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***Interactive comment on “Diversity of cultivated and metabolically active aerobic anoxygenic phototrophic bacteria along an oligotrophic gradient in the Mediterranean Sea” by C. Jeanthon et al.***

**Anonymous Referee #1**

Received and published: 17 June 2011

Title: "Diversity of cultivated and metabolically active aerobic anoxygenic phototrophic bacteria along an oligotrophic gradient in the Mediterranean Sea"

by C. Jeanthon et al.

This manuscript describes the diversity of Aerobic Anoxygenic Phototrophic (AAP) bacteria along an oligotrophic gradient in the Mediterranean Sea in summer 2008 based on AAP cultivation (phylogenetically analysed by 16S rRNA), and molecular pufM mRNA analyses. The pufM transcript were reverse transcribed, cloned and sequenced. This

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manuscript is a companion study of Lamy et al. (2011), also submitted to Biogeosciences. The authors isolated 52 AAP strains, phylogenetically affiliated to the Alphaproteobacteria. In contrast, most of the *pufM* clones generated were affiliated to the Gammaproteobacteria. Highest *pufM* transcript diversity was detected in the ultra-oligotrophic eastern basin, which fits well into results of Lamy et al., who detected highest bacteriochlorophyll concentrations within this area. Finally, the authors highlight the discrepancy between culture-based and molecular methods, and propose that this demonstrates the existing gaps in AAP ecology.

#### General comments:

After all, this study is not ground-braking. Neither the detected discrepancy, nor this kind of approach is really new. However, it is solid science which contributes some new insights into AAP distribution and diversity in the Mediterranean Sea and is worth to be published.

#### Specific comments:

Material & Methods: Please described in detail from which stations clone libraries were gained. This is not clear to me only from Fig. 1. What is the meaning of both RNA-based *pufM* libraries in Fig. 1?

Fig. 2 and also within the text (4432, line 1): To my knowledge *Erythrobacter* is an alpha-4, *Roseovarius* an alpha-3 proteobacterium, not vice versa. Please check this and change accordingly.

Page 4437, line 24: Please mention the transcripts which were analysed in these studies, they differ from *pufM*.

#### Technical comments:

Page 4437, line 16: ...BChl-a synthesis... Page 4438, line 29: ... abundance. Moreover... Table 2: *Roseovarius halotolerans*

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