

## ***Interactive comment on “Benthic communities in the deep Mediterranean Sea: exploring microbial and meiofaunal patterns in slope and basin ecosystems” by K. Sevastou et al.***

**Anonymous Referee #3**

Received and published: 4 February 2013

The paper by Sevastou et al. investigated the spatial patterns of microbial and meiofaunal communities in slope and basin ecosystems in the deep Central-Eastern Mediterranean Sea. The paper is based on a large dataset collected in the framework of different research projects. Authors investigated total meiofaunal and copepod abundance, meiofaunal diversity (as richness of higher taxa and nematodes as genus richness) and microbial diversity in relation to the bathymetric gradient in two habitats: slope and basin. In general results reported here confirmed previous investigations, the novelty is mostly related to the comparison of spatial patterns for meiofauna and bacteria. In my opinion, the paper can be published after a major revision. In particular, authors should stress the different patterns between meiofauna and bacteria. In the present form, the

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paper appears mainly focused on meiofauna while bacteria have been marginally investigated. The two benthic components should be integrated, in the present version of the paper they appear two independent part of the story. I understand that most of the dataset is based on meiofaunal data but I think that also bacteria should be valorized, and the comparison could be the basis of novel aspects for the paper. Main criticisms: Analyses focused only on the bathymetric gradient. The scientific value of the paper could be improved investigating the role of latitude, longitude and trophic sources. Depth explains up to 60% for nematode diversity but the variance explain for the other components is limited suggesting that other aspects should be considered. Microbial communities: data of abundance could be included in the paper to be consistent with meiofauna. The number of replicates is not reported for each sampling station. Please clarify. Results and Discussion are very long. In my opinion, these two sections should be revised stressing the attention on the main results. I would suggest to revise the order of the results, in particular all results of DISTML analyses could be moved at the end of the description of the results on meiofauna and bacteria. I find repetitive and not useful for the reading of the text, the division in the paragraph: 3.2 and 3.3. I would suggest to investigate abundance, diversity and DISTML results. Discussion should be reduced and fluent, stressing the comparison between meiofaunal and bacterial patterns. Minor revisions: Abstract: Pag 1, lines 25-27: the higher meiofaunal abundance and richness . . . . highlights the effect of productivity on benthic patterns. Pag 2, lines: . . . differentiation diversity . . . Please explain the meaning. In my opinion, the authors should be consistent along the text to indicate turnover diversity or changes in taxa and genera composition. Material and Methods I would suggest to add the depths range in the text in line 26, pag 5. Pag 5, line 31: . . . sediment surface. . . , the top 1 cm or more? Please explain. Pag 6, line 9: after Rose Bengal add “counted” and sorted to . . . .

Results In general I would suggest to add standard deviation in the description of data. Pag 10: Check the order of figure. Figure 4B and Figure 4C is after Figure 5A, please revise. Pag 11, line 26: What is diversity change? Table 2 and 3: I would suggest the p level as asterisk: \*, \*\*, \*\* and ns not significant to make the reading of the tables

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more easy and immediate. Figure 2: I would suggest to start the Y axis from 60% to highlight the contribution of different minor taxa. Figure 4: Add regression lines. Are the equations significant? Figure 7: is not clear, maybe could be deleted.

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Interactive comment on Biogeosciences Discuss., 9, 17539, 2012.

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