

DISTRIBUTION AND ACTIVITIES OF PROKARYOTES IN THE WATER COLUMN OF THE TYRRHENIAN SEA

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Abstract

Tyrrhenian Sea is a poorly studied part of the Mediterranean Sea. During the CIESM-SUB1 multidisciplinary cruise in April 2006, we studied hydrostatic pressure effect on the prokaryotic activities and the structure of communities. Results show an important aminopeptidase and phosphatase activities in the deep sea. Community structure has been studied using two approaches: CARD-FISH and cloning/sequencing. The main result shows an increase of *Archaea* population according to the depth. *Euryarchaeota* (group II *Archaea*) dominates deep-sea waters of Tyrrhenian Sea. Preliminary results of cloning/sequencing have shown that gamma-Proteobacteria (*Bacteria*) are dominant in deep sea among Bacteria.

Keywords : *Bacteria, Biodiversity, Deep Sea Ecology, Deep Sea Processes, Tyrrhenian Sea.*

The CIESM-SUB1 cruise is the first survey of a long term project aimed to study, through a multidisciplinary approach, the main diversity patterns of a poorly investigated area of the Mediterranean Sea, namely the Southern Tyrrhenian area up to the Sardinia-Sicily Channels. Results shown thereafter are focused on the understanding of hydrostatic pressure effects on the prokaryotic activities and the structure of communities.

The sampling area is located off the Gulf of Napoli up to the Sardinia-Sicily channel and sampling was done on board the R/V *Universitatis*. Three water masses [1] can be well identified by Theta-S diagram as:

- Surface Water (SW), originated from Atlantic waters
- Levantine Intermediate Water (LIW), originated from the eastern basin older than the deep water masses
- Western Mediterranean Deep Water (WMDW) originated from the surface waters of the Gulf of Lion.

Samples were collected at 5 stations at 3 depths (20, 500, 3000m) with Niskin bottles. In parallel, deep-sea water samples were collected via high-pressure bottles (HPBs) to maintain deep-sea samples at the in situ conditions (pressure, temperature ; for more details see [2]).

strated for the Pacific Ocean [4] and the North Atlantic [5]. However, in the Tyrrhenian Sea, the dominant archaeal group was the Euryarchaea rather than the Crenarchaea [4- 6] suggesting a peculiar structure of the prokaryotic community of the Tyrrhenian Sea.

Preliminary data on the impact of hydrostatic pressure indicate a selective response of some members of the prokaryotic community, however, data analysis is still in progress.

References

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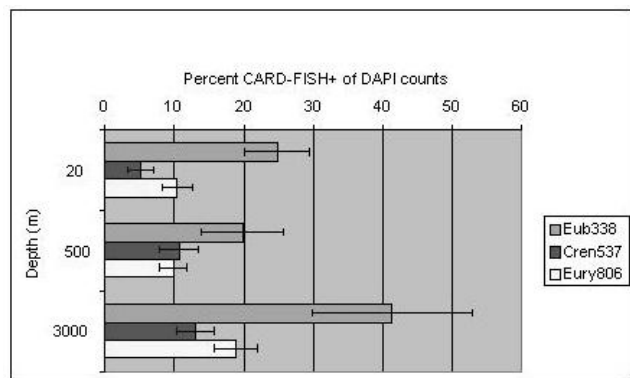


Fig. 1. Distribution of Bacteria, Crenarchaea, Euryarchaea at 20m, 500m and 3000m depths of the Tyrrhenian Sea in April 2006 as percent CARD-FISH⁺ of DAPI counts. Bars represent mean of 5 stations (+/- standards errors).

Aminopeptidase and phosphatase activity showed maximum rates in the surface water and minimum rates in the LIW, while the WMDW was characterized by high rates. These rates were in the same range than those measured in the Ionian Sea [3]. However, both aminopeptidase and phosphatase rates in the deep-sea waters were in the same range than those in the surface waters. Measurements obtained at in situ pressure conditions were higher than those obtained under atmospheric pressure. This suggests that a substantial part of the prokaryotic community is adapted to high pressure conditions.

The CARD-FISH data shows that archaeal numbers (sum of Crenarchaea and Euryarchaea, figure 1) increased with depth as previously demon-