Deep Ocean microbial communities in the South Adriatic Pit

*Marino Korlević[1], Danny Ionescu[2], Paolo Paliaga[1], Tina Šilović[1], Rudolf Amann[2], Mirjana Najdek[1], Sandi Orlić[1]**
[1]Center for Marine Research, Ruđer Bošković Institute, G. Paliaga 5, 52210 Rovinj, Croatia
[2]Max Planck Institute for Marine Microbiology, Celsiusstrasse 1, 28359 Bremen, Germany
*Corresponding author: sandi.orlic@irb.hr

Introduction:

The Adriatic Sea is a semi enclosed basin in the Northeastern Mediterranean with a shelf that extends from its northernmost part to the Split-Gargano transect. Its deeper southern part is characterized by the circular, 1243 m deep South Adriatic Pit (SAP). Adriatic ecosystems are influenced by regular water exchange with the Eastern Mediterranean through the strait of Otranto. Levantine Intermediate water and Ionian Surface Water flow into the Adriatic along its eastern border. The volume of this flow is greater in winter but changes from year to year depending on climate oscillations that occur from the Adriatic to the Southeast Mediterranean. In this study we used pyrosequencing of the 16S rRNA gene and DGGE to study the water column above the SAP in comparison to a station closer to the shore (300 m depth) (Fig. 1).

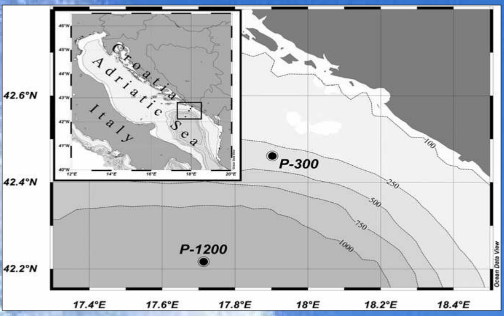

Fig. 1. Sampling stations in the Southern Adriatic: P1200-1200 m depth, P300-300 m depth (Batistić et al., 2012, doi:10.1016/j.csr.2011.01.004).

Conclusion:

- **Station P1200 has 4 distinct bacterial communities: surface (0 -10 m), shallow (75-200 m), intermediate (400-800 m) and deep (1000 -1200 m).**
- **Bacteria characteristic to the deep ocean are found at the station P1200 despite its “shallow” nature.**
- **Deltaproteobacteria nitrite oxidizing bacteria (*Nitrospinaceae*) are commonly found in deep waters at P1200.**
- **No bacterial ammonia oxidizer was found suggesting that ammonia oxidation is probably carried out by Archaea.**

Results:

The total bacterial number at stations P300 and P1200 ranged between $1.1x10^5$-$1.8x10^5$ and $6.7x10^4$-$3.3x10^5$, respectively (Fig. 3). Flow cytometry counts showed a *Synechococcus* peak at 10 m and a *Prochlorococcus* peak at 100 m in both stations (Fig. 4). DGGE analysis of the P1200 samples showed 4 distinct communities: surface (0 and 10 m), shallow deep (75, 100 and 200 m), intermediate depth (400, 600 and 800 m) and deep (1000 and 1200 m) (Fig. 5). A similar pattern was obtained by cluster analysis of the pyrosequencing data. Taxonomic analysis of the sequencing data showed a depth related distribution of the various phylogenetic groups (Fig. 6).

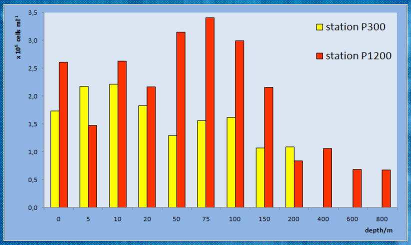

Fig. 3. Total bacteria counts at stations P300 and P1200.

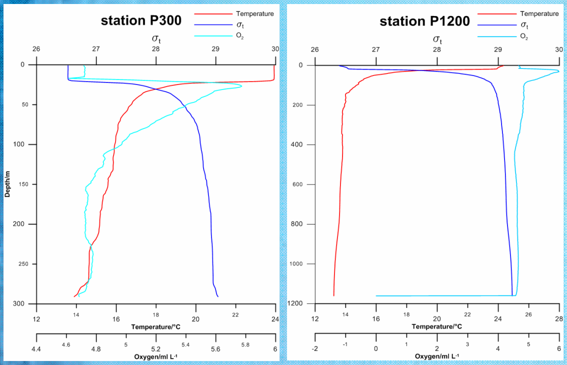

Fig. 2. Temperature, σ_t and O_2 at stations P300 and P1200.

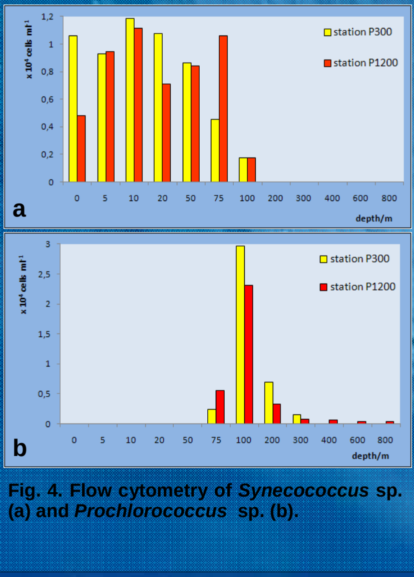

Fig. 4. Flow cytometry of *Synecococcus* sp. (a) and *Prochlorococcus* sp. (b).

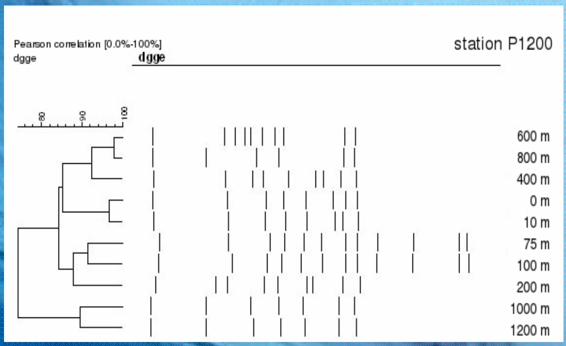

Fig. 5. Pearson correlation of DGGE data from station P1200.

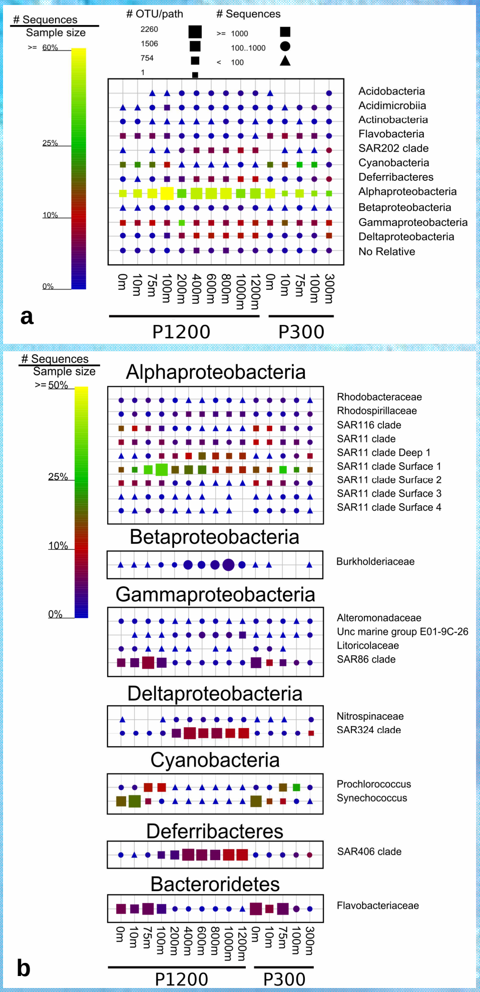

Fig. 6. Pyrosequencing data of major prominent phylogenetic groups at class (a) and family (b) resolution. Symbol color represents sequence frequency; size represents inner diversity (number of OTUs); shape represents general number of sequences in the specific taxonomic path (numeric data shown for class level only).

Aknowledgment:

This work is part of the BABAS scientific project no. 02.05/38 funded by the Croatian Science Foundation. We would like to thank the crew of the R/V Naše more for assistance during sampling.