

Reply to the Referee 3 comments.

We thank the referee for taking time to revise the proposed manuscript. Our replies are reported in italics below each of the Referee comments.

The authors analyzed the distribution patterns of planktonic bacterial community through the water column and across different water masses in the whole Mediterranean Sea by determining bacterial community composition using Automated Ribosomal Intergenic Sequence Analysis (ARISA). They used bacterial community composition, prokaryotic abundance and environmental variables (i.e., positions, depth, salinity, Temperature dissolved oxygen, PO₄, NO₃ and NO₂) from the cruise to show bacterial diversity is correlated to different water masses across the water column of the eastern and western Mediterranean Sea. Overall, the manuscript is well written and clear with a few exceptions noted below.

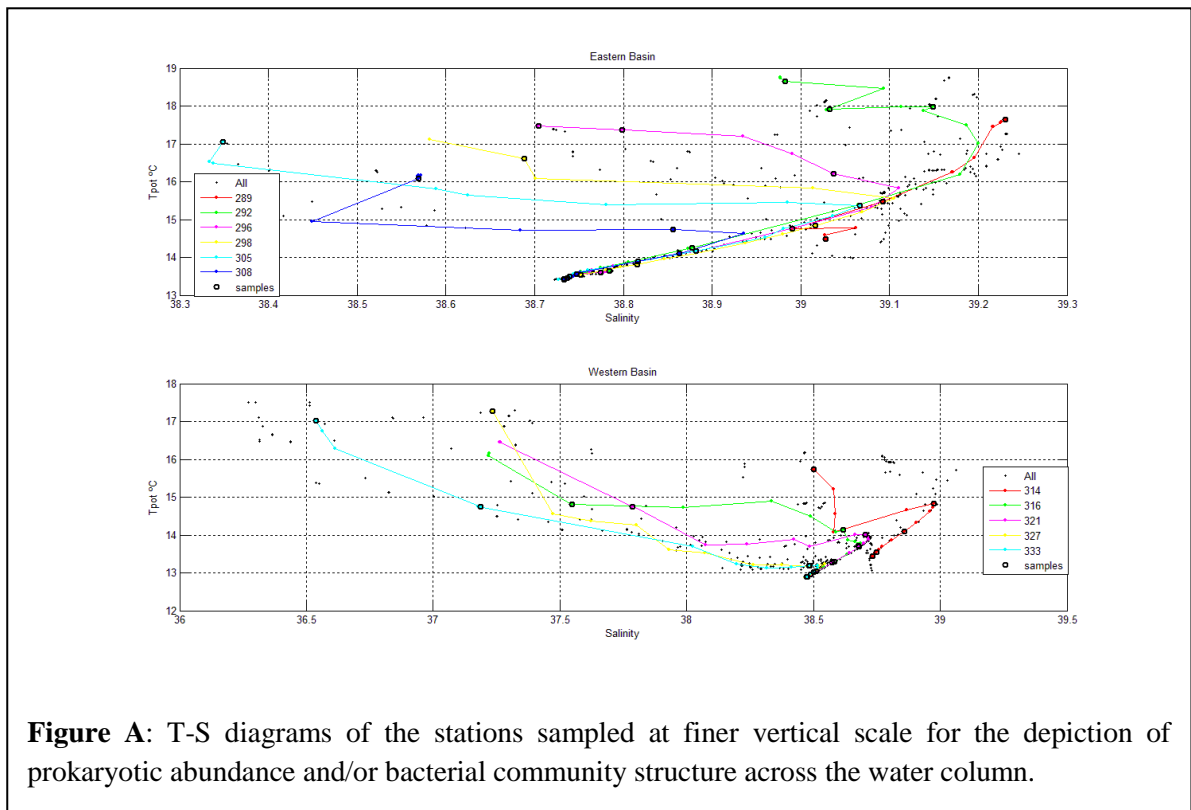
Two points concerned are 1) the authors have used the physico-chemical factors to characterize water masses which excludes temporal changes in bacterial substrate quality in a given water body. DOM/POM quality could be a good factor for the age of a given water body in the aphotic zone. It would be helpful to have more data on primary production, Chl.a, DOM/POM quality.

We agree with the referee about the importance of DOM/POM quality and additional data concerning primary productivity, however we did not have the opportunity to perform such a complete chemical characterization of the seawater samples analyzed by microbiological methods in the present study. Nonetheless, we implemented the discussion of the available nutrient data (section 3.1) and added a paragraph discussing the results obtained by Rahav et al (2013). They studied nitrogen fixation and its contribute to primary productivity and chlorophyll concentration on a set of surface water samples collected during the same sampling cruise (Meteor M84/3) from which our samples were collected.

2) There is no definition of “water masses” in the manuscript. It may be possible that sampling points have identical temperature and salinity despite that they are not hydrologically connected on a relevant time scale. The authors need to assess the definition of water masses much better or describe data set on how water masses are moving in this sampling region to test the relationship between bacterial community dynamics and water masses.

We agree with the referee about the importance to provide more data on the characterization of the different water masses in the sampled area. Figure A included in this file shows the T/S diagrams illustrating that indeed different water masses were sampled across the water column of the eight stations selected for the finer vertical scale investigation. To clarify the differences between the different seawater samples we also revised section 3.1, improving the discussion of those physico-chemical parameters that are used for water masses identification. Moreover, to provide a framework of the characteristics of the sampled water we added the Supplementary Figure 1 showing a section of salinity in the Mediterranean Sea recorded during the Meteor cruise M84/3, where the samples collected and analyzed for bacterial community structure and/or prokaryotic abundance are indicated.

However, the main topic of the paper was a microbiological study that did not aspire to provide an exhaustive oceanographic survey. That said, we tried to highlight the hypothetical nature of the correlation between bacterial community structure and water masses, the former being statistically related to those physical parameters (i.e. temperature, salinity) generally used to identify different water masses.



Minor suggestion: It would be great to show a similarity matrix for the entire individual sample determined by ARISA in the Mediterranean Sea. This figure makes clear for readers regarding the patterns and similarity of bacterial community composition in the Mediterranean Sea.

Patterns and similarity of bacterial community composition between the investigated sites were illustrated in different Figures (Fig.3-4-5) in the submitted manuscript. All these Figures graphically showed: in (a) panel the similarity between the samples and their distribution as nMDS (non-metric multidimensional scaling) plot and in (c) panel the distribution of the samples observed by ARISA fingerprinting overlaid with the environmental variables explaining the clustering of the samples. Graphic distance between the samples is inversely related to their similarity. We trust that this type of graphic representations of the similarity patterns are more intuitive and easy to catch for readers thus, to avoid the presentation of redundant data analysis, we prefer to show the similarity between bacterial communities as reported above.