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Interactive comment on "Phytoplankton community structure in the VAHINE MESOCOSM experiment" *by* K. Leblanc et al.

Anonymous Referee #2

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This manuscript provides results of the changes in phytoplankton community composition during a mesocosm experiment in Low Nutrient, Low Chlorophyll waters in the Southwest Pacific. The primary objective was to stimulate a bloom of N2-fixing cyanobacteria through PO$ addition and track the resulting particulate carbon fluxes resulting either directly for the N2-fixing organisms (including those associated with diatoms) or indirectly through the diazotrophs providing a source of fixed, reduced nitrogen to the enclosed system. The manuscript by Leblanc et al. provides a thorough overview of the changes in non-diazotroph phytoplankton communities within three replicate mesocosms during three phases of development. Phase one of the analysis follows a spike of PO4 to each mesocosm that was meant to stimulate N2-fixation. The second phase corresponded with a transition from N2-fixing cyanobacteria to non-N2-fixers, following the depletion of the PO4 spike. From the data presented, there ap-

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pears to by some rather complex dynamics of the phytoplankton communities not only throughout the duration of the experiment but among the mesocosms. For example, it is apparent that mesocosm 3 achieved higher amounts of phytoplankton biomass during phase 2 of the experiment associated with increases in pico- and nano-eukaryotes that were not replicated in the other experiments. In addition, the substantial increase in phycoerythrin in mesocosm 3 that was somewhat replicated in the control sampling but not found in the other incubations is somewhat perplexing.

I found the article well-written and for the most part, the methods used seem applicable for the general objectives of the paper in detailing the phytoplankton taxonomy transitions throughout the bloom. The manuscript is more of a descriptive account of the phytoplankton successions rather than being able to provide definitive reasoning as to why certain groups of phytoplankton changed in abundance when they did. Noticeably absent are the changes in abundance in N2-fixers at the same resolution as what is presented for the non-diazotroph phytoplankton groups apart from phase averages in N2-fixation rates in figure 11 and gene expression data in the supplemental. Although I gather this is due to another paper that will be part of the same special issue describing these results (Turk-Kubo et al. 2015). In addition, it is also surprising that chlorophyll concentrations do not necessarily provide much insight into the phytoplankton composition dynamics. In fact, during the peak abundance of the C. closterium around days 15 and 16, chlorophyll concentrations remained quite low. Chlorophyll concentrations seem to be better correlated with pico and nano-eukaryotes that bloomed near the end of phase 2 of the observation period. In addition, the conversion to carbon biomass presented in Figure 10 was rather unsatisfactory. It would have been interesting to compare these biomass estimates with those that were exported to determine whether similar proportions exist between the two or if there is a preferential export of certain groups (e.g. diatoms etc.). Thus in some regards, I find the results presented to be somewhat incomplete. However, as part of a special issue dedicated to the VAHINE mesocosm experiment, this manuscript does constitute an important contribution to describing the overall outcomes. Although further support and discussion on principle

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factors governing the transitions observed in phytoplankton group successions would benefit the manuscript immensely.

Specific Comments:

Line 62 – Given the primary outcome was to determine whether a diazotroph bloom would increase C export fluxes to depth, I am curious to know if this was the case. Although I can imagine this will be presented in other papers (possibly lead by Bonnet?), perhaps a short discussion as to whether this was the case would add value to this manuscript. Clearly, the resulting changes in non-diazotroph abundances would have also contributed to the overall outcome in influencing C export potential.

Line 79 – So do the authors think that the transition from DDAs to cyanobacterial N2-fixers may have influenced the phytoplankton composition somehow?

Line 161 – Include the volumes settled for micro-phytoplankton enumeration.

Line 170 – It is unfortunate that cell volume estimates of diatoms counted were not measured as this can vary substantially for a given species. It should therefore be noted that these C biomass estimates be taken with extreme caution.

Line 218 – . . .were comprised of between. . .

Line 347 – It is surprising there is little discussion of Si limitation of diatom growth. Clearly with Si concentrations below 2 uM, this would favor very lightly silicified species (such as C. closterium) or non-diatom phytoplankton groups. I would guess that after PO4 addition, Si is a major regulator of diatom growth (as well as possibly Fe).

Line 400 – Is there evidence to support this hypothesis within the scientific literature? Why would C. closterium have such a higher NH4 affinity. It's likely more related to their low Si requirements relative to other diatoms.

Line 409 – It's also very likely that these dinoflagelates were mixotrophic. Gyrodinium/Gymnodinium are well known to exhibit heterotrophy within low nutrient envi-

ronments when this mode is more favorable.

Line 463 – Indeed, this might be the case for a number of phytoplankton groups and not just Synechococcus.

Line 515 – remove “to “ in benefited to the entire. . .

Line 517 – observed by, not on.

Line 518 – More precisely, what are these clear implications for the efficiency of C export by DDN? What groups were exported?

Figure 5 – Missing M labels of panels to be consistent with other figures.

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