

***Interactive comment on* “Role of environmental factors for the vertical distribution (0–1000 m) of marine bacterial communities in the NW Mediterranean Sea” by J. F. Ghiglione et al.**

Anonymous Referee #1

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In their study entitled "Role of environmental factors for the vertical distribution (0–1000m) of marine bacterial communities in the NW Mediterranean Sea", Ghiglione et al. attempt to link environmental metadata to the composition of the bacterial component of the marine microbial community in one vertical profile sample in the Mediterranean Sea. This effort seems appropriate for Biogeosciences readers and shows interest at present time.

My main concern lies into the lack of hypothesis of this study, though the authors indicate (p.2134, l.24–27) that they "hypothesized that the combination of high-throughput diversity composition assessments in combination with in-depth environmental param-

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eters measurements and appropriate multivariate statistical analyses should shed light on the actual factors responsible for bacterioplankton communities shifts with depth". To my opinion this is not a hypothesis; this simply describes their approach. An appropriate hypothesis would test the strength of each measurable environmental factor to shape the community distribution.

Also, despite the fact they aim to (p. 2135, l. 14-17) "determine the consistency of the vertical distribution of bacterial communities during the late summer-autumn transition period by using multivariate non-parametric statistical methods", I could not read any result or discussion point relating the temporal pattern of the observed vertical distributions. It seemed this was treated elsewhere in Biogeosciences (Mevel et al. 2008). This objective should therefore be clearly discussed or removed from the introduction.

Unfortunately, while reading this manuscript, I had the feeling the authors used methodical statistics to extract potential meanings from their results, which seemed predisposed to support inaccurate conclusions. Fortunately (or not?), the concluding remarks ending the manuscript remain vague and repeat the general opinion concerning this question: there is no single factor shaping microbial communities but rather complex interactions of multiple factors.

Though the manuscript is generally well written, I noticed the authors tended to overestimate the extent of their analysis, their techniques and their results. Their approach is far from being the first analysis linking environmental metadata to microbial community profiles, and I would urge the authors to go back to the recent literature on this subject. Bacteria, though essential for the biogeochemistry of the marine environment are linked to a more complex network than physico-chemical parameters or phytoplankton diversity, including virus mortality, grazing activity and competition for nutrients. This should not come last in the concluding remarks but first in the discussion part. Moreover, CE-SSCP combines the worst from all fingerprinting techniques (i.e. PCR biases, impossible taxonomic inference, lack of reproducibility outside the same lab…etc) and scrapes the surface of the abundant members of the com-

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munity. This should be discussed in regards to the current literature on the subject and completed with deeper analysis of the samples.

Interactive comment on Biogeosciences Discuss., 5, 2131, 2008.

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