

Interactive comment on “Biogeography of planktonic microbial communities across the whole Mediterranean Sea” by F. Mapelli et al.

Anonymous Referee #1

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The manuscript by Mapelli et al. is an interesting work looking at the biogeography of bacterioplankton across the entire Mediterranean Sea. Overall, I believe that the quality of the data set is good, providing a synoptic view of the distribution of bacterioplankton communities in the Mediterranean Sea, and trying to link it to changes in environmental parameters. The authors have also done a good job when synthesizing and presenting the data. However, I believe that some particular issues should need to be further clarified before this manuscript can be accepted for publication in Ocean Science.

The authors use several times the word “diversity”, but they used ARISA as the molecular fingerprinting technique of choice. ARISA is a good tool for analyzing differences in community structure but it is not sensitive enough for analyzing the full richness and diversity of a natural community (as shown by the last generation sequencing

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techniques). Therefore I suggest being cautious with the use of those words in the manuscript.

In the Results and Discussion section (particularly in 3.4) they write about the differences between the eastern and western basin in terms of bacterioplankton community composition, and they try to link it to variations in water masses. However, they did not characterize the specific water masses and their distribution. Therefore, it is difficult to clearly establish a link between water masses and the bacterioplankton community structure.

Another possible explanation for the differences found in bacterioplankton communities between both basins could be related to the variations found in phytoplankton communities between both basins. There are numerous reports about the strong link that exists between phytoplankton and bacterioplankton communities, where changes in phytoplankton abundance or community structure provokes changes in bacterioplankton community structure, many times due to changes in the DOM quality/quantity provoked by those changes in phytoplankton.

A clearer explanation of the stations covered is required. There are stations in the supplementary table that were not included in Fig.1. Moreover, the legend of Fig. 1 is not clear to me: “Stations where both bacterial abundance and community composition (ARISA fingerprinting) were determined are indicated by encircle dots and station numbers. Underlined stations numbers indicate those stations were only the bacterial abundance was measured”. But, what are the single dots? I would remove the stations that were not sampled for parameters used in this manuscript, if that is the case. I would also try to mark clearly in that Fig.1 the 8 stations that were used for the finer vertical scale profiling of bacterioplankton communities.

I am missing the rationale about why those 8 stations were selected for the finer scale profiling. Authors should include some words about it if they have not done so already.

A clean rewrite by a good editor would help throughout.

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