.

Figure 5: The reading of this figure could be simplified by a colour code for the different compartments. We color-coded the flows mentioned (Figure 5).

Figure 8b: via instead of vi on the fourth panel. Fixed

In Supplements:
Figure S1-S5: Some labels of y-axis on figures S1 S5 S6 are cut and grey lines are visible. How are the model outputs and observations normalized? Are they both divided the observed means? Please indicate units of the model/observations errors. Fixed the figures and legends (Figures S2-6)

L 117: "Kim et al. in prep" : Is it the same article as Kim et al. in review? Yes, it is the same article as the attached GMD manuscript (Kim et al. 2021). Fixed throughout the manuscript.

L 209: Do you mean June 1, 2012 instead of June 1, 2011? Fixed

Tables S2-S6: Please indicate units of the parameters. Fixed