

Interactive comment on “The effects of decomposing invasive jellyfish on biogeochemical fluxes and microbial dynamics in an ultraoligotrophic sea” by Tamar Guy-Haim et al.

Anonymous Referee #2

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The paper of Guy-Haim et al. provides new information on the impact that the decomposition of jellyfish's carcasses can have on nutrients dynamics and on the bacteria living in sediments and in surrounding waters. The study focuses in particular on the jellyfish *Rhopilema nomadica*, a non indigenous species that has established in recent decades in some regions of the eastern Mediterranean, where swarms of this species are regularly reported with detrimental effects for different activities of high economical relevance. An experimental set-up is built to allow measuring nutrients and dissolved oxygen as well as assessing bacteria abundance, productivity and composition, throughout different phases of the carcasses' decomposition process. Results show that jellyfish degradation determines significant changes in nutrients supply, oxy-

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gen concentration/ph and in the composition and abundance of bacteria living in the sediments and in the above water.

Overall the study addresses a highly relevant scientific question, providing a significant contribution towards a better understanding of the impact of jellyfish blooms on biogeochemical fluxes. Research outcomes here presented can be used to improve current ecosystem models, implementing the effects of jellyfish blooms, more specifically blooms of *R. nomadica*, on biogeochemical fluxes and on the first levels of the trophic web (i.e. bacterial communities).

The paper is quite comprehensive, though needs some revisions in the description of the methods and possibly in the presentation of some results. In particular session 2.6 should include more details on the numerical methods here adopted, as the reader is not necessarily familiar with the R routines indicated in the text and need to understand what has been done with the data. For instance it should be mentioned on which data set (supposedly 30 + 30 groups shown in Fig. 7 and fig. C1?) the diversity indices have been calculated and possibly why these three specific diversity indices (Chao, Shannon and Simpson) have been selected. Also, it should be indicated the dimension of the matrix (N metabolic functions/pathways X P observations) analysed by PCA, which should not include “rare” metabolic functions, i.e. lines with too many zeros, to prevent bias in the results of the analysis. Finally, Figure 8 should be redone using symbols and labels that would allow reading at least the key variables discussed in the text.

Further comments that should be also addressed before publication in Biogeoscience are listed here below:

- line 166: Table 2 should be cited instead of Table 1. -line 173: here it should be indicated that the NO₃ concentration in JF2 is different from the other stations and possibly the reason for it should be discussed.

-Lines 302-307: this sentence is unclear and should be further revised. In particular it is not clear whether the chlorophyll maximum in late-spring summer is a recurrent

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event that does usually follow records of jellyfish blooms. Unless the two events can be chronologically connected, the sentence here drafted should be changed or deleted; -Line 314: in the first and second parentheses *Synechococcus* and *Prochlorococcus* should be respectively indicated (in other words, the two parentheses have been inverted). - Lines 324-325: I suggest to revise the text along the following lines: "In the shallow waters of the EMS the peak of bacterial production observed in summer is possibly associated with the swarms of *R. nomadica*, which are frequently (regularly?) observed in this season" -Lines 363-365: this sentence needs further revision, as the study does not really measure decomposition dynamics in the Mediterranean, which would imply measurements done in situ. The study does rather measure nutrients and dissolved oxygen released by remineralisation of *R. nomadica* carcasses and the potential impact of this on the bacterial community.

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