

We thank the reviewer for his/her helpful comments. Detailed response to each comment is provided below:

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 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.

Reply: In the revised version of the manuscript all concerns of the reviewer were addressed and his/her suggestions were taken into consideration. Nevertheless, we need to point out that more emphasis was inevitably given initially to the meiobenthic communities due to the lower availability of bacterial data compared to meiobenthic data from the specific region (no microbial abundance data are available, microbial diversity data are from fewer stations compared to meiofauna). In our attempt to avoid, as much as possible, this unequal presentation of meiofaunal and microbial communities according to the reviewer's suggestions, the following actions were taken:

(i) in the revised version of the manuscript we decided to include a new figure, similar to Figure 2 of the initial version of the manuscript, which presents the microbial community composition on the level of large taxonomic groups, and relevant paragraphs have been added in both the results and the discussion sections. Two more references by Quaiser et al. 2008 and Jones et al. 2009 have also been added.

(ii) a new figure (similar to Figure 6) illustrating bacterial species estimator Chao1 has also been added.

(iii) we have corrected, rewritten and rephrased certain parts of the results and the discussion, as indicated by the reviewer in the following comments; we have included more information regarding the microbial component and we have tried to integrate the two components (meiofauna vs microbes).

(iv) we have explored diversity patterns of the two investigated benthic components in the limited number of stations from which both meiobenthic and bacterial samples exist, with a view to include new aspects of diversity patterns in the discussion.

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.

Reply: As explained in the manuscript, our main goal in this study is to investigate and compare patterns of the smaller benthic components (meiofauna and microbiota) in relation to two different marine habitats, basins and slopes. Yet we included depth as a factor in the analyses because it is well known that it affects benthic community patterns. Although we have considered initially the possibility of exploring latitudinal and longitudinal patterns of the studied groups, we rejected this option for two main reasons: firstly, because we believe that our data are very limited with regard to latitude and longitude (i.e. they only cover the central-eastern part of the Mediterranean); and secondly, because a number of such extensive studies covering the entire Mediterranean basin have been published very recently (e.g. Danovaro et al. 2008, Danovaro et al. 2009, Gambi et al 2010). For these reasons we felt that it would not be appropriate to repeat a latitudinal and longitudinal approach with a more restricted, in terms of geographical coverage, dataset. Moreover, if we were to include these aspects in our study that would have to be restricted exclusively to major meiofaunal taxa, which would render the manuscript rather unbalanced.

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.

Reply: Following also relevant suggestions from Reviewer 2, in the revised manuscript we make an attempt to investigate and discuss the observed benthic patterns also in relation to other environmental parameters, particularly food availability, which has been found in all our previous studies in the E. Mediterranean to have the strongest positive correlation with benthic communities (Tselepides et al 2000, Tselepides & Lampadariou 2004, Polymenakou et al 2005, Lampadariou & Tselepides 2006, Lampadariou et al 2009).

Microbial communities: data of abundance could be included in the paper to be consistent with meiofauna.

Reply: Unfortunately, data on bacterial abundances are not available and thus are not presented. All samples were collected onboard and kept frozen for molecular analysis and no samples were collected and preserved for counting. Frozen samples cannot be used for bacteria counting and thus the collected frozen samples were only processed for pyrosequencing.

The number of replicates is not reported for each sampling station. Please clarify.

Reply: The supplementary table TS1 was amended in order to include in the last column the number of replicated samples per station and type of data. For meiofaunal major taxa analysis three sediment cores were used for most of the stations (>75%), while for nematode analysis 50% of the stations were based on a single sample. Microbial analysis was based on 3-4 sediment cores from each station that were merged in a single sample.

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.

Reply: We have taken into consideration all the suggestions of the reviewer as well as relevant suggestions from Reviewer 2 and we hope that in the revised manuscript we managed to address all issues and to resolve the structure problems indicated by the two reviewers.

Minor revisions:

Abstract: Pag 1, lines 25-27: the higher meiofaunal abundance and richness . . . highlights the effect of productivity on benthic patterns.

Reply: We did not make any change because we could not understand what the suggestion of the reviewer was (the text repeated by the reviewer is exactly as written in the manuscript).

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.

Reply: As explained in the Methods section (p. 7, l. 10) differentiation diversity is the rate of change in species composition. Throughout the text it is presented as beta or delta diversity to indicate variability within levels of habitats (basin, slope) and within levels of depth ranges. Turnover diversity, on the other hand, is used in our study always to indicate variability between levels of habitats and depth ranges. We use the wording “changes in taxa/genera composition” as is widely used in many text books in order to avoid repetition of the same words in the same sentence/paragraph. In the revised version of the manuscript, though, we reconsider the use of this phrase.

Material and Methods I would suggest to add the depths range in the text in line 26, pag 5.

Reply: Added.

Pag 5, line 31: . . . sediment surface. . . , the top 1 cm or more? Please explain.

Reply: Samples for microbial analysis were from the first 2 cm of the sediment and for meiofaunal and nematode analyses from the top 5 cm. This information was added in the text.

Pag 6, line 9: after Rose Bengal add “counted” and sorted to . . .

Reply: Corrected

Results In general I would suggest to add standard deviation in the description of data.

Reply: In Figure 3 the standard deviation are presented. In Figure 4, the standard deviations exist only for the meiobenthic abundance as for the rest (major meiofaunal, nematode and bacterial diversity) analyses was performed after pooling of data or merging of samples (in the case of microbial community samples). For the same reason, standard deviation was not also illustrated in Figure 5. Nevertheless, we added relevant information, whenever possible, in the text as well.

Pag 10: Check the order of figure. Figure 4B and Figure 4C is after Figure 5A, please revise.

Reply: We will make the changes accordingly.

Pag 11, line 26: What is diversity change?

Reply: Differentiation diversity is considered to reflect changes in inventory diversity. In that sense it was used in this heading to suggest that this section will refer to differentiation diversity and community structure, two interrelated aspects of communities. Nevertheless, as a follow up on a previous comment on the repeatability and usefulness of paragraphs 3.2 and 3.3, we have modified the results and paragraphs headers hoping to have made things clearer.

Table 2 and 3: I would suggest the p level as asterisk: \*, \*\*, \*\*\* and ns not significant to make the reading of the tables more easy and immediate.

Reply: Usually, the asterisks are provided to indicate different levels of statistical significance when the F values are not provided. Here, we have chosen to give both values in order for the reader to be able to check the output raw data of the analyses. Nevertheless, we could change the tables as suggested, provided that the editor and the other two reviewers will not mind that this type of data will be removed from the revised manuscript

Figure 2: I would suggest to start the Y axis from 60% to highlight the contribution of different minor taxa.

Reply: Modified as suggested.

Figure 4: Add regression lines. Are the equations significant?

Reply: Bathymetric trends for all variables presented in Figure 4 were tested using DISTLM, and not parametric regression, the results of which are presented in the relevant sub-sections of the Results. Although we are not convinced that trendlines would add value to the figure/results, we will explore if this possibility is feasible when using DISTLM routine for regression analysis.

Figure 7: is not clear, maybe could be deleted.

Reply: We could not understand to what specifically the reviewer refers to with regard to clarity of the figure, nevertheless, we will try to better visualise the output of the plots.

## References

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