

Interactive comment on “Distribution of Arctic and Pacific copepods and their habitat in the northern Bering Sea and Chukchi Sea” by H. Sasaki et al.

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We really appreciate thoroughly giving comments and helpful suggestion to our study by anonymous referee #1. We have answered all the comments made by the referee #2. RC, AR and RS stand for Referees comment, Authors response and Revised sentence, respectively. We hope that our explanations and revise plan are acceptable and satisfactory. In addition, I will change the abbreviations of large and small Arctic copepods (Coparc L and CoparcS) to CopLarc and CopSarc, respectively. I carefully proofread English and revise the manuscript before the submission of the revised version.

[RC1] Figure 1 is not as informative as I expect. The authors described different water

C9778

masses in the northern Bering and Chukchi Seas (Table 1). However, the interactions of these water masses, especially during the summer season when zooplankton samplings were conducted, are not well demonstrated and described. In Figure 1, consider adding more features for better illustrations of this shallow and highly advective system: 1) ocean bathymetry as colored background or contour lines; 2) locations and names of geographical places, e.g., St. Lawrence Island, Bering Strait, Herald Shoal, Herald Canyon, Hanna Shoal, Barrow Canyon; 3) arrows demonstrating dominant summer circulation patterns, including Alaska Coastal Current, Anadyr Water, Bering Shelf Water, Siberian Coastal Current etc. Excellent examples are shown by Grebmeier 2012 Figure 1, Day et al. 2013 Figure 1 and Spall et al. 2014 Figure 1 (Spall, M. A., Pickart, R.S., Brugler, E.T., Moore, G.W.K., Thomas, L., Arrigo, K.R., 2014. Role of shelfbreak upwelling in the formation of a massive under-ice bloom in the Chukchi Sea. Deep. Res. Part II, 105, 17–29. doi:10.1016/j.dsr2.2014.03.017).

[AR1] We appreciate for giving us helpful comments to revise Figure 1. Thank you for the information and helpful excellent examples. I will revise Figure 1 as the reviewer suggested. Please check the figure and its caption [RS1].

[RS1] Figure 1. Study area and sampling stations in the northern Bering Sea and Chukchi Sea during the summers of 2007, 2008 and 2013. The symbols denote the sampling stations where NORPAC net and CTD water samplings were conducted. The color scale indicates bottom water depth (m). Modified from figure presented in Spall et al. (2014) and Grebmeier et al. (2015).

[RC2] The calculation of vertical density gradient and variability of depth of maximum density gradient are not straightforward to me. Was the density gradient at the each depth calculated by the difference between 1 m above and 1 m below the specific depth using a central difference scheme? Then, how about the most top and bottom depths? How variable are the depths of maximum density gradient, from year to year and from station to station? The depths of maximum density gradient further determine mean values of temperature, salinity and chlorophyll, and later statistical analyses.

C9779

From readers' perspective, it may be helpful to spatially illustrate Table 3 explanatory variables at all stations using colored dots. If allowed by the journal, consider including these figures as supplementary materials.

[AR2] We are sorry for not sufficiently explaining the calculation of vertical density gradient and variability of depth of maximum density gradient. The answer for the first question, "Was the density gradient at the each depth calculated by the difference between 1 m above and 1 m below the specific depth using a central difference scheme?" is "No". We calculated a vertical density gradient at a specific depth using 2m-mean densities just above and below the specific depth. This calculation was conducted at all depths except at the top, second top, bottom and second bottom depths. Then we evaluated maximum density gradient and the depth of maximum density gradient at each profile. Further, we calculated temperature; salinity and chlorophyll-a concentration averaged at the upper and the bottom layers. We revised the manuscript to explain the methods more straightforwardly. We further added maps of Table 3 environmental variables (Figure A1–A4 in Supplementary Materials).

[RS-2] We divided the water column into two layers; i.e., the layers above and under the pycnocline and defined them as the upper and bottom layers, respectively. The density (ρ) was calculated from temperature and salinity measured by CTD profiles with a vertical data resolution of 1 m. Then, we calculated vertical density gradient (dp/dD) at a specific depth using 2m-mean densities just above and below the specific depth. This calculation was conducted at all depths except at the top, second top, bottom and second bottom depths. Then we evaluated maximum density gradient (dp/dD_{max}) and defined the depth of dp/dD_{max} at each profile, and defined the depth of dp/dD_{max} as pycnocline of the profile. We also defined the layers of above and under the pycnocline as the upper and the bottom layers, respectively. In this approach, to examine the water mass properties at the upper and bottom layers, environmental variables (temperature, salinity and log-transformed chlorophyll a) were vertically averaged within the upper and bottom layers and defined as TUPP, TBOT, SUPP, SBOT, Chl aUPP and Chl

C9780

aBOT, respectively (see Table 3 and Figure A1–A4 in Supplementary Materials).

[RC3] The sea ice concentration (SIC) of 50% seems a bit arbitrary. The conventional sea ice studies used 15% to represent an ice free or open water region. I know this threshold value is probably too small for the months from June to August in this region. A better explanation of this would be valuable. For instance, how sensitive are the anomaly timing of sea ice retreat and the GAM results to this threshold? For instance, will SIC thresholds of 60% or 40% change the overall conclusion regarding the impact of early ice retreat on zooplankton abundance? Since ice retreat timing is very critical for the marine ecosystem, I would like to see figures showing spatial distribution of the climatological mean sea ice retreat date of 1991-2013 (one panel) and the anomaly of sea ice retreat at all sampling locations in 2007, 2008 and 2013 (similar to Figure 3 and 4 except color dots representing anomaly days).

[AR3] We appreciate for helpful comments. As you suggested, we made the climatological mean sea ice retreat date of 1991-2013 (Figure 2) and the anomaly of sea ice retreat at all sampling locations in 2007, 2008 and 2013 (Figure 3). Furthermore, we tried to reconstruct GAM using the anomaly of sea-ice retreat date (aTSR) with SIC thresholds of 10–50%. The definition of "non-ice-covered pixel" actually causes the absolute TSR, but calculating the anomaly of aTSR has less impact on the result of GAMs. The correlation charts with aTSR thresholds of 50 % and that of 10–40 % are shown in Figure 4. In addition, the smaller SIC thresholds (10–30%) sometimes lead to derive unrealistic TSR because of microwave contamination from lands in late season especially in the near-shore area. Using aTSR with 40% and 50%, sea-ice retreat date was slightly different depend on threshold. Because several outliers affect the result of GAM when we use the threshold of 40 %, we use the threshold of 50 % in this study. We are so sorry for lacking the description. We will add more explanation on revised manuscript.

[RC4] In Section 3.2 Copepods abundance, the authors should try to use statistical tests (e.g., ANOVA or T-test) to compare spatial and inter-annual differences in cope-

C9781

pod abundance of three groups.

[AR4] We appreciate for helpful suggestion. I tried to use statistical test to compare spatial and inter-annual differences in copepod abundance of three groups. In our case, we did the non-parametric Kruskal-Wallis tests because the abundance of copepods of each group was not assumed its normality. The result of Kruskal-Wallis tests showed no inter-annual difference in sampling station, and the abundance of Arctic small copepods ($p > 0.5$). The abundance of Arctic large and Pacific copepods was different among years ($p < 0.001$). However, these differences in abundance of them could be regarded as the cause of habitat environment in each year because there were no inter-annual differences in the sampling stations, spatially.

[RC5] I had a really hard time in interpreting Figure 5 and consequently understanding Section 3.3 Habitats of copepods. In Section 2.3, the authors described that GAM used additive smoothing functions. But throughout the paper, the forms of smoothing functions for the explanatory variables were mystery to authors, which made the interpretations of functional responses of copepod abundance (i.e. independent variables) to explanatory variables in Figure 5 almost impossible. To me, the GAM here looked more like a black box and for the sake of best model fitting to the observation. This authors need to explain more thoroughly GAM underlying assumptions and result interpretations.

[AR5] We are sorry for not explaining well enough about Figure 5. In GAM, for instance in the Model of Arctic large copepods (Coparc-L, e.q. 1.1)

$$\text{Coparc-L} \sim s(\text{aTSR})+s(\text{PC1})+s(\text{PC2})+s(\text{PC3})+s(\text{Chl.aUPP})+s(\text{Chl.aBOT})+s(\text{Bdepth}) + \varepsilon \quad (1.1)$$

where aTSR, PC1–3, Chl.aUPP, Chl.aBOT, Bdepth are explanatory (independent) variables which affect the abundance of Coparc-L. $s(\text{XXX})$ is a smoothing function for each variable as similar role as a regression coefficient in a regression model. However, we don not have a direct access to a mathematical expression because it is summarized

C9782

the smooth function in several parts of scatter plot. In GAM plot, small circles show the standardized residuals where a constant term is ε . In Figure 5, the horizontal axes show the range of each independent variable and the vertical axes show the estimated smoother for them. The estimated smoother converts the explanatory variable to fit the models, so it shows positive effects for response variables and the magnitude of its effects when estimated smoother is positive, and vise versa. I will add this explanation on the figure description. [RS-5] Figure 5. GAM plot of the best model in each copepod groups: large Arctic (Coparc-L), small Arctic (Coparc-S) and Pacific (Coppac) copepods. The horizontal axes show the explanatory variable: the anomaly of the timing of sea-ice retreat (aTSR), principal component score (PC1–3) averaged log-transformed chlorophyll a concentration within the layer above and below pycnocline, (Chl aUPP and Chl aBOT) and bottom depth (Bdepth). Shade area represents 95% confidence intervals. The vertical axes indicate the estimate smoother for the abundance of copepods. The estimated smoother converts the explanatory variable to fit the models, so it shows positive effects for response variables and the magnitude of its effects when estimated smoother is positive, and vise versa. Short vertical lines located on the x axes of each plot indicate the values at which observations were made.

[RC6] I am also interested to know whether early ice retreat (and ocean warming) could also allow *C. glacialis* to develop much faster in 2007 than in 2008 and 2013. Of course, such analysis requires other information on zooplankton biomass and stage composition, which were not included in this study and probably not lab analyzed.

[AR6] We appreciate for helpful suggestion. I am also interested to know the abundance and development of *C. glacialis* in response to earlier sea-ice retreat. The prediction of the abundance of *C. glacialis* response to only earlier sea-ice retreat might be possible. However, we don't have the detailed information of zooplankton biomass and stage composition as referee a reviewed. Therefore, we are sorry that it is difficult to investigate the development of *C. glacilis* in response to much earlier sea ice retreat.

[RC7] The authors should proofread the paper to correct all typos. Just provide

C9783

a few examples of typo corrections in bolded below: Page 18672 Line-4: six water massesâPage 18674 Line-7: accumulate more lipidsâPage 18674 Line-10: cold IMW and DW in spring Page 18674 Line-14: Pacific zooplanktonâPage 18675 Line-27: A plausible explanation

[AR7] We appreciate for indicating them. We are sorry for my misspelling. I will proof-read the paper to correct typos.

Figure captions

Figure 1. Study area and sampling stations in the northern Bering Sea and Chukchi Sea during the summers of 2007, 2008 and 2013. The symbols denote the sampling stations where NORPAC net and CTD water samplings were conducted. The color scale indicates bottom water depth (m). Modified from figure presented in Spall et al. (2014) and Grebmeier et al. (2015).

Figure 2. Climatological mean sea ice retreat date of 1991-2013.

Figure 3. The anomaly of sea ice retreat at all sampling locations in 2007, 2008 and 2013 based on daily passive microwave sea ice concentrations using a threshold of 40%.

Figure 4. Correlation charts of with aTSR thresholds of 50 % vs. 0–40 %.

Figure A1. Maximum density gradient (10^{-3} kg m⁻¹) at each sampling station.

Figure A2. Horizontal distributions of temperature (°C) averaged within the upper (TUPP, top panels) and the bottom (TBOT, bottom panels) layers at each sampling station in 2007 (left panels), 2008 (middle panels) and 2013 (right panels).

Figure A3. Same as figure A2 but for salinity (SUPP and SBOT).

Figure A4. Same as figure A2 but for Chlorophyll-a concentration (ChlaUPP and ChlaBOT).

C9784

Please also note the supplement to this comment:

<http://www.biogeosciences-discuss.net/12/C9778/2016/bgd-12-C9778-2016-supplement.pdf>

Interactive comment on Biogeosciences Discuss., 12, 18661, 2015.

C9785

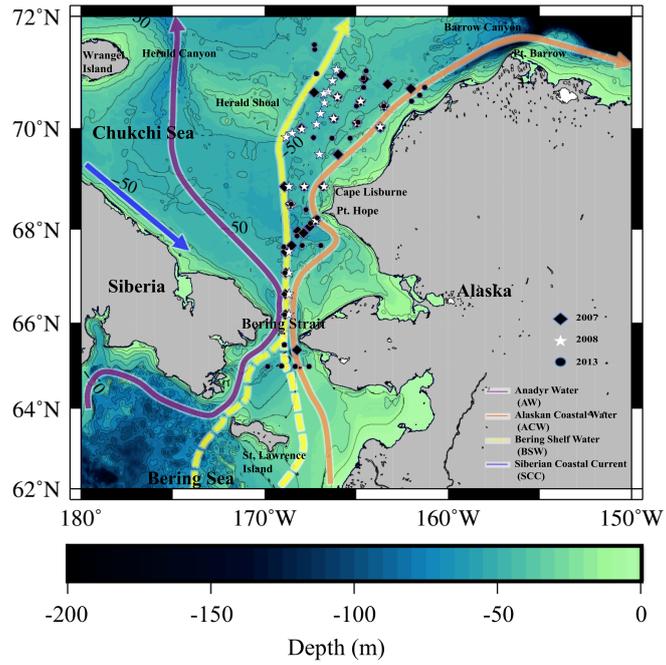


Fig. 1. Study area and sampling stations in the northern Bering Sea and Chukchi Sea during the summers of 2007, 2008 and 2013.

C9786

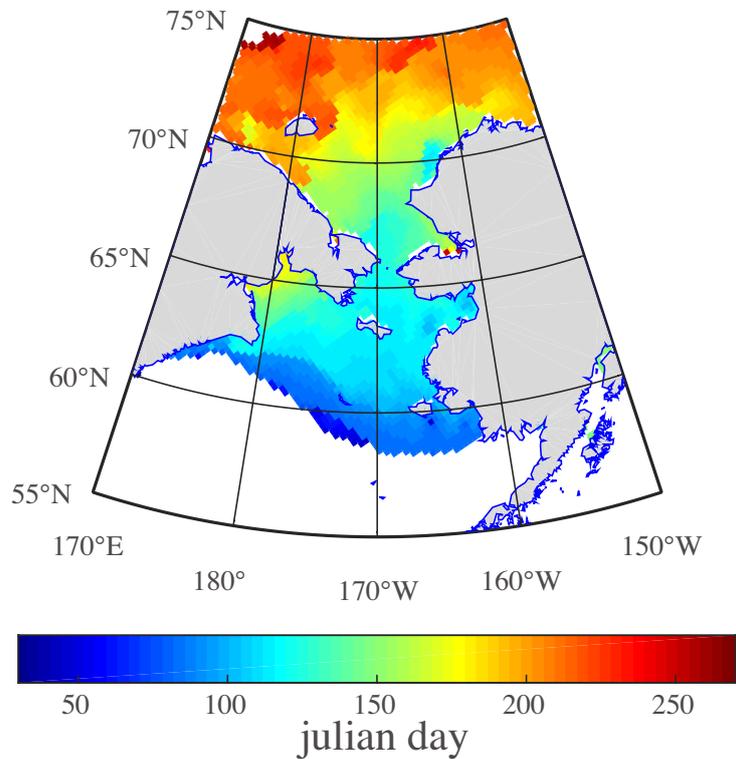


Fig. 2. Climatological mean sea ice retreat date of 1991-2013.

C9787

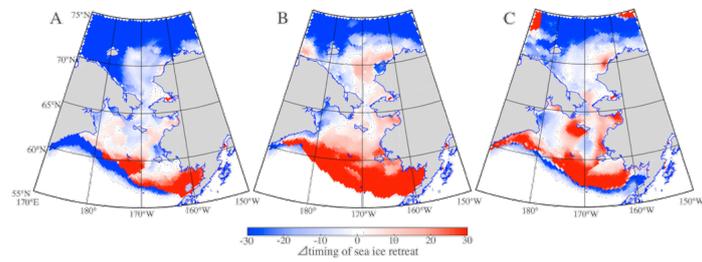


Figure 3

Fig. 3. The anomaly of sea ice retreat at all sampling locations in 2007, 2008 and 2013 based on daily passive microwave sea ice concentrations using a threshold of 40%.

C9788

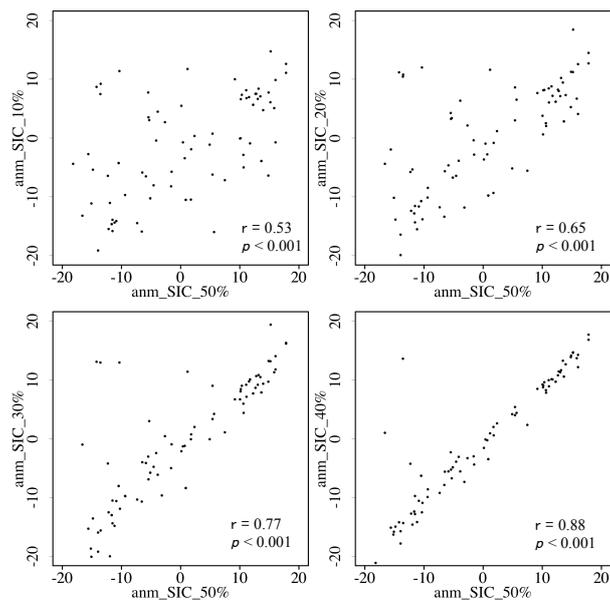


Figure 4

Fig. 4. Correlation charts of with aTSR thresholds of 50 % vs. 0–40 %.

C9789