

Interactive
Comment

***Interactive comment on* “Contribution of picoplankton to the total particulate organic carbon (POC) concentration in the eastern South Pacific” by C. Grob et al.**

Anonymous Referee #1

Received and published: 19 June 2007

Review of MS-NR: bgd-2007-0024 By Grob et al.

General comments This manuscript describes an attempt to assess the contribution of different picophytoplanktonic groups (Prochlorococcus, Synechococcus and picoeukaryotes) as well as bacterioplankton to particle beam attenuation (c_p) and particulate organic carbon (POC) along a transect in the eastern South Pacific. To accomplish such objective, flow cytometric measurements were used to constraint approximations of single cell optical properties. The results obtained show that picophytoeukaryotes represent a significant fraction of phytoplankton c_p along the studied transect. Moreover, despite the dominance of non-vegetal particles over the total c_p values, it is also

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper

shown that phytoplankton are responsible for most of the spatial variations of c_p in the study area.

These conclusions are of interest because they emphasize the potential importance of picoeukaryotes in the cycling of carbon in the South Pacific. However, despite the technique used in this paper (flow cytometry to sort cells and to constraint optical theory) has been already applied in other studies, to my knowledge it has never been directly validated. What I mean is that although the authors claim to be able to partition the bulk c_p signal, it has yet to be demonstrated that the sum of the parts obtained equals (within the uncertainty of the technique) the bulk c_p measurement. I understand that this validation would be a daunting or even an impossible task because not all particles can be accounted for. Nevertheless, because of this impossibility, I believe it is the responsibility of the authors 1) to warn the reader about this drawback and 2) to provide the uncertainty estimates of their predicted values in greater detail.

Note also that Kitchen and Zaneveld [LO 1992, 37(8):1680-1690] studied the effect of modeling the optical properties of single cells as layered spheres and concluded that “the effect of high-index-of-refraction outer shells in optical models of natural phytoplankton populations increases scattering at all angles except the very near-forward by *more than one order of magnitude*”. This conclusion suggests that the simple anomalous diffraction approximation used in the current manuscript may have severely underestimated the c_p for each modeled group and as a consequence severely overestimated the contribution of detritus to c_p .

Specific comments I would suggest the authors to analyze how the contributions of each group to the total c_p are affected by: 1) the uncertainties around the regression lines presented in figure 3a and 3b (the regression should ideally account for the uncertainties in both x and y values); 2) the uncertainties in the abundances of each group (size distributions were measured rather single values); 3) the assumption that $c_{het}=2c_{bact}$ (Claustre et al 1999 report a range of values from 1.8 to 2.4); 4) the assumption of $n=1.05$ for all groups (note that the c_{euk}/c_{veg} may not be influenced, but the con-

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper

tribution of e.g. c_{euk}/c_p may and as a consequence the estimate of c_{det} could change); the typical range of n would at least span from 1.03 to 1.08 [e.g. fig 10 in Stramski et al 1995 JGR, 100(C7):13295-13307]; 5) the assumption that the size of Prochlorococcus and Synechococcus are constant and equal to the sizes measured from a few samples (page 1469 lines 17-19); 6) the assumption that the size of bacterioplankton is 0.5 μm (see ranges reported in Table 2); 7) the assumption that Prochlorococcus intracellular carbon content is equal to that of Synechococcus; 8) the fact that Prochlorococcus size was measured only for one population; 9) the fact that the average FLS of the available data points for Synechococcus and Prochlorococcus was taken as a constant signal along the transect.

Another important comment. Section 3.3 is very confusing. Here is what I understood. On page 1475 lines 8-17, the authors state “we used two different approaches to estimate the picophytoeukaryotes carbon biomass: (1) from intracellular carbon content (Figs. 7b; see Sect. 2.1) and (2) calculating c_{euk} contribution to c_p , the latter assumed to be equivalent to POC (see Sect. 2.2). Both approaches gave very similar results”. But at this point of the manuscript I cannot see any figure or table showing these “very similar results”. Also fig. 7b shows the contribution of the predicted beam-c value for each group to the total c_p . There is nothing related to “intracellular carbon content” in Fig. 7b. So I assumed that there is a typo and that the authors are referring to fig 9 where they present a comparison between $c_{euk}:c_{veg}$ and $\text{carbon}_{euk}:\text{carbon}_{veg}$. Next they state “The above provides strong support for the use of optical techniques and theory to determine picophytoeukaryotes contribution **to POC**, under the sole condition of using actual mean cell sizes.” If indeed there is the above typo, then I have the impression that this statement is a misinterpretation of the results. Figure 9b provides support for the use of optical techniques and theory to determine picophytoeukaryotes contribution **to photosynthetic carbon biomass, NOT to particulate organic carbon**. $c_{euk}:c_p$ and (eukaryotic carbon):POC depend also on other assumptions among which those related to the the size and refractive index of bacteria and the relationship between c_{bact} and c_{het} . So either the authors forgot to show part of their results or the

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper

results are misinterpreted.

Technical corrections Abstract. The abstract should be revised after providing estimates of the uncertainties in the contributions of the different groups to the c_p and POC.

Abstract: define Tchl_a

Page 1466, line 13: “The error associated to abundances determined using flow cytometry is <5%.” Can you provide a reference for this statement? Is this uncertainty estimate valid also when you had to fit a Gaussian curve to the data?

Page 1467, line 6: define “actual sizes”.

Page 1467, lines 19-21. The authors state that the single point for which they have size measurements and FLS is important because it represents the cell size of a natural Prochlorococcus population. I agree with them. However, they should also recognize that the uncertainties around this part of the regression line are large and that they should be propagated through their calculations.

Page 1469, line 8: the word “detritus” to define the unexplained part of the c_p is dangerous. The real contribution of detritus was never measured in this study, nor in the previous studies. I suggest to call this quantity with a name that recalls the unaccounted c_p .

Page 1469, lines 21-22: which were the conditions in which you used the nearest sample value? How many times did you have to use the nearest sample value?

Page 1469, eq. (5): what are the uncertainties related to the coefficient 500?

Page 1469, line 20: that they use always local noon time data may be important with respect to the result that the value adopted for real part of the refractive index seems to be not important. Maybe this topic could be briefly discussed.

Results: please include uncertainties for all your calculations.

Page 1473, line 15-16: “Cyanobacteria and bacterioplankton attenuation coefficients, on the other hand, varied only according to their abundances”. Shouldn't we expect that since for these groups only mean sizes were used?

Page 1477, line 1: the reference to Li 2007 is missing.

Page 1477, line 9-10: “Picophytoeukaryotes were the only group to vary independently from Tchl_a, suggesting that the factors controlling picophytoplankton population, such as sinking, sensibility to radiation, grazing, viral infection,” Actually, from Fig 8a, it seems that Euk_carbon_biomass correlates with Tchl_a (although it is difficult to say for sure, because the different symbols are hard to distinguish). Please use a different symbol to represent Euk_carbon_biomass. If the above fact is verified, how can the discrepancy between table 1 and fig 8a be explained?

Page 1479, lines 24-25: “Our results indicate that Tchl_a and c_p would be equally useful estimates of photosynthetic carbon biomass in the open ocean, where it is mainly constituted by picophytoplankton (<3 μm)”. Would this statement be valid also for the data presented in figure 2? (Compare MAR and all-but-MAR data). Clearly, intracellular dvchl_a content is higher in the MAR data which implies that, at least for Prochlorococcus in the South Pacific, Tchl_a=chl_a+dvchl_a is not a good indicator of biomass.

Fig. 3b: the units of the y-axis are missing.

Fig. 5: “as a function of temperature”. Is it “surface temperature” or “integrated temperature”?

Fig. 7a and 7c are very difficult to read after printing. For example it is impossible to distinguish c_{proc} from c_{euk} from c_{syn} . It may be more useful for the reader to see the partitioning for the stations H, G, EG and W. By reducing the number of stations it would be also possible to plot the uncertainties associated with each prediction. Also in the caption there is a reference to section 3.4. This section does not exist.

Fig. 8: Proc is indistinguishable from Euk. From Fig. 8a one can see that there is not a

[Full Screen / Esc](#)[Printer-friendly Version](#)[Interactive Discussion](#)[Discussion Paper](#)

negative correlation between *Synechococcus* carbon biomass and *Tchl*_a. What I see is a flat relationship up to $\log(\text{Tchl}_a) = -1.2$ and then a vertical relationship between the two variables. I would also indicate better that the variables plotted are log-transformed (e.g. there is no “log” in the y-axis).

Also it is somewhat surprising that there is a rather strong relationship between *Syn* abundance and *Tchl*_a ($r=0.82$, Table 1), but in Fig. 8a there is no relationship between *Syn_carbon_biomass* and *Tchl*_a. Since $\text{Syn_carbon_biomass} = (\text{Syn_abundance} * \text{Syn_carbon_per_cell})$, this discrepancy would imply that the carbon per cell in this group varied in a systematic manner with abundance. However in the supplementary material we learn that “we took the average of the available data points as the mean FSC signal for *Prochlorococcus* and *Synechococcus* along the transect”. Thus a single value of FLS was used from which the intracellular carbon content of *Syn* was estimated (Fig 3b). So how can this discrepancy explained? It may be useful to see a plot of the relationship between the variables used to construct table 1. How about a plot of the correlation matrix (see fig 3.3 pag 85 of <http://cran.stat.ucla.edu/doc/contrib/grafi3.pdf>)?

Supplementary material.

Page 1: “eliminating the signal’s outliers at both ends” How exactly?

Page 1: “For picophytoeukaryotes, the whole Coulter’s size distribution was used to calculate the arithmetical mean for cell size”. Wouldn’t it be better to use a weighted mean?

Page 1: “volume distribution of particles standardized to 1 956;μm” This is not clear.

Interactive comment on Biogeosciences Discuss., 4, 1461, 2007.

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper