

Interactive
Comment

Interactive comment on “Diazotroph community succession during the VAHINE mesocosms experiment (New Caledonia Lagoon)” by K. A. Turk-Kubo et al.

Anonymous Referee #2

Received and published: 20 July 2015

General comments:

In an extensive mesocosm experiment, the authors use quantitative PCR to monitor the abundance/succession of nine diazotrophic phylotypes over a 23-day period following a dissolved inorganic phosphate fertilization event. In addition to reporting the observed abundances of these nine diazotrophs over time, the authors use the data to calculate net growth rates of the individual phylotypes as well as changes in their relative abundances (using the total abundances of the nine phylotypes as a proxy for the entire diazotrophic community). Hence, the data describe the dynamics of some important groups of diazotrophs and are indeed interesting and important for the prediction of the fate of fixed N in this system.

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However, I find it somewhat problematic that there are no indications of whether these nine phylotypes are important in this system. The manuscript deals with community succession and it would have been preferable to have some analyses of the actual diazotrophic communities present in the mesocosms and in the lagoon itself during the experiment (e.g. a *nifH* clone library or similar). An accompanying manuscript in preparation is mentioned (Berthelot et al. 2015 in prep). It is however, unclear whether the reader can find information on the composition of the diazotrophic community in this paper. Is this the case? And what were the overall findings regarding the community composition if that is the case? On several occasions, e.g. p. 12, l. 12-16; p. 18, l.11-12; Figure 2, the authors talk about abundances of specific phylotypes as fractions of the total diazotrophic community. Such deductions cannot be made as it is unknown/unlikely whether the nine selected primer/probe sets collectively target the entire community. I suggest addressing this matter and supplying a short general description of the present community as well as the relative abundances of the quantified phylotypes if these data are available. If they are not I would strongly suggest making these data if there are DNA left from the study. Alternatively, are there previous data describing the community in this location?

Nonetheless, the data do show significant changes in the dynamics and relative abundances of the monitored phylotypes as a function of the fertilization event (and temperature), which in itself is novel and interesting.

Specific comments:

p. 12, l. 12-16: I disagree with the use of the term total diazotroph community since the community as such is not investigated. Do the authors have any data describing the relative abundance of this sequence compared to total *nifH* sequences – maybe in the in prep paper?

p. 18, l.11-12: As above

p. 20, l. 16-19: As above

Figure 2: As above

Technical comments:

p. 2, l. 11: “unicellularcyanobacterial”

p. 5, l. 15: Delete “the” in “understand the how”

p. 5, l. 19-20: Move parentheses start to surround the 2015

p. 6, l. 10: As above

p. 20, l. 6: change “NO3” to “NO3-“ (may want to check throughout the MS)

p. 20, l. 21: change “NH4” to “NO4+“ (may want to check throughout the MS)

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