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Biogeosciences Discussions

Interactive comment on "Quantifying the structure of the mesopelagic microbial loop from observed depth profiles of bacteria and protozoa" *by* T. Tanaka et al.

Anonymous Referee #2

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Comments on the ms. entitled: "Quantifying the structure of the mesopelagic microbial loop from observed depth profiles of bacteria and protozoa"

This ms. uses already published data of deep vertical profiles of bacteria and protists in the NW Mediterranean to generate some conclusions on the carbon flow available to zooplankton, and on the main mode of control of the bacterial populations. The calculations are done using a simple steady-state model, and correspond to the exploitation of already-collected data to learn more about the system.

But I don't like the ms. First, the model is unclear (or is not well explained), it does not fit very well to the data, and finally the conclusions are either vague or uninformative. For example, to cite that "HNF are the important remineralizers", is a vague statement. Everyone knows that it is bacterial activity what remineralizes organic matter. But, if bacteria are close to their carrying capacity and viruses are not actively removing bac-

teria, HNF predation can play this role, then stimulating remineralization. What does this ms. add to this contention? I'm afraid little. That bacteria are "controlled by both bottom-up and top-down" is an uninformative statement. The final paragraph points to a "change in paradigm" claiming that bacteria would not be the main remineralizers, but HNF would. This is really a daring statement since it's based in unmeasured bacterial and flagellate growth efficiencies, estimated with large uncertainties, uncertainties that are not reported.

The ms. has slightly more than 2 pages (˜50 lines) of "Results and discussion". However, it has 4 figures and 2 tables. How can someone explain 6 elements in 50 lines, and on top of that, add a discussion with references to the literature ? This is, obviously, impossible. In a revised vs. this ms. needs either an expanded text, or reduced elements. Figures 2 and 4 have already been published in one way or another.

I had trouble with the model, which I assume is explained in Thingstad 2000, particularly equations 1-3. The way in which the model is exposed in this ms. requires an act of faith. These equations are far from self-evident, and must be explained. To me is not valid to refer to a model that was explained somewhere else with no further explanations. As an example, the ms. requires sentences of the type: "in a steady-state situation, the production of new bacterial biomass (BP) will be compensated by the losses to predators and viruses, and this can be rationalized as BP = alpha*B*H + delta*B, being alpha and delta...." . By the way, I don't get why the mortality to HNF is dependent on both B and H abundance while the mortality to viruses is not dependent upon V density. This is so because the model has some element I can't grasp ? or is so because you have adapted the model to fit the data you have, and you don't have the V data ? More on the model: It took me a few hours to follow all the reasoning (and assumptions, and deletions) in page 417, lines 1-15. And I did spot a few strange things: BP/B is regressed against H, and estimates for something as complicated as "alphaC/Yh " obtained from the slope, and (alphaCdeltaBV/YhalphaH) from the intercept. Then, some magic to obtain these 5 variables (constants ?) out of 2. Sorry, I

BGD

1, S277–S281, 2004

Interactive Comment

already lost faith on the unexplained, so I need more explanations. Similarly, because BP and B data are not available simultaneously, the authors use the “average” B, when they had reported large seasonal variations in B in one of their former ms. How much the estimates of the 5 variables are dependent on these variability that is recognized to exist but then deleted ? All in all, how much of the conclusions depend on the magic exercises ? Does it matter if YC is assumed to be equal to YH ? What happens if it is not ? Still more, if, according to Fig 4 and Table 1, the regressions between BP/B and H are not particularly good, then the parameters have large errors. How can all these large errors allow you to make inferences about the “true” values of C transfer to viruses and HNF ? In other words: what happened to the errors in Table 1 that were lost in their transfers to Table 2 ????

I’m afraid the paper can’t be published as is. It’s of really little help to fellow scientists, it does not threaten any “established paradigm”, and the other conclusions from the model (that viruses and HNF are similar loss factors for B, that “a full microbial web” exists in the mesopelagic,...) are either not fully supported by the data, or had been reported before.

Other comments

- Is the title really saying what’s the ms. all about ? Are you “quantifying” the structure of the microbial loop ? Or else you are modeling the flows of C through bacteria available to be used by larger organisms ? I think the title reflects little of what the ms. is about. You equate “structure of the microbial loop” to “the trophic link between bacteria and zooplankton”. I think this is not obvious but rather confusing. Just to offer an argument against this equation, if it happens to exist multiple trophic step between bacteria and “zooplankton” such as those reported by Wikner & Hagström (1988, MEPS 50: 137-145) or Calbet et al. (2001, AME 23: 283-292), then “the structure of the ML” according to you, i.e. bacteria and protozoan abundance, will no longer reflect how much C is available to larger zooplankton.

BGD

1, S277–S281, 2004

Interactive Comment

- I consider inappropriate the use of “microbial loop” associated to “structure”. The authors know well that the concept of the microbial loop referred to the potential transfer of bacterial C to upper trophic levels and thus, had a connotation of dynamics. Once we have learned that things are quite more complex to what it was explained in the Azam et al. paper, I think we should refer to the “structure of the microbial food web”, instead of “loop”. I understand that in the context of this ms. you are trying to estimate the amount of bacterial C available to higher trophic levels, but this, to me, has nothing to do with the structure of the microbial loop. Finally, and in terms of dynamics, you should realize that you did not measure any rate here, and that all rates derive from the steady-state assumption. You should be careful in not overstating anything given that you didn’t measure H nor C grazing rates.

- As far as I know the idea that roughly the same amount of bacterial production goes to viruses and to bacteria is the “default” knowledge. The message, then, is that in the mesopelagic things are equal than in the epipelagic. Isn’t that ? In fact, do we need the use of a model to arrive to that conclusion ? Can’t that be derived from the analysis of the ratios of F to B in different layers ?

- The description of the site dynamics was not clear (page 415, lines 24-27). Exported DOC is roughly 3x exported POC, but I could not understand the text “Annual fluxes of... in the mesopelagic...” Are those the values of what is entering the mesopelagic ? Then, the values of 75% and 100% “of those from the euphotic layer” what do they mean ? I guess that the message is that most C is exported as DOC, but require clarifications.

- page 416, l. 21. Alpha in units of (L nmol C-1 d-1) ???

- page 417, l. 19. If HNF decrease more than B with depth, then the ratio B:F is higher in the mesopelagic than in the epipelagic. Unless F feed more efficiently on B in the mesopelagic (could be, bacteria seem to be larger, Patching & Eardly 1997 DSR 44: 1655, and HNF more active in the mesopelagic Cho et al. 2000), one could easily

BGD

1, S277–S281, 2004

Interactive Comment

assume that H are less important as regulators of B in the mesopelagic than in the epipelagic. Do these data fit with your models ? This type of discussion I'm missing.

- Figure 3. These data have already been published, and thus I don't see the point in repeating them. They are strange: dilution with < 0.2 μm water tests for bottom-up dependence of B ? In my experience, we always get growth when we dilute, among other things because the DOC field might be enriched. I don't see the point of this figure, especially if already published.

- page 418, line 11. Well, I could possibly say that "the not-very good relationships in eqs 4 and 5 imply that the assumed steady-state model does not generally apply to the mesopelagic". I would be as correct as you are in your sentence.

- Do you really believe that BGE is 19-39% after having read the del Giorgio & Cole reviews ????? that seems absolutely unrealistic. And why should BGE be high and FGE be as low as 1% ?

- The key to your assertion that HNF function as remineralizators depends on the FGE. I would like to see here estimates of the error associated to the value of 1%, and a thorough revision of the literature on FGE. Or else, the sentence should be deleted.

- Table 2 and pg. 418, l. 20. On talking about viruses and H as sources of mortality for B, it is needed to offer error estimates, not just one single value.

- The data by Cho could be exploited in your models, since they did measure FGR and some other of the factors in your equations.

- page 418, l. 22. How do you know that F feeding on bacteria produces POC and not DOC ?

Interactive comment on Biogeosciences Discussions, 1, 413, 2004.