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## ***Interactive comment on “Specific rates of leucine incorporation by marine bacterioplankton in the open Mediterranean Sea in summer using cell sorting” by A. Talarmin et al.***

### **Anonymous Referee #2**

Received and published: 21 October 2010

#### General comments

The manuscript by Talarmin et al. investigates the in situ metabolic activities of dominant groups of bacterioplankton across the Mediterranean Sea, both at cellular and population level, using radioactively labeled amino acid tracer and flow cytometry sorting. This work represents a considerable data set and allows drawing some interesting hypotheses and conclusions regarding the role of the different players of the bacterioplankton. I only have a few questions, comments and suggestions listed below.

Specific comments 1) One of the main interest of this work is the large range of samples collected along the transect of stations encompassing a large longitudinal gradient in

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the Mediterranean Sea. This point could be emphasized a bit more in the text showing the originality of the work.

2) Has any phylogenetic characterization of the LNA and HNA populations been done, at least for a few samples, using for example in situ hybridization after cell sorting? It would have been interesting for the discussion to have an idea of the diversity found in these populations, how this diversity varies across the Mediterranean Sea and with depth, and how it differs/compares with already known HNA/LNA populations from other environments. Similar metabolic relevance of the LNA population in the Atlantic ocean (for example, i.e. Schattenhofer et al., EM, 2009 or Mary et al., AME, 2006 mentioned in the introduction but wrong reference used in the Reference section, should be changed) for a large range of samples along a transect has also been shown using similar method. This population was mainly composed of SAR11 cells. It would be then interesting to see if such a dominance is found in the Mediterranean Sea.

3) Material and methods. Not sure it is necessary to mention the 3 enrichment experiments (A, B, C) if only one was used for this work. Just describe the experiment B. Is there any references for the TCA method that could be quoted to simplify the text?

4) In this work, labeled amino acids were added at saturating concentrations. How does this compare with nonperturbing tracer concentrations used in other works mentioned in the manuscript? It is known that the use of high concentration of leucine can as a result, elevate the ambient concentrations of amino acids in seawater and the activities of some groups of bacteria could be overestimated because of their ability to use the added compound as an alternative nutrient.

5) Again, has any molecular characterization of the HNA+ population been done? Thus, it would very interesting to discuss the results, especially in terms of nutrient response and distribution.

Technical corrections p6554: SyBR Green commercial solution is usually 10000x concentrated so the dilution is probably more. p6559: "15+/-31%" Is that correct??? P6561

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Line 3: Remove “Dealing with abundances” P6569. Line 3: Should it be “incubation in the light” rather than in the dark?

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Interactive comment on Biogeosciences Discuss., 7, 6545, 2010.

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7, C3410–C3412, 2010

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